EURING Analytical Meeting & Workshop

Apr 17-21, 2023 - Montpellier, France

Book of abstracts

Monday 17th April

Conference introduction

09:00 – 09-15

Amphithéâtre Délégation CNRS

09:15-09:45	**Alison Johnston**	**Plenary**: People and birds: The challenges and power of citizen science data in ornithology
09:45 – 10:00		*Break*

Abundance in space

10:00 – 11:00

Chair: Brett **McClintock**
Amphithéâtre Délégation CNRS

10:00	Riki **Herliansyah**	Animal density estimation for unmarked populations using a spatially explicit model
10:12	Rahel **Sollmann**	Mt or not Mt: Temporal variation in detection probability in spatial capture-recapture models
10:24	Murray **Efford** (remote)	Robust sampling designs for spatially explicit capture-recapture
10:36	Ehsan **Moqanaki**	Population-level determinants of density for a historically persecuted large carnivore
10:48	Ana **Sanz-Pérez**	Estimating demographic parameters and abundance of the Pyrenean Brown bear population using open SCR
11:00 - 11:15		*Break*

Abundance estimation for management

11:15 – 12:03

Chair: Erlend **Nilsen**
Amphithéâtre Délégation CNRS

11:15	Rachel **McCrea** (remote)	Evaluating and correcting for the effect of dependence in the integrated analysis of removal and capture-recapture data
11:27	Leslie **Skora**	Estimating brown bear abundance along salmon spawning streams in Katmai National Park, Alaska
11:39	Amy **Davis** (remote)	A multi-method dynamic removal model for evaluation of abundance and management effectiveness overtime
11:51	Yiran **Wang** (remote)	Bayesian genetic mark-recapture methods for estimating seasonal river run size of stock populations
12:03 – 13:30		*Lunch break* — *CEFE experimental field*

Novel approaches to abundance estimation

13:30 – 14:30

Chair: Mahdieh **Tourani**
Amphithéâtre Délégation CNRS

13:30	Charles **Yackulic**	Sharing abundance: Integrating long-term count data with short-term capture-recapture data in a marginalized multistate Jolly-Seber framework
13:42	Diego **Rondon**	A Bayesian Multi-state model for estimating the effect of inbreeding and age on population dynamics
13:54	Rémi **Fraysse**	Modelling misidentifications in capture-recapture experiments
14:06	Rishika **Chopara** (remote)	A framework for goodness-of-fit testing in ecological modelling
14:18	Michelle **Kissling**	Aligning statistical and biological populations for abundance estimation
14:30 – 14:45		*Break*

Causal inference for management

14:45 – 15:45

Chair: Thomas **Riecke**
Amphithéâtre Délégation CNRS

14:45	Romuald **Hounyèmè** (remote)	From responses of macroinvertebrate metrics to the definition of reference thresholds
14:57	Daniel **Fink** (remote)	Estimating spatially explicit population trajectories with citizen science data and double machine learning
15:09	Allison **Binley**	Redistributing resources from monitoring to action: Quantifying the value of citizen science data in conservation decision making
15:21	Annabelle **Stanley**	Making informed decisions for private lands conservation under uncertainty and spatial complexity: A case study on the Northern Bobwhite
15:33	Priyanjana **Pramanik**	What-if thinking in conservation policy research: Expanding the use of synthetic controls
15:45-15:57		*Break*

Advances in monitoring

15:57 – 17:09

Chair: Marc **Kery**
Amphithéâtre Délégation CNRS

15:57	Yoba **Alenga**	Bat sonotype as a novel insight into the Congo Basin Rainforest dynamic
16:09	Philip **Patton**	The effect of fully automated animal recognition on mark-recapture estimates
16:21	Gaël **Bardon**	RFIDeep: unfolding the potential of deep learning for radio-frequency identification
16:33	Clark **Rushing**	Estimation of seasonal survival and migration phenology of migratory birds from automated telemetry data using continuous-time multi-state models
16:45	Erlend **Nilsen**	Structured citizen science as a means to monitor wildlife populations
16:57	Philipp **Boersch-Supan**	Modelling life cycle-event phenology using biometrics collected by citizen science ringers
17:09 – 17:30		*Break*

Honorary plenary talk

17:30-18:15	Emmanuelle **Cam**	30 years of data collection, capture-mark-recapture (CMR) modeling and teaching: what is seen matters, what is unseen matters as much, and sometimes we estimate quantities that are unobservable

Amphithéâtre Délégation CNRS

Ice-breaker

18:30-23:00

CEFE experimental field

Tuesday 18th April

Announcements

08:45 – 09-00

Amphithéâtre Délégation CNRS

09:00-09:30	**Matthieu Paquet**	**Plenary:** Estimating immigration and density dependence using Integrated Population Models
09:30 – 09:48		*Break*

Movement and habitat selection

09:48 - 10:48

Chair: Richard **Chandler**

Amphithéâtre Délégation CNRS

09:48	Clara **Panchaud**	Accounting for animal movement in spatial capture-recapture
10:00	Janelle **Badger** (remote)	Integrating movement data into mark recapture analysis: Case study of false killer whale (*Pseudorca crassidens*) abundance estimation around the main Hawaiian Islands
10:12	Sara **Gomez**	Linking variation in juvenile meerkat foraging behaviour to growth rates and survival later in life: a biologging and state space modelling approach
10:24	Guillaume **Souchay**	Follow the yellow brick road: Using does to find the leverets
10:36	Brett **McClintock**	A multistate Langevin diffusion for inferring behavior-specific habitat selection and utilization distributions
10:48 - 11:15		*Break*

Connectivity

11:15 – 12:03

Chair: Charles **Yackulic**

Amphithéâtre Délégation CNRS

11:15	Matthew **Gonnerman** (remote)	An individual based model trained on multiple data sources estimates population connectivity for harvested eastern wild turkeys
11:27	Maëlis **Kervellec**	Mapping connectivity from non-invasive surveys with spatial capture-recapture models: A focus on the Pyrenean brown bear population
11:39	Killian **Gregory**	An integrated framework to combine migratory connectivity and demographic data
11:51	Lise **Viollat**	Animal demography in motion: Integration of individual spatial component in demographic variability of Bonelli eagle
12:03 – 13:30		*Lunch break* — *CEFE experimental field*

Natal dispersal and migration

13:30 – 14:18

Chair: Michelle **Kissling**

Amphithéâtre Délégation CNRS

13:30	Paul **Acker**	Capture-recapture animal model for quantitative genetic decomposition of variance in seasonal migration versus residence
13:42	Rita **Fortuna**	Using a multistate capture-recapture animal model to estimate additive genetic variance in early-life seasonal movement
13:54	Charly **Souc**	A multi-event CMR analysis applied to reveals the influence of the natal colony for age-specific movement patterns of the Yellow-legged gull (*Larus michahellis*)
14:06	Richard **Chandler**	Directional natal dispersal in a trailing-edge population of black-throated blue warblers
14:18 – 14:45		*Break*

Phenology

14:45 – 15:45

Chair: Paul **Acker**

Amphithéâtre Délégation CNRS

14:45	James **Clarke**	Accounting for phenology and varying spatial scales in the production of UK butterfly abundance estimates using citizen science data
14:57	Simon **English**	Quantifying phenology and migratory behaviours of hummingbirds using single-site dynamics and mark-detection analyses
15:09	Fabian **Ketwaroo**	How to walk the BeeWalk: Modelling Bumblebee citizen science data
15:21	Edel **Lheureux**	Distinguish the biological process from the observation process in a tagging-recapture experiment to study the migration phenology of the Atlantic salmon (*Salmo salar*)
15:33	Paul **Cuchot**	Not all resident birds reproduce earlier in warmer springs: inferring habitat-dependency of phenological sensitivity to temperature using a bayesian sigmoid modelling approach applied to constant ringing effort sites
15:45-15:57		*Break*

Drivers of vital rate variation

15:57 – 17:09

Chair: Chloé Rebecca **Nater**

Amphithéâtre Délégation CNRS

15:57	Sarah **Cubaynes**	Modeling the impacts of canine distemper virus on the Yellowstone wolf population
16:09	Ana **Payo-Payo** (remote)	Long-lasting effects of harsh early-life conditions on adult survival of a long-lived vertebrate
16:21	Camille **Schatz**	Intra- and interspecific demographic variation in two phylogenetically related seabirds
16:33	Rachel **Bergeron**	Post-weaning survival in kangaroos is high and constant until senescence: Implications for population dynamics
16:45	Morgane **Gicquel**	Age-related survival in the European cranes population
16:57	Emilienne **Grzegorczyk**	Is hidden demographic heterogeneity a common phenomenon?
17:09 – 17:30		*Break*

Poster session

17:30-20:00

Hall Délégation CNRS

Wednesday 19th April

Announcements

08:45 – 09-00

Amphithéâtre Délégation CNRS

09:00-09:30	Aline Magdalena **Lee**	**Plenary:** The magic of mark-recapture

09:30 – 09:48 *Break*

Vital rates across space and time

09:48 - 10:48

Chair: Paul **Conn**

Amphithéâtre Délégation CNRS

09:48	Chloé Rebecca **Nater**	An integrated distance sampling model to estimate variation in demographic rates across space and time
10:00	Fränzi **Korner-Nievergelt**	Demographic indices from constant ringing effort sites in Switzerland
10:12	Cyril **Milleret**	Mapping population-level mortality risks of an emblematic and controversial large carnivore, the wolf
10:24	Brady **Mattsson**	Importance of biases associated with ground counts of nestlings in an arboreal nester, the red kite (*Milvus milvus*)
10:36	Johanna **Faure**	The post-release survival of a deep-sea skate caught as bycatch by demersal longline fishery in Crozet, Southern Ocean

10:48 - 11:15 *Break*

Survival and movement in context

11:15 – 12:03

Chair: Michael **Schaub**

Amphithéâtre Délégation CNRS

11:15	Maria **Dzul**	Can “true” survival be without global resights: it depends on “true” movement
11:27	Saskia **Schirmer**	Seasonal and spatial explicit survival estimates - Combining the multinomial reencounter model with an individual-based temporal model
11:39	Jaume-A. **Badia-Boher**	Evaluating permanent emigration and subsequent biases in survival in territorial raptors using spatial capture-recapture methods: the case of the Bonelli's eagle
11:51	Murray **Christian**	Accurately estimating the demographic contribution of immigration: a southern elephant seal case study

12:03 – 13:30 *Lunch break* *CEFE experimental field*

Excursions

13:30 – 19:00

Thursday 20th April

Announcements

08:45 – 09-00

Amphithéâtre Délégation CNRS

09:00-09:30	Marlène **Gamelon**	**Plenary:** Biotic interactions matter: how intra- and interspecific competition shape vital rates and population dynamics

09:30 – 09:48 *Break*

Individual heterogeneity, sociality, and kinship

09:48 - 11:00

Chair: Sarah **Cubaynes**

Amphithéâtre Délégation CNRS

09:48	Matthew **Silk**	Demographic models of social networks
10:00	Javier **Klaich**	Estimating individual survival under a social network analysis when detection is imperfect
10:12	Christophe **Barbraud**	Selection against immigrants: demographic evidence and testing the familiarity hypothesis in seabirds
10:24	Paul **Conn**	Using close-kin mark-recapture to estimate abundance and survival of bearded seals in Alaska
10:36	Thomas **Riecke**	Estimating latent fitness heterogeneity using structural equation models
10:48	Blanca **Sarzo** (remote)	Justice for the weaklings! Survivorship bias in individual heterogeneity CMR models

11:00 - 11:15 *Break*

Distribution and conservation of rare and endangered species

11:15 – 12:03

Chair: Frédéric **Barraquand**

Amphithéâtre Délégation CNRS

11:15	Brett **Sandercock**	Estimating den use and reproductive rates of arctic fox with multistate occupancy models
11:27	Sarah **Bauduin**	Using occupancy to monitor populations. Case study: the wolf in France
11:39	Anaïs **Dasnon**	Estimating seabird populations breeding in sparse colonies in remote areas
11:51	Fabiola **Iannarilli** (remote)	Leveraging sharing of camera trap data to inform biodiversity conservation at large scales

12:03 – 13:30 *Lunch break* *CEFE experimental field*

Novel approaches for species distributions

13:30 – 14:30

Chair: Guillaume **Souchay**

Amphithéâtre Délégation CNRS

13:30	Marc **Kéry**	Integrated distance sampling models for simple point counts
13:42	Javier **Fernández-López**	A unified framework for estimating animal abundance from hunting statistics: the thinned Poisson Point Process model
13:54	John **Grider**	A novel method for estimating pathogen presence, prevalence, load, and dynamics at multiple scales during a disease outbreak
14:06	Florian **Lasgorceux**	Inferring niche models with unknown sampling effort estimated from opportunistic data
14:18	Jamie **Sanderlin** (remote)	Innovations for biodiversity monitoring using acoustic methods in the southwestern United States: What does this mean for rare species?

14:30 – 14:45 *Break*

Communities and species interactions

14:45 – 15:45

Chair: Rahel **Sollmann**

Amphithéâtre Délégation CNRS

14:45	Divyajyoti **Ganguly**	Three's company: Integrating detection data from multiple methods to examine meso-carnivore co-occurrence in India
14:57	Julie **Louvrier**	How much data do you need to detect co-occurrence with multi-species occupancy models: A simulation study
15:09	Prashant **Mahajan**	Interspecific interactions and co-existence among canids in the semi-arid landscape of western India
15:21	Matt **Metz**	Estimating the abundance of wolf-killed prey through multiple detection methods in a mark-recapture framework
15:33	Frédéric **Barraquand**	The various concepts of independence in integrated population models

15:45-15:57 *Break*

Species movement, life history, and detectability

15:57 – 17:09

Chair: Brett **Sandercock**

Amphithéâtre Délégation CNRS

15:57	Kasper **Thorup**	Historical changes in migration patterns
16:09	Jacob **Davies**	Quantitative year-round modelling of the movements of European waterfowl populations
16:21	Emmanuel **Adebija**	Testing avian body size conformity to Bergmann's and Allen's rules along a latitudinal gradient in Nigeria
16:33	Christophe **Botella**	A dynamic species distribution model fitted to heterogeneous occurrences explains a plant invasion trajectory
16:45	Brandon **Edwards**	Estimating landbird detectability from autonomous recording unit data
16:57	Gonçalo **Ferraz**	Decline in avian detection more evident than secondary forest colonization in a 30-year old Amazon forest disturbance frontier

Gala diner

19:00-23:00

Gazette Café - 6 rue Levat 34000 Montpellier

Friday 21st April

Announcements

09:00 – 09:15

Amphithéâtre Délégation CNRS

09:15-09:45	Todd **Arnold**	**Plenary:** Density dependence, individual heterogeneity, and demographic compensation: new approaches to age-old questions

09:45 – 10:00 *Break*

Management and conservation I

10:00 - 10:48

Chair: Thomas **Riecke**

Amphithéâtre Délégation CNRS

10:00	Stephen **Gregory**	Power analysis for real-World sampling strategies
10:12	Michael **Schaub**	Lessons to be learned by comparing fisheries stock assessment methods (SAMs) with integrated population models (IPMs)
10:24	Benjamin **Debetencourt**	Estimating chimpanzee demography, social structure and territory range with camera trap data in Moyen Bafing National Park, Guinea
10:36	Liam **Bailey**	Monitoring changes in carrying capacity through time to assess conservation outcomes in a large social carnivore

10:48 - 11:15 *Break*

Management and conservation II

11:15 – 12:03

Chair: Julie **Louvrier**

Amphithéâtre Délégation CNRS

11:15	Kylee **Dunham** (remote)	Design and evaluation of long-term monitoring programs to inform annual life cycle modeling, conservation, and adaptive harvest management of migratory waterfowl in North America
11:27	Chris **Sutherland** (remote)	Opposite effects of global and local density-dependent dispersal on metapopulation stability and persistence
11:39	Eva **Conquet**	Effects of season-density interactions on the vital rates of an African lion population
11:51	Nicolas **Strebel**	Multi-species population indices for sets of species that include disappearing or newly occurring species

12:03 – 13:30 *Lunch break* *CEFE experimental field*

Workshops

13:30 – 17:30

Animal Movement Modeling

Instructors:
Mevin **Hooten**, Devin **Johnson**, Brett **McClintock**, Juan **Morales**

Grande Salle Réunion CEFE

Integrated Models in Population Ecology + Species Distribution Modeling

Instructors:
Marc **Kéry,** Michael **Schaub,** Nicolas **Strebel**

Amphithéâtre Délégation CNRS

An Introduction to Close-Kin Mark-Recapture

Instructors:
Paul **Conn**

Salle Polyvalente CEFE

Monday 17th April

09:15-09:45 **Alison Johnston** **Plenary**: People and birds: The challenges and power of citizen science data in ornithology

People and birds: The challenges and power of citizen science data in ornithology

Alison Johnston

Dr Alison Johnston is a Reader in Statistics, based at the Centre for Research in Ecological and Environmental Modelling at the University of St Andrews, UK. She is an ecological statistician with broad interests in how we can use creative analytical methods to learn more about the natural world, to understand the drivers of ecological changes, and to prioritise conservation action. Most of her research has focussed on birds, with particular emphasis on citizen/community science data, however she has also worked with a broad range of other data including mark-recapture data, nest data, tagging data, aerial survey data, and acoustic data. She uses a combination of both statistical and machine learning methods.

Humans have a close relationship with birds, which has led to a long history of citizen/community science data contributing to ornithological advances. However, the last couple of decades have seen a rapid expansion in observational data collected by volunteers in ornithology, driven by the growth of simpler and more flexible projects that allow a broad spectrum of participation. The resulting datasets have huge power to expand our knowledge of bird distributions, migration routes, and population trends. However, to extract reliable ecological knowledge, we need to address the numerous challenges that arise from these data and that can bias the ecological inference. It also requires the development and application of robust analytical approaches to account for these sources of variation during data analysis. However, this work requires us to understand people and how they relate to and record birds. Overall, there is a huge potential to use these large, messy, observational datasets to fill gaps in our ornithological knowledge and strengthen ecological inference using CS data. To achieve these goals, we need to develop robust analytical approaches, built on the foundation of the relationship between people and birds.

Abundance in space

10:00 – 11:00 *Amphithéâtre Délégation CNRS*

10:00 Riki **Herliansyah** Animal density estimation for unmarked populations using a spatially explicit model

Animal density estimation for unmarked populations using a spatially explicit model

Riki Herliansyah, Ruth King, Dede A. Rahman, Stuart King

Obtaining abundance and density estimates is typically a particularly important aspect within wildlife conservation and management. To monitor such wildlife populations, the use of motion-sensor camera traps is becoming increasing more popular due to its non-invasive nature and efficiency. When animals can be uniquely identified from camera images, spatial capture-recapture (SCR) models are often used for obtaining population density estimation. However, animal identification is not always feasible in practice due to poor quality images and/or individuals not having uniquely identifiable physical characteristics. Spatially explicit models for unmarked individuals permit the estimation of animal density when individuals cannot be uniquely identified. In this study, we consider the motivating-large dataset relating to barking deer (Muntiacus muntjak) collected in Ujung Kulon National Park (UKNP), Indonesia. The barking deer data was collected by 77 units of camera traps over 9 weeks of sampling occasions during the dry season in (May-June) 2014. We fit the camera-trap data to spatial count models using a more efficient Bayesian algorithm to obtain the population density. We extend the model by including a categorical covariate information, habitat structures, and assess how this covariate may affect in detecting individuals.

10:12 Rahel **Sollmann** Mt or not Mt: Temporal variation in detection probability in spatial capture-recapture models

Mt or not Mt: Temporal variation in detection probability in spatial capture-recapture models

Sollmann, R. Department of Ecological Dynamics, Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany

A premise of closed capture-recapture (CR) modeling is that you need to account for variation in detection probability, p, to obtain unbiased estimates of abundance. Detection probability can vary over time (model Mt), among individuals (Mh), or due to behavioral response to capture (Mb). Foundational work on closed CR models suggested that models are fairly robust to violating the assumption of p being constant in time.

Spatial capture-recapture (SCR) has replaced traditional CR in many applications. SCR models can account for the same sources of variation in p as traditional CR models, as well as for variation across detectors. SCR is particularly useful for wide-ranging and rare species, but data for such species, however, are often sparse, making it necessary to prioritize among sources of variation in p. On the other hand, with increasing computational ability to fit models to large data sets, we also have to consider computational expense of increasing model complexity. It stands to reason that SCR should be similarly robust to violation of the assumption of p being constant in time, but this has not been evaluated.

Here, I use simulations to investigate accuracy in estimates of abundance and density-covariate relationship from SCR models when temporal variation in baseline detection probability, p0, is ignored. I simulate data under three scenarios: a logit-linear decline in p0 with (1) a covariate that is the same for all detectors (e.g., 'date' in a survey where all detectors are operated at the same time); (2) a covariate that varies over time and space; and (3) a covariate that varies over time and space and whose spatial variation is correlated with a covariate affecting density. For all scenarios, I fit the data-generating model (Mt) and a model with fixed p0 over time (M0); for scenarios 2 and 3, I fit an additional model using the local average of the time varying covariate as a predictor for p (i.e., accounting for spatial but not temporal variation in p0; Ms).

I found that in all scenarios, estimates of abundance under Mt and M0 were, on average, very similar, with median relative difference <1% in scenarios 1 and 3, and 6% in scenario 2. Similarly, in scenarios 2 and 3, median relative differences in abundance estimates between Mt and Ms were <1%; but the range of differences was much narrower under Ms than under M0 (max. relative difference 7% and 13%, respectively). Estimates of the density-covariate relationship under Mt and M0 were, on average, very similar (median relative difference of <1%) in scenario 1 only; in scenarios 2 and 3, model Ms (but not M0) led to very similar estimates as Mt.

Results suggest that when data are limited or adding temporal variation in p0 is computationally costly, inference on density from SCR models is valid as long as spatial variation in p0 is properly accounted for.

10:24 Murray **Efford** Robust sampling designs for spatially explicit capture-recapture

Robust sampling designs for spatially explicit capture–recapture

Efford, M. G. Department of Mathematics and Statistics, University of Otago, Dunedin, New Zealand.

Spatially explicit capture–recapture (SECR) has proven to be a robust and flexible method for surveying animal populations with natural marks or that are amenable to marking. Population density may be estimated by fitting a spatial detection model to the histories of individual visitation to detectors placed arbitrarily within the study area. Optimal placement of detectors is a topic of ongoing research. Recent papers promote model-based algorithms that distribute detectors to maximize a criterion predictive of estimate precision. I illustrate by simulation that such methods lack robustness to unmodeled patterns in density because they do not attempt to be spatially representative. I suggest two systematic designs for balanced sampling of large regions that also provide enough recaptures to fit the SECR detection model. These are a grid of intersecting lines with detectors spaced closely along lines ('lacework'), and a widely spaced grid with supplementary detectors at close spacing ('supplemented grid'). For aggregated populations both designs out-performed, by the criterion of root-mean-square error, a layout algorithmically optimized for precision. Systematic and other balanced designs protect against departures from model assumptions.

10:36 Ehsan **Moqanaki** Population-level determinants of density for a historically persecuted large carnivore

Population-level determinants of density for a historically persecuted large carnivore

Moqanaki, E.M. Faculty of Environmental Sciences and Natural Resource Management, Norwegian University of Life Sciences, P.O. Box 5003, 1432 As, Norway – ehsan.moqanaki@gmail.com
Milleret, C. Faculty of Environmental Sciences and Natural Resource Management, Norwegian University of Life Sciences, P.O. Box 5003, 1432 As, Norway
Dupont, P. Faculty of Environmental Sciences and Natural Resource Management, Norwegian University of Life Sciences, P.O. Box 5003, 1432 As, Norway
Broseth, H. Department of Terrestrial Ecology, Norwegian Institute for Nature Research, PB 5685 Torgarden, 7485 Trondheim, Norway
Bischof, R. Faculty of Environmental Sciences and Natural Resource Management, Norwegian University of Life Sciences, P.O. Box 5003, 1432 As, Norway

Using country-wide non-invasive genetic sampling data and custom spatial capture-recapture models, we quantify the population-level factors shaping the current density distribution of the wolverine Gulo gulo across the Scandinavian Peninsula. We show that a combination of historical and current environmental conditions explain the Scandinavian wolverine's population density today. Specifically, our analysis reveals that distance from the relic range, where the wolverine population survived historical persecution in the alpine borderland between Norway and Sweden, has a significant negative impact on wolverine density. However, the strength of this effect varies in management zones that differ in terms of the target number of annual wolverine reproductions, as well as their environmental conditions. Consequently, the wolverine's ability to recolonize Scandinavia varies across the species' historical range. Wolverine density is currently lowest in the southern parts of Norway and Sweden. We discuss our results in the context of differences in management goals and national legislation and obligations in Norway and Sweden. We stress that a fully coordinated monitoring and management of this transboundary wolverine population is needed.

10:48 Ana **Sanz-Pérez** Estimating demographic parameters and abundance of the Pyrenean Brown bear population using open SCR

Estimating demographic parameters and abundance of the Pyrenean Brown bear population using open SCR

Sanz-Pérez, Ana - Department of Ecological Dynamics. Leibniz Institute of Zoo and Wildlife Research, Berlin & Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals. University of Barcelona, Barcelona
Sazatornil, Victor - Conservation Biology Group. Forest Science and Technology Centre of Catalonia, Solsona
Palazón, Santiago - Fauna and Flora Service, Generalitat de Catalunya. Carrer del Foc, 57, 08038 Barcelona, Spain
Sentilles, Jerome - Équipe Ours, Office Français de la Biodiversité, Impasse de la Chapelle, 31800 12 Villeneuve-de Rivière, France
Quenette, Pierre-Yves – Équipe Ours, Office Français de la Biodiversité, Impasse de la Chapelle, 31800 12 Villeneuve-de Rivière, France
Afonso Jordana, Ivan - Conselh Generau d'Aran. Plaça d'Aran, 1-2, 25530 Vielha, Spain
Jato, Ramón - Departamento de Operaciones, SARGA - Gobierno de Aragón, Avda Ranillas, 5 Edificio A 3ª Planta, 50018 Zaragoza , Spain
Elósegui Irurtia, Miguel Mari - Servicio de Biodiversidad, Sección de Espacios Naturales y Especies 21 Amenazadas, Gobierno de Navarra-Nafarroako Gobernua, Pamplona-Iruñea, Spain
Sollmann, Rahel - Department of Ecological Dynamics. Leibniz Institute of Zoo and Wildlife Research, Berlin

Large carnivores are slowly recolonizing human-dominated landscapes, yet anthropogenic pressures and species intrinsic characteristics hold back populations expansion and keep their populations at low densities. Local governments are tasked with management that ensure large carnivores' persistence, which is usually hampered by the challenge of monitoring elusive species in heterogenous landscapes, and through differing monitoring programs across political borders. Open Spatial Capture Recapture (OPSCR) addresses the above issues by allowing the integration of data from multiple sources and modelling spatial variation in density and demographic parameters. The Pyrenean Brown bear (*Ursus actos*) is a transnational critically endangered population that has expanded since the progressive reintroduction of ten individuals starting in the nineties. Here, we integrate data from camera traps and hair snags from Spain, France, and Andorra during 2017-2021 within an OPSCR model to estimate density and demographic parameters of Pyrenean brown bears. We extend the OPSCR model to an age-structured model, which allowed us to perform age-dependent inference and improve parameter estimation. Our results show high overall bear survival, with adult survival (Mean (SD) = 0.91 (0.03)) being higher than subadult (Mean (SD) = 0.84 (0.06)) and cub (Mean (SD) = 0.88 (0.07)) survival. Brown bear abundance increased from 55 individuals (95%BCI = 47-65) in 2017 to 75 individuals (95%BCI = 59-100) in 2021, confirming the recovery of the population. Areas that were further from the origin of the population presented lower density than areas at the core, suggesting future room for population expansion. Our OPSCR model can be further extended to forecast the expansion of the Brown bear population in the Pyrenees in a spatially explicit manner and estimate spatial variation in survival. In the face of the imminent growth of this endangered population and the challenges that this expansion will bring, our results will assist in management decisions across political borders. Our age-structured OPSCR model may help improve the estimation of density and demographic parameters of other elusive mammal populations.

Abundance estimation for management

11:15 – 12:03 *Amphithéâtre Délégation CNRS*

11:15 Rachel **McCrea** Evaluating and correcting for the effect of dependence in the integrated analysis of removal and capture-recapture data

Evaluating and correcting for the effect of dependence in the integrated analysis of removal and capture-recapture data

Mccrea, R.S. Department of Mathematics and Statistics, Lancaster University, England
Frost, F. Department of Mathematics and Statistics, Lancaster University, England

Conservation translocations are being increasingly used in the conservation of threatened species and as part of ecological restoration programmes (Bickerton et al, 2022). Robust estimates of abundance are essential for meaningful conservation decision-making and the impact of translocations on source populations needs to be understood. Within this talk I will present a modelling framework where capture-recapture is combined with removal/depletion methodology (Zhou et al, 2019). I will demonstrate that an exact likelihood is possible when individual level information is available, and I will show how a standard integrated population modelling approach (Frost, et al, 2022), which assumes independence between component data sets, can be adapted to provide an approximate likelihood when individual level data is not available. This approach, as well as providing a valuable tool for estimating the abundance of source populations post translocation, also motivates a new direction of research for overcoming issues of dependence of data within a standard integrated population modelling framework.

Bickerton, K., Ewen, J.G., Canessa, S., Cole, N., Frost, F., Mootoocurpen, R. and McCrea, R.S. (2022) Estimating population size of translocated populations: a modification of the Jolly-Seber model. Submitted.
Frost, F., McCrea, R.S., King, R., Gimenez, O. and Zipkin, E. (2022) Integrated population models: Achieving their potential. Journal of Statistical Theory and Practice. In press.
Zhou, M., McCrea, R.S., Matechou, E., Cole. D.J. and Griffiths, R.A., (2019) Removal models accounting for temporary emigration. Biometrics. 75, 24-35.

11:27 Leslie **Skora** Estimating brown bear abundance along salmon spawning streams in Katmai National Park, Alaska

Estimating brown bear abundance along salmon spawning streams in Katmai National Park, Alaska

Skora, L. Department of Environmental Conservation, University of Massachusetts, Amherst, USA.
Wilson, T. Massachusetts Cooperative Fish and Wildlife Research Unit, U.S. Geological Survey, Department of Environmental Conservation, University of Massachusetts, Amherst, USA.

Monitoring wildlife populations is difficult especially in remote places such as Katmai National Park and Preserve in southwest Alaska. Here accessibility, harsh weather, and limits to staff and funding make it difficult to monitor one of the largest brown bear populations in the world. Katmai is specifically tasked with maintaining a high concentration of brown bears that rely on a large salmon return. Over the past few decades, Katmai has conducted aerial surveys counting brown bears congregating along salmon spawning streams. These counts provide a standardized, long-term, non-invasive record of brown bears throughout the park. But, without further analysis and context, these counts do not inform managers on how bear abundance is changing. I propose using these counts of brown bears in an N-mixture modeling framework to estimate trends in brown bear abundance.

The N-mixture model framework uses repeated counts of unmarked individuals to estimate abundance while correcting for imperfect detection. Incorporating time of year covariates will provide further insight into shifting use of salmon streams throughout the year. Preliminary results estimate abundance in Katmai National Preserve at 500 bears. Understanding seasonal and annual trends in brown bear abundance will

allow managers to better understand the health and fluctuations of the ecosystem, better allocate limited park resources to mitigate negative human-bear conflict zones, and better inform hunt management in Katmai National Preserve.

11:39 Amy **Davis** A multi-method dynamic removal model for evaluation of abundance and management effectiveness overtime

A multi-method dynamic removal model for evaluation of abundance and management effectiveness overtime

Amy J. Davis[1], Randy Farrar[2], Brad Jump[3], Parker Hall[4], Travis Guerrant[5], Kim M. Pepin[1]*

1.National Wildlife Research Center, Wildlife Services, Animal and Plant Health Inspection Service, United States Department of Agriculture, 4101 Laporte Ave., Fort Collins, CO, 80521, USA
2.Wildlife Services, Animal Plant Health Inspection Service, United States Department of Agriculture, Puxico, MO,
3.Wildlife Services, Animal Plant Health Inspection Service, United States Department of Agriculture, Marshfield, MO, 65706
4.Wildlife Services, Animal Plant Health Inspection Service, United States Department of Agriculture, Gainesville, FL, 32641
5.Wildlife Services, Animal Plant Health Inspection Service, United States Department of Agriculture, Columbia, MO, 65202
**Corresponding author email: Amy.J.Davis@USDA.GOV*

Evaluating the efficacy of management actions to control invasive species is crucial for maintaining funding and to provide feedback for the continual improvement of management efforts. However, it is often difficult to assess the efficacy of control methods due to limited resources for monitoring. We expanded on removal models to estimate abundance, evaluate management effectiveness, and evaluate population growth over time from a combination of removal activities (e.g., trapping, ground shooting) using only data collected during removal efforts (method of removal, date, location, number of animals removed, and effort). This dynamic approach allows for abundance estimation at discrete time points and the estimation of population growth between removal periods. To test this approach, we simulated over a million conditions. Our estimates were unbiased (within 10% of truth) 81% of the time and were correlated with truth 91% of the time. Overall, this method performs well, particularly at monitoring trends in abundances over time. We applied this method to removal data of feral swine (*Sus scrofa*) from Mingo National Wildlife Refuge in Missouri from December 2015 to September 2019. Populations fluctuated over time but showed marked declines in the last 3-6 months corresponding to increased removal pressure. In Mingo NWR the target monthly removal rate needed to cause a population decline is 18%. Our method provides advancement over traditional removal modeling approaches because it can be applied to evaluate management programs that use a broad range of removal techniques concurrently and whose management effort and spatial coverage vary across time.

11:51 Yiran **Wang** Bayesian genetic mark-recapture methods for estimating seasonal river run size of stock populations

Bayesian genetic mark-recapture methods for estimating seasonal river run size of stock populations

Yiran, W. Department of Statistics and Actuarial Science, University of Waterloo, Waterloo, Canada
Martin, L. Department of Statistics and Actuarial Science, University of Waterloo, Waterloo, Canada
Audrey, B. Department of Statistics and Actuarial Science, University of Waterloo, Waterloo, Canada

Population size estimation is an important topic in wildlife research and fisheries management. With the development of the genetic techniques, the genetic mark-recapture (GMR) becomes a popular method to estimate population size. By combining genetic data on the relative abundance of species from a sample with population counts obtained for a subset of the species, GMR allows the estimation of the total population size and the contributions of each species. This is typically done with a type of Lincoln-Petersen estimator which provides an asymptotically unbiased estimate for the total population size. However, few studies have addressed the issue that the accompanying variance estimator does not account for all the uncertainty in the genetic samples. As a result, this approach can suffer from a significantly underestimated variance, especially when the relative proportions in the genetic sample differ from those in the population. In this paper, we propose a novel Bayesian GMR framework to resolve this issue. The Bayesian framework can explicitly incorporate the uncertainties in the genetic sample and readily lends itself to combining additional sources of data into a single model, such as capture-recapture data or telemetry data, which are also frequently used to estimate population size. The effectiveness of the new method is investigated via simulation studies and used to estimate the abundance of Sockeye Salmon in the Taku River.

Novel approaches to abundance estimation

13:30 – 14:30 *Amphithéâtre Délégation CNRS*

13:30 Charles **Yackulic** Sharing abundance: Integrating long-term count data with short-term capture-recapture data in a marginalized multistate Jolly-Seber framework

Sharing abundance: Integrating long-term count data with short-term capture-recapture data in a marginalized, multistate jolly-seber framework

Yackulic, C.B. U.S. Geological Survey, Southwest Biological Science Center, Grand Canyon Monitoring and Research Center, Flagstaff, AZ, USA
Saracco, J.F. The Institute for Bird Populations, Petaluma, CA 94953 USA
Korman, J. Ecometric Research Inc. and Institute of Oceans and Fisheries, University of British Columbia, 3560 W 22nd Ave., Vancouver, BC V6S 1J3, Canada.
Dzul, M. U.S. Geological Survey, Southwest Biological Science Center, Grand Canyon Monitoring and Research Center, Flagstaff, AZ, USA

For many species of birds and other animals, there exist long time-series of count data that provide information about changes in relative abundance (e.g., Breeding Bird Survey data). In recent years, integrated population models have been introduced that combine these count data with capture-recapture data collected concurrently. Most integrated population models estimate survival using capture-recapture or dead recovery data and share this parameter with a sub-model describing changes in abundance to estimate productivity or recruitment. Here we develop an alternative approach that borrows heavily from the original parameterization of the Jolly Seber (JS) model, shares both abundance and survival, and allows for estimation of abundance at the scale of the capture-recapture study during periods when only count data are available (provided a sufficient period during which both data are collected). Computationally efficient implementation of this integrated framework relies on analyzing capture-recapture data using a marginalized approach, parameterizing the JS model in terms of recruitment, tracking abundance over the longer time series as a continuous latent variable, and linking counts to the latent abundance with either negative binomial or Poisson distributions.

We investigate the value of this approach in a variety of circumstances through simulation studies and then fit a version of this model to long-term dataset illustrating how integration allows for improved inferences under certain conditions. We begin by comparing two versions of our modified JS model to version based on the super population approach. Precision, coverage, and bias of recruitment, survival and capture probability are indistinguishable when comparing a super-population JS to a modified JS model that estimates the size of the unmarked population and focuses on capture of unmarked individual. A second version that estimates total abundance and capture of both marked and unmarked individuals is computationally quicker and performs similarly when capture probability is low and total population size is reasonably large. However, this version leads to decreased precision when total population size is small, and/or capture probability is high. In the integrated model, count data is most informative when unexplained variation in survival and capture probability is relatively small, there is substantial interannual variation in recruitment, newly recruited individuals can be distinguished (and counted) separately from survivors, and/or there are counts in both the breeding and nonbreeding season. Applications to real data sets illustrate how integrating long-term count data with intensive mark-recapture leads to improved inferences regarding drivers of recruitment, an important demographic parameter that can vary substantially over time in some species and may be difficult to characterize during short term studies.

13:42 Diego **Rondon** A bayesian multi-state model for estimating the effect of inbreeding and age on population dynamics

A Bayesian Multi-state model for estimating the effect of inbreeding and age on population dynamics

Diego Rondon[a], Samu Mantyniemi[c], Jouni Aspi[b], Laura Kvist[b], Mikko J. Sillanpää[a]
[a]Research Unit of Mathematical Sciences, University of Oulu, Oulu, Finland
[b]Research Unit of Ecology and Genetics, University of Oulu, Oulu, Finland
[c]Natural Resources Institute Finland, Helsinki, Finland

Multi-state modeling has been considered a useful technique for estimating population sizes and transition probabilities, removing the assumption that all individuals need to be seen at the start of the study, makes it a very useful technique to study wild animals or in cases where capture and tracking are challenging. In this research, an open simulated population where the inbreeding coefficient and the age of individuals affected reproduction and survival rate over different scenarios is created, random samples of individuals are taken and a Multistate model is built, where the transition probabilities are modeled as a function of covariates vial Generalized Linear Models. Our main goal is to correctly estimates population sizes and survival probabilities via data augmentation.

13:54 Rémi **Fraysse** Modelling misidentifications in capture-recapture experiments

Modelling misidentifications in capture-recapture experiments

Rémi Fraysse

Capture–recapture studies widely use environmental DNA samples or camera traps for animal identification. Both these techniques can lead to misidentifications. These errors, leading to more than one "identity" being associated with a single animal, tend to result in substantial overestimation of population size or underestimation of survival. Deleting low-quality samples is a solution but it can lead to the elimination of large amount of data and it might be preferable to model the misidentifications.

Link et al. (2010) have described a framework for a latent multinomial model. In this framework, observed histories frequencies $\boldsymbol{y}$ are a known linear transformation $\boldsymbol{y} = \boldsymbol{A}\,\boldsymbol{x}$ of latent histories' frequencies $\boldsymbol{x}$ that follow a multinomial distribution. This model when little data is available (i.e. a low capture rate), quickly becomes weakly identifiable, in particular for the probability of misidentification. We looked into two ways of adding information in order to improve the performances of the model in these cases.

First, using simulations, we tested the impact of an informative prior on the probability of misidentifying an individual. Such a prior can be obtained through a test of the identification protocol with known individuals. We show that an unbiased strong informative prior allow for acceptable estimates of population size in situations where the use of an uninformative prior leads to a relative bias over 60%.

On another hand, we extended the model to include data relative to the eDNA samples. The first approach was to add the quality of the observed genotype associated with a capture as a covariate of identification in the model. This work still in progress can open the way to define more robust model with the addition of information coming from eDNA samples.

14:06 Rishika **Chopara** A framework for goodness-of-fit testing in ecological modelling

A framework for goodness-of-fit testing in ecological modelling

Rishika Chopara

Goodness-of-fit (GOF) testing is vital to statistical analysis, as it allows us to validate the reliability of any statistical inference we make. In many modern capture-recapture models, such as spatial capture-recapture, effective methods of assessing GOF remain unresolved.

In many statistical models, the deviance is used to assess GOF by comparing it against a Chi-squared distribution. However, in some situations (e.g. when dealing with sparse counts) the deviance does not have a Chi-squared distribution, even approximately, yielding such tests unusable. In principle, the true distribution for the deviance is computable, however in practice it is often intractable. We show that when dealing with a Poisson response, we can accurately approximate the true underlying distribution of the deviance using a Gamma distribution. Using this approximation, we enhance the usability and power of GOF tests while retaining the familiarity and convenience of the deviance statistic.

Using a range of capture-recapture models for illustration, we show how our method can be used to accurately approximate the distribution of the deviance when dealing with various levels of data sparsity. With this approach, we aim to provide an accessible and effective GOF testing framework for complex modelling scenarios such as spatial capture-recapture.

14:18 Michelle **Kissling** Aligning statistical and biological populations for abundance estimation

Aligning statistical and biological populations for abundance estimation

Kissling, M.L. Wildlife Biology Program, University of Montana, Missoula, USA.
Lukacs, P.M. Wildlife Biology Program, University of Montana, Missoula, USA.
Nesvacil, K. Padre Island National Seashore, National Park Service, Corpus Christi, Texas, USA.
Gende, S.M. National Park Service, Glacier Bay Field Station, Juneau, Alaska, USA.
Pendleton, G.W. Alaska Department of Fish and Game, Juneau, Alaska, USA.

Ideally, a statistical population is the same as or accurately represents its corresponding biological population, or a superpopulation. In practice, they do not always align in space and/or time, which can lead to biased inference. A population mismatch is often handled analytically as temporary emigration, an oddly vague process with statistical and/or biological drivers that usually are confounded. Most abundance models that account for temporary emigration rely on spatial or temporal replicates with periods of closure or the ability to identify individuals during sampling. Therefore, these models often are not suitable for species that are highly mobile, non-territorial, difficult to recapture or resight, or use dynamic habitats, as is the case for many marine species. We developed a hierarchical Bayesian integrated model for the Kittlitz's murrelet (*Brachyramphus brevirostris*), a highly mobile, non-colonial, ice-associated seabird that is patchily distributed across coastal Alaska and eastern Russia. Our model combines datasets from boat-based surveys and telemetry flights to estimate superpopulation abundance by accounting for all components of overall detection: probability of presence (p_p), probability of availability (p_a), and probability of detection (p_d). We used telemetry location data to estimate p_p and line transect distance sampling data to estimate p_d; we separately determined that p_a was nearly 1 using dive behavior data. By estimating p_p directly, we were able to account for temporary emigration from the sampled area, which changed with shifting icefloes between sampling occasions. Across a 6-year period, p_p explained most (79%) of the variation in overall detection probability, averaging 0.50 (SD=0.02; range=0.33–0.75), but was not predictable using five environmental covariates available to us. In years when two boat surveys were conducted, our model reduced coefficients of variation (CV) of annual abundance estimates by 30% (range=25–31); in the year with only one boat survey, the CV increased by 27%, underscoring the importance of within-year replication when p_p is highly variable. By explicitly accounting for all components of overall detection probability, especially p_p, we reduced variation of the across-year trend estimate by 5%. Although temporary emigration of murrelets from our study area appears to be random, its high variability, if ignored, reduces power to detect and diagnose population changes of this ice-associated species and could introduce confusion in integrated population models. Our model presented here is simple, flexible, and effective in generating unbiased and precise abundance estimates of highly mobile species that occupy dynamic habitats where other open population models are not feasible.

Causal inference for management

14:45 – 15:45 *Amphithéâtre Délégation CNRS*

14:45 Romuald **Hounyèmè** From responses of macroinvertebrate metrics to the definition of reference thresholds

From responses of macroinvertebrate metrics to the definition of reference thresholds

Romuald Hounyèmè 1,2,3*, Florence Le Ber 4, Daouda Mama 3 and Christine Argillier 1,2
*(1) * ED251, Aix-Marseille University, CEREGE, Europole de l'Arbois BP80, Aix-en-Provence, 13545, France. (4) ENGEES, 1 Quai Koch, 67070 Strasbourg*
(2) AQUA-UMR RECOVER, INRAE, 3275 route de Cézanne CS 40061, Aix-en-Provence, 13182, France.
(3) LHA-INE, University of Abomey-Calavi, 01BP: 526, Cotonou, Benin
**romualdaurel1@yahoo.fr*

The present study focused on the use of benthic macrofauna to define the reference state of an anthropized lagoon (Nokoué-Benin) from the responses of relevant metrics to proxies. The approach used is a combination of a joint species distribution model and Bayesian networks. The joint species distribution model was used to select the relevant metrics and generate posterior probabilities that were then converted into posterior response probabilities for each of the quality classes (pressure levels), which will constitute the conditional probability tables allowing the establishment of the probabilistic graph representing the different causal relationships between metrics and pressure proxies. For the definition of the reference thresholds, the predicted responses for low pressure levels were read via probability density diagrams. Observations collected during high and low water periods spanning 03 consecutive years (2004-2006), sampling 33 macroinvertebrate taxa present at all seasons and sampling points, and measurements of 14 environmental parameters were used as application data. The study demonstrated reliable inferences, selection of 07 relevant metrics and definition of quality thresholds for each environmental parameter. The relevance of the metrics as well as the reference thresholds for ecological assessment despite the small sample size, suggests the potential for wider applicability of the approach for aquatic ecosystem monitoring and assessment programs in developing countries generally characterized by a lack of monitoring data.

14:57 Daniel **Fink** Estimating spatially explicit population trajectories with citizen science data and double machine learning

Estimating spatially explicit population trajectories with citizen science data and double machine learning

Daniel Fink[1], Alison Johnston[2], Matt Strimas-Mackey[1], Tom Auer[1], Wesley M. Hochachka[1], Shawn Ligocki[1], Lauren Oldham Jaromczyk[1], and Orin Robinson[1]
[1]Cornell Lab of Ornithology, Cornell University, Ithaca, NY 14850, USA.
[2]School of Mathematics and Statistics, University of St Andrews, St Andrews KY16 9SS, UK.
**Corresponding author. daniel.fink@cornell.edu*

Citizen and community-science (CS) datasets have great potential for estimating interannual patterns of population change given the large volumes of data collected globally every year. Yet, the flexible protocols that enable many CS projects to collect large volumes of data typically lack the structure necessary to keep consistent sampling across years. This leads to interannual confounding, as changes to the observation process over time are confounded with changes in species population sizes.

In this presentation we discuss how double machine learning can be used to estimate population trajectories while adjusting for the interannual confounding common in citizen science data. Double Machine Learning is statistical framework that uses off-the-shelf machine learning methods to estimate population change and the propensity scores used to adjust for confounding discovered in the data. Machine learning makes it possible to use large feature sets to identify and adjust for confounding and model heterogeneity in population change.

To illustrate the approach, we estimated species trajectories of relative abundance using data from the citizen science project eBird. eBird engages large numbers of participants who each decide where, when, and how to conduct surveys. Like many other citizen science projects, the flexibility of the eBird protocol has given rise to an evolving, heterogenous observation process where interannual confounding is a central concern when estimating population change. We used a simulation study to assess the ability of the method to estimate spatially varying trajectories in the face of real-world confounding. Results show how population trajectories can be recovered while distinguishing between different spatial patterns of population change. These results add to a growing literature demonstrating how innovations in causal inference can unlock ecological information from citizen science data.

15:09 Allison **Binley** Redistributing resources from monitoring to action: Quantifying the value of citizen science data in conservation decision making

Redistributing resources from monitoring to action: quantifying the value of citizen science data in conservation decision making

Allison D. Binley, Department of Biology, 1125 Colonel By Drive, Carleton University, Ottawa ON, K1S 5B6 Canada
Jeffrey Hanson, Department of Biology, 1125 Colonel By Drive, Carleton University, Ottawa ON, K1S 5B6 Canada
Orin Robinson, Cornell Lab of Ornithology, Cornell University, Ithaca, NY 14850 USA
Mark Reynolds, The Nature Conservancy, San Francisco, California 94105 USA
Gregory Golet, The Nature Conservancy, Chico, California 95928 USA
Joseph R. Bennett, Department of Biology, 1125 Colonel By Drive, Carleton University, Ottawa ON, K1S 5B6 Canada

Citizen science data can serve as an effective means to collect vast quantities of data in a cost-efficient manner. This may prove invaluable to conservation efforts, as using crowd-sourced data to inform decisions can allow managers to redirect limited funds towards action rather than monitoring. Here, we aimed to quantitatively explore the potential benefits of using citizen science data for setting conservation priorities in an applied conservation setting. Using data from the BirdReturns conservation program implemented by The Nature Conservancy in central California, rice farms were prioritized for conservation action based on the modeled probability of detection of seven shorebird species using two datasets: eBird citizen science data, and monitoring data collected through professional surveys conducted by the Nature Conservancy. The value of these prioritizations was assessed using an integrated dataset that combined both the community and professionally collected data as a benchmark. Prioritizations conducted using the professional monitoring data were subject to a monitoring penalty, where the cost of monitoring was deducted from the overall budget, leaving less remaining to pay for conservation action. Prioritizations were then run across a range of different available budgets. We predicted that decisions based solely on eBird data would be preferable at lower budgets given that more money can be spent on action rather than monitoring, but that the more targeted professional monitoring may provide better value at larger budgets. Contrary to these predictions, prioritizing detections across all seven species based on the model using eBird data resulted in the greatest overall value across all budgets. The difference was greatest at lower budgets, but prioritizations based on eBird data consistently performed better until the budget was sufficiently large enough so that all properties could be enrolled in the program. Furthermore, prioritizations based on citizen science data performed comparably to those based on the integrated model (i.e., the best available information). Even when the monitoring penalty was removed from the professional monitoring prioritization, allowing for a more direct comparison of information content, the eBird prioritization performed comparably or better than professional monitoring. This demonstrates that, in this case study, eBird citizen science data matched or surpassed the capacity of professional monitoring data to inform conservation decisions. This study quantified the trade-offs between monitoring and action, to better illustrate to conservation managers the potential risks associated with unnecessary data collection. In this case study, there was no benefit to spending money on professional monitoring at any budget. Using citizen science data, resources can be redistributed towards actions that will directly benefit biodiversity, ultimately resulting in better overall outcomes.

15:21 Annabelle **Stanley** Making informed decisions for private lands conservation under uncertainty and spatial complexity: A case study on the Northern Bobwhite

Making informed decisions for private lands conservation under uncertainty and spatial complexity: A case study on the Northern Bobwhite

Annabelle E. Stanley, Georgia Cooperative Fish and Wildlife Research Unit, Warnell School of Forestry and Natural Resources, University of Georgia
James Martin, Warnell School of Forestry and Natural Resources, University of Georgia
Edwige Bellier, Department of Natural Resources Science, University of Rhode Island
Jeffrey Hepinstall-Cymerman, Warnell School of Forestry and Natural Resources, University of Georgia
John M. Yeiser, U. S. Fish and Wildlife Service, Division of Migratory Bird Management
Clinton T. Moore, U.S. Geological Survey, Georgia Cooperative Fish and Wildlife Research Unit, Warnell School of Forestry and Natural Resources, University of Georgia

Agri-environment schemes across the globe offer financial incentives to encourage private landowners to engage in conservation. In the U.S., certain incentive programs at the state and federal levels are used to increase the amount and quality of habitat available on managed ecosystems for declining bird species. For the Northern Bobwhite (*Colinus virginianus*), such programs include the Environmental Quality Incentive Program of the U.S. Department of Agriculture. Sponsoring agencies have finite budgets and must make discrete choices about whether to enroll prospective participants. Because decision making in a context of spatial complexity and uncertainty is inherently difficult, the problem of selecting participants is sometimes cast into simplified scoring rubrics that mask the assumed underlying relationships between actions and bird response. We developed a prototype decision framework for selecting enrollees and compared its performance to the status quo approach of scoring applicants. Our framework is built on a spatially explicit and individual-based Northern Bobwhite population model that includes biological processes of survival, productivity, and dispersal. We simulated the model on randomly generated landscapes and property boundaries from landscapes identified as focal regions for the Northern Bobwhite. Enrollees were assumed to implement habitat management actions taken from a list of actions. We used a genetic algorithm to construct and evaluate portfolios of participant selection, where better portfolios were those that predicted more birds within imposed constraints of cost. We conducted optimizations for varying levels of connectivity, alternative hypotheses about scale of effect on actions, and different degrees of controllability of participant actions. We computed expected Northern Bobwhite abundance for each optimal solution, and we compared performance of the solutions against the status quo scoring framework.

15:33 Priyanjana **Pramanik** What-if thinking in conservation policy research: Expanding the use of synthetic controls

What-if thinking in conservation policy research: expanding the use of synthetic controls

Pramanik, P. Wildlife Biology and Conservation Programme, National Centre for Biological Sciences, Bangalore, India.

Counterfactual thinking assesses what would have happened in the absence of an intervention, enabling us to estimate program impact, but such methods have not been commonly used in conservation. I examine the use of one of these methods – synthetic controls – to evaluate program impact on forest cover change through a systematic review. My review finds a dearth of evidence from India, where deforestation is of pressing concern. This paucity of evidence may be part of a wider trend, as recent systematic reviews of conservation interventions include only 1-2 studies from India. In an ongoing analysis, I am using remotely sensed forest cover data to look at the performance of protected areas in India, seeking to provide a proof of concept of the use of synthetic controls. There is a need for increased use of rigorous evaluation of conservation interventions to promote evidence-based conservation practices. Program evaluations could benefit from synthetic controls in suitable contexts, making use of readily available satellite data to create vegetation indices and map forest cover change.

Advances in monitoring

15:57 – 17:09

Amphithéâtre Délégation CNRS

15:57 Yoba **Alenga** Bat sonotype as a novel insight into the Congo Basin Rainforest dynamic

Bat sonotype as a novel insight into the Congo Basin Rainforest dynamic

Yoba, A.S. Faculty of Sciences, University of Kisangani, Democratic Republic of the Congo
Mande, C. Faculty of Sciences, University of Kisangani, Democratic Republic of the Congo
Gembu, G. C. Faculty of Sciences, University of Kisangani, Democratic Republic of the Congo
Laudisoit, A. Ecohealth Alliance, 520 8th Avenue, 10018 New York, NY, United States of America

Tropical forest ecosystems are undergoing an exponential regression of their surface areas with subsequent habitat loss and fragmentation. The effects of such disturbances on bats are quite significant, even leading to a decline in populations. In order to ensure the maintenance of bat populations, it is thus important to preserve their habitats. This involves highlighting preferential habitats but also factors related to their foraging sites.

We have combined acoustic surveys and capture-mark-recapture methods to study relationships between bats and their preferred habitats and also to identify functional role of bats captured or recorded in their habitat. A total of 42 bats were captured, belonging to 13 species, including 5 species of frugivorous bats and 8 insectivorous bats.

The frugivorous bats - namely the species *Scotonycteris bergmansi*, *Casinycteris arginnis*, *Myonycteris torquata* and *Epomops franqueti* - were associated with dispersal of 16 plant species in the Yangambi Man and Biosphere Reserve (*Aidia micrantha*, *Allanblackia floribunda*, *Anonidium mannii*, *Barteria nigritana*, *Canarium schweinfurthii*, *Coelocaryon preussi*, *Dacryodes edulis*, *Mammea africana*, *Maranthes glabra*, *Microdesmis yanfungana*, *Musanga cecropioides*, *Pycnanthus angolensis*, *Staudtia gabonensis*, *Strombosia grandifolia*, *Strombosiopsis tetrandra* and *Panda oleosa*) while the species *Megaloglossus woermanni* ensures the pollination of the species *Maranthes glabra.*

Acoustic monitoring revealed the presence of 11 sonotypes namely of the following species: *Chaerephon pumilus*, *Macronycteris gigas*, *Macronycteris vittatus*, *Doryrhina cyclops*, *Rhinolophus fumigatus*, *Neoromicia nana/Scotophilus dinganii*, *Pipistrellus nanulus*, *Pipistrellus rueppellii*, *Nycteris arge*, *Myotis bocagii* and *Glauconycteris superba.*

The type of habitat (primary forest) significantly increases the foraging activity of bats. A medium to high density of the understorey and a medium opening of the canopy have a significant influence on bat activity and call structure. Complementarity of acoustic monitoring and capture is crucial to understand the mechanisms governing aggregation of bats assemblages in order to assess their activity and the ecosystem services they provide.

16:09 Philip **Patton** The effect of fully automated animal recognition on mark-recapture estimates

The effect of fully automated animal recognition on mark recapture estimates

Patton, P.T. Hawai‘i Institute of Marine Biology, University of Hawai‘i at Manoa, Kane‘ohe, Hawai‘i
Bejder, L. Hawai‘i Institute of Marine Biology, University of Hawai‘i at Manoa, Kane‘ohe, Hawai‘i

Baird, R.W. Cascadia Research Collective, Olympia, Washington, USA
Oleson, E.M. Pacific Islands Fisheries Science Center, NOAA Fisheries, Honolulu, Hawai'i

Estimating abundance or vital rates via mark-recapture requires recognizing the same individual over time. This step demands time and expertise in some cases, e.g., photo-id of cetaceans with natural markings. As a result, in conjunction with the rapid development of deep learning, photo-id systems are being developed that are fully automated, i.e., they predict the individual label with minimal input from the user. The error rates of these systems may differ from those of traditional approaches, meaning that the same set of photos processed manually and automatically may produce different encounter histories. Here, we study the effect that these differences may have on demographic estimates from capture-recapture models, and how the effect might vary across situations. To that end, we modeled encounter histories that were generated through manual matching and two different automated methods. We compared these methods using two catalogs that differed by species, which affects the predictive performance of the automated tools, and sampling design, which affects the modeling approach. Additionally, we studied these effects using Monte Carlo simulation. We found that the error rate drives differences in estimates of abundance and survival, which appear most sensitive to incorrect matches, i.e., false positives. In some situations, the differences in demographic estimates were negligible, meaning that the potential benefits of fully automated systems could outweigh the costs for similar catalogs. With these results in mind, we offer some guidance to practitioners who are considering transitioning to fully automated systems from manual approaches. In doing so, we account for tradeoffs that may exist between potential bias introduced by the model and the reduced cost of processing photos.

16:21 Gaël **Bardon** RFIDeep: unfolding the potential of deep learning for radio-frequency identification

RFIDeep: unfolding the potential of deep learning for radio-frequency identification

Gaël Bardon1,2, Robin Cristofari3, Alexander Winterl4, Denis Allemand1, Téo Barracho2,5, Claire Ceresa1, Nicolas Chatelain2, Julien Courtecuisse2, Flavia A.N. Fernandes6, Benjamin Friess2, Michel Gauthier-Clerc7, Jean-Paul Gendner2, Yves Handrich2, Aymeric Houstin1,2,8, Adélie Krellenstein2,4, Nicolas Lecomte5, Charles-Edouard Salmon2, Emiliano Trucchi6, Benoit Vallas2,9, Emily Wong8,10, Daniel P. Zitterbart4,8* & Céline Le Bohec1,2*
1 - Centre Scientifique de Monaco, Département de Biologie Polaire, Monaco, Principality of Monaco
2 - Université de Strasbourg, CNRS, IPHC UMR 7178, Strasbourg, France
3 - University of Turku, Turku, Turun Yliopisto, Finland
4 - Department of Physics, Friedrich-Alexander-University Erlangen-Nürnberg Erlangen, Germany
5 - Canada Research Chair in Polar and Boreal Ecology, Department of Biology, University of Moncton, Moncton, NB, Canada
6 - Department of Life and Environmental Sciences, Marche Polytechnic University, Ancona, Italy
7 - Université de Genève – Faculté des Sciences, Genève, Switzerland
8 - Applied Ocean Physics and Engineering, Woods Hole Oceanographic Institution, Woods Hole, MA, United States of America
9 - Réserve Nationale des Terres Australes Françaises, TAAF, Saint-Pierre, La Réunion, France
10 - Stanford University, Stanford, CA, USA

1. Automatic monitoring of wildlife is becoming a critical tool in the field of ecology. In particular, radio-frequency identification (RFID) is now a widespread technology to assess the phenology, breeding, and survival of many species. RFID generates massive and complex datasets with little to no fast and accurate data processing pipelines yet available. Deep learning approaches have been used to overcome similar problems in other scientific fields and hence might bear the potential to easily overcome analytical challenges and unlock the full potential of RFID studies.

2. Here, our aim is to present a deep learning workflow, coined "RFIDeep", to derive ecological features, such as breeding status and output, from RFID mark-recapture data. To demonstrate the performance of RFIDeep with complex datasets, we used long-term automatic monitoring of a long-lived seabird breeding in densely packed colonies, i.e., king penguins (*Aptenodytes patagonicus*).

3. To determine individual breeding status and phenology at the individual level and for each breeding season, we first developed a one-dimensional convolution neural network (1D-CNN) architecture. Second, to account for variance in breeding phenology and technological limitations of field data acquisition, we added a new data augmentation step mimicking a shift in breeding dates and missing detections (i.e., missing RFID recaptures). Third, to identify segments of the breeding activity used during classification, we also included a visualisation tool, allowing users to understand what is usually considered a "black box" step of deep learning. With these three steps, we achieved a high accuracy for all breeding parameters (breeding status accuracy = 95.1%; phenological accuracy = 87.2%; breeding success accuracy = 97.3%).

4. RFIDeep has unfolded the potential of artificial intelligence for tracking changes in animal populations, multiplying the benefit of automated mark-recapture monitoring of undisturbed wildlife populations. RFIDeep's code is open source to facilitate their use, adaptation, or enhancement in a wide variety of species. In addition to a tremendous time saving, our study shows the capacities of CNN models to blindly detect ecologically meaningful patterns in data through visualisation techniques seldom used in ecology.

16:33 Clark **Rushing** Estimation of seasonal survival and migration phenology of migratory birds from automated telemetry data using continuous-time multi-state models

Estimation of seasonal survival and migration phenology of migratoyr birds from automated telemetry data using continuous-time, multi-state models

Rushing, C.S. Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA
Cooper, N.W. Migratory Bird Center, Smithsonian Conservation Biology Institute, Washington, DC, USA
Yanco, S.W. Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT, USA
Marra, P.P. Department of Biology, Georgetown University, Washington, DC, USA

Estimating seasonal survival and movement rates of migratory birds has long been a primary goal of ornithologists, as these rates are central to population dynamics and conservation. New methods for tracking birds across their annual cycle, in particular the growth of the Motus tracking network, are providing novel sources of data that can shed light on these important vital rates. Motus data present several challenges and opportunities for robust estimation of survival and movement. First, detections occur in continuous time. Although it is possible to bin detections and use discrete-time models, continuous-time modeling approaches avoid the loss of information and arbitrary intervals caused by binning. Second, detections by the Motus network are conditional on both the location of towers and the movement of tracked birds. Estimation of parameters from Motus data therefore requires explicit consideration of spatial variability in the detection process. Third, dead individuals cannot be detected and uncertainty in the state of unobserved individuals must be accounted for, which may be particularly difficult in areas with low tower density. We describe a continuous-time, multi-state model that allows for estimation of seasonal survival rates and the timing of movement between geographic areas, while accounting for spatial variation in the detection of birds. Using both simulations and detections of Kirtland's Warblers (*Setophaga kirtlandii*) during winter, spring, and summer, we demonstrate that this modeling approach can provide reliable estimates of seasonal survival and migration phenology. We also discuss challenges and future opportunities for continued development of models for Motus data.

16:45 Erlend **Nilsen** Structured citizen science as a means to monitor wildlife populations

Structured citizen science as a means to monitor wildlife populations

Nilsen, E.B. Norwegian Institute for Nature Research, Trondheim, Norway AND Nord University, Faculty of Bioscience and Aquaculture, Norway
Rød-eriksen, L. Norwegian Institute for Nature Research, Trondheim, Norway
Berge, S. Norwegian Institute for Nature Research, Trondheim, Norway
Vang, R. Norwegian Institute for Nature Research, Trondheim, Norway
Kjønsberg, M. Inland Norway University of Applied Sciences, Evenstad, Norway
Johnsen, K. Inland Norway University of Applied Sciences, Evenstad, Norway

Citizen science (CS) data is becoming increasingly important for global biodiversity monitoring and assessments, and there has been a massive increase in the volume of CS data shared openly through global facilities such as those operated by the Global Biodiversity Information Facility (GBIF). However, because traditional CS programs are based mainly on convenience sampling designs, interpretation of the data could be challenging. Here, we present what we call a structured citizen science program for grouse species (in particular willow ptarmigan *Lagopus lagopus*) in Norway known as "*Hønsefuglportalen*". At the core, the program is a based on a line transect distance sampling data collection protocol, where volunteer personnel search predetermined transect lines using pointing dogs to locate the birds. The program brings together managers, landowners, hunters and scientist in a common effort to monitor species populations. The program offers common field protocols, data flow pipelines, reporting templates and training courses for volunteer field personnel as well as managers and landowners that should interpret and utilize the output into their management schemes. On a larger scale the program is however less structured, as there is no mandatory monitoring of these species by landowners in Norway. As of 2022, the total effort was close to 10.000km of line transect surveys annually, resulting in more than 8000 annual observations of single birds or broods. The program is built around principles for open, transparent and reproducible science, and data are shared via GBIF based on the event core data model. This allow other stakeholders as well as other researchers to scrutinize the data collected through the program, but also re-use the data for other purposes. So far, the data has been used for a wide range of scientific research questions. In this talk, we will present how the program is organized, how manage the data pipeline between field data collection and open data published at GBIF, and how the data available from GBIF contain information that is sufficient for classical and novel distance sampling models and integrated population models.

16:57 Philipp **Boersch-Supan** Modelling life cycle-event phenology using biometrics collected by citizen science ringers

Modelling life cycle-event phenology using biometrics collected by citizen science ringers

Boersch-Supan, PH, British Trust for Ornithology, Thetford, United Kingdom
Hanmer, H, British Trust for Ornithology, Thetford, United Kingdom
Robinson, RA, British Trust for Ornithology, Thetford, United Kingdom

The study of phenology, the timing of species' annual life-cycle events, has allowed for a better understanding of fundamental ecosystem processes. Shifts in the timing of life-cycle events can have important population implications directly, or provide information about the mechanisms driving population trajectories, especially if phenological shifts differ between life-cycle events. Phenological analyses usually focus on the timing of particular events, e.g. dates of first appearance. However, for many phenomena exact dates of particular events are more difficult to observe than the state of the system itself. For example, a bird ringer may record whether an individual is in active moult, but not the onset or completion date of moult. Such observations categorize an organism's state and are often encoded as discrete, ordered classes or (semi-)continuous progression scores. A plethora of statistical models have been developed by ecologists to infer dates of interest from such data, often framed around taxon-specific applications. Many of these models are special cases of categorical or censored regression models.

We describe parallels between existing modelling approaches and apply Bayesian inference to this class of models, with the aim to make full use of information from repeated observations of individuals where available. Our focus is on the estimation of avian life-cycle event phenology from biometric data such as brood patch scores or moult observations (Boersch-Supan et al. 2022 arXiv; Hanmer et al. 2022 Biol Lett), which are often collected during bird ringing or recapture, and which can provide crucial information about mechanistic drivers of vital rates inferred from mark-recapture analyses. For moult data we provide the R package 'moultmcmc' which makes use of fast Hamiltonian Monte Carlo samplers, whereas models for other data types can be estimated using general purpose regression software.

We illustrate our modelling approaches with applications to multiple datasets: Demonstrating how climate driven phenological shifts identify failure points in the annual cycle of an endangered Afro-Palearctic migrant - the Willow Warbler (Phylloscopus trochilus), how weather and resource availability influence annual cycle scheduling in a nomadic Eurasian finch - the Eurasian Siskin (Spinus spinus), as well as highlighting outstanding challenges in measuring and modelling phenology using southern African passerines as examples.

Honorary plenary talk
17:30-18:15 Emmanuelle **Cam**

30 years of data collection, capture-mark-recapture (CMR) modeling and teaching: what is seen matters, what is unseen matters as much, and sometimes we estimate quantities that are unobservable

Amphithéâtre Délégation CNRS

30 years of data collection, capture-mark-recapture (CMR) modeling and teaching: what is seen matters, what is unseen matters as much, and sometimes we estimate quantities that are unobservable

Emmanuelle Cam

Dr. Emmanuelle Cam has been a professor at the University of Western Britanny (Brest, France) since 2017. She is a population ecologist who combines fieldwork and statistical modeling to address the demographic processes underlying population dynamics. She is involved in a kittiwake (Rissa tridactyla) monitoring program based on individually marked birds (1979 to the present). The primary theme of her research focuses on variation in individual decisions (breeding or not, timing of breeding, mate and site fidelity) according to ontogenetic factors and social or environmental conditions, and on individual responses to changing conditions. She teaches courses on population dynamics, evolutionary ecology, applied modeling for conservation biology, and a specific course on modeling for the conservation of marine megafauna (International Master of Science in Marine Biological Resources). Before that (2002-2017) she was an associate professor and then a professor at the University of Toulouse (France). Prior to 2017 she was a post-doctoral fellow with the biometry group at Patuxent Wildlife Research Center (U.S.A), with the Center for Wildlife Ecology at Simon Fraser University (Canada), and with the Ecology and Evolution group at the Mediterranean Institute for Advanced Studies (Spain). She has MSc degree (1993) and a PhD in ecology (1997) from Pierre and Marie Curie University in (Paris, France).

In the 20th century, the probability of a young biologist with a basic training in statistics successfully building the CMR models required to address ambitious hypotheses based on ecological or evolutionary theory was small. The situation has changed thanks to the amazing dynamism of researchers involved in the development of CMR models, pieces of software, courses offered in universities and workshops worldwide, and the publication of papers and textbooks. EURING Analytical meetings have played a large part in the sustained dynamics of the community of statisticians and biologists using CMR models. As a user, studying how to design CMR models brings you more than 'recipes' to overcome problems inherent in imperfect detection of marked individuals. For example, any piece of software designed to build CMR models includes tools to conduct model selection based on Information Criteria because leading researchers have popularized this approach to assess hypotheses about the processes that give rise to data. Kendall and Gould (2002) published an opinion paper focused on the curriculum of wildlife students and highlighted difficulties that are still true: 'Relating statistics to scientific methodology is a good idea in any case... However, the more this is necessary, the fewer statistical topics can be covered. In addition, by teaching scientific methods in a statistics course, we have found students can misinterpret the differences between scientific hypotheses and statistical hypotheses.' The constant innovation in CMR modeling has widened the gap between modern concepts and techniques and the basic training of students. Teaching CMR modeling is a fantastic means of opening the students' minds to complex ideas: 'what is seen matters, what is unseen matters, and sometimes you estimate quantities that remain unobservable even if you use the most efficient tools of investigation of micro- and macroscopic processes governing the state of Nature.' The integration of occupancy and CMR models within the common framework of hidden Markov models, combined with flexible programming languages has created an imposing background that leads to numerous publications that even the most 'statophobic' student can't ignore today. Long-term monitoring programs of individually marked animals have tremendously benefited from innovation in CMR modeling: ecological or evolutionary hypotheses that were impossible to address can now be evaluated. New results have raised new questions and highlighted new obstacles. From the biologist's viewpoint, some innovations in CMR modeling such as the estimation of model parameters that are impossible to measure even with perfect detectability can be difficult to advocate in the ecology or evolution literature due to a lack of familiarity of many biologists with the way we draw inferences about ecological or evolutionary hypotheses using data and CMR models, and because there is ongoing debate in biology concerning the interpretation of some models. This sheds light on the twofold challenge that biologists must overcome and that teachers must help students overcome: the more powerful the technology becomes (fast computers, flexible programming languages, efficient algorithms to estimate the parameters of complex models), the deeper our understanding of the conceptual foundations of both ecology or evolution and statistics must be.

Tuesday 18th April

09:00-09:30 **Matthieu Paquet** **Plenary:** Estimating immigration and density dependence using Integrated Population Models

Estimating immigration and density dependence using Integrated Population Models

Matthieu Paquet

Dr. Matthieu Paquet is interested in behavioral ecology and population dynamics and aims to better understand and predict population fluctuations by integrating information on interactions within (e.g. parental effects and social behaviour) as well as among species (e.g. competition and predation), notably using Integrated Population Models.

By combining several data sources that contain information on demographic parameters and population size, Integrated Population Models (IPMs) have allowed us to i) jointly estimate population size and demographic parameters, and therefore density dependent effects on the demographic parameters, ii) estimate parameters for which explicit data is hard to collect (e.g. immigration), and iii) estimate the contribution of demographic parameters (and to some extent population size and other covariates) to variation in population growth, in a unified statistical framework. I will briefly review recent developments, and pinpoint some challenges, in the use of IPMs for estimating immigration and (intra and interspecies) density dependence, and their potential importance as drivers of population dynamics.

Movement and habitat selection
09:48 - 10:48

Amphithéâtre Délégation CNRS

09:48 Clara **Panchaud** Accounting for animal movement in spatial capture-recapture

Accounting for animal movement in spatial capture-recapture

Panchaud, C. University of Edinburgh
King, R. University of Edinburgh
Borchers, D. University of St Andrews
Worthington, H. University of St Andrews
Durbach, I. University of St Andrews

Estimating wildlife populations abundance is essential for conservation and management. Capture-recapture surveys using camera traps are often used to obtain data sets which are then analyzed by methods such as spatially explicit capture-recapture (SECR) models. Traditional SECR introduces spatial correlation by assuming that animals are more likely to be seen near their latent activity center, providing more robust population estimates. However, SECR assumes that the probability of being observed at a trap depends solely on the (unobserved) activity center location and not on any previously observed trap locations. We argue that this assumption does not always hold, as it assumes that individuals may essentially teleport between consecutive sightings. We propose a new model that removes the teleportation by incorporating memory within a continuous time form of SECR model. This new model defines the density of the location of an individual via an OU process that depends both on the observed locations and the unknown activity center. We consider a simulation study in order to demonstrate the performance of the memory model before considering applications to real data, comparing the results with the standard SECR model.

10:00	Janelle **Badger**	Integrating movement data into mark recapture analysis: Case study of false killer whale (*Pseudorca crassidens*) abundance estimation around the main Hawaiian Islands

Integrating movement data into mark recapture analysis: case study of false killer whale (*Pseudorca crassidens*) abundance estimation around the main hawaiian islands

Janelle Badger, Devin Johnson, Robin Baird, Amanda Bradford, Michaela Kratofil, Erin Oleson

Monitoring natural populations requires data that can be extremely difficult to collect when the animals are rare, cryptic, or inaccessible. Surveys often only encompass a small portion of a population's range due to difficult terrain or inclement weather. Thus, to maximize encounters, sampling efforts may be largely opportunistic. The resulting sparse and spatially-biased data may be difficult to model, standardize across years, and incorporate into a management framework. In many monitoring programs, however, there are usually multiple threads of data that, though each may have its own deficiencies, can be synthesized to reveal important ecological processes. Currently, surveys for the insular population of false killer whales (*Pseudorca crassidens*) around the main Hawaiian Islands are almost exclusively conducted on leeward sides of the islands due to sighting and safety concerns. This sampling bias limits the ability to fully assess population abundance and trends of this endangered population. Here, we used 16 years (2000–2015) of a longitudinal photo ID mark-recapture dataset containing 141 known false killer whale individuals along with telemetry data from 43 individuals to fit a quasi-spatial mark-recapture model that uses the information from telemetry data to address the sampling bias. Utilization distributions (UDs) were estimated from each GPS track and then combined into social cluster UDs. We then fit a dynamic factor analysis to the sighting data to mix cluster-level UDs according to individual observation trends. The interaction between these approximated individual UDs and kernel densities of yearly survey efforts was incorporated into a state-space Jolly-Seber population model to estimate abundance of false killer whales around the main Hawaiian Islands. Our method resulted in more robust and precise abundance estimates than previous mark-recapture analyses on these data. Future accommodation of additional data types, such as passive acoustics, into this framework can allow for integration of disparate data sets collected in monitoring programs to enhance our understanding of elusive populations.

10:12	Sara **Gomez**	Linking variation in juvenile meerkat foraging behaviour to growth rates and survival later in life: a biologging and state space modelling approach

Linking variation in juvenile meerkat foraging behaviour to growth rates and survival later in life: a biologging and state space modelling approach

Gomez, S. University of Montpellier, France.
Borger, L. Swansea University, Gales.
Rotics, S. Cambridge University, England.
Matthiopoulos, J. Glasgow University, Scotland.

In the wild, individuals often vary in their efficiency in acquiring food and energy, and in the patterns of growth and reproduction across their life history, with conditions at one life stage often carrying over and affecting the patterns and success later in life. For this reason, understanding how differences in early life stages can impact lifetime trajectories remains essential in population demography studies. However, reconstructing and linking fine-scale behavioural differences of wild animals to their energetic consequences and realized daily growth rates is mostly lacking for wild animals. Here, we tackle this using biologging data and weight data recovered on a free-living meerkat population from emergency to late life, coupled within an energy-based framework. By focusing on the transition of juveniles to independent foragers, we will highlight how this key life stage is impacting individual growth and survival.

Using 50 Hz accelerometer data on 46 pups we created classification rules allowing to accurately determine sub-second resolution individual behavioural time budgets during the transition period. We linked these individual time budgets to frequently measured weight data using a hierarchical Bayesian state-space model run in JAGS and R. This model allows us to (1) reconstruct the unobserved complete hourly weight curves during transition to independent foragers, (2) estimate individual foraging efficiency over this period (in grams of food acquired per hour spent foraging) and (3) estimate how individual characteristics are affecting foraging efficiency. In a second step, we linked these individual foraging efficiency estimates to growth and survival further in life in order to understand in which way transition to independence is a crucial stage in meerkat life.

Individuals markedly varied in their weight and weight trajectories, with the model closely matching empirical data, reconstructing over-night weight loss and daily weight gains (and losses), based on the observed individual foraging budgets. Individual foraging efficiency also strongly differed between juveniles. The later was closely correlated with juvenile weight at the start of the independence period (3 months old) and with weights later in life, i.e., 6 months old. This result suggests a strong impact and carry-over of early-life, when pups are fed by the adults and are taught how to find and process food. On the other hand, there is no relation between foraging efficiency and the 12 months old weights which means that, even if it has impact on growth until 6 months old, foraging efficiency during the transition to independence is not carrying over effect up to 12 months. Indeed, as foraging is a crucial behaviour in survival, it is expected that individuals will either catch up in terms of foraging or not survive. With this study, we can say that the state-space model implemented, coupled with the detailed life history meerkat data available, is a real opportunity to understand how changes in behaviour through different life-stages can be scaled up to survival and population demography.

10:24	Guillaume **Souchay**	Follow the yellow brick road: Using does to find the leverets

Follow the yellow brick road: Using does to find the leverets

Souchay, G. Office Français de la Biodiversité - Research Department, Wildlife Health and Agricultural ecosystem functioning, Nantes, France.
Hole, G. Office Français de la Biodiversité - Research Department, Wildlife Health and Agricultural ecosystem functioning, Nantes, France.
Mauvy, B. Office Français de la Biodiversité - Research Department, Wildlife Health and Agricultural ecosystem functioning, Clermont-Ferrand, France.
Marchandeau, S. Office Français de la Biodiversité - Research Department, Wildlife Health and Agricultural ecosystem functioning, Nantes, France.
Ruette, S. Office Français de la Biodiversité - Research Department, Wildlife Health and Agricultural ecosystem functioning, Nantes, France.

Farmlands have experienced a global loss of biodiversity, with a decrease for all taxa. The main reasons involve change in the habitat due to intensification of agriculture over several decades. These changes can impact differently the species, depending on their need and how they can adapt to these changes.

These changes at the species level should impact interspecific relationship, especially predation, and for the equilibrium at the ecosystem level. In temperate area, any change in small mammals can have detrimental effect for birds and mammals on the same trophic levels or above.

In France, evolution of the structure of habitat might have negative impact on rodents, and decrease in rabbits and partridges' species have been documented. During the same period, some indicators suggest that generalist predators have increased over time.

We thus propose to study trophic relationships, focusing on the European hares, perhaps the last alternative species still not decreasing in France. This species is very common in France and an alternative prey for lots of predators. Despite a relative stability of the population, we found a decrease in breeding success of the species over the last decade, probably resulting from a decreasing in leveret survival. The main hypothesis is a higher vulnerability to predation related to both landscape and agricultural practices changes in farmlands.

The first step of our programme is to identify litters' place and to evaluate potential sources of mortality, based on a GPS survey of does. We equipped 10 does with GPS collars in 2022, with fixes during suckling time. The survey occurred from February to late September.

Based on literature, we propose to study recursive moment in GPS tracking data to detect suckling area, to improve leveret survey and to identify mortality risk, associated to predation and/or agricultural practices.

10:36	Brett **McClintock**	A multistate Langevin diffusion for inferring behavior-specific habitat selection and utilization distributions

A multistate langevin diffusion for inferring behavior-specific habitat selection and utilization distributions

Mcclintock, B. T. Marine Mammal Laboratory, Alaska Fisheries Science Center, NOAA-NMFS, Seattle, WA USA
Lander, M. E. Marine Mammal Laboratory, Alaska Fisheries Science Center, NOAA-NMFS, Seattle, WA USA

The identification of important habitat and the behavior(s) associated with it is critical to conservation and place-based management decisions. Behavior also links life-history requirements and habitat use, which is key to understanding why animals use certain habitats. Wildlife population studies often use tracking data to quantify habitat selection and/or utilization distributions, but they typically do not account for behavior (e.g., foraging, migrating, reproduction). This can result in erroneous inferences and potentially ineffective management decisions. To address current deficiencies in approaches for inferring behavior-specific habitat selection and utilization distributions, we develop a habitat-driven Langevin diffusion for animals that exhibit distinct movement behavior states. Our multistate model combines many of the desirable properties of the Langevin movement model (e.g., continuous time, closedform stationary distribution) with the inferential machinery of hidden Markov models to simultaneously estimate behavioral states along with their corresponding habitat selection coefficients and utilization distributions. The model can be customized, fitted, assessed, and simulated using R package `momentuHMM`. Simulation experiments demonstrated that the model worked well under a range of sampling scenarios as long as observations were of sufficient temporal resolution. Our simulations also demonstrated the importance of accounting for different behaviors and the misleading inferences that can result when these are ignored. We highlight some of the potential advantages and challenges of the multistate Langevin diffusion using Steller sea lion (***Eumetopias jubatus***) satellite telemetry data that have served as an illustrative example for previous habitat selection analyses. Unlike previous singlestate analyses of this marine central-place forager, the multistate model was able to link foraging-type movements to steeper offshore slopes that are believed to enhance prey concentrations. To our knowledge, this is the first single-stage approach for estimating behavior-specific habitat selection and utilization distributions from tracking data that can be readily implemented with user-friendly software. As certain behaviors are often more relevant to specific conservation or management objectives, practitioners can use the multistate Langevin diffusion to help inform the identification and prioritization of important habitats.

Connectivity

11:15 – 12:03 *Amphithéâtre Délégation CNRS*

11:15 Matthew **Gonnerman** An individual based model trained on multiple data sources estimates population connectivity for harvested eastern wild turkeys

An individual based model trained on multiple data sources estimates population connectivity for harvested eastern wild turkeys

Matthew Gonnerman, Stephanie A. Shea, Kelsey Sullivan, Pauline Kamath, Erik Blomberg

The administrative boundaries used in wildlife management are often a product of political and social influence, with less direct reliance on biological criteria, such as individual dispersal. Individual based models (IBM) offer an approach for combining multiple data sources to build and calibrate models of animal movement, from which inferences on the likely degree of connectively among management units can be made. We built an IBM describing wild turkey spring seasonal movements, which simulated individual responses to landscape connectivity and identified connectivity dynamics between harvest management districts in Maine, USA. Our IBM was built initially from GPS tracking data from individuals (N=24) marked in a subset of focal study areas, and we calibrated it with coarser harvest reporting (N=74) and nesting (N=91) data which had broader scale availability. Finally, we used available abundance estimates to quantify district-specific immigration and emigration rates, and assessed connections among management districts following principles of migratory connectivity. We found that male turkeys were more likely to initiate seasonal movements than females but were also less selective in their settling decisions, resulting in similar rates of immigration between sexes. We calculated a low degree of migratory connectivity between management districts which, in combination with the substantial number of boundary crossings observed, indicated a more diffuse distribution of turkeys with limited correlation between winter and spring districts. While defining management regions for such a dispersed population may be difficult, information on the total number of turkeys moving between districts can delineate where immigration is strongest and therefore which management districts share the most animals and should therefore be considered as a singular unit. Transition probabilities between districts can identify uneven immigration patterns and therefore where source-sink populations likely exist, so that harvest regulations can be considered with both in mind.

11:27 Maëlis **Kervellec** Mapping connectivity from non-invasive surveys with spatial capture-recapture models: A focus on the Pyrenean brown bear population

Mapping connectivity from non-invasive surveys with spatial capture-recapture models: A focus on the Pyrenean brown bear population

Kervellec, M. CEFE, University of Montpellier, CNRS, EPHE, IRD, Montpellier, France
Milleret, C. Faculty of Environmental Sciences and Natural Resource Management, Norwegian University of Life Sciences, Ås, Norway
Vanpé, C. Équipe Ours, Office Français de la Biodiversité, Impasse de la Chapelle, 31800 Villeneuve-de Rivière, France
Quenette, P-Y. Équipe Ours, Office Français de la Biodiversité, Impasse de la Chapelle, 31800 Villeneuve-de Rivière, France
Sentilles, J. Équipe Ours, Office Français de la Biodiversité, Impasse de la Chapelle, 31800 Villeneuve-de Rivière, France
Palazón, S. Fauna and Flora Service, Department of Territory and Sustainability, Dr. Roux, 80. 08017 Barcelona, Spain
Jordana, I. A. Departament de territòri, paisatge e gestion ambientau, Conselh Generau d'Aran, Plaça d'Aran 1-2, 25530 Vielha, Spain
Jato, R. Departamento de Producción y Asistencias Técnicas, Sociedad Aragonesa de Getión Agroambiental, S. L. U., Ctra HUV-Fornillos, 22195 Fornillos de Apiés, Huesca, Spain
Elósegui irurtia, M. M. Servicio de Biodiversidad, Sección de Espacios Naturales y Especies Amenazadas, Gobierno de Navarra-Nafarroako Gobernua, Pamplona-Iruñea, Spain
Gimenez, O. CEFE, CNRS, University of Montpellier, EPHE, IRD, Montpellier, France

Management plans require to map connectivity to delineate the habitat accessible to small populations. However, connectivity is challenging to quantify, especially for elusive and wide-ranging species, because we lack the data to properly quantify it. When available, GPS data are used to follow the movements of some individuals. Otherwise based on encounter data, spatial capture-recapture models can simultaneously estimate density and connectivity in the sense of the space used by an individual throughout a monitoring session. In this case, the issue is often that structured monitoring prospects just areas of regular presence. We integrate structured monitoring from hair snag and opportunistic surveys from depredations on livestock to map the connectivity of the transboundary Pyrenean brown bear (Ursus arctos) population. Integrating opportunistic monitoring allowed us to extend the study area to the whole population, especially to part of the massif where the presence of bears is sparse. Based on detections and non-detections of individuals, we estimated a resistance parameter showing that roads impede their movements. Brown bear home range size is reduced up to two-fold in area with high road length. Spatial capture-recapture models offer a flexible framework to integrate data over multiple countries and type of surveys to inform the management of a reintroduced population.

11:39 Killian **Gregory** An integrated framework to combine migratory connectivity and demographic data

An integrated framework to combine migratory connectivity and demographic data

Gregory, K. A. CEFE, Univ. Montpellier, CNRS, EPHE, IRD, Montpellier, France.
Francesiaz, C. OFB, DRAS, Juvignac, France.
Jiguet, F. CESCO, MNHN-CNRS-Sorbonne Université, Paris, France.
Besnard, A. CEFE, Univ Montpellier, CNRS, EPHE-PSL University, IRD, Montpellier, France.

As they periodically move between breeding and non-breeding populations, migratory birds draw connexions between different parts of the world. These links, which are referred to as migratory connectivity, are key to understand how environmental changes and anthropogenic pressures in a localised region may affect the global population dynamics of a migratory species. Considering migratory connectivity in population dynamics models is therefore crucial to fully understand the declining trends of migratory species. Besides, a decrease or an increase in population numbers may lead to the loss or the establishement of migratory routes, changing how breeding and non-breeding populations are connected through time. The temporal dynamics of populations may thus in turn also affect migratory connectivity. While current population models are beginning to include static descriptions of migratory connectivity to account for seasonal interactions, a full understanding of this complex interplay between migratory connectivity and population dynamics calls for an integrated analysis of connectivity and demographic data. Here, we extended the reach of recent migratory connectivity models to develop a methodological framework allowing for a formal integration of connectivity and population models. The performance of the model was first assessed on simulated data. The model was then used to estimate both migratory connectivity and demographic parameters on a large scale from various types of data for two species of conservation concern in Europe, namely the Ortolan Bunting (*Emberiza hortulana*) and the Eurasian Curlew (*Numenius arquata*), known to differ in their migration patterns. Preliminary results suggest that our integrated framework did not improve connectivity and survival estimates when they were already supported by a large amount of connectivity data. However, it benefited from the properties of integrated population models to estimate demographic parameters that were not directly informed by the data, by taking advantage of the high precision and accuracy of the parameters obtained from the connectivity models. The connectivity and demographic parameters that could be estimated for the Ortolan Bunting and the Eurasian Curlew were consistent with previous descriptions. This work serves as a proof of concept for flexible analytical frameworks that integrate both migratory connectivity and population dynamics data, making the next step towards a comprehensive understanding of migration processes.

11:51 Lise **Viollat** Animal demography in motion: Integration of individual spatial component in demographic variability of Bonelli eagle

Animal demography in motion: integration of individual spatial component in demographic variability of Bonelli eagle

Lise Viollat1,2,3 Aurélien Besnard1, Alexandre Millon2, Cécile Ponchon3, Alain Ravayrol4
1. CEFE, Univ Montpellier, CNRS, EPHE-PSL University, IRD, Montpellier, France
2. Aix Marseille Université, Institut Méditerranéen Biodiversité et Ecologie marine et continentale, CNRS, IRD, Avignon Université, Technopôle Arbois-Méditerranée, Aix-en-Provence
3. CEN PACA, Maison de la Crau 2, Place Léon Michaud - 13310 Saint-Martin de Crau cecile.ponchon@cen-paca.org
4. La Salsepareille, 3 bis rue vieille commune 34800 Clermont l'Hérault lasalsepareille@orange.fr

Life histories of individuals involve movements at different temporal and spatial scales and it's one of the key behaviors to better understanding how animals use and response to their environments. Movement has direct consequence on the survival and fitness of individuals and may have major consequences on population dynamics. Only few studies have assessed the impact of individuals movement on the population dynamics. We examined the link between movement and demography of a territory and sedentary long-lived raptor, the Bonelli eagle (*Aquilla fasciata*). Between 2008 and 2019, 47 individuals (26 males and 21 females) have been equipped with GPS logger, supported by an intensive demographic monitoring program that allowed us to know the annual fecundity of each individual. We assess if the characteristic of individuals and territory, as well as local climatic conditions shape daily movement of Bonelli eagle inside their territory and if those daily movement of individuals at different period through the years affect their survival and breeding success. Daily movements, travelled distances and habitat use vary between days and period that shows different behavioral. Results shows individual heterogeneity of daily movement due to territorial and individual characteristic, as well as survival and breeding success.

Natal dispersal and migration

13:30 – 14:18 *Amphithéâtre Délégation CNRS*

13:30 Paul **Acker** Capture-recapture animal model for quantitative genetic decomposition of variance in seasonal migration versus residence

Capture-recapture animal model for quantitative genetic decomposition of variance in seasonal migration versus residence

Acker, P.[1], Daunt, F.[2], Burthe, S. J.[2], Wanless, S.[2], Harris, M. P.[2], Newell, M.[2], Swann, R.[3], Morley T.I.[4], and Reid, J. M.[1,4]

[1] Centre for Biodiversity Dynamics, NTNU, Trondheim, Norway.
[2] Centre for Ecology & Hydrology, Bush Estate, Midlothian, UK.
[3] Highland Ringing Group, Tain, UK.
[4] School of Biological Sciences, University of Aberdeen, Aberdeen, UK.

Global changes are rapidly altering patterns of spatio-seasonal environmental variability. Populations might respond to resulting perturbations through combinations of plasticity and micro-evolution. Predicting such responses requires quantifying environmental and genetic components of variance in key traits. Migration vs. residence is one such key trait that allows individual animals escape from temporarily deteriorating local conditions, and shapes spatio-seasonal population dynamics. However, decomposition of variance underlying this trait has not been fully achieved, preventing evaluation of potentials of wild populations to overcome environmental changes. More generally, major analytical advances are still required to dissect eco-evolutionary responses in traits expressed as alternative life-history states (also including e.g. dispersal vs. philopatry, breeding vs. non-breeding, etc.). These can be conceptualised as threshold traits, where a latent continuous liability yields one or the other phenotype when below or above some threshold. Non-linearity in threshold traits implies that strictly additive effects on liability interact to generate nonadditive effects on phenotypes. However, exact solutions for quantifying all resulting interaction variances on the phenotypic scale are not yet available. Moreover, while additive genetic and environmental variances in latent liability can be estimated using binomial 'animal' models, this task is complicated by observation failure in wild populations. Here, joint capture-recapture animal models (CRAMs) are required, but general CRAMs applicable to any dichotomous trait remain to be developed. Accordingly, we devised a novel multistate CRAM for decomposition of variance in liability for migration vs. residence. We fitted this model to 12 years of large-scale year-round ring-resighting and >30 years of pedigree data from a wild population of adult European shags (*Gulosus aristotelis*). Further, we derived and applied formulas enabling full decomposition of non-linear phenotypic variance. Our results reveal considerable additive genetic, permanent individual, and temporary environmental variance in liability for adult migration vs. residence. We further show that substantial gene-by-environment interactions emerge on the phenotypic scale, effectively causing among-individual variation in migratory plasticity. Finally, we illustrate how these effects shape phenotypic dynamics through multiscale dissection of temporal changes in response to known episodes of selection. We thereby highlight how the interplay of plasticity, selection, and micro-evolution generate complex eco-evolutionary dynamics of migration vs. residence.

13:42 Rita **Fortuna** Using a multistate capture-recapture animal model to estimate additive genetic variance in early-life seasonal movement

Using a multistate capture-recapture animal model to estimate additive genetic variance in early-life seasonal movement

Fortuna R., Centre for Biodiversity Dynamics, Institutt for Biologi, NTNU, Trondheim, 7034, Norway
Acker P. Centre for Biodiversity Dynamics, Institutt for Biologi, NTNU, Trondheim, 7034, Norway
Ugland C., Centre for Biodiversity Dynamics, Institutt for Biologi, NTNU, Trondheim, 7034, Norway
Burthe S.J., UK Centre for Ecology & Hydrology, Midlothian, UK
Newell M.A., UK Centre for Ecology & Hydrology, Midlothian, UK
Morley T.I., School of Biological Sciences, University of Aberdeen, Aberdeen, AB24 2TZ, United Kingdom
Wanless S., UK Centre for Ecology & Hydrology, Midlothian, UK
Harris M.P., UK Centre for Ecology & Hydrology, Midlothian, UK
Daunt F., UK Centre for Ecology & Hydrology, Midlothian, UK
Reid J.M., Centre for Biodiversity Dynamics, Institutt for Biologi, NTNU, Trondheim, 7034, Norway; School of Biological Sciences, University of Aberdeen, Aberdeen, AB24 2TZ, United Kingdom

One of the main current challenges in biological research is to predict populations' evolutionary potential to respond to rapid changes in the environment. For rapid evolutionary responses to occur, key phenotypic traits that could mediate an 'escape' from harsh conditions must be genetically variable and heritable. Moreover, potential for micro-evolution should be estimated at different stages of a species life cycle, since selection processes can be different for juveniles and adults. In partially migratory species, residents and migrants will be temporarily exposed to different environments and selective pressures, and migrants can spatially escape severe conditions. Even though seasonal movement can directly affect fitness and population dynamics, it has rarely been considered in eco-evolutionary studies, and has been primarily studied in adult individuals which typically show highly repeatable migratory strategies. Here, we estimated additive genetic variance in early-life seasonal movement in a partially migratory long-term monitored population of European shags (*Gulosus aristotelis*) in Scotland. To estimate genetic variation and heritability in migratory strategies, we had to simultaneously model 1) seasonal movements from multi-year individual-based data, while accounting for spatial and temporal variation in detection, 2) genetic relationships between phenotype-informative individuals, and 3) migration vs residence as a binary threshold trait on a continuous liability latent scale, on which additive genetic variance is estimated. We used 8 years of resighting data of individually marked individuals during their first year of life, and >35 years of pedigree data for this population, and developed a multistate capture-recapture animal model to estimate additive genetic effects on individuals' liability to stay resident or migrate, using the Bayesian software *Stan*. We found that migratory strategies vary substantially within and among juveniles during their first year of life, and that migratory decisions can happen soon after fledging. Our results also indicate considerable additive genetic variance in migratory strategies, and hence potential for rapid evolution of early-life movement. Altogether, these findings illustrate how early-life eco-evolutionary processes can shape spatio-seasonal population dynamics.

13:54 Charly **Souc** A multi-event CMR analysis applied to reveals the influence of the natal colony for age-specific movement patterns of the Yellow-legged gull (*Larus michahellis*)

A multi-event CMR analysis applied to reveals the influence of the natal colony for age-specific movement patterns of the Yellow-legged gull (*Larus Michahellis*).

Souc, C. MIVEGEC, CNRS, Montpellier, France.
Blanchon, T. Tour du Valat, Research Institute for the Conservation of Mediterranean Wetlands Arles, France.
Vittecoq, M. Tour du Valat, Research Institute for the Conservation of Mediterranean Wetlands, Arles, France.
Choquet, R. CEFE, CNRS, Montpellier, France.
McCoy, K. MIVEGEC, CNRS, Montpellier, France.

The yellow-legged gull (*Larus michahellis*) is a common seabird species around the Mediterranean coast, well adapted to exploit human-associated resources. As this species can carry a range of infectious agents, some of specific public health concern, understanding its movement ecology can provide essential information for predicting disease risk and pathogen emergence. This study aimed to characterize movement between three large areas in France based on opportunistic data from volunteer observers. It included the encounter histories of 5158 birds marked at fledging between 1999 and 2004 at 14 colonies in southern France and resighted for 10 years. Recapture heterogeneity was detected among individuals so we defined a model using two classes of individuals with different resighting probabilities. Using a multi-event model similar to the model of (Peron et al, 2010), we found that young individuals had greater mobility than older individuals. However, the spatial extent of juvenile movements depended on natal colony location, with a strong difference in the proportion of sedentary individuals between colonies less than 50 km apart. Colony quality or local population dynamics may explain these differences. Indeed, young birds from colonies with strong juvenile survival probabilities (~0.75) appear to be more sedentary than those from colonies with low survival probabilities (~0.36). These results indicate that young birds are likely to frequent areas where exposure to environmental stresses is different from that of adults. These young birds are also likely to be more important dispersers of avian disease than older birds, and this propensity may be conditioned by local reproductive success, which may itself depend on the presence of environmental stresses. The heterogeneity of capture also raises the question of the local source of this heterogeneity, which will imply the need to track these birds locally with GPS to understand the cause of it. The method used to correct for capture heterogeneity in this study is thus an example that can inspire other studies facing heterogeneity in their data.

Peron G, Crochet P-A, Choquet R, Pradel R, Lebreton J-D, Gimenez O. Capture-recapture models with heterogeneity to study survival senescence in the wild. Oikos. 2010;119:524–32.

14:06 Richard **Chandler** Directional natal dispersal in a trailing-edge population of black-throated blue warblers

Directional natal dispersal in a trailing-edge population of black-throated blue warblers

Heather Gaya[1], Robert Cooper[1], Clay Delancey[1], Jeff Hepinstall-Cymerman[1], Betsy Kurimo-Beechuk[2], Will Lewis[1], Sam Merker[3], and Richard Chandler[1]
1 Warnell School of Forestry and Natural Resources, University of Georgia, Athens GA, USA
2 College of Veterinary Medicine, University of Georgia, Athens GA, USA
3 Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA

Warming temperatures are predicted to shift trailing-edge breeding ranges to higher latitudes and elevations. Little information is available to determine if climate-induced range shifts are the result of reduced survival and reproductive rates or directional dispersal. We used mark-recapture data to model natal dispersal and adult dispersal of black-throated blue warblers (*Setophaga caerulescens*) in the Southern Appalachian Mountains in North Carolina, USA. Young black-throated blue warblers tended to move upslope towards cooler and wetter locations unless they were born at the highest elevation sites. In contrast, adult birds exhibited strong site fidelity and rarely dispersed between sites regardless of climate characteristics. Our findings suggest that this trailing-edge population of black-throated blue warblers is gradually shifting upslope, and the speed of these movements is likely moderated by natal dispersal.

Phenology

14:45 – 15:45 *Amphithéâtre Délégation CNRS*

14:45 James **Clarke** Accounting for phenology and varying spatial scales in the production of UK butterfly abundance estimates using citizen science data

Accounting for phenology and varying spatial scales in the production of UK butterfly abundance estimates using citizen science data

Clarke, J.A. Statistical Ecology at Kent, National Centre for Statistical Ecology, School of Mathematics Statistics and Actuarial Science, University of Kent, UK
McCrea, R.S. Department of Mathematics and Statistics, Lancaster University, UK
Dennis, E.B. Butterfly Conservation, Manor Yard, East Lulworth, Wareham, Dorset, UK
Morgan, B.J.T. Statistical Ecology at Kent, National Centre for Statistical Ecology, School of Mathematics Statistics and Actuarial Science, University of Kent, UK

Over the past four decades, three-quarters of UK butterfly species have declined in abundance, distribution or both. Butterflies respond quickly to habitat and climatic change, hence their population status is a valuable biodiversity indicator. Analysis of long-term butterfly monitoring datasets has provided some of the world's best evidence of the biological impacts of climate change, including major phenological and distribution shifts, evolutionary responses and the impacts of extreme events.

Long-term citizen-science count data allows for the estimation of abundance estimates in the UK. However, currently population trends are assessed only at the national scale, and it has been shown that there is spatial variation in flight periods within a species across the UK. Butterflies have also been shown to be emerging earlier with warmer spring temperatures. This, as well as the spatial differences in phenology, have yet to be modelled when producing abundance trends. We show how the current framework to produce abundance estimates, the generalised abundance index (GAI), developed by Dennis et al. 2016 (*Biometrics*), can be adapted to account for spatial and temporal variation in flight periods. We demonstrate the efficacy of varying spatial scales in producing robust estimates of abundance. The use of this model should allow for more strategic planning and land management across regions of the UK, and, at a smaller scale, for site managers at protected sites across the UK. We hope that this work will aid conservation of UK butterflies as well as be used in a wider context for similar citizen-science datasets across Europe to understand and mitigate declines in butterflies.

14:57 Simon **English** Quantifying phenology and migratory behaviours of hummingbirds using single-site dynamics and mark-detection analyses

Quantifying phenology and migratory behaviours of hummingbirds using single-site dynamics and mark-detection analyses

Simon English

Nuanced understanding of seasonal movements of partially migratory birds is paramount to species and habitat conservation. Using nascent statistical methods, we identified migratory strategies of birds outfitted with radio-frequency identification (RFID) tags detected at RFID feeders in two sites in California, USA. We quantified proportions of migrants and residents and the seasonal phenology for each movement strategy in Allen's and Anna's hummingbirds; we also validated our methodology by fitting our model to obligate migratory black-chinned hummingbirds. Allen's and Anna's hummingbirds exhibited characteristics of facultative migratory behaviour. We also quantified apparent annual survival for each migratory strategy and found that residents had significantly higher probabilities of apparent survival. Low survival estimates for migrants suggest that a high proportion of birds in the migrant group permanently emigrated from our study sites. Considered together, our analyses suggest that hummingbirds in both northern and southern California sites partake in diverse and highly plastic migratory behaviours. Our assessment elucidates the dynamics underlying idiosyncratic migratory behaviours of two species of hummingbirds, in addition to describing a framework for similar assessments of migratory behaviours using the multi-state open robust design with state uncertainty (MSORD-SU) model and single-site dynamics.

15:09 Fabian **Ketwaroo** How to walk the BeeWalk: Modelling Bumblebee citizen science data

How to walk the BeeWalk: Modelling Bumblebee Citizen Science Data

Fabian Ketwaroo, Eleni Matechou, Richard Comont
University of Kent

Bumblebees are extraordinarily important components of the ecosystem, providing pollination services of vast economic impact and functioning as indicator species for changes in climate or land use. Declines, either of distribution or abundance, are thus of serious concern from agricultural and economic viewpoints as well as from a conservation point of view. The Beewalk citizen science scheme was established by Bumblebee Conservation Trust to monitor the abundance of bumblebees in the UK. Volunteers walk along transects counting the number of bumblebees they detect and identifying their species and caste, where possible. However, the resulting data are incredibly sparse, introducing a computational challenge on a spatial scale. Consequently, we develop a novel Bayesian dynamic mixture model for Beewalk citizen science data that accounts for sparsity and enables spatio-temporal modelling. This framework produces invaluable information on caste-specific and area-specific demographic parameters such as phenology and relative abundance, amongst others. In addition, we implement an efficient Bayesian variable selection approach to identify important predictors on a subset of demographic parameters. We present the performance of this modelling framework via a simulation study and we also present the results obtained by analysing the latest Beewalk dataset.

15:21 Edel **Lheureux** Distinguish the biological process from the observation process in a tagging-recapture experiment to study the migration phenology of the Atlantic salmon (*Salmo salar*)

Distinguish the biological process from the observation process in a tagging-recapture experiment to study the migration phenology of the Atlantic salmon (*Salmo salar*)

Edel Lheureux 1, Buoro Mathieu1, Prévost Etienne1
1Université de Pau et des Pays de l'Adour, e2s UPPA, INRAE, ECOBIOP, 64310, St Pée-sur-Nivelle, France

The phenology of migration in Atlantic salmon (Salmo salar) is influenced by both abiotic and biotic factors allowing the species to respond to environmental changes. The phenology of seaward migration is especially important because a fish's body size and date of arrival at sea influence its subsequent survival and growth at sea. Changes in river growth conditions (affecting size at departure) or environmental determinants of migration can thus disrupt the synchronisation of the departure and the arrival conditions (mismatch/mistiming) with potential consequences on population dynamics. However, the processes underlying phenology migration remain poorly understood due to incomplete data and/or an inadequate statistical approach. Data collected in natural environments, for example, are subject to variations in the observation process which can mask or bias the results of underlying biological processes. This is especially important when a factor (such as discharge) influences both the observation (e.g. trap efficiency) and the biological process (triggering migration decision) potentially leading to misinterpretation. My ultimate goal is to assess how the environmental factors (temperature, discharge...) and the individual variations (size, growth...) influence the migration phenology of the Atlantic salmon using a long-term tagging/recapture experiment of Atlantic salmon juveniles in the Scorff river (Brittany, France). To that end, I propose a Bayesian model that explicitly separates the observational (capture at traps) and dynamic (migration) processes, as well as the different effects of the environmental factors.

15:33 Paul **Cuchot** Not all resident birds reproduce earlier in warmer springs : inferring habitat-dependency of phenological sensitivity to temperature using a bayesian sigmoid modelling approach applied to constant ringing effort sites

Not all resident birds reproduce earlier in warmer springs: inferring habitat-dependency of phenological sensitivity to temperature using a bayesian sigmoid modelling approach applied to constant ringing effort sites

Cuchot, P. Centre d'écologie fonctionnelle et évolutive, Montpellier, CNRS, France.
Henry, P-Y. Mécanismes adaptatifs et évolution, MNHN, Brunoy, France.
Teplitsky, C. Centre d'écologie fonctionnelle et évolutive, Montpellier, CNRS, France.

Phenological plasticity is a major mechanism of response to global change often characterised by an earlier reproduction in warmer years for bird species. Plasticity varies between populations and is affected by environmental features such as the forest type. We still know little about factors limiting or promoting the expression of phenological plasticity but large scale monitoring allows investigating the determinants of between-site differences in phenological plasticity to temperature. We developed a flexible method, based on the study of the change in the capture probability of young vs adult individuals throughout spring and early summer. We tested the effect of forest cover, which quantify the quality of the environment, on (1) the phenology and (2) its plasticity in response to local temperature of two well known species : the blue tit *Cyanistes caeruleus* and the great tit *Parus major,* relying on the French constant effort site monitoring and satellite images. We expected that populations located in their optimal environment (here forest) relying on less diverse, but more abundant resources, would be more able to adjust their breeding phenology according to environmental cues (here temperature). According to those predictions, tits populations are more sensitive to temperature in sites with a denser cover of forest. Phenology is also later in these populations, in line with previous results from fine scale laying date monitoring. The provided model allowed us to assess tit phenology but can also be useful for the study of other breeding parameters such as breeding success or breeding synchronicity.

Drivers of vital rate variation

15:57 – 17:09 *Amphithéâtre Délégation CNRS*

15:57 Sarah **Cubaynes** Modeling the impacts of canine distemper virus on the Yellowstone wolf population

Modeling the impacts of canine distemper virus on the Yellowstone wolf population

Sarah Cubaynes[1]*, Ellen E. Brandell[2], Daniel R. Stahler[3], Douglas W. Smith[3], Emily S. Almberg[4], Susanne Schindler[5], Robert K. Wayne[6], Andrew P. Dobson[7], Bridgett M. vonHoldt[7], Daniel R. MacNulty[8], Paul C. Cross[9], Peter J. Hudson[2], Tim Coulson[10]

[1] CEFE, Univ Montpellier, CNRS, EPHE-PSL University, IRD, Montpellier, France
**Corresponding author. Email: sarah.cubaynes@cefe.cnrs.fr*
[2] Center for Infectious Disease Dynamics, Department of Biology, Pennsylvania State University; State College, Pennsylvania, USA. 16802.
[3] Yellowstone Center for Resources; Yellowstone National Park, WY 82190, USA.
[4] Wildlife Division, Montana Fish Wildlife & Parks; 1400 S 19th Avenue, Bozeman, Montana, USA.
[5] School of Biological Sciences, University of Bristol; Bristol, U.K.
[6] Department of Ecology and Evolutionary Biology, UCLA Ecology & Evolutionary Biology; 2312 Life Sciences Building, BOX 951606, Los Angeles, CA, USA.
[7] Department of Ecology and Evolutionary Biology; 106A Guyot Hill, Princeton, New Jersey, USA.
[8] Department of Wildland Resources and Ecology Center, Utah State University; Logan, Utah, USA.
[9] U.S. Geological Survey, Northern Rocky Mountain Science Center, 2327 University way; Suite 2, Bozeman, Montana, USA.
[10] Department of Biology, University of Oxford; Mansfield Road, Oxford, OX1 3SZ, UK.

We analyzed longitudinal data collected on wolves' survival, reproduction, morphology, genetics and epidemiological status in Yellowstone National Park from 1998 to 2020. Our aim was to estimate vital rates and assess the impact of canine distemper virus (CDV) outbreaks on the population. We used estimated survival rate and reproductive success to parametrize a two-sex population projection model structured by genotype. Our results showed that exposure to CDV alters survival rate, reproductive success, and the relative fitness of wolves with different genotypes. We found that an increased survival advantage of heterozygote black wolves exposed to the virus compensates for the reduced fertility of black females when disease outbreaks are frequent. Simulations using the population projection model predicted that varying frequency of CDV outbreaks can generate fluctuating selection that alter population growth as well as the optimal mating behavior. These results were supported by field observations from Yellowstone and cross-sectional data that we collected from 12 populations across the North American. In addition to demographic impacts of the virus on the population, the frequency of disease outbreaks could be responsible for the observed cline in coat color seen across North America, and explain why Yellowstone wolves mate disassortatively.

16:09 Ana **Payo-Payo** Long-lasting effects of harsh early-life conditions on adult survival of a long-lived vertebrate

Long-lasting effects of harsh early-life conditions on adult survival of a long-lived vertebrate

Payo-Payo, A. School of Biological Sciences, Aberdeen, UK.
Sanz-Aguilar, A. Universitat de les Illes Balears, Palma, Spain.
Oro, D. CEAB, Blanes, UK.

Early life conditions, especially in long-lived organisms, can have both immediate and long-lasting effects in vital traits generating demographic structure across cohorts. Multiple non-exclusive hypotheses have been proposed to explore this question. For instance, the silver spoon, the viability selection or the predictive adaptive response hypothesis, predict that long lasting effects resulting from harsh early conditions could be negative, positive or vary with current environmental conditions, respectively. We use an 18-year capture–mark–recapture dataset on adult Audouin's gulls *Ichthyaetus audouinii* to test for these different hypotheses while accounting for age, breeding experience and large-scale dispersal. Audouin's gull cohorts experiencing harsh conditions during early life (i.e. nestling period and first winter) are known to experience lower first year survival. Here, we show that early life conditions also explained a large proportion (54%) of adult survival variation among cohorts. However, adulthood cohorts experiencing poor early life conditions had higher adult survival, in accordance with the viability selection hypothesis. Our results also show that apparent inexperienced breeders showed lower survival than experienced ones. Moreover, adult survival decreased with age. These results could suggest an increased cost of reproduction for deferred breeders, individual quality differences or survival senescence in this population. Overall, our study highlights the importance of early development, age and breeding experience as potential factors generating heterogeneity of survival between cohorts. Understanding the mechanisms driving responses to early life conditions at different life stages is fundamental to understanding the long-term dynamics of wild populations.

16:21 Camille **Schatz** Intra- and interspecific demographic variation in two phylogenetically related seabirds

Intra- and interspecific demographic variation in two phylogenetically related seabirds

Schatz Camille, Centre d'Etudes Biologiques de Chizé UMR 7372, CNRS, Villiers en Bois, France.
Delord Karine, Centre d'Etudes Biologiques de Chizé UMR 7372, CNRS, Villiers en Bois, France.
Barbraud Christophe, Centre d'Etudes Biologiques de Chizé UMR 7372, CNRS, Villiers en Bois, France.

Today seabirds are one of the most threatened groups of birds, especially albatrosses which suffer additional mortality due to bycatch in fisheries, disease and impact of introduced predators, resulting in population declines. Successful conservation programs require estimations of demographic parameters, which are possible through the study of long-time series of capture–recapture data. However, the demography of several albatross species and populations remain poorly known. Here, we estimated multiple demographic s parameters (survival probability, return probability, breeding probability, breeding success probability and population growth rate) for four populations of two closely related species of albatrosses: Sooty Albatrosses (*Phoebetria fusca*) and Light-Mantled Sooty Albatrosses (*Phoebetria palpebrata*) from two different biomes (subtropical and subantarctic). Data were collected from 1966 to 2021 during several decades for each population on Amsterdam Island for Sooty Albatrosses, Kerguelen Island for Light-Mantled Sooty Albatrosses and Crozet Island for both species. Both species are quasi-biennial breeders. We thus used multievent mark–recapture models to account for quasi-biennial breeding and for dealing with non-breeding individuals and state uncertainty.

16:33 Rachel **Bergeron** Post-weaning survival in kangaroos is high and constant until senescence: Implications for population dynamics

Post-weaning survival in kangaroos is high and constant until senescence: implications for population dynamics

Rachel Bergeron[1], Gabriel Pigeon[1,2], David M. Forsyth[3], Wendy J. King[1,4] and Marco Festa-Bianchet[1,4]
[1]Département de biologie, Université de Sherbrooke, Sherbrooke, QC, Canada
[2]Institut de recherche sur les forêts, Université du Québec en Abitibi-Témiscamingue, Rouyn-Noranda, QC, Canada
[3]New South Wales Department of Primary Industries, Orange, NSW, Australia
[4]Research School of Biology, The Australian National University, Acton, ACT, Australia
Email: rachel.bergeron@usherbrooke.ca
Twitter: @rachelbergeron_ @festa_bianchet

Large herbivores typically have consistently high prime-aged adult survival and lower, more variable, juvenile and senescent survival. Many kangaroo populations undergo greater fluctuations in density than other large herbivores, but age- and sex-specific survival of kangaroos and its response to environmental variation remain poorly estimated. We used long-term capture-mark-recapture data on 920 individuals to investigate the survival component of eastern grey kangaroo (*Macropus giganteus*) population dynamics. Forage availability and population density were monitored quarterly and included as predictors of survival in Bayesian Cormack-Jolly-Seber models. Annual survival probabilities were estimated for 5 age classes: 0 years (juveniles), 1–2 years (sub-adults), 3–6 years (prime-aged adults), 7–9 years (pre-senescent adults), and ≥ 10 years (senescent adults). Survival of juveniles varied widely during our 12-year study, ranging from 0.07–0.90 for females and 0.05–0.92 for males. Sub-adult survival was 0.80–0.93 for females and 0.75–0.85 for males, while that of prime-aged adults was ≥ 0.94 for females and ≥ 0.83 for males, despite large fluctuations in forage and density. The survival of pre-senescent adults spanned 0.86–0.93 for females and 0.60–0.86 for males. Senescent survival was variable, at 0.49–0.90 for females and 0.49–0.80 for males. Male survival was significantly 40 lower than female survival in prime-aged and pre-senescent adults, but not in other age classes. Although most models supported by WAIC selection included one or a combination of environmental covariates, none of these covariates individually had a discernable effect on survival. Temporal variability in overall survival appeared mostly due to changes in survival of juvenile and senescent kangaroos. Kangaroo survival patterns are similar to those of ungulates, suggesting a strong role of sex-age structure on population dynamics.

16:45 Morgane **Gicquel** Age-related survival in the European cranes population

Age-related survival in the European cranes population

Gicquel, M. Grimsö Wildlife Research Station, Department of Ecology, Swedish University of Agricultural Sciences, SE-73091 Riddarhyttan, Sweden.
Nilsson, L. Grimsö Wildlife Research Station, Wildlife Damage Center, Department of Ecology, Swedish University of Agricultural Sciences, SE-73091 Riddarhyttan, Sweden.
Low, M. Department of Ecology, Swedish University of Agricultural Sciences, SE-75007 Uppsala, Sweden.
Nowald, G. Kranichschutz Deutschland, NABU-Kranichzentrum, Lindenstraße 27, D-18445 Groß Mohrdorf, Germany.
Alonso, J.C. Department of Evolutionary Ecology, Museo Nacional de Ciencias Naturales, Consejo Superior de Investigaciones Científicas (CSIC), José Gutiérrez Abascal 2, E-28006 Madrid, Spain.
Månsson, J. Grimsö Wildlife Research Station, Wildlife Damage Center, Department of Ecology, Swedish University of Agricultural Sciences, SE-73091 Riddarhyttan, Sweden.

The common crane (*Grus grus*) is an iconic flagship species. Since its inclusion in the highest protection category in the Birds Directive in 1979, the European population has known a rapid recovery, resulting in recent population estimates along the Western European flyway of around 500 000 individuals. The transition from threatened to abundant can be viewed as a conservation success, however, the success also comes with a cost. In some regions, cranes cause damage to agricultural crops and there are also increased observations of cranes preying on eggs and chicks of other vulnerable wetland bird species. These conservation conflicts have raised the question of what can be expected in the future regarding the population numbers of common cranes. Knowing demographic parameters, such as survival and recruitment is very important to be able to understand and predict population dynamics. For instance, variation in survival probability across age classes can give information on population dynamics such as the number of new recruits that will survive to maturity, or the impact of management measures. However, for cranes, basic relevant ecological knowledge is still largely lacking.

Thanks to the collaboration of 15 countries and extensive ringers' team effort in Europe, thousands of cranes have been banded with colour rings and hundreds of thousands of resighting have been registered. The collected data on European banded cranes includes about 5 000 individuals ringed since 1979, and more than 190 000 resightings registered in 30 countries (most of the data were obtained by iCORA; internet-based Crane Observation Ring Archive). The European cranes demographic project aims to conduct a first thorough, scientifically rigorous analysis of individual survival by using the colour banding and re-sighting data of European cranes. The first goal is to determine the variation in survival among different age classes, the annual survival probabilities and the longevity of individual cranes, but also the probability of survival to first migration, using CMR (Capture-Mark-Recapture) methods in a Bayesian framework. Here, we will present a summary of the data collected, the methods used, as well as some preliminary results of the study. In conclusion, knowledge about survival will not only lead to an increased understanding of the general ecology and demography of this species but will also be important from a conservation and management perspective and help develop more accurate predictive population models in the future.

16:57 Emilienne **Grzegorczyk** Is hidden demographic heterogeneity a common phenomenon?

Is hidden demographic heterogeneity a common phenomenon?

Grzegorczyk Emilienne, Office Français de la Biodiversité, Service Conservation et Gestion Durable des Espèces Exploitées, Villiers-en-Bois, France*
Schatz Camille, Centre d'Etudes Biologiques de Chizé, UMR 7372, CNRS, Villiers-en-bois, France
Francesiaz Charlotte, Office Français de la Biodiversité, Service Conservation et Gestion Durable des Espèces Exploitées, Juvignac, France
Pradel Roger, Centre d'Ecologie Fonctionnelle et Evolutive, UMR 5175, CNRS, Montpellier, France
Barbraud Christophe, Centre d'Etudes Biologiques de Chizé, UMR 7372, CNRS, Villiers en Bois, France
Souchay Guillaume, Office Français de la Biodiversité, Service Santé de la Faune et Fonctionnement des Ecosystèmes Agricoles, Nantes, France
Caizergues Alain and Le Rest Kévin, Office Français de la Biodiversité, Service Conservation et Gestion Durable des Espèces Exploitées, Nantes, France
Guillemain Matthieu, Office Français de la Biodiversité, Service Conservation et Gestion Durable des Espèces Exploitées, Arles, France
Champagnon Jocelyn, Tour du Valat, Research institute for conservation of Mediterranean wetlands, 13200 Arles, France
Eraud Cyril, Office Français de la Biodiversité, Service Conservation et Gestion des Espèces à enjeux, Villiers-en-Bois, France
**** Presenting author***

Individual heterogeneity is the breeding ground for selection and thus evolution. But it also has its importance in population dynamics, where heterogeneity is often translated as simple categories as age class or sex. Few studies have considered hidden heterogeneity, defined as persistent individual variation beyond obvious groups.

In our study we looked for hidden individual heterogeneity in survival rates of seven harvested bird species: Common Teal (Anas crecca), Mallard (Anas platyrhynchos), Common Pochard (Aythya ferina), Common Snipe (Gallinago gallinago), Common quail (Coturnix coturnix) and Blackbird (Turdus merula). We used Capture-Mark-Recapture data spanning from 1953 to 2020 with datasets ranging from 10 to 65 seasons and 61 432 individuals ringed.

Our multievent models showed hidden heterogeneity for survival in most species even though the inter-individual variance for survival rate was quite small in some species. We also looked for variables that could explain the observed individual heterogeneity, such as morphological traits or migration phenology.

The evaluation of the degree of hidden heterogeneity is essential in population management, particularly for game species. Indeed, heterogeneity can directly affect the capacity of a population to compensate for all or part of the harvest. Moreover, evaluating hidden heterogeneity in all birds' species is more globally important for their long-term conservation. Indeed, this diversity is crucial for population to adapt to the multiple environmental challenges they are currently facing.

Poster session

17:30-20:00 *Hall Délégation CNRS*

Jaume-A. **Badia-Boher** 17:30-20:00

Evaluating the effectiveness of raptor reintroduction strategies using individual-based population viability analyses

Jaume-Adria Badia-Boher*1, Antonio Hernández-Matías1, & Joan Real1
1Grup de Biologia de la Conservació, Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Universitat de Barcelona (UB), Barcelona, Catalonia, Spain.
**jabadia@ub.edu*

Reintroductions are an extended tool to prevent extinctions, although their overall success rate is low. Assessing the efficiency and cost-effectiveness of different reintroduction strategies may help identify and promote efficient practices. Captive breeding is widely used in animal reintroductions, although concerns have been raised about relatively high failure rates and economic costs. Here, we compared the effectiveness of two strategies simultaneously used in the reintroduction of the Bonelli's eagle on the island of Mallorca: the release of 1) captive-bred chicks, and 2) wild-reared, translocated non-juveniles. To do so, we estimated the main vital rates for individuals released by both strategies and used them to perform population viability analyses to assess their overall performances. The use of wild-reared non-juveniles showed a trend with higher numbers of breeding pairs 10 years after the end of releases (14.75 pairs, 95% CI 4–25 vs. 11.21 pairs, 95% CI 2–24) and was the only strategy that prevented extinction in the long term. Following this, based on cost estimations of every strategy and different reintroduction budgets, we assessed the cost-effectiveness of releasing wild-reared non-juveniles compared with two captive-breeding alternatives: Releasing chicks either originally from breeding programmes or extracted from nests in natural populations. Again, releasing wild-reared non-juveniles was the only strategy that prevented long-term extinction in all economic scenarios (i.e., low-budget scenario 21.49 pairs, 95% CI 2–25). The use of chicks sourced from captive-breeding programmes did not guarantee long-term persistence even in high-budget scenarios (14.50 pairs, 95% CI 0–25). Releasing wild-reared non-juveniles boosts early recruitment to the breeding population and early reproduction, which can be key for reintroduction success. However, in some scenarios, post-release effects can be stronger in wild-reared individuals, especially because of high translocation stress and post-release dispersal. Hence, we recommend undertaking careful evaluation of the pros and cons of every strategy and embracing adaptive management to choose best strategies.

Jocelyn **Champagnon** 17:30-20:00

Survival of a long-distance migratory bird is affected by wintering climate in africa

J. Champagnon[1], S. Hodic, P. Marin Prado[2], P. Vera
[1]Tour du Valat, Research institute for the conservation of Mediterranean wetlands, France
[2] Grupo Ornitológico – Gotur, Spain
[3]Servicio de Conservación de Ambientes Acuáticos, València, Spain

Afro-Palearctic migrants are in decline across Europe and these declines are of high conservation concern. Wintering conditions in Africa are found to be of great significance for population limitation of long-distance migrants. Wintering conditions may affect population growth through direct effect on survival in wintering grounds but limited studies tested the impact of climatic factors on the survival rate of species because it requires long-term dataset using capture-recapture methods. The collared pratincole is an insectivorous and strictly migratory bird that nests in Europe in grasslands and steppes. It remains very dependent on wetlands for insect feeding. It is found in the savannahs where it occurs in West Africa, mainly in the Sahel. In this study, we used a mark-recapture dataset of 13 years collected on breeding ground in L'Albufera Spain to confirm that survival of collared pratincole varied over years. Then we found that NDVI index (a remotely sensed measures of vegetation based on primary production) in December in West Africa explained 62% of the residual variation in survival with a positive effect of density of vegetation on annual survival probability. Our study suggests that decline of western European population of collared pratincoles is driven by dryer winters in Sahel over the last decades, explaining temporal trend of annual survival probability and consequently, the decline of this western European population. The pratincole is a good candidate as a sentinel of declining Afro-Palearctic migrants.

Remi **Choquet** 17:30-20 :00

Implementation of new tests for classes heterogeneity in program U-CARE

Rémi Choquet
Center of Functional ecology and evolution, CNRS, 1919 route de Mende, Montpellier, France

The program U-CARE (Choquet et al., 2009) computes the goodness of fit of the multistate Arnason-Schwarz(A-S) model. This program tests for some violations of the assumption that individuals have the same rates for survival, transition and capture. In particular, U-CARE have some particular and well-known tests for detecting transient individuals and trap effect on individuals. However although these effects are used routinely in population dynamic analysis, heterogeneity could have a more wider form making the choice of the model difficult when overdispersion is detected. This situation may occurs when two groups of individual have different vital rates or behaviour. Thus the authors of Jeyam et al., 2018, 2020) have recently proposed two new tests for detecting heterogeneity of classes in both transition and capture. These new tests have been implemented in program U-CARE as additional tools to help the biologist to make the choice between severals candidate models with heterogeneity.

Choquet, R., Lebreton, J.-D., Gimenez, O., Reboulet, A.-M., & Pradel, R. (2009). U-CARE: Utilities for performing goodness of fit tests and manipulating CApture-REcapture data. Ecography, 32(6). https://doi.org/10.1111/j.1600-0587.2009.05968.x
Jeyam, A., McCrea, R., & Pradel, R. (2020). Assessing heterogeneity in transition propensity in multistate capture–recapture data. Journal of the Royal Statistical Society: Series C (Applied Statistics), 69(2), 413–427. https://doi.org/10.1111/rssc.12392
Jeyam, A., McCrea, R. S., Bregnballe, T., Frederiksen, M., & Pradel, R. (2018). A Test of Positive Association for Detecting Heterogeneity in Capture for Capture-Recapture Data. Journal of Agricultural, Biological, and Environmental Statistics, 23(1), 1–19. https://doi.org/10.1007/s13253-017-0315-4

Ana **Couto** 17:30-20:00

Power analysis to assess the use of very high frequency (VHF) radio tags to address critical knowledge gaps in seabirds' movement, connectivity with offshore wind, and population consequences

A. Couto[1], A. Butler[1], K. Newman[1,2], E.L. Jones[1], L. Wright[2]
[1] Biomathematics and Statistics Scotland, Edinburgh, UK
[2] School of Mathematics, University of Edinburgh, Edinburgh, UK
[3] RSPB Centre for Conservation Science, Bedfordshire, UK

Many countries, including the UK, are increasing the pace of deployment of offshore wind installations to meet the requirements of ambitious renewables energy targets. The British Energy Security Strategy (April 2022) seeks to deliver 50GW from offshore wind by 2030, whilst maintaining high environmental standards. To help achieve this goal, the cumulative impacts of offshore wind turbines on protected seabirds such as Black-legged kittiwake (Rissa tridactyla), which are a prioritised consenting risk, must be characterised and understood. Three key knowledge gaps require investigation, which are (1) juvenile and immature survival rates, (2) movement of individuals between colonies and (3) year-round connectivity between seabird Special Protection Areas (SPAs) and offshore wind farms.

Whilst an increasing body of ongoing research aims to tackle these issues, some key knowledge gaps cannot be adequately addressed by current approaches. For example, while Geographical Positioning Systems (GPS) and satellite tracking devices provide detailed spatio-temporal data on animal movements, they cannot be deployed long-term on most seabirds due to animal welfare and licensing issues (e.g., breaching the recommended weight threshold for tags on birds), thus restricting data collection to adults during the breeding season.

A potential technical solution is the Motus automated radio telemetry network. Very high frequency (VHF) Motus radio tags are smaller and lighter than GPS devices, and could be deployed on leg-rings for multi-year periods, thereby generating intra- and inter-annual data on movement and survival. Moreover, networks of Motus receivers automatically detect the presence of tagged birds within range, allowing the collection of informative data on direction of movements, connectivity and survival at inaccessible colonies more readily than GPS methods.

This project aims to assess the use of the Motus system to address the three key knowledge gaps identified above. Initially, a power analysis will be developed to determine the number of tagged individuals and receiver configuration required to (a) estimate survival for different age-classes using capture-mark-recapture models, (b) estimate dispersal, and using this to investigate the characteristics of metapopulations, and (c) quantify connectivity through the use of network analysis.

Karine **Delord** 17:30-20:00

Long-term monitoring of seabird species in the French Southern Territories

Karine Delord, Dominique Joubert, Charles-Andre Bost, Yves Cherel,
Henri Weimerskirch[1], Christophe Barbraud
Centre d'Études Biologiques de Chizé, UMR 7372 du CNRS-La Rochelle Université, 79360 Villiers-en-Bois, France

Long-term ecological datasets are pivotal to evaluate changes that affect the structure and functioning of ecosystems due to environmental variations. It is now established that we are facing a period of rapid climate change due to human activities and that we shall face even more rapid changes during the 21st century. This change in climate is accompanied with increasing human activities such as fisheries or habitat variations that are already affecting marine ecosystems. Therefore, understanding processes through which these changes affect seabirds and marine ecosystems has become a major issue for ecologists. In addition it is the prerequisite to be able to make robust projections on future impacts. The research program of our team in the French Southern Territories uses seabirds as indicators of global changes in the marine ecosystems of the Southern Ocean. Through a network of four observatories from the Antarctic to sub-tropical biomes, started in the late 1950s, the populations of ~25 species of marine top predators and their distribution at sea are monitored. Individual based long-term information (capture-mark-recapture, tissue sampling, bio-logging, phenotypic sampling), combined with continuous records of population sizes, at-sea survey and with specific studies carried out on an annual base, are used to describe temporal trends and to understand the processes though which climate and human induced environmental stressors affect seabird populations and marine ecosystems. Then three main types of data have enriched the database: demographic, tracking and more recently stable isotopes. These processes are integrated in population models to make scenarii on the effects of future environmental changes on Southern Ocean seabirds, as well as to propose conservation measures to limit the impact of fisheries and introduced predators on populations. All these information are today centralized in a long-term database on the demography and spatial distribution of Southern Ocean top predators, making a unique information system.

E.H.J. **De Vries** 17:30-20:00

Multi-state survival modelling as part of an Adaptive Flyway Management Programme for the barnacle goose

De Vries, E.H.J. (Lisenka), Dutch Centre for Avian Migration and Demography, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands; Department of Animal Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands; Department of Theoretical and Computational Ecology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, The Netherlands.
Van der Jeugd, H.P., Dutch Centre for Avian Migration and Demography, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands; Department of Animal Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands.
Nolet, B.A., Department of Animal Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands; Department of Theoretical and Computational Ecology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, The Netherlands.
Jongejans, E., Department of Animal Ecology and Physiology, Radboud University, Nijmegen, The Netherlands; Department of Animal Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands.

Human impact on the environment has allowed several goose species in Europe to expand their breeding range and drastically increase their population numbers. Originally breeding in Arctic Russia, the Russia/Germany & Netherlands flyway population has expanded their breeding range to original stopover sites in the Baltic and wintering sites in the North Sea area since the 1970s. Along with the concurrent rapid population growth, this has led to increasing conflicts with humans because of agricultural damage and air safety risks. To facilitate agreement between range states on management and conservation of the population, an International Single Species Management Plan (ISSMP) and subsequent Adaptive Flyway Management Programme (AFMP) were developed under the Agreement on the Conservation of African-Eurasian Migratory Waterbirds (AWEA).

Although mark-recapture data of barnacle geese suggests a limited degree of dispersal, the sub-populations within the flyway are currently treated as separate in the AFMP. To gain insight into the degree of dispersal between subpopulations of this flyway, a multi-state model has been developed using the program E-SURGE. Input for these models are mark-recapture-resighting-recovery data of metal- and colour-ringed barnacle geese. The temporal and spatial difference in (re)capture and resighting probability between the three subpopulations as well as the high occurrence of recoveries due to derogation and hunting within parts of the flyway have led us to deviate from a "traditional" multi-state model. By including site-dependent dead recoveries, the survival probability in this model is depended on site of arrival, rather than the site of departure.

The resulting estimates on dispersal are then used as building blocks for subpopulation specific Integrated Population Models.

Oliver **Gimenez** 17:30-20:00

Trends in capture-recapture: Ecological questions and methods over the past decade

Olivier Gimenez, National Centre for Scientific Research, France
Rachel Mccrea, University of Kent, UK

Ruth King, University of Edinburgh, UK

Studying wildlife populations is challenging because not all individuals can be captured, identified and monitored exhaustively. Capture-recapture (CR) is a powerful framework to quantify demography and population dynamics of animal and plant populations, while explicitly accounting for the issue of imperfect detection.

The past decade has seen an explosion in the developments and applications of CR in statistics, conservation biology, ecology and evolution. We review the scientific CR literature over the 2009-2019 period and analyzed > 5000 papers using bibliometric and textual analyses. In particular, we used topic modelling to identify hot topics.

We discuss recent applications of CR, including the study of life-history trade-offs and senescence, threats to biodiversity like climate change and overexploitation, dominance and parental care, foraging and anti-predation vigilance, resistance and tolerance to pathogens, overall providing a better understanding of changes in population size and composition and useful insights for management and conservation.

We also review recent CR methods. The last decade has seen much progress in how to mark and recapture animals with non-invasive methods, in particular camera trapping and genetic tagging. We have seen an uptake of state-space and hidden Markov models to estimate i) transitions between states (survival, dispersal, breeding or infection) and ii) the hidden states (disease/hybrid prevalence, sex ratio, home ranges locations). Also, there has been a growing interest in combining CR data with other sources of information on demography using integrated models.

We suggest future research and model development. New technologies produce new and more data with, e.g., drones, e-DNA, PIT tags and bioacoustics. In this context, survey design will remain important to collect data in ways that can inform ecological questions. We anticipate a growing interest in studying species interactions with community ecology and the assimilation of data using continuous CR models. Other avenues of research will be spatial CR models and the combination of CR data with even more sources of information, including data on unmarked animals and telemetry data. We suspect hidden Markov models will become a unifying framework for data integration. Last, cross-fertilization between disciplines will continue, including between ecology and climate science, artificial intelligence with deep learning for signal processing and machine learning for inference, and statistics and computer science for data combination and the analysis of big data.

The data and code are available on GitHub for reproducibility,
https://github.com/oliviergimenez/appendix_capturerecapture_review

Amélie **Hoste** 17:30-20:00

Estimation of life-history traits of an European eel stock in a mediterranean drainage channel through long-term capture-mark-recapture monitoring

Hoste[1,2], A., Bouchard[3], C., Poggiale[2], J.-C., Nicolas[1], D.
[1] Tour du Valat, Arles, France
[2] UMR 7294 (MIO), Aix-Marseille Université, Marseille, France
[3] UMR Ecobiop, UPPA – INRAe, Saint Pée sur Nivelle, France

Since the 1980s, the European eel (*Anguilla anguilla*) has suffered a 95% decline in recruitment overall its European and north-African spatial distribution area. This diadromous migrative fish spawns at sea and come into continental waters, either marine, brackish or freshwater, to grow for two to more than 25 years depending on the habitat conditions and localisation. Indeed, the growth of European eels varies according to latitude with a faster growth in the southern part of their distribution than in the northern part. Numerous studies of Atlantic eel stocks have been carried out, while the Mediterranean ones remain less known despite their high settlement potential and shorter growth time. Yet, 48% of Mediterranean wetlands have disappeared during the last 50 years. It is therefore essential to understand whether the remaining Mediterranean environments are favourable for the production of future genitors, both in terms of quantity and quality. Especially that Mediterranean lagoons could represent half of the reproductive stock. In fact, they are dynamic environments that may consist of a mosaic of diverse habitats and whose physico-chemical and hydrological characteristics may change drastically over time. Based on a rare long-term survey of more than 20 years, we aim to understand the evolution of Mediterranean sub-population life-history traits. Since 2001, a capture-mark-recapture monitoring has been carried out inside the River Rhône Delta (France) within an artificial drainage channel that is connected to a vast brackish pond (the Vaccarès lagoon). Using Bayesian multi-state models of capture-mark-recapture, we aim to analyse the evolution of demographic parameters such as survival, mortality, and growth rate according to the eel stage over time and the potential influence of the environment on these parameters. A total of 5995 eels were tagged with a percentage of recapture up to 21%. The majority has been recaptured only once (74%) and four individuals were captured 10 to 15 times. Individuals are tracked for 1 year in average, with a maximum of 12 years. Preliminary results suggest a low mortality rate over the period studied. Moreover, the degree of territoriality of individuals is examined based on the amplitude of their spatial movements within our study area.

Norbert **Ngameni-Tchamadeu** 17:30-20:00

Benthic macroinvertebrates as bioindicators of water quality in view of the construction of a hydropower dam on the dibombe river in cameroon

Norbert Tchamadeu Ngameni[1]*, Daniel Brice Nkontcheu Kenko [1,2] and Louis Nforbelie Ngwa
[1]Department of Animal Biology, Faculty of Science, University of Dschang, Dschang, Cameroon.
[2]Department of Animal Biology and Conservation, Faculty of Science, University of Buea, Buea, Cameroon.
[3]Pinnacle Group Cameroon, Pinnacle Consulting Services, Yaoundé, Cameroon
**Corresponding author, E-mail: norbert.ngameni@univ-dschang.org Tel: +237 675 00 31 80*

Intensive and incessant disruptions in watercourses such as dams have become frequent in Cameroon due to the growing demand for hydroelectric power. This usually results in severe deterioration of ecosystem services on which local communities highly depend. The purpose of this study was to highlight the expected changes in macroinvertebrate community structures of the Dibombé river due to flow stressors induced by a Hydropower Plant (HPP) during its construction and operation phases. Sampling was carried out during the month of April 2021 in seven sampling stations along a five-kilometre stretch of the river. Data collected involved habitat characteristics, physicochemical properties of water, and macroinvertebrate diversity. In total, 346 individuals of macroinvertebrates belonging to 2 phyla, 3 classes, 8 orders, 18 families and 29 genera/species were collected. Insects were the most abundant taxon with many orders, while Crustaceans and Molluscs were less represented with only one order each. The presence of the pollutant-sensitive families was undoubtedly favoured by the absence of anthropogenic activities. The Dibombé river is of great importance for the conservation of many benthic taxa that are intolerant to anthropogenic stress. However, these organisms could disappear with the construction of HPP. Analysis of environmental variables show that Dibombé river has good ecological status, with important canopy coverage, well oxygenated and very low mineralized waters. However, the construction of HPP could affect macroinvertebrates through modification of natural flow regimes and changes in stream physicochemical characteristics.

Femke **Pflüger** 17:30-20:00

Assessing the effectiveness of EU Special Protection Areas in Germany using semi-structured citizen science data and occupancy models

***PFLÜGER[1,2], F., FRANK[1,2], C., BUSCH[2], M.,* WAHL[2], J., DRÖSCHMEISTER, R., SUDFELDT[2], C., KAMP[1,2], J.**
[1] Department of Conservation Biology, University of Göttingen, Göttingen, Germany
[2] Dachverband Deutscher Avifaunisten (DDA), Münster, Germany
[3] Federal Agency for Nature Conservation (BfN), Bonn, Germany

Special Protection Areas (SPA), as part of the European Union's Natura 2000 network, aim to conserve and restore target species and their habitats. While the general effectiveness of SPA in conserving biodiversity has been demonstrated, it is largely unknown how designation and site management affect the trends of bird populations and their conservation status on the national level, including Germany. This is partly due to a lack of structured long-term monitoring data for rather rare target species. Citizen science data, which are increasingly used in applied ecological research and conservation planning, may be a promising data source to fill this gap. However, the lack of a standardized monitoring protocol entails several challenges and can lead to biased inference. We used semi-structured checklist data of several target breeding bird species from the online database ornitho.de collected over an 11-year period across Germany. To account for variable survey effort and imperfect detection, we run occupancy models on refined datasets and incorporated habitat information to correct for potential confounding effects. We applied matching techniques to select control sites that had similar habitat composition and mean abundance at the time of SPA designation and derived trends in occupancy inside and outside SPA. Finally, we compared the resulting trends with those from structured monitoring programs to test the credibility of our approach. We will discuss the potential of checklists from citizen-science databases for estimating trends under a hierarchical modelling framework and to assess the effectiveness of SPA.

Tonio **Schaub** 17:30-20:00

High-resolution sampling and barometric altimetry substantially improve the accuracy of height data from bird-borne GPS tags

Tonio Schaub[1,2,3,4], Alexandre Millon[1], Caroline de Zutter[2], Ralph Buij[5], Joël Chadœuf[6], Simon Lee[7,8], Aymeric Mionnet[9], & Raymond Klaassen[3,4]
[1] Aix Marseille Univ, CNRS, IRD, Avignon Univ, Mediterranean Institute of Ecology and Biodiversity (IMBE), France
[2] Engie Lab CRIGEN, France
[3] University of Groningen, Netherlands
[4] Dutch Montagu's Harrier Foundation, Netherlands
[5] Wageningen Environmental Research, Netherlands
[6] French National Institute for Agriculture, Food, and Environment (INRAE), France
[7] Natural England, UK
[8] University of Exeter, UK
[9] LPO Champagne-Ardenne, France

In the context of rapidly increasing development of wind energy and power line infrastructure, collecting accurate data on flight height of birds is becoming particularly important to assess the collision risk with these vertical structures. GPS tags potentially represent a powerful tool to collect flight height data of individual birds, yet this is hindered by multiple sources of error in the GPS altitude data. While analytical procedures have been developed to account for this error, it remains crucial to increase the accuracy in raw altitude data from GPS tags.

Here, we study to what extent collecting GPS tracking data in high temporal resolution (GPS fix interval of 1-3 s) on the one hand, and calibrated barometric data from pressure loggers integrated in GPS tags on the other hand, improves the accuracy of the resulting height data compared to conventional "low-resolution" GPS tracking (fix intervals ≥ 5 min). Using data from GPS tags from three manufacturers deployed on four raptor species in France and the Netherlands, we estimate the vertical accuracy based on a) the height recorded during periods where the birds were stationary on the ground (true height above ground is zero), b) the proportion of negative height values and c) the deviation of GPS and barometric height. We also describe recurrent error patterns, propose methods to further increase accuracy and assess the effect of residual error for practical questions such as the time spent at rotor height of wind turbines. Last, we discuss the advantages and disadvantages of the two approaches regarding their suitability for different research questions and practical aspects of data collection.

Preliminary results indicate that high-resolution GPS data had a substantially higher vertical accuracy than low-resolution GPS data (mean absolute error for stationary periods: 3.8 m vs. 30.2 m). Accuracy of barometric data was intermediate, with no difference between high- and low-resolution sampling (mean absolute error: 8.1 vs. 7.2 m). Final results will be presented at the conference.

Mahdieh **Tourani** 17:30-20:00

Climate-dependent responses of mammalian community to land use across the United States

TOURANI, Mahdieh
Department of Wildlife, Fish, and Conservation Biology, University of California, Davis, USA – mahdieh.tourani@mso.umt.edu

Biologists generally categorize species into three groups based on how they respond to land use: species that have readily adapted and now specialize in anthropogenic habitats; those that are restricted to natural environments; and habitat generalists. However, recent studies suggest that different populations of the same species may respond differently to habitat conversion. That is, in some areas, species may readily occupy anthropogenic habitats whereas, in others they may not. Understanding the contexts in which species can be conserved alongside humans in working landscapes, and when protected areas are essential, is key to designing effective conservation plans for wildlife in the Anthropocene. Here, we apply community occupancy models to a large-scale, mammal camera trapping dataset, Snapshot USA, with over 2000 sites distributed across the United States, asking two key questions. First, are species' responses to the forest and anthropogenic habitats (i.e., agriculture and urban areas) consistent across their range or do they act as habitat specialists, or habitat generalists in some regions but not others? Second, can spatial variation in climatic conditions explain variation in species' responses to habitat conversion? We found that the average mammal community's response to natural and anthropogenic habitats is variable and that this variation is mediated by climate. Even though our approach looks at static distribution, land use and climate patterns, these findings suggest that climate change will interact with land use in its impact on biodiversity, and that vegetation cover may play an increasingly important role in protecting mammals from warming climates. These results could provide major insight into how mammals can be most effectively conserved under a changing climate.

David **Vallecillo** 17:30-20:00

Combining two independent counting programmes to improve abundance estimates

David Vallecillo, Matthieu Authier, Matthieu Guillemain, Colin Bouchard, Jocelyn Champagnon

In the context of wildlife population declines, increasing computer power and advances in statistics can help improve estimates of population sizes while considering imperfect detection of individuals. Model-based data integration are particularly relevant to take advantage of independent protocols in order to understand population dynamics more reliably. Here we present a state-space model with an error process modelled on the log scale to evaluate wintering waterfowl numbers in the Camargue, southern France, while taking a conditional probability of detection into consideration. Conditional probability of detection corresponds to estimation of detection probabilities index relative to the value set for one of the parameters. The overall high probability of detection of waterfowl (gregarious species), the large number of sites (wetlands within the Camargue delta) and years monitored (44) made it possible to combine both terrestrial and aerial surveys (which constituted spatially and temporally replicated counts) to estimate a conditional probability of detection, while accounting for false-positive counting errors and changes in observers over the study period. The model estimates abundance indices of wintering Common Teal, Mallard and Common Coot, all species abundant in the area. We found that raw counts were underestimated compared to the predicted population size. The model-based data integration approach as described here seems like a promising solution that takes advantage of as much as possible of the data collected from several methods.

Ghais **Zriki** 17:30-20:00

Efficient marking of *Drosophila suzukii*: an important tool for the development of Sterile Insect Technique

Léa Tregoat--Bertrant, Pierre-Yves Poupart, Rémy Blois, Ghais Zriki
Centre Technique Interprofessionnel des Fruits et Légumes (CTIFL), 751 Chemin de Balandran, 30127 Bellegarde, France

The Sterile Insect Technique (SIT) is a biocontrol method applied as a key element in Area-Wide insect pests management programs. SIT consist in sequential and regular massif releases of sterile males into a specific area where they mate with fertile females that lay inviable eggs. The wild population in the field incorporate progressively the sterility and then collapse. Mark-Release-Recapture is an important tool for the employment of SIT and assess its efficiency in the field. Markers should be inexpensive, easily applicable and detectable on millions of mass-reared insects. The Spotted-winged *Drosophila suzukii* (SWD) is a major pest of soft-skinned fruit world-wide. The development and the employment of SIT to control SWD have been investigated during the last five years. The suitability of many marking methods like using fluorescent dust and animal protein have been evaluated for SWD. The objective of the present study was to investigate -under lab conditions- the persistence of abdomen coloration after the ingestion of colored artificial diet. Three food dyes were tested among them the Indigotine (blue colorant) was the most effective dyes with over 90% of flies showing abdomen coloration after 24h feeding-period on the colored diet. The coloration mean persistence under lab condition was around four days. The diet coloration method is easy to apply, and coloration is easily detectable with naked eye, nevertheless, coloration persistence is relatively low. This marking method may be used for SIT application when colored flies are recaptured shortly after released.

Wednesday 19th April

09:00-09:30 Aline Magdalena **Lee** **Plenary:** The magic of mark-recapture

The magic of mark-recapture

Aline Magdalena Lee

Dr. Aline Magdalena Lee is an associate professor and researcher at the Center for Biodiversity Dynamics at the Norwegian University of Science and Technology. Previously, she has been based at the University of California, Berkeley, and the University of Aberdeen, Scotland. Her main research interest is understanding stochastic population and extinction dynamics within ecological communities. She has worked with a wide range of species and systems, ranging from marine fish and daphnia to birds and ungulates. Combining theoretical modeling with empirical data analysis is a central theme in her research. She has a particular fondness for *methods that can extract additional information from limited data, and for studies that attempt to uncover general ecological processes while also teaching us about specific systems and species. She regularly uses mark-recapture models and integrated population models in her work, alongside other methods.*

Methods for analyzing mark-recapture data have developed rapidly in recent decades and the amount and type of information that can be extracted from such data is constantly increasing. At times, it can seem almost like magic. How can users that don't necessarily understand all the details of the underlying math and coding be sure their analyses are in fact doing what they think they are? How do we know whether we can trust our results? In this presentation I will use examples from my work to discuss a few of the magical things that methods such as integrated population modeling and multievent modeling can achieve, while demonstrating some ways that we can test whether our results are in fact telling us what we think they are.

Vital rates across space and time

09:48 - 10:48 *Amphithéâtre Délégation CNRS*

09:48 Chloé Rebecca **Nater** An integrated distance sampling model to estimate variation in demographic rates across space and time

An integrated distance sampling model to estimate variation in demographic rates across space and time

Chloé R. Nater, James A. Martin, Erlend B. Nilsen

Demographic rates vary in space and time in response to environmental conditions. Determining the drivers of variation in demographic rates – including to what degree they operate across large spatial scales or are localized effects – is central to implementing effective conservation measures and sustainable harvest strategies. In Norway, recreational hunting of willow ptarmigan is a popular and culturally highly valued pastime. Hunters and other volunteers contribute to collating the knowledge necessary for sustainable harvest management by collecting data through a nation-wide line transect monitoring programme. New data is made openly accessible every year and constitutes the base for abundance estimation but methodology for quantifying variation in underlying vital rates has been lacking so far. We develop a spatially-explicit integrated distance sampling model that combines long-term nation-wide line transect data with a few small local telemetry and brood survey datasets. The model not only efficiently estimates population size across Norway, but provides unique insights into how survival and reproduction vary across space and time and the environmental drivers responsible for that variation.

10:00 Fränzi **Korner-Nievergelt** Demographic indices from constant ringing effort sites in Switzerland

Demographic indices from constant ringing effort sites in Switzerland

Fränzi Korner-Nievergelt, Saskia Schirmer, Jacques Laesser, Jan von Rönn
Swiss Ornithological Institute, Seerose 1, CH – 6204 Sempach, Switzerland

Constant ringing effort sites aim at informing monitoring programs on demographic parameters such as breeding success and survival for getting a better understanding of why populations may change. We use a multi-site mark-recapture model with a robust design on two different temporal scales, the capture session and the season. We estimate apparent survival, the probability to be a transient visitor at the site and the recapture-probability. From the model, we derive the size of first-year and adult population per species within the vicinity of the constant ringing effort sites to obtain an index for breeding success, i.e. the ratio of first-year and adult individuals.

10:12 Cyril **Milleret** Mapping population-level mortality risks of an emblematic and controversial large carnivore, the wolf

Mapping population-level mortality risks of an emblematic and controversial large carnivore, the wolf

Cyril Milleret, Pierre Dupont, Soumen Dey, Henrik Brøseth, Jonas Kindberg, Mikael Åkesson, Petter Wabakken, Barbara Zimmermann, Richard Bischof

The dynamics of wildlife populations arise from individual life histories, which in turn are influenced by the spatial and temporal dynamics of resources and pressures, often shaped by humans. Quantifying spatial variation in vital rates, particularly survival, is therefore a central topic in ecology and has direct relevance for wildlife management and conservation. Yet, population-level inferences about spatial variation in survival remain elusive. We applied an open-population spatial capture-recapture model (OPSCR) to an extensive dataset from a decade of range-wide non-invasive genetic sampling of wolves (*Canis lupus*) in Scandinavia. Using this approach, we were able to estimate and map spatial variation in multiple sources of mortality, while accounting for imperfect detection. Our results revealed substantial variation in wolf mortality across space and time. Because our OPSCR model was able to simultaneously estimate density and its effect of mortality, we were able to demonstrate the effect of spatial variation in wolf density on cause-specific mortality. Management and conservation - like wildlife population dynamics - are spatially explicit and require information at the scale at which interventions are typically implemented. Our study provides a way to do so, by mapping cause-specific mortality and offering a better understanding of the factors driving spatial variation in survival.

10:24 Brady **Mattsson** Importance of biases associated with ground counts of nestlings in an arboreal nester, the red kite (*Milvus milvus*)

Importance of biases associated with ground counts of nestlings in an arboreal nester, the red kite (*Milvus milvus*)

Mattsson, B.J. Institute of Wildlife Biology and Game Management, Department of Integrative Biology and Biodiversity Research, University of Natural Resources and Life Sciences, Vienna, Austria
Sollmann, R. Department of Ecological Dynamics, Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany

Counting nestlings of arboreal species from the ground is common practice, but these counts can be biased high or low, and can lead to biased estimates of reproductive output. In some studies, nestlings are counted during ringing, which offers the opportunity to compare ground-based to climb-based counts. We investigated bias in ground-based nestling counts, its causes, and its implication for population projections with data from 26 red kite nests visited with ground and nest-based counts during 2021 and 2022 in central Europe. Two ground-based counts resulted in undercounting, and five resulted in overcounting the number of nestlings. As the true number of nestlings increased, obtaining an accurate ground count became less likely; no other nest or observation attribute affected the probability of accuracy. Average number of nestlings was slightly lower for ground counts (2.04 vs. 2.16 in climb counts). We used both values along with published demographic parameters for *M. milvus* to project populations 50 years into the future using stochastic simulations over 1000 iterations, and we found that effects differed between growing and declining populations. In growing populations, projected abundance in year 50 averaged 305 (SD 279) more individuals when using average number of nestlings from true counts compared to that from ground counts (mean N_{50}=1045 vs 739). Examining this difference in declining populations, projected final abundance averaged 2.2 (SD 12) more individuals (mean N_{50}=13 vs 15). To address this bias, we use paired ground and nest counts to construct multinomial distributions that probabilistically link true (here, nest count) to observed (here, ground count) number of nestlings. Using this multinomial correction, the estimated average number of nestlings from ground counts and subsequent population projections were unbiased. Finally, we repeated the above simulations under 4 levels of uncertainty for average number of nestlings: (1) none, (2) standard error of the mean number of nestlings, (3) standard error from our multinomial estimation approach, and (4) same as (3) but also accounting for uncertainty in multinomial probabilities. As expected, the coefficient of variation (CV) of population size N (SD over 1000 iterations, divided by N) at year 50 was much higher for scenarios 2-4 (>165% and >95% in growing and declining populations, respectively) than for scenario 1 (≤25% and ≤70% in growing and declining populations, respectively). The CV was however similar across scenarios that incorporated uncertainty. Accounting for apparently minor biases associated with ground counts is important for ensuring accurate estimates of abundance and population dynamics especially for increasing populations. We show how collecting paired data on ground-based and climb-based counts enables accounting for ground-count bias. This could be particularly important for informing conservation decisions in projects aimed at recovering depleted populations.

10:36 Johanna **Faure** The post-release survival of a deep-sea skate caught as bycatch by demersal longline fishery in Crozet, Southern Ocean

The post-release survival of a deep-sea skate caught as bycatch by demersal longline fishery in Crozet, Southern Ocean

Faure, J. Laboratoire de Biologie des Organismes et Ecosystèmes Aquatiques (BOREA), UMR 8067 – MNHN, CNRS, IRD, SU, UCN, UA, 75005 Paris, France.
Massiot-granier, F. Laboratoire de Biologie des Organismes et Ecosystèmes Aquatiques (BOREA), UMR 8067 – MNHN, CNRS, IRD, SU, UCN, UA, 75005 Paris, France.
Peron, C. Laboratoire de Biologie des Organismes et Ecosystèmes Aquatiques (BOREA), UMR 8067 – MNHN, CNRS, IRD, SU, UCN, UA, 75005 Paris, France.
Authier, M. Observatoire Pelagis, UAR 3462 CNRS-LRUniv, 5 allée de l'Océan 17000 La Rochelle
Plard, F. Observatoire Pelagis, UAR 3462 CNRS-LRUniv, 5 allée de l'Océan 17000 La Rochelle

Bycatch, the non-intentional catch of non-commercial or protected species in commercial fisheries, is a major threat to many marine megafauna species. Skates, cartilaginous fish belonging to the order Rajiforms, are often bycaught in demersal longline fisheries. The post-release survival of skates discarded is largely unknown but is paramount to assess stock status and implement effective bycatch management. The aim of this study was to estimate the survival rate of the most abundant bycaught skate species, the whiteleg skate (*Amblyraja taaf*), in the Patagonian toothfish longline fishery in Crozet Archipelago, Southern Ocean. A tagging program was initiated in 2020 to assess post-release survival of this poorly-known skates whose IUCN conservation status is data-deficient. We used capture-mark-recapture models to estimate both survival and detection probabilities of tagged skates. These models are rarely used in fisheries research because of low recapture rates and single recapture opportunities. Based on 3000 individuals tagged with conventional tags, we investigated in a Bayesian framework the effects of the depth of capture (ranging from 500 to 2,000 meters deep), total length and presence of injury on post-release survival of tagged individuals. Our hypotheses are reduced survival rates for small individuals, individuals with injuries and those bycaught in deeper depths. We illustrate the challenges of addressing knowledge gaps in deep-sea skate species with low recapture rates, gaps which must be filled for enabling the effective conservation of data-poor species.

Survival and movement in context

11:15 – 12:03 *Amphithéâtre Délégation CNRS*

11:15 Maria **Dzul** Can "true" survival be without global resights: it depends on "true" movement

Can "true" survival be without global resights: it depends on "true" movement

Dzul, M. U.S. Geological Survey, Southwest Biological Science Center, Grand Canyon Monitoring and Research Center, Flagstaff, AZ, USA
Yackulic, C. U.S. Geological Survey, Southwest Biological Science Center, Grand Canyon Monitoring and Research Center, Flagstaff, AZ, USA

Survival is a key life history parameter that often informs management decisions. Estimating "true" survival in field settings is often difficult because survival estimates are confounded with permanent emigration from the study area. Models that combine intensive capture data from a study area (hereafter the 'capture site') with resighting data from a broader geographic area are designed to separate true survival from permanent emigration. Such models often assume that all individuals have equal resight probabilities, an assumption that may not be realistic for widely dispersing species or species that inhabit large geographic ranges. While these models are increasingly being applied, there has been limited assessment of how violation of assumptions affects inferences. Here we use simulation to evaluate survival bias from a Barker joint live-recapture/live-resight model under different movement and study design scenarios. We simulate three movement scenarios (home-ranging movements, cauchy dispersal and uniform dispersal) and six study design scenarios. The six resight scenarios differ in the site selection for resight sites: 1) global, 2) random, 3) fixed sites (including the capture site), 4) fixed sites (excluding the capture site), 5) random and fixed combinations (including the capture site as a fixed site), and 6) random and fixed combinations (excluding the capture site as a fixed site). Simulation results indicate that using fixed sites can lead to substantial bias in survival probabilities under cauchy movement and home-range movement, and that the direction of the bias will be based on whether or not the capture site is included during the resight interval. When the capture site is always visited during resight, resight probabilities are over-estimated and survival probabilities underestimated. When the capture site was never visited during resight, resight probabilities were under-estimated and survival overestimated. When movement was uniform, survival estimates were unbiased for all sampling designs. We conclude that while the Barker model is a good choice for estimating survival during long, continuous resight intervals, using the Barker model to group resights from a large geographic region with heterogeneous resight probabilities may be problematic for survival estimation under realistic sets of conditions.

11:27	Saskia **Schirmer**	Seasonal and spatial explicit survival estimates - Combining the multinomial reencounter model with an individual-based temporal model

Seasonal and spatial explicit survival estimates - Combining the multinomial reencounter model with an individual-based temporal model

Saskia Schirmer, Jan von Rönn, Fränzi Korner-Nievergelt
Swiss Ornithological Institute, Seerose 1, CH – 6204 Sempach, Switzerland

Migratory species experience a wide range of influences from sometimes very distant locations at different times. Describing the resulting differences in seasonal and local survival is desirable to better understand the population ecology and evolution of migratory species and to better protect them. However, many available datasets contain only very incomplete information on seasonal space use by individuals. For example, in mark-dead-reencounter datasets, individuals are only detected once at thesite and in the season they died in. We therefore combine the population-based multinomial reencounter model to describe migratory connectivity between seasons with an individual-based time-dependent dead-reencounter model that estimates seasonal survival and recapture probability. Under the constraint that individuals show site-fidelity in all seasons and use the same migration route for fall and spring migration, we obtain seasonal and local explicit survival estimates, recapture probabilities, and migratory connectivity distributions from this modelcombination. This model also allows us to estimate survival and migratory connectivity for species with complex life histories. We demonstrate this using the osprey Pandion haliaetus as an example.

11:39	Jaume-A. **Badia-Boher**	Evaluating permanent emigration and subsequent biases in survival in territorial raptors using spatial capture-recapture methods: the case of the Bonelli's eagle

Evaluating permanent emigration and subsequent biases in survival in territorial raptors using spatial capture-recapture methods: the case of the Bonelli's eagle

Jaume-Adria Badia-Boher*1, Joan Real1, Francesc Parès1,
& Antonio Hernández-Matías1
1Grup de Biologia de la Conservació, Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Universitat de Barcelona (UB), Barcelona, Catalonia, Spain.
**jabadia@ub.edu*

Robust estimates of survival are essential in order to perform reliable evaluations of population dynamics and conservation status. Survival is usually estimated using capture-mark-recapture analyses, but most study designs and modelling frameworks cannot distinguish between mortality and emigration from the study area. This can be especially important in territorial raptors, as tagging usually is focused on fledglings that may move far away from their birthplaces to breed and not return to their study sites throughout their lives. This phenomenon - known as permanent emigration - can lead to negatively biased estimates of survival, and consequently, wrong assumptions of the study population's status, which can ultimately lead to implementing ineffective conservation actions. Here, we estimate permanent emigration in the regionally threatened Catalan Bonelli's eagle population taking advantage of a long-term intensive ringing and monitoring scheme. Since monitoring schemes were active in neighbouring populations in the Iberian Peninsula and France throughout the course of our study, we were able to detect those individuals born in Catalonia and recruited elsewhere. Such a degree of detail in the monitoring of contiguous populations is infrequent in most species and provides an excellent opportunity to evaluate dispersal processes and estimate permanent emigration. We applied multistate capture-recapture methods to quantify the magnitude of permanent emigration in the population and assess its potential bias on survival estimation. In addition, we discussed and presented potential approaches to address this issue using recent developments in spatial capture-mark-recapture. Our results illustrate that omitting permanent emigration may lead to an underestimation of survival of sufficient magnitude to skew population predictions. Overall, we highlight the need to improve our understanding of permanent emigration in capture-recapture studies and to develop robust methods to account for this potential source of bias.

11:51	Murray **Christian**	Accurately estimating the demographic contribution of immigration: a southern elephant seal case study

Accurately estimating the demographic contribution of immigration: a southern elephant seal case study

Christian, M. Marion Island Marine Mammal Program, Department of Zoology and Entomology, University of Pretoria, South Africa
Oosthuizen, W.C. Centre for Statistics in Ecology, the Environment and Conservation, Department of Statistical Sciences, University of Cape Town
De Bruyn, P.J.N. Marion Island Marine Mammal Program, Department of Zoology and Entomology, University of Pretoria, South Africa

Integrated Population Models (IPMs) provide a powerful tool for understanding population dynamics. Coupled with transient Life Table Response Experiments (tLTREs), they offer ecologists the possibility of decomposing the temporal variance in realised population growth rates into contributions due to vital rates and population structure. This framework has great potential to identify important drivers of population change, but this potential is tempered by the vulnerability of key estimands to bias. IPMs often contain parameters that are inestimable using any one data source alone, such as immigration, and these are easily biased by model misspecification. Moreover, the tLTRE contributions of these 'additional parameters' are often overestimated, as they tend to absorb residual variance of the model. Goodness-of-fit therefore plays a crucial role, but is difficult to assess for IPMs.

In this talk we explore these issues in the context of a long-term study of southern elephant seals on Marion Island, South Africa. We built a Bayesian IPM using 39 years of mark-recapture, fecundity and count data, and performed tLTRE analyses with the posterior estimates. We used a multi-event model for the mark-recapture data to account for intermittent breeding (temporary emigration), and incorporated immigration as an additional parameter. The tLTRE analysis indicated that immigration is the most important driver of the

Thursday 20th April

09:00-09:30	Marlène **Gamelon**	**Plenary:** Biotic interactions matter: how intra- and interspecific competition shape vital rates and population dynamics

Biotic interactions matter: how intra- and interspecific competition shape vital rates and population dynamics

Marlène Gamelon

Dr. Marlène Gamelon is a researcher at the Centre National de la Recherche Scientifique (CNRS) in the Biometry and Evolutionary Biology Lab (LBBE) in Lyon, France and at the Centre for Biodiversity Dynamics at the University of Science and Technology (NTNU) in Trondheim, Norway. She is a population ecologist interested in understanding how free-ranging animal populations respond to environmental changes, including abiotic (climate conditions), anthropogenic (harvest), and biotic (intra- and interspecific interactions) factors. She uses modelling approaches to study how these factors shape phenotypic traits, demographic rates and population growth rate. Her research primarily relies on individual long-term monitoring of natural populations of birds and mammals, with implications in conservation and management.

Understanding components of intra- and interspecific competition is a major goal in ecological studies. Classical approaches for the analyses of density dependence typically consider equal responses and contribution of all individuals to density dependence. However, in age-structured populations, individuals of different ages may differ in their responses to changes in population size and how they contribute to density dependence affecting the growth rate of the whole population. Based on the long-term individual monitoring of sympatric competing species at several locations across Europe, we analyzed capture-mark-recapture data to assess how vital rates (e.g. survival, reproduction) and population growth rate of the focal species are affected by intra- and interspecific competition. We provide evidence for age-dependent responses and effects of intra- and interspecific competition. Accounting for both age structure and biotic interactions greatly improve predictions of annual variations in population size.

Individual heterogeneity, sociality, and kinship

09:48 - 11:00 *Amphithéâtre Délégation CNRS*

09:48	Matthew **Silk**	Demographic models of social networks

Demographic models of social networks

Silk, M.J. CEFE, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France
Gimenez, O.A. CEFE, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France

The fitness consequences of individual social behaviour are linked to an animal's social environment. Consequently, patterns of social behaviour are closely tied to demographic change and population density. Social networks can quantify social structure from individual to population scales, providing a natural way to integrate social behaviour and its demographic consequences. However, a key challenge is that demographic studies in natural populations must deal with population turnover and missing data; issues social network approaches are rarely designed for. We outline how social networks can be incorporated in demographic models and identify the steps needed to achieve this. We then introduce genNetDem, a tool capable of generating simulated co-capture datasets representative of a broad range of animal societies, and demonstrate its use by testing our ability to detect social network effects on survival in capture-recapture data. Together, this provides a roadmap for future developments in integrating social and population ecology.

10:00 Javier **Klaich** Estimating individual survival under a social network analysis when detection is imperfect

Estimating individual survival under a social network analysis when detection is imperfect

Klaich, M.J. Facultad de Ciencias Naturales y de la Salud, Universidad Nacional de la Patagonia San Juan Bosco, Puerto Madryn, Chubut, Argentina.

The way and strength in which two individuals (i.e. a dyad) are associated represent the basis of the social network analysys. Associations between individuals in social or gregarious species determine the social structure of the population. This structure remains in the population by natural selection due to it maximizes a component of the individual survival. When groups are small, it is easy to keep track of all individuals and their associations on each sampling occasion. When this is the case, social network analysis techniques become in a useful tool for testing hypotheses about the effect of social structure on individual survival. However, as either the sample size increase or individual behavior turn in cryptic type, detection probability becomes less than 1. As already shown in the bibliography, when detection is imperfect and heterogeneous with respect to association state of a dyad, the estimated probability that two individuals are in association is biased. When imperfect and heterogeneous detection is taking into account, it is possible to infer and visualize an unbiased social network. In addition, the estimated association transition probabilities are capable of characterizing the dynamics of the social structure of the population. However, these methods assume both demographic and geographic closure. In this work, a model is proposed for estimating the individual apparent survival conditional on the association state of a dyad when detection is imperfect and heterogeneous. The individual apparent survival conditioned to the dyad´s association state, is defined as the probability that individual *i* survives from occasion *t* to (*t+1*) and remains in the study area given the association state with the individual *j* at the occasion *t*. To analyses the dyadic data, a state-space modeling was implemented. Four states were considered for each dyad, both individuals are alive in association, both individuals are alive in non-association, one individual is alive and the other is dead and both individuals are dead. Given the underlying states, a dyad can be recaptured as both individuals in association, both individuals in non-association, only one individual, or none of both individuals are detected. The state-space model was built on the basis of the combination of 3 equations. First, the joint survival state equation specifies if both, only one or none individual survive from t to t+1 conditional on the dyadic state at occasion t. Second, if both individuals survived, the dyadic state equation specifies the association state for both individuals at occasion t+1 conditional on association state at occasion t. And third, the observation equation specifies the observation of the dyad at time t given its state at the same occasion. A simulation study was carried out in order to evaluate the performance of the proposed model under different scenarios. As an example, the model was applied to real data set of Commerson´s Dolphin (*Cephallorhynchus commersonii*) sampled in Patagonia Argentina. Finally, the application of the proposed method for testing hypotheses about the effect of social structure on individual survival and the possible model extensions are discussed.

10:12 Christophe **Barbraud** Selection against immigrants: demographic evidence and testing the familiarity hypothesis in seabirds

Selection against immigrants: demographic evidence and testing the familiarity hypothesis in seabirds

Barbraud Christophe, Centre d'Etudes Biologiques de Chizé UMR 7372, CNRS, Villiers en Bois, France.
Delord Karine, Centre d'Etudes Biologiques de Chizé UMR 7372, CNRS, Villiers en Bois, France.

Immigration is a major demographic parameter shaping population dynamics and is an important driver of eco-evolutionary patterns, but the fitness consequences for individuals following their settlement to a new population (immigrants) remain poorly tested in wild animal populations, particularly among long-lived species. Using long-term capture-mark-recapture data over a 32-year period for three seabird species (wandering albatross *Diomedea exulans*, southern fulmar *Fulmarus glacialoides*, snow petrel *Pagodroma nivea*) and multi-state capture-recapture models, we show that i) immigrants and residents differ in demographic parameters and ii) immigrants have a lower fitness than residents. Across all species, immigrants made on average -9-29% fewer breeding attempts, had 5-31% fewer fledglings, had 2-16% lower breeding success and produced 6-46% fewer recruits. Female immigration and male residency were also favored through differences in sex-specific breeding performance. We provide evidence for selection against immigrants in wild populations of long-lived species and our results are consistent with female-biased dispersal in birds being driven by asymmetric limiting resources and the competitive ability of dispersers *versus* non-dispersers. We test the lack of familiarity hypothesis to explain these fitness differences by investigating how demographic parameters and fitness vary with time since arrival and environmental variability.

10:24 Paul **Conn** Using close-kin mark-recapture to estimate abundance and survival of bearded seals in Alaska

Using close-kin mark-recapture to estimate abundance and survival of bearded seals in Alaska

Conn, P.B. Marine Mammal Lab, NOAA Alaska Fisheries Science Center, Seattle, USA
Taras, B.D. Alaska Department of Fish and Game, Statewide Marine Mammals, retired, Fairbanks, USA.
Bravington, M.V. CSIRO Marine Lab, Hobart, Australia.
Quakenbush, L. Alaska Department of Fish and Game, Arctic Marine Mammal Program, Fairbanks, USA
Kilian, A. *Diversity Arrays Technology Pty Ltd, University of Canberra, Bruce, ACT, Australia*
Lang, A.R. Southwest Fisheries Science Center, NOAA-Fisheries, La Jolla, USA
Bryan, A. Alaska Department of Fish and Game, Arctic Marine Mammal Program, Fairbanks, USA

Close-kin mark-recapture (CKMR) provides a framework for estimating abundance and adult survival using frequencies of kinship relationships observed in animal samples. In this study, we used ~1,800 genetic samples from indigenous harvested bearded seals gathered over a ~20 year period to obtain DNA and estimate age. A ~3,000 locus single nucleotide polymorphism (SNP) panel was developed, and all samples were genotyped and sexed. Kin relationships were ultimately established for 1,484 seals at 2,569 loci resulting in 2 parent-offspring and 18-25 half-sibling or grandparent-grandchild pairs (depending on modeling assumptions). We then used a sequence of age-structured CKMR models embodying different assumptions about data and population structure to estimate mean abundance throughout our study period and to update a prior distribution for survival-at-age. Estimates of bearded seal abundance ranged from 200,000-400,000 depending on the assumptions used. These estimates are smaller, but of similar magnitude to those obtained through aerial surveys (~500,000 seals) and confidence intervals had substantial overlap. Although the observed frequencies of kinship relationships were considerably less than recommended for CKMR estimation, we were encouraged by our results and the ecological insights possible even with a limited dataset. We plan to increase seal harvest data collection to further refine estimates and increase precision going into the future.

10:36 Thomas **Riecke** Estimating latent fitness heterogeneity using structural equation models

Estimating latent fitness heterogeneity using structural equation models

Riecke, T.V., Swiss Ornithological Institute, Sempach, Switzerland
Schaub, M., Swiss Ornithological Institute, Sempach, Switzerland

Understanding individual heterogeneity in demographic performance has long been recognized as a central problem in evolutionary and population ecology. Critically, recent research has demonstrated that existing approaches (i.e., multivariate normal distributions) to estimating correlated individual heterogeneity in Bernoulli traits often do not accurately estimate variance in demographic performance among individuals or correlations among demographic traits. We use real and simulated data with structural equation modeling approaches to estimate latent heterogeneity in fitness among individuals rather than individual hetereogeneity in each demographic component and correlations among parameters. With the simulated data, we compare the performance of structural equation models to data-generating multivariate normal approaches. Structural equation models estimate relationships between demographic components more reliably, particularly when the number of releases or study occasions are reduced. Thus, our approach is more reliable for estimating relationships among demographic parameters when correlated heterogeneity exists, and may allow for more accurate inference. We then apply these models to two long-term capture-recapture and fecundity datasets collected on pied flycatcher (Ficedula hypoleuca) and dipper (Cinclus cinclus) populations breeding in Switzerland. We demonstrate strong relationships between individual-level survival probability and fecundity, and senescent decline in both survival and fecundity in both populations. We discuss potential extensions and limitations of these methods, and suggest that they may be broadly useful for modeling individual heterogeneity in fitness with capture-reencounter and fecundity data.

10:48 Blanca **Sarzo** Justice for the weaklings! Survivorship bias in individual heterogeneity CMR models

Justice for the weaklings! Survivorship bias in individual heterogeneity CMR models

Blanca Sarzo, Ruth King, Rachel McCrea, and Fränzi Korner-Nievergelt

"Survivorship bias" arises when conclusions are drawn conditional on only the surviving individuals, whilst failing to correct for those individuals who have not survived. This issue has been well studied in many fields such as economy, construction, forestry, health, etc. (Czeisler et al., 2021; Cooke et al., 2003) but less well explored within the context of capture-mark-recapture studies (CMR). The survivorship bias can be immediately observed in individual heterogeneity models that are commonly fitted to capture-recapture data. This bias is manifested within these studies in that weaker individuals are more likely to die at younger ages compared to stronger individuals who may survive longer within the study period. In other words, the weaker individuals are less likely to be observed within the study period, compared to the stronger individuals, potentially leading to biased estimates, dependent on the sampling strategy.

To illustrate this, we present a simulation study where an algorithm to correct the survivorship bias is implemented for individual heterogeneity CMR models, considering that individuals may have different ages when they are first marked. We highlight the necessity of careful interpretation of the model parameters as well as the problem of survivorship bias when individual heterogeneity is included within this context.

Cooke, B., W. Miller, and J. Roland (2003). Survivorship bias in tree-ring reconstructions of forest tent caterpillar outbreaks using trembling aspen. Tree-Ring Research 59, 29–36.

Czeisler, M. E., J. F. Wiley, C. A. Czeisler, S. M. Rajaratnam, and M. E. Howard (2021). Uncovering survivorship bias in longitudinal mental health surveys

Distribution and conservation of rare and endangered species

11:15 – 12:03 *Amphithéâtre Délégation CNRS*

11:15 Brett **Sandercock** Estimating den use and reproductive rates of arctic fox with multistate occupancy models

Estimating den use and reproductive rates of arctic fox with multistate occupancy models

Sandercock, B.K. Department of Terrestrial Ecology, Norwegian Institute for Nature Research, Norway
Eide, N. Department of Terrestrial Ecology, Norwegian Institute for Nature Research, Norway

Flagstad, Ø. Rovdata, Norwegian Institute for Nature Research, Norway
Rød-Eriksen, L. Department of Terrestrial Ecology, Norwegian Institute for Nature Research, Norway
Ulvund, K. Department of Terrestrial Ecology, Norwegian Institute for Nature Research, Norway

Arctic fox (*Vulpes lagopus*) are a species of conservation concern in mountain areas of Fennoscandia where populations are threatened by a variable climate, damping of rodent cycles, and competition with red fox (*V. vulpes*). Population monitoring in Norway includes annual surveys of breeding activity at known den sites and estimation of population size from DNA sampling of scat. Here, we used multistate occupancy models to model patterns of den use and to evaluate the status of arctic foxes in relation to recovery targets from a joint action plan for Scandinavia. The two key targets for 2035 include a viable population of ≥1000 adults and ≥250 breeding pairs in years with good food resources. Den sites were visited by observers during the 6-month period of Mar-Aug and detections were recorded as signs of tracks or digging, or the number of adults or pups sighted. Den status was then coded each month as unoccupied (0), occupied by a breeding pair (1), or a confirmed breeding attempt (2). The total sample from 2001 to 2022 included >9,500 visits to >800 den sites. Arctic foxes had secretive behavior and the monthly probability of detection for occupied dens was p1=0.33-0.66, but was higher if an occupied den produced pups p2>0.94. The probability of correctly classifying a den as producing pups was delta=0 in Mar-May but then increased to delta=0.25-0.71 after emergence of the young in Jun-Aug. Our results indicate that 3-4 monthly visits would be needed to confirm den occupancy with high confidence (p*>0.96), and visits during the summer months are needed to confirm production of young. The annual probabilities of den occupancy steadily increased from psi1=0.15 to 0.41 during a period of population recovery. On the other hand, the conditional probability of occupancy that pups were produced if a den was occupied was highly variable. The estimates ranged from psi2=0 to >0.4 but were linked to regional variation in rodent numbers. Overall, we estimate the national population status to be up to psi1×psi2=60 breeding pairs of arctic foxes in the mountain areas of mainland Norway. Multistate occupancy models provided a useful tool for making efficient use of monitoring data for a species of conservation concern in remote mountain areas.

11:27	Sarah **Bauduin**	From abundance to occupancy as an indicator to monitor the French wolf population

Using occupancy to monitor populations. Case study: the wolf in France

Bauduin, S. Service Conservation et Gestion des Espèces à Enjeux, Direction de la recherche et de l'appui scientifique, Office Français de la Biodiversité, Juvignac, France.
Gimenez, O. CEFE, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France.
Duchamp, C. Service Conservation et Gestion des Espèces à Enjeux, Direction de la recherche et de l'appui scientifique, Office Français de la Biodiversité, Gap, France.
Drouet-Hoguet, n. Service Conservation et Gestion des Espèces à Enjeux, Direction de la recherche et de l'appui scientifique, Office Français de la Biodiversité, Gières, France

In France, and in Europe, the gray wolf is protected under the Bern convention and the Habitats Directive. A monitoring of the population state and trend are necessary to evaluate the species conservation status and adapt its management. Today, France is monitoring its wolf population using a demographic indicator: an estimation of the population size. Population size is estimated with a capture-mark-recapture (CMR) model using genetic data. However, as the population keeps growing over time, it becomes more and more difficult to obtain reliable estimates because of the CMR limits for large population at large scale (i.e., time and monetary costly). A way to assess the changes for such population is to rely on a spatial indicator to evaluate changes in the distribution of the species over a defined area. We used occupancy modeling to estimate each year the area occupied by the wolf in France. We compared the changes over time of this indicator with those of the demographic indicator and tested its sensitivity to detect wolf permanent presence appearance or disappearance. The indicator is better at informing on wolf settlement than disappearance though. This indicator can inform, at the scale of the country, how much area of occupancy the wolf gains or losses from year to year. At a local scale, it can also indicate if an area became colonized or extinct. This spatial indicator may be completed by an estimate of demographic parameters such as survival to make a full evaluation of the species status.

11:39	Anaïs **Dasnon**	Estimating seabird populations breeding in sparse colonies in remote areas

Estimating seabird populations breeding in sparse colonies in remote areas

Dasnon, A. Centre d'Etudes Biologiques de Chizé, CNRS UMR7372, Villiers en Bois, France ; Réserve Naturelle Nationale des Terres Australes Françaises, TAAF, Saint-Pierre, France
Lesage, C. Réserve Naturelle Nationale des Terres Australes Françaises, TAAF, Saint-Pierre, France
Barbraud, C. Centre d'Etudes Biologiques de Chizé, CNRS UMR7372, Villiers en Bois, France

Getting reliable and precise knowledge about population sizes and distribution is urgent for species management and conservation in the context of the current massive loss of biodiversity. While monitoring techniques have rapidly evolved for the last decades, many animal populations remain unknown. Seabirds are among the most threatened bird species worldwide and many of their populations are still not evaluated.

While population distribution and abundance of conspicuous species that breed in large colonies such as albatrosses and large penguins are now well known, knowledge about abundance of sparsely distributed seabird populations is still lacking for many species breeding in remote sites. The Kerguelen archipelago hosts around 33 breeding seabird species and for most of these species reliable population size estimates are lacking. Among these, Kerguelen shags and eastern rockhopper penguins breed in sparse and small to medium sized colonies along the coastline of remote and isolated islands, most often in rocky habitat or in cliffs. Their count remains challenging and their populations were never accurately estimated.

Here, we model presence and abundance of these two species as a function of several environmental variables and estimate their populations all along the Kerguelen coastline. We combined several heterogeneous presence-absence and colony counts datasets obtained from field surveys made at Kerguelen between 2010 and 2022. We used generalised additive models (GAM) to model the occurrence, and hurdle GAM to model the abundance of Kerguelen shags and penguins populations. The detection probability was estimated using data from prospections

led along the same coastline portion in 2011 and 2014. GAM allowed us to model non-linear relationships between the occurrence/abundance and the environmental factors and to take account of potential spatial auto-correlation.

The occurrence of the Kerguelen shags increased around relatively high elevation on the coast (70m), around moderately deep bathymetry (-45m), with increasing distance to open-sea, decreasing distance to the nearest rockhopper penguins colony and with absence of cats. Their abundance increased around 100m elevation and with decreasing wind influence. The occurrence of the rockhopper penguins increased with increasing elevation and with moderate wind influence. Their abundance increased around 40m elevation, with increasing bathymetry, increasing distance to the nearest shag colony and increasing sea surface temperature.

Detection probabilities were contrasted according to the method of survey and ranged from 0.76 to 0.84 for penguins and from 0.63 to 0.88 for shags. The Kerguelen shags and rockhopper penguins occurrence models had fairly decent discriminating abilities (AUC = 0.77 and 0.73 respectively) and the hurdle models had Pearson correlation coefficients of 0.43 and 0.50 respectively. While hurdle models had relatively low performances, they could gave a good indication of the distributions of both species along the Kerguelen coastline, allowing future surveys and management actions to be adapted.

11:51 Fabiola **Iannarilli** Leveraging sharing of camera trap data to inform biodiversity conservation at large scales

Leveraging sharing of camera trap data to inform biodiversity conservation at large scales

IANNARILLI Fabiola, Center for Biodiversity and Global Change and Department of Ecology and
Evolutionary Biology, Yale University, New Haven, CT, USA
JETZ Walter, Center for Biodiversity and Global Change and Department of Ecology and
Evolutionary Biology, Yale University, New Haven, CT, USA

Although the spatial-temporal extent of the impacts of anthropogenic activities on biodiversity has considerably increased in the last few decades, our ability to assess the effects of these activities on species at such large scales has lagged behind. Yet, advancements in technology and statistical methods, and new initiatives that promote data sharing create opportunities to fill this gap. Occupancy is one of the main criteria to define species status within the IUCN Red List Categories, however, too often trends in occupancy at large scales are only established qualitatively. We present an approach that allows a statistically-based and robust assessment of population and species status at large spatial scales. We leverage camera trap data shared by different organizations through the recently established platform Wildlife Insights to assess which are the main types of human disturbance that drive range-wide trends in occupancy in several species of mammals and birds. Pooling data across projects, we created species-specific datasets containing information collected in different areas within the range of each species and over multiple years. We then applied single-species Bayesian hierarchical occupancy models to estimate local and range-wide trends in occupancy as a function of different proxies of human disturbance, including changes in forest cover and human population density. Finally, we used these estimates to assess which species were most affected and what were the traits that characterized them. Our results can inform the management and conservation of many species at a scale beyond the single protected area, network, or political jurisdiction. We emphasize that this advancement in understanding trends at large scales can be made possible only by researchers and organizations willing to share their data and by initiatives, such as Wildlife Insights, that work to facilitate data sharing. Our modelling exercise is, thus, also an example of what collaboration among scientists can achieve for preserving global biodiversity.

Novel approaches for species distributions

13:30 – 14:30 *Amphithéâtre Délégation CNRS*

13:30 Marc **Kéry** Integrated distance sampling models for simple point counts

Integrated distance sampling models for simple point counts

Kéry, M. Swiss Ornithological Institute, Seerose 1, 6204 Sempach, Switzerland
Royle, J.A. USGS Eastern Ecological Science Center, Laurel, 20708 Maryland USA
Hallman, T. Department of Biology and Chemistry, Queens University of Charlotte, North Carolina USA
Robinson, W.D. Oak Creek Lab of Biology, Department of Fisheries, Wildlife, and Conservation Science, Oregon State University, Corvallis, Oregon USA
Strebel, N. Swiss Ornithological Institute, Seerose 1, 6204 Sempach, Switzerland
Kellner, K.F. Department of Fisheries and Wildlife, Michigan State University, East Lansing, Michigan USA

Point counts (PCs) are widely used in biodiversity surveys, but despite numerous advantages, simple PCs suffer from several problems: detectability, and therefore abundance, is unknown; systematic spatiotemporal variation in detectability produces biased inferences, and unknown survey area prevents formal density estimation and scaling-up to the landscape level. We introduce integrated distance sampling (IDS) models that combine distance sampling (DS) with simple PC or detection/nondetection (DND) data and capitalize on the strengths and mitigate the weaknesses of each data type. Key to IDS models is the view of simple PC and DND data as aggregations of latent DS surveys that observe the same underlying density process. This enables estimation of separate detection functions, along with distinct covariate effects, for all data types. Additional information from repeat or time-removal surveys, or variable survey duration, enables separate estimation of the availability and perceptibility components of detectability. IDS models reconcile spatial and temporal mismatches among data sets and solve the above-mentioned problems of simple PC and DND data. To fit IDS models, we provide JAGS code and the new IDS() function in the R package unmarked. Extant citizen-science data generally lack adjustments for detection biases, but IDS models address this shortcoming, thus greatly extending the utility and reach of these data. In addition, they enable formal density estimation in hybrid designs, which efficiently combine distance sampling with distance-free, point-based PC or DND surveys. We believe that IDS models have considerable scope in ecology, management, and monitoring.

13:42 Javier **Fernández-López** A unified framework for estimating animal abundance from hunting statistics: the thinned Poisson Point Process model

A unified framework for estimating animal abundance from hunting statistics: the thinned Poisson Point Process model

Fernández-López, J. CEFE, Université Montpellier, CNRS, EPHE, IRD, Montpellier, France / Universidad Complutense, Madrid, Spain
Illanas, S. IREC, CSIC-UCLM-JCCM, Ciudad Real, Spain
Blanco-Aguiar, JA. IREC, CSIC-UCLM-JCCM, Ciudad Real, Spain
Vicente, J. IREC, CSIC-UCLM-JCCM, Ciudad Real, Spain
Acevedo, P. IREC, CSIC-UCLM-JCCM, Ciudad Real, Spain
Gimenez, O. CEFE, Université Montpellier, CNRS, EPHE, IRD, Montpellier, France

Reliable estimates of species distribution and abundance are key elements for wildlife conservation and management. However, this basic information is not always easy to obtain due either to logistical constraints and/or intrinsic difficulties inherent to the studied species. Harvest data (the number of animals culled during a hunting season) are often systematically collected by Government departments or agencies and they can be considered as "observations" that emerge from animal abundance through an observational process (hunting events). In this study we used the discrete thinned Poisson Point Process (PPP) as underlying model in a hierarchical framework to obtain wild boar abundance estimates in Castilla – La Mancha (Spain). Animal abundance was related to climate and land cover, while the PPP thinning rate (which can be seen as the mortality due to hunting activities) was related to hunting management and hunting ground size. We followed a "change-of-support" strategy to reconcile harvest data from different hunting ground sizes and to downscale abundance predictions to 2 km^2 cell grid. Model predictions were visually assessed in calibration plots by dividing harvest data in calibration and validation data sets. All analyses were conducted through Bayesian inference in NIMBLE. Average mortality rate due to hunting activities in Castilla – La Mancha was 0.33 (0.16 – 0.69) which was in accordance with hunting efficiency in other Spanish regions. Total wild boar abundance for Castilla – La Mancha region was estimated at 368,500 (340,121 – 396,170), mainly distributed in areas with high forest coverage. Model predictions were in agreement with other local abundance measures obtained by independent methodologies (random encounter models and distance sampling). Our study unified existing approaches for hunting yield modeling, and allows obtaining reasonable estimates of absolute animal abundance from harvest data by modeling mortality due to hunting activities.

13:54	John **Grider**	A novel method for estimating pathogen presence, prevalence, load, and dynamics at multiple scales during a disease outbreak

A novel method for estimating pathogen presence, prevalence, load, and dynamics at multiple scales during a disease outbreak

Grider, J.F. Colorado Cooperative Fish and Wildlife Research Unit, Colorado State University, Fort Collins, CO, USA
Udell, B.J. USGS, Fort Collins Science Center, Fort Collins Colorado, USA
Reichert, B.E. USGS, Fort Collins Science Center, Fort Collins Colorado, USA
Frick, W.F. Bat Conservation International, 500 North Capital of Texas Highway, Building 1, Austin, TX, USA
Cheng, T.L. Bat Conservation International, 500 North Capital of Texas Highway, Building 1, Austin, TX, USA
Kendall, W.L. U.S. Geological Survey, Colorado Cooperative Fish and Wildlife Research Unit, Colorado State University, Fort Collins, CO, USA

The use of eDNA and qPCR to monitor the presence and spread of pathogens has become common; however, quantitative frameworks that consider both the observation process and dynamics in the pathogen presence and load are lacking. This can be especially problematic in the early stages of disease progression, where low level detections are treated as 'inconclusive' and excluded from analyses. Alternatively, a monitoring framework that uses qPCRs Ct score to inform the detection process would be able to make use of all the collected data and provide more robust inferences in the early stages of disease progression. To better estimate pathogen presence, prevalence, and spread within a population, we developed a multi-scale, dynamic occupancy hurdle model (MSDOHM) that estimated the probability of a site and sample being occupied, and the amount of pathogen given presence. The model utilized data gathered during sampling for the pathogen *Pseudogymnoascus destructans* on North American bats. We evaluated pathogen presence using qPCR, which allowed us to account for pathogen load by equating the Ct score of qPCR runs to pathogen load in the sample. We modeled site level initial occupancy given space; and site persistence and colonization rates given time, space, and site level pathogen load from the previous time step. We estimated site level prevalence while accounting for detectability, using the proportion of the population vulnerable to infection as a predictor of prevalence, and days since the onset of hibernation and pathogen load within the sample as a predictor of the detection probability. To assess the ability of the dynamic occupancy hurdle model to estimate pathogen spread, we compared model results to outputs from 1) a dynamic distribution models that did not include a detection process and 2) inferences based on raw presence absence data (which is the current method for assessing pathogen presence). Initial results indicate that estimates of site level pathogen presence for the MSDOHM were 6 and 15% higher than those of the dynamic distribution models and raw presence absence data, respectively. Additionally, the MSDOHM's utilization of Ct scores to infer pathogen load and detectability at the site and individual level gives disease managers more insight into the potential threat of the pathogen on a population. Our findings indicate that a failure to account for spatial spread and detection probability of a pathogen could lead to an underestimation of its presence and prevalence, making management of disease outbreaks more challenging.

14:06	Florian **Lasgorceux**	Inferring niche models with unknown sampling effort estimated from opportunistic data

Inferring niche models with unknown sampling effort estimated from opportunistic data

Lasgorceux, F. BioSP, INRAE, UR BioSP, Avignon, France.
Papaix, J. BioSP, INRAE, UR BioSP, Avignon, France.
Bunz, Y. Parc national des Ecrins, Domaine de Charance, Gap, France.
Combrisson, D. Parc national des Ecrins, Domaine de Charance, Gap, France.
Opitz, T. BioSP, INRAE, UR BioSP, Avignon, France.

Managers/wardens of natural areas are increasingly using species databases which are supplied in an opportunistic way (presence-only data). These data often provide good spatio-temporal coverage but suffer from acquisition-related biases due to the lack of a strict observation protocol, which leads to a heterogeneous and unknown sampling effort. In this study, we propose strategies to model and estimate the sampling effort in these large datasets and we assess the insights gained by explicitly taking into account the sampling effort in species distribution models. We here promote the idea that the variability in numbers of observations, aggregated over observers and species, provides a useful proxy for the varying sampling effort. Therefore, we first predict the number of observations of a chosen taxonomic group without differentiating the species it contains by developing a point-process model defined in a Bayesian setting, more precisely a spatio-temporal Log-Gaussian Cox Process accounting for spatial and seasonal variability. The a posteriori distribution of the expected number of observations (i.e., of the point process intensity function) is then used as a proxy of the sampling effort when estimating species-specific properties in a second step. For this purpose, we draw random samples of this a posteriori distribution and include them as covariates in the species-specific distribution to take into account the heterogeneous spatio-temporal sampling of the data. Species-specific distribution models are also based on Log-Gaussian Cox Processes that further include covariates for characterizing the species-specific niche. The structure of the estimated niche and the amount of information added by including the proxy of the sampling effort are studied through model comparisons. The estimation of models is carried out through Bayesian inference using the INLA-SPDE approach. We present results from a case study of a large opportunistic database of bird observations by expert observers in the Ecrins National Parc in the French Alps.

14:18 Jamie **Sanderlin** Innovations for biodiversity monitoring using acoustic methods in the southwestern United States: What does this mean for rare species?

Innovations for biodiversity monitoring using acoustic methods in the southwestern United States: What does this mean for rare species?

Sanderlin, J.S. Rocky Mountain Research Station, USDA Forest Service, Flagstaff, AZ, USA
Jones, G.M. Rocky Mountain Research Station, USDA Forest Service, Albuquerque, NM, USA
Wood, C.M. Center for Conservation Bioacoustics, Cornell Lab of Ornithology, Cornell University, Ithaca, NY, USA
Stein foster, V. Kaibab National Forest, USDA Forest Service, Williams, AZ, USA
Strohmeyer, B.E. Rocky Mountain Research Station, USDA Forest Service, Flagstaff, AZ, USA

With a high diversity of birds in the southwestern United States region and multiple stressors on these populations (e.g., climate change, drought, wildfire), there is a need for monitoring approaches that provide cost-effective information on population status across broad scales. One of the biggest monitoring challenges is the ability to efficiently allocate samples of species in space and time with limited budgets. This is less of a challenge with common species but becomes more problematic with rare species. Most broad-scale monitoring programs do well at tracking common species, yet many species have insufficient observations to detect trends with standard monitoring protocols. However, rare species tend to be of more interest in conservation and management applications. An additional logistical challenge is that as budgets are reduced, fewer personnel are available to accomplish monitoring on the ground leading to increased safety considerations, especially with night work. Wildlife monitoring technologies like passive acoustic surveys show great promise in overcoming these challenges to monitor multiple species at the same time using new innovative automated data processing methods for multiple species. Passive acoustic surveys can be used to monitor wildlife communities, including multiple focal species, and behaviors using one approach at reduced costs and over larger areas. We will discuss current pilot study efforts in the southwest United States targeting specific questions to help guide decisions for a regional monitoring program based in acoustic monitoring, in the broader context of similar efforts occurring in other regions across National Forest Systems. Our pilot study on the Kaibab National Forest focused on both methodological and ecological questions, using a design with co-located passive acoustic surveys and point count surveys of unmarked individuals. We used multi-species occupancy models to estimate both individual species- and community-level metrics (occupancy, species richness) with both detection methods separately. Additionally, we used an approach to find an optimal design with both detection methods using a constrained optimalization framework (maximum precision of species richness and occupancy probability of focal species, given a fixed budget). We will discuss monitoring implications of these results in the context of a broader effort on the Kaibab National Forest to integrate point count and eBird data for estimating species distributions of forest focal species in relation to management activities with the potential of integrating an additional data source from passive acoustic surveys.

Communities and species interactions

14:45 – 15:45 *Amphithéâtre Délégation CNRS*

14:45 Divyajyoti **Ganguly** Three’s company: Integrating detection data from multiple methods to examine meso-carnivore co-occurrence in India

Three’s company: integrating detection data from multiple methods to examine meso-carnivore co-occurrence in India

Ganguly, D. Post graduate program in Wildlife Biology and Conservation, National Centre for Biological Sciences, Bangalore, India
Srivathsa, A. DST INSPIRE Fellow, National Centre for Biological Sciences, Bangalore, India
Vasudev, D. Conservation Initiatives, Guwahati, India
Ramakrishnan, U. Associate Professor, National Centre for Biological Sciences, Bangalore, India

Carnivores are important components of the ecosystem. Yet, studying them can be challenging because they are typically secretive, elusive, and difficult to detect. Studies of carnivores in the tropics are therefore limited by insufficient data. In resource-restricted landscapes which are also prone to intensive human use, the inherently low densities of carnivores are associated with even lower detectability rates. Assessing the interplay amongst co-occurring carnivores as well as human–carnivore interactions is crucial in such landscapes, so as to better inform conservation and management. We assessed the impact of ecological and anthropogenic factors on intraguild co-occurrence and species interactions in a meso-carnivore community in the semi-arid landscape of Kutch, India. The study area of 800 km^2 was surveyed for four months in the dry season (February–May 2022) using a combination of camera trap and scat surveys. In total, 950 camera trap nights and 374 km of scat surveys provided 531 independent detections of 12 carnivore species. Carnivore site use and co-occurrence were assessed for four meso-carnivore species for which the surveys yielded sufficient data ─ Golden jackal (*Canis aureus*), Jungle cat (*Felis chaus*), Indian fox (*Vulpes bengalensis*) and Desert cat (*Felis silvestris ornata*). We combined spatially and temporally replicated detection data by using site-specific survey effort and survey-specific detection type as covariates. We undertook a three-stage modelling workflow. In the first step, we explored species–habitat associations using single-species occupancy models. Next, species co-occurrence patterns and associated impacts of free-ranging dogs—a competitor for carnivores that is associated with human presence—were assessed using multi-species occupancy models. Finally, we tested the influence of anthropogenic factors (distance to settlement, road density and number of wind turbines) measured as a single index, the Human Impact index, on species presence and co-occurrence. We found that open savanna was the most used habitat for three of the four meso-carnivores. We found no support for the impact of free-ranging dogs on species presence or interactions (except in the case of Indian fox and desert cat, where there was evidence for increased spatial segregation). However, human impact negatively influenced the presence of Golden jackal and Indian fox, and the co-occurrence between five of the six species pairs, leading to increased spatial segregation. Considered in context, our results suggest that rapid increase in the human footprint in the study landscape can engender competition for limited space, especially in the case of carnivore pairs with similar habitat requirements. In the long term, this could lead to local extinctions of socially subordinate species or habitat specialists, and thereby result in a more simplified, homogenized meso-carnivore community. Our study exemplifies the use of multiple sources of data to assess complex patterns of species co-occurrence in human-use landscapes, particularly in scenarios where the species occur in low densities, and, the unavailability of resources or personnel imposes logistical constraints.

14:57	Julie **Louvrier**	How much data do you need to detect co-occurrence with multi-species occupancy models: A simulation study

How much data do you need to detect co-occurrence with multi-species occupancy models: a simulation study

Louvrier, J. CEFE, University of Montpellier, CNRS, EPHE, IRD, Montpellier, France
Fidino, M. Department of Conservation and Science, Lincoln Park Zoo, Chicago, IL, 60614, USA
Gimenez, O. CEFE, University of Montpellier, CNRS, EPHE, IRD, Montpellier, France

Species interactions shape animal communities but they are difficult to study on the field, particularly due to imperfect species detection. Occupancy models, which explicitly account for such imperfect detection, were initially developed with single-species parametrization. Occupancy models have recently been developed to two or more interacting species by Rota et al. (2016), and these models have been broadly used to assess predator-prey interactions or species competition. In our study we investigated the performance of the occupancy model accounting for two interacting species in different settings based on the number of visits, sites, and level of interaction. We also investigated the performance of such model in comparison with a null model, in which no co-occurrence is accounted for. We found that parameters were estimated with little or no bias in all simulation scenarios. Precision of the estimates increased with the number of sites visited. In terms of inference however, the two-species model did not perform better than the null model except in cases where a species displays a strong avoidance of the other species. The fact that we could not detect a significant signal for species co-occurrence when it is in fact occurring, is a critical issue for the application of multispecies occupancy models and highlights the need to develop further models capable of detecting co-occurrence in situations where the interaction level is mild.

15:09	Prashant **Mahajan**	Interspecific interactions and co-existence among canids in the semi-arid landscape of western India

Interspecific interactions and co-existence among canids in the semi-arid landscape of western India

Mahajan P.

Competition among animals (interference or exploitative) can severely affect population dynamics of subordinate species. On contrary dominant predator can also facilitate smaller carnivore through carrion provisioning. Therefore, apex predator can influence population structure of an entire carnivore guild through positive and negative interactions and can help in species specific management. Indirect evidences for wolf, jackal, fox and hyaena (due to similar behavioural and ecological requirements) were collected in an occupancy framework. To investigate potential interactions among canids, the Ψ^{BA} parameterization of a single-season two-species co-occurrence models were conducted to make pairwise assessments of conditional occupancy among canids. Size differences drive canid interspecific interactions. Wolves being the dominant predators suppressed hyaena and jackal populations which resulted in an indirect net benefit to other smaller mesocarnivores like fox, which may have been due to carrion provisioning. Wolves therefore caused cascade of negative and positive interactions throughout an entire canid guild. Intraguild interactions are complex ecological processes that change species demography. Understanding community-level interactions is the first step in determining how species coexist. In conservation and management efforts to restore or reduce apex predator populations, the potential for apex predators to influence more than one competitively dominant mesocarnivore should be considered.

15:21	Matt **Metz**	Estimating the abundance of wolf-killed prey through multiple detection methods in a mark-recapture framework

Estimating the abundance of wolf-killed prey through multiple detection methods in a mark-recapture framework

Metz, M. Yellowstone Center for Resources, National Park Service, Yellowstone National Park, WY, USA
Smith, D. Yellowstone Center for Resources, National Park Service, Yellowstone National Park, WY, USA
Lukacs, P. Wildlife Biology Program, Department of Ecosystem and Conservation Science, W.A. Franke College of Forestry and Conservation, University of Montana, Missoula, MT, USA
Williams, S. Panthera, Missoula, MT, USA
Stahler, D. Yellowstone Center for Resources, National Park Service, Yellowstone National Park, WY, USA
Hebblewhite, M. Wildlife Biology Program, Department of Ecosystem and Conservation Science, W.A. Franke College of Forestry and Conservation, University of Montana, Missoula, MT, USA

Estimating the abundance of predator kills is fundamental to evaluating predator-prey dynamics. For example, predator kill rate, i.e., the number of kills per predator per unit time, is a foundational predation metric that influences both the predator and prey populations. The ability to estimate predator kill rate, however, begins with estimating the number of predator kills. Here, we developed an abundance estimator that leveraged independent detection of wolf (*Canis lupus*)-acquired ungulates through three field methods – aerial observation, ground observation, and GPS cluster searches. We specifically estimated the number of ungulate carcasses for 408 unique wolf pack-sessions, which each typically lasted 30 days, in Yellowstone National Park in a Bayesian mark-recapture model, using the technique of data augmentation. Through our Bayesian abundance model, we accounted for biological processes, detection probability, and sampling effort. For instance, we tested for the importance of, and then included, pack size, mean carcass size, and seasonality in our biological process model because these covariates each had an underlying influence on the number of carcasses acquired during a pack-session. We similarly tested for covariates (i.e., carcass size, distance from observer, openness of landscape, pack size, proportion of pack with radiocollars, viewshed) that affected detection probability, doing so while allowing covariate effects to differ across methods. Finally, we sampled differently across pack-sessions, with 11% of pack-sessions monitored by all three methods, 23% monitored by the ground and airplane, <1% by GPS cluster searches and the airplane, and 65% by only the airplane. Moreover, individual methods could not always operate on each day of a sampling period. For example, the airplane was often unable to fly due to weather. As such, we included sampling effort in our model through the concept of availability, i.e., whether it was possible for a carcass to be detected by a particular method. We specifically leveraged knowledge of realized method-specific effort during a pack-session to define availability for the augmented data. The summation of our modeling efforts resulted in carcass abundance increasing from the naïve number of 2,498 to the estimated number of 5,713, an increase of 128%. How much estimates increased during a pack-session was fundamentally affected by the methods that had been employed. For example, GPS cluster searches had the highest detection probability ($p = 0.92$; 90% CI: 0.88 – 0.94) for detecting a carcass. As such, estimates for pack-sessions that included a GPS collar increased relatively little (19%). Conversely, our estimates increased from the naïve detections by 67% for those pack-sessions monitored by the ground and airplane, and 321% for those monitored by only the airplane. The much larger increase for those pack-sessions monitored by only the airplane was also driven by that detection method being the most variable in effort, thus lowering availability. Our study ultimately showed that accounting for detection probability and sampling effort was critical for estimating the number of wolf kills. Yet, the magnitude of that importance depended on the type of methods employed to detect the carcasses.

15:33 Frédéric **Barraquand** The various concepts of independence in integrated population models

The various concepts of independence in Integrated Population Models

Barraquand F., Institute of Mathematics of Bordeaux, CNRS and University of Bordeaux, Talence, France.

Integrated population models (IPMs) combine several data types such as capture-mark-recapture, reproduction surveys, and population counts (each with their associated submodels) into a single statistical framework. An assumption of independence between these different data types is usually made. Several works have even investigated the robustness of IPMs to deviations from independence, considering that the same individuals could contribute to multiple data types, since individuals that are marked or surveyed at the nest are often among those that are counted in the field. However, this is not the concept of independence that matters to such demographic modelling. Instead, what matters from a statistical perspective is probabilistic independence: $P(A \text{ and } B) = P(A)P(B)$ for two random variables A and B representing data (or parameters in some contexts). Contrary to a widespread perception, probabilistic non-independence does not automatically result from collecting data on the same physical individuals. Conversely, while there can be good reasons for non-independence of IPM submodels in the probabilistic sense (e.g. individuals that are easier to capture are also easier to count, higher survival for individuals that have a high fecundity), these relations do not seem to be included in IPMs whose robustness to non-independence is being investigated. Furthermore, many IPMs are implemented in a computational Bayesian framework that does not require statistical independence between datasets, in contrast to their representation as a product of likelihoods which permeates the literature. In this talk, I will survey the various independence concepts used in IPMs, try to make sense of them by getting back to first principles, and finally revisit recommendations pertaining to component data independence, from both data collection and modelling perspectives.

Species movement, life history, and detectability

15:57 – 17:09 *Amphithéâtre Délégation CNRS*

15:57 Kasper **Thorup** Historical changes in migration patterns

16:09 Jacob **Davies** Quantitative year-round modelling of the movements of European waterfowl populations

Quantitative year-round modelling of the movements of European waterfowl populations

Davies, J.G., BTO Scotland, Beta Centre (Unit 15), Stirling University Innovation Park, Stirling, FK9 4NF

Gargallo, G., Catalan Ornithological Institute, ES-08019 Barcelona, Spain
Robinson, R.A. & Baillie, S.R., BTO, The Nunnery, Thetford, Norfolk, IP24 2PU

At a continental scale, much of the work describing the movement of birds from one location to another has been qualitative. However, many applications require quantification of bird movement. Here, we used ring-recovery data from the EURING databank to quantify long-distance (migratory or cold weather) and local bird movement for 12 species of waterfowl.

For the long-distance movement analysis, we estimated movement between any pair of grid cells in Europe, for any pair of consecutive months. A key challenge is that due to the spatial unevenness of ringing and recovery effort, ring-recovery pairs were not available for all combinations of grid cells, even when birds were known to move between those grid cells. We addressed this by fitting Bayesian spatial models in INLA, which shared information between adjacent origin cells on the proportion of birds moving to a given destination cell.

We also characterised local (<200km) bird movements within Europe using Weibull kernels, fitted by season and by ecoregion. Our estimates of long-distance and local bird movements were then combined with spatial bird abundance estimates (from EuroBirdPortal) by partner organisations, to parameterise a prototype epidemiological model for the spread of high-pathogenicity avian influenza.

Our analyses provide a novel assessment of seasonal flux in patterns of bird movements across Europe, with potentially wide application to migration studies. Here, we present our analytical approach, our movement estimates, and discuss remaining challenges. One remaining challenge is that, even where ring-recovery pairs allow estimation of the proportion of birds moving between grid cells, variation in ringing effort or recovery effort can bias this estimate. We discuss ongoing work to resolve this issue, by using ringing totals and other data to quantify variation in ringing and recovery effort, and by informing the model with spatial abundance estimates.

16:21 Emmanuel **Adebija** Testing avian body size conformity to Bergmann’s and Allen’s rules along a latitudinal gradient in Nigeria

Testing avian body size conformity to Bergmann’s and Allen’s rules along a latitudinal gradient in Nigeria

Adebija, E.- A.P. Leventis Ornithological Research Institute, Jos, Nigeria
Chaskda, A.- A.P. Leventis Ornithological Research Institute, Department of Zoology University of Jos, Nigeria
Ivande, S.- Global Center for Species Survival, Indianapolis Zoo, USA
Nwaogu, C.-Fitzpatrick Institute of African Ornithology, South Africa

Two important eco-geographical rules that have attracted global attention over the years are Bergmann's and Allen's rules. Bergmann's rule posits that endotherms in colder environments should have a smaller surface area to volume ratio (and thus, larger) than those in warmer environments, while Allen's rule posits that the body appendages of species in warmer environments should be longer than those in colder environments. These rules have been proved and disproved many times due to inconsistencies in body size differences along latitudinal gradients. In this study, we tested whether body size variation in the Northern Red Bishop (*Euplectes franciscanus*) – a widespread species inhabiting different latitudes, conforms to Bergmann's and Allen's rules in Nigeria, West Africa. Nigeria provides a unique Afro-tropical environment where temperature and precipitation vary differently across locations. Using mist net trapping, I sampled 209 Northern Red Bishops in 11 locations across latitudes 70 to 120 N in Nigeria. I took wing length, bill length, tarsus length, and body mass measurements. Surface area to mass ratio (estimated as the product of wing length and tarsus length divided by body mass) was used as a relative measure of body size, and residual appendage size was obtained from the linear regression of body appendages against body mass while bioclimatic variables, elevation and food availability were used as predictor variables. Linear mixed effect model shows that variation in surface area to mass ratio and body appendages of Northern Red Bishop did not vary significantly across latitude except for appendage wing length that varied positively in females alone. Elevation was the only significant predictor of body size in our study and was only significant in females and did not conform to the pattern predicted by Bergmann's rule. Also, wing length significantly varied with predictor variables, whereas other body appendages did not. Our study suggests that Northern Red Bishop varies in their adaption to environmental pressure in males and females; also, we found that several environmental variables influence body morphology differently. Therefore, we recommend that to understand better how Bergmann's and Allen's rules affect species, detailed information on the species' life history to be studied is required. A comparative morphometric analysis and translocation experiment may also be required further validate this rule.

16:33 Christophe **Botella** A dynamic species distribution model fitted to heterogeneous occurrences explains a plant invasion trajectory

A dynamic species distribution model fitted to heterogeneous occurrences explains a plant invasion trajectory

Christophe Botella (1), Pierre Bonnet (2), Cang Hui (3,4), Alexis Joly (5), David M. Richardson (1,6)
1: Centre for Invasion Biology (CIB), Department of Botany & Zoology, Stellenbosch University, Stellenbosch 7602, South Africa
2: Botany and Modeling of Plant Architecture and Vegetation (AMAP), CIRAD, CNRS, INRAE, IRD, University of Montpellier, 34398 Montpellier, France
3: Centre for Invasion Biology, Department of Mathematical Sciences, Stellenbosch University, Stellenbosch 7602, South Africa;
4: Biodiversity Informatics Unit, African Institute for Mathematical Sciences, Cape Town 7945, South Africa;
5: Inria, LIRMM, University of Montpellier, France;
6: Department of Invasion Ecology, Institute of Botany, The Czech Academy of Sciences, 252 43 Průhonice, Czech Republic

Plant invasions generate massive ecological and economic costs worldwide. Predicting their spatial dynamics is crucial to the design of effective management strategies and the prevention of invasions. Earlier studies highlighted the crucial role of long-distance dispersal in explaining the speed of many invasions. In addition, invasion speed depends highly on the duration of its lag phase, which may depend on the scaling of fecundity with age, especially for woody plants, even though empirical proof is still rare. Spatially explicit dynamic population models can explicitely account for the roles of human-mediated long-distance dispersal and age-dependent fecundity in reconstructing the past invasion trajectory of woody plant. However, given the duration of lag phases and invasions in plants, standardised observational data covering the temporal and spatial scales required to fit dynamic models are rarely available. We developped a Bayesian dynamic species distribution model fitted to prense-only data from heterogeneous datasets using a state-space modeling approach. We use our model to explore the roles of long-distance dispersal and age-structured fecundity in the transient invasion dynamics of Plectranthus barbatus, a woody plant invader in South Africa. Our lattice-based model accounts for both short and human-mediated long-distance dispersal, as well as age-structured fecundity. We fitted our model on opportunistic occurrences, accounting for the spatio-temporal variations of the sampling effort and the variable detection rates across datasets. The Bayesian framework enables us to integrate a priori knowledge on demographic parameters and control identifiability issues. The model revealed a massive wave of spatial spread driven by humanmediated long-distance dispersal during the first decade and a subsequent drastic population growth, leading to a global equilibrium in the mid-1990s. Without long-distance dispersal, the maximum population would have been equivalent to 30% of the current equilibrium population. We further identified the reproductive maturity at three years old, which contributed to the lag phase before the final wave of population growth. Our results highlighted the importance of the early eradication of weedy horticultural alien plants around urban areas to hamper and delay the invasive spread.

16:45 Brandon **Edwards** Estimating landbird detectability from autonomous recording unit data

Estimating landbird detectability from autonomous recording unit data

Edwards, Brandon P.M. Department of Biology, Carleton University, Ottawa, Canada & Alberta Biodiversity Monitoring Institute, University of Alberta, Edmonton, Canada.
Knight, Elly C. Alberta Biodiversity Monitoring Institute, University of Alberta, Edmonton, Canada.
Docherty, Teegan D.S. Boreal Avian Modelling Project, University of Alberta, Edmonton, Canada.
Bennett, Joseph R. Department of Biology, Carleton University, Ottawa, Canada.
Smith, Adam C. Canadian Wildlife Service, Environment and Climate Change Canada, Ottawa, Canada.
Hedley, Richard W. Government of Alberta, Edmonton, Canada.
Bayne, Erin. Department of Biology, University of Alberta, Edmonton, Canada.

The NA-POPS project is an initiative to estimate detection probabilities for all landbird species in North America. These detection probabilities, which are the product of a bird's availability and perceptibility, can be used to integrate disparate datasets into a common standard, generate density and population estimates, or inform value of information analyses. The probabilities are estimated from human-conducted point counts via either removal sampling, distance sampling, or both. Autonomous recording units (ARUs) are increasingly used for acoustic monitoring of wildlife, especially in remote regions such as Canada's boreal forest, where human surveys are more expensive. Hundreds of thousands of ARUs deployed across Canada and have collected data on populations of hundreds of species of birds by conventional means. Recently, methods have been developed for analyzing ARU data to estimate the direction and distance to a singing bird by making use of localization techniques and sound pressure level curves from grids of ARUs. By estimating the distance to a bird based on the sound pressure of the bird song in an ARU recording, we can estimate perceptibility with distance sampling methods, while also recording time to first detection to estimate availability with removal sampling very accurately. This extra information makes it possible to integrate ARU data with human survey data into the NA-POPS project. Here, we develop and demonstrate the analytical methods to integrate ARU data with the traditional human surveys, using several example migratory bird species that breed in Canada's boreal forest. We evaluate key differences in estimates of availability and perceptibility obtained from traditional point counts and from ARUs. Finally, we provide potential research directions to further facilitate the integration of ARU and human point counts, and provide recommendations for further data collection using ARUs.

16:57 Gonçalo **Ferraz** Decline in avian detection more evident than secondary forest colonization in a 30-year old Amazon forest disturbance frontier

Decline in avian detection more evident than secondary forest colonization in a 30-year old Amazon forest disturbance frontier

Ferraz, G. Departamento de Ecologia, Universidade Federal do Rio Grande do Sul, Brazil.
Wood, F.O.S.S. Instituto de Biociências, Universidade Federal do Rio Grande do Sul, Brazil.
De Camargo, U. Mindhive Oy, Mikkeli, Finland.
Kéry, M. Swiss Ornithological Institute, Sempach, Switzerland.

When the large-scale field experiment of the Biological Dynamics of Forest Fragments Project was implemented in the central Brazilian Amazon, 43 years ago, thousands of hectares of old growth forest were cleared for cattle pasture, leaving a set of 1-, 10- and 100- ha forest islands in its midst, which were the focus of much subsequent research. The cleared area, surrounded by old-growth that still covers hundreds of kilometers to the north, east and west, was soon abandoned by ranchers giving place to an equal area of secondary forest that has been re-colonized by plants and animals from the adjacent old growth. We compared the bird fauna of old growth and secondary forest based on a 5-year acoustic sample of 151 sites, starting in 2010. One third of the sites were located in secondary forest with up to 30 years of age, while the remaining two thirds were in old growth. One of us processed the resulting 10,950 hours of audio recordings with an automated identification algorithm aimed at a set of 62 species which produced the most reliable identification models. Processing originated a matrix with the probability of each species vocalization being present in each recording minute. By imposing a 0.9 probability threshold for detection, we built a detection/non-detection matrix with information about all species and years, with replicate samples within the year for all sampled sites. In order to test the prediction that secondary forest was accumulating species while old growth was at an equilibrium state throughout the five years of our study, we built a multi-species occupancy dynamic model that was fit to detection data in a Bayesian framework. Our model treated species as random effects and made it possible to estimate species-specific as well as community-wide effects of time and habitat on colonization, persistence, occupancy, and detection probabilities. In agreement with previous observations, most species persisted in and colonized old growth sites with higher probability than secondary forest. Contrary to our prediction, however, we could not detect a temporal trend toward increasing occupancy, persistence, or colonization in the secondary growth. What we did find was a decline in detection probability, which was evident at the community level as well as for one third of the species. This decline may be the result of behavior or demographic changes motivated by recent environmental change across forest types.

Friday 21st April

09:15-09:45 Todd **Arnold** **Plenary:** Density dependence, individual heterogeneity, and demographic compensation: new approaches to age-old questions

Density dependence, individual heterogeneity, and demographic compensation: new approaches to age-old questions

Todd Arnold

Dr. Todd Arnold is a Morse Distinguished Teaching Professor in the Department of Fisheries, Wildlife and Conservation Biology at the University of Minnesota, USA. He received his Ph.D. in Zoology from Western University in Ontario, Canada, where he conducted dissertation research on the adaptive significance of clutch size in American coots. Current research interests focus on developing better methods of estimating population size of secretive wildlife, estimation of population vital rates such as nest success and annual survival, and development of integrated population models to better guide conservation activities.

Understanding the impacts of human harvest on population dynamics was a key motivation behind the development of modern tag-recovery models, and the general framework can be expanded to address any source of natural or anthropogenic mortality of interest. Mortality sources are considered additive if they lead to a net reduction in annual survival that cannot be ameliorated over the course of the annual cycle, or fully compensatory if the reduction is completely ameliorated through increases in natural survival. Compensation can also occur if harvest mortality falls disproportionately upon frail individuals that were less likely to survive anyway. Additive and compensatory mortality are reference points along a continuum, and methods to estimate partial compensation are sorely needed. I review previous analytical approaches and propose an alternative method that estimates annual survival as a function of harvest mortality. If harvest or other anthropogenic mortality sources are seasonally restricted, then models that allow annual mortality to be partitioned into seasonal hazard rates (rather than annual survival probabilities) further facilitates assessment of compensatory mechanisms, as do integrated population models (IPMs) that allow compensation to occur via other vital rates (e.g., fecundity or immigration). IPMs also facilitate direct assessment of density-dependent relationships that might promote demographic compensation. However, identifying demographic compensation is complicated by temporal and individual variation in vital rates, and I hope to inspire audience members to help address many of the remaining important questions.

Management and conservation I

10:00 - 10:48

Amphithéâtre Délégation CNRS

10:00	Stephen **Gregory**	Power analysis for real-World sampling strategies

Power analysis for real-World sampling strategies

Stephen Gregory^ & Jon Barry^^
^ Centre for Environment, Fisheries and Aquaculture Science, Weymouth; University of Bournemouth, Bournemouth
^^ Centre for Environment, Fisheries and Aquaculture Science, Lowestoft

Power analysis is used to estimate the probability of detecting change, such as a decline, in a target variable, such as a marine invertebrate population, in response to a planned disturbance, such as an offshore wind farm development. The use of power analysis is increasingly common, but in most cases, these uses are restricted to simple sampling strategies, such as those assuming that samples are collected prior to the planning and are spatially-independently. For a variety of reasons, including logistical and financial constraints, many sampling strategies are rarely so simple. A power analysis that ignores these additional complexities will violate the underlying statistical models and yield biased results. In this paper we present updates to R package emon that extends basic power analysis to better account for complex sampling strategies. The updates are numerous and include procedures to: help choose a statistical distribution for your data, including assuming no fixed distribution, accounting for spatial non-independence in samples, and using data from existing samples. To deliver these procedures, emon now uses procedures, such as vectorisation and parallelisation, to maximise computational efficiency and minimise run time. In addition to these updates, we have substantially improved and extended the emon documentation, including tools to encourage reproducibility and repeatability in power analysis reporting among emon users, such as offshore wind farm developers.

10:12	Michael **Schaub**	Lessons to be learned by comparing fisheries stock assessment methods (SAMs) with integrated population models (IPMs)

Lessons to be learned by comparing fisheries stock assessment methods (SAMs) with integrated population models (IPMs)

Michael Schaub[1], Mark N. Maunder[2], Marc Kéry[1], Eiren K. Jacobson[3], James T. Thorson[4], André E. Punt[5]
[1] Swiss Ornithological Institute, Sempach, Switzerland
[2] Inter-American Tropical Tuna Commission/Center for the Advancement of Population Assessment Methodology, USA
[3] Centre for Research into Ecological and Environmental Monitoring School of Mathematics and Statistics University of St Andrews, UK
[4] Habitat and Ecosystem Process Research program, Alaska Fisheries Science Center, National Marine Fisheries Service, NOAA, Seattle, WA, USA
[5] School of Aquatic and Fishery Sciences, Box 355072, University of Washington, USA

Stock Assessment Methods (SAMs) and Integrated Population Models (IPMs) are respectively applied in aquatic and terrestrial systems to estimate abundance and demographic rates in a population of interest. The approaches are fundamentally very similar, but they tend to be used to address different goals with different sources of data. SAMs are typically applied to assess levels of sustainable exploitation, while IPMs are used to study population dynamics or to inform conservation. The most common data sources for SAMs are harvest data (volume and stage/size structure) while IPMs make extensive use of individual longitudinal data. The two approaches have historically been considered as separate disciplines, resulting in a loss of shared visions, practices and progress. We review them to identify common elements and differences, with a view to identifying key lessons that would benefit population ecology more generally. Our premise is that the same statistical methods for parameter estimation, model validation, diagnostics, decision analysis and forecasting (including population viability analysis) should be used irrespective of whether the application is aquatic or terrestrial, or the goal is exploitation or conservation.

10:24 Benjamin **Debetencourt** Estimating chimpanzee demography, social structure and territory range with camera trap data in Moyen Bafing National Park, Guinea

Estimating chimpanzee demography, social structure and territory range with camera trap data in Moyen Bafing National Park, Guinea

Debetencourt, B. Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany
Boesch, C. Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany

Precise estimates of population dynamics are required for effective conservation of wild animal populations. It is especially difficult to obtain such precise estimates using traditional, large-scale methods on threatened species—such as non-human great apes—that have slow reproductive rates, and thus muted short-term variation in population density and structure. To gain a better understanding of demography in these populations, previous research has typically undertaken a long and slow process of habituation. While habituation may allow researchers to produce fine-grained data on a population's demography, such research can be prohibitively slow, and may have important impacts on the studied population. Recently, researchers have begun to collect camera trap data to study wild animal populations in an efficient and non-invasive way. Here, we collected camera trap data continuously over a year-long period to monitor an unhabituated population of critically endangered West African chimpanzees (Pan troglodytes verus) in Moyen Bafing National Park, Guinea. To collect this data, we used an array of 100 camera traps that were opportunistically placed to increase the probability of capture in a 100 km2 area. We identified 228 individuals occupying the area through their unique facial features. Our camera trap data make clear that these individuals belong to 6 closed communities—4 communities seem to be near-completely sampled, while 2 communities were peripheral to our sampled area and therefore few individuals were captured. Through estimation of minimum convex polygons on the sample space, we were able to describe the minimum home range for the main communities. Using spatially explicit capture-recapture models, we find that population density is high, with 1.69 individuals per km2 (1.46-1.96), making the Moyen Bafing region a critical territory for West African chimpanzee conservation. Compared to other chimpanzee communities living in a similar environment (mosaic forest), we also demonstrated that the Bafing population has small territories for their community size. Alongside this, we described in detail the demographic composition of the main communities that we have identified, and use Bayesian social network analysis to understand population structure. Predictions from our network analyses suggest that the social bonds within our populations were structured by sex homophily, with male chimpanzees being more likely to be captured together. Our research showcases the potential of camera traps for studying the demographic composition of chimpanzee populations with precision without the drawbacks inherent to habituation. We continue to monitor these populations using a subset of the 100 cameras used in this study, providing us with a potential first estimate of vital rates for the Bafing population.

10:36 Liam **Bailey** Monitoring changes in carrying capacity through time to assess conservation outcomes in a large social carnivore

Monitoring changes in carrying capacity through time to assess conservation outcomes in a large social carnivore

Bailey, L.D.1,2, Höner, O.P.2, Courtiol, A.1
Department of Evolutionary Genetics, Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany
Department of Evolutionary Ecology, Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany

Increasing population abundance is often the primary goal of conservation management. However, without quantifying changes in environmental conditions it can be difficult to accurately identify cases of conservation success. Population growth is possible under improving, static, or even declining environmental conditions. If we want to identify successful conservation outcomes, we need to measure both changes in population abundance as well as the underlying environmental conditions that may be responsible for population abundance trends.

Carrying capacity is a useful single metric that can be used to assess environmental conditions, incorporating the effects of multiple environmental variables relevant for a target population. By relaxing the classical assumption of static carrying capacity and allowing carrying capacity to vary over time, we have the potential to quantify changing environmental conditions in conjunction with changes in population abundance.

In this study, we use an individual-based model to quantify carrying capacity through time in a large social carnivore that has experienced recent population growth, the spotted hyena (*Crocuta crocuta*). Our study site has been the target of conservation actions over the past two decades; however, it is unclear whether these actions can explain observed recovery. We use 26 years of detailed demographic data of uniquely identifiable individuals to build robust vital rate models that parameterise our individual-based model. We use our method to understand how carrying capacity of spotted hyenas has changed over time and how this can explain observed population growth.

Carrying capacity of hyenas showed large inter-annual variation, likely due to outbreaks of disease. However, we found no evidence of positive or negative trends in carrying capacity, indicating that environmental conditions have remained relatively stable over time. Similarly, we observed no improvement in survival and reproduction. We conclude that population growth in our study area is likely a result of historical improvements in environmental conditions before the start of the project, rather than evidence of more recent conservation success. The discrepancy between trends in population abundance and carrying capacity is likely the result of demographic lag, which will be more likely in long-lived species, like hyenas.

Using time-varying carrying capacity as a measure of environmental conditions provided key insights into our population that could not be obtained by observing trends in population abundance alone. Monitoring environmental conditions in conjunction with population abundance will be key to more accurately identify successful conservation outcomes and understand the drivers of success. Such an approach will contribute towards the goal of evidence-based conservation.

Management and conservation II

11:15 – 12:03 *Amphithéâtre Délégation CNRS*

11:15 Kylee **Dunham** Design and evaluation of long-term monitoring programs to inform annual life cycle modeling, conservation, and adaptive harvest management of migratory waterfowl in North America

Design and evaluation of long-term monitoring programs to inform annual life cycle modeling, conservation, and adaptive harvest management of migratory waterfowl in North America

Kylee D. Dunham, Eastern Ecological Science Center, U.S. Geological Survey
J. Andrew Royle, Eastern Ecological Science Center, U.S. Geological Survey
James E. Lyons, Eastern Ecological Science Center, U.S. Geological Survey
Patrick K. Devers, Division of Migratory Bird Management, U.S. Fish and Wildlife Service

Much of our current understanding of migratory bird ecology and successful management is based on capturing and releasing birds with bands (i.e., rings) and subsequent re-encounters with the marked individuals through live recaptures, resights, or dead recoveries. Banding, or ringing, has been a critical component of waterfowl conservation and management in North America. However, the amount of data collected per marked bird can be low in space and time due to low encounter rates resulting in poor parameter estimation and potentially inefficient monitoring efforts. Recent advancements in wildlife marking technology, crowdsourcing, citizen science platforms, and analytical methods offer new opportunities to advance migratory bird conservation and management. We reviewed the current waterfowl banding programs used to inform the adaptive harvest management plan and explored alternative marking technologies (i.e., Motus tags) and their potential for supplementing the current monitoring programs. We measured the utility of alternative marking technologies and analytical methods using structured decision-making principles considering the financial costs, logistical challenges, and the number of additional parameters (i.e., migration phenology) that could be estimated for combinations of marking technologies, study design, and analytical method. We evaluated the performance, benefits, and costs of alternative monitoring programs and provide recommendations on future funding needs and allocation to support and advance the North American waterfowl adaptive harvest management plan.

11:27	Chris **Sutherland**	Opposite effects of global and local density-dependent dispersal on metapopulation stability and persistence

Opposite effects of global and local density-dependent dispersal on metapopulation stability and persistence

Sutherland, C. University of St Andrews, St Andrews, Scotland
Elston, D. Biomathematics and Statistics Scotland, Aberdeen, Scotland
Lambin, X. University of Aberdeen, Aberdeen, Scotland

In this work, we integratively progress two fundamental issues in spatial population ecology using a Bayesian implementation of a demographically informed spatial occupancy model. First, we quantify spatiotemporal variability in effective dispersal as an emergent multi-scale combination of density-dependent emigration at the scale of local source populations and density dependent immigration at the metapopulation scale. We then build upon established theoretical work to describe the implications of such dual-scale dependency on the dynamics and long-term persistence of a dispersal-driven spatially structured population that functions as a classic metapopulation.

11:39	Eva **Conquet**	Effects of season-density interactions on the vital rates of an African lion population

Effects of season-density interactions on the vital rates of an African lion population

Conquet, Eva. Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, Switzerland.
Paniw, Maria. Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, Switzerland; Department of Conservation and Global Change, Doñana Biological Station (EBD-CSIC), Seville, Spain.
Borrego, Natalia. Department of Ecology, Evolution, and Behavior, University of Minnesota, Saint Paul MN, USA; Department for the Ecology of Animal Societies, Max Planck Institute of Animal Behavior, Konstanz, Germany.
Nater, Chloé. R. Centre for Biodiversity Dynamics, Norwegian University of Science and Technology NTNU, Trondheim, Norway; The Norwegian Institute for Nature Research (NINA), Trondheim, Norway.
Cozzi, Gabriele. Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, Switzerland.
Packer, Craig. Department of Ecology, Evolution, and Behavior, University of Minnesota, Saint Paul MN, USA.
OzguL, Arpat. Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, Switzerland.

Environment-density interactions have important effects on vital rates and population dynamics. Additionally, in social species, the effects of density can be strongly influenced by sociality. For example, vital rates can show various responses to density depending on whether density is measured at the level of social groups or the population. Vital-rate responses to density measures can also differ depending on social status. The demography of the African lion (Panthera leo), a social species, is largely shaped by sociality. However, studies assessing density dependence in lion populations have thus far focused on assessing the response of vital rates to single measures of density, without accounting for the effects of multiple measures of density taken at different levels of social organization. Moreover, studies have seldom investigated lion vital-rate responses to interactions between the environment and different measures of density. This is despite the strong seasonality in environmental conditions and prey availability experienced by our study lion population in the Serengeti National Park (SNP), Tanzania. To fill this knowledge gap, we aimed to understand how a socially-explicit consideration of density and its interaction with environmental seasonality affect vital rates in a population of lions in the SNP. Using 30 years of capture-recapture data on 1347 lions and dead recovery data on 101 of these individuals, we estimated lion survival and between-stage transition rates using a Bayesian multistate capture-recapture model to account for imperfect detection. To fit this model, we used a NIMBLE custom likelihood function based on the structure of the lion life cycle, allowing us to decrease the computational load of our model. In addition, we used Bayesian GLMMs to estimate reproduction probability and litter size. Using these models, we tested for various season-specific effects of intra- and extra-group density measures and of habitat type (grassland or woodland). Effects of both intra- and extra-group measures of density were prevalent in our lion population and showed seasonal patterns for key vital rates. For example, resident-male survival increased more strongly with coalition size in the dry season compared to the wet season. Moreover, adult-female abundance affected old-subadult survival slightly negatively in the dry season, but positively in the wet season. We also found seasonal differences in habitat effects, with survival decreasing in the woodland in the wet season for most life-history stages. Overall, our results highlight the importance of accounting for environmentdensity interactions as well as a socially explicit consideration of density when assessing the effects of density dependence on vital rates. A better understanding of such complex effects of density on vital rates could help improve the accuracy of population projections, possibly benefitting populations of social species beyond the Serengeti lion.

Multi-species population indices for sets of species that include disappearing or newly occurring species

Fränzi Korner, Nicolas Strebel (presenting), Thomas Sattler
Swiss Ornithological Institute, Sempach, Switzerland

Multi-species indices (MSI) summarize the relative population size development of a group of species over time. Species-wise relative population sizes are condensed to one single value per time unit. The resulting simplified information on population development are widely used to inform environmental policies. Many of the currently used MSIs are based on the geometric mean. One desired property of the geometric mean in the context of MSIs is that positive and negative relative changes are weighted equally. The Achilles' heel of such MSIs is that the geometric mean is not defined if the population of at least one species is zero. One common workaround is therefore to base MSIs on a selection of common species only whose populations never drop to zero. By default, this leads to species selections that are biased in terms of rarity. Another workaround is to truncate small population sizes or replace population sizes of zero by small non-zero values for MSI calculation. However, such workarounds exhibit an arbitrary influence on the geometric mean MSI. Disappearance or emergence of species is a natural process whose probability increases with longer time series. To summarize the population development of a group of species, a method is needed that can cope with zero values and that is not based on arbitrary decisions like replacing zeros by some small values.

The compound Poisson and the negative binomial model can be used for that purpose. They allow obtaining an MSI that have similar features as the geometric mean, including weighting halving and doubling of a species' population equally. These two statistical models can handle zero values in population sizes and thus accommodate newly occurring and temporarily or permanently disappearing species. We compare different aspects of the two statistical models with the geometric mean for MSI calculation using simulated and real-world data. Also, we seek to appropriately include different sources of uncertainty in MSI calculation.

The negative binomial model relies on annual absolute population sizes, while the compound Poisson model and the geometric mean can be calculated based on relative population sizes. The MSI resulting from the compound Poisson model is influenced more than the other two methods by trends of species showing a low interannual variance, thus downweighing species with strong year-to-year changes. The negative binomial MSI is less sensitive to trends in rare species compared with the other two methods, and similarly sensitive to trends in abundant species as the geometric mean. While the two new MSIs have the advantage that they are not arbitrarily influenced by newly appearing and disappearing species, both do not weight all species equally.

Our recommendation is to replace the geometric mean MSI with either compound Poisson or negative binomial MSI in cases where some of the considered species have a population size of zero in some years. Further, we recommend providing additional information alongside the MSIs, e.g., by indicating the number of disappearing and newly occurring species in addition to the MSI.

Workshops

13:30 – 17:30

Animal Movement Modeling 13:30 – 17:30

Animal Movement Modeling

Mevin Hooten, Devin Johnson, Brett McClintock, Juan Morales

The study of animal movement has always been a key element in ecological science because it is inherently linked to critical processes that scale from individuals to populations and communities to ecosystems. Rapid improvements in biotelemetry data collection and processing technology have given rise to a variety of statistical methods for characterizing animal movement. This workshop provides an overview of the types of statistical models used to study individual-based animal movement based on telemetry data. This workshop on animal movement modeling is intended for wildlife biologists, quantitative ecologists, and statisticians who seek a deeper understanding of modern animal movement models. In the workshop, we present a wide variety of modeling approaches using a consistent notation. We organize the models into groups based on how they treat the underlying spatio-temporal process of movement. The primary groups of models covered are: point process models, discrete-time models, and continuous-time models. We also highlight connections among approaches to facilitate a broader view of animal movement analysis and its associations with traditional spatial and temporal statistical modeling. The workshop will draw on examples and material from the recent textbook: Hooten, M.B., D.S. Johnson, B.T. McClintock, and J.M. Morales. (2017). Animal Movement: Statistical Models for Telemetry Data. Chapman and Hall/CRC.

Integrated Models in Population Ecology + Species Distribution Modeling 13:30 – 17:30

Integrated Models in Population Ecology + Species Distribution Modeling

Marc Kéry, Michael Schaub, Nicolas Strebel

Data integration has been one of the dominant trends in ecological statistics during the last 30 years. By data integration we mean the use of different data types that are informative about the same underlying process in the form of a joint likelihood. Such data integration in an integrated model (IM) makes very much sense ("use all the available information in an estimation task"), typically leads to more precise parameter estimates, and sometimes lets one estimate a parameter that is not estimable from each data set alone. Among the audience of the EURING analytical meetings, integrated population models (IPMs) may be the best-known instance of an IM, but exactly the same data integration principles apply also for a large number of IMs that have been described in the species distribution modeling (SDM) field, e.g., for occupancy and N-mixture models. We present the principles of data integration that underlie all IMs and then provide illustrations from the SDM and IPM fields using JAGS. Participants will walk away with a good understanding of what IMs are, pointers to further resources, why we build IMs and how, and with a stock of sample R and JAGS code for some typical IMs that they may adapt for their own projects.

An Introduction to Close-Kin Mark-Recapture 13:30 – 17:30

An Introduction to Close-Kin Mark-Recapture

Paul Conn

Close-kin mark-recapture (CKMR) is a recently developed approach for estimating abundance and life history parameters (e.g., adult survival, recruitment schedules) from genetic samples. Unlike traditional mark-recapture estimators (including non-invasive approaches that use genetics to individually identify animals), CKMR does not require that animals be released or recaptured after marking. It thus seems like a potential holy grail for fish and wildlife agencies, in the sense that CKMR models can be fitted directly to data from angler or hunter harvest samples. In this workshop, I introduce CKMR to a statistical audience familiar with capture-recapture models, but perhaps not with genetic data or CKMR models. I emphasize overall concepts, underlying assumptions, and the types of models that can be fitted to kinship data. I will also muse a little bit about applying CKMR to bird populations, which to my knowledge has not been attempted yet. Modeling will be illustrated in R and in Template Model Builder (TMB).