31
JAN.
2013

de 11h à 12h

SÉMINAIRE

Inference of natural selection on human transcription factor binding sites

Adam Siepel
Professor, Biological Statistics & Computational Biology,Cornell University, USA

http://compgen.bscb.cornell.edu/~acs/Quelques références représentatives:· Guertin MJ*, Martins AL*, Siepel A, Lis JT. Accurate prediction of inducible transcription factor binding intensities in vivo. PLoS Genetics, 2012;8(3):e1002610.· Lindblad-Toh K, Garber M, Zuk O, Lin MF, Parker BJ, et. al. (63 co-authors). A high-resolution map of evolutionary constraint in the human genome based on 29 eutherian mammals. Nature 478(7370):476-482, 2011.· Gronau I, Hubisz MJ, Gulko B, Danko CG, Siepel A. Bayesian inference of ancient human demography from individual genome sequences. Nature Genetics 43(10):1031-1034, 2011.· Lowe CB, Kellis M, Siepel A, Raney B, Clamp M, Salama SR, Kingsley D, Lindblad-Toh K, Haussler D. Three different periods of regulatory innovation during vertebrate evolution. Science 333(6045):1019-1024, 2011.· Hubisz MJ, Pollard KS, Siepel A. PHAST and RPHAST: Phylogenetic analysis with space/time models. Briefings in Bioinformatics 12(1):41-51, 2011.· Vinar T, Brejova B, Song G, Siepel A. Reconstructing histories of complex gene clusters on a phylogeny. J Comput Biol 17(9):1267-1279, 2010.· Pollard KS, Hubisz MJ, Rosenboom K, Siepel A. Detection of non-neutral substitution rates on Mammalian phylogenies. Genome Res, 20:110-121, 2010.· Siepel A. Phylogenomics of primates and their ancestral populations. Genome Res, 19:1929-1941, 2009.· Kosiol C, Vinar T, da Fonseca RR, Hubisz MJ, Bustamante CD, Nielsen R, Siepel A. Patterns of positive selection in six mammalian genomes. PLoS Genet, 4(8):e1000144, 2008..

URL de la page : https://lbbe.univ-lyon1.fr/fr/agenda/inference-natural-selection-human-transcription-factor-binding-sites?is_pdf=true