Package ‘mosaic’

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Title Mosaic: calculates the ’mosaicity’ of a one dimensional hybrid zone

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Depends R (>= 2.4)

Description This package uses likelihood to fit step-wise models to one dimensional hybrid zone data, and to estimate the ’mosaicity’ of the hybrid zone.

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URL http://www.zoology.ubc.ca/prog/mosaic

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fit.mosaic  Fit a Mosaic Model Using Maximum Likelihood

Description

This function fits a step-wise model to data from a one dimensional hybrid zone.

Usage

fit.mosaic(data, sig.level, N=50, ngens=100, s=5, p.mutate=0.1, p.sex=1, p.rec=0.25, verbose=TRUE)
Arguments

**data**
a data frame where columns represent genotype frequencies and rows correspond to patches in a one dimensional hybrid zone dataset. See `hybrid.zone` for a sample dataset and more information

**sig.level**
desired significance level for the number of steps fit by the model

**N**
the ’population size’ used in the genetic algorithm (a larger population will typically result in a more accurate best fit model, but also will increase the calculation time)

**ngens**
number of generations to run the genetic algorithm for (more generations will typically result in a more accurate best fit model, but also will increase the calculation time)

**s**
strength of selection used in the genetic algorithm

**p.mutate**
mutation rate (e.g., probability of moving the location of a step in a model during reproduction in the genetic algorithm

**p.sex**
probability of sexually recombining two models to create permuted offspring models in the genetic algorithm

**p.rec**
a real number between 0 and 0.5 which denotes the probability that recombination occurs between two model step locations in a sexual event in the genetic algorithm

**verbose**
a logical value indicating the level of output as the algorithm runs

Author(s)

LKM & RGF

References


See Also

`plotMosaic` for plotting fitted models, `mosaicity` for summing step heights of models, `hybrid.zone` for a sample dataset, and `make.mosaic.logLik` for computing likelihoods.

Examples

```r
## Not run:
data(hybrid.zone)
res <- fit.mosaic(hybrid.zone, 0.05)
plot(res)
mosaicity(hybrid.zone, best.model)
## End(Not run)
```
hybrid.zone  

**Example (simulated) Hybrid Zone**

**Description**

A sample hybrid zone with 30 patches.

**Usage**

```r
hybrid.zone
```

**Format**

A data frame where columns represent genotype frequencies and rows correspond to patches.

**Author(s)**

LKM & RGF

**Source**

part of simulations used in M’Gonigle and FitzJohn 2010, simulated data.

**References**


**Examples**

```r
data(hybrid.zone)
hybrid.zone
```

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**make.mosaic.logLik Compute likelihoods**

**Description**

Returns a function which returns the likelihood of each possible step (partial likelihoods for all partitions are computed and cached to speed up future calculations).

**Usage**

```r
make.mosaic.logLik(d)
```

**Arguments**

- `d` a hybrid zone dataset as described in `hybrid.zone`
mosaicity

Author(s)
LKM & RGF

References

mosaicity

Sums the step heights of a best fit model.

Description
Returns the ‘mosaicity’ score of a model \( m \) corresponding to hybrid zone dataset \( d \).

Usage
mosaicity(d, m)

Arguments
d
  a hybrid zone dataset as defined in \( \text{fit.mosaic} \)
m
  a model as defined in \( \text{fit.mosaic} \)

Author(s)
LKM & RGF

References

See Also
plotMosaic for plotting fitted models, hybrid.zone for a sample dataset, and make.mosaic.logLik for computing likelihoods.

Examples
## Not run:
data(hybrid.zone)
res <- fit.mosaic(hybrid.zone, 0.05)
best.model <- res[[length(res)]]$best.model
mosaicity(hybrid.zone, best.model)
## End(Not run)
**plotMosaic**

Plots a Mosaic Fit

**Description**

`plotMosaic` plots a hybrid dataset along with a specified model. `plot` can be applied directly to the output of `fit.mosaic` and by default plots the dataset and most likely best fit model. If `nsteps` is specified it plots a best fit model with `nsteps` steps.

**Usage**

```r
plotMosaic(d, m, pch=20, lcol="blue", ...)  # S3 method for class 'mosaic':
plot(x, nsteps=NULL, ...)  # when using plot
```

**Arguments**

- `d`: a hybrid zone data set as defined in `fit.mosaic`
- `m`: a model as defined in `fit.mosaic`
- `pch`: plot style of hybrid zone data
- `lcol`: line color of best fit model
- `nsteps`: number of steps
- `x`: object of class `mosaic`
- `...`: additional arguments to `plotMosaic` (when using `plot`) and from `plotMosaic` to the underlying `plot` functions.

**Author(s)**

LKM & RGF

**References**


**Examples**

```r
## Not run:
data(hybrid.zone)
res <- fit.mosaic(hybrid.zone, 0.05)
plot(res)
plotMosaic(hybrid.zone, res[[length(res)]]$best.model)
## End(Not run)
```
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