

# Kaikoura09 Program

## Saturday 7<sup>th</sup> Feb

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

## Sunday 8<sup>th</sup> Feb

08:45 – 09:15	<b>Registration</b>
09:15 – 09:20	<b>Greetings and opening</b>
09.20 – 10:00	<b>[Complexities of evolution]</b> <i>Chair: Barbara Holland</i>  09:20–09:40 Michael Charleston, Mixing models for phylogenetic estimation with large heterogeneous data sets  9:40–10:00 Liat Shavit*, The process of evolution and long-branch attraction – no rates about it!
10:00 – 10.40	<b>Morning break</b>
10:40 – 12:00	<b>[Phylogenetic Theory I : Algebra and Combinatorics]</b> <i>Chair: Charles Semple</i> 10:40–11:00 Steffen Klaere, Algebraic invariants  11:00–11:20 Beáta Faller*, Optimizing phylogenetic diversity for cluster systems  11:20–11:40 Stefan Grünewald, On the Chain Reduction Conjecture  11:40–12:00 Radu Mihaescu, Combinatorics of least squares trees
12:00 – 14:00	<b>Lunch</b>
14:00 – 15:00	<b>[Rates and Dates]</b> <i>Chair: David Penny</i> 14:00–14:20 Stephane Guindon, New methods for molecular dating.  14:20–14:40 Simon Hills*, Calibrating molecular clocks with a wealth of paleontological data  14:40–15:00 Matt Phillips, Molecular dating suggests the echidna is a terrestrial platypus
15:00 – 15.30	<b>Afternoon break</b>
15:30 – 16.30	<b>[Applications I]</b> <i>Chair: Michael Charleston</i> 15:30–15:50 Russell Gray, Four things linguistics can tell geneticists about Pacific genetics  15:50–16:10 Rob Lanfear, A comparison of likelihood and Bayesian approaches to comparing hypotheses of Hox cluster evolution  16:10–16:30 Ellen Nisbet, Using phylogenetics to trace the domestication of horses
17:30	<b>Dinner - cooked seafood provided</b>

## Monday 9th Feb

<b>08:55 – 09:00</b>	<b>Greeting and notices</b>
<b>09:00 – 10:30</b>	<b>[Phylogenomics]</b> <i>Chair: David Bryant</i> 09:00–09:30 Andreas Dress, New approaches to alignment-free comparative sequence analysis  09:30–09:50 Benny Chor, Genomic DNA k-mers Distributions: Models and Modalities  09:50–10:10 Melanie Abeysondera*, Building phylogenetic trees with the spectral envelope covariance  10:10–10:30 Arndt von Haeseler, The effect of a single substitution on an alignment pattern
<b>10:30 – 11:00</b>	<b>Morning break</b>
<b>11:00 – 12:00</b>	<b>[Population processes I]</b> <i>Chair: Mike Steel</i> 11:00–11:20 James Degnan, probabilities of ranked gene trees given species trees under coalescence  11:20–11:40 David Bryant, Demographic inference from SNPs and AFLPs  11:40–12:00 Joseph Heled*, Doing better than BEST in BEAST - species trees from multi individual, multi locus data
<b>12:00 – 14:00</b>	<b>Lunch</b>
<b>14:00 – 15:00</b>	<b>[Diversity]</b> <i>Chair: Charles Semple</i> 14:00–14:20 Lindell Bromham, Phylogenies for communities  14:20–14:40 Magnus Bordewich, Selecting taxa to maximize biodiversity  14:40–15:00 Binh Nguyen*, Uncovering the origins of genetic diversity within a species
<b>15:00 – 15:30</b>	<b>Afternoon break</b>
<b>15:30 – 16:30</b>	<b>[Applications II]</b> <i>Chair: Chris Simon</i> 15:30–15:50 Louis Ranjard, Bird song evolution in the North Island saddleback  15:50–16:10 Gillian Gibb*, Untangling Pelecaniformes: The phylogeny of pelecaniformes using mitochondrial DNA  16:10–16:30 Meg Woolfit, Rates and patterns of evolution in mutualistic and parasitic endosymbionts
	<b>Dinner (own arrangements)</b>

## Tuesday 10<sup>th</sup> Feb

<b>All day</b>	<b>Excursions</b>
	<b>Dinner (own arrangements)</b>
<b>19:30 – 20:00</b>	<b>Refreshments, discussions</b>
<b>20:00 – 20:45</b>	<b>Special Talk:</b> Bill Martin, Hydrothermal vents and the origin of life <i>Chair: David Penny</i>

## Wednesday 11<sup>th</sup> Feb

<b>08:55 – 09:00</b>	Greeting and notices
<b>09:00 – 10:30</b>	<b>[Phylogenetic theory II: Methods and models]</b> <i>Chair: Mike Steel</i> 09:00–09:30 Olivier Gascuel, Distance-based serial phylogenies  09:30–9:50 Mareike Fischer*, Curious properties of Maximum Parsimony in estimating evolutionary trees  9:50–10:10 Lars Jermiin, Shuffle: A tree-independent application to detect and visualize rate-heterogeneity across sites  10:10–10:30 Shlomo Moran, Towards optimal distance functions for stochastic substitutions Models
<b>10:30 – 11:00</b>	<b>Morning break</b>
<b>11:00 – 12:00</b>	<b>[Population processes II]</b> <i>Chair: Alexei Drummond</i> 11:00–11:20 Sidney Markowitz*, Modeling the emergence of genetic coding in the prebiotic environment [ <i>Revised abstract</i> ]  11:20–11:40 Tanja Stadler, A character-dependent birth-death model with application to HIV  11:40–12:00 Raaz Sainudiin, Lumpings of a Kingman-Tajima $n$ -coalescent
<b>12:00 – 14:00</b>	<b>Lunch</b>
<b>14:00 – 15:00</b>	<b>[Recombination and networks]</b> <i>Chair: Mike Hendy</i> 14:00–14:20 Alethea Rea*, Estimating recombination rates.  14:20–14:40 Neil Gemell, The mitochondrial bottleneck and inheritance of mitochondrial heteroplasmy in chinook salmon ( <i>Oncorhynchus tshawytscha</i> ).  14:40–15:00 Regula Rupp, Depth- $k$ networks
<b>15:00 – 15:30</b>	<b>Afternoon break</b>

<b>15:30 – 16:30</b>	<p><b>[Applications III]</b> <i>Chair: Russel Gray</i></p> <p>15:30–15:50 Peter Waddell, The fit of mammalian sequence data to phylogenetic model</p> <p>15:50–16:10 Phil Novis, Conflicting phylogentic signal from chloroplast data in the green algae</p> <p>16:10–16:30 Chris Simon, Glacial refugia in a maritime temperate climate: Cicada (<i>Kikihia subalpina</i> complex) mtDNA phylogeography in New Zealand</p>
<b>17:30</b>	<b>BBQ at Kaikoura Winery</b>

### Thursday 12<sup>th</sup> Darwin's Day: origins and outlook

<b>08:55 – 09:00</b>	<b>Greeting and notices</b>
<b>09:00 – 10:20</b>	<p><b>[Session I]</b> <i>Chair: Bill Martin</i></p> <p>09:00–09:30 David Penny, If only Darwin had a PC – the <i>One</i> Question</p> <p>09:30–10:50 Barbara Holland, Robust consensus methods for summarising phylogenetic trees</p> <p>09:50–10:20 Daniel Huson. SplitsTree4, MEGAN, Dendroscope, MetaSim und DarwinRocks!</p>
<b>10:20 – 10:50</b>	<b>Morning break</b>
<b>10:50 – 11:50</b>	<p><b>[Session II]</b> <i>Chair: Daniel Huson</i></p> <p>10:50–11:20 Alan Cooper, Reconstructing the past (literally) using ancient DNA</p> <p>11:20–11:50 Mark Suchard, Bayesian Phylogeography findings its root</p>
<b>11:50</b>	<b>Closing comments, lunch</b>