



Sveriges lantbruksuniversitet
Swedish University of Agricultural Sciences

**Department of Animal Breeding
and Genetics**

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Computational modelling of genomic inbreeding and homozygosity islands in extremely small populations

Goal

The project aims to use formal models to simulate the expected patterns of genomic inbreeding and homozygosity islands in extremely small populations under selection, such as companion animal breeds.

Background

Extremely effectively small populations, such as companion animal breeds like dogs as well as small isolated natural populations, have high levels of inbreeding while experiencing strong selection on particular traits. These processes both give genomic signatures in the forms of runs of homozygosity, and regions of reduced diversity, respectively. However, the joint presence of both effects complicates detection. Regions ("islands") frequently covered by runs of homozygosity may be due to selection on particular loci.

Project description

This project will combine computational models of the dog genome with inferred population histories from dog breeds to generate predictions of the background distribution of runs of homozygosity and run of homozygosity islands, in situations with and without locus-specific selection. The simulations can be compared against real data, and be packaged up in a reproducible software package for empirical use.

Useful previous knowledge: Some background in population, quantitative or evolutionary genetics. R programming. Interest in inbreeding and/or selection.

Start time: Flexible

Contact

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