

Package ‘scrm’

January 27, 2015

Type Package

Title Simulating the Evolution of Biological Sequences

Version 1.3-3

Date 2014-11-17

Description A coalescent simulator that allows the rapid simulation of biological sequences under neutral models of evolution.

URL <https://github.com/scrm/scrm-r>

License GPL (>= 3)

Depends R (>= 3.1.0)

Imports Rcpp (>= 0.11.2)

Suggests testthat (>= 0.9.0), knitr, ape

SystemRequirements C++11

VignetteBuilder knitr

LinkingTo Rcpp

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NeedsCompilation yes

Repository CRAN

Date/Publication 2014-11-18 11:19:58

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scrm-package

Simulating the evolution of biological sequences

Description

The Sequential Coalescent with Recombination Model (SCRM) is an approximation of the Ancestral Recombination Graph. It can be used to simulate the neutral evolution of chromosomes/biological sequences subject to possibly complicated population structure. The program *scrm* is an implementation of this model that is designed to act as a drop-in replacement for the widely adopted coalescent simulator *ms*. This package contains *scrm* along with a convenient R interface.

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See Also

- [scrm](#) for details on how to use *scrm*,
- `vignette('scrm-Arguments')` for an overview of command line arguments and
- `vignette('scrm-TreesForApe')` for an example on using genealogies simulated with *scrm* with package 'ape'.

scrm

Simulate the evolution of biological sequences

Description

This function provides an interface for calling *scrm* from R. The command line options are passed via the `args` argument. The vignette 'scrm-Arguments' contains details about the available options. Summary statistics are converted into an R format. Additionally, there is an option to write the original command line output into a file.

Usage

```
scrm(args, file = "")
```

Arguments

<code>args</code>	A string containing the command line arguments for <i>scrm</i> . Look at <i>scrm</i> 's vignette for a description of available arguments.
<code>file</code>	If provided, <i>scrm</i> will additionally write its output into a file with the given file, using an <i>ms</i> -like text output.

Value

A named list of summary statistics. Most summary statistics are again a list, where each entry contains the value for one locus. For the site frequency spectrum, the summary statistic is a matrix, where each row contains the spectrum for one locus.

Seeding

The R version of *scrm* uses random number from R's random generator. Therefore, the `'-seed'` argument of the command line version will be ignored, and no seed is given in the output. Use the R function [set.seed](#) prior to calling this function to ensure reproducibility of results.

See Also

- `vignette('scrm-Arguments')` for an overview of commandline arguments and
- `vignette('scrm-TreesForApe')` for an example on using genealogies simulated with *scrm* with package `'ape'`.

Examples

```
# 5 Chromosomes with 100 bases each with recombination and mutation
sum_stats <- scrm('5 1 -r 5 100 -t 5 -T -L')
str(sum_stats)

# Simulate the site frequency spectrum at 3 loci. For each locus
# 10 Chromosomes of 1Mb length are sampled from two populations with
# migration inbetween.
scrm('10 3 -r 400 1000000 -l 100000 -I 2 4 6 0.5 -t 300 -oSFS')$sfs
```

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