

# Abstracts: Oral Presentations

## Eighth International Hole-Nesting Birds Conference

### *Session 1: Behaviour*

#### Keynote

Date: Tuesday 31 October, 2017  
Time: 09:15 – 10.00  
Room: Seminar Room

### **Social processes in a community of Paridae**

Author: **Ben C. Sheldon**

Affiliation: Edward Grey Institute of Field Ornithology, Department of Zoology,  
University of Oxford, Oxford, United Kingdom

Many processes of interest in natural populations have a social dimension, from foraging and mate selection, to territoriality and competition. Particularly in the non-breeding season, when population structure is more fluid than during breeding, many species form social groups of variable extent, size and permanence. In this talk I will describe the development of an empirical framework for studying large-scale social behaviour of tits in Wytham, near Oxford. I will highlight practical, statistical and conceptual challenges in the development of this work. I will then highlight some of the key questions that we have addressed in this work relating to individual differences in social behaviour, and how these influence population structure. I will conclude by discussing how this work has enabled us to develop an experimental focus on the way that novel information is transmitted and becomes established within wild populations.

Date: Tuesday 31 October, 2017  
Time: 10:00 – 10:20  
Room: Seminar Room

### On the use of heterospecific information in birds

Presenting author: **Tore Slagsvold**

Authors: **Tore Slagsvold<sup>1</sup>, Karen L. Wiebe<sup>1,2</sup>**

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In the wild, essential information may be transferred among individuals in order to increase foraging efficiency, avoid predators, or choose breeding habitats and sites. Much is known about the transfer of information within species but much less among species. Recent experiments on the use of heterospecific information in hole-nesting birds purport to show that two migratory species, the pied *Ficedula hypoleuca* and collared *F. albicollis* flycatchers use cues from a resident species, the great tit *Parus major*, to adjust nest site choice. This was shown by manipulating white markings around the entrance holes of nest boxes used by tits in the field and observing that the flycatchers apparently took the markings into account when choosing their own nest box, the type of box chosen depending on the clutch size of the tit. Although the idea is intriguing, we suggest that there are fundamental reasons to doubt that flycatchers can obtain substantial fitness benefits by doing so. We argue that available cues for flycatchers may be uninformative and costly to assess, and that there is actually little evidence for such assessment. In particular, we argue that the most critical assumption fails, namely video filming shows that the flycatchers rarely enter tit nests to assess clutch size because they risk being injured or even killed by the tit owner. We hope that our arguments, and new preliminary results from the field, will broaden the array of hypotheses for data purportedly showing the use of heterospecific information. We suggest that aggression by the tits could be an alternative explanation for the observed nest site choices of the flycatchers.

Date: Tuesday 31 October, 2017  
Time: 10:35 – 10:55  
Room: Seminar Room

## Evolutionary dynamics in wild birds: from single populations to multiple species

Presenting author: **Jesús Martínez-Padilla**

Authors: **Jesús Martínez-Padilla<sup>1</sup>, C. Camacho<sup>2</sup>, A. Estrada<sup>3</sup>, F. Garcia-Gonzalez<sup>2</sup>, D. Canal<sup>2</sup>, R. Early<sup>4</sup>, V. Jennings<sup>5</sup>, J. le Vaillant<sup>1</sup>, J. Potti<sup>2</sup>**

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Natural selection is the main mechanism driving evolution and therefore the hub for understanding biodiversity. Natural selection operates on phenotypes when its variance and fitness are associated at the across-individual level. As an outcome, evolution is detected when the frequency distribution of a given trait or genes changes over time or space. However, environmental conditions are permanently changing across time and space, often in an unpredictable manner, which dilutes genetically fixed phenotype/fitness correlations. In this talk, I will show some insights on the evolutionary dynamics of secondary sexual, morphological and life-history traits, jumping from a single population of a long-term monitored population of pied flycatchers (*Ficedula hypoleuca*) in a Mediterranean region, to a biogeographical and multi-species perspective. Our results suggest that population density and variance in temperature during laying date can be the main agents of selection acting on the expression of secondary sexual traits and laying date, respectively. In addition, not only micro-evolutionary processes but dispersal can promote population differentiation at micro-geographical scales through a phenotype-dependent dispersal within our population of pied flycatchers. At a biogeographical scale, biogeographical tools can help us out to understand the evolutionary dynamics of phenotypic traits in wild bird populations. Our findings suggest that the evolutionary potential of morphological traits decreases at maximum and minimum values of environmental favourability. Overall, the aim of this talk is to describe the role that environmental conditions may have on the evolutionary dynamics of different phenotypes, not just in specific populations, but in multiple populations and species, making use of analytical tools from the field of biogeography.

Date: Tuesday 31 October, 2017  
Time: 10:55 – 11:15  
Room: Seminar Room

## Diurnal patterns of the production and use of food-related information in Parid flocks

Presenting author: **Friederike Hillemann**

Authors: **Friederike Hillemann<sup>1</sup>, E. F. Cole<sup>1</sup>, S. C. Keen<sup>1,2</sup>, B. C. Sheldon<sup>1</sup>, D. R. Farine<sup>1,3,4</sup>**

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Wintering songbirds have been widely shown to make economic decisions when foraging. Recent studies have also shown that songbirds manage predation risk on the one hand and resource uncertainty on the other by switching from prioritizing food discovery in the morning to exploiting known patches later in the day. In this study, we ask whether the communication of food availability and the use of social information to find food also differ throughout the day. First, we assessed temporal variation in food-related vocal information in foraging flocks of tits (Paridae) using audio recordings at feeding stations. Vocal activity was highest in the morning and decreased into the afternoon, and calling behaviour was inversely correlated with foraging flock size. Next, we experimentally tested the underlying causes for the diurnal calling pattern. We set up bird feeders with or without a playback of calls from tit species, either in the morning or in the afternoon, and compared latency until feeder discovery, accumulation of flock members, and total number of birds visiting the feeder. Irrespective of time of day, playbacks had a strong effect on all three response measures, compared to silent control trials, demonstrating that tits will readily use vocal information to improve food detection throughout the day. We suggest that, as the day progresses and foraging group sizes increase, the costs of producing calls at the food source (competition and attraction of predators) outweigh the benefits of recruiting group members (e.g. safety in numbers), causing the observed decrease in vocal activity into the afternoon.

## Session 1: Behaviour

Date: Tuesday 31 October, 2017  
Time: 11:15 – 11:35  
Room: Seminar Room

### **Adaptations of birds to tree holes: insights from long-term studies in primeval conditions**

Presenting author: **Tomasz Wesółowski**

Authors: **Tomasz Wesółowski<sup>1</sup>**

Affiliations: <sup>1</sup>Laboratory of Forest Biology, Wrocław University, Wrocław, Poland

To understand biological adaptations of organisms one has to study them in proper evolutionary context, i.e. in conditions to which the organisms have been adapted. As the hole-nesting birds have been adapting to breed in tree holes, if we wish to comprehend functional importance of different aspects of their behaviour and ecology, we should study them nesting in tree holes. Conditions for such observations are rarely met in heavily transformed European forests, but one can still find them in the Białowieża National Park (Eastern Poland), where last fragments of pristine European lowland forest have survived. All the abiotic and biotic processes leading to hole formation and decay still operate there, and diversity and abundance of tree holes is not reduced by human management. An entire assemblage of nest predators using diverse detection and attack techniques occurs there as well. Numerous studies of hole nesting birds breeding in such conditions were carried out there during the last 40 years. Here I shall summarize some results of this work, concentrating on the evolutionary (adaptive) questions. I shall introduce tree holes as a biological opportunity, follow with listing challenges of successful breeding in such places (predation, soaking, darkness, microclimate). Then, I shall show diversity of solutions used by individual bird species to cope with these problems. Finally I shall present some questions still without answers and shall stress an urgent need to preserve the last pieces of European pristine forest as indispensable evolutionary and ecological laboratories.

Date: Tuesday 31 October, 2017  
Time: 11:35 – 11:55  
Room: Seminar Room

## Personality-related differences in response to habitat in Mediterranean blue tits

Presenting author: **Eva Serrano-Davies**

Authors: **Eva Serrano-Davies<sup>1</sup>, Yimen G. Araya-Ajoy<sup>2</sup>, Niels J. Dingemanse<sup>3</sup>, Juan José Sanz<sup>4</sup>**

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Habitat-specific selection pressures have been widely recognized but whether selection favours different personality types in different habitats has rarely been evaluated. This study aimed to test whether personality-related differences in annual reproductive success differed between two populations of blue tits (*Cyanistes caeruleus*) occupying different Mediterranean habitats (oakwood and pinewood). We measured exploration and parental provisioning behaviours and used a path analysis to ask how the interplay between these two behavioural traits affected reproductive success in each of these two habitats. We found that blue tits breeding in the pinewood were slow-exploring compared to blue tits breeding in the oakwood, suggesting the occurrence of personality-related differences in settlement, or behavioural plasticity in response to habitat. Exploration behaviour and feeding rates were positively associated, suggesting that they affect each other or that there is an environmental factor affecting both traits simultaneously. Finally, fast explorers were favoured in the pinewood, while there was no selection acting on exploration behaviour in the oak habitat. These findings emphasize the importance of integrating habitat selection, plasticity and personality in the study of behavioural evolution.

Date: Tuesday 31 October, 2017  
Time: 11:55 – 12:40  
Room: Seminar Room

## **Body temperature and immune defence**

Author: **Jan-Åke Nilsson**

Affiliation: Department of Biology, Lund University, Lund, Sweden

The first line of defence against invading pathogens, the acute phase response of the vertebrate immune system, involves a suit of behavioural and physiological responses, collectively called sickness behaviours. In mammals, this response is often characterized by a rapid, metabolically costly onset of fever. The use of fever in birds is much less known. It seems as if “large” birds, e.g. ducks also attain fever but results from small passerines are much more variable. This might be due to the much more flexible body temperature regulation of small birds. A roosting blue tit during winter may decrease its body temperature by around 8 °C to reduce the energy expenditures during a time with restricted access to food and low ambient temperatures. We found that the acute phase response did not induce fever during these circumstances as the birds did not increase their body temperature above daytime values. However, they had higher body temperatures than control birds roosting in the same ambient temperature environment. Furthermore, during the day they reduced body temperature and these different strategies will be discussed in the light of making full use of energy savings during night and avoid being overheated during the day. Another, hypothesis considered is the potential for a span of body temperatures where the function of other parts of the immune reaction would be optimized.

Date: Tuesday 31 October, 2017  
Time: 12:40 – 13:00  
Room: Seminar Room

### Interaction types between four genera of haemoparasites in blue tit females

Presenting author: **Anna Dubiec**

Authors: **Anna Dubiec<sup>1</sup>, Adam Krupski<sup>1</sup>**

Affiliations: <sup>1</sup>Museum and Institute of Zoology, Polish Academy of Sciences, Warsaw, Poland

Host individuals commonly get infected with a vast array of parasites. Concurrent infections set the opportunity for interactions between parasites, which may arise either directly or indirectly. The outcome of these interactions – neutral, synergistic or antagonistic – may affect the host individual as it may translate into the size of its parasite community. Despite growing interest in identifying interaction types between different parasites, this field is still largely unexplored. Here, interaction types between four genera of common avian haemoparasites – *Plasmodium*, *Haemoproteus*, *Leucocytozoon* and *Trypanosoma* – were studied in a hole-nesting passerine, the blue tit (*Cyanistes caeruleus*). In contrast to previous studies, which examined interactions between these parasites in a single time point, the probability of infection with a given parasite was examined as a function of the presence of infection with other parasites assessed at an earlier stage of the nesting period. Because interactions between parasites may be affected by the environment they occupy, i.e. the quality of the host, this host characteristic was diversified by exposing adult females during the incubation and nestling period to different levels of infestation with fleas – a common ectoparasite of cavity nesting passerines. In the majority of cases, the interaction between different haemoparasite genera was neutral. However, the synergistic interaction was identified between *Haemoproteus* and *Leucocytozoon* as well as *Trypanosoma* and *Leucocytozoon* and the antagonistic interaction between *Haemoproteus* and *Plasmodium*. Contrary to expectations, the interactions between haemoparasites were similarly expressed in females exposed to low and high flea infestation level except for *Plasmodium*-*Trypanosoma*. This study suggests that the composition of the haemoparasite community in bird populations may shape the frequency of infection with individual parasite genera as well as the rate of multiple infections.

Date: Tuesday 31 October, 2017  
Time: 14:30 – 14:50  
Room: Seminar Room

## **Distinct foraging behaviours differently constrain the physiological state in a hole-nesting seabird, the Scopoli's shearwater (*Calonectris diomedea*)**

Presenting author: **Roger Colominas-Ciuró**

Authors: **Roger Colominas-Ciuró<sup>1</sup>, M. Cianchetti-Benedetti<sup>2</sup>, L. Michel<sup>2</sup>, G. Dell'Omo<sup>3</sup>, P. Quillfeldt<sup>2</sup>**

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It is expected that activities which require a high use of energy could generate high oxidative unbalance and stress, and negatively influence both the physiological state and the immune system of individuals. In the present study, we have compared two breeding periods with different energetic demands (incubation and chick rearing) in the hole-nesting and shallow-diving seabird species, the Scopoli's shearwater (*Calonectris diomedea*). Since chick rearing involves higher demanding activities, we predicted a higher oxidative unbalance (higher oxidative damage and lower antioxidant defences) and stress (Heterophil/Lymphocyte ratio), and lower triglycerides and non-esterified fatty acids, as well as a worse immunological state during chick rearing than during incubation. Fieldwork was conducted in the largest colony of Scopoli's shearwater on Linosa Island (35°51'33"N, 12°51'34"E), Italy, during the breeding season of 2016 and, apart from blood samples extraction, birds were equipped with Axy-depth data-loggers (Technosmart Europe S.r.l.). Surprisingly, incubating adults had their oxidative status unbalanced showing significantly lower antioxidant levels than those rearing chicks. In contrast, adults rearing chicks showed higher H/L ratio and lower triglycerides and non-esterified fatty acids compared to those incubating eggs, suggesting that both periods differently unbalance breeder's physiological state. Differential foraging effort could explain such results since shearwaters adjust their foraging location depending on the breeding period, performing longer foraging trips during incubation than during chick rearing. Consequently, this causes an oxidative status imbalance during incubation although results in a better physiological state, thanks to the high quality preys that might encountered (unavailable at the colonies vicinity during chick rearing). However, chick rearing appears to be more stressful due to chick demands (e.g. chick feeding). Our results therefore show the importance of examining physiological markers to assess breeding cycle differences and how foraging behaviour explains them.

## Session 2: Physiology

Date: Tuesday 31 October, 2017  
Time: 14:50 – 15:10  
Room: Seminar Room

### Effects of urban environment on health in the great tits

Presenting author: **Sylvie Massemin**

Authors: **S. Massemin<sup>1</sup>, M. Millet<sup>2</sup>, A. Boos<sup>1</sup>, E. Rojas<sup>1</sup>, S. Zahn<sup>1</sup>, M. Del Nero<sup>1</sup>**

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How urban stressors such as chemical pollution or food availability can affect the ecological and physiological traits of birds is important to understand the mechanisms by which birds can colonize urban environment. To highlight how species can adapt to urban constraints, we studied the fitness of the Great tit (*Parus major*) during three years along an urban gradient around Strasbourg (France). Three areas were followed on this gradient (one in Strasbourg, two outside). We showed that they were different according to the atmospheric and ground pollution, the food availability and the vegetation cover around the nests. In the town (few food, less polycyclic aromatic hydrocarbons and pesticides), few great tits pairs bred, adults were smaller and reproductive success of these birds was lower compared to the two other areas. We will present results concerning oxidative stress and telomere attrition as physiological parameters in adults and fledglings. In addition, we will propose an international collaboration on the great tits as an urban ecological and physiological observatory.

Date: Tuesday 31 October, 2017  
Time: 15:10 – 15:30  
Room: Seminar Room

## Interaction between genetic effects and experimentally manipulated pre-hatching hormonal conditions

Presenting author: **Szymon Drobnik**

Authors: **Szymon Drobnik<sup>1,2</sup>, Dorota Lutyk<sup>1</sup>, Katarzyna Janas<sup>1</sup>**

Affiliations: <sup>1</sup>Institute of Environmental Sciences, Jagiellonian University in Kraków, Krakow, Poland  
<sup>2</sup>Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden

Maternal effects shape phenotypic traits in many organisms providing them with effective means of responding to environmental heterogeneity experienced by their mothers. Maternal effects are mediated through a wide array of mechanisms, and hormonal mediators are important examples thereof. Bird mothers deposit various hormones in their eggs' yolks to influence the traits of their offspring. Since maternal effects were repeatedly demonstrated to interact with additive genetic effects, maternal effects may provide one of possible mechanisms of genotype-by-environment interactions. Here, we experimentally test this possibility by manipulating yolk levels of two important hormones (testosterone and corticosterone) in developing embryos of the blue tit inhabiting a long-term monitored wild population. Hormones levels were manipulated by injecting eggs with three types of solutions (sham injection; testosterone solution; corticosterone solution). Subsequently, the eggs were cross-fostered between nests arranged in triplets and chicks were assigned to their eggs by hatching them in an incubator. Offspring traits were analysed using an animal model. Our results show that the expression of additive genetic effects in morphological and condition-dependent traits in this species depends on the elevated levels of yolk steroid hormones: steroids affected both the amount of observed genetic variance in traits and genetic correlations within traits between experimental groups. It indicates that maternal hormones may significantly contribute to generating and maintaining genotype-by-environment interactions, which in turn contribute to the maintenance of genetic variance in naturally selected traits.

## Session 3: Population Dynamics

### Keynote

Date: Tuesday 31 October, 2017  
Time: 15:45 – 16:30  
Room: Seminar Room

## Age-specific contributions to the dynamics of hole-nesting birds

Author: **Marlène Gamelon**

Affiliation: Centre for Biodiversity Dynamics, Department of Biology,  
Norwegian University of Science and Technology, Trondheim,  
Norway

Classical approaches for the analyses of density dependence assume that all the individuals in a population equally respond and equally contribute 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. Here, we apply the concept of critical age classes, i.e. a specific scalar function that describes how one or a combination of several age classes affect the demographic rates negatively, in order to examine how total density dependence acting on the population growth rate depends on the age-specific population sizes. In a 38-year dataset of an age-structured great tit (*Parus major*) population, we find that the age classes including the youngest breeding females were the critical age classes for density regulation. These age classes correspond to new breeders that attempt to take a territory and that have the strongest competitive effect on other breeding females. They strongly affected population growth rate and reduced recruitment and survival rates of all breeding females. We also show that depending on their age class, females may differently respond to varying density. In particular, the negative effect of the number of breeding females was stronger on recruitment rate of the youngest breeding females. These findings question the classical assumptions that all the individuals of a population can be treated as having an equal contribution to density regulation and that the effect of the number of individuals is age independent. Our results improve our understanding of density regulation in natural populations.

## Session 3: Population Dynamics

Date: Tuesday 31 October, 2017  
Time: 16:30 – 16:50  
Room: Seminar Room

### **The importance of conservation measures for pied flycatchers breeding in the boreal landscape dominated by forest management**

Presenting author: **Toni Laaksonen**

Authors: **Toni Laaksonen<sup>1</sup>**

Affiliations: <sup>1</sup>Department of Biology, University of Turku, Turku, Finland

It is known that the number of available cavities is often limiting the abundance of secondary hole-nesting animals. The great majority of population studies of hole-nesting birds are however conducted in nest box populations in relatively small areas, and we tend to have a poor idea of how severe the limitation is in the landscape scale. This is particularly the case in the heavily managed boreal forests of northern Europe, where we have a limited understanding of even how many cavities there are for the whole community of hole-nesters. Here, I will address the following questions: 1) how many natural cavities suitable for secondary hole-nesting birds there are in the forest-dominated landscape of Finland; how many of them may be available for the pied flycatcher, an obligate hole-nesting bird that is a long-distance migrant and the last to arrive at the scene; and 3) what is the importance of different conservation measures for this species. I will address these questions primarily by using preliminary data from surveys searching for natural cavities in SW Finland, supplement with line transect and nest box data. The results are useful in putting the ecological and behavioural studies of nest-hole breeding birds into a context outside the restricted study sites and in considering the state of the managed forests for the hole-nesting community.

Date: Tuesday 31 October, 2017  
Time: 16:50 – 17:10  
Room: Seminar Room

## Impact of urbanization on abundance and phenology of caterpillars and consequences for breeding in an insectivorous bird

Presenting author: **Gábor Seress**

Authors: **Gábor Seress<sup>1</sup>, Tamás Hammer<sup>1</sup>, Veronika Bókony<sup>2</sup>, Ernő Vincze<sup>3</sup>, Bálint Preiszner<sup>4</sup>, Ivett Pipoly<sup>1</sup>, Csenge Sinkovics<sup>3</sup>, Karl L. Evans<sup>5</sup>, András Liker<sup>1,3</sup>**

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Urbanization can have marked effects on plant and animal populations' phenology, population size, predator-prey interactions and reproductive success. These aspects are rarely studied simultaneously in a single system, and some are rarely investigated, e.g. how insect phenology responds to urban development. Here, we study a tri-trophic system of trees – phytophagous insects (caterpillars) – insectivorous birds (great tits) to assess how urbanization influences i) the phenology of each component of this system, ii) insect abundance and iii) avian reproductive success. We use data from two urban and two forest sites in Hungary, central Europe, collected over four consecutive years. Despite a trend of earlier leaf emergence in urban sites there is no evidence for an earlier peak in caterpillar abundance. Thus, contrary to the frequently stated prediction in the literature, the earlier breeding of urban bird populations is not associated with an earlier peak in food availability. Despite this the seasonal dynamics of caterpillar biomass exhibited striking differences between habitat types with a clear peak in forests, and several much smaller peaks in urban sites. Caterpillar biomass was 8.5 to 24 times higher in forests than urban sites during the period when great tits were raising their first broods. This higher biomass was not associated with taller trees in forest sites, or with tree species identity, and occurred despite most of our focal trees being native to the study area. Urban great tits laid smaller clutches, experienced more frequent nestling mortality from starvation, and reared fewer offspring (of lower body mass) to fledging age. Our study strongly indicates that food limitation is responsible for reduced avian reproductive success in cities, which is driven by reduced availability of the preferred nestling diet, i.e. caterpillars, rather than phenological shifts in the timing of peak food availability.

## Session 5: Movement

### Keynote

Date: Wednesday 1 November, 2017  
Time: 09:00 – 09:45  
Room: Seminar Room

### Individual variation in dispersal in great tits

Author: **Erik Matthysen**

Affiliation: Evolutionary Ecology Research Group, University of Antwerp, Antwerp, Belgium

Dispersal is the “glue” that holds spatially structured populations together, but it is also a crucial life-history trait. While dispersal can be easily characterized as distance between birth and breeding, the underlying mechanisms contributing to dispersal are manifold and often remain poorly understood. In this presentation I review work by our group and others on unravelling the contribution of environmental, genetic and social factors on individual variation in dispersal, using the great tit (*Parus major*) as a case study. Most of our work was carried out in a patchy population consisting of small woodland fragments, while other studies have focused on larger continuous woodlands. Variation in dispersal can to some extent be explained by environmental factors such as population density and habitat structure. Conditions in early life also play a role; for example, we showed earlier that family movements guided by parents influence dispersal decisions later in life. Several studies have now confirmed that dispersal also has a heritable component. I will show how this analysis can be extended to test for heritable variation in the different phases of the dispersal process (leaving, transfer, and settlement). Finally, I will discuss the role of personality-related variation in explaining variation in dispersal, both at the phenotypic and genotypic level.

## Session 5: Movement

Date: Wednesday 1 November, 2017  
Time: 09:45 – 10:05  
Room: Seminar Room

### **Spatio-temporal variation in emigration and immigration is density-dependent in a house sparrow metapopulation**

Presenting author: **Yimen Araya-Ajoy**

Authors: **Ranke, P. S.<sup>1</sup>, Araya-Ajoy, Y. G.<sup>1</sup>, Ringsby, T. H.<sup>1</sup>, Pärn, H.<sup>1</sup>, Saatoglu, D.<sup>1</sup>, Rønning, B.<sup>1</sup>, Jensen, H.<sup>1</sup>, Wright, J.<sup>1</sup>, Sæther, B.-E.<sup>1</sup>**

Affiliations: <sup>1</sup>Centre for Biodiversity Dynamics, Department of Biology, Norwegian University of Science and Technology, Trondheim, Norway

We studied dispersal dynamics on 11 islands across 22 years in a house sparrow (*Passer domesticus*) metapopulation in northern Norway. There was considerable spatial heterogeneity in dispersal within the metapopulation. Outer islands farther from the mainland and with a harsher environment had higher dispersal rates compared to the inner islands with a more benign environment closer to the mainland. On the inner islands, the proportion of emigrants was negatively related to population size. Conversely, on the outer islands, emigration increased with population size. The relationship between immigration and population size was not so clear, but there was a trend suggesting that immigration was lower in islands with larger populations. Heterogeneity in dispersal rates in our system therefore suggests active attraction (less emigration and more immigration) towards larger populations on the more stable inner islands. However, in the outer islands there was more emigration and less immigration in islands with larger populations, suggesting source-sink dynamics. Such spatial heterogeneity in dispersal dynamics will have substantial demographic and evolutionary consequences in the metapopulation.

Date: Wednesday 1 November, 2017  
Time: 10:05 – 10:25  
Room: Seminar Room

## Advancement of spring arrival in a long-term study of a passerine bird: sex, age and environmental effects

Presenting author: **Luis Cadahia**

Authors: **Luis Cadahía<sup>1</sup>, Antonieta Labra<sup>1,2</sup>, Endre Knudsen<sup>1</sup>, Anna Nilsson<sup>1</sup>, Helene M. Lampe<sup>1</sup>, Tore Slagsvold<sup>1</sup>, Nils Chr. Stenseth<sup>1</sup>**

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<sup>2</sup>Instituto de Ciencias Biomédicas, Facultad de Medicina, University of Chile, Santiago, Chile

In migratory birds, mistimed arrival might have negative consequences for individual fitness, causing population declines. This may happen if arrival time is not synchronized with breeding time, especially when earlier springs favour earlier reproduction. We studied spring arrival time to the breeding areas in a pied flycatcher *Ficedula hypoleuca* population in southern Norway during a 30-year period (1985–2014). We investigated trends in arrival both for the entire population and for different population fractions (e.g., early vs. late arrivals). We also studied sex and age class differences, along with repeatability of arrival. Finally, we explored how arrival is influenced by environmental conditions at the areas birds use throughout the year, using mixed-effects models and quantile regressions with individual-based data. Spring arrival advanced over five days, at a similar rate through the entire population. Males and adult birds arrived earlier than females and yearlings. Arrival was significantly repeatable for males and females. Birds arrived earlier in years with high temperature and rainfall at the breeding grounds, and low NDVI both on the Iberian Peninsula and in central Europe. Later fractions of the population showed a steeper response to these environmental variables. This intra-population heterogeneity in the responses to the environment probably stems from a combination between the different selection pressures individuals are subject to and their age-related experience. Our results highlight the importance of studying how migration phenology is affected by the environment not only on the breeding grounds but also on the other areas birds use throughout the year.

## Session 6: Speciation

### Keynote

Date: Wednesday 1 November, 2017  
Time: 10:40 – 11:25  
Room: Seminar Room

### **Speciation in hole-nesting birds: any general lessons so far?**

Author: **Anna Qvarnström**

Affiliation: Department of Ecology and Genetics, Uppsala University, Uppsala, Sweden

There is a general agreement that the evolution of new species that can co-exist requires both ecological divergence and the development of reproductive isolation. Key questions in speciation research are therefore under which geographical conditions ecological divergence occurs (i.e. during allopatry or at secondary contact) and whether and how ecological divergence is associated with the development of reproductive isolation. The typical strong competition for limiting nest sites among hole nesting birds means that we may expect competition-driven ecological character displacement at secondary contact. In a young *Ficedula* hybrid zone on Öland, Sweden we find that pied flycatchers rapidly are displaced from their preferred breeding habitat by collared flycatchers and that this process is linked with the build-up of both habitat and temporal isolation. I will show some examples of how we use genomic methods to reveal the underlying genetic changes and discuss how these findings may contribute to our general understanding of speciation in hole-breeding birds.

## Session 6: Speciation

Date: Wednesday 1 November, 2017  
Time: 11:25 – 11:45  
Room: Seminar Room

### The Blue Tit

Presenting author: **Martyn Stenning**

Authors: **Martyn Stenning<sup>1</sup>**

Affiliations: <sup>1</sup>University of Sussex, Brighton, United Kingdom

Sporting a mix of blue, yellow, white, green and black, the unmistakable blue Tit *Cyanistes* spp. reflect the colours of a planet affected by a burgeoning human population. Fortunately, blue tits are adapting well to modern humanity, taking advantage of our propensity to feed birds in our gardens and provide boxes for them to nest in. Blue tits are one of only a few bird taxa that show a current increase in numbers. In turn, this charismatic little cavity nester proves to be an excellent model for biological research, and currently features in around 100 new scientific publications every year. This book is the result of a personal quest by author Martyn Stenning to bring some of these discoveries together into one accessible volume.

The Blue Tit begins by inviting readers into the intimate life of our bird as it attempts to reproduce, describing the many proximate challenges faced by Blue Tits when rearing offspring. The story moves on to the fluid state of Blue Tit variant classification across a native Palearctic range and progresses into population structure, life-time ecology and an exploration of ultimate factors that determine Blue Tit breeding success. It culminates with an in-depth exploration of Blue Tit research and concludes with a genial selection of personal anecdotes and an overview of Blue Tit appearances in folklore and poetry.

The talk will focus in on blue tit evolutionary history, speciation and current taxonomy, which is in a state of flux. Several published authors have analysed blue tit DNA in order to refine the understanding of blue tit evolutionary history, but this has raised almost as many questions as answers. There are currently eight recognised species of *Cyanistes* and 21 subspecies named and reported in Avibase, which is an online repository of current taxonomic authorities.

## Session 6: Speciation

Date: Wednesday 1 November, 2017  
Time: 11:45 – 12:05  
Room: Seminar Room

### **Citizen science for the study of hole-nesting birds: UK examples and emerging opportunities**

Presenting author: **Malcolm Burgess**

Authors: **Malcom Burgess<sup>1,2</sup>, Ken Smith<sup>3</sup>, Dave Leech<sup>4</sup>**

Affiliations: <sup>1</sup>RSPB Centre for Conservation Science, The Lodge, Sandy, Bedfordshire, United Kingdom  
<sup>2</sup>PiedFly.Net, Yarnar Wood, Bovey Tracey, Devon, United Kingdom  
<sup>3</sup>15 Roman Fields, Chichester, W. Sussex, United Kingdom  
<sup>4</sup>British Trust for Ornithology, The Nunnery, Thetford, Norfolk, United Kingdom

Some hole-nesting birds are among the most well studied species of passerine in the world, in large part because of the ease of monitoring these during the breeding season in purpose designed nest-boxes. Most hole-nesting bird research originates from nest box schemes at single or small numbers of sites. Because of the challenges of finding nests it rarely involves birds using natural nest sites. The potential for increased participation of citizen scientists, and use of citizen collected data, in relation to studies of hole-nesting bird research is huge. Such involvement can increase our ability to monitor and study both common and rare hole-nesting species over much wider areas than at present. Citizen scientists can also be motivated to collect information for other taxa relating to hole-nesting bird studies, such as recording the phenology of vegetation and invertebrate abundance. To illustrate this potential we highlight several examples from the UK.

The British Trust for Ornithology run several citizen science schemes, including the Nest Record Scheme that monitors several thousand hole-nesting bird nests annually. PiedFly.Net is a regional network that co-ordinates monitoring of 47 nestbox schemes across SW England, using these data in collaborative research across Europe. Woodpecker-network helps citizen scientists monitor hard to find woodpecker nests through loaning specialist nest inspection equipment. These networks also organise monitoring of other taxa that relates to these hole-nesting birds, for example invertebrate phenology and abundance. Many new and emerging techniques and technologies, such as DNA bar-coding for diet studies, provide many new opportunities for involving citizen scientists that will enable us to address new questions over large areas.

## Session 7: Genetics & Genomics

### Keynote

Date: Wednesday 1 November, 2017  
Time: 13:30 – 14:15  
Room: Seminar Room

## The significance of genetic variation in wild tit populations

Author: **Jon Slate**

Affiliation: Department of Animal and Plant Sciences, University of Sheffield,  
Sheffield, United Kingdom

We use extensive data from a long-term study of great tits (*Parus major*) in the UK and the Netherlands to better understand how genetic signatures of selection translate into variation in fitness and phenotypes. We found that genomic regions under differential selection contained candidate genes for bill morphology, and used genetic architecture analyses to confirm that these genes, especially the collagen gene COL4A5, explained variation in bill length. COL4A5 variation was associated with reproductive success which, combined with spatiotemporal patterns of bill length, suggested ongoing selection for longer bills in the UK. Finally, bill length and COL4A5 variation were associated with usage of feeders, suggesting that longer bills may have evolved in the UK as a response to supplementary feeding.

Date: Wednesday 1 November, 2017  
Time: 14:15 – 14:35  
Room: Seminar Room

## Avian ecological epigenetics: what do we know about DNA methylation in hole-breeding passerines

Presenting author: **Kees van Oers**

Authors: **Kees van Oers<sup>1</sup>**

Affiliations: <sup>1</sup>Department of Animal Ecology, Netherlands Institute of Ecology, Wageningen, The Netherlands

The past decade has seen an increasing interest in studying epigenetic mechanisms such as DNA methylation. This attention is present in both geneticists and non-geneticists interested in the mechanisms explaining variation in gene expression. For geneticists, the search for the hereditary mechanisms underlying quantitative traits traditionally focussed on the identification of underlying genomic polymorphisms such as SNPs, but this has not been very fruitful. It has now become clear that epigenetic mechanisms, such as DNA methylation, can consistently alter gene expression over multiple generations. Non-geneticists found out that these methylation patterns are prone to changes and such changes may be transmitted over generations. DNA methylation may therefore be an explanation for non-genetic inheritance such as maternal effects.

Much of what we know however, is based on studies on plants and mammals, mainly humans and laboratory strains. This raises the question whether the knowledge we have from these model systems can be generalized over species or classes and urges for a better understanding of the function of the methylome in passerine birds. In this talk I will first give a background on the current status of epigenetic research in passerines. I will follow this up by using the great tit (*Parus major*) as a case study to show i) the structure and function of the methylome ii) the relative role of induced versus inherited variation in methylation and iii) some methodological considerations for analysing DNA methylation.

Identification of variation in DNA methylation and changes in variation over time offer a great opportunity to combine genetic and non-genetic studies. Hole-breeding passerines could be ideal ecological model species for studying epigenetic mechanisms in natural populations.

Date: Wednesday 1 November, 2017  
Time: 14:35 – 14:55  
Room: Seminar Room

## Consequences of demographic processes for genetic drift in house sparrows

Presenting author: **Henrik Jensen**

Authors: **Henrik Jensen<sup>1</sup>, Marlene Wæge Stubberud<sup>1,2</sup>, Ane Marlene Myhre<sup>1</sup>, Helle Tessand Baalsrud<sup>1,2</sup>, Håkon Holand<sup>1</sup>, Thomas Kvalnes<sup>1</sup>, Ingerid Julie Hagen<sup>1</sup>, Henrik Pärn<sup>1</sup>, Thor Harald Ringsby<sup>1</sup>, Bernt-Erik Sæther<sup>1</sup>**

Affiliations: <sup>1</sup>Centre for Biodiversity Dynamics, Department of Biology, Norwegian University of Science and Technology, Trondheim, Norway  
<sup>2</sup>Centre for Ecological and Evolutionary Synthesis, Department of Biosciences, University of Oslo, Oslo, Norway

Effective population size ( $N_e$ ) and the ratio between effective and census population size ( $N_e/N$ ) are important measures of the long-term viability and evolutionary potential of a population because they reflect how fast genetic variation is lost due to genetic drift. Identifying the demographic processes that affect  $N_e$  and  $N_e/N$  most may therefore improve our understanding of 1) how demography affects drift, and 2) the relative importance of drift and selection for the fixation probability of alleles. In this study we use individual genotype and fitness data from natural house sparrow (*Passer domesticus*) populations in Norway to estimate  $N_e/N$  using demographic and genetic methods. We found that demographic  $N_e/N$  was most sensitive to demographic variance, especially among older individuals. Also, individual reproductive values (that determine demographic variance) were most sensitive to variation in fecundity. Importantly, genetic  $N_e/N$  increased with immigration rates, and genetic  $N_e$  were generally much larger than demographic  $N_e$ , probably because immigration affected genetic processes more than demographic processes within local populations. Our results suggest that sensitivity analysis is an important tool in linking ecological and genetic processes, and that even low levels of gene flow may have important consequences for the interpretation of genetic estimates of  $N_e$ .

Date: Wednesday 1 November, 2017  
Time: 14:55 – 15:15  
Room: Seminar Room

## Estimating heritability and response to selection in the presence of phenotypic error

Presenting author: **Erica Ponzi**

Authors: **Erica Ponzi<sup>1,2</sup>, Lukas F. Keller<sup>1</sup>, Timothee Bonnet<sup>1</sup>, Stefanie Muff<sup>1,2</sup>**

Affiliations: <sup>1</sup>Institute of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, Switzerland  
<sup>2</sup>Biostatistics, Epidemiology, Biostatistics and Prevention Institute, University of Zurich, Zurich, Switzerland

Quantitative genetic analyses, such as the estimation of heritability or the response to selection, require measurements of phenotypic traits across multiple generations. This may be especially challenging in wild animal populations, where the measurement precision can suffer considerably.

Such imprecision leads to measurement error in phenotypic trait records, which is a possible cause for bias in the estimation of quantitative genetic parameters. Consequently, quantities that are derived from these estimates such as heritability and quantitative trait dynamics, are potentially biased as well.

Here we use simulated pedigrees to investigate the effect of phenotypic measurement error on the heritability of phenotypic traits and on their response to selection and we propose a method to take such error into account when fitting the animal model by adding a random effect to the model structure. In our simulated pedigrees, this correction provides estimates for parameters of interest which are unbiased with respect to the real simulated ones.

One of the main conclusions is that measurement error biases quantities that involve phenotypic variances, and that the error should therefore be modeled when interest centers around heritability and predictive models of evolutionary change, as estimated by the breeder's equation. Thanks to the proposed method, accounting for the error is relatively straightforward and merely requires the inclusion of an additional variance component in the animal model, which can be estimated if a certain type of “close” repeated measurement are available, while more “distant” repeats are used to isolate permanent environmental effects. Finally, we discuss why the Robertson-Price identity is robust against phenotypic measurement error, namely because it involves only genetic covariances that do not depend on random phenotypic fluctuations.

Date: Wednesday 1 November, 2017  
Time: 15:30 – 16:15  
Room: Seminar Room

## Quantitative genetics and genomics of life-history traits in a wild bird population

Author: **Phillip Gienapp**

Affiliation: Department of Animal Ecology, Netherlands Institute of Ecology,  
Wageningen, The Netherlands

Quantitative genetics, which assumes that traits are determined by many loci with small effects, has long been successfully used in domestic and natural populations to understand and predict evolutionary change. Especially the development and implementation of the so-called 'animal model', a mixed model fitting genetic relatedness among individuals, has advanced its study in wild, pedigreed populations. The advancements in molecular genetic tools have now allowed genotyping many individuals for thousands of markers, which has opened the possibility to identify loci underlying traits even in wild populations of 'non-model' species. While some studies were able to find the loci underlying traits in wild populations, a number of other studies were less successful. An obvious explanation is limited power related to sample size or number of markers but other potential explanations are genotype-by-environment interactions or the trait being truly polygenic. Another potentially highly useful application of high-density markers in wild populations is to estimate relatedness directly from markers instead from the pedigree, which should – in theory – yield more accurate estimates of quantitative genetic parameters and also allow such studies in virtually any species. I will here illustrate the application of quantitative genetics, genomics and 'pedigree-free' quantitative genetics in a long-term study population of great tits.

Date: Wednesday 1 November, 2017  
Time: 16:15 – 16:35  
Room: Seminar Room

## Reversal of response to artificial selection on body size in a wild passerine

Presenting author: **Thomas Kvalnes**

Authors: **Thomas Kvalnes<sup>1</sup>, Thor Harald Ringsby<sup>1</sup>, Henrik Jensen<sup>1</sup>, Ingerid Julie Hagen<sup>1</sup>, Bernt Rønning<sup>1</sup>, Henrik Pärn<sup>1</sup>, Håkon Holand<sup>1</sup>, Steinar Engen<sup>2</sup>, Bernt-Erik Sæther<sup>1</sup>**

Affiliations: <sup>1</sup>Centre for Biodiversity Dynamics, Department of Biology, Norwegian University of Science and Technology, Trondheim, Norway

<sup>2</sup>Centre for Biodiversity Dynamics, Department of Mathematical Sciences, Norwegian University of Science and Technology, Trondheim, Norway

A general assumption in quantitative genetics is the existence of an intermediate phenotype with higher mean individual fitness in the average environment than more extreme phenotypes. Here we investigate the evolvability and presence of such a phenotype in wild bird populations from an eleven-year experiment with four years of artificial selection for long and short tarsus length, a proxy for body size. The experiment resulted in strong selection in the imposed directions. However, artificial selection was counteracted by reduced production of recruits in offspring of artificially selected parents. This resulted in weak natural selection against extreme trait values. Significant responses to artificial selection were observed at both the phenotypic and genetic level, followed by a significant return towards pre-experimental means. During artificial selection, the annual observed phenotypic response closely followed the predicted response from quantitative genetic theory ( $r_{\text{years}} = 0.96$ ,  $r_{\text{cohorts}} = 0.56$ ). The rapid return to pre-experimental means was induced by three interacting mechanisms: selection for an intermediate phenotype, immigration and recombination between selected and unselected individuals. The results of this study demonstrates the evolvability of phenotypes and that selection may favour an intermediate phenotype in wild populations.

Date: Wednesday 1 November, 2017  
Time: 16:35 – 16:55  
Room: Seminar Room

### Gene expression linked to timing of reproduction in the great tit

Presenting author: **Veronika N. Laine**

Authors: **Veronika N. Laine<sup>1</sup>, Irene Verhagen<sup>1</sup>, Christa Mateman<sup>1</sup>, Agata Pijl<sup>1</sup>, Kees van Oers<sup>1</sup>, Phillip Gienapp<sup>1</sup>, Marcel E. Visser<sup>1</sup>**

Affiliations: <sup>1</sup>Department of Animal Ecology, Netherlands Institute of Ecology, Wageningen, The Netherlands

Climate change, one of the major threats to biodiversity, has globally resulted in shifts in seasonal timing, varying between species and across taxonomic groups. The differences in shifts or advancements in seasonal timing, often lead to mismatches in timing between trophic levels. The great tit (*Parus major*) has advanced its seasonal timing, but fails to match with the more advanced shift of their caterpillar food. This mismatch of offspring needs and caterpillar abundance has major fitness consequences and, as earlier laying females now do better, there is strong natural selection for earlier laying. It is important to know which genes are contributing to evolutionary adaptation to a changing world. In order to investigate the genetic basis of laying date more, we generated selection lines for early and late laying and sequenced the whole transcriptomes of 12 pools of F1 birds for early and late egg laying. We had two tissues, hypothalamus and liver, and three different time points before and after laying the first eggs and two temperature treatments (warm and cold). We described several genes being differentially expressed between time points in great tits and showed also that there is differential expression of genes between liver and hypothalamus. Many of the differentially expressed genes in liver were bird specific related to egg laying e.g. the VTG2 (vitellogenin 1) and APOV1 (apovitellenin 1) and in hypothalamus many of the differentially expressed genes were linked to metabolism and signalling related gene-ontology groups. Furthermore, there was a significant interaction between temperature and time point in hypothalamus. A better understanding of gene expression patterns can contribute greatly to our understanding of molecular evolutionary processes in natural populations, and hence to assess the adaptive potential of species to cope with environmental change.

## Session 9: Life History

### Keynote

Date: Thursday 2 November, 2017  
Time: 09:00 – 09:45  
Room: Seminar Room

## Ongoing adjustment of flycatcher phenology in response to climate change: evolution in action?

Author: **Christiaan Both**

Affiliation: Conservation Ecology Group, Groningen Institute of Evolutionary Life Sciences, University of Groningen, Groningen, The Netherlands

Long-term nest box studies have illuminated how populations have been responding to climate change over the past half century. Most attention has been on breeding phenology, and across Europe, populations of tits and flycatchers varied in trends in laying date, which is partly related to local trends in spring temperature. These responses were not in all cases sufficient, most notably leading to trophic mismatches in Dutch populations of tits and pied flycatchers. In this talk I concentrate on how pied flycatchers have been able to respond to ongoing warming. As a long-distance migrant, they lack information while on their African wintering ground on the progress of spring at the breeding grounds. Despite this lack of information, flycatchers have progressively advanced both arrival date at the breeding grounds, and their breeding dates. Individually plasticity in spring arrival dates is very small, as is plasticity of laying date to temperature. This individual plasticity is unable to explain the population trend in laying dates over the years, and flycatchers lay at present earlier with the same temperatures than 30 years ago. This suggests an evolutionary response. The past directional selection for earlier arrival likely comes from the increased mismatch with the caterpillar peak, but also from increasingly beneficial conditions encountered upon arrival. We show that local survival of females increased over the years, and is correlated with spring temperatures in the year of arrival. Yet it is unclear whether this is linked to (genetic) variation in arrival dates. Relatively colder springs during the 10 years seem to have enabled flycatchers to catch up with the food peak, reducing selection for early breeding, and stabilizing population numbers.

## Session 9: Life History

Date: Thursday 2 November, 2017  
Time: 09:45 – 10:05  
Room: Seminar Room

### The evolutionary ecology of passerines in the Anthropocene

Presenting author: **Marta Szulkin**

Authors: **Marta Szulkin<sup>1</sup>**

Affiliations: <sup>1</sup>Wild Urban Evolution & Ecology Lab, Centre of New Technologies,  
University of Warsaw, Warsaw, Poland

Urban areas currently occupy approximately 3% of the Earth's surface, and more than half of the human population worldwide lives in cities. Yet our understanding of natural variation, response to selection and adaptation of wildlife living in urban environments is limited. Indeed, virtually all long-term studies of vertebrates investigated in the wild and used as cornerstone in evolutionary ecology research were started in natural environments characterised by limited human interference. There is thus a considerable gap in our understanding of the dynamics of organismal trait variation, selection and response to selection in an urban setting. As urban space is an environment with conspicuously altered ecological dynamics relative to original natural habitat, more insight into the evolutionary ecology of free-living animals in urban environments is needed. Moreover, urbanisation is also a statistically powerful and fascinating framework to study evolutionary and ecological processes since the process lends itself to multiple replicate experimental setups. I will here present 2 years of life-history and fitness data collected in a gradient of urbanisation to highlight (i) the need for a greater consensus in quantifying urbanisation and its effect on fitness and (ii) the importance of studying gradients of environmental change rather than urban-rural dichotomies to detect non-linear responses to urbanisation.

Date: Thursday 2 November, 2017  
Time: 10:05 – 10:25  
Room: Seminar Room

## **Complete brood loss in blue tits is almost always associated with the sudden and permanent disappearance of a parent**

Presenting author: **Peter Santema**

Authors: **Peter Santema<sup>1</sup>, Bart Kempenaers<sup>1</sup>**

Affiliations: <sup>1</sup>Max Planck Institute for Ornithology, Department of Behavioural Ecology and Evolutionary Genetics, Seewiesen, Germany

Blue tits (*Cyanistes caeruleus*) are a model species in ecological and evolutionary research and a key parameter of interest in many studies is the number of nestlings that survive until fledging. Not much is known, however, about what causes mortality during the nestling period. Using data from a long-term nest box study on blue tits, we found that in almost all nests that suffered complete brood mortality one of the parents had suddenly disappeared during the nestling stage. In contrast, nests with partial brood failure were only rarely associated with the disappearance of a parent, although more often so when a large proportion of the nestlings died. Parents that disappeared during the nestling stage were rarely seen again and almost never returned to breed. In contrast, parents that remained after their partner disappeared were equally likely to be observed again or return to breed as parents of nests where both parents stayed. Of the nests where both parents stayed, the likelihood of being seen again or returning to breed was unrelated to nestling mortality. Visit rates at nests where a parent disappeared were no different from those of nests where both parents stayed, up to the point where the parent disappeared. Interestingly, visit rates then increased if the remaining parent was female, but remained unchanged when the remaining parent was male. Taken together, our results show that, in contrast to nests with partial brood failure, nest with complete brood failure are almost always associated with the sudden and permanent disappearance (probable death) of one of the parents. Complete brood failure and partial brood loss are thus distinct processes that require different functional explanations.

## Session 9: Life History

### Keynote

Date: Thursday 2 November, 2017  
Time: 10:40 – 11:25  
Room: Seminar Room

## Layers of variance in the parental care of hole-nesting birds and what they might mean

Author: **David F. Westneat**

Affiliation: Department of Biology, University of Kentucky, United States

Many phenotypic traits vary at multiple scales, including within and among individuals. I will describe analyses arising from our 26-year and ongoing study of reproductive performance in House Sparrows, plus two studies on provisioning in great tits and pied flycatchers. In sparrows, various metrics of parental provisioning behaviour show complex patterns of within- and among-individual variance. This variance can be ascribed to three major sources: within-individual plasticity with vaguely known causes, among-individual variance in mean parental care, the causes of which are also unknown, and unexplained residual variance that may have its own within- and among-individual patterning. Parental care is responsive to several well-known factors, including brood size and nestling age. These two interact to affect care, do so differently for males and females, and at least for nestling age, individuals vary in responsiveness. Results from several types of brood manipulations, in sparrows and the other hole-nesting species, have begun to flesh-out the details of plasticity and the direct and indirect effects of behavioural shifts on residual variance. Manipulations of nestling age in house sparrows revealed rapid and symmetrical adjustments to multiple metrics of provisioning behaviour. Brood size manipulations in all three species have confirmed many previous studies but intersected some predictions from theory in odd ways. For example, the predicted effects of brood size manipulations may depend on subtle differences in the shapes of benefit and cost curves. In two recent studies, we uncovered major year effects, supporting this idea. In another example, we tested that the possibility that parents are managing stochastic variance when provisioning offspring, but we encountered difficulties because changes in mean provisioning trickled down to affect residual variances. These fine-grained shifts in the behaviour of parent birds provide new opportunities to learn more about both the mechanisms and functional consequences of plasticity and individuality.

## Session 9: Life History

Date: Thursday 2 November, 2017  
Time: 11:25 – 11:45  
Room: Seminar Room

### Structural nest cavity modification using stones

Presenting author: **Nathanial Warning**

Authors: **Nathanial Warning<sup>1</sup>**

Affiliations: <sup>1</sup>Maryland Department of Natural Resources, Annapolis, Maryland, United States

There is a growing recognition that birds facultatively alter the nest environment in versatile ways. Nest modification using stones is a rare nest construction technique used by birds from five Passerine families occurring in arid, rocky environments. I compared nest structures among three cavity-nesters: black wheatear (*Oenanthe leucura*), blackstart (*Oenanthe melanura*), and rock wren (*Salpinctes obsoletus*) and reviewed possible functions of stone arrangements, including nest stabilization, nest dryness, and predator deterrence. I measured 78 rock wren nests and found that the area of the cavity blocked by stones was significantly correlated ( $r = 0.67$ ,  $P < 0.01$ ) with the size of the cavity opening, suggesting that occlusion of the cavity entrance is one driver of stone use in this species. The few studies examining the use of stone structures in cavity nests show that their use could serve multiple functions and allow birds to nest in a wider variety of sites.

Date: Thursday 2 November, 2017  
Time: 11:45 – 12:05  
Room: Seminar Room

### Family planning under social competition

Presenting author: **Rienk Fokkema**

Authors: **Rienk Fokkema<sup>1</sup>, Joost M. Tinbergen<sup>1</sup>, Richard Ubels<sup>1</sup>**

Affiliations: <sup>1</sup>Groningen Institute for Evolutionary Life Sciences, University of Groningen, Groningen, The Netherlands

Competition is an essential part of evolution. Animals compete over resources as food, partners and breeding sites. Individuals with characteristics that enable them to outcompete others and gain access to vital resources will be able to produce more offspring and thereby contribute more to future generations. Experimental research on great tits (*Parus major*) showed that the family size that parents raise can negatively affect their future survival probability in areas with high competitive pressure. The hypothesis was formulated that family size may negatively affect the competitive ability of parents in later life. Under competition it may thus be more favourable for parents to raise smaller families. The focus of our research was to experimentally test this hypothesis in a great tit nest box population. We manipulated family size by reducing or enlarging broods, relative to a control group. Next, we measured parental competitive ability both in winter and in the following spring by experimentally increasing the level of competition for vital resources as winter food, winter roosting boxes and breeding boxes. We found evidence that the manipulated family size had a negative effect on the probability of parents to 1) claim food in winter and 2) claim deeper breeding boxes which were safer from nest predation during the next spring. This evidence is consistent with the hypothesis that family size negatively affects the competitive ability of parents. This work contributes our understanding of how social mechanisms, such as competition, can shape individual reproductive behaviour. This knowledge is essential to predict how animals will respond to changes in their ecological environment.

## Session 10: Climate Change

### Keynote

Date: Thursday 2 November, 2017  
Time: 13:30 – 14:15  
Room: Seminar Room

### Hole-nesting passerines in a warming world

Author: **Marcel E. Visser**

Affiliation: Department of Animal Ecology, Netherlands Institute of Ecology,  
Wageningen, The Netherlands

Spring temperatures are increasing due to climate change and this has had profound effects on the spring phenology of many organisms. These shifts in phenology however vary substantially among species, with predatory species shifting only at half the rate as their prey. This leads to so-called phenological mismatches: the phenology of predators and their prey get out of synchrony. I will give an overview of these mismatches, the evolutionary consequences and the population consequences using data from our long-term study on great tits. I will present the updated version of our paper from 1998 and will show that after a period in which the mismatch was increasing over time, there is now a period in which the mismatch gets smaller again. I will present data of birds, caterpillars and trees to show that to understand such patterns we need to take the phenology of the entire food chain into account. Next, I will switch gears and focus more in detail on potential for genetic change in response to selection on timing of reproduction in great tits. We have been studying the genetics and physiology underlying timing of reproduction by creating selection lines of early and late reproducing great tits, using genomic rather than phenotypic selection. We breed great tits of these selection lines under controlled conditions and look at their lay dates as well as at RNA expression. As a final step we have introduced selection line eggs into our wild population and in 2018 we will have the first F4 offspring breeding in the wild and we can then measure their fitness depending on their timing of reproduction. In contrast to for instance egg or chick swapping manipulations, these birds need to make the full costs of laying early, which should provide us with an unbiased measure of fitness.

Date: Thursday 2 November, 2017  
Time: 14:15 – 14:35  
Room: Seminar Room

## An experimental increase of nestbox temperature during egg-laying affects maternal effects and nestling health in great tits

Presenting author: **Josefa Bleu**

Authors: **Josefa Bleu<sup>1</sup>, Claudy Haussy<sup>2</sup>, Simon Agostini<sup>3</sup>, Frédéric Angelier<sup>4</sup>, Clotilde Biard<sup>2</sup>**

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<sup>3</sup>CEREEP-Ecotron Ile-de-France, UMS 3194, École Normale Supérieure, St-Pierre-les-Nemours, France  
<sup>4</sup>Centre d'Etudes Biologiques de Chizé, CNRS, 79360, Villiers en Bois, France

Prenatal maternal effects can be a source of phenotypic plasticity and may play a role in adaptation to climate change. However, we do not know how far temperature could influence such effects, if at all. We studied the influence of temperature during egg laying on maternal reproductive investment, on egg characteristics, and on the phenotype of nestlings. We expected temperature to have an effect, as it influences maintenance costs for females, who can also use it as a cue of the advancement of the breeding season. We experimentally increased night-time nestbox temperatures by approximately 1°C throughout the entire laying period in great tits (*Parus major*). Clutch size was negatively correlated with laying date in heated females. Also, heated females did not delay incubation after clutch completion as frequently as control females did. Egg content (androgen yolk concentration and lysozyme concentration in the albumen) and egg mass were not affected by the heating treatment. Yet, last-laid eggs in clutches from control nestboxes had a thicker eggshell than last-laid eggs from heated nestboxes, suggesting a decrease of maternal investment with the heating treatment. Finally, nestlings' blood sedimentation rate, which is an indicator of acute infections and inflammatory diseases, was positively correlated with hatching date in control broods. This suggests that nestlings were of lower quality in late-hatched broods than in early-hatched broods. This seasonal effect was not detected in heated nests. Our results show that a small increase in temperature during laying can influence breeding strategy and nestling characteristics. These results suggest that birds used temperature as a cue of seasonal advancement to adjust breeding phenology, with beneficial effects on nestling health. To better understand the consequences of maternal adjustments during egg laying, it would be interesting to combine studies with heating treatment during different periods of the breeding cycle.

## Session 10: Climate Change

Date: Thursday 2 November, 2017  
Time: 14:35 – 14:55  
Room: Seminar Room

### **Do responses to temperature vary spatially in the great tit (*Parus major*)?**

Presenting author: **Liam D. Bailey**

Authors: **Liam D. Bailey<sup>1</sup>, Martijn van de Pol<sup>1</sup>, Marcel E. Visser<sup>1</sup>**

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Phenological shifts in response to increasing global temperatures are well documented in a range of plant and animal species, with potential consequences for individual fitness. The hole-nesting great tit (*Parus major*) is a particularly well documented example, where timing of egg laying is important to allow synchronisation between offspring development and local food peaks. Previous studies have demonstrated that temperature affects breeding phenology in great tits, but it is not immediately clear whether all populations are sensitive to the same temperature window. Furthermore, it is unclear whether the strength of such responses are uniform across the species' range as other factors may mediate the relationship between phenology and temperature. For example, it is hypothesised that photoperiod will be a more relevant driver of lay date at higher latitudes.

We present an ongoing collaborative study involving an inter-population comparison of laying date responses to temperature. The great tit represents one of the best study species for this topic, with an extensive network of monitored populations. In each population, we use a newly developed method to determine the window at which temperature most strongly influences laying date. We then determine the strength of the relationship between temperature and phenology for each population and test for spatial patterns across the species' range. We will test how other variables, such as photoperiod and habitat type, help explain spatial patterns in temperature sensitivity. In this presentation, we discuss preliminary results and outline our future research goals.

Differences in temperature sensitivity across great tit populations of Europe may lead to varying levels of phenological mismatch between offspring development and food peaks. Studying how temperature sensitivity of laying date varies across the species' range will give us a better understanding of how different populations may be affected by ongoing global climate change.



Date: Thursday 2 November, 2017  
Time: 14:55 – 15:15  
Room: Seminar Room

## Eco-evolutionary dynamics of a sexually selected trait in a Mediterranean population of pied flycatchers

Presenting author: **Valeria Jennings**

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To understand the evolutionary dynamics of phenotypic traits and the potential of populations to adapt to changing environmental conditions, it is essential to identify the factors that best explain variation in selection. This is particularly relevant for sexually selected traits since they are directly associated to reproductive success, and environmental change can modify their frequency distribution over time by influencing such association. The effects of climate change on eco-evolutionary dynamics have often been investigated, but whether climate is a proximate cause of evolutionary change or its effect is related to other agents of selection has been little explored. Thus, there is a need for a systematic approach dedicated to finding the best abiotic or biotic factors driving selection on the expression of secondary sexual traits in wild populations. We use long-term data gathered from a population of pied flycatchers in which the sexually-selected male white forehead patch has steadily increased in mean size over 30 years. We first show that climate has no direct effect on the expression of patch size but is instead mediated by population density. Secondly, we find that viability and fecundity selection on male patch size can be driven by climate or population density, respectively. Specifically, we find opposing trends of viability and fecundity selection in relation to population density. This suggests that individuals with larger patches face a different life-history trade-off as a function of population density. A behavioural interpretation of this is that the ornament cost is density-dependent, so males with a larger patch may switch their investment from reproduction to survival as population density increases. We suggest that evolutionary dynamics of this sexual trait in our population is driven more by intrinsic (intra-sexual) than extrinsic (climatic) factors although a potential indirect effect of climate on population demography cannot be ruled out.

Date: Thursday 2 November, 2017  
Time: 15:30 – 15:50  
Room: Seminar Room

## Phenological sensitivity to climate change is higher in resident than in migrant bird populations among European cavity breeders

Presenting author: **Jelmer M. Samplonius**

Authors: **Jelmer M. Samplonius<sup>1</sup>, Lenka Bartošová<sup>2</sup>, Malcolm D. Burgess<sup>3,4</sup>, Andrey V. Bushuev<sup>5</sup>, Tapio Eeva<sup>6</sup>, Elena V. Ivankina<sup>7</sup>, Anvar B. Kerimov<sup>5</sup>, Indrikis Krams<sup>8,9</sup>, Toni Laaksonen<sup>6</sup>, Marko Mägi<sup>8</sup>, Raivo Mänd<sup>8</sup>, Jaime Potti<sup>10</sup>, János Török<sup>11</sup>, Miroslav Trnka<sup>2</sup>, Marcel E. Visser<sup>12</sup>, Herwig Zang<sup>13</sup>, Christiaan Both<sup>1</sup>**

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Many organisms adjust their reproductive phenology in response to climate change, but phenological sensitivity to temperature may vary between species. For example, resident and migratory birds have vastly different annual cycles, which can cause differential temperature sensitivity at the breeding grounds, and may affect competitive dynamics. Currently however, adjustment to climate change in resident and migratory birds have been studied separately or at relatively small geographical scales with varying time series durations and methodologies. Here, we studied differential effects of temperature on resident and migratory birds using annual mean first egg laying dates (hereafter laying date) from ten European nest box schemes between 1991 and 2015 that had data on at least one resident tit species and at least one migratory flycatcher species. We found that both tits and flycatchers advanced laying in response to spring warming, but resident tit populations advanced more strongly in relation to temperature increases than migratory flycatchers. These different temperature responses have already led to a divergence in laying dates between tits and flycatchers of on average 0.7 days per decade over the current study period. Interestingly, this divergence was stronger at lower latitudes where the interval between tit and flycatcher phenology is smaller and winter conditions can be considered more favourable for resident birds. This could indicate that phenological adjustment to climate change by flycatchers is increasingly hampered by competition with resident species. Indeed, we found that tit laying date had an additional effect on flycatcher laying date after controlling for temperature, and this effect was strongest in areas with the shortest interval between both species groups. Combined, our results suggest that the differential effect of climate change on species groups with overlapping breeding ecology affects the phenological interval between them, potentially affecting interspecific interactions.

## Session 10: Climate Change

Date: Thursday 2 November, 2017  
Time: 15:50 – 16:10  
Room: Seminar Room

### **Seasonal decline in fitness: its causes and its relation to warmer springs in northern wheatears**

Presenting author: **Tomas Pärt**

Authors: **Tomas Pärt<sup>1</sup>, Debora Arlt<sup>1</sup>, Jonas Knape<sup>1</sup>, Matt Low<sup>1</sup>, Meit Öberg<sup>1</sup>**

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We investigated 20-year trends in spring timing, breeding time, selection for breeding time and annual demographic rates of northern wheatears. Both thermal progression of spring and breeding time of wheatears advanced in time during the study period, but despite breeding on average 7 days earlier with respect to date, wheatears bred about 4 days later with respect to thermal spring progression. Over the same time period selection for breeding time changed from distinct within-season advantage of early breeding to no or very weak advantage. During the same time period demographic rates (nest success, fledgling production, recruitment, adult survival) and nestling weight declined markedly, by 16-79%. In contrast to the breeding mismatch hypothesis, these dramatic changes in demographic rates and patterns of selection for early breeding were not related to the annual estimates of the thermal timing of breeding. Other analyses suggest a large part of the seasonal decline in fitness is likely driven by a corresponding deterioration of breeding conditions and we therefore suggest a general deterioration of the breeding environment may reduce the benefit of being early and reduce annual demographic rates.