

THE EFFECT OF THE DEMOGRAPHIC HISTORY AND SAMPLING SCHEME ON THE DETECTION OF SPURIOUS BOTTLENECKS IN FRAGMENTED AND STRUCTURED POPULATIONS

L. Chikhi^{1,2}, B.D. V. Sousa^{1,3}, P. Luisi^{1,4}, B. Goossens^{5,6}, M. A. Beaumont⁷.

¹ CNRS, EDB (Lab. Evolution et Diversité Biologique), UMR CNRS/UPS 5174, Toulouse, France, ² Instituto Gulbenkian de Ciência, Oeiras, Portugal, ³ Centro de Biologia Ambiental, FCUL, Lisbon, Portugal, ⁴ INSA de Toulouse, Toulouse, France, ⁵ School of Biosciences, Cardiff Univ., Cardiff, UK, ⁶ Sabah Wildlife Department, Wisma Muis, Kota Kinabalu, Malaysia, ⁷ School of Animal and Microbial Sciences, Univ. Reading, Reading, U.K.

Presenter's Email: chikhi@igc.gulbenkian.pt

Molecular data contain information on the recent evolutionary history of populations and much of the work carried out today owes to the work of the theoreticians who demonstrated that it was possible to use genetic data to detect departures from equilibrium conditions (e.g. panmitic population/mutation-drift equilibrium) and interpret them in terms of deviations from neutrality or stationarity. The detection of population size changes has usually been carried out under the assumption that samples were obtained from populations that can be approximated by a Wright-Fisher model (i.e. assuming panmixia, demographic stationarity, etc.). However, natural populations are usually part of spatial networks and are interconnected through gene flow. We simulated genetic data under n-island and stepping-stone models. The simulated populations were thus stationary and not subject to any population size change. We varied the level of gene flow between populations and the scaled mutation rate. We also used several sampling schemes. We then analyzed the simulated samples using the Bayesian method implemented in the MSVAR program to detect and quantify putative population size changes. Our results show that all three factors (genetic differentiation, genetic diversity and the sampling scheme) play a role in generating bottleneck signals. We also suggest an ad hoc method to counter this effect. The confounding effect of population structure and of the sampling scheme has practical implications for many conservation studies. Indeed, several studies may have overestimated or incorrectly detected bottlenecks in endangered species.

Keywords: Bottlenecks, population structure, genetic diversity, sampling scheme