Bachelor or Master thesis BIOVIT 2021/22

Topic/Title

Imputation to whole genome sequencing (WGS) for fine mapping and genomic selection in A. salmon

Summary

Use of whole genome sequence data (WGS) is expected to improve identification of quantitative trait loci (QTL) and prediction of genomic breeding values. However, sequencing of large number of individuals is not cost efficient. An alternative is to use genotype imputation. It involves whole genome sequencing of few key individuals, while most individuals are genotyped with a small subset of genome-wide distributed markers (low-density genotyping panel). These sequence data are then used to impute the non-genotyped markers for the individuals genotyped at low-density. The objective of this study was to determine accuracy of WGS imputation in Atlantic salmon (*Salmo salar*) and their application for genome-wide association studies (GWAS) and genomic predictions.

Recently, a new genome assembly for Atlantic salmon is released (NCBI GeneBank reference: GCA_905237065.2), which is constructed using long-read sequencing technologies and expected to improve the quality of genomic resource as well as their applications, including genotype imputation. Whole genome sequence data for ~300 individuals and SNP-chip data from close relatives is available for this task.

Subject area

Genotype imputation, genomic selection, whole genome sequence (WGS), fine mapping

Language thesis

English

Bachelor or Master thesis

Masters

Credits

30/60 ECTS

Project/company

Nofima

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