Package 'DEEPR'

February 19, 2015

Version 0.1

Date 2015-01-08

Title Dirichlet-multinomial Evolutionary Event Profile Randomization
(DEEPR) test

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Description
Tests for, and describe differences in event count profiles in groups of reconstructed cophylogenies

Depends R (>= 3.0), dirmult

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

Date/Publication 2015-01-12 23:03:29

R topics documented:

DEEPR   *Test two cophylogeny event count matrices*

Description

This command provides a way to test for differences in event count profiles among two groups of
reconstructed cophylogenies.

Usage

```
DEEPR(group_1, group_2, perm_number = 999)
```

Arguments

group_1	A matrix of event counts for the first group of cophylogenies. Rows represent individual cophylogenies. Columns represent counts for specific event types.
group_2	A matrix of event counts for the second group of cophylogenies. Rows represent individual cophylogenies. Columns represent counts for specific event types.
perm_number	The number of permutations to be performed. By default 999 permutations are performed.

Details

A Dirichlet-multinomial model is fit to each of the groups, such that the two groups can be described by their respective model parameters, and a Log-Likelihood Ratio Test (LLRT) can be performed to compare the two models. A permutation test is performed by repeatedly generating new groups by random sampling of the originals, without replacement. As with the original two groups, the LLRT statistic is calculated for each permutation. In doing so, a distribution or LLRT values is obtained and a p-value is estimated.

Value

p_value	The p value of the test.
group_1_pi	Estimated event probabilities for group 1
group_2_pi	Estimated event probabilities for group 2
group_1_alphas	Estimated Dirichlet parameters for group 1
group_2_alphas	Estimated Dirichlet parameters for group 2
group_1_theta	Estimated overdispersion parameter for group 1
group_1_theta	Estimated overdispersion parameter for group 2

Author(s)

The package was written by Mark T Merilo, with contributions to the statistical methodology and biological considerations from R. Ayesha Ali, and Sarah J. Adamowicz.

Examples

```
#Specify the cophylogeny event datasets to use
#In this example event counts are artificially generated
groupA<-simCophy(c(1,1,1,1), 20)
groupB<-simCophy(c(1,1,1,5), 20)

#Compare cophylogeny groups
#Here an extremely small permutation number is used here to shorten example run time
#A permutation number of 999 is recommended for real analysis.
DEEPR(groupA,groupB,9)
```

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simCophy   *Generate simulated cophylogeny event counts*

Description

This command provides a way to generate simulated matrices representing sets of cophylogeny event counts.

Usage

```
simCophy(group_alphas = c(1,1,1,1), cophy_number = 20, mean_event_count = 33)
```

Arguments

group_alphas   Set of Dirichlet alpha parameter for cophylogeny group

cophy_number   Number of simulated cophylogeny event profiles to be generated in the group

mean_event_count

                The expected number of total event counts per simulated cophylogeny

Details

From specified Dirichlet parameters, a set of multinomial probabilities are generated. A total number of co-evolutionary events are generated from a Poisson distribution in order to introduce variation in the number of events per cophylogeny. These events are then distributed among the sets of multinomial probabilities previously generated.

Value

group_events   A matrix of cophylogeny event counts. Each row represents a single reconstructed cophylogeny and each column represents specific event type counts.

Author(s)

Mark T Merilo <mmerilo@uoguelph.ca>

Examples

```
#Generate a simulated event count set with specified Dirichlet parameters
#and desired number of simulated cophylogenies
simCophy(c(1,1,1,5), 20)
```

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