

Poster presentation

Bioinformatics in phylogeography: analytical methods and applications

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Phylogeographic approach focuses in the description and interpretation of relationships between the genealogy of populations or closely related species, estimated from DNA sequences, and the corresponding geographic distributions. Bioinformatics implementation of coalescent theory predictions has been in the forefront of this field for some years now, which, on the other hand, has important practical applications such as in conservation genetics and epidemiology. Sampling and field work is followed by obtaining data in the wet lab (usually a longer-than-expected period) and by the use a panoply of computer programs to determine phylogenetic relationships of the sequences and/or specimens collected, estimating gene flow within populations, inferring historical events and population dynamics. Different methodologies implemented in several computer packages are available. For the average Ph-student, several questions soon arise: what methodology and which programs to use? Assumptions and limitations of those? How to assess the reliability of the results obtained? We present data on studies focused in the phylogeography and population dynamics of beetles endemic to the Canary Islands. Inferences obtained of inter-island colonisations; population expansions and restricted gene flow within particular islands are assessed in the light of available ecology and geology data of the archipelago. The results obtained show the benefits and potential perils of this approach applied to low-vagility organisms in oceanic islands.