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| gdm\_ext.sigtest(gdm\_ext) | R Documentation |

Perform Significance Test with a Data Table for a Generalized Dissimilarity Model

Description

gdm\_ext.sigtest is used to perform a monte carlo type significance test on a GDM composite data table and create a suite of output diagnostic files. Potentially significant predictors can be derived from the test and these could be used for input to gdm.fit.

Usage

gdm\_ext.sigtest(dllpath, wdpath, datatable, outname,

iterations=100, do\_geo=TRUE)

Arguments

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| dllpath | a string containing the full path to the GDM4Rext.dll support library |
| wdpath | a string containing the path to the GDM workdirectory where the processing will take place. |
| datatable | a data frame containing the GDM modelling data. |
| outname | a string containing the name of the output diagnostic file set. |
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| iterations | number of iterations to perform on each predictor to determine significance |
| do\_geo | include the geographic distance predictor. |
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Details

gdm\_ext.sigtest performs a montecarlo significance test on a set of potential GDM predictors in order to determine the relative significance of the potential predictors in a GDM data table. Significance is determined by calculating the proportion of time that a random shuffling of each predictor exceeds the deviance explained for a baseline GDM model.

Outputs are write as a file suite into the wdpath using the outname as the primary filename.

Outname.txt will contain all the GDM modelling parameters.

Outname\_LOG.txt contains the updates processing times for each predictor. This file can be opened at anytime during processing with notepad to ascertain the current progress by where the current predictor is in the predictor list.

Outname\_SIG.csv contains the diagnostics for each predictor being tested. It is a comma delimited text file where column[1] contains the predictor index (geographic distance will always have the index=0), column[2] contains the predictor name, column[3] contains the number of iterations done, column[4] contains the baseline % deviance explained, column[5] contains the P-Value which is the proportion of shuffles that exceeded the baseline deviance explained and columns 6 and 7 contain the minimum and maximum differences in those values that did exeed (for diagnostic purposes).

Value

gdm\_ext.sigtest returns null.

Author(s)

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References

Ferrier, S., Manion, G., Elith, J. and Richardson, K. (2007) Using generalized dissimilarity modelling to analyse and predict patterns of beta diversity in regional biodiversity assessment. *Diversity and Distributions* 13: 252-264

See Also

gdm.fit, gdm.summary, gdm.plot, gdm.transform, gdm.predict

Examples

##

dllpath <- “d:\\mydlls\\GDM4Rext.dll”

workdir <- “d:\\outputs”

mytable = read.csv(“d:\\mytablepath.csv”)

gdm\_ext\_sigtest(dllpath, workdir, mytable, “sigout”, iterations=250)

##