

Subject Area: Advanced Methods in Biotechnology and Biodiversity

Subject: Practical bioinformatics

Level: III-PhD

Year: I-IV

Semester: 1-2

Speciality: N/A

Status: Facultative

ECTS: 2

Department(s): Genetics

Cooperating Department:

Form of teaching (Number of hours; Form of assessment: Exam or Credit)

Lectures:	Seminars/Conversatoria	Practicals:	Total:
4		26	30

Staff:

SUBJECT COORDINATOR: Mirosław Kwaśniewski PhD

LECTURE/CONVERSATORIA: Mirosław Kwaśniewski PhD

PRACTICALS: Mirosław Kwaśniewski PhD, Damian Gruszka PhD

Contents:

Organization and content of biological databases, local and Internet accessible tools for bioinformatics.

LECTURES:

Identification of genomic functional elements, identification of DNA regulatory elements, identification of homologous proteins, prediction of proteins function.

PRACTICALS:

Database search for flower formation-related genes in Arabidopsis, preparation of a local database of flower formation-related genes using the Jellyfish software, analysis of expression pattern of flower formation-related genes with use of publicly available databases of Arabidopsis microarray data, analysis of co-expression with flower formation-related marker genes, identification of presumably functional *cis*-acting elements in promoters of co-expressed genes by using the Gibbs method and promoter conservation analysis in orthologous systems, design of promoter-deletion experiment for functional characterization of identified *cis* elements, design of primers for validation of flower-related expression of candidate genes using qPCR method.

Methods and forms of teaching:

Lectures with the use of computer presentations.

Practicals carried out by individual students using computers aided data analysis.

Requirements: Basic knowledge of genetics, biochemistry and cell biology.

Literature (maximum 5, preferably recent sources, all in English):

1. David W. Mount. 2001. Bioinformatics: Sequence and Genome Analysis, Cold Spring Harbor Laboratory Press
2. Arvidsson S, Kwasniewski M, Riano-Pachon DM and Mueller-Roeber B. 2008. QuantPrime – a flexible tool for reliable high-throughput primer design for quantitative PCR. BMC Bioinformatics. 9(1):465
3. Hruz T, Laule O, Szabo G, Wessendorp F, Bleuler S, Oertle L, Widmayer P, Gruissem W and P Zimmermann. 2008. Genevestigator V3: a reference expression database for the meta-analysis of transcriptomes. Advances in Bioinformatics Article ID 420747, doi:10.1155/2008/420747
4. Toufighi K, Brady SM, Austin R, Ly E and Provart NJ. 2005. The Botany Array Resource: e-Northerns, Expression Angling, and promoter analyses. Plant J. 43 :153-63.