

Package ‘LPmerge’

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Title Integrating linkage maps with linear programming

Version 1.3

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Description Software to create a synthetic consensus (or composite) map by minimizing the mean absolute error between intervals in the linkage maps and the corresponding intervals in the consensus map. This minimization is performed subject to the constraint that the ordering of the markers in the linkage maps is preserved, which is amenable to linear programming. When marker order is not consistent across the linkage maps, a minimum set of ordinal constraints is deleted to resolve the conflicts.

Depends Rglpk, Matrix

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Lazyload yes

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LPmerge	<i>Integrating linkage maps with linear programming.</i>
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Description

Software to create a consensus (or composite) map by minimizing the mean absolute error between intervals in the linkage maps and the corresponding intervals in the consensus map. This minimization is performed subject to the constraint that the ordering of the markers in the linkage maps is preserved, which is amenable to linear programming. When marker order is not consistent across the linkage maps, a minimum set of ordinal constraints is deleted to resolve the conflicts.

Usage

```
LPmerge(Maps, max.interval = 3, weights = NULL)
```

Arguments

<code>Maps</code>	List of T genetic maps for a single linkage group. Each genetic map is a data frame with two columns: the first column contains the marker names, the second column contains the map position.
<code>max.interval</code>	Whole number specifying the maximum interval size between bins to include in the objective function.
<code>weights</code>	Numeric array of length T , used to differentially weight the maps in the objective function.

Details

Map positions in the i th linkage map are denoted by y_i , and consensus map positions are denoted by x . Within linkage map i , the markers are ordered from $j = 1$ to M_i , and the map distance between the j th and $(j+q)$ th markers is $y_i(j+q) - y_i(j)$. Letting $u(j; i)$ denote the consensus map bin containing marker j from map i , the corresponding distance in the consensus map is $x(u(j+q; i)) - x(u(j; i))$. The total error across T maps with maximum interval size K is

$$\sum_{i=1}^T W_i N_i^{-1} \sum_{q=1}^K \sum_{j=1}^{M_i} |x(u(j+q; i)) - x(u(j; i)) - [y_i(j+q) - y_i(j)]|$$

where $N_i = \sum_{q=1}^K \sum_{j=1}^{M_i} 1$ is the number of error terms for map i , and W_i are the weights (equal to 1 by default). At the end of linkage map, where the sum $j+q$ exceeds M_i , the expression is evaluated as if the map were circular rather than linear. These "wrap-around" error terms keep the total consensus map length commensurate with the average length of the linkage maps.

Linear inequality constraints are used to ensure the marker order in the consensus map is consistent with the order in the linkage maps. When the linkage maps are not consistent, a minimum set of constraints is deleted to resolve the conflicts. See Chancerel et al. for details. The deleted constraints are printed to the standard output.

One way to select the maximum interval size K is based on the principle of minimizing the root mean-squared error (RMSE) between the consensus map and the linkage maps. The RMSE for each linkage map, and the overall mean, is displayed for convenience. Since the consensus map length can vary with K , this is another factor to consider when selecting this parameter.

Value

A data frame containing the consensus map and the component linkage maps.

References

Chancerel et al.

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)
ans <- LPmerge(Maps,max.interval=3)
```

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