Package ‘GenomeAdmixR’

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Type Package

Title Simulate Admixture of Genomes

Version 2.1.1

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 (2020) <doi:10.1101/2020.10.19.343491>.

License GPL (>= 2)

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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 2.1.1 - 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
ancestry_module

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


ancestry_module

Creates a module to start simulations tracking local ancestry

Description

Module to perform simulations based on local ancestry
calculate_allele_frequencies

Usage

ancestry_module(
    input_population = NA,
    number_of_founders = 2,
    initial_frequencies = NA,
    morgan = 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.

morgan
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

---

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
)
calculate_average_ld

Arguments

- `source_pop`: Population for which to estimate allele frequencies
- `locations`: A vector indicating the locations (in Morgan) where to calculate the allele frequencies.
- `progress_bar`: 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

```r
data_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
**calculate_dist_junctions**

**Description**

collect the full distribution of junctions in the population

**Usage**

```r
calculate_dist_junctions(pop)
```

**Arguments**

- `pop` object of the class `population`

**Value**

a list with two entries: LD and r_squared

**calculate_fst**

**Description**

The FST value between two populations is calculated, given a number of markers. Markers are superimposed upon the (known) ancestry along the chromosome for all sampled individuals. Markers can be chosen to be regularly spaced, or randomly distributed.

**Usage**

```r
calculate_fst(
    pop1,
    pop2,
    sampled_individuals = 10,
    number_of_markers = 100,
    random_markers = FALSE
)
```
**Arguments**

- `pop1` Population object
- `pop2` Population object
- `sampled_individuals` Number of individuals to base the FST upon. Individuals are randomly drawn from each population, a lower number speeds up calculations.
- `number_of_markers` Number of markers along the chromosome used to calculate FST metrics.
- `random_markers` If TRUE, markers are randomly spaced along the chromosome, if FALSE, markers are equidistantly spaced along the chromosome.

**Details**

Uses the function `wc` from the package `hierfstat` to calculate the FST. The function `wc` computes the Weir and Cockerham F statistic.

**Value**

FST value

**Examples**

two_populations <- simulate_admixture(
    module = ancestry_module(),
    migration = migration_settings(migration_rate = 0.01,
        population_size = c(100, 100)))

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)
**calculate_ld**

**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

**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, morgan = 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, morgan = 1),
  pop_size = 1000,
  total_runtime = 10)

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

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()

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_genomeadmixr_data

function to generate artificial genomeadmixr_data

Description

function to generate artificial genomeadmixr_data
create_iso_female

function to simulate creation of an isofemale line

create_iso_female 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**

A subset of sequencing data from the *Drosophila Genetics Reference Panel*

---

**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](http://dgrp2.gnets.ncsu.edu/data.html).

**Usage**

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

**Format**

genomeadmixr_data object

**References**

Examples

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

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.
iso_female_sequence

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

input_data 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)
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.
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.

---

**load_population**

*Load a population from file*

---

**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, an R 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.
plot.individual

Description

function to convert plink style (ped/map) data to genome_admixr_data

Usage

plink_to_genomeadmixr_data(ped_data, map_data, chosen_chromosome)

Arguments

ped_data result of read.table(ped_file, header = F)
map_data result of read.table(map_file, header = F)
chosen_chromosome chromosome of choice

Value

genomeadmixr_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

plots a chromosome

Description

This function plots a chromosome in the range \([\text{xmin}, \text{xmax}]\). Colors indicate different ancestry.

Usage

\[\text{plot\_chromosome}(\text{chrom}, \text{xmin} = 0, \text{xmax} = 1)\]

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

```r
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**

```r
plot_difference_frequencies(
  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 ggplot2 object

**Examples**

```r
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)
```
**plot_dist_junctions**

```r
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**

```r
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**

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

**Arguments**

- `result` An object which is the result of `select_population` or `create_population_selection`, being a list with four properties: population, frequencies, initial frequencies and final frequencies
- `locations` A vector indicating the locations (in Morgan) where to calculate the allele frequencies.
- `progress_bar` Displays a progress_bar if TRUE. Default value is FALSE
Value

a ggplot2 object

Examples

```r
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

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

Arguments

- **frequencies**: A tibble containing four columns: time, location, ancestor, frequency. Typically one of the items returned by `create_population_selection` or `select_population` when the user specifies `track_frequency`.
- **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

```r
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

```r
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)
```

Description

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

Usage

```r
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

```r
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)
```
print.genomeadmixr_data

    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

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

x    individual
...
other arguments
print.population  

print a population object

Description

prints the contents of a population nicely

Usage

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

Arguments

- `x`: input population
- `...`: other arguments

Value

No return value

read_input_data  

read sequence data from file to be used in simulation

Description

Create data in a format that can be used by GenomeAdmixR

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>file_names</td>
<td>names of input files</td>
</tr>
<tr>
<td>type</td>
<td>type of data, options are 'ped' and 'vcf'</td>
</tr>
<tr>
<td>chosen_chromosome</td>
<td>GenomeAdmixR simulates only a single chromosome.</td>
</tr>
<tr>
<td>number_of_snps</td>
<td>number of snps to be loaded from file, default is to load all snps</td>
</tr>
<tr>
<td>random_snps</td>
<td>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).</td>
</tr>
<tr>
<td>verbose</td>
<td>give verbose output</td>
</tr>
</tbody>
</table>

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.

Description

Saves a population to file for later use

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>population</td>
<td>Object of class population</td>
</tr>
<tr>
<td>file_name</td>
<td>Name of the file to save the population</td>
</tr>
<tr>
<td>compression</td>
<td>By default, the population is compressed to reduce file size. See for more information saveRDS</td>
</tr>
</tbody>
</table>

Details

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

Value

No return value
sequence_module

create sequence module

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,
  morgan = 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 genomeadmixr_data. Either a single dataset is provided, or a list of multiple genomeadmixr_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**

```r
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 `module_ancestry` or `module_sequence`.

- **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: location 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
simulate_ancestry

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

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_ancestry(
  input_population = NA,
  pop_size = NA,
  number_of_founders = 2,
  initial_frequencies = NA,
  total_runtime = 100,
  morgan = 1,
  num_threads = 1,
simulate_ancestry

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: location 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**

```r
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**

- `input_population_1`  
  Potential earlier simulated population used as starting point for the simulation. If not provided by the user, the simulation starts from scratch.

- `input_population_2`  
  Potential earlier simulated population used as starting point for the simulation. If not provided by the user, the simulation starts from scratch.
**pop_size**
Vector containing the number of individuals in both populations.

**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.

**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: location 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.
simulate_sequence

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 

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_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 genomeadmixr_data. Either a single dataset is provided, or a list of multiple genomeadmixr_data 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 recombination_rate 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: location 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, these markers are 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
simulate_sequence_migration

Usage

```r
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

- **input_data_population_1**: Genomic data used as input, should be created by the function `create_input_data` or by the function `combine_input_data`
- **input_data_population_2**: Genomic data used as input, should be created by the function `create_input_data` or by the function `combine_input_data`
- **pop_size**: Vector containing the number of individuals in both populations.
- **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 recombination_rate 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: location 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_genomeadmixr_data

function to convert ped/map data to genome_admixr_data

Description

function to convert ped/map data to genome_admixr_data

Usage

simulation_data_to_genomeadmixr_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

genomeadmixr_data object ready for simulate_admixture_data

vcfR_to_genomeadmixr_data

function to convert a vcfR object to genome_admixr_data

Description

function to convert a vcfR object to genome_admixr_data

Usage

vcfR_to_genomeadmixr_data(
  vcfR_object,
  chosen_chromosome,
  number_of_snps = NA,
  random_snps = TRUE,
  verbose = FALSE
)

)
write_as_plink

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

geneadmixr_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 "geneadmixr_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

this function doesn’t return anything.
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