

Bioinformatics - a user's approach

13-16 March 2007, Wageningen University, The Netherlands

Instructors: Prof. dr. J. Leunissen (Bioinformatics, Wageningen University, NL) & Dr. David Judge (Genetics, University of Cambridge, UK)

Aim: The aim of this course is to present a *hands-on* approach to bioinformatics utility software for computing novices. The course will provide an overview of available software, discuss some of the ideas behind the approaches and tackle some common tasks.

Content: There will be a mixture of lectures and frequent practical sessions. The course has many practical examples which try to follow typical mini projects so that the relevance is apparent. Topics that will be addressed during the morning and afternoon sessions include accessing, searching and retrieval information from various Internet Data Resources (e.g. non-sequence databases, the Genome Database, clinical databases, sequence databases, etc.); Sequence analysis and alignment (e.g. BLAST, dotplot, ORF identification and translation, restriction maps; primer design, etc.); Advanced sequence analysis (e.g. scoring matrices, genetic code scoring, chemical similarity, observed substitutions, etc.); Database mining (e.g. BLAST, FASTA, BLITZ, etc); Gene, identification (e.g. Genscan, etc.), prediction and annotation, as well as Computational protein analysis (e.g. proteins sequence analysis, paralogous and orthologous sequences, primary and secondary structure, sequence motifs and domains, multiple sequence alignments, tertiary and quaternary structure, etc).

Level: Novice

Length: 4 full days, from 13 – 16 March 2007

Time: 9.30 am till about 17.30 pm

Location: Room PC-20, Agrotechnion (building no. 309), Bomenweg 4, 6703HD, Wageningen, The Netherlands.

Fee: € 150,-- for PhD's with approved iTSP's of EPS, VLAG, PE&RC and WIAS, and postdocs of EPS; all others € 250,--

Registration: course-registration@graduateschool-eps.info , mentioning course Bioinformatics.