

Multiple Sequence Alignment

Monday January 12, 2015

- 8:00–8:50 *Check-In/Light Breakfast (Hosted by IPAM)*
- 8:50–9:00 *Welcome and Opening Remarks*
- 9:00–9:40 **Tandy Warnow** (University of Illinois at Urbana-Champaign)
Overview
- 10:00–10:15 *Break*
- 10:15–10:55 **Martin Weigt** (Université de Paris VI (Pierre et Marie Curie))
Coevolutionary modeling of protein sequences: Inference of 3D structure and mutational landscapes
- 11:15–11:30 *Break*
- 11:30–12:10 **Alexandre Bouchard-Cote** (University of British Columbia)
MSA using Divide-and-Conquer Sequential Monte Carlo
- 12:30–2:30 *Lunch (on your own)*
- 2:30–3:10 **Cedric Notredame** (Center for Genomic Regulation)
Grabbing High Hanging Fruits From the Tree Of Life
- 3:30–4:00 *Break*
- 4:00–4:40 *Participants: Open Problems and Computational or Scientific Challenges*
- 5:00–6:30 *Poster Session & Reception (Hosted by IPAM)*

Tuesday January 13, 2015

- 8:00–9:00 *Check-in/Breakfast (hosted by IPAM)*
- 9:00–9:40 **Sebastien Roch** (University of Wisconsin-Madison)
A survey of theoretical results on the TKF model
- 10:00–10:15 *Break*
- 10:15–10:55 **Steven Evans** (University of California, Berkeley (UC Berkeley))
Recovering a tree from the lengths of random subtrees
- 11:15–11:30 *Break*

(Tuesday schedule continued on next page)



(Tuesday schedule continued from previous page)

- 11:30–12:10 **Ari Loytynoja** (University of Helsinki)
Phylogeny-aware alignment with sequence graphs
- 12:30–2:30 *Lunch (on your own)*
- 2:30–3:10 **Mark Ragan** (University of Queensland)
Phylogenetics without multiple sequence alignment
- 3:30–4:00 *Break*
- 4:00–5:00 *Short talks by Participants*

Wednesday January 14, 2015

- 8:00–9:00 *Check-in/Breakfast (hosted by IPAM)*
- 9:00–9:40 **Nick Grishin** (UT Southwestern Medical School)
Pushing the limits of sequence profile similarity search and alignment
- 10:00–10:15 *Break*
- 10:15–10:55 **Noah Daniels** (Massachusetts Institute of Technology)
Structure-based multiple sequence alignments
- 11:15–11:30 *Break*
- 11:30–12:10 **Olivier Lichtarge** (Baylor College of Medicine)
Evolution versus disease: the calculus of life
- 12:30–2:30 *Lunch (on your own)*
- 2:30–3:10 **Jinbo Xu** (Toyota Technological Institute at Chicago)
Graphical models of multiple protein sequence alignment
- 3:30–4:00 *Break*
- 4:00–4:40 **Patricia Babbitt** (University of California, San Francisco (UCSF))
Back to the Beginning: Which sequences to align?

Thursday January 15, 2015

- 8:00–9:00 *Check-in/Breakfast (hosted by IPAM)*
- 9:00–9:40 **Jim Leebens-Mack** (University of Georgia)
Plant gene family circumscription, multiples sequence alignment and phylogenomic analysis
- 10:00–10:15 *Break*

(Thursday schedule continued on next page)

(Thursday schedule continued from previous page)

- 10:15–10:55 **Siavash Mir arabbaygi** (University of Texas at Austin)
Co-estimation of sequence alignments and trees
- 11:15–11:30 *Break*
- 11:30–12:10 **Nam-phuong Nguyen** (University of Illinois at Urbana-Champaign)
New HMM-based Methods in Sequence Alignment, Phylogenetics, and Metagenomics
- 12:30–2:30 *Lunch (on your own)*
- 2:30–3:10 **Elena Rivas** (Howard Hughes Medical Institute)
Parameterizing sequence alignment with an explicit evolutionary model reduces homologous overextension artifacts
- 3:30–4:00 *Break*
- 4:00–5:00 *Short talks by Participants*

Friday January 16, 2015

- 8:00–9:00 *Check-in/Breakfast (hosted by IPAM)*
- 9:00–9:40 **Scott Schmidler** (Duke University)
The Cutoff Phenomenon in Evolutionary Models for Sequence Alignment
- 10:00–10:15 *Break*
- 10:15–10:55 **Benjamin Redelings** (Duke University)
Erasing Errors Due to Alignment Ambiguity When Estimating Positive Selection
- 11:15–11:30 *Break*
- 11:30–12:10 **Adam Godzik** (Sanford-Burnham Medical Research Institute)
Analysis and multiple alignments of periodic proteins
- 12:30–2:30 *Lunch (on your own)*
- 2:30–3:10 **Jian Peng** (University of Illinois at Urbana-Champaign)
Distances between protein sequence alignments
- 3:30–4:30 *Open Problems and Discussion*

