

Package ‘GenomeAdmixR’

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Type Package

Title Simulate Admixture of Genomes

Version 2.1.13.2

Description Individual-based simulations forward in time, simulating how patterns in ancestry along the genome change after admixture. Full description can be found in Janzen (2021) <[doi:10.1111/2041-210X.13612](https://doi.org/10.1111/2041-210X.13612)>.

License GPL (>= 2)

URL <https://github.com/thijsjanzen/GenomeAdmixR>

BugReports <https://github.com/thijsjanzen/GenomeAdmixR/issues>

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Contents

GenomeAdmixR-package	3
ancestry_module	5
calculate_allele_frequencies	6
calculate_average_ld	7
calculate_dist_junctions	7
calculate_fst	8
calculate_heterozygosity	9
calculate_ld	9
calculate_marker_frequency	10
combine_input_data	11
create_artificial_genomeadmixr_data	12
create_iso_female	12
dgrp2.3R.5k.data	13
iso_female_ancestry	14
iso_female_sequence	15
load_population	16
migration_settings	17
plink_to_genomeadmixr_data	18
plot.individual	18
plot_chromosome	19
plot_difference_frequencies	20
plot_dist_junctions	21
plot_frequencies	21
plot_joyplot_frequencies	22
plot_over_time	23
plot_start_end	24
print.genomeadmixr_data	25
print.individual	26
print.population	26
read_input_data	27
save_population	28
sequence_module	28
simulate_admixture	29
simulate_ancestry	31
simulate_ancestry_migration	32
simulate_sequence	35
simulate_sequence_migration	36
simulation_data_to_genomeadmixr_data	39
vcfR_to_genomeadmixr_data	39
write_as_plink	40
Index	41

Description

Individual-based simulations forward in time, simulating how patterns in ancestry along the genome change after admixture. The simulation assumes Wright-Fisher dynamics, e.g. random mating and non-overlapping generations. In the simulation, instead of specific alleles, local ancestry is tracked, thus assuming that local molecular data can always be uniquely traced back to one of the founding individuals (populations). The package provides functionality to perform such simulations, but also to perform post-hoc statistical analyses and to visualize the obtained results. Version 2.1.13 - Added support for machines without TBB

Version 2.1.12 - Update to C++17

Version 2.1.11 - Replaced `Rf_error` with `Rcpp::stop()`

Version 2.1.10 - Fixed memory bug, improved documentation

Version 2.1.9 - updated `tbb::task_scheduler_init` to `tbb::global_control`

Version 2.1.7 - Improve documentation

Version 2.1.6 - check classes with `inherits`

Version 2.1.5 - Removed debugging output

Version 2.1.4 - Only output when `verbose = TRUE`

Version 2.1.3 - Changed DOI link in description

Version 2.1.2 - Improved testing

Version 2.1.1 - Removed GNU make dependency

Version 2.1 - Removed error in `calculate_allele_frequency`

Version 2.0.1 - Moved migration outside the modules

Version 2.0 - Added `ancestry_module` and `sequence_module` to distinguish between implementations of the model

Version 1.2 - Added example sequencing data

Version 1.2 - Added the option to load sequence data for admixing

Version 1.1 - Fixed a minor bug with `plot_joyplot_frequencies`

Version 1.1 - Improved tests

Version 1.1 - Improved recombination code (again)

Version 1.0 - Release associated with bioRxiv submission, to be found here: <https://doi.org/10.1101/2020.10.19.343491>

Version 0.66 - Improved recombination code, about twice as fast

Version 0.65 - Added testing and added logo

Version 0.64 - Reduced cyclomatic complexity

Version 0.63 - Updated random number generation

Version 0.62 - Updated to Roxygen

Version 0.61 - Added `plot_over_time`

Version 0.60 - Added admixture with migration

Version 0.59 - Updated frequency code under the hood

Version 0.58 - Renamed to GenomeAdmixR

Version 0.58 - Collapsed and improved many functions

Version 0.57 - Added function to generate admixed individuals

Version 0.56 - Added starting frequencies to `'simulate_admixture'`

Version 0.55 - Extended `'calculate_marker_frequency'` to handle a vector of locations

Version 0.55 - Increased accuracy of choosing a random position for recombination, this should

prevent the rare bug fixed in version 0.54
Version 0.54 - Fixed a MAJOR bug regarding recombination: in rare cases, a crossover position could be picked on an existing junction, due to the limited number of digits in uniform()
Version 0.54 - Improved plot_difference_frequencies to handle modified input
Version 0.53 - Added multiplicative_selection
Version 0.52 - Added plot_difference_frequencies
Version 0.51 - Added tajima's d calculation
Version 0.50 - Added simulated_admixture until
Version 0.49 - Added 'simulate' to cpp
Version 0.48 - Added a general 'simulate' function
Version 0.47 - Changed the effect of migration
Version 0.46 - Added joyplot & increase_ancestor
Version 0.45 - Removed create_two_populations
Version 0.44 - Added tracking regions
Version 0.43 - Fixed bugs in select_population
Version 0.42 - Added initial and final frequency tables
Version 0.41 - Added multiple marker support
Version 0.40 - Collapsed selection functions
Version 0.39 - Added support for non-additive selection
Version 0.38 - Added track frequencies
Version 0.37 - Removed selection on regions
Version 0.36 - Added progress_bar option
Version 0.35 - Added calculate_marker_frequency
Version 0.34 - Added selection_markers
Version 0.33 - Fixed bugs in selection
Version 0.32 - Moved Fish.h code to Fish.cpp
Version 0.31 - Changed random number generator to R based
Version 0.30 - Added Recombination = 1 code
Version 0.29 - Changed internal junction representation: removed .left
Version 0.28 - Reverted to Agner Fog Random number generation
Version 0.27 - Speed up return types
Version 0.26 - Added class verification code
Version 0.25 - Squashed plotting bug
Version 0.24 - Removed Output.cpp
Version 0.23 - Removed number_of_founders from calc_allele_spectrum
Version 0.22 - Added save and load functions
Version 0.21 - Changed random-seed management
Version 0.20 - Removed superfluous code
Version 0.19 - Removed number_of_founders from Fst and LD code
Version 0.18 - Start of tracking changes

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References

Janzen T, Diaz F. Individual-based simulations of genome evolution with ancestry: The GenomeAdmixR R package. *Methods Ecol Evol.* 2021; 12: 1346–1357. <https://doi.org/10.1111/2041-210X.13612>

ancestry_module	<i>Creates a module to start simulations tracking local ancestry</i>
-----------------	----------------------------------------------------------------------

Description

Module to perform simulations based on local ancestry

Usage

```
ancestry_module(  
  input_population = NA,  
  number_of_founders = 2,  
  initial_frequencies = NA,  
  morgans = 1,  
  markers = NA,  
  track_junctions = FALSE  
)
```

Arguments

input_population	Potential earlier simulated population used as starting point for the simulation. If not provided by the user, the simulation starts from scratch.
number_of_founders	Number of unique ancestors / ancestries to be tracked in the simulation
initial_frequencies	A vector describing the initial frequency of each ancestor / ancestry. By default, equal frequencies are assumed. If a vector not summing to 1 is provided, the vector is normalized.
morgans	Length of the genomic stretch simulated, expressed in Morgan (e.g. the number of crossovers during meiosis)
markers	A vector of locations of markers, with the location in Morgan. Ancestry at these marker positions is tracked for every generation.
track_junctions	Tracks the average number of junctions over time if TRUE

Value

list with type = "Ancestry". Can be used in simulate_admixture.

`calculate_allele_frequencies`*Calculate allele frequencies*

Description

Calculate for a number of regularly spaced markers the relative frequency of each ancestor in the population.

Usage

```
calculate_allele_frequencies(  
  source_pop,  
  locations = seq(0, 1, length.out = 100),  
  progress_bar = FALSE  
)
```

Arguments

<code>source_pop</code>	Population for which to estimate allele frequencies
<code>locations</code>	A vector indicating the locations (in Morgan) where to calculate the allele frequencies.
<code>progress_bar</code>	Displays a progress_bar if TRUE. Default value is TRUE

Details

Markers are equidistantly spaced, with a distance of `step_size` in between them.

Value

A tibble containing the allele frequencies

Examples

```
number_founders = 20  
wildpop = simulate_admixture(  
  module = ancestry_module(number_of_founders = 20, morgan = 1),  
  pop_size = 1000,  
  total_runtime = 10,  
  num_threads = 1)  
  
freq_output <- calculate_allele_frequencies(wildpop,  
                                           progress_bar = TRUE)  
  
require(ggplot2)  
ggplot(freq_output, aes(x=location, y = frequency,  
                       col = as.factor(ancestor))) +  
  geom_line()
```

calculate_average_ld *Calculates the ld between two alleles*

Description

calculate the average ld between two loci

Usage

calculate_average_ld(alleles_pos_1, alleles_pos_2)

Arguments

alleles_pos_1 alleles at locus 1

alleles_pos_2 alleles at locus 2

Value

a list with two entries: LD and r_squared

calculate_dist_junctions
collect the full distribution of junctions in the population

Description

calculates the distribution of junctions across the population

Usage

calculate_dist_junctions(pop)

Arguments

pop object of the class 'population'

Value

vector with two entries per individual, each indicating the number of junctions in the respective chromosomes


```
FST <- calculate_fst(pop1 = two_populations$population_1,
                    pop2 = two_populations$population_2,
                    sampled_individuals = 10,
                    number_of_markers = 100,
                    random_markers = TRUE)
```

calculate_heterozygosity
Calculate heterozygosity

Description

Calculate the average population level heterozygosity

Usage

```
calculate_heterozygosity(source_pop, locations, progress_bar = FALSE)
```

Arguments

source_pop	Population for which to estimate allele frequencies, or a list of individuals for which to calculate average heterozygosity
locations	A vector indicating the locations (in Morgan) of markers for which to calculate the heterozygosity
progress_bar	Displays a progress_bar if TRUE. Default value is TRUE

Value

A tibble containing the heterozygosities

calculate_ld	<i>Calculate linkage disequilibrium statistics This function calculates two matrices, once containing all pairwise linkage disequilibrium (ld) values, and one matrix containing all pairwise r statistics</i>
--------------	----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

Description

Calculate linkage disequilibrium statistics This function calculates two matrices, once containing all pairwise linkage disequilibrium (ld) values, and one matrix containing all pairwise r statistics

Usage

```
calculate_ld(pop, sampled_individuals = 10, markers = NA, verbose = FALSE)
```

Arguments

pop	focal population
sampled_individuals	Number of individuals randomly sampled to calculate the LD matrices
markers	vector of markers. If a single number is used, that number of markers is randomly placed along the genome.
verbose	display verbose output, default is FALSE.

Value

An object containing two items:

ld_matrix	Pairwise ld statistics for all markers
rsq_matrix	Pairwise rsq statistics for all markers

Examples

```
wildpop = simulate_admixture(
  module = ancestry_module(number_of_founders = 10, morgans = 1),
  pop_size = 1000,
  total_runtime = 10)

ld_results <- calculate_ld(pop = wildpop,
  markers = 10)

plot(ld_results$ld_matrix~ld_results$dist_matrix,
  pch = 16,
  xlab="Distance between markers",
  ylab = "Linkage Disequilibrium")
```

calculate_marker_frequency

Calculate allele frequencies at a specific marker location

Description

Calculate the relative frequency of each ancestor in the population at a specific marker location

Usage

```
calculate_marker_frequency(pop, location)
```

Arguments

pop	Population for which to estimate allele frequencies at the given marker
location	A vector or scalar of location(s) along the chromosome for which allele frequencies are to be calculated. Locations are in Morgan.

Value

A tibble containing the frequency of each present ancestor at the provided location. Ancestors with frequency = 0 are dropped out of the table. The tibble contains three columns: location, ancestor and frequency.

Examples

```
wildpop = simulate_admixture(
  module = ancestry_module(number_of_founders = 20, morgans = 1),
  pop_size = 1000,
  total_runtime = 10)

avg_frequencies <- calculate_marker_frequency(pop = wildpop,
                                             location = 0.5)

frequencies <-
  calculate_marker_frequency(pop = wildpop,
                             location = seq(0.4, 0.5, by = 0.01))
require(ggplot2)
ggplot(frequencies, aes(x = location, y = frequency, col = ancestor)) +
  geom_step()
```

combine_input_data	<i>combine sequence data that was previously read from file into a population</i>
--------------------	-----------------------------------------------------------------------------------

Description

Create data in a format that can be used by GenomeAdmixR, entries are sampled randomly from each input data set, with replacement. Probability of sampling from each input data set is driven by the input frequencies, and total number of individuals sampled is driven by pop_size.

Usage

```
combine_input_data(input_data_list, frequencies = NA, pop_size)
```

Arguments

input_data_list	list where each entry is the result of create_input_data
frequencies	frequency of each entry in the list in the starting population
pop_size	intended population size

Value

the input data entries are combined to one single population that can be used to seed simulate_admixture_data. Output is identical to create_input_data

create_artificial_genomeadmixture_data
function to generate artificial genomeadmixture_data

Description

function to generate artificial genomeadmixture_data

Usage

```
create_artificial_genomeadmixture_data(  
  number_of_individuals,  
  marker_locations,  
  used_nucleotides = 1:4,  
  nucleotide_frequencies = NA  
)
```

Arguments

number_of_individuals
number of individuals

marker_locations
location of markers, either in bp or Morgan

used_nucleotides
subset or full set of [1/2/3/4] (reflecting a/c/t/g)

nucleotide_frequencies
frequencies of the used nucleotides, if not provided, equal frequencies are assumed.

Value

genomeadmixture_data object ready for simulate_admixture_data

create_iso_female *function to simulate creation of an isofemale line*

Description

create_isofemale simulates the creation of an isofemale line through extreme inbreeding.

Usage

```

create_iso_female(
  module = ancestry_module(),
  n = 1,
  inbreeding_pop_size = 100,
  run_time = 2000,
  num_threads = 1,
  verbose = FALSE
)

```

Arguments

module	Source population from which isofemales are generated
n	Number of isofemales to be generated
inbreeding_pop_size	Population size of the population used to generate homozygous individuals
run_time	Maximum runtime used for inbreeding
num_threads	number of threads. Default is 1. Set to -1 to use all available threads
verbose	Displays verbose output if TRUE. Default value is FALSE

Details

To create an isofemale, two individuals are randomly picked from the source population. Using these two individuals, a new population is seeded, of size `inbreeding_pop_size`. Then, this population is allowed to inbreed until either `run_time` is reached, or until all individuals are homozygous and genetically identical, whatever happens first.

Value

A list of length `n`, where each entry is a fully homozygous isofemale.

dgrp2.3R.5k.data	<i>A subset of sequencing data from the Drosophila Genetics Reference Panel</i>
------------------	---------------------------------------------------------------------------------

Description

This data set contains sequences from the 3R chromosome. Included are 4603 SNPs with at least 0.05 minor allele frequency, sequenced across 410 isofemale lines. Sequences were downloaded from <http://dgrp2.gnets.ncsu.edu/data.html>.

Usage

```
data("dgrp2.3R.5k.data")
```

Format

genomeadmixr_data object

References

Mackay, T., Richards, S., Stone, E. et al. The *Drosophila melanogaster* Genetic Reference Panel. *Nature* 482, 173–178 (2012). <<https://doi.org/10.1038/nature10811>>

Examples

```
data("dgrp2.3R.5k.data")
simulate_admixture(
  module = sequence_module(molecular_data = dgrp2.3R.5k.data),
  pop_size = 100,
  total_runtime = 10)
```

iso_female_ancestry *Create isofemale*

Description

Creates isofemale individuals, given a population

Usage

```
iso_female_ancestry(
  source_pop = NA,
  n = 1,
  inbreeding_pop_size = 100,
  run_time = 2000,
  morgan = 1,
  num_threads = 1,
  verbose = FALSE
)
```

Arguments

source_pop	Source population from which isofemales are generated
n	Number of isofemales to be generated
inbreeding_pop_size	Population size of the population used to generate homozygous individuals
run_time	Maximum runtime used for inbreeding
morgan	Size of the chromosome in Morgan (e.g. the number of crossovers during meiosis)
num_threads	number of threads. Default is 1. Set to -1 to use all available threads
verbose	Displays verbose output if TRUE. Default value is FALSE

Details

To create an isofemale, two individuals are randomly picked from the source population. Using these two individuals, a new population is seeded, of size `inbreeding_pop_size`. Then, this population is allowed to inbreed until either `run_time` is reached, or until all individuals are homozygous and genetically identical, whatever happens first.

Value

A list of length `n`, where each entry is a fully homozygous isofemale.

`iso_female_sequence` *Create isofemale*

Description

Creates isofemale individuals, given a population

Usage

```
iso_female_sequence(
  input_data = NA,
  n = 1,
  inbreeding_pop_size = 100,
  run_time = 2000,
  morgan = 1,
  recombination_rate = NA,
  num_threads = 1,
  verbose = FALSE
)
```

Arguments

<code>input_data</code>	Source population from which isofemales are generated
<code>n</code>	Number of isofemales to be generated
<code>inbreeding_pop_size</code>	Population size of the population used to generate homozygous individuals
<code>run_time</code>	Maximum runtime used for inbreeding
<code>morgan</code>	Size of the chromosome in Morgan (e.g. the number of crossovers during meiosis)
<code>recombination_rate</code>	rate in cM / Mbp, used to map recombination to the markers. If the <code>recombination_rate</code> is not set, the value for Morgan is used, assuming that the markers included span an entire chromosome.
<code>num_threads</code>	number of threads. Default is 1. Set to -1 to use all available threads
<code>verbose</code>	Displays verbose output if TRUE. Default value is FALSE

Details

To create an isofemale, two individuals are randomly picked from the source population. Using these two individuals, a new population is seeded, of size `inbreeding_pop_size`. Then, this population is allowed to inbreed until either `run_time` is reached, or until all individuals are homozygous and genetically identical, whatever happens first.

Value

A list of length `n`, where each entry is a fully homozygous isofemale.

load_population	<i>Load a population from file</i>
-----------------	------------------------------------

Description

Loads a population that has previously been written to file.

Usage

```
load_population(file_name)
```

Arguments

file_name	Name of the file to save the population
-----------	-----------------------------------------

Details

This function is a wrapper for `readRDS`.

Value

A population object

See Also

[save_population](#)

migration_settings *Function to manage settings associated with migration*

Description

creates a list with settings associated with migration.

Usage

```
migration_settings(
  migration_rate = NA,
  stop_at_critical_fst = FALSE,
  critical_fst = NA,
  population_size = c(100, 100),
  initial_frequencies = list(c(1, 0), c(0, 1)),
  generations_between_update = 10,
  sampled_individuals = 10,
  number_of_markers = 100,
  random_markers = TRUE
)
```

Arguments

migration_rate Rate of migration between the two populations. Migration is implemented such that with probability m (migration rate) one of the two parents of a new offspring is from the other population, with probability $1-m$ both parents are of the focal population.

stop_at_critical_fst option to stop at a critical FST value , default is FALSE

critical_fst the critical fst value to stop, if stop_simulation_at_critical_fst is TRUE

population_size vector of population sizes, one size for each population

initial_frequencies A list describing the initial frequency of each ancestor in each population. Each entry in the list contains a vector with the frequencies for all ancestor. The length of the vector indicates the number of unique ancestors. If a vector not summing to 1 is provided, the vector is normalized.

generations_between_update The number of generations after which the simulation has to check again whether the critical Fst value is exceeded

sampled_individuals Number of individuals to be sampled at random from the population to estimate Fst

number_of_markers Number of markers to be used to estimate Fst

random_markers Are the markers to estimate Fst randomly distributed, or regularly distributed? Default is TRUE.

Value

list with migration associated settings. To be used to pass on migration settings to `simulate_admixture`.

```
plink_to_genomeadmrx_data
      function to convert plink style (ped/map) data to genome_admrx_data
```

Description

function to convert plink style (ped/map) data to `genome_admrx_data`

Usage

```
plink_to_genomeadmrx_data(
  ped_data,
  map_data,
  chosen_chromosome,
  verbose = FALSE
)
```

Arguments

<code>ped_data</code>	result of <code>read.table(ped_file, header = F)</code>
<code>map_data</code>	result of <code>read.table(map_file, header = F)</code>
<code>chosen_chromosome</code>	chromosome of choice
<code>verbose</code>	verbose output

Value

`genomeadmrx_data` object ready for `simulate_admixture_data`

```
plot.individual      plot the genome of an individual
```

Description

visualise ancestry blocks on both chromosomes

Usage

```
## S3 method for class 'individual'
plot(x, cols = NA, ...)
```

Arguments

x	object of type individual
cols	colors for the different ancestors
...	other arguments

Value

No return value

plot_chromosome	<i>plots a chromosome</i>
-----------------	---------------------------

Description

This function plots a chromosome in the range [xmin, xmax]. Colors indicate different ancestry.

Usage

```
plot_chromosome(chrom, xmin = 0, xmax = 1)
```

Arguments

chrom	object of type chromosome, typically a table with two columns. The first column indicates the start of an ancestry block (location in Morgan), the second column indicates the ancestry type.
xmin	minimum value of the range, default = 0.
xmax	maximum value of the range, default = 1.

Value

No return value

Examples

```
wildpop = simulate_admixture(
  module = ancestry_module(number_of_founders = 10, morgan = 1),
  pop_size = 1000,
  total_runtime = 10)

isofemale <- create_iso_female(
  module = ancestry_module(input_population = wildpop,
                           morgan = 1),
  n = 1,
  inbreeding_pop_size = 100,
  run_time = 10)

plot_chromosome(chrom = isofemale[[1]]$chromosome1)
```

```
# and a detail of the chromosome:
plot_chromosome(chrom = isofemale[[1]]$chromosome1,
                xmin = 0.4,
                xmax = 0.6)
```

```
plot_difference_frequencies
```

Plot the change in frequency between the start and end of a simulation

Description

This function plots the change in frequency of one or multiple ancestors after performing a simulation.

Usage

```
plot_difference_frequencies(
  results,
  picked_ancestor = "ALL",
  picked_population = 1
)
```

Arguments

results	An object which is the result of <code>simulate_admixture</code> being a list with four properties: population, frequencies, initial_frequencies and final frequencies
picked_ancestor	Default is "ALL", where different colors indicate different ancestors. Alternatively, for clarity, the user can specify a specific ancestral allele, and only that allele is plotted
picked_population	If multiple populations were simulated (in the case of <code>simulate_admixture_migration</code>), which population should be plotted? Default is <code>population_1</code> .

Value

a ggplot2 object

Examples

```
s <- 0.1
select_matrix <- matrix(nrow = 1, ncol = 5)
select_matrix[1, ] <- c(0.25, 1.0, 1 + 0.5 * s, 1 + s, 0)

markers <- seq(from = 0.2, to = 0.3, length.out = 100)

selected_pop <- simulate_admixture(
  module = ancestry_module(number_of_founders = 10,
```

```
                                morgan = 1,  
                                markers = markers),  
                                pop_size = 1000,  
                                total_runtime = 11,  
                                select_matrix = select_matrix)  
require(ggplot2)  
plot_difference_frequencies(results = selected_pop,  
                            picked_ancestor = "ALL")
```

plot_dist_junctions *plot the distribution of junctions*

Description

plots the distribution of junctions in the population using base R

Usage

```
plot_dist_junctions(pop)
```

Arguments

pop of the class 'population'

Value

No return value

plot_frequencies *Plot the frequencies of all ancestors along the genome.*

Description

This function plots the frequency of all ancestors after performing a simulation.

Usage

```
plot_frequencies(  
  result,  
  locations = seq(0, 1, length.out = 100),  
  progress_bar = FALSE  
)
```

Arguments

result	An object which is the result of <code>select_population</code> or <code>create_population_selection</code> , being a list with four properties: <code>population</code> , <code>frequencies</code> , <code>initial_frequencies</code> and <code>final_frequencies</code>
locations	A vector indicating the locations (in Morgan) where to calculate the allele frequencies.
progress_bar	Displays a <code>progress_bar</code> if TRUE. Default value is FALSE

Value

a `ggplot2` object

Examples

```
pop <- simulate_admixture(
  module = ancestry_module(number_of_founders = 4),
  pop_size = 1000,
  total_runtime = 11)
require(ggplot2)
plot_frequencies(result = pop)
```

`plot_joyplot_frequencies`

make a joy plot of the distribution of allele frequencies within a region

Description

This function plots the distribution of allele frequencies within a region over time, making use of a 'joyplot'

Usage

```
plot_joyplot_frequencies(
  frequencies,
  time_points,
  picked_ancestor = "ALL",
  picked_population = 1
)
```

Arguments

frequencies	A tibble containing four columns: <code>time</code> , <code>location</code> , <code>ancestor</code> , <code>frequency</code> . Typically one of the items returned by <code>create_population_selection</code> or <code>select_population</code> when the user specifies <code>track_frequency</code> .
time_points	A sequence of time points for which the user wants to create the joyplot

picked_ancestor

Default is "ALL", where different colors indicate different ancestors. Alternatively, for clarity, the user can specify a specific ancestral allele, and only that allele is plotted

picked_population

If multiple populations were simulated (in the case of simulate_admixture_migration), which population should be plotted? Default is population_1.

Value

a ggplot object

Examples

```
s <- 0.01
select_matrix <- matrix(nrow = 1, ncol = 5)
select_matrix[1, ] <- c(0.25, 1.0, 1 + 0.5 * s, 1 + s, 0)

markers <- seq(from = 0.2, to = 0.3, length.out = 100)

selected_pop <- simulate_admixture(
  module = ancestry_module(number_of_founders = 10,
                           morgan = 1,
                           markers = markers),
  pop_size = 1000,
  total_runtime = 11,
  select_matrix = select_matrix)

require(ggplot2)
plot_joyplot_frequencies(frequencies = selected_pop$frequencies,
  time_points = 0:11,
  picked_ancestor = "ALL")

# joyplot frequencies returns a ggplot object, so we can
# add extra elements:
plot_joyplot_frequencies(frequencies = selected_pop$frequencies,
  time_points = 0:11,
  picked_ancestor = "ALL") +
  ggplot2::xlab("Location") +
  ggplot2::ylab("Generations")
```

plot_over_time

Plot the frequencies of all ancestors over time

Description

This function plots the frequency of all ancestors over time at a specific location on the chromosome, after performing a simulation.

Usage

```
plot_over_time(frequencies, focal_location)
```

Arguments

frequencies A tibble containing four columns: time, location, ancestor, frequency. A fifth column population can be included if the tibble is the result of `simulate_admixture_migration`.

focal_location Location (in Morgan) where to plot the allele frequencies.

Value

a ggplot2 object

Examples

```
pop <- simulate_admixture(
  module = ancestry_module(number_of_founders = 10,
                           markers = 0.5),
  pop_size = 1000,
  total_runtime = 11)
require(ggplot2)
plot_over_time(frequencies = pop$frequencies,
              focal_location = 0.5)
```

<code>plot_start_end</code>	<i>Plot both the starting frequencies and the final frequencies in one plot</i>
-----------------------------	---------------------------------------------------------------------------------

Description

This function plots the distribution of both the starting and the final frequencies in one plot

Usage

```
plot_start_end(results, picked_ancestor = "ALL", picked_population = 1)
```

Arguments

results An object which is the result of `simulate_admixture`, being a list with four properties: population, frequencies, initial_frequencies and final frequencies

picked_ancestor Default is "ALL", where different colors indicate different ancestors. Alternatively, for clarity, the user can specify a specific ancestral allele, and only that allele is plotted

picked_population If multiple populations were simulated (in the case of `simulate_admixture_migration`), which population should be plotted? Default is population_1.

Value

a ggplot object

Examples

```
markers <- seq(from = 0.2, to = 0.3, length.out = 100)

pop <- simulate_admixture(
  module = ancestry_module(number_of_founders = 3,
                            morgan = 1,
                            markers = markers),
  pop_size = 1000,
  total_runtime = 11)
require(ggplot2)
plot_start_end(pop,
               picked_ancestor = "ALL")
plot_start_end(pop,
               picked_ancestor = 1)
```

```
print.genomeadmixr_data
```

print an individual to the console

Description

prints an object of class genomeadmixr_data to the console

Usage

```
## S3 method for class 'genomeadmixr_data'
print(x, ...)
```

Arguments

x	individual
...	other arguments

Value

No return value

`print.individual` *print an individual to the console*

Description

prints an object of class `individual` to the console

Usage

```
## S3 method for class 'individual'  
print(x, ...)
```

Arguments

<code>x</code>	individual
<code>...</code>	other arguments

Value

No return value

`print.population` *print a population object*

Description

prints the contents of a population nicely

Usage

```
## S3 method for class 'population'  
print(x, ...)
```

Arguments

<code>x</code>	input population
<code>...</code>	other arguments

Value

No return value

read_input_data	<i>read sequence data from file to be used in simulation</i>
-----------------	--------------------------------------------------------------

Description

Create data in a format that can be used by GenomeAdmixR

Usage

```
read_input_data(  
  file_names,  
  type,  
  chosen_chromosome,  
  number_of_snps = NA,  
  random_snps = TRUE,  
  verbose = FALSE  
)
```

Arguments

file_names	names of input files
type	type of data, options are 'ped' and 'vcf'
chosen_chromosome	GenomeAdmixR simulates only a single chromosome.
number_of_snps	number of snps to be loaded from file, default is to load all snps
random_snps	if a subset of all snps has to be taken, should these be sampled sequentially (e.g. the first 100 snps) or randomly (100 randomly sampled snps) (examples are for 'number_of_snps' = 100).
verbose	give verbose output

Value

list with two properties: `genomes` a matrix with the sequence translated to numerics, such that [actg] corresponds to [1234], and missing data is represented with "-". Rows in the matrix correspond to chromosomes, and columns represent bases. Two consecutive rows represent an individual, such that rows 1-2 are individual, rows 3-4 are one individual etc. `markers` corresponds to the locations of the markers (in bp) on the chosen chromosome.

save_population	<i>Save a population to file</i>
-----------------	----------------------------------

Description

Saves a population to file for later use

Usage

```
save_population(population, file_name, compression = TRUE)
```

Arguments

population	Object of class population
file_name	Name of the file to save the population
compression	By default, the population is compressed to reduce file size. See for more information saveRDS

Details

This function functions as a wrapper for the base function saveRDS.

Value

No return value

sequence_module	<i>create sequence module</i>
-----------------	-------------------------------

Description

creates a sequence module, which contains all relevant information in order to perform a simulation based on sequence data.

Usage

```
sequence_module(  
  molecular_data = NA,  
  initial_frequencies = NA,  
  morgans = 1,  
  recombination_rate = NA,  
  markers = NA,  
  mutation_rate = 0,  
  substitution_matrix = matrix(1/4, 4, 4)  
)
```

Arguments

- `molecular_data` Genomic data used as input, should be of type `genomeadmixture_data`. Either a single dataset is provided, or a list of multiple `genomeadmixture_data` objects.
- `initial_frequencies` A vector describing the initial contribution of each provided input data set to the starting hybrid swarm. By default, equal frequencies are assumed. If a vector not summing to 1 is provided, the vector is normalized.
- `morgan` Length of the molecular sequence in Morgan (e.g. the number of crossovers during meiosis), alternatively, the recombination rate can be used, see below.
- `recombination_rate` rate in cM / Mbp, used to map recombination to the markers. If the `recombination_rate` is not set, the value for Morgan is used, assuming that the markers included span an entire chromosome.
- `markers` A vector of locations of markers, these markers are tracked for every generation.
- `mutation_rate` the per base probability of mutation. Default is 0.
- `substitution_matrix` a 4x4 matrix representing the probability of mutating to another base (where $[1/2/3/4] = [a/c/t/g]$), conditional on the event of a mutation happening. Default is the JC69 matrix, with equal probabilities for all transitions / transversions.

Value

sequence module object, used as starting point for `simulate_admixture`.

`simulate_admixture` *Individual based simulation of the breakdown of contiguous ancestry blocks.*

Description

Individual based simulation of the breakdown of contiguous ancestry blocks, with or without selection. Simulations can be started from scratch, or from a predefined input population.

Usage

```
simulate_admixture(
  module = ancestry_module(),
  pop_size = 100,
  total_runtime = 100,
  migration = migration_settings(),
  select_matrix = NA,
  multiplicative_selection = TRUE,
  verbose = FALSE,
  num_threads = 1
)
```

Arguments

module	Chosen module to simulate, either created with <code>module_ancestry</code> or <code>module_sequence</code> .
pop_size	The number of individuals in the population. If the number is larger than the number of individuals in the input population (if provided), additional individuals are sampled randomly from the input population to reach the intended size.
total_runtime	Number of generations
migration	settings associated with migration, should be created with migration_settings
select_matrix	Selection matrix indicating the markers which are under selection. If not provided by the user, the simulation proceeds neutrally. If provided, each row in the matrix should contain five entries: <ul style="list-style-type: none"> • location of the marker under selection (in Morgan) • fitness of wildtype (aa) • fitness of heterozygote (aA) • fitness of homozygote mutant (AA) • Ancestral type that represents the mutant allele A
multiplicative_selection	Default: TRUE. If TRUE, fitness is calculated for multiple markers by multiplying fitness values for each marker. If FALSE, fitness is calculated by adding fitness values for each marker.
verbose	Verbose output if TRUE. Default value is FALSE
num_threads	number of threads. Default is 1. Set to -1 to use all available threads

Value

A list with: population a population object, and three tibbles with allele frequencies (only contain values of a vector was provided to the argument markers: `frequencies`, `initial_frequencies` and `final_frequencies`). Each tibble contains four columns, `time`, `location`, `ancestor` and `frequency`, which indicates the number of generations, the location along the chromosome of the marker, the ancestral allele at that location in that generation, and finally, the frequency of that allele.

Examples

```
# local ancestry simulation
two_populations <- simulate_admixture(
  module = ancestry_module(number_of_founders = 3,
                           morgan = 0.8),
  migration = migration_settings(
    migration_rate = 0.01,
    population_size = c(100, 100)),
  total_runtime = 10)

# sequence simulation
data(dgrp2.3R.5k.data)

sequence_population <-
  simulate_admixture(
    module = sequence_module(molecular_data = dgrp2.3R.5k.data,
```

```

        recombination_rate = 0.2,
        mutation_rate = 1e-5),
pop_size = 1000,
total_runtime = 10)

```

simulate_ancestry	<i>Individual based simulation of the breakdown of contiguous ancestry blocks.</i>
-------------------	------------------------------------------------------------------------------------

Description

Individual based simulation of the breakdown of contiguous ancestry blocks, with or without selection. Simulations can be started from scratch, or from a predefined input population.

Usage

```

simulate_ancestry(
  input_population = NA,
  pop_size = NA,
  number_of_founders = 2,
  initial_frequencies = NA,
  total_runtime = 100,
  morgans = 1,
  num_threads = 1,
  select_matrix = NA,
  markers = NA,
  verbose = FALSE,
  track_junctions = FALSE,
  multiplicative_selection = TRUE
)

```

Arguments

input_population	Potential earlier simulated population used as starting point for the simulation. If not provided by the user, the simulation starts from scratch.
pop_size	The number of individuals in the population. If the number is larger than the number of individuals in the input population (if provided), additional individuals are sampled randomly from the input population to reach the intended size.
number_of_founders	Number of unique ancestors
initial_frequencies	A vector describing the initial frequency of each ancestor. By default, equal frequencies are assumed. If a vector not summing to 1 is provided, the vector is normalized.
total_runtime	Number of generations

morgan	Length of the chromosome in Morgan (e.g. the number of crossovers during meiosis)
num_threads	number of threads. Default is 1. Set to -1 to use all available threads
select_matrix	Selection matrix indicating the markers which are under selection. If not provided by the user, the simulation proceeds neutrally. If provided, each row in the matrix should contain five entries: <ul style="list-style-type: none"> • location of the marker under selection (in Morgan) • fitness of wildtype (aa) • fitness of heterozygote (aA) • fitness of homozygote mutant (AA) • Ancestral type that represents the mutant allele A
markers	A vector of locations of markers (relative locations in [0, 1]). If a vector is provided, ancestry at these marker positions is tracked for every generation.
verbose	Verbose output if TRUE. Default value is FALSE
track_junctions	Track the average number of junctions over time if TRUE
multiplicative_selection	Default: TRUE. If TRUE, fitness is calculated for multiple markers by multiplying fitness values for each marker. If FALSE, fitness is calculated by adding fitness values for each marker.

Value

A list with: population a population object, and three tibbles with allele frequencies (only contain values of a vector was provided to the argument markers: frequencies, initial_frequencies and final_frequencies. Each tibble contains four columns, time, location, ancestor and frequency, which indicates the number of generations, the location along the chromosome of the marker, the ancestral allele at that location in that generation, and finally, the frequency of that allele.

simulate_ancestry_migration

Individual based simulation of the breakdown of contiguous ancestry blocks in two populations linked by migration

Description

Individual based simulation of the breakdown of contiguous ancestry blocks, with or without selection. Simulations can be started from scratch, or from a predefined input population. Two populations are simulated, connected by migration

Usage

```
simulate_ancestry_migration(
  input_population_1 = NA,
  input_population_2 = NA,
  pop_size = c(100, 100),
  initial_frequencies = list(c(1, 0), c(0, 1)),
  total_runtime = 100,
  morgan = 1,
  num_threads = 1,
  select_matrix = NA,
  markers = NA,
  verbose = FALSE,
  track_junctions = FALSE,
  multiplicative_selection = TRUE,
  migration_rate = 0,
  stop_at_critical_fst = FALSE,
  critical_fst = 0.1,
  generations_between_update = 100,
  sampled_individuals = 10,
  number_of_markers = 100,
  random_markers = TRUE
)
```

Arguments

<code>input_population_1</code>	Potential earlier simulated population used as starting point for the simulation. If not provided by the user, the simulation starts from scratch.
<code>input_population_2</code>	Potential earlier simulated population used as starting point for the simulation. If not provided by the user, the simulation starts from scratch.
<code>pop_size</code>	Vector containing the number of individuals in both populations.
<code>initial_frequencies</code>	A list describing the initial frequency of each ancestor in each population. Each entry in the list contains a vector with the frequencies for all ancestor. The length of the vector indicates the number of unique ancestors. If a vector not summing to 1 is provided, the vector is normalized.
<code>total_runtime</code>	Number of generations
<code>morgan</code>	Length of the chromosome in Morgan (e.g. the number of crossovers during meiosis)
<code>num_threads</code>	number of threads. Default is 1. Set to -1 to use all available threads
<code>select_matrix</code>	Selection matrix indicating the markers which are under selection. If not provided by the user, the simulation proceeds neutrally. If provided, each row in the matrix should contain five entries: <ul style="list-style-type: none"> • location of the marker under selection (in Morgan) • fitness of wildtype (aa)

- fitness of heterozygote (aA)
- fitness of homozygote mutant (AA)
- Ancestral type that represents the mutant allele A

markers A vector of locations of markers (relative locations in [0, 1]). If a vector is provided, ancestry at these marker positions is tracked for every generation.

verbose Verbose output if TRUE. Default value is FALSE

track_junctions Track the average number of junctions over time if TRUE

multiplicative_selection
Default: TRUE. If TRUE, fitness is calculated for multiple markers by multiplying fitness values for each marker. If FALSE, fitness is calculated by adding fitness values for each marker.

migration_rate Rate of migration between the two populations. Migration is implemented such that with probability m (migration rate) one of the two parents of a new offspring is from the other population, with probability $1-m$ both parents are of the focal population.

stop_at_critical_fst
option to stop at a critical FST value , default is FALSE

critical_fst the critical fst value to stop, if stop_simulation_at_critical_fst is TRUE

generations_between_update
The number of generations after which the simulation has to check again whether the critical Fst value is exceeded

sampled_individuals
Number of individuals to be sampled at random from the population to estimate Fst

number_of_markers
Number of markers to be used to estimate Fst

random_markers Are the markers to estimate Fst randomly distributed, or regularly distributed? Default is TRUE.

Value

A list with: population_1, population_2 two population objects, and three tibbles with allele frequencies (only contain values of a vector was provided to the argument markers: frequencies, initial_frequencies and final_frequencies. Each tibble contains five columns, time, location, ancestor, frequency and population, which indicates the number of generations, the location along the chromosome of the marker, the ancestral allele at that location in that generation, the frequency of that allele and the population in which it was recorded (1 or 2). If a critical fst value was used to terminate the simulation, and object FST with the final FST estimate is returned as well.

simulate_sequence	<i>Individual based simulation of the breakdown of contiguous ancestry blocks.</i>
-------------------	------------------------------------------------------------------------------------

Description

Individual based simulation of the breakdown of contiguous ancestry blocks, with or without selection. Simulations can be started from scratch, or from a predefined input population.

Usage

```
simulate_sequence(
  input_data = NA,
  pop_size = NA,
  initial_frequencies = NA,
  total_runtime = 100,
  morgan = 1,
  recombination_rate = NA,
  num_threads = 1,
  select_matrix = NA,
  markers = NA,
  verbose = FALSE,
  multiplicative_selection = TRUE,
  mutation_rate = 0,
  substitution_matrix = matrix(1/4, 4, 4)
)
```

Arguments

input_data	Genomic data used as input, should be of type <code>genomeadmixr_data</code> . Either a single dataset is provided, or a list of multiple <code>genomeadmixr_data</code> objects.
pop_size	Vector containing the number of individuals in both populations.
initial_frequencies	A vector describing the initial contribution of each provided input data set to the starting hybrid swarm. By default, equal frequencies are assumed. If a vector not summing to 1 is provided, the vector is normalized.
total_runtime	Number of generations
morgan	Length of the chromosome in Morgan (e.g. the number of crossovers during meiosis)
recombination_rate	rate in cM / Mbp, used to map recombination to the markers. If the <code>recombination_rate</code> is not set, the value for Morgan is used, assuming that the markers included span an entire chromosome.
num_threads	number of threads. Default is 1. Set to -1 to use all available threads

select_matrix	Selection matrix indicating the markers which are under selection. If not provided by the user, the simulation proceeds neutrally. If provided, each row in the matrix should contain five entries: <ul style="list-style-type: none"> • location of the marker under selection (in Morgan) • fitness of wildtype (aa) • fitness of heterozygote (aA) • fitness of homozygote mutant (AA) • Ancestral type that represents the mutant allele A
markers	A vector of locations of markers (relative locations in [0, 1]). If a vector is provided, ancestry at these marker positions is tracked for every generation.
verbose	Verbose output if TRUE. Default value is FALSE
multiplicative_selection	Default: TRUE. If TRUE, fitness is calculated for multiple markers by multiplying fitness values for each marker. If FALSE, fitness is calculated by adding fitness values for each marker.
mutation_rate	the per base probability of mutation. Default is 0.
substitution_matrix	a 4x4 matrix representing the probability of mutating to another base (where [1/2/3/4] = [a/c/t/g]), conditional on the event of a mutation happening. Default is the JC69 matrix, with equal probabilities for all transitions / transversions.

Value

A list with: population a population object, and three tibbles with allele frequencies (only contain values of a vector was provided to the argument markers: frequencies, initial_frequencies and final_frequencies. Each tibble contains four columns, time, location, ancestor and frequency, which indicates the number of generations, the location along the chromosome of the marker, the ancestral allele at that location in that generation, and finally, the frequency of that allele.

simulate_sequence_migration

Individual based simulation of the breakdown of contiguous ancestry blocks in two populations linked by migration

Description

Individual based simulation of the breakdown of contiguous ancestry blocks, with or without selection. Simulations can be started from scratch, or from a predefined input population. Two populations are simulated, connected by migration

Usage

```
simulate_sequence_migration(
  input_data_population_1 = NA,
  input_data_population_2 = NA,
  pop_size = c(100, 100),
  total_runtime = 100,
  morgan = 1,
  recombination_rate = NA,
  num_threads = 1,
  select_matrix = NA,
  markers = NA,
  verbose = FALSE,
  multiplicative_selection = TRUE,
  migration_rate = 0,
  stop_at_critical_fst = FALSE,
  critical_fst = NA,
  generations_between_update = 100,
  sampled_individuals = 10,
  number_of_markers = 100,
  random_markers = TRUE,
  mutation_rate = 0,
  substitution_matrix = matrix(1/4, 4, 4)
)
```

Arguments

<code>input_data_population_1</code>	Genomic data used as input, should be created by the function <code>create_input_data</code> or by the function <code>combine_input_data</code>
<code>input_data_population_2</code>	Genomic data used as input, should be created by the function <code>create_input_data</code> or by the function <code>combine_input_data</code>
<code>pop_size</code>	Vector containing the number of individuals in both populations.
<code>total_runtime</code>	Number of generations
<code>morgan</code>	Length of the chromosome in Morgan (e.g. the number of crossovers during meiosis)
<code>recombination_rate</code>	rate in cM / Mbp, used to map recombination to the markers. If the <code>recombination_rate</code> is not set, the value for <code>morgan</code> is used, assuming that the markers included span an entire chromosome.
<code>num_threads</code>	number of threads. Default is 1. Set to -1 to use all available threads
<code>select_matrix</code>	Selection matrix indicating the markers which are under selection. If not provided by the user, the simulation proceeds neutrally. If provided, each row in the matrix should contain five entries: <ul style="list-style-type: none"> • location of the marker under selection (in Morgan) • fitness of wildtype (aa)

- fitness of heterozygote (aA)
- fitness of homozygote mutant (AA)
- Ancestral type that represents the mutant allele A

markers A vector of locations of markers (relative locations in [0, 1]). If a vector is provided, ancestry at these marker positions is tracked for every generation.

verbose Verbose output if TRUE. Default value is FALSE

multiplicative_selection
Default: TRUE. If TRUE, fitness is calculated for multiple markers by multiplying fitness values for each marker. If FALSE, fitness is calculated by adding fitness values for each marker.

migration_rate Rate of migration between the two populations. Migration is implemented such that with probability m (migration rate) one of the two parents of a new offspring is from the other population, with probability 1-m both parents are of the focal population.

stop_at_critical_fst
option to stop at a critical FST value , default is FALSE

critical_fst the critical fst value to stop, if stop_simulation_at_critical_fst is TRUE

generations_between_update
The number of generations after which the simulation has to check again whether the critical Fst value is exceeded

sampled_individuals
Number of individuals to be sampled at random from the population to estimate Fst

number_of_markers
Number of markers to be used to estimate Fst

random_markers Are the markers to estimate Fst randomly distributed, or regularly distributed? Default is TRUE.

mutation_rate the per base probability of mutation. Default is 0.

substitution_matrix
a 4x4 matrix representing the probability of mutating to another base (where $[1/2/3/4] = [a/c/t/g]$), conditional on the event of a mutation happening. Default is the JC69 matrix, with equal probabilities for all transitions / transversions.

Value

A list with: population_1, population_2 two population objects, and three tibbles with allele frequencies (only contain values of a vector was provided to the argument markers: frequencies, initial_frequencies and final_frequencies. Each tibble contains five columns, time, location, ancestor, frequency and population, which indicates the number of generations, the location along the chromosome of the marker, the ancestral allele at that location in that generation, the frequency of that allele and the population in which it was recorded (1 or 2). If a critical fst value was used to terminate the simulation, and object FST with the final FST estimate is returned as well.

simulation_data_to_genomeadmrx_data
function to convert ped/map data to genome_admrx_data

Description

function to convert ped/map data to genome_admrx_data

Usage

```
simulation_data_to_genomeadmrx_data(  
  simulation_data,  
  markers = NA,  
  verbose = FALSE  
)
```

Arguments

simulation_data	result of simulate_admixture
markers	vector of locations of markers (in Morgan). If no vector is provided, the function searches for marker locations in the simulation_data.
verbose	provide verbose output (default is FALSE)

Value

genomeadmrx_data object ready for simulate_admixture_data

vcfr_to_genomeadmrx_data
function to convert a vcfr object to genome_admrx_data

Description

function to convert a vcfr object to genome_admrx_data

Usage

```
vcfr_to_genomeadmrx_data(  
  vcfr_object,  
  chosen_chromosome,  
  number_of_snps = NA,  
  random_snps = TRUE,  
  verbose = FALSE  
)
```

Arguments

vcfr_object result of vcfr::read.vcfr
 chosen_chromosome
 chromosome of choice
 number_of_snps number of snps to be loaded from the vcf file, default is to load all snps
 random_snps if a subset of all snps has to be taken, should these be sampled sequentially (e.g. the first 100 snps) or randomly (100 randomly sampled snps) (examples are for 'number_of_snps' = 100).
 verbose if true, print progress bar

Value

genomeadmixr_data object ready for simulate_admixture_data

write_as_plink *function to write simulation output as PLINK style data*

Description

function to write simulation output as PLINK style data

Usage

```
write_as_plink(
  input_pop,
  marker_locations,
  file_name_prefix,
  chromosome = 1,
  recombination_rate = 1
)
```

Arguments

input_pop input population, either of class "population" or of class "genomeadmixr_data"
 marker_locations
 location of markers, in bp
 file_name_prefix
 prefix of the ped/map files.
 chromosome chromosome indication for map file
 recombination_rate
 recombination rate in cM / kb

Value

No return value

Index

- * **datasets**
 - dgrp2.3R.5k.data, 13
- ancestry_module, 5
- calculate_allele_frequencies, 6
- calculate_average_ld, 7
- calculate_dist_junctions, 7
- calculate_fst, 8
- calculate_heterozygosity, 9
- calculate_ld, 9
- calculate_marker_frequency, 10
- combine_input_data, 11
- create_artificial_genomeadmixr_data, 12
- create_iso_female, 12
- dgrp2.3R.5k.data, 13
- GenomeAdmixR (GenomeAdmixR-package), 3
- GenomeAdmixR-package, 3
- iso_female_ancestry, 14
- iso_female_sequence, 15
- load_population, 16
- migration_settings, 17, 30
- plink_to_genomeadmixr_data, 18
- plot.individual, 18
- plot_chromosome, 19
- plot_difference_frequencies, 20
- plot_dist_junctions, 21
- plot_frequencies, 21
- plot_joyplot_frequencies, 22
- plot_over_time, 23
- plot_start_end, 24
- print.genomeadmixr_data, 25
- print.individual, 26
- print.population, 26
- read_input_data, 27
- save_population, 16, 28
- sequence_module, 28
- simulate_admixture, 29
- simulate_ancestry, 31
- simulate_ancestry_migration, 32
- simulate_sequence, 35
- simulate_sequence_migration, 36
- simulation_data_to_genomeadmixr_data, 39
- vcfR_to_genomeadmixr_data, 39
- write_as_plink, 40