



## **BIO692 – Introduction to Genome-Wide Association Studies (GWAS)**

**Lecturers:** Thomas Wicker (IPMB)  
**Location:** Botanical Garden, University of Zurich  
**Dates:** 20-22.05.2025  
**Credit Points:** 1 ECTS

### **Course Description:**

In this course, we will discuss one of the main tools for identifying genes that underlie natural phenotypic variation: genome-wide association studies (GWAS). At the beginning of the course, we will provide an introduction to GWAS and a brief introduction to the computer language R. Then, we will introduce the principles of genetic mapping of target genes and the genetic and statistical background on which GWAS are based. The course has a strong practical component, and students will gain experience analyzing real data on the computer. At the end of the course, students will be able to interpret GWAS results and carry out their own analyses with their own data. We will also discuss basic concepts (and challenges) in population genetics and genomics. Before the course starts, the students will be asked to complete basic R tutorials. Depending on the number of students, we can provide laptops with the necessary software installed for most or all students. Those students who want to use their own laptops should inform us, so that we can instruct them to install basic software packages on their computers.

### **Course Program:**

The topics covered include:

- Gene mapping approaches
- Interpreting GWAS results
- Identifying promising candidate genes for functional analysis
- Assessing genetic diversity in population data

### **Prior Knowledge:**

A background in genetics is required. Before the course, we will email you with instructions for installing the required software on your computer, if you want to use your own laptop. In addition, we will ask you to complete one or two (brief) R tutorials. Any other previous experience with R will be beneficial.

**Number of Participants:** At a maximum, 12 students

### **Individual Performance:**

This 3-day course will be split between lectures and tutorials. Required: reading (~4-8 or more hours), attendance, and active participation during the course (24 hours).

**Credit Points:** 1 ECTS

**NB:** The course is open to PhD students. Priority will be given to students in Evolutionary Biology and the Plant Sciences. Interested Master's students should contact the instructors.