Bachelor Project

Restricted Maximum Likelihood-Method for Genomic Prediction

Duration: 4 months
Mentors at USI: Prof. Olaf Schenk (USI), Fabio Verbosio
Working place: Lugano, Switzerland

Prerequisites

The requirements are knowledge of MATLAB plus the basics of the BSc courses Introduction to Computational Science and Numerical Computing. During the BSc project, you will be working together with the researchers at the ICS and will have the chance to get familiar with the most important libraries used in numerical linear algebra.

This project aims at the investigation of the state-of-the-art restricted maximum-likelihood method techniques analyzing the details of the different frameworks currently used. In addition, it will be possible to examine performance, advantages, and limitations of the available software. The computing language used will be MATLAB - while it will be possible to use the statistical language R as well - according to the student preferences. The requirements are knowledge of MATLAB plus the basics of Introduction to Computational Science and Numerical Computing. During the BSc project, you will be working together with the researchers at the ICS and will have the chance to get familiar with the most important libraries used in numerical linear algebra.

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In genetics, genomic prediction provides a powerful tool for animal and plant breeding. This process aims at the improvement of breed selection, reducing costs. The mathematical models regulating such process are "mixed models," since they include both fixed and random effects, and the equations describing the model are called "mixed model equations" (MMEs). The MMEs are solved in order to compute the maximum-likelihood estimates for the parameters describing the model. What characterizes MMEs in genomic prediction is the presence of a heterogeneous type of coupling structure between the effects. The different environments in which the genome is studied affect the genomic markers in a sparse or dense way, meaning that the matrices describing the MMEs are dense, but present large sparse blocks. This particular structure has led to the development of a sparse-dense solver for large-scale datasets.

Contact information and application

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