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October 2, 2017

Dear Editor

We present our article "AnaCoDa: Analyzing Codon Data with Bayesian mixture models" to be considered for publication as an application note in Bioinformatics. The authors (Cedric Landerer, Alexander Cope, Russell Zaretzki, and Michael A. Gilchrist) developed a software package to aid researchers with analyzing coding sequence and ribosome footprinting data. The software provides a fitting and analysis mechanism for multiple published and unpublished models and is readily accessible via the R scripting language.

AnaCoda allows for the estimation of biologically relevant parameters like mutation bias or ribosome pausing time, depending on the model employed. Bayesian estimation of parameters is performed using an adaptive Metropolis-Hasting within Gibbs sampling approach. Models implemented in AnaCoda are currently able to handle gene coding sequences and ribosome footprinting data. However, the flexible framework implemented using Rcpp, combining C++ with an R interface, allows for the implementation of models for other data types(e.g. phylogenetic data).

AnaCoda is a versatile R package that provides a useful set of tools of interest to the fields of molecular evolution and translation dynamics. The software will be submitted to CRAN for easy access and long term availability.

The authors declare no competing interests and all authors have approved the manuscript for submission.

The submitted material has neither been published nor is under considera-

tion for publication by other journals.

with best regards

Cedric Landerer