

# Genomic data improve coalescent inference across a range of demographic parameters and life-histories

Michael Hart<sup>1</sup>, Vanessa Guerra<sup>1</sup>, Maria Byrne<sup>2</sup>, and Jon Puritz<sup>3</sup>

<sup>1</sup>Simon Fraser University

<sup>2</sup>University of Sydney

<sup>3</sup>University of Rhode Island College of Arts and Sciences

September 12, 2020

## Abstract

Understanding the demographic context for population divergence and speciation in the sea often requires distinguishing the contributions of mutation, isolation, and gene flow on temporal or geographical scales where those diverse processes may not achieve equilibrium conditions. Coalescent isolation-with-migration (IM) models can meet this need for non-equilibrium modelling of genetic variation, but the quality of IM model parameter estimation depends on the breadth of genome sampling. Here, we describe three improvements in IM parameter estimates based on hundreds of loci from RNA-seq assemblies relative to previously published results based on few loci in two sea star study systems that differ in the tempo of population divergence. (1) Precision of all model parameter value estimates (with narrow posterior distributions) was vastly better in both study systems and resolved uncertainty around one key parameter in each. (2) Maximum likelihood estimates of some model parameters were broadly similar to previously published estimates, but with greater precision we obtained more realistic values for some parameters that were consistent with expectations based on the biogeography of the organisms. (3) We found non-zero but demographically trivial gene flow in one study system where we previously estimated gene flow to be zero, and modest symmetrical gene flow ( $2Nm < 1$ ) in a second study system where we previously estimated gene flow to be massive ( $2Nm \sim 10$ ) and asymmetrical. Improved understanding through judicious application of genome-wide sampling in replication studies as shown here may improve the information needed for biodiversity management and conservation.

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