

# Teaching Statement

Martin Mascher

Biology is evolving into a computational science. High-throughput methods in the lab and in the field generate datasets whose size and complexity preclude their easy analysis with ready-made software tools on desktop computers. Scientific computing will become a crucial skill for plant scientists. My primary aim as an academic teacher will be to equip future plant geneticists and breeders with the computational skills to analyze the data they generate. During my Ph.D. studies, I have mentored two M.Sc. students in expression data analysis and database development. My research group at IPK Gatersleben currently unites scientists from diverse backgrounds: an anthropologist, a plant pathologist, a plant geneticist and a bioinformatician. This poses the dual challenge of inspiring enthusiasm for genetics in computer scientists on the one hand and teaching hands-on data analysis skills to researchers with no formal computational training on the other hand. Although I have not had the opportunity to teach classes at IPK Gatersleben - a non-university research center - I did develop course materials and exercises for genetic data analysis in Unix and R for in-coming lab members without a computational background or for local collaborators wishing to analyze their own data. My diverse background ensures that I am qualified to teach a variety of courses at the intersection of statistics, computer science and plant genetics. Specifically, I would be interested in designing and teaching the following courses.

## **Introduction to plant genomics**

This course would provide an overview of both the algorithms and software tools currently applied in plant genomics. Topics to be covered include: genome sequencing and assembly, genetic mapping, and various methods in transcriptomics. Students will be given several small homework exercises to complete during the course that are relevant to each of the topics covered (such as aligning sequences, constructing a genetic map, and finding differentially expressed genes). This class is intended as an introduction for plant genetics majors, but could easily be adapted to graduate students or more advanced undergraduates by adding a basic instruction into scripting with R and Python for data analysis and visualization.

## **Population and statistical genomics**

A graduate level course focusing on the quantitative analysis of genomic data in crop plants. This course will provide sufficient background to students so that they may conduct research in this area. A thorough overview of both data and models in gene mapping, population genetics and characterization of plant genetic diversity will be brought together with the statistical and computational tools necessary for the analysis of whole genomes and large-scale resequencing or genotyping datasets. The course will cover QTL mapping, genome-wide association scans, and the analysis of population structure. A combination of lectures, readings of current literature, and hands-on computer tutorials will familiarize the

students with a variety of computational and statistical techniques to enable them to conduct an original analysis on a self-chosen topic.

### **The evolution of our crops**

An undergraduate course intended for non-majors, the aim would be to relate important advances in plant domestication research to an audience interested in human history and evolution in general. Mixing readings from popular science and introductory texts on genetics, this course would cover three main areas: basic plant genetics, the evolution of crops under domestication, and utilization of genetic variation in crops and their wild relatives in breeding. Additional topics covered under these major headings will include the conservation of plant genetic diversity and the evolution of crop pathogens and resistances. This course will foster critical thought about the role of scientific plant breeding for global food security.