Package 'DAGGER'

July 2, 2014

Title Consensus genetic maps

Version 1.4

Author Jeffrey Endelman

Maintainer Jeffrey Endelman <j.endelman@gmail.com>

Description Integrates the information from multiple linkage maps to
create a consensus directed graph, which is then linearized to produce a consensus map.

Depends Rglpk, quadprog, Matrix

License GPL-3

LazyLoad yes

Repository CRAN

Date/Publication 2011-08-05 06:10:02

NeedsCompilation no

R topics documented:

DAGGER *Consensus genetic maps*

Description

Integrates the information from multiple linkage maps to create a consensus directed graph, which is then linearized to produce a consensus map.

Usage

```
DAGGER(Maps,Linearize=TRUE,method="QP",rescale=TRUE,
       MapFilename=NULL,GraphFilename=NULL,GraphDistances=FALSE)
```

Arguments

Maps	List of linkage maps. Each linkage map is a data frame with two columns: the first column contains the marker names, the second column contains the map positions.
Linearize	If TRUE (default), DAGGER will linearize the consensus graph provided it is acyclic.
method	Specifies the linearization method: either "QP" (default) for quadratic programming or "LP" for linear programming.
rescale	If TRUE (default), the consensus map is rescaled to equal the mean length of the linkage maps.
MapFilename	Specifies the name of the output file for the consensus map.
GraphFilename	Specifies the name of the output file for the consensus graph.
GraphDistances	If FALSE (default), the consensus graph is simplified and edge weights are not included in the output file.

Details

DAGGER first merges the linkage maps to create a consensus directed graph, in which the vertices are marker bins and there is an edge for every map interval between adjacent bins in the linkage maps.

DAGGER next checks whether the consensus graph is acyclic by identifying the strongly connected components. Cycles represent ordering conflicts between the linkage maps, which must be resolved by the user before DAGGER will produce a consensus map. DAGGER will write the non-singleton strongly connected components to the output GraphFilename in a format for visualization with the software Graphviz dot (http://www.graphviz.org).

If the consensus graph is acyclic, it can be written to GraphFilename in one of two ways. When the argument GraphDistances == TRUE, all of the edges and their weights are shown, which conveys the information used to linearize the graph. When GraphDistances == FALSE, the edge set is reduced to the minimum necessary to show the ordering of the markers, and no edge weights are shown. This edge reduction preserves the ordinal equivalency of the consensus graph with the

linkage maps (there is a path from vertex v to vertex w if and only if bin v precedes bin w in one of the linkage maps).

If Linearize == TRUE (and the consensus graph is acyclic), a linear consensus map is produced that is ordinally consistent with the consensus graph and contains minimum error relative to the linkage maps. The consensus map can be written to the output MapFilename, arranged by marker bin. It will also be returned by the function as a data frame with two columns: marker name and map position.

Value

If Linearize == TRUE, DAGGER returns either a dataframe containing the consenus map or NULL if the linkage maps had ordering conflicts. If Linearize == FALSE, DAGGER returns a logical value indicating whether the consensus graph was acyclic.

References

Endelman, J.B. (in press) New algorithm improves fine structure of the barley consensus SNP map. BMC Genomics.

Examples

```
#generate two pseudo-linkage maps, each with 500 markers out of 1000 possible
m1 <- c(0,sort(sort(runif(1000),index.return=TRUE)$ix[1:500]))
m2 <- c(0,sort(sort(runif(1000),index.return=TRUE)$ix[1:500]))
Maps <- list()
Maps[[1]] <- data.frame(marker=m1,map=m1)
Maps[[2]] <- data.frame(marker=m2,map=m2)
ConsensusMap.LP <- DAGGER(Maps,method="LP")
ConsensusMap.QP <- DAGGER(Maps,method="QP")
```

Index