

SOUTH 2012 - PROGRAM

- UPDATED 23 JANUARY 2012



Sunday 29 January

17:00 – 20:00 Registration and reception (Edward Percival Marine Lab)

Monday 30 January [Phylogenetic models and methods]

09:00–09:25 Registration

09:25–09:30 Greetings and opening

Session 1 [Chair: Mike Steel]

09:30–09:50 DAVID LIBERLES

Towards a general model for duplicate gene retention and loss

09:50–10:10 Aaron Kleinman*

The size of common subtrees of pairs of phylogenetic trees

10:10–10:30 Remco Bouckaert

Beast 2

10:30–11:00 Morning break

Session 2 [Chair: Michael Charleston]

11:00–11:20 Mareike Fischer

The impact of ‘non-heredity’ on tree reconstruction in practice

11:20–11:40 Joe Zhu*

Clade probabilities under neutral evolutionary models

11:40–12:00 Lars Jermiin

MtArt-2012: A new MtArt model of amino acid substitutions

12:00–14:00 Lunch

Session 3 [Chair: Mareike Fischer]

14:00–14:20 Ruriko Yoshida

Nonparametric estimation of phylogenetic tree distributions

14:20–14:40 Denise Kuhnert*

Inferring epidemiological parameters while reconstructing phylogenetic histories

14:40–15:00 Bennet McComish*

Multiple optima of likelihood on trees from real data

15:00–15:30 Afternoon break

- Session 4** [Chair: Lars Jermiin]
- 15:30–15:50 Barbara Holland
Distance corrections for Dollo data
- 15:50–16:10 Chieh-His Wu*
Bayesian model selection of substitution models and their site assignments
- 16:10–16:30 Stephane Guindon
From trajectories to averages: an improved description of the heterogeneity of substitution rates along lineages
- 17:00–19:00 Dinner -- cooked seafood barbeque (on-site).
- 19:00–19:30 David Penny
What are the next set of unsolved problems for genomics and evolution?

Tuesday 31 January [Phylogenetic Networks]

- 09:25–09:30 Greeting and notices
- Session 1** [Chair: Charles Semple]
- 09:30–09:50 Jennifer Hoyal Cuthill
Cophylogenetics and the study of bacterial lateral gene transfer
- 09:50–10:10 Simone Linz
Picking cherries to merge phylogenetic trees into a temporal network
- 10:10–10:30 Michael Charleston
Practical approaches to cophylogenetic analysis
- 10:30–11:00 Morning break
- Session 2** [Chair: Stephane Guindon]
- 11:00–11:20 Leo van Iersel
Approximating the minimum number of reticulations needed to explain two conflicting gene trees
- 11:20–11:40 Josh Collins*
Finding maximal acyclic agreement forests
- 11:40–12:00 Anthony Poole
Illuminating the twilight zone of sequence similarity: use of phylogenetic networks of protein structure for classification of superfamilies

12:00-14:00 Lunch

Session 3 [Chair: Simone Linz]

14:00-14:20 Charles Semple
Realizing phylogenetic networks with local information

14:20-14:40 Louis Ranjard
Estimating dispersal from genealogies

14:40-15:00 Jonathan Mitchell*
Distinguishing convergence in phylogenetic models

15:00-15:30 Afternoon break

Session 4 [Chair: Leo van Iersel]

15:30-15:50 Jessica Leigh
Where now for haplotype networks? A review and some open problems

15:50-16:10 David Bryant
Where now for phylogenetic networks? A review and some open problems

Discussion [Chairs: Barbara Holland, David Bryant]

16:10-16:50 Discussion [Phylogenetic networks]

17:00 Peninsula walk to view seals (low tide= 18:01, 0.6m)

Dinner (own arrangements)

Wednesday 1 February

All day Excursions, discussions

Dinner (own arrangements)

19:30 – 20:00 Refreshments, discussions

20:00 – 20:45 Slide show/talk: Leo van Iersel (volunteer work in Africa)

Thursday 2 February

09:00–9:10 Greeting and notices

Session 1 [Phylogenetic theory; Chair: Raaz Sainudiin]

09:10–09:30 Katherine St John

Walks of treespace

09:30–9:50 Helen Shearman*

A comparison of phylogenetic diversity and maximum minimum distance

09:50–10:10 David Marshall

Difficulties with tree-length estimation in likelihood-based phylogenetic analyses

10:10–10:30 Jeremy Sumner

Is the general time-reversible model bad for molecular phylogenetics?

10:30- 11:00 Morning break

Session 2 [Population processes; Chair: Anthony Poole]

11:00–11:20 Joseph Heled

The coalescent and local mixing

11:20–11:40 Stefan Prost*

Implementing demographic models in the study of human history in the Pacific

11:40–12:00 Raaz Sainudiin

Ancestries of recombining population pedigrees

12:00–14:00 Lunch

Session 3 [Structure; Chair: Stefan Klaere]

14:00–14:20 Scott Schmidler

Bayesian protein structure alignment and phylogeny

14:20–14:40 Paul Gardner

Annotating a plethora of RNA motifs

14:40–15:00 Afternoon break

- Session 4** [Real biology; Chair: Paul Gardner]
15:00–15:20 Chris Simon
A more detailed look at species swarms in the NZ cicada genus *Kikihia*
15:20–15:40 Nicole Gruenheit
Transcriptomics of NZ alpine plants
15:40–16:00 Bojian Zhong*
Systematic error in seed plant phylogenomics

18:00 Dinner at Tutis restaurant (35 Beach Road)

Friday 3 February

- 09:25–09:30 Greeting and notices
- Session 1** [Chair: Katherine St John]
09:30–09:50 Stefan Gruenwald
The quartet distance between phylogenetic trees
09:50–10:10 Steffen Klaere
Goodness of fit tests in phylogeny
10:10–10:30 Gillian Gibb
Next generation mitogenomics: new results from modern and fossil xenarthrans

10:30–10:50 Morning break
- Session 2** [Chair: David Penny]
10:50–11:10 Michael Woodhams
The triangle inequality and additivity in phylogenetic distances
11:10 –11:30 Simon Hills
Marrying molecules and morphology in marine molluscs
11:30 –11:50 Mike Steel
Peculiar properties of a polarity ‘pully principle’
11: 50 –12:00 Closing comments

12:00 Lunch