

Stochastic Methods in Evolutionary Biology

Project Description:

This postdoctoral project will be part of an ongoing collaboration between mathematics and evolutionary biology at Uppsala University, which seeks to develop advanced mathematical modeling and computational methods to resolving some of the many remaining challenges in evolutionary biology modeling and data analysis.

The project builds on the long and successful tradition of using stochastic models in population genetics. The Wright-Fisher reproduction model and diffusion processes obtained under scaling of time and population size provide a solid theoretical framework. Complementary approaches are based on random coalescent processes, which trace the evolutionary dynamics backwards in time towards a common ancestor in the “tree of life”. Additional methods apply branching processes and random tree models to improve our understanding of how species are interrelated. Innovative stochastic methods in this field are essential to analyze the statistical patterns of variation in sequence and genome data, shaped by the fundamental evolutionary forces in nature.

An ongoing study focuses on time-dependent estimates of molecular evolutionary rates, and the implications of time-dependence for inferences of adaptive evolution. A second ongoing project is devoted to modeling trait-dependent evolution on a random species tree. A unifying aspect of the current projects is the mathematical study of dN/dS , the ratio of nonsynonymous and synonymous substitutions, a widely used measure in evolutionary genetic studies to investigate the extent to which selection modulates gene sequence evolution.

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Recent publications and preprints related to the project:

Carina F. Mugal, Jochen B.W. Wolf, Ingemar Kaj (2014). *Why time matters: codon evolution and the temporal dynamics of dN/dS* . *Molecular Biology and Evolution* 31, 212-231.

Carina F. Mugal, Ingemar Kaj (2016). *The non-equilibrium allele frequency spectrum in a Poisson random field framework*. *Theoretical Population Biology* 111, 51-64.

K. Bartoszek, S. Glémin, I. Kaj, M. Lascoux (2017). *The Ornstein-Uhlenbeck process modeling evolution of interacting populations*. Submitted.

D. Tahir, M. Lascoux, S. Glemin, I. Kaj (2017). *Modeling trait-dependent evolution on a random species tree*. Manuscript in preparation.