Genome-wide association studies of agronomic traits using individual plants from segregating populations of European maize landraces

Supervised by:

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Background

Using individual plants from segregating populations for proven breeding tools such as genome-wide association studies will be of great interest in the near future. This is due to falling costs associated with genotyping and phenotyping of plants used for breeding research. More so, working with segregating populations will drastically increase genetic gain in time amongst other benefits. This concept then leads us to a groundbreaking approach of looking at the use of phenotypic and genotypic data from large numbers of individual plants for selection and breeding.
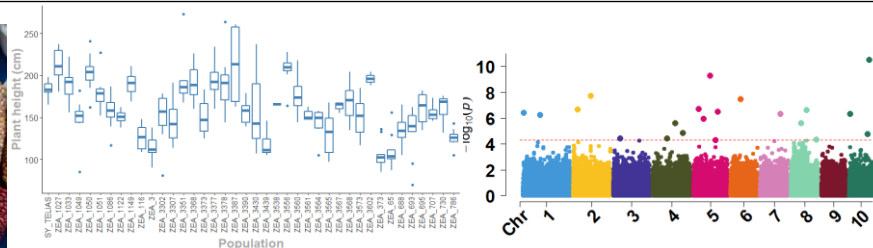
Thesis objectives

- Phenotyping and Phenotypic data analysis
- SNP-calling from individual-plants
- GWAS: marker-trait association of important agronomic traits

Requirements

- Appreciable knowledge of quantitative genetics and population genetics
- Proficiency in working with R (e.g. coursework in statistical genetics and/or data analysis with R)
- Basic knowledge of the Linux command line
- Readiness to code and handle big data

Application

Please send your CV and motivation letter to Prof. Dr. Stefan Scholten (stefan.scholten@uni-goettingen.de) and/or Leke Victor Aiyesa (lekevictor.ayiesa@uni-goettingen.de).