Katedra aplikovanej informatiky FMFI UK,
Katedry genetiky a biochémie PriF UK
a občianske združenie *NATURA*
v spolupráci so
Slovenskou spoločnosťou pre biochémiu a molekulárnu biológiu

Vás pozývajú na 78. prednášku v rámci Kuželových seminárov:

Adam Siepel

Cornell University, USA

Bayesian inference of ancient human demography from individual genome sequences

ktorá sa uskutoční **9. marca 2011** (streda) o **14:00**

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

http://www.naturaoz.org/seminare.html
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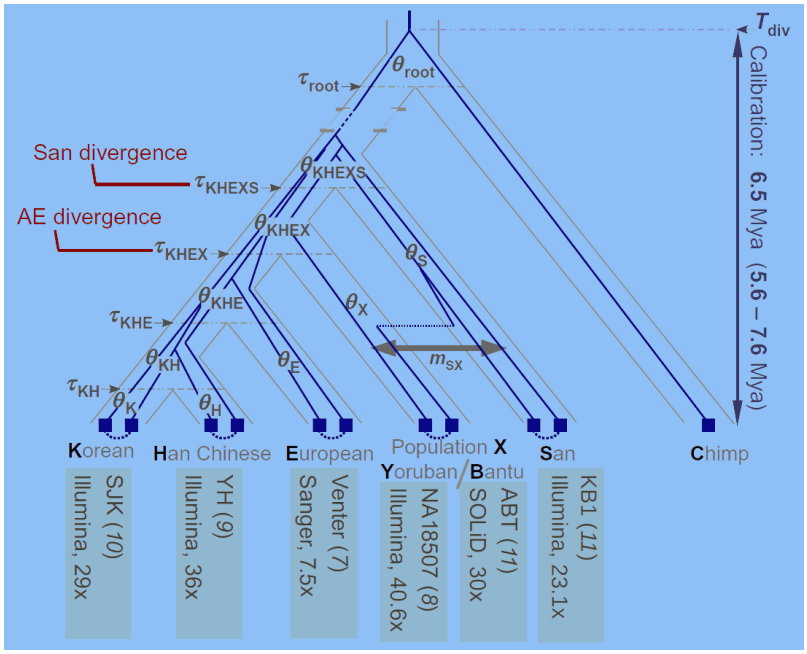
*hostiteľ: dr. Tomáš Vinař, Katedra aplikovanej informatiky FMFI UK

Dr. Adam Siepel is an Associate Professor in the Department of Biological Statistics and Computational Biology at Cornell University. His research focuses on comparative genomics, particularly of mammals, and includes a mixture of statistical modeling, algorithms development, software implementation, and scientific discovery. Siepel received a B.S. in Agricultural and Biological Engineering from Cornell in 1994, then worked in software development for bioinformatics for several years in the late 1990s, first at Los Alamos National Laboratory and then at the National Center for Genome Resources in Santa Fe. In 2001, he received an M.S. in Computer Science from the University of New Mexico, and, in 2005, a Ph.D. in Computer Science from UC Santa Cruz. Siepel is a winner of a Microsoft Research New Faculty Fellowship, a Packard Fellowship, a Sloan Fellowship, and a National Science Foundation CAREER Award. He currently serves as an associate editor for PLoS Computational Biology, on the Program Committee of the RECOMB computational biology conference, and as an associate director for the Cornell Center for Comparative and Population Genomics (3CPG). He has also served on the editorial board of Genome Research, on review panels for the National Science Foundation and the National Institutes of Health, and on advisory committees for the National Human Genome Research Institute. Siepel teaches courses in computational genomics and machine learning at Cornell, and is a member of the graduate fields of Computational Biology, Computer Science, Biometry, Applied Mathematics, and Genetics & Development.

Synopsis of the lecture:



Complete genome sequences are now available for individuals from several major human population groups. Here we describe an effort to estimate key evolutionary parameters from the complete genome sequences of six individuals from six different populations. Employing a Bayesian approach based on coalescent theory, we extracted information about ancestral population sizes, divergence times, and migration rates from inferred genealogies at many neutrally evolving loci from across the genome. To analyze data from human individuals, we modified previous methods to account for gene flow between populations and to integrate over possible phasings of diploid genotypes. We also developed a custom pipeline for genotype inference to mitigate possible biases from heterogeneous sequencing technologies, coverage levels, and read lengths. We estimate that the most recent common ancestral population of modern humans lived 108-157 thousand years ago (kya) and had an effective size of ~9,000, and that Eurasian and West African populations diverged 38-64 kya.

Recent publications:

Hubisz, M.J., Lin, M.F., Kellis, M., Siepel, A. (2011). Error and error mitigation in low-coverage genome assemblies. *PloS One*. **14**: e17034.

Pollard, K.S., Hubisz, M.J., Rosenbloom, K.R., Siepel, A. (2010). Detection of nonneutral substitution rates on mammalian phylogenies. *Genome Res*. **20**: 110-121.

Siepel, A. (2009). Phylogenomics of primates and their ancestral populations. *Genome Res*. **19**:1929-1941.

Kosiol, C., Vinař, T., da Fonseca, R.R., Hubisz, M.J., Bustamante, C.D., Nielsen, R., Siepel, A. (2008). Patterns of positive selection in six mammalian genomes. *PloS Genet*. **4**: e1000144.