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2009 : April 2009 - Fast Breaking Papers : François Rousset

FAST BREAKING PAPERS - 2009

April 2009



François Rousset talks with ScienceWatch.com and answers a few questions about this month's Fast Breaking Paper in the field of Environment/Ecology.



Article Title: GENEPOP ' 007: a complete re-implementation of the GENEPOP software for Windows and Linux

Authors: Rousset, F
 Journal: MOL ECOL RESOUR
 Volume: 8
 Issue: 1
 Page: 103-106
 Year: JAN 2008

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 * Univ Montpellier 2, CNRS, UM2, Inst Sci Evolut,CC 065, F-34095 Montpellier 5, France.

SW: Why do you think your paper is highly cited?

This paper is highly cited because it describes the successor of the software Genepop, already widely used in several branches of genetics. Part of Genepop's success derives from its well-established methods, thoroughly tested algorithms, and its convenient input file format which has been endorsed by several other softwares.

SW: Does it describe a new discovery, methodology, or synthesis of knowledge?

Genepop'007 includes some relatively recent statistical developments, but is used mostly for not-so-new methods. In particular, it implements computer algorithms allowing testing of the independence between two variables, each of which takes discrete values (categorical variables). The initial target application of Genepop was the analysis of highly polymorphic genetic markers where the number of categories for one or both variables can be large.

Computer algorithms available 15 years ago were comparatively slow when the number of categories was large. Despite some improvements in alternative algorithms, the ones implemented in Genepop'007 remain competitive today.

SW: Would you summarize the significance of your paper in layman's terms?

The paper describes software that makes it easy to perform a number of data analyses, in particular, quantifying the extant of genetic exchanges between different populations.

SW: How did you become involved in this research, and were there any problems along the way?

"The software is used in conservation science and medical genetics, and as such, it can guide the application of policies in these different fields."

I became involved in this research as a collaboration with Michel Raymond, the past co-developer of Genepop (also from the Institute of Evolutionary Sciences in Montpellier). It fitted well with my then-growing interest in statistical and theoretical issues related to what has become my other main research program, the evolution of social behaviors and related ecological traits.

SW: Where do you see your research leading in the future?

Genepop is actively maintained, but most of my current research on quantifying genetic exchanges involves a distinct class of algorithms based on coalescent theory, i.e., on properties of genealogical trees of ancestors of a sample. These computer-intensive algorithms are being developed as a new software, Migraine, written in collaboration with Raphaël Leblois (currently at the Museum of Natural History in Paris).


SW: Do you foresee any social or political implications for your research?

The software is used in conservation science and medical genetics, and as such, it can guide the application of policies in these different fields. However, I am not aware that it has been prominently involved in any social or political debate.

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KEYWORDS: PARTIAL MANTEL TESTS; GENETIC DIFFERENTIATION; MAXIMUM-LIKELIHOOD; PERMUTATION TESTS; F-STATISTICS; POPULATION; FREQUENCY; ALLELES.



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