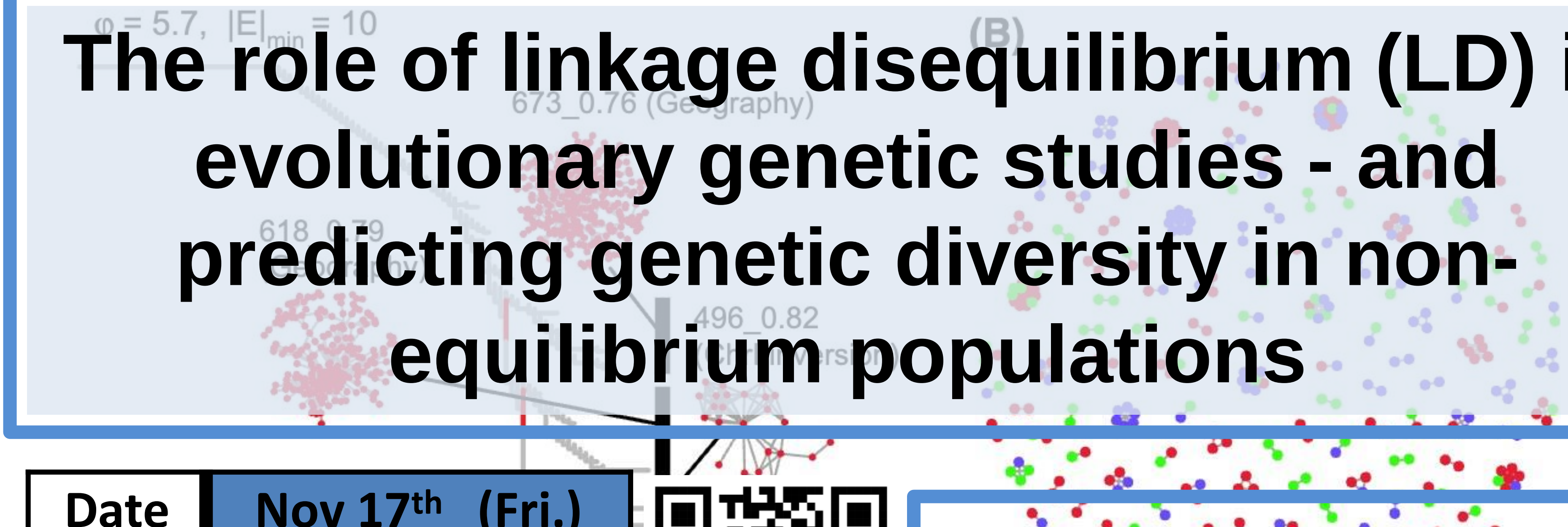
E&B Seminar Series

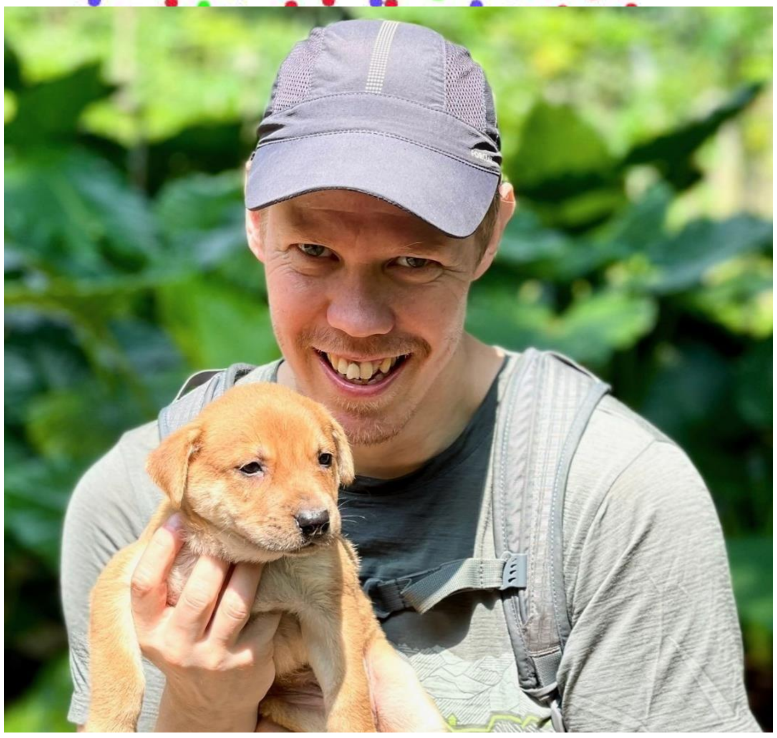
The role of linkage disequilibrium (LD) in evolutionary genetic studies - and predicting genetic diversity in non-equilibrium populations



Date	**Nov 17th (Fri.)**
Time	**16:00 (UTC+8)**
Venue	**3N01 & Zoom**

Abstract

Linkage disequilibrium (LD) estimates non-random allelic associations between loci across genomes. Using LD network analyses (LDna) correlated sets of loci can be partitioned into groups reflecting distinct evolutionary genetic processes and phenomena. Here I will give an overview of how LDna can be utilised in evolutionary genetic research to de-novo study chromosomal rearrangements and sex chromosome evolution as well as to increase statistical power in genome wide association studies, QTL-mapping and when detecting signatures of natural selection in population genomic data. Secondly, using two-dimensional continuous space simulations modelled after the grey reef sharks in the coral triangle, I will outline methods that aim to predict patterns of genetic diversity in equilibrium populations as well as in populations that recently have undergone range expansions.



While Petri may have been brewed in Finland he was definitely bottled in Sweden. He started his career in Sweden studying the ecology and genetics of parallel evolution in marine periwinkles under the wings of Kerstin Johannesson. During his postdoctoral research in UK, Czech Republic, Norway and most recently six years in Helsinki, Finland (in Juha Merilas lab) before moving to HK, he studied evolutionary genetics in a diverse set of species, such as malaria mosquitoes in SE Asia, grey sparrows and three and nine-spined sticklebacks. He has a particular interest in method development and publishing research on how not to analyse data.