Katedra aplikovanej informatiky
Fakulty matematiky, fyziky a informatiky UK,
Katedry biochémie a genetiky
Prírodovedeckej fakulty UK,
a občianske združenie *NATURA*
v spolupráci so
Slovenskou spoločnosťou pre biochémiu a molekulárnu biológiu

Vás pozývajú na 72. prednášku v rámci Kuželových seminárov:

Dr. Carolin Kosiol

Institute of Population Genetics
University of Veterinary Medicine Vienna

Detecting natural selection with empirical codon models

ktorá sa uskutoční **27. novembra 2009** (piatok) o **14:00**

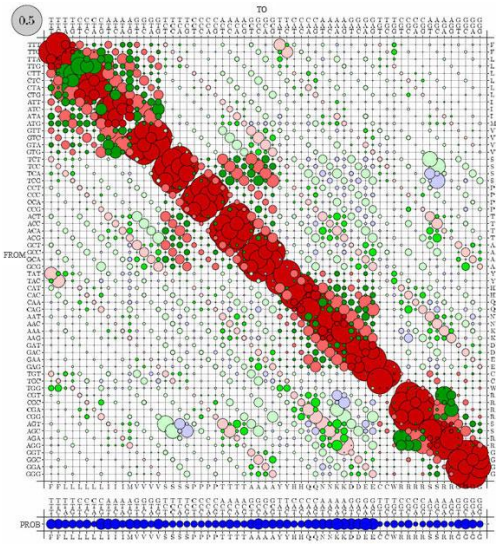
v miestnosti **CH1-222** Prírodovedeckej fakulty UK

http://www.naturaoz.org/seminare.html

Dr. Carolin Kosiol

Education:
1993-1999: Studies in Maths, Physics and Philosophy, Mainz University, Germany
1999-2000: MSc High Perfomance Computing, Trinity College Dublin, Ireland
2000-2002: Trinity Centre of High Performance Computing, Dublin, Ireland
2002-2006: PhD, European Bioinformatics Institute and Cambridge University, UK
(Thesis title: Markov Models for Protein Sequence Evolution,
supervisor: Dr. Nick Goldman)

Research Experience:
2006-2008: Postdoctoral Research, Cornell University, USA
(Advisors: Drs. Adam Siepel and Carlos D. Bustamante)
2009-present: Group Leader in Bioinformatics, Institute of Population Genetics, Veterinary Medical University Vienna, Austria.



The statistical modelling of the evolutionary process is of great importance when performing systematic studies, because it enables us to make inferences about evolutionary relationships of genes, proteins and genomes and organisms of particular interest and to study the processes and pressures of molecular evolution itself. The estimation of empirical codon models sheds new light on recently discussed questions about biological pressures and processes acting during codon sequence evolution. Dr. Kosiol´s results show that modelling the evolutionary process is improved by allowing for single, double and triple nucleotide changes; the affiliation between DNA triplets and the amino acid they encode is a main factor driving evolution; and the nonsynonymous-synonymous rate ratio is a suitable measure to classify substitution patterns observed for different proteins. However, comparing models estimated from genomic data and polymorphism data indicates that double and triple changes are not instantaneous. This new view of how codon evolution proceeds leads to consequences for selection studies. Dr. Kosiol will discuss that under the new empirical codon model purifying selection is less purifying and that cases of positive selection are observed weaker than under the standard codon models.

Recent publications:

1. Anisimova M, **Kosiol C**. (2009). Investigating protein-coding sequence evolution with probabilistic codon substitution models. *Molecular Biology and Evolution* 26: 255-271.
2. **Kosiol C**, Vinar T, da Fonseca RR, Hubisz MJ, Bustamante CD, Nielsen R, and Siepel A. (2008). Patterns of positive selection in six mammalian genomes. *PLoS Genetics* 4: e1000144.
3. Blekhman R, Man O, Herrmann L, Boyko AR, Indap A, **Kosiol C**, Bustamante CD, Teshima KM and Przeworski M. (2008). Natural selection on genes that underlie human disease susceptibility. *Current Biology* 18: 883-889.
4. Rhesus Macaque Genome Sequencing and Analysis Consortium. (2007). Evolutionary and biomedical insights from the rhesus macaque genome. *Science* 316: 222-234.
5. **Kosiol C**, Holmes I, and Goldman N. (2007). An empirical codon model for protein sequence evolution. *Molecular Biology and Evolution* 24: 1464-1479.