



Mardi 18 novembre 2025, 11:00

Grande salle + visio.

LAVA: A METHOD FOR IDENTIFYING LOCAL ADAPTATION IN STRUCTURED POPULATIONS

par

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- 🧠 Demonstrating that natural selection drives phenotypic divergence requires distinguishing adaptive change from neutral differentiation caused by genetic drift. Accurately modeling these expectations under complex population structures remains challenging. The commonly used Q_{st} - F_{st} approach quantifies population genetic structure using F_{st} as the neutral baseline, but this summary statistic fails to capture non-uniform patterns of relatedness across metapopulations.
- 🧠 We developed LogAV and its R implementation LAVA, that build on a method, Driftsel, developed by Ovaskainen *et al.* (2011). LogAV uses relatedness matrices to infer between- and within-population ancestral additive genetic variances under a mixed-effects framework. Under neutrality, these variance estimates are expected to be equal; significant differences indicate selection. We evaluate LAVA's performance alongside Q_{st} - F_{st} and Driftsel across multiple population structures and selection strengths.
- 🧠 Our results demonstrate that while all methods perform well under simple island models, methods accounting for population structure (Driftsel and LAVA) show superior power under non-isotropic structures, particularly when selective gradients do not align with demographic patterns. LAVA maintains proper calibration with consistently low false positive rates across diverse scenarios, whereas Q_{st} - F_{st} and Driftsel exhibit poor calibration under certain structures.