

Article in the Science Journal Bioinformatics Advances Details the Release of Open Source Bioinformatics Software Tool

The ExRec Open Platform Is Designed to Accelerate Research in Phylogenomics

RIVERSIDE, CALIFORNIA, USA, March 20, 2024 /EINPresswire.com/ -- A recent article in the journal [Bioinformatics Advances](#) details the release of a new open source bioinformatics software tool designed to accelerate research in computational phylogenomics. The article, entitled "[ExRec: a python pipeline for generating recombination-filtered multilocus datasets](#)" by Sam McCarthy Potter and Professor Bryan Jennings, presents the ExRec software package. ExRec was designed to filter out the adverse effects of recombination in genome-scale DNA sequence datasets. By filtering datasets in this manner, ExRec may allow researchers to obtain better estimates of key parameters in the reconstructed Tree of Life such as speciation times, historical migration rates, and population sizes.

The ExRec package contains five standalone programs: a core program that automatically performs recombination filtering on genome-scale datasets plus four file conversion applications that make the software user-friendly. The original code was written in the popular software language Python.

According to Sam McCarthy Potter, "one of the greatest challenges with developing ExRec was designing a program that can accommodate various input file variants that are being used by





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research scientists. Given its user-friendliness and suite of useful features, I believe ExRec will help the research community resolve the current debate as to whether or not recombination filtering procedures are needed to improve the quality of genome-scale datasets."

According to Professor Jennings, "when I was a postdoctoral fellow studying the evolutionary diversification of Australian songbirds, I spent several days manually doing what ExRec can do in seconds -- and error free. If we eventually conclude that recombination filtering

is an important data-cleaning step in phylogenomic studies, then ExRec will make an important contribution to the field."

Sam McCarthy Potter

Samuel McCarthy Potter, is a Researcher in the Haim Lab in the Department of Microbiology and Immunology, the Carver College of Medicine, at the University of Iowa. He is a biology graduate from Carleton College, Northfield, Minnesota with a background in bioinformatics, genetic engineering and computer programming. His experience working with and developing open source bioinformatics tools has given him a perspective looking at broader trends in genetics and the future use of computers in the field of biology. He is dedicated to the application of computer science to solve bio-engineering problems. He is particularly interested in developing algorithms to help assign personalized medication. He is focused on combining his interest in biology and bioinformatics to contribute to research that allows identification of specific infections from laboratory use to clinical treatment options.

Dr. W. Bryan Jennings

Dr. W. Bryan Jennings is a Principal Investigator in the Department of Evolution, Ecology, & Organismal Biology at the University of California, Riverside and a Senior Research Associate in the Department of Vertebrates, National Museum of Brazil. He received a PhD in Ecology, Evolution, & Behavior from the University of Texas at Austin, in 2002. For his doctoral and postdoctoral work, he studied the diversification of Australian lizards and birds using genomic data at the University of Washington and Harvard University. Recent research by he and his students has focused on the evolution and conservation of vertebrates in the Mojave Desert and Redwood Forests of the western United States, and in the Brazilian Atlantic Rainforests. He and his students have also been developing bioinformatics tools for acquiring and refining phylogenomic datasets. He is the author of the book "Phylogenomic Data Acquisition: Principles and Practice".

Link to the article:

<https://academic.oup.com/bioinformaticsadvances/article/3/1/vbad174/7455250?searchresult=1>

Link to the software:

<https://github.com/Sammccarthypotter/ExRec>

Bioinformatics Advances

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ExRec

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