

Package ‘gromovlab’

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Title Gromov-Hausdorff Type Distances for Labeled Metric Spaces

Maintainer Volkmar Liebscher <volkmar.liebscher@uni-greifswald.de>

Author Volkmar Liebscher

Description Computing Gromov-Hausdorff type l^p distances for labeled metric spaces. These distances were introduced in V.Liebscher, Gromov meets Phylogenetics - new Animals for the Zoo of Metrics on Tree Space. preprint arXiv:1504.05795, for phylogenetic trees but may apply to much more situations.

Imports methods,igraph, ape, glpkAPI , quadprog, cluster, stats

Depends R (>= 2.15.1)

License GPL (>= 2)

NeedsCompilation no

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gromovdist	<i>Gromov-Hausdorff-type distances of labelled metric spaces</i>
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Description

The function `gromovdist` calculates the matched Gromov- ℓ^p distances of two metrics on a finite space X :

$$D_p(\rho_1, \rho_2) = \inf\{\|(|d(\phi_1(x), \phi_2(x))|)_{x \in X}\|_p\}.$$

There, the infimum is taken over all isometric embeddings ϕ_1 of (X, ρ_1) , ϕ_2 of (X, ρ_2) into a common metric space (Y, d) . Only $1 \leq p \leq \infty$ is considered.

At the basis is the reformulation of the metric as value of a convex program, see Liebscher (2015).

Methods for various classes are provided:

- `dist`, `dissimilarity` which are distance matrices.
- `matrix` for matrices containing the individual distances of the elements of X .
- `igraph` for connected graphs. The metric on the nodes or just the leaves (nodes of degree 1) of the graph is the length of the shortest path.
- `phylo` for phylogenetic trees. Again the metric is induced by the graph.

Usage

```
gromovdist(d1, d2=NULL, type="l1", p=NULL, ...)

## S3 method for class 'list'
gromovdist(d1, d2=NULL, type="l1", p=NULL, ...)
## S3 method for class 'multiPhylo'
gromovdist(d1, d2=NULL, type="l1", p=NULL, ...)
## S3 method for class 'phylo'
gromovdist(d1, d2=NULL, type="l1", p=NULL, ...)
## S3 method for class 'dist'
gromovdist(d1, d2=NULL, type="l1", p=NULL, ...)
## S3 method for class 'dissimilarity'
gromovdist(d1, d2=NULL, type="l1", p=NULL, ...)
## S3 method for class 'matrix'
gromovdist(d1, d2=NULL, type="l1", p=NULL, ...)
## S3 method for class 'igraph'
gromovdist(d1, d2=NULL, type="l1", p=NULL, leavesonly=TRUE, ...)
```

Arguments

<code>type</code>	type of metric to use
<code>d1, d2</code>	distance object(s).
<code>p</code>	if <code>type="lp"</code> the value of p . If not supplied, $p = 2$ is used.
<code>leavesonly</code>	compute the distances between the leaves of the graph/tree only?
<code>...</code>	further parameters

Details

type="l1" yields $p = 1$

type="l2" yields $p = 2$

type="linfinity" yields $p = \infty$

type="lp" is for (not so efficient) computation using [constrOptim](#) for arbitrary $1 \leq p < \infty$

If d1 is a list, the distance matrix between all elements of the list is computed. It is represented as an object of class `dissimilarity`, see [dissimilarity.object](#).

The distance is only computed for that part of the objects where the labels are present in both objects. If there are no labels the elements are numbered consecutively.

Value

The distance (one numeric) or a distance matrix for the `list` and `multiPhylo` methods

Author(s)

Volkmar Liebscher

References

V.Liebscher, Gromov meets Phylogenetics - new Animals for the Zoo of Metrics on Tree Space. preprint 2015 arXiv:1504.05795

See Also

[dist](#), [dissimilarity.object](#), [phangorn-package](#), [igraph-package](#), [constrOptim](#).

Examples

```
library("ape")
tr1<-rtree(n=10)
tr2<-rtree(n=10)
gromovdist(tr1,tr2,"l1")
gromovdist(tr1,tr2,"l2")
#thesame, but slower
gromovdist(d1=tr1,d2=tr2,type="lp",p=2)
gromovdist(tr1,tr2,"linf")
```

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