

## 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*

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- 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*

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- 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*

