



ABSTRACTS USER STORIES

LifeWatch.be Users & Stakeholders Meeting

Day 1 – Thursday January 25th 2018

Catrein: towards a cameratrap research infrastructure

Jim Casaer¹, Jolien Wevers², Natalie Beenaerts², Stijn Van Hoey³, Peter Desmet³ & Tanja Milotic³

¹ Research Institute for Nature and Forest (INBO)

² Centre for Environmental Sciences – Hasselt University (UHasselt)

³ LifeWatch team

In recent years, the use of camera traps has become increasingly popular for monitoring wildlife behaviour, abundance and community structure. Camera traps allow for continuous non-invasive monitoring of species communities, without disturbing the animals. Compared to other monitoring methods, they require minimal staff input, and recent quality improvements have made camera traps reliable research instruments. Nonetheless, not only do camera traps generate large quantities of pictures, one also has to identify species as well as number of individuals on those pictures. In order to allow both long-term biodiversity monitoring and local research projects, data sharing is a prerequisite. Therefore, data collection, storage and metadata processing have to be standardized and well documented.

The project aims at providing the hardware (a set of high quality camera traps that can be used in different projects), in combination with a platform that allows the project management, as well as annotation of camera trap images. Furthermore, a data pipeline will be developed to publish camera trap images as open data and provide archiving of the data.

The presentation will consist of two parts. In the first part we will present the current use of camera traps for wildlife monitoring, its advantages and limitations, the LifeWatch camera hardware, the use of the selected platform, the first projects using the infrastructure and future plans. In the second part we will present the application of the research infrastructure in the largest (long-term) current project which is studying the space use of wild boar in National Park Hoge Kempen.

DNA Barcoding for Forensics

Stijn Desmyter¹

¹ National Institute for Forensics (NICC)

The Belgian National Institute for Forensics (NICC) and BOPCO are running a long-term collaboration on DNA barcoding for forensic entomology. Necrophagous insects play an essential role in the accurate estimation of the post mortem interval of deceased persons. Unequivocal species identification of flies and beetles is crucial for case work interpretation. Multiple projects were started to develop the molecular identification of insects with forensic interest. Protocols and reference databases were established for forensically important diptera and coleoptera species of which identification is very difficult and requires strong taxonomic expertise. The COI gene as a molecular diagnostic tool for species identification was evaluated for Sarcophagidae (diptera) and Staphylinidae (coleoptera).

Besides data basing reference sequences, also more particular issues in DNA barcoding of forensic entomology are tackled. In order to overcome the failure of the barcoding standard COI gene to discriminate between two forensically important close-related blowfly species (*Lucilia caesar* and *L. illustris*), a broad spectrum of nuclear and mitochondrial DNA markers was evaluated. Besides, the observed intercontinental divergence between the COI gene sequences of the North American and West European blow fly species *Phormia regina* was further studied on other mitochondrial and nuclear markers in relationship to their morphological characteristics.

The collaboration between both institutes resulted also in a study of dog mitochondrial DNA. Dogs are very popular pets and as such, they often could act as “silent witnesses” in forensic casework. Dog hair found on a crime scene may provide a link between victims and suspects. The project studied the genome variation and frequencies in the Belgian dog population, with reference to former studies. Due to the outcome of this study, the practice of dog hairs in forensic case work has been made possible.

Detection and identification of mosquito species (Culicidae) in Belgium

Wim Van Bortel¹

¹ Institute of Tropical Medicine (ITM)

Mosquitoes and mosquito-borne diseases pose an increasing threat to animal and human health in temperate regions. Important drivers for the introduction and spread of exotic mosquito species are the significant increase in international trade and tourism, along climatic and ecological changes. Acquiring knowledge of the occurrence of both endemic and exotic mosquito species is an essential step towards understanding the potential risk of mosquito-borne diseases in Belgium. A critical step in this process is the correct identification of the collected mosquito species which can be done using morphological and molecular criteria.

In the framework of the MODIRISK project, “Mosquito vectors of disease: spatial biodiversity, drivers of change, and risk” financed by the Belgian Science Policy (2007-2010), the use of DNA barcoding for Belgian mosquitoes (Diptera: Culicidae) was assessed. Overall, the study showed that DNA barcoding offers a

reliable framework for mosquito species identification in Belgium except for some closely related species. This study was done in collaboration with the Joint Experimental Molecular Unit (JEMU) of the Royal Belgian Institute of Natural Sciences (RBINS) and the Royal Museum for Central Africa (RMCA).

In the context of the MEMO project, “Monitoring of exotic mosquitoes in Belgium” funded by Belgian federal authorities and federated entities (2017-2020), the Barcoding facility for Organisms and tissues of Policy COncern (BopCo project - the Belgian federal in-kind contribution to LifeWatch), collaborates with the Institute of Tropical Medicine to validate the morphological identification of mosquitoes using DNA-based methods. A workflow for the molecular identification of the Belgian mosquito species has been developed for this purpose.

Both examples show the importance of the detection and the reliable and rapid DNA-based identification of mosquito species in Belgium.

Saigas on the brink: multi-disciplinary analysis of the factors influencing mass mortality events

Sarah Robinson¹ (for Kock et al.)

¹ Imperial College London

In 2015 more than 200,000 saiga antelopes died at calving aggregations over a period of three weeks in Central Kazakhstan. The proximate cause of death is confirmed as haemorrhagic septicaemia caused by the bacterium *Pasteurella multocida* type B. This organism, which is a commensal living in the respiratory tract, may have been triggered to virulence by environmental factors. We investigated the influence of such factors on the probability of a mass mortality event at saiga calving sites, using cases from 2015 (and two other years in which these events have occurred) and controls from unaffected calving aggregations over a 30-year period. The predictor variables used were generated from a suite of gridded climatic datasets and from vegetation and snow anomaly data provided by the LifeWatch LW-WB webGIS project. Our results suggest that there was unusually high relative humidity and temperature in the days leading up to the mortality event; temperature and humidity anomalies were also observed in the two previous similar events in the same region. The modelled influence of environmental covariates is consistent with known drivers of haemorrhagic septicaemia.

The LifeWatch data indicated that spring greenup was unusually late in 2015 but not at all mortality sites, and that such patterns were not observed during other recorded mortality events. These data helped to eliminate alternative hypotheses concerning triggers linked to nutrition and vegetation phenology. Given the saiga population’s vulnerability to mass mortality and the likely exacerbation of climate-related and environmental stressors in future, management of risks to population viability such as poaching and viral livestock disease is urgently needed, as well as robust ongoing veterinary surveillance. A multidisciplinary approach is needed to research mass mortality events under rapid environmental change.

The use of ecotopes for the biodiversity conservation: the case of Violet Copper (*Lycaena helle*)

Jessica Delangre¹

¹ Ardenne et Gaume ASBL

In this study, the ecotope database developed by the Lifewatch-WB project was used to design a conservation plan for the violet copper (*Lycaena helle*). A map of habitat quality was generated by a species distribution model (GAM), and combined with connectivity constraints to identify priority areas for the violet copper conservation. In a preliminary test, the sensitivity of spatial conservation prioritization output to connectivity parameterization was assessed in a subset of the study area (the Amblève basin). The proposed priority areas varied according to the types of connectivity included in the analysis. This highlights the importance of the ecological model underlying the spatial prioritization process. For this species, matrix connectivity was the most efficient way of accounting for connectivity while still focusing conservation efforts in areas of intermediate to high habitat quality. This method was thus applied to prioritize agri-environment schemes over the whole distribution range of *Lycaena helle* in Wallonia.

ANTABIS: feedback and perspectives from a long-term user

Huw Griffiths¹

¹ British Antarctic Survey (BAS)

ANTABIS consists of a network of interconnected initiatives building on recent biodiversity informatics technologies. The network includes websites, servers, but also people, organisations, and various stakeholder benefiting from free and open access to primary data, code, and information. This presentation will give an overview of the existing components of the network and unveil potential, long-term projects.

EMODnet Biology as a user of the LifeWatch infrastructure

Simon Claus¹

¹ Flanders Marine Institute (VLIZ)

The EMODnet biology data portal provides free access to data on temporal and spatial distribution of marine species and species traits from all European regional seas. EMODnet Biology is part of the EU funded European Marine Observation and uses different components developed under the LifeWatch taxonomic Backbone such as the World Register of Marine Species and the European Ocean Biogeographic Information System. EMODnet biology collaborates closely with regional sea commissions, transatlantic partnerships, industry, conservation and management organisations to steer the development of key biological data products.

Day 2 – Friday January 26th 2018

Towards a qualitative spatial sensor network for long-term observation of harbour porpoises

Elisabeth Debusschere¹, Bob Rumes², Jolien Goossens¹, Jan Reubens¹ & Klaas Deneudt¹

¹ Flanders Marine Institute (VLIZ)

² Royal Belgian Institute of Natural Sciences (RBINS)

Harbour porpoises (*Phocoena phocoena*) are the most common marine mammal in the Belgian part of the North Sea (BPNS), and are protected by both national and EU law. Echolocation is their tool for navigation and foraging within their habitat, and their echolocation clicks can be recorded by hydrophones. In 2015, the Belgian LifeWatch observatory (as part of Flanders contribution to the LifeWatch European Research Infrastructure) started with the passive acoustic monitoring of harbour porpoises using C-PODs (Chelonia). The aim is to set-up a long-term monitoring of harbour porpoises in the BPNS in order to gain knowledge on their spatial and temporal distribution across the BPNS.

Creating a qualitative spatial sensor network is a learning process in terms of equipment, mooring type, locations, sound analysis, etc. Having long-term funding is a major advantage which allows evaluation and optimization of the design. Key in this process are discussions with peers and in-depth data analysis. Therefore, a three-day workshop was organized in October 2017, bringing together a community of C-POD users, statisticians, students and other scientists. Two main issues were identified: noise of the mooring chain was reducing the quality of the recorded echolocation and the northwest of the BPNS was a blind spot in the spatial network.

Acting upon these issues, a successful test with an acoustic release bottom mooring frame was conducted and in the near future, all surface moorings will be replaced by acoustic release frames installed on the bottom. Secondly, an extra station will be added to the spatial sensor network in the NW region of the BPNS. Furthermore, to complete the spatial sensor network covering both shallow and deep stations, a collaboration with OD nature was set up which will add a shallow station for the long-term monitoring.

This exercise was extremely useful and will be repeated in two years. Having a qualitative spatial network will allow us to better address a number of policy-related research questions and promotes scientific collaboration.

Is this for (r)eel? Permanent fish tracking in Flanders with acoustic telemetry

Ine Pauwels¹

¹ Research Institute for Nature and Forest (INBO)

As part of the Flemish contribution to LifeWatch, a permanent acoustic receiver network for fish tracking has been established in the Belgian Part of the North Sea (BPNS), the Scheldt Estuary, and several rivers and canals in Belgium.

The network (<http://lifewatch.be/en/fish-acoustic-receiver-network>) is a cooperation between the Flanders Marine Institute (VLIZ), the Research Institute for Nature and Forest (INBO), and the Ghent University Marine Biology Research Group (UGent – MARBIOL), and currently consists of 190 receivers, allowing the study of the movements and habitat use of marine, freshwater and diadromous fish.

Since 2010, data have been collected of 13 species, specifically 4 marine species (Atlantic cod *Gadus morhua*, common dab *Limanda limanda*, European plaice *Pleuronectes platessa*, lemon sole *Microstomus kitt*), 3 freshwater species (chub *Squalius cephalus*, common carp *Cyprinus carpio*, wels catfish *Silurus glanis*) and 6 diadromous species (Atlantic salmon *Salmo salar*, European eel *Anguilla anguilla*, European flounder *Platichthys flesus*, river lamprey *Lampetra fluviatilis*, sea lamprey *Petromyzon marinus*, Twaite shad *Alosa fallax*). The receivers in the BPNS allowed the first observation of southward migrating silver eels in the North Sea. These eels were tagged with acoustic transmitters in three river catchments in Western Europe (Belgium, Germany and The Netherlands) and passed the Dutch–Belgian coast during spawning migration (Huisman et al. 2016).

This and other interesting acoustic network results indicate the importance and benefits of permanently tracking individual fish at multiple spatial scales. In this presentation we present the state of the art and unfold the future perspectives of the LifeWatch acoustic fish tracking network in Flanders.

GPS-tracking migration and foraging movements of Western Marsh Harrier *Circus aeruginosus* breeding in the Low Countries

Wouter Vansteelant¹

¹ Montagu's Harrier Foundation

A substantial part of the Western Marsh Harrier *Circus aeruginosus* population in Flanders (150 pairs) and the Netherlands (1200-1500 pairs) breeds in agricultural landscapes. And while this species is of conservation concern (Annex 1 EU Birds Directive), we do not know what are the main bottlenecks in the annual cycle of this migratory species, nor do we know how they use agricultural landscapes for breeding and foraging. To address these knowledge gaps, researchers started tracking Marsh Harriers with GPS-loggers in 2012 and 2013 respectively (www.uva-bits.nl).

All harriers tracked for at least one year migrated to relatively wet areas in the savannahs of West Africa, moving between multiple wintering sites at repeatable times across multiple years. Migration appeared

to be much more challenging in spring, with nearly all birds engaging in long stop-overs before and after the desert crossing, travelling a longer westward route over the Sahara (often tracking the Atlantic coast) which in turn caused a stronger convergence of harriers at Gibraltar in spring than in autumn. We discuss the causes and consequences of the challenging spring migration using additional tracking data from Swedish Marsh Harriers. We also highlight the importance of West-African and North-African stop-over and wintering sites for flyway-scale conservation of this species.

Research into foraging strategies at the breeding grounds is still ongoing. In this presentation we will introduce working hypotheses on how (semi-)natural habitat types, crop types and land use activities (e.g. harvest) may affect prey availability for Marsh Harriers in Flemish and Dutch agricultural landscapes. And we will explore how landscape configuration may then generate contrasting movement patterns between Flemish and Dutch agricultural landscapes.

From GPS data to daily decisions in 2 sympatric gull species

Jan Baert^{1,2}

¹ Terrestrial Ecology Unit (TEREC) – Ghent University (UGent)

² Antwerp University (UA)

Larus gulls are puzzling scientists and policy makers alike. Their high degree of behaviour plasticity allows them to thrive in urbanised areas. Still, individuals appear to be highly specialised in where they go and what food sources they prefer. But how do individuals develop this specialisation over time, how do they adapt to changes in food sources by human activities, and what are the costs and benefits of an individual's decisions throughout its entire lifetime?

Since 2013, 127 Lesser Black-backed Gulls (*Larus fuscus*) and 48 Herring Gulls (*Larus argentatus*) breeding in the port areas of Ostend, Zeebrugge and Vlissingen have been fitted with UvA-BiTS GPS-trackers. At present, this unique long-term dataset is used in 3 MSc, 4 PhD and one postdoctoral projects to study daily decisions in various stages of the life cycle such as the negotiation in parental investments within pairs, changes in daily foraging decisions or the selection of wintering areas.

The high spatio-temporal resolution of the obtained data has thereby not only allowed us to identify where these gulls forage, but also estimate costs associated with daily foraging decisions. This is essential for understanding the currency at which pairs negotiated their parental investment, how individuals change their foraging decisions over time, and how the costs of long-distance migration can be offset by foraging in favourable environments. This detailed understanding of daily decisions does not only address several key questions within movement and behaviour ecology, but also provides data to support policy makers in managing gull populations along the Belgian coast.

Long-term monitoring of Climate change effects on short vegetation

Tom De Dobbelaer¹

¹ Research Institute for Nature and Forest (INBO)

In 2017, the INBO (Research Institute for Nature and Forest) started to expand its long-term monitoring research to open vegetation types in Natura2000 sites with the co-funding of the Flemish LifeWatch project.

The goal of this project is to get a better understanding of climate change effects in a broad range of open vegetation types, by collecting biotic and abiotic data according to the Ecosystem Integrity principles.

Five sites within the European Long-Term Ecological Research (LTER) network (<http://www.lter-europe.net/>) were selected and will be equipped with weather stations, groundwater level sensors and soil moisture/temperature sensors by the end of 2018. Automated data logging and transmission are used to minimize manual intervention and disturbance of the sites and make data collection in inaccessible areas possible. The project will collaborate with other networks as LifeWatch groundwater monitoring network (using automatic GPRS loggers), ICP-Forests, ICOS an LTER to maximize data exchange and provisioning.

Building and using the MarineSPEED benchmark dataset

Samuel Bosch¹

¹ UNESCO/IOC Project Office for IODE, Ocean Biogeographic Information System (OBIS)

We present here MarineSPEED, a benchmark dataset for marine species distribution modelling. Using this dataset, we showed that while temperature is a relevant predictor of global marine species distributions, considerable variation in predictor relevance is linked to the species distribution modelling (SDM) set-up. This benchmark dataset (MarineSPEED) was created by combining records from OBIS and GBIF with environmental data from Bio-ORACLE and MARSPEC and taxonomic information from WoRMS. Predictor relevance was analysed under different variations of SDMs for all combinations of predictors from eight correlation groups.

Linking occurrences, traits and the environment to map the diversity of marine life

Tom Webb¹

¹ University of Sheffield

Significant openly available datasets on the occurrences, taxonomy, and biology of marine organisms, and the environment they live in, makes it possible for anyone to explore marine biodiversity at an unprecedented scale using open source tools. Although these databases are immensely valuable by themselves, by linking them together and enriching them with data from other sources we can gain major new insights into how marine diversity is distributed in space, how it changes through time, and how it responds to a range of human pressures. In this talk I will demonstrate the potential of matching data on the occurrence, biological traits, and physical environment of marine species using newly developed open source tools.