

# Package ‘TDAvec’

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**Type** Package

**Title** Vector Summaries of Persistence Diagrams

**Version** 0.1.1

**Description** Tools for computing various vector summaries of persistence diagrams studied in Topological Data Analysis. For improved computational efficiency, all code for the vector summaries is written in 'C++' using the 'Rcpp' package.

**License** GPL (>= 2)

**Encoding** UTF-8

**Imports** Rcpp (>= 1.0.9), TDA, microbenchmark

**LinkingTo** Rcpp

**Suggests** knitr

**VignetteBuilder** knitr

**NeedsCompilation** yes

**RoxygenNote** 7.2.0

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**Repository** CRAN

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 computeECC

*A Vector Summary of the Euler Characteristic Curve*


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### Description

Vectorizes the Euler characteristic curve

$$\chi(t) = \sum_{k=0}^d (-1)^k \beta_k(t),$$

where  $\beta_0, \beta_1, \dots, \beta_d$  are the Betti curves corresponding to persistence diagrams  $D_0, D_1, \dots, D_d$  of dimensions  $0, 1, \dots, d$  respectively, all computed from the same filtration

### Usage

computeECC(D, maxhomDim, scaleSeq)

### Arguments

D	matrix with three columns containing the dimension, birth and death values respectively
maxhomDim	maximum homological dimension considered (0 for $H_0$ , 1 for $H_1$ , etc.)
scaleSeq	numeric vector of increasing scale values used for vectorization

### Value

A numeric vector whose elements are the average values of the Euler characteristic curve computed between each pair of consecutive scale points of  $\text{scaleSeq}=\{t_1, t_2, \dots, t_n\}$ :

$$\left( \frac{1}{\Delta t_1} \int_{t_1}^{t_2} \chi(t) dt, \frac{1}{\Delta t_2} \int_{t_2}^{t_3} \chi(t) dt, \dots, \frac{1}{\Delta t_{n-1}} \int_{t_{n-1}}^{t_n} \chi(t) dt \right),$$

where  $\Delta t_k = t_{k+1} - t_k$

### Author(s)

Umar Islambekov

### References

1. Richardson, E., & Werman, M. (2014). Efficient classification using the Euler characteristic. *Pattern Recognition Letters*, 49, 99-106.

**Examples**

```

N <- 100
set.seed(123)
# sample N points uniformly from unit circle and add Gaussian noise
X <- TDA::circleUnif(N,r=1) + rnorm(2*N,mean = 0,sd = 0.2)

# compute a persistence diagram using the Rips filtration built on top of X
D <- TDA::ripsDiag(X,maxdimension = 1,maxscale = 2)$diagram

scaleSeq = seq(0,2,length.out=11) # sequence of scale values

# compute ECC
computeECC(D,maxhomDim=1,scaleSeq)

```

computePES

*A Vector Summary of the Persistent Entropy Summary Function***Description**

For a given persistence diagram  $D = \{(b_i, d_i)\}_{i=1}^N$ , `computePES()` vectorizes the persistent entropy summary (PES) function

$$S(t) = - \sum_{i=1}^N \frac{l_i}{L} \log_2 \left( \frac{l_i}{L} \right) 1_{[b_i, d_i]}(t),$$

where  $l_i = d_i - b_i$  and  $L = \sum_{i=1}^N l_i$ . Points of  $D$  with infinite death value are ignored

**Usage**

```
computePES(D, homDim, scaleSeq)
```

**Arguments**

D	matrix with three columns containing the dimension, birth and death values respectively
homDim	homological dimension (0 for $H_0$ , 1 for $H_1$ , etc.)
scaleSeq	numeric vector of increasing scale values used for vectorization

**Value**

A numeric vector whose elements are the average values of the persistent entropy summary function computed between each pair of consecutive scale points of  $\text{scaleSeq} = \{t_1, t_2, \dots, t_n\}$ :

$$\left( \frac{1}{\Delta t_1} \int_{t_1}^{t_2} S(t) dt, \frac{1}{\Delta t_2} \int_{t_2}^{t_3} S(t) dt, \dots, \frac{1}{\Delta t_{n-1}} \int_{t_{n-1}}^{t_n} S(t) dt \right),$$

where  $\Delta t_k = t_{k+1} - t_k$

**Author(s)**

Umar Islambekov

**References**

1. Atienza, N., Gonzalez-Díaz, R., & Soriano-Trigueros, M. (2020). On the stability of persistent entropy and new summary functions for topological data analysis. *Pattern Recognition*, 107, 107509.

**Examples**

```

N <- 100
set.seed(123)
# sample N points uniformly from unit circle and add Gaussian noise
X <- TDA::circleUnif(N,r=1) + rnorm(2*N,mean = 0,sd = 0.2)

# compute a persistence diagram using the Rips filtration built on top of X
D <- TDA::ripsDiag(X,maxdimension = 1,maxscale = 2)$diagram

scaleSeq = seq(0,2,length.out=11) # sequence of scale values

# compute PES for homological dimension H_0
computePES(D,homDim=0,scaleSeq)

# compute PES for homological dimension H_1
computePES(D,homDim=1,scaleSeq)

```

computePI

*A Vector Summary of the Persistence Surface***Description**

For a given persistence diagram  $D = \{(b_i, p_i)\}_{i=1}^N$ , `computePI()` computes the persistence image (PI) - a vector summary of the persistence surface:

$$\rho(x, y) = \sum_{i=1}^N f(b_i, p_i) \phi_{(b_i, p_i)}(x, y),$$

where  $\phi_{(b_i, p_i)}(x, y)$  is the Gaussian distribution with mean  $(b_i, p_i)$  and covariance matrix  $\sigma^2 I_{2 \times 2}$  and

$$f(b, p) = w(p) = \begin{cases} 0 & y \leq 0 \\ p/p_{max} & 0 < p < p_{max} \\ 1 & y \geq p_{max} \end{cases}$$

is the weighting function with  $p_{max}$  being the maximum persistence value among all persistence diagrams considered in the experiment. Points of  $D$  with infinite persistence value are ignored

**Usage**

```
computePI(D, homDim, xSeq, ySeq, res, sigma)
```

**Arguments**

D	matrix with three columns containing the dimension, birth and persistence values respectively
homDim	homological dimension (0 for $H_0$ , 1 for $H_1$ , etc.)
xSeq	numeric vector of increasing x (birth) values used for vectorization
ySeq	numeric vector of increasing y (persistence) values used for vectorization
res	resolution parameter (or grid size). For example, if res=10 and the birth values are not all equal, a $10 \times 10$ grid is constructed for vectorization
sigma	standard deviation of the Gaussian

**Value**

A numeric vector whose elements are the average values of the persistence surface computed over each cell of the two-dimensional grid constructed from  $xSeq=\{x_1, x_2, \dots, x_n\}$  and  $ySeq=\{y_1, y_2, \dots, y_m\}$ :

$$\left( \frac{1}{\Delta x_1 \Delta y_1} \int_{[x_1, x_2] \times [y_1, y_2]} \rho(x, y) dA, \dots, \frac{1}{\Delta x_{n-1} \Delta y_{m-1}} \int_{[x_{n-1}, x_n] \times [y_{m-1}, y_m]} \rho(x, y) dA \right),$$

where  $dA = dx dy$ ,  $\Delta x_k = x_{k+1} - x_k$  and  $\Delta y_j = y_{j+1} - y_j$

**Author(s)**

Umar Islambekov

**References**

1. Adams, H., Emerson, T., Kirby, M., Neville, R., Peterson, C., Shipman, P., ... & Ziegelmeier, L. (2017). Persistence images: A stable vector representation of persistent homology. *Journal of Machine Learning Research*, 18.

**Examples**

```

N <- 100
set.seed(123)
# sample N points uniformly from unit circle and add Gaussian noise
X <- TDA::circleUnif(N,r=1) + rnorm(2*N,mean = 0,sd = 0.2)

# compute a persistence diagram using the Rips filtration built on top of X
D <- TDA::ripsDiag(X,maxdimension = 1,maxscale = 2)$diagram

# switch from the birth-death to the birth-persistence coordinates
D[,3] <- D[,3] - D[,2]
colnames(D)[3] <- "Persistence"

res <- 5 # resolution or grid size

# compute PI for homological dimension H_0
minPH0 <- min(D[D[,1]==0,3]); maxPH0 <- max(D[D[,1]==0,3])
ySeqH0 <- seq(minPH0,maxPH0,length.out=res+1)

```

```

sigma <- 0.5*(maxPH0-minPH0)/res
computePI(D,homDim=0,xSeq=NA,ySeqH0,res,sigma)

# compute PI for homological dimension H_1
minBH1 <- min(D[D[,1]==1,2]); maxBH1 <- max(D[D[,1]==1,2])
minPH1 <- min(D[D[,1]==1,3]); maxPH1 <- max(D[D[,1]==1,3])
xSeqH1 <- seq(minBH1,maxBH1,length.out=res+1)
ySeqH1 <- seq(minPH1,maxPH1,length.out=res+1)
sigma <- 0.5*(maxPH1-minPH1)/res
computePI(D,homDim=1,xSeqH1,ySeqH1,res,sigma)

```

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computePL

*A Vector Summary of the Persistence Landscape Function*


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### Description

Vectorizes the persistence landscape (PL) function constructed from a given persistence diagram. The  $k$ th order landscape function of a persistence diagram  $D = \{(b_i, d_i)\}_{i=1}^N$  is defined as

$$\lambda_k(t) = k \max_{1 \leq i \leq N} \Lambda_i(t), \quad k \in N,$$

where  $k$ max returns the  $k$ th largest value and

$$\Lambda_i(t) = \begin{cases} t - b_i & t \in [b_i, \frac{b_i+d_i}{2}] \\ d_i - t & t \in (\frac{b_i+d_i}{2}, d_i] \\ 0 & \text{otherwise} \end{cases}$$

### Usage

```
computePL(D, homDim, scaleSeq, k)
```

### Arguments

D	matrix with three columns containing the dimension, birth and death values respectively
homDim	homological dimension (0 for $H_0$ , 1 for $H_1$ , etc.)
scaleSeq	numeric vector of increasing scale values used for vectorization
k	order of landscape function. By default, k=1

### Value

A numeric vector whose elements are the values of the  $k$ th order landscape function evaluated at each point of  $\text{scaleSeq} = \{t_1, t_2, \dots, t_n\}$ :

$$(\lambda_k(t_1), \lambda_k(t_2), \dots, \lambda_k(t_n))$$

### Author(s)

Umar Islambekov

## References

1. Bubenik, P. (2015). Statistical topological data analysis using persistence landscapes. *Journal of Machine Learning Research*, 16(1), 77-102.
2. Chazal, F., Fasy, B. T., Lecci, F., Rinaldo, A., & Wasserman, L. (2014, June). Stochastic convergence of persistence landscapes and silhouettes. In *Proceedings of the thirtieth annual symposium on Computational geometry* (pp. 474-483).

## Examples

```

N <- 100
set.seed(123)
# sample N points uniformly from unit circle and add Gaussian noise
X <- TDA::circleUnif(N,r=1) + rnorm(2*N,mean = 0,sd = 0.2)

# compute a persistence diagram using the Rips filtration built on top of X
D <- TDA::ripsDiag(X,maxdimension = 1,maxscale = 2)$diagram

scaleSeq = seq(0,2,length.out=11) # sequence of scale values

# compute persistence landscape (PL) for homological dimension H_0 with order of landscape k=1
computePL(D,homDim=0,scaleSeq,k=1)

# compute persistence landscape (PL) for homological dimension H_1 with order of landscape k=1
computePL(D,homDim=1,scaleSeq,k=1)

```

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computePS

*A Vector Summary of the Persistence Silhouette Function*


---

## Description

Vectorizes the persistence silhouette (PS) function constructed from a given persistence diagram. The  $p$ th power silhouette function of a persistence diagram  $D = \{(b_i, d_i)\}_{i=1}^N$  is defined as

$$\phi_p(t) = \frac{\sum_{i=1}^N |d_i - b_i|^p \Lambda_i(t)}{\sum_{i=1}^N |d_i - b_i|^p},$$

where

$$\Lambda_i(t) = \begin{cases} t - b_i & t \in [b_i, \frac{b_i+d_i}{2}] \\ d_i - t & t \in (\frac{b_i+d_i}{2}, d_i] \\ 0 & \text{otherwise} \end{cases}$$

Points of  $D$  with infinite death value are ignored

## Usage

```
computePS(D, homDim, scaleSeq, p)
```

**Arguments**

D	matrix with three columns containing the dimension, birth and death values respectively
homDim	homological dimension (0 for $H_0$ , 1 for $H_1$ , etc.)
scaleSeq	numeric vector of increasing scale values used for vectorization
p	power of the weights for the silhouette function. By default, $p=1$

**Value**

A numeric vector whose elements are the values of the  $p$ th power silhouette function evaluated at each point of  $\text{scaleSeq}=\{t_1, t_2, \dots, t_n\}$ :

$$(\phi_p(t_1), \phi_p(t_2), \dots, \phi_p(t_n))$$

**Author(s)**

Umar Islambekov

**References**

1. Chazal, F., Fasy, B. T., Lecci, F., Rinaldo, A., & Wasserman, L. (2014). Stochastic convergence of persistence landscapes and silhouettes. In Proceedings of the thirtieth annual symposium on Computational geometry (pp. 474-483).

**Examples**

```
N <- 100
set.seed(123)
# sample N points uniformly from unit circle and add Gaussian noise
X <- TDA::circleUnif(N,r=1) + rnorm(2*N,mean = 0,sd = 0.2)

# compute a persistence diagram using the Rips filtration built on top of X
D <- TDA::ripsDiag(X,maxdimension = 1,maxscale = 2)$diagram

scaleSeq = seq(0,2,length.out=11) # sequence of scale values

# compute persistence silhouette (PS) for homological dimension H_0
computePS(D,homDim=0,scaleSeq,p=1)

# compute persistence silhouette (PS) for homological dimension H_1
computePS(D,homDim=1,scaleSeq,p=1)
```



**Description**

For a given persistence diagram  $D = \{(b_i, d_i)\}_{i=1}^N$ , `computeVAB()` vectorizes the Betti Curve

$$\beta(t) = \sum_{i=1}^N w(b_i, d_i) 1_{[b_i, d_i)}(t),$$

where the weight function  $w(b, d) \equiv 1$

**Usage**

`computeVAB(D, homDim, scaleSeq)`

**Arguments**

D	matrix with three columns containing the dimension, birth and death values respectively
homDim	homological dimension (0 for $H_0$ , 1 for $H_1$ , etc.)
scaleSeq	numeric vector of increasing scale values used for vectorization

**Value**

A numeric vector whose elements are the average values of the Betti curve computed between each pair of consecutive scale points of `scaleSeq` =  $\{t_1, t_2, \dots, t_n\}$ :

$$\left( \frac{1}{\Delta t_1} \int_{t_1}^{t_2} \beta(t) dt, \frac{1}{\Delta t_2} \int_{t_2}^{t_3} \beta(t) dt, \dots, \frac{1}{\Delta t_{n-1}} \int_{t_{n-1}}^{t_n} \beta(t) dt \right),$$

where  $\Delta t_k = t_{k+1} - t_k$

**Author(s)**

Umar Islambekov, Hasani Pathirana

**References**

1. Chazal, F., & Michel, B. (2021). An Introduction to Topological Data Analysis: Fundamental and Practical Aspects for Data Scientists. *Frontiers in Artificial Intelligence*, 108.
2. Chung, Y. M., & Lawson, A. (2022). Persistence curves: A canonical framework for summarizing persistence diagrams. *Advances in Computational Mathematics*, 48(1), 1-42.

**Examples**

```

N <- 100
set.seed(123)
# sample N points uniformly from unit circle and add Gaussian noise
X <- TDA::circleUnif(N,r=1) + rnorm(2*N,mean = 0,sd = 0.2)

# compute a persistence diagram using the Rips filtration built on top of X
D <- TDA::ripsDiag(X,maxdimension = 1,maxscale = 2)$diagram

scaleSeq = seq(0,2,length.out=11) # sequence of scale values

# compute vector of averaged Bettis (VAB) for homological dimension H_0
computeVAB(D,homDim=0,scaleSeq)

# compute vector of averaged Bettis (VAB) for homological dimension H_1
computeVAB(D,homDim=1,scaleSeq)

```

---

computeVPB

*A Vector Summary of the Persistence Block*


---

**Description**

For a given persistence diagram  $D = \{(b_i, p_i)\}_{i=1}^N$ , `computeVPB()` vectorizes the persistence block

$$f(x, y) = \sum_{i=1}^N 1_{E(b_i, p_i)}(x, y),$$

where  $E(b_i, p_i) = [b_i - \frac{\lambda_i}{2}, b_i + \frac{\lambda_i}{2}] \times [p_i - \frac{\lambda_i}{2}, p_i + \frac{\lambda_i}{2}]$  and  $\lambda_i = 2\tau p_i$  with  $\tau \in (0, 1]$ . Points of  $D$  with infinite persistence value are ignored

**Usage**

```
computeVPB(D, homDim, xSeq, ySeq, tau)
```

**Arguments**

D	matrix with three columns containing the dimension, birth and persistence values respectively
homDim	homological dimension (0 for $H_0$ , 1 for $H_1$ , etc.)
xSeq	numeric vector of increasing x (birth) values used for vectorization
ySeq	numeric vector of increasing y (persistence) values used for vectorization
tau	parameter (between 0 and 1) controlling block size. By default, tau=0.3

**Value**

A numeric vector whose elements are the weighted average values of the persistence block computed over each cell of the two-dimensional grid constructed from  $xSeq=\{x_1, x_2, \dots, x_n\}$  and  $ySeq=\{y_1, y_2, \dots, y_m\}$ :

$$\left( \frac{1}{\Delta x_1 \Delta y_1} \int_{[x_1, x_2] \times [y_1, y_2]} f(x, y) wdA, \dots, \frac{1}{\Delta x_{n-1} \Delta y_{m-1}} \int_{[x_{n-1}, x_n] \times [y_{m-1}, y_m]} f(x, y) wdA \right),$$

where  $wdA = (x + y)dxdy$ ,  $\Delta x_k = x_{k+1} - x_k$  and  $\Delta y_j = y_{j+1} - y_j$

**Author(s)**

Umar Islambekov, Aleksei Luchinsky

**References**

1. Chan, K. C., Islambekov, U., Luchinsky, A., & Sanders, R. (2022). A computationally efficient framework for vector representation of persistence diagrams. *Journal of Machine Learning Research\_23*, 1-33.

**Examples**

```
N <- 100
set.seed(123)
# sample N points uniformly from unit circle and add Gaussian noise
X <- TDA::circleUnif(N,r=1) + rnorm(2*N,mean = 0,sd = 0.2)

# compute a persistence diagram using the Rips filtration built on top of X
D <- TDA::ripsDiag(X,maxdimension = 1,maxscale = 2)$diagram

# switch from the birth-death to the birth-persistence coordinates
D[,3] <- D[,3] - D[,2]
colnames(D)[3] <- "Persistence"

# construct one-dimensional grid of scale values
ySeqH0 <- unique(quantile(D[D[,1]==0,3],probs = seq(0,1,by=0.2)))
tau <- 0.3 # parameter in [0,1] which controls the size of blocks around each point of the diagram
# compute VPB for homological dimension H_0
computeVPB(D,homDim = 0,xSeq=NA,ySeqH0,tau)

xSeqH1 <- unique(quantile(D[D[,1]==1,2],probs = seq(0,1,by=0.2)))
ySeqH1 <- unique(quantile(D[D[,1]==1,3],probs = seq(0,1,by=0.2)))
# compute VPB for homological dimension H_1
computeVPB(D,homDim = 1,xSeqH1,ySeqH1,tau)
```

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