

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.