Stochastic **P**rocesses **I**n **E**vo**L**ution and **E**cology

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Multiple merger coalescent model selection for whole genome cod data

Multiple merger coalescents (MMCs) have long been suggested as appropriate models for the genetic diversity of organisms with skewed offspring distributions, such as many marine and microbial species. They predict an excess of low frequency mutations relative to the Kingman coalescent, similarly to other phenomena such as historical population growth. However, their predictions for the full site frequency spectrum differ from the Kingman coalescent even under fairly arbitrary demographic scenarios. I will describe joint work with Einar Arnason, Katrin Halldorsdottir, and Bjarki Eldon, in which we assessed the extent to which several prominent MMC families were able to explain the genetic diversity of cod populations sampled around Iceland. The Kingman coalescent provides a poor fit even under non-parametric, best-fit demographies or simple models of population structure. More surprisingly, so does the Beta-coalescent, which has often been seen as a natural candidate model for skewed offspring reproduction. Instead, an MMC model by Durrett & Schweinsberg for recurrent selective sweeps provides a remarkably good fit only a few free parameters. Our results are informative of possible mechanisms giving rise to the skewed and shallow genealogies observed among cod.

Speaker: Dr Jere Koskela (University of Warwick)
Time: Monday, 24.04.23, 4 P.M. CET

The lecture will be held online. Interested? Link available from Jochen Blath
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