

# Package ‘scrm’

February 14, 2022

**Type** Package

**Title** Simulating the Evolution of Biological Sequences

**Version** 1.7.4-0

**Author** Paul Staab [aut, cph],  
Zhu Sha [aut, cph],  
Dirk Metzler [aut, cre, cph, ths],  
Gerton Lunter [aut, cph, ths]

**Maintainer** Dirk Metzler <metzler@bio.lmu.de>

**Description** A coalescent simulator that allows the rapid simulation of biological sequences under neutral models of evolution. Different to other coalescent based simulations, it has an optional approximation parameter that allows for high accuracy while maintaining a linear run time cost for long sequences. It is optimized for simulating massive data sets as produced by Next-Generation Sequencing technologies for up to several thousand sequences.

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

**BugReports** <https://github.com/scrm/scrm-r/issues>

**License** GPL (>= 3)

**Depends** R (>= 3.1.0)

**Imports** Rcpp (>= 0.11.2)

**Suggests** ape, knitr, rmarkdown, testthat (>= 0.9.0)

**SystemRequirements** C++11

**VignetteBuilder** knitr

**LinkingTo** Rcpp

**RoxygenNote** 6.1.0

**NeedsCompilation** yes

**Repository** CRAN

**Date/Publication** 2022-02-14 09:00:02 UTC

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### 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 an R interface.

### Author(s)

Paul Staab, Zhu Sha, Dirk Metzler & Gerton Lunter

Maintainer: Paul Staab <develop@paulstaab.de>

### 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'.

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### 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

args	A string containing the command-line arguments for scrm. Look at scrms vignette for a description of available arguments.
file	If provided, scrm will additionally write its output into a file with the given file, using an ms-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 command line arguments and
- `vignette('scrm-TreesForApe')` for an example on using genealogies simulated with *scrm* with package 'ape'.

## Examples

```
set.seed(789)
# 5 Chromosomes with 100 bases each with recombination and mutation
sum_stats <- scrm('5 1 -r 3.1 100 -t 1.5 -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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