

Center for Inference and Dynamics of Infectious Diseases Seminar

## Recent advances in methods for detecting adaptation in protein-coding DNA

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Pelton Auditorium, Weintraub Building

Fred Hutchinson Cancer Research Center

Refreshments will be served; registration is not necessary to attend this event



**Abstract:** Statistical modelling of the long-term evolution of protein-coding DNA is an active area of research in molecular phylogenetics. Several recent works have adopted a mutation-selection framework, whereby the substitution process is specified from a set of parameters controlling a point-mutation process, and another set of (potentially site-specific) parameters controlling the probability of fixation of mutations. We have previously discussed using such a model as "a more relevant background against which to distinguish positive selection" (Rodrigue, Philippe & Lartillot, PNAS, 2010), and have recently used simulations to illustrate the potential of the approach (Rodrigue & Lartillot, MBE, 2017). This lecture will outline the rationale of such a model, present results of its large-scale applications over several thousand protein-coding genes, and discuss on-going expansions to the mutation-selection framework.



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