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Title: Very spatial indeed: trying to take (spatial) structure into account in population genetics inference

Abstract: "Genetic data are increasingly used to infer some aspects of the recent evolution of populations (time of population split, population expansions or contractions, admixture, etc.). Statistical methods have been developed during the 1990s to that aim, but most of them tend to ignore population structure and assume that the samples obtained in the field come from isolated (no gene flow exchanged with other populations) and random mating (no "substructure") populations. While such assumptions are probably legitimate under some conditions, they can be problematic and can lead to biased inference. Indeed there is an increasing recognition that population structure (spatial or not) can generate false signals of demographic change, or of selection. In our group we have been interested in reconstructing the recent history of endangered species subjected to habitat loss and fragmentation. In parallel to the analysis of real data sets we have been using simulation-based approaches to test the robustness of existing methods and to determine whether population bottlenecks could indeed be detected. I will present an overview of our research on that theme and a quick summary of the results obtained in the last few years."