

# 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 Bioinformatics 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