

# 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.

**License** GPL (>=2)

**URL** <http://www.zoology.ubc.ca/prog/mosaic>

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fit.mosaic

*Fit a Mosaic Model Using Maximum Likelihood*

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## 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**

<code>data</code>	a data frame where columns represent genotype frequencies and rows correspond to patches in a one dimensional hybrid zone dataset. See <a href="#">hybrid.zone</a> for a sample dataset and more information
<code>sig.level</code>	desired significance level for the number of steps fit by the model
<code>N</code>	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)
<code>ngens</code>	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)
<code>s</code>	strength of selection used in the genetic algorithm
<code>p.mutate</code>	mutation rate (e.g., probability of moving the location of a step in a model during reproduction in the genetic algorithm)
<code>p.sex</code>	probability of sexually recombining two models to create permuted offspring models in the genetic algorithm
<code>p.rec</code>	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
<code>verbose</code>	a logical value indicating the level of output as the algorithm runs

**Author(s)**

LKM &amp; RGF

**References**

M'Gonigle, L.K., FitzJohn, R.G. 2010. Assortative Mating and Spatial Structure in Hybrid Zones. *Evolution*: 64: 444–445.

**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**

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

## End(Not run)
```

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`hybrid.zone`*Example (simulated) Hybrid Zone*

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**Description**

A sample hybrid zone with 30 patches.

**Usage**

```
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**

M'Gonigle, L.K., FitzJohn, R.G. 2010. Assortative Mating and Spatial Structure in Hybrid Zones. *Evolution*: 64: 444-445.

**Examples**

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

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`make.mosaic.logLik` *Compute likelihoods*

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**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**

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

**Arguments**

`d` a hybrid zone dataset as described in [hybrid.zone](#)

**Author(s)**

LKM &amp; RGF

**References**

M’Gonigle, L.K., FitzJohn, R.G. 2010. Assortative Mating and Spatial Structure in Hybrid Zones. *Evolution*: 64: 444–445.

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`mosaicity`*Sums the step heights of a best fit model.*

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**Description**

Returns the 'mosaicity' score of a model `m` corresponding to hybrid zone dataset `d`.

**Usage**

```
mosaicity(d, m)
```

**Arguments**

<code>d</code>	a hybrid zone dataset as defined in <a href="#">fit.mosaic</a>
<code>m</code>	a model as defined in <a href="#">fit.mosaic</a>

**Author(s)**

LKM &amp; RGF

**References**

M’Gonigle, L.K., FitzJohn, R.G. 2010. Assortative Mating and Spatial Structure in Hybrid Zones. *Evolution*: 64: 444–445.

**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)
```

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plotMosaic	<i>Plots a Mosaic Fit</i>
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### 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

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

### Arguments

d	a hybrid zone data set as defined in <code>fit.mosaic</code>
m	a model as defined in <code>fit.mosaic</code>
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 <code>plotMosaic</code> (when using <code>plot</code> ) and from <code>plotMosaic</code> to the underlying <code>plot</code> functions.

### Author(s)

LKM & RGF

### References

M'Gonigle, L.K., FitzJohn, R.G. 2010. Assortative Mating and Spatial Structure in Hybrid Zones. *Evolution*: 64: 444-445.

### Examples

```
## 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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