

Methods for detection of recent population subdivisions

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Abstract

Potential subdivision events in populations can have a wide range of causes: from natural disasters like bushfires that isolate communities, to anthropogenic disturbances like infrastructure projects cutting through a population's habitat. Due to the unpredictability inherent in events like bushfires, or even for predictable events such as property development, populations affected by these potential subdivisions are often not studied until after the event, making it extremely hard to assess negative conservation impacts without the benefit of prior data. This paper aims to apply population genetics methods to assess whether it is possible to accurately assess the impact a potential subdivision event can have on the genetic makeup of a population, especially when one has no data prior to such an event. Differentiation measures, such as F_{st} , might be used for detecting whether a population has been subdivided. However, these measures often take dozens of generations to show a significant change from zero (i.e., no differentiation), especially in larger populations. In this paper we present a more sensitive method, which is suitable for detecting subdivision effects within a few generations of the event and which can be applied without prior data. We test this method using both simulated data, and genetic data from a population of koalas impacted by a railroad infrastructure development.

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