

**Code:** 03-2-07

## **STATISTICAL ANALYSIS OF BIOLOGICAL DATA**

**ECTS:** 5

**Course coordinator:** Prof. Dr. Andrej Blejec

**Lecturers:** Prof. Dr. Andrej Blejec

**No. of hours:** 125

**Lectures:** 10

**Seminar:** 10

**Lab. work:** 20

**Other:** 85

### **2. Entry requirements:**

At least 3 to 5 ECTS gained in basic statistics in previously completed studies.

### **3. Objectives of the course and intended learning outcomes : (competences)**

Educational aims: The student builds on understanding of statistical methods with more demanding methods required in research work. The stress is on conceptual understanding of methods, comparability of methods for various problems and independent analysis of data with the aid of up-to-date software (R).

Intended learning outcome: The student is trained for as independent as possible selection of suitable methods and analysis of problems with which he or she is dealing. The achieved knowledge will help him or her in communication with statistical experts and with suitable inclusion of statistical results in reports and scientific articles.

### **4. Syllabus outline:**

1. Review of basic statistical methods and their use for the analysis of data. Statistical testing of assumptions. Methods of studying the dependence of phenomena.
2. Basis of use of the environment for analysis of data »R«. Types of data, preparation and arrangement of data. Entry and extraction of data, exchange of data with other programme environments. Graphic presentation of data. Preparation of own functions. Statistical distribution and simulation of data. Analysis of data with R.
3. Review of methods of multivariate analysis. Basic concepts of linear algebra for use in statistics of multidimensional data. Vector algebra, matrices and matrix calculation, concept of own values and own vectors. Statistical and geometric interpretation of concepts of linear algebra. Method of main components, discrimination analysis, factorial analysis, classifying in groups, visualisation of data.
4. Statistical background to analysis of micronets. Plan of experiment, preparation of data, methods for removing background noise, normalisation of data, analysis of differential expression, graphic presentation and visualisation of results, analysis of networks, linkage with databases and ontologies on the internet.
5. Selected methods for data analysis. The selection of special methods will be adapted to the orientation and field of work of students.

## **5. Literature (in the case of books and monographs, study sources are only selected chapters from them):**

- Venables WN: An Introduction to R, 2008,
- <http://cran.r-project.org/doc/manuals/R-intro.pdf>
- McGarigal K, Cushman S, Stafford S, 2000, Multivariate Statistics for Wildlife and Ecology Research, Springer, ISBN 0-387-98642-1.
- Schena M in Knudsen S, 2004 Guide to Analysis of DNA Microarray Data: Microarray Analysis Set, Willey-Liss, ISBN: 9780471678533
- Various internet sources.

## **6. Teaching methods:**

- lectures,
- laboratory exercises,
- consultations,
- seminar tasks.

## **7. Assessment methods:**

- seminar task,
- oral examination.

## **8. References:**

### **Blejec Andrej**

1. PIPAN, Tanja, BLEJEC, Andrej, BRANCELJ, Anton. Multivariate analysis of copepod assemblages in epikarstic waters of some Slovenian caves. Hydrobiologia (Den Haag), 2006, št. 559, p. 213-223, graf. prikazi. [COBISS.SI-ID 24875053] JCR IF: 1.049, SE (45/79), marine & freshwater biology, x: 1.325
2. FIŠER, Cene, BININDA-EMONDS, O. R. P., BLEJEC, Andrej, SKET, Boris. Can heterochrony help explain the high morphological diversity within the genus Niphargus (Crustacea: Amphipoda)?. Org. divers. evol. (Print), 2008, vol. 8, no. 2, p. 146-162. <http://dx.doi.org/10.1016/j.ode.2007.06.002>. [COBISS.SI-ID 1748559] JCR IF (2006): 1.127, SE (30/34), evolutionary biology, x: 3.202
3. ROTTER, Ana, HREN, Matjaž, BAEBLER, Špela, BLEJEC, Andrej, GRUDEN, Kristina. Finding differentially expressed genes in two-channel DNA microarray datasets: how to increase reliability of data preprocessing. Omics (Larchmt. N.Y.), 2008, vol. 12, no. 3, 12 p., [in press]. <http://dx.doi.org/10.1089/omi.2008.0032>. [COBISS.SI-ID 1888847] JCR IF (2006): 2.056, SE (61/140), biotechnology & applied microbiology, x: 2.589, SE (79/131), genetics & heredity, x: 3.644