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SÉMINAIRE

Inference of natural selection on human transcription factor binding sites

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<http://compugen.bsccb.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..