Methods of Metabolomics, Proteomics and Signaling in Plant Physiology

1. <u>Lecturer:</u> Samoilov Andrii Myhaylovych, senior lecturer of the department of plant and microorganism physiology and biochemistry.
2. Status: optional for masters.
3. Course, semester: 1th academic year, 2th semester.
4. Number of credits – 4, general academic hours – 120, labs – 44; self-study – 76.
5. Preliminary requirements: basics of Biochemistry, Microbiology, Genetics, Biotechnology, Molecular Biology, Plant Physiology and Biochemistry
6. <u>Description of the course:</u> the main purpose of the special lab practice is to form practical skills and ability to use methods of bioinformatics in the study and analysis of the proteome, genome, metabolome or signaling systems of plants, and to work with metabolic, genetic and protein databases; to find, process and analyze biological information; to simulate biological molecules and analyze their structure and function. Within the special practice basic bioinformatic methods, work with online resources and software packages are trained.

   <u>Sections:</u> 1) Work with database, search and analysis of the proteome, genome and metabolome of plants. 2) Modeling the spatial structure of biomolecules and study their properties and functions in the proteome, metabolome and signaling roles.

   <u>Knowledge and skills:</u>
   - Work with genomic databases
   - Work with proteomic bases
   - Work with metabolic bases
   - Work with software packages and online services of analysis of biological data
   - Mathematical and statistical models in bioinformatics
   - Search for genes, proteins and metabolic signaling pathways and analyze their structural and functional relationships;
   - Use of biological databases and software to analyze biological information;
   - Use of bioinformatics methods in related areas of biology.
7. Course organization: lab practice. Forms of control: tests, lab protocols.
8. Language: Ukrainian.
9. Educational and methodological support: program, schedule of classes, educational and multimedia presentations, methodical complex, guidelines for practice.

   <u>Studentbooks:</u>
   1. *Леск А.М.* Введение в биоинформатику. – М.: БИНОМ, 2009. – 324 с.
   2. *Дурбин Р., Эдди Ш. и др.* Анализ биологических последовательностей. – М.: Изд-во Ин-та компьютерных исследований, 2006. – 480 с.
   3. *Хельтье Х.-Д. и др.* Молекулярное моделирование. Теория и практика. – М.: БИНОМ, 2010. – 320 с.
   4. *Jin Xiong* Essential Bioinformatics. – Cambridge University Press, 2006. – 362 p.
   5. http://www.ncbi.nlm.nih.gov/guide/training-tutorials/
   6. http://www.ncbi.nlm.nih.gov/home/learn.shtml
   7. http://www.ensembl.org/info/website/tutorials/index.html
   8. http://pdb101.rcsb.org/#Posters-Exhibits
   9. http://genome.ucsc.edu/training/index.html