

Combi Seminar

Wednesday, 3.7.18 | 1:30 | Foegen Auditorium



Dr. Erick Matsen

Associate Member, Fred Hutchinson Cancer Research Center
<http://matsen.fhcrc.org/>

“Beyond random-walk Markov chain Monte Carlo for Bayesian phylogenetics”

Bayesian posterior distributions on phylogenetic trees remain difficult to sample despite decades of effort. The complex discrete and continuous model structure of trees means that recent statistical samplers developed for Euclidean space are not applicable to the phylogenetic case. Thus, we are left with random-walk Markov Chain Monte Carlo with uninformed tree modification proposals. These methods traverse tree space slowly because phylogenetic posteriors are concentrated on a small fraction of the very many possible trees.

In this talk, I will describe our recent work moving beyond random walk MCMC sampling of posterior distributions on phylogenetic trees. This includes

- (1) an online sequential Monte Carlo algorithm that can update existing posterior inferences when additional sequences arrive,
- (2) an extension of Hamiltonian Monte Carlo to simultaneously explore discrete and continuous aspects of tree space using gradients,
- (3) "phylogenetic topographer," a strategy to systematically map out the posterior distribution and provide an approximate posterior weight, and
- (4) a successful "factored" representation of tree posterior distributions that points the way to new opportunities.

Questions? Contact Brian Giebel at bgiebel@uw.edu or visit the Combi website at <http://www.gs.washington.edu/news/combi.htm>

The University of Washington is committed to providing access, equal opportunity and reasonable accommodations in its services, programs, activities, education and employment of individuals with disabilities. To request disability accommodations contact the Disability Services Office at least ten days in advance at: 206.543.6450/V, 206.543.6452/TTY, 206.685.7264 (FAX), or e-mail at dso@u.washington.edu