

Zapraszamy na kurs zamawiany (15-21.04.2011):

Introduction to Bioinformatics

WYKŁADOWCA: Dr JC Nebel (Kingston University, Wlk. Brytania)

osoba kontaktowa na PWr: Dr hab. inż. Małgorzata Kotulska

Inżynierii Biomedycznej i Pomiarowej, WPPT, D1-115

TERMINY ZAJĘĆ

15.IV.2011 (pt) godz. 17.00-18.30 (2h) sala 304/D1, wykład

15.IV.2011 (pt) godz. 19.00-20.30 (2h) sala 012/D1, lab

18.IV.2011 (pn) godz. 17.00-18.30 (2h) sala 204/A1, wykład

18.IV.2011 (pn) godz. 19.00-20.30 (2h) sala 012/D1, lab

19.IV.2011 (wt) godz. 17.00-18.30 (2h) sala 204/A1, wykład

19.IV.2011 (wt) godz. 19.00-20.30 (2h) sala 012/D1, lab

20.IV.2011 (śr) godz. 17.00-18.30 (2h) sala 012/D1, lab

20.IV.2011 (śr) godz. 19.00-20.30 (2h) sala 204/A1, wykład

21.IV.2011 (czw) godz. 17.00-18.30 (2h) sala 204/A1, wykład

21.IV.2011 (czw) godz. 19.00-20.30 (2h) sala 012/D1, lab

MODULE SUMMARY (INDICATIVE)

AIMS

- To provide students with basic knowledge of bioinformatics methods such as sequence alignment, evolutionary tree building and structure prediction.
- To prepare students for analysing requirements of bioinformatics users, writing their own bioinformatics applications and using specialised software.

LEARNING OUTCOMES: on successful completion of the module, students will be able to:

- State and explain the motivations for using bioinformatics
- Explain the digital nature of genetic information
- Describe and compare various bioinformatics algorithms and their potential use in other fields
- Be able to analyse and describe the requirements of bioinformatics users
- Enumerate the principal software and databases for bioinformatics
- Comment on research papers on topics associated with bioinformatics
- Apply the knowledge gained to research and development in bioinformatics

CURRICULUM CONTENT (INDICATIVE)

- Digital nature of genetic information: the central dogma (DNA, RNA and proteins);
- Sequence alignment: graphical comparison, dynamic programming and multiple alignments;
- Evolutionary tree building: clustering and neighbour joining methods;
- Structure prediction and classification: statistical, 3D simulation and 3D alignment techniques;
- Data mining and classification: machine learning approaches;
- Applications of bioinformatics: DNA fingerprinting, taxonomy, gene therapy, GMO, drug design;
- Social, economical and ethical issues that arise in bioinformatics