

PhyloGroup 9
Friday 11 December 2009
EBI, Hinxton

Programme

- 10:00 - 10:25 *Coffee on arrival*
- 10:30 - 10:55 Minh Anh Thi Nguyen (CIBIV)
Evaluating the goodness of fit between a phylogenetic model and an alignment
- 10:55 - 11:20 Ari Loytynoja (EMBL-EBI)
Progressive alignment of sequence graphs with insertion-deletion history
- 11:20 - 11:45 Simon Whelan (Manchester)
A phylogenetic method for inferring rate shifts during the evolution of plastids
- 11:45 - 12:10 Martin Taylor (EMBL-EBI)
Simultaneous mutations and the one-step birth of RNA stem structures
- 12:10 - 13:10 *Lunch*
- 13:10 - 13:35 Daniel Money (Manchester)
Characterising the phylogenetic tree-search problem
- 13:35 - 14:00 Radoslaw Suchecki (UEA)
A new tool for triplet-based phylogenetic network reconstruction
- 14:00 - 14:25 Mareike Fischer (CIBIV)
Hereditary maximum parsimony trees - or not so hereditary ones
- 14:25 - 14:50 Anne Kupczok (Vienna)
Consequences of different null models on the tree shape bias of supertree methods
- 14:50 - 15:20 *Tea and biscuits*
- 15:20 - 15:45 Samir Bhatt (Oxford)
Site frequency based methods for detecting viral adaptation
- 15:45 - 16:10 Seena Shah (NIMR, MRC)
Analysis of host-parasite incongruence in Papillomavirus evolution using importance sampling
- 16:10 - 16:35 Asif Tamuri (NIMR, MRC)
Identifying changes in selective constraints: host shifts in influenza
- 16:35 - 17:00 Mario dos Reis (NIMR, MRC)
Host adaptation and pandemic potential of influenza viruses

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Participants

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