

SYMPOSIUM

Next Generation Comparative Phylogenomics

4 June 2014 – Centre Médical Universitaire (CMU), Geneva - Auditorium C150

9:30-9:40	Ioannis Xenarios <i>SIB Swiss Institute of Bioinformatics, Switzerland</i> Welcome
Session I:	Methods for Phylogenomics Chair: Evgeny Zdobnov
9:40-10:25	Des Higgins <i>Conway Institute, University College Dublin, Ireland</i> "Making accurate multiple sequence alignments of very large numbers of protein sequences"
10:25-11:10	Eyal Privmann <i>Institute of Evolution, University of Haifa, Israel</i> "Alignment reliability, alignment filtering, and their effect on downstream evolutionary analyses"
11:10-11:40	Coffee
11:40-12:25	Maria Anisimova <i>Institute of Applied Simulations, Zurich University of Applied Sciences (ZHAW), and Computer Science Department, Swiss Federal Institute of Technology (ETH), Zurich, Switzerland</i> "Current standards in phylogenomics as applied to sequences with tandem repeats"
12:25-13:45	Lunch break
Session II:	Applied Phylogenomics Chair: Michel Milinkovitch
13:45-14:30	Vincent Daubin <i>Biometry and Evolutionary Biology laboratory (LBBE), National Center for Scientific Research (CNRS), Lyon, France</i> "Genomes as documents of evolutionary history"
14:30-15:15	Shinichi Sunagawa <i>European Molecular Biology Laboratory (EMBL), Heidelberg, Germany</i> "Quantitative metagenomics of the human gut and ocean microbiome"
15:15-15:45	Coffee
15:45-16:30	Margarida Cardoso Moreira <i>Center for Integrative Genomics, University of Lausanne, Switzerland</i> "Functional evolution of mammalian genomes"
16:30-17:00	Panel discussion Moderator: Marc Robinson-Rechavi "Thousands of phylogenies with thousands of species, then what?"