Package 'PopPsiSeqR'

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Type Package

Title Process and Visualize Evolve & Resequence Experiments

Version 1.0.0

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Description Handle data from evolve and resequence experiments. Measured allele frequencies (e.g., from variants called from high-throughput sequencing data) are compared using an update of the PsiSeq algorithm (Earley, Eric and Corbin Jones (2011) <doi:10.1534/genetics.111.129445>). Functions for saving and loading important files are also included, as well as functions for basic data visualization.

URL https://github.com/csoeder/PopPsiSeq, https://github.com/csoeder/PopPsiSeqR

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Encoding UTF-8

RoxygenNote 7.3.2

Imports rtracklayer, GenomicRanges, ggplot2, dplyr, S4Vectors, magrittr, ggbio, withr, utils, patchwork, tidyr, rlang, devtools

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

BugReports https://github.com/csoeder/PopPsiSeqR/issues

NeedsCompilation no

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Repository CRAN

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Contents

`export.freqshft` *Save the shifted frequencies*

Description

Save the shifted frequencies

Usage

```
export.freqshft(frequency_shifts, output_file)
```

Arguments

`frequency_shifts`	table of allele frequency shifts, as output by freqShifter()
`output_file`	path to savefile

Value

nothing

Examples

```
merged_frequencies.filename <- system.file("extdata",
"merged_frequencies.example_data.tbl", package = "PopPsiSeqR")
frequencies.bg <- import.freqtbl(merged_frequencies.filename)
frequency_shifts.bg <- freqShifter(frequencies.bg)
export.freqshft(frequency_shifts.bg , tempfile())
```

`freqShifter` *Frequency Shift Calculator*

Description

This function accepts a GRanges object containing allele frequencies from two parental populations and an offspring population. It then polarizes each variant site and calculates how the offspring has shifted from equilibrium.

Usage

```
freqShifter(freqbed_in)
```

Arguments

`freqbed_in`	in goes the file containing the grouped frequency measurements (extended bed format)

Value

per-site PopPsiSeq frequency shifts

polarization of alleles

At each variant site, either the selected parent or the backcrossed parent might have the alternate allele at a higher frequency than the other (sites in which they have the same allele frequency are not informative and are assumed to have been filtered out). To regularize the data, each site was independently polarized, which is to say, the alternate and reference alleles were reassigned ad hoc to make the selected parent population have the higher frequency.

putting the offspring in context

At each site, the offspring's allele frequency is compared to the hypothetical equilibrium frequency expected by simply averaging the parents' frequencies. This is reported as the mean_oriented_shift; also reported is the distance to fixation in each direction (max_oriented_shift, min_oriented_shift), and the difference between parental allele frequencies (AF_difference)

Examples

```
merged_frequencies.filename <- system.file("extdata",
"merged_frequencies.example_data.tbl", package = "PopPsiSeqR")
frequencies.bg <- import.freqtbl(merged_frequencies.filename)
frequency_shifts.bg <- freqShifter(frequencies.bg)
```

`import.freqtbl` *Load Merged Allele Frequency Table*

Description

This function accepts as input a path to a BED file containing allele frequency and returns a GRanges object ready for the freqShifter function.

Usage

```
import.freqtbl(freqtbl_filename)
```

Arguments

`freqtbl_filename`
: file containing the allele frequencies as an extended BED6+ file

Value

frequency table as bedgraph

input format

This function accepts as input a path to a file in an extended BED6+ format; specifically,

'chrom start end name score strand reference_allele alternate_allele selected_parent_count selected_parent_allele_frequency backcrossed_parent_count backcrossed_parent_allele_frequency offspring_count offspring_allele_frequency'

eg,

'chr2L 8517 8518 0 0 + G A 8 0 16 0.25 8 0.25'

Some of these fields (name, score, strand, reference_allele, alternate_allele, selected_parent_count, backcrossed_parent_count, offspring_count) are required as placeholders but not used in the current PopPsiSeq algorithm This format is the output of joining and filtering the output of vcftools' –freq output; see vignette for details

Examples

```
merged_frequencies.filename <- system.file("extdata",
"merged_frequencies.example_data.tbl", package = "PopPsiSeqR")
frequencies.bg <- import.freqtbl(merged_frequencies.filename)
```

import.smvshift *Load Smoothed Frequency Shift*

Description

Load Smoothed Frequency Shift

Usage

```
import.smvshift(filename, selected_parent = "sim", backcrossed_parent = "sec")
```

Arguments

filename	file containing the allele frequencies as an extended BED6+ file; see vignette for formatting
selected_parent	name of the First Parent (that which is Selected for)
backcrossed_parent	name of the Second Parent (that which is Backcrossed to)

Value

loaded data as a bedgraph

Examples

```
windowed_shifts.filename <- system.file("extdata",
"windowed_shifts.example_data.bed", package = "PopPsiSeqR")
windowed_shifts.bg <- import.smvshift(windowed_shifts.filename)
```

subTractor *Subtractor*

Description

Subtractor

Usage

```
subTractor(
  data_one,
  data_two,
  treament_name = "pseudoparent",
  field = "avg_simward_AFshift",
  hoarder = FALSE
)
```

Arguments

data_one	first bedfile
data_two	second bedfile
treament_name	what column is the independent variable
field	what column is the variable being compared
hoarder	whether or not to retain the other data

Value

GRanges of the difference

Examples

```
 lab_sechellia.filename <- system.file("extdata",
"wild_sechellia.example_data.bed", package = "PopPsiSeqR")
lab.bg <- import.smvshift(lab_sechellia.filename)
lab.bg$sechellia <- "lab"
wild_sechellia.filename <- system.file("extdata",
"lab_sechellia.example_data.bed", package = "PopPsiSeqR")
wild.bg <- import.smvshift(wild_sechellia.filename)
wild.bg$sechellia <- "wild"
sub.traction <- subTractor(lab.bg, wild.bg ,treament_name = "sechellia")
```

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windowedFrequencyShift.plotter

Data displayer

Description

Data displayer

Usage

```
windowedFrequencyShift.plotter(
  windowed_shift,
  selected_parent = "sim",
  backcrossed_parent = "sec",
  contigs = c("chr2L", "chr2R", "chr3L", "chr3R"),
  main_title = "popPsiSeq results",
  ref_gen = "droSim1",
  primary_aesthetic = ggplot2::aes(),
  envelope_aesthetic = ggplot2::aes(),
  ancestral_aesthetic = ggplot2::aes()
)
```

Arguments

windowed_shift	GRanges containing windowed data (as loaded by import.smvshft)
selected_parent	Name of the selected-for population
backcrossed_parent	Name of the backcrossed-too population
contigs	What contigs to display
main_title	What to call the plot
ref_gen	Name of the reference genome
primary_aesthetic	Primary aesthetic
envelope_aesthetic	envelope aesthetic
ancestral_aesthetic	ancestral aesthetic

Value

a ggbio plot object

Examples

```
windowed_shifts.filename <- system.file("extdata",
"windowed_shifts.example_data.bed", package = "PopPsiSeqR")
windowed_shifts.bg <- import.smvshift(windowed_shifts.filename)
windowedFrequencyShift.plotter(windowed_shifts.bg)
```

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