2018 Phylogenomics Software Symposium
Institut des Sciences de l'Evolution – Montpellier
University of Montpellier, Louis Thaler room (Building 22)

Schedule

1:00-1:10 PM: Opening remarks (Fabien Condamine, Lisa Pokorny, and Tandy Warnow)

1:10-2:30 PM: Algorithms for Phylogenomics (17 minutes per talk, 3 minutes Q&A)
- **Carolin Kosiol** (St. Andrews), IQ-TREE-PoMo: Polymorphism-aware tree estimation
- **Siavash Mirarab** (University of California at San Diego), Coalescent-based species tree estimation
- **Erin Molloy** (University of Illinois at Urbana-Champaign), Scaling species tree estimation methods to large datasets using NJMerge
- **Luay Nakhleh** (Rice), Phylogenetic Network Estimation

2:30-2:40: Break

2:40-3:40 PM: Algorithms for Multiple Sequence Alignment and Gene Tree Estimation (17 minutes per talk, 3 minutes Q&A)
- **Tandy Warnow** (University of Illinois at Urbana-Champaign), Large-scale multiple sequence alignment
- **Mike Nute** (University of Illinois at Urbana-Champaign), Benchmarking Bali-Phy
- **Eric Tannier** (INRIA, University of Lyon), Treerecs with Seaview: gene tree inference from alignment to reconciliation, with a graphical interface

3:40-4:10 PM: Coffee Break

4:10-5:30 PM: Contributed Talks (7 minutes per talk, 3 minutes for Q&A)
- **Dominic Bennett** (University of Gothenburg), supersmartR: Towards a modular pipeline for phylogenetic tree construction in the R language
- **Nicola de Maio** (European Bioinformatic Institute (EMBL-EBI)), BADTRIP: reconstructing transmission from within-host SNPs (PDF)
- **Jan Kim** (Kew Royal Botanic Gardens), High Throughput Multigene Phylogeny: Tools for Tackling the Plant and Fungal Trees of Life
- **Elise Lauterbur** (Stony Brook University), OrthoCapture: Facilitating Gene Capture Probe Creation for Non-Model Organisms
- **Uyen Mai** (Rice University) TreeShrink: Fast and Accurate Detection of Outlier Long Branches in Collections of Phylogenetic Trees
- **Benoit Morel** (Heidelberg Institute for Theoretical Studies), ParGenes, an integrated tool for model selection and maximum likelihood (ML) based phylogenetic inference on thousands of independent MSAs on clusters and supercomputers
- **Sanna Olsson** (Forest Research Centre (CIFOR) INIA, Madrid), Demographic history and molecular adaptation of the Pinus halepensis-brutia complex
- **Lisa Pokorny** (Kew Royal Botanic Gardens), Building the Plant Tree of Life: A Proof of Concept for Flowering Plant Families

5:30-6:00 PM: Discussion and Closing Remarks