



Multiple Sequence Alignment

January 12 – 16, 2015

ORGANIZING COMMITTEE: Jim Leebens-Mack (University of Georgia) , Sebastien Roch (University of Wisconsin-Madison), Tandy Warnow (University of Texas at Austin)

Scientific Overview

In multiple sequence alignment (MSA), a set of nucleotide or amino-acid sequences are "aligned" through the addition of spaces or rearrangement of individual sequences. An alignment gap indicates a possible loss or gain of an element, and rearrangements account for inversions or translocations (particularly important for genome alignments); thus evolutionary inference of the insertion and deletion, translocation and inversion processes is inherent in MSA. MSA estimation is also closely tied to phylogenetic estimation – an area with connections to probability theory, geometry, algebra, and graph theory. MSA estimation also informs protein function and structure prediction, and thus has strong connections to structural biology. However, these disciplines approach MSA estimation very differently. As a result, a variety of techniques have been explored, including combinatorial optimization, biophysical models of protein structure, machine learning, and probabilistic models of evolution. Despite active research in MSA estimation, many challenges persist. The research community is addressing these through improved mathematical formalization of MSA estimation; development of sophisticated and biologically meaningful models of sequence evolution that include insertions, deletions, and rearrangements; and design of new methods that have good mathematical properties and empirical performance for large datasets. This workshop will engage researchers from different fields, including mathematicians, statisticians, evolutionary biologists, structural biologists, and computer scientists, with the aim of integrating diverse viewpoints, improving mathematical foundations, and developing new and more powerful methods for estimating MSAs.

Confirmed Speakers

Patsy Babbitt (UCSF), **Alexandre Bouchard-Cote** (Univ. of British Columbia), **Leonore Cowen** (Tufts), **Aaron Darling** (Univ. of Technology, Sydney), **Charlotte Deane** (Oxford), **Roland Dunbrack** (Fox Chase Cancer Ctr.), **Sean Eddy** (HHMI), **Steve Evans** (UC Berkeley), **Adam Godzik** (Sanford-Burnham), **Nick Goldman** (EMBL-EBI), **Nick Grishin** (UT Southwestern), **Jotun Hein** (Oxford), **Mark Holder** (Univ. of Kansas), **Jim Leebens-Mack** (Univ. of Georgia), **Olivier Lichtarge** (Baylor), **Cedric Notredame** (Ctr. for Genomic Regulation), **Mark Ragan** (Univ. of Queensland), **Benjamin Redelings** (Duke), **Elena Rivas** (HHMI), **Sebastien Roch** (Wisconsin-Madison), **Kimmen Sjolander** (UC Berkeley), **Tandy Warnow** (UT Austin)

Participation

Additional information about this workshop, including links to register and to apply for funding, can be found on the webpage listed below. Encouraging the careers of women and minority mathematicians and scientists is an important component of IPAM's mission, and we welcome their applications.

<http://www.ipam.ucla.edu/programs/msa2015>

