

UNIL MSc course:
"Genes: from sequence to function 2009"

- Sven Bergmann (SB)
- Carlo Rivolta (CR)
- Johann Weber (JW)
- Roman Chrast (RC)

Course Concept

- Main goal: Introduction to how *knowledge on genes affecting phenotypes* is commonly generated.
- Survey two common *genetic screening approaches* for identifying genetic variants causally related to a particular phenotype:
- [Linkages studies](#) (use family pedigrees in order to identify genetic regions that segregate in family members affected by a particular trait)
- [Genome Wide Association Studies](#) (use profiles of many genetic variants for individuals in a large population)
- Analysis of [Expression studies](#) also uses high-throughput data, but here the observables are at the level of the transcripts.
- Different methods may individually lead to candidate genes, but [Integrative analysis](#) of the vast amounts of data may refine them and teach you about systems properties of the regulatory networks.
- Target Prioritization that makes use of the exiting knowledge accumulated on public repositories is always useful, before embarking on focused [Functional studies](#).

Course Schedule

- 16/09 10:00-12:00 **Introduction (SB)**
- 17/09 10:00-12:00 **Genomic studies: theory (CR)**
- 23/09 10:00-12:00 **Genome Wide Association Studies (SB)**
- 28/09 13:00-15:00 **Expression studies 1 (JW)**
- 28/09 15:00-17:00 **Expression studies 2 (JW)**
- 05/10 13:00-15:00 **Genomic studies: databases and tools 1 (CR)**
- 05/10 15:00-17:00 **Genomic studies: databases and tools 2 (CR)**
- 12/10 13:00-15:00 **Integrative Analysis 1 (SB)**
- 12/10 15:00-17:00 **Integrative Analysis 2 (SB)**
- 26/10 13:00-15:00 **Genomic studies: exercises 3 (CR)**
- 27/10 13:00-15:00 **Functional studies 1 (RC)**
- 27/10 15:00-17:00 **Functional studies 2 (RC)**

Course Information

- **Organizers:**
Sven.Bergmann@unil.ch (021-6925452)
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- **Online information:**
<http://www2.unil.ch/cbg> under Teaching
- **Venue: Biophore BIO/2917b**
(unless arranged otherwise)

Course wiki under <http://www2.unil.ch/cbg>

The screenshot shows a web browser displaying the course wiki page. The page title is "UNIL MSc course: 'Genes: from sequence to function 2009'". The content includes:

- Coordinators:** Carlo Rivolta and Sven Bergmann
- Lecturers:** Sven Bergmann (SB), Carlo Rivolta (CR), Johann Weber (JW) and Roman Chrast (RC)
- Concept of the course:** The lectures give an introduction to how knowledge on genes affecting phenotypes is commonly generated. After a general introduction we survey two common screening approaches that can help identifying genetic variants that are potentially causally related to a particular phenotype under investigation. Linkages studies use family pedigrees in order to identify genetic regions that segregate in family members affected by a particular trait. Genome Wide Association Studies (GWAS) use profiles of many genetic variants for individuals in a large population to reveal those that are associated with the phenotypes measured for these individuals. These approaches screen for interesting regions in the DNA, which may or may not contain genes in the same or opposing transcripts (DNA). In contrast, the analysis of Expression studies also uses high-throughput data, but here the observables are at the level of the transcripts. The different methods may individually lead to candidate genes, but *integrative analysis* of the vast amounts of data generated at different levels may also be pursued to refine them and learn more about systems properties of the regulatory networks. Whatever the approach leading to a list of candidates a *Target Prioritization* that makes use of the exiting knowledge accumulated on public repositories is always useful, before embarking on focused *Functional studies*.
- Lectures:**
 - + 16/09 10:00-12:00 Introduction (SB)
 - + 17/09 10:00-12:00 Genomic studies: theory (CR)
 - + 23/09 10:00-12:00 Genome Wide Association Studies (SB)
 - + 28/09 13:00-15:00 Expression studies 1 (JW)
 - + 28/09 15:00-17:00 Expression studies 2 (JW)
 - + 05/10 13:00-15:00 Genomic studies: databases and tools 1 (CR)
 - + 05/10 15:00-17:00 Genomic studies: databases and tools 2 (CR)
 - + 12/10 13:00-15:00 Integrative Analysis 1 (SB)
 - + 12/10 15:00-17:00 Integrative Analysis 2 (SB)
 - + 26/10 13:00-15:00 Genomic studies: exercises 3 (CR)