

	June 25 Wednesday Substitution models	June 26 Thursday Parameter estimation	June 27 Friday Statistical alignment	June 28 Saturday Power of the methods	June 29 Sunday Advanced models
8:30-9:10	Registration starts at 8:00 Greetings of the director 9:00 Announcements: 9:05	Alexei Drummond: <i>Non-parametric modeling of population history using the coalescent</i>	Ian Holmes: <i>Transducers: an emerging probabilistic framework for modeling indels on trees</i>	Bhalchandra Thatte: <i>Convergence of the TKF91 model</i>	Jens Lagergren: <i>Bayesian Gene/Species Tree Reconciliation and Orthology Analysis Using MCMC</i>
9:10-9:50	Bret Larget: <i>Markov chain Monte Carlo algorithms for the Bayesian analysis of phylogenetic trees</i>	Marc Suchard: <i>Fast, accurate and simulation-free stochastic mapping: effective tests for evolutionary innovation</i>	Rahul Satija: <i>Statistical alignment and rate heterogeneity</i>	Istvan Miklos: <i>Speed of convergence of MCMC methods</i>	Miklos Csuros: <i>Intron evolution</i>
9:50-10:10	Coffee break	Coffee break	Coffee break	Coffee break	Coffee break
10:10-10:50	Gerton Lunter: <i>A nucleotide substitution model with nearest-neighbour interactions</i>	Gerton Lunter: <i>Probabilistic whole-genome alignments reveal high indel rates in the human and mouse genomes</i>	Istvan Miklos: <i>Protein structure prediction with statistical alignment</i>	Dirk Metzler: <i>Galton-Wattson process and statistical alignment</i>	Ben Redelings: <i>Modelling indel hotspots when inferring alignments</i>
10:50-11:30	Alexei Drummond: <i>Relaxing the molecular clock for phylogenetic inference</i>	Jeff Thorne: <i>Adding Phenotype and Population Genetics to Interspecific Evolution</i>	Rune Lyngsoe: <i>Statistical alignment with spannoids</i>	Mike Steel: <i>Some mathematical aspects of Bayesian phylogenetics</i>	Bret Larget: <i>Bayesian analysis of metazoan mitochondrial genome arrangements</i>
11:30-12:10	Istvan Miklos: <i>Gain, loss, duplication model</i>	Ian Holmes: <i>XRate: a fast prototyping, training and annotation tool for phylo-grammars</i>	Ian Holmes: <i>Discovery, alignment and reconstruction of structured RNA</i>	Marc Suchard: <i>Temporal-spatial smoothing in phylogenetics</i>	Dirk Metzler: <i>MCMC RNA structure prediction</i>
12:10-14:00	Lunch	Lunch	Lunch	Lunch	Lunch

	June 25 Wednesday	June 26 Thursday	June 27 Friday	June 28 Saturday	June 29 Sunday
14:00-15:00	Georgia Tsagkogeorga: <i>Updating tunicate phylogeny: Bayesian analysis of 18S rRNA sequences</i> Bastien Boussau: <i>Parallel adaptations to high temperatures in the Archean Eon</i>	Vladimir N. Minin: <i>Bayesian phylogenetic mapping of recombination hot-spots</i> Yosef E. Maruvka: <i>New methods for inferring ancient migration rates, using genetics variation, applied to prehistoric human migration</i>	Elena Rivas: <i>Probabilistic phylo-genetic inference with insertions and deletions</i> Alexander V. Alekseyenko: <i>Wagner and Dollo: a stochastic duet by composing two parsimonious solos</i>	Discussion: The power of the methods	Discussion: What's next?
15:00-15:30	Coffee break	Coffee break	Coffee break	Coffee break	Coffee break
15:30-17:00	Software demos: MrBayes, BEAST, XRate	Discussion: The state-of-the-art of modelling the molecular evolution	Bengt Autzen: <i>The 'star-tree paradox' in Bayesian phylogeny</i> Software demos: Statistical alignment software packages	Informal discussions	Informal discussions
17:00-19:00	Wine & cheese party	Informal discussions	Informal discussions		
19:00-		Dinner	Dinner	River trip	Dinner