

Package ‘mph’

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Description A fast approach to compute approximate persistent homology using a multiscale approach

Title Multiscale persistent homology

Depends R (>= 2.10)

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R topics documented:

multiscale.rips	1
Index	3

multiscale.rips	<i>Multiscale Rips Persistent Homology</i>
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Description

A multiscale approach to compute Rips persistent homology.

Usage

```
multiscale.rips.ipca( X, epsGMRA, maxD, single = FALSE )
```

Arguments

X	Data set. Each row is a data point
epsGMRA	Accuracy of GMRA approximation
maxD	Highest dimensionality of simplicies to insert into the filtration
single	Compute single scale TRUE or FALSE

Value

Persistent diagram, matrix with first column birth, second column death times and a third column at which scale the death happened.

Author(s)

Samuel Gerber

Examples

```
##Noisy circle example
phi <- runif(100)*2*pi
arc <- cbind(cos(phi), sin(phi)) * (1+rnorm(length(phi)) * 0.1)

dgm <- multiscale.rips.ipca(X = arc, epsGMRA = 0, maxD = 2);

plot(x = dgm[,1], y = dgm[,2], xlim = c(0, max(dgm[,1:2])), ylim = c(0, max(dgm[,1:2])),
     asp=1, pch=19)
abline(0, 1)
```

Index

*Topic **multi-**
scale,persistence,homology,topology
multiscale.rips, 1

multiscale.rips, 1