

The bigger picture of population genomics

January 5 2012

Not so long ago it was the work of many years to sequence the genome of a single organism: the human genome project, for example, took many laboratories a total of 13 years to complete. The availability of so-called next-generation sequencing methods makes it easy – and comparatively cheap – to sequence DNA, although sequencing the large number of individuals required for population genetics studies is still time-consuming and costly and has thus been restricted to few organisms.

The group of Christian Schlötterer of the Institute of [Population Genetics](#) at the University of Veterinary Medicine, Vienna has shown previously that pooling samples enables [population genetics](#) studies to be undertaken at significantly reduced costs. Despite the wide applicability and obvious power of the method, however, it has so far proven possible to apply next-generation sequencing at the scale of populations to only few model systems. The problem lies in the interpretation of the data. And this is where the latest work from Schlötterer's group comes in. Robert Kofler, Ram Vinay Pandey and Schlötterer now report the development of a software package – catchily termed "PoPoolation2" – that makes it possible even for non-experts to compare populations.

The package offers a wide range of statistical methods to determine how the frequencies of particular forms – termed alleles – of genes vary between populations. The program has been tested on the sequences of a single chromosome from two distinct populations of the fruit fly *Drosophila melanogaster* and the results confirm that the program can correctly predict the levels of divergence between the samples. As

Schlötterer says, "PoPoolation2 helps us compare the allele frequencies between populations. It will enable us quickly and cheaply to compare how populations of different species have adapted differently to their environments, giving us better information on the big picture of evolution in practice."

More information: The paper 'PoPoolation2: Identifying differentiation between populations using sequencing of pooled DNA samples (Pool-Seq)' by Robert Kofler, Ram Vinay Pandey and Christian Schlötterer is published in the current issue of the journal *Bioinformatics* and is available online at [bioinformatics.oxfordjournals. ... tics.btr589.full.pdf](https://www.bioinformatics.oxfordjournals.org/doi/full/10.1093/bioinformatics/btr589)

Provided by University of Veterinary Medicine -- Vienna

Citation: The bigger picture of population genomics (2012, January 5) retrieved 4 July 2024 from <https://phys.org/news/2012-01-bigger-picture-population-genomics.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.