My Interview

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Contents

1 How I can contribute to the SAPPHIRE project

1.1 Update the `glottodist` with different metrics other than Gower's distance

We can implement other kinds of metrics like listed in [Boriah et al., 2008], Take Eskin's distance as an example:

$$S_k(X_k, Y_k) = \begin{cases} 1 & \text{if } X_k = Y_k \\ \frac{n_k^2}{n_k^2+2} & \text{otherwise} \end{cases}$$

1.2 The Hausdorff distance of two datasets

The **Hausdorff distance** is a qunatity to measure the distance between two subsets of a metric space.

Definition 1.1 (Hausdorff distance)**.** Let X and Y be two subsets of a metric space (M, d). The Hausdorff distance $d_H(X, Y)$ is given by

$$d_H(X, Y) = \max\left\{\sup_{x\in X} d(x, Y), \sup_{y\in Y} d(X, y)\right\},$$

where $d(x, Y) := \inf_{y\in Y} d(x, y)$.

More than that, we can take the **Gromov-Hausdorff distance**, which measures the difference between two different datasets, into account.

1.3 Topological data analysis (TDA)

Using topological data analysis methods to analyze the `glottodata`

- Linguistic data analysis: [Port et al., 2018], [Port et al., 2022]
- Spatial data: [Feng et al., 2022]

1.4 Spectral graph theory methods

Construct a graph from the `glottodata` and analyse the graph, for example, analyse the spectrum of the Laplacian operator of the graph or apply heat kernel analysis methods [Ortegaray et al., 2021] to analyse the `glottodata`.

2 Some codes

2.1 Load the `wals` datasets

```
library(glottospace)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(TDAstats)
library(sf)
```

```
## Linking to GEOS 3.10.2, GDAL 3.4.1, PROJ 8.2.1; sf_use_s2() is TRUE
```

```
# load the dataset wals
wals <- glottoget("wals")
```

```
#select the data wrt Aouth America
wals_sam <- subset(wals, continent == "South America")
wals_asia <- subset(wals, continent=="Asia")
```

```
# Define a function select.features to get all features of dataset that the percentage of
# NA values is less than the threshold a
count.na <- function (dataset, feature.name) {
  num.features <- length(st_drop_geometry(dataset))
  return(sum(is.na(dataset[[feature.name]])) / nrow(dataset))

}

select.features <- function(dataset, feature_names, a) {
  counts <- c()
  for (x in feature_names) {
    counts <- append(counts, count.na(wals_sam, x))
  }
  result <- t(as.matrix(counts[counts<0.5]))
  colnames(result) <- feature_names[which(counts<0.5)]

  return(result)
}
```

```
feature_names <- colnames(wals_sam)[-c(1, 194:208)]
select.features(wals_sam, feature_names, 0.5)
```

```
##         81A   82A    83A       86A   129A
## [1,] 0.4875 0.425 0.4125 0.4833333 0.4875
```

```
glottodata.wals <- function (continent_name) {
  structure <- glottocreate_structuretable(varnames = c("81A","82A", "83A", "86A", "129A"))
structure$type <- rep("factor", 5)
  wals_data <- subset(wals, continent == continent_name)
  data <- select(wals_data, 'glottocode', '81A', '82A', '83A', '86A', '129A')
  data.df <- st_drop_geometry(data)

  data.df$`81A` <- as.factor(data.df$`81A`)
  data.df$`82A` <- as.factor(data.df$`82A`)
  data.df$`83A` <- as.factor(data.df$`83A`)
  data.df$`86A` <- as.factor(data.df$`86A`)
  data.df$`129A` <- as.factor(data.df$`129A`)

  data.unique <- match(unique(data.df$glottocode),
                           data.df$glottocode)
  data.df.unique <- data.df[data.unique, ]
  glottodata <- glottocreate_addtable(data.df.unique, structure,
                                      name="structure")
  return(glottodata)
}

glottodata_sam <- glottodata.wals("South America")
glottodata_asia <- glottodata.wals("Asia")
```

2.2 The Hausdorff distance

```
overlap.dist <- function (x, y){
  sum(x != y) / length(x)
}

overlap.x.Y.dist <- function(x, Y) {
  result <- c()
  for (i in 1:nrow(Y)) {
    result <- append(result, overlap.dist(x, Y[i,]))
  }
  return(min(result))
}

overlap.supX.Y.dist <- function(X, Y) {
  result <- c()
  for (i in 1:nrow(X)) {
    result <- append(result, overlap.x.Y.dist(X[i, ], Y))
  }
  return(max(result))
}

overlap.hausdorff.dist <- function(X, Y) {
  X <- glottoclean(X)
  structure <- X[["structure"]]
  X <- glottosimplify(X)
  X <- tibble::column_to_rownames(X, "glottocode")
```

```
  X <- data.frame(lapply(X, as.character),
                                stringsAsFactors = FALSE)
  X[is.na(X)] <- "unknown"

  Y <- glottoclean(Y)
  Y <- glottosimplify(Y)
  Y <- tibble::column_to_rownames(Y, "glottocode")
  Y <- data.frame(lapply(Y, as.character),
                                  stringsAsFactors = FALSE)
  Y[is.na(Y)] <- "unknown"


  result <- max(overlap.supX.Y.dist(X, Y), overlap.supX.Y.dist(Y,X))
  return(result)
}
```

Compute the Hausdorff distance between South America and Asia:

```
overlap.hausdorff.dist(glottodata_asia, glottodata_sam)
```

```
## Missing values recoded to NA
##
## Missing values recoded to NA
```

```
## [1] 0.6
```

2.3 TDA

2.3.1 The linguistic syntactic data of South America and Asia

```
glottodist_sam <- glottodist(glottodata_sam)
```

```
## Missing values recoded to NA
```

```
## All variables have two or more levels (excluding NA)
```

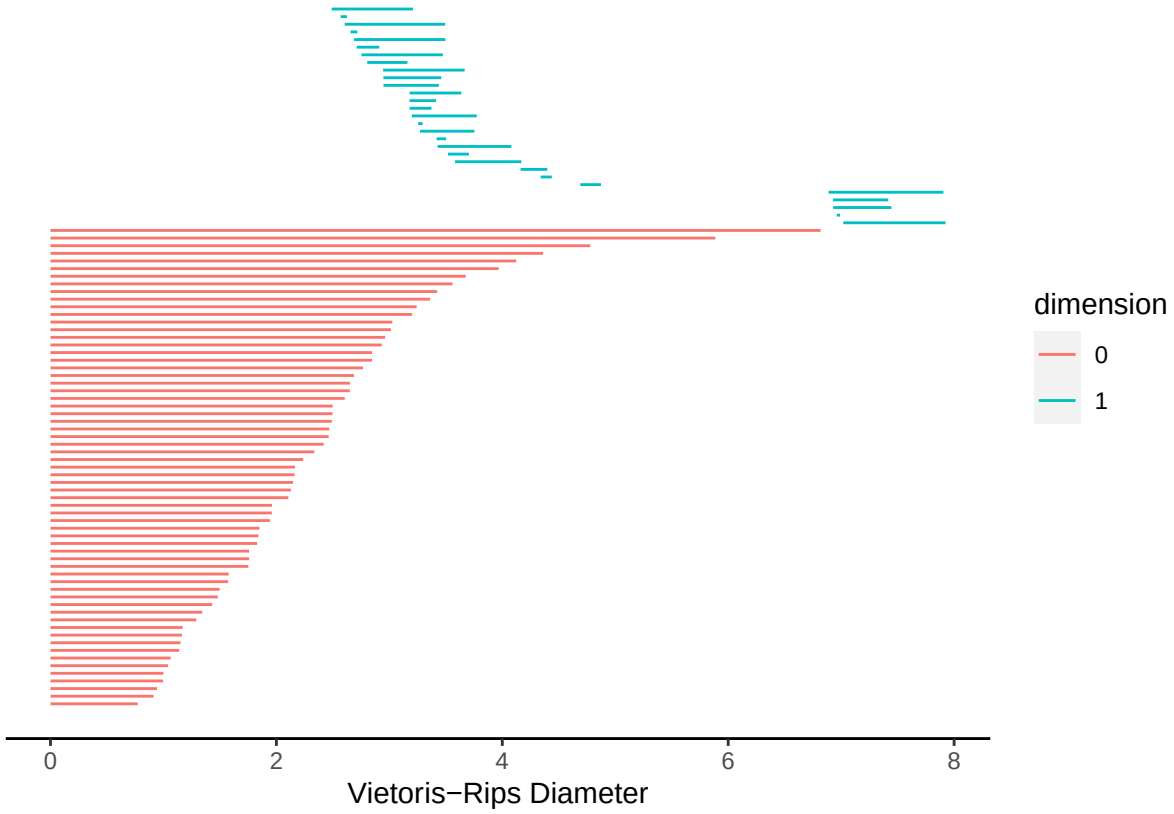
```
glottodist_sam[is.na(glottodist_sam)] <- 0

glottodist_asia <- glottodist(glottodata_asia)
```

```
## Missing values recoded to NA
##
## All variables have two or more levels (excluding NA)
```

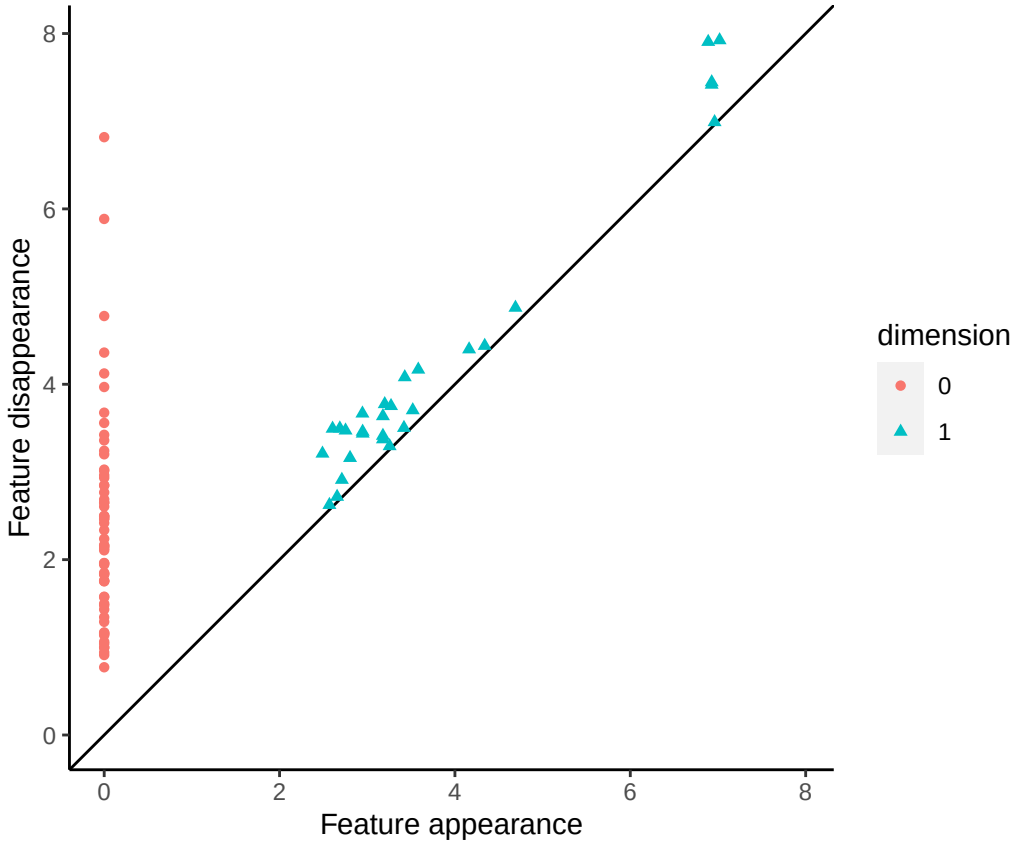
```
glottodist_asia[is.na(glottodist_asia)] <- 0
```

The persistence barcode and persistence diagram of South America language syntactic structures

```
sam.phom <- calculate_homology(glottodist_sam)

par(mfrow=c(1,2))
plot_barcode(sam.phom)
```

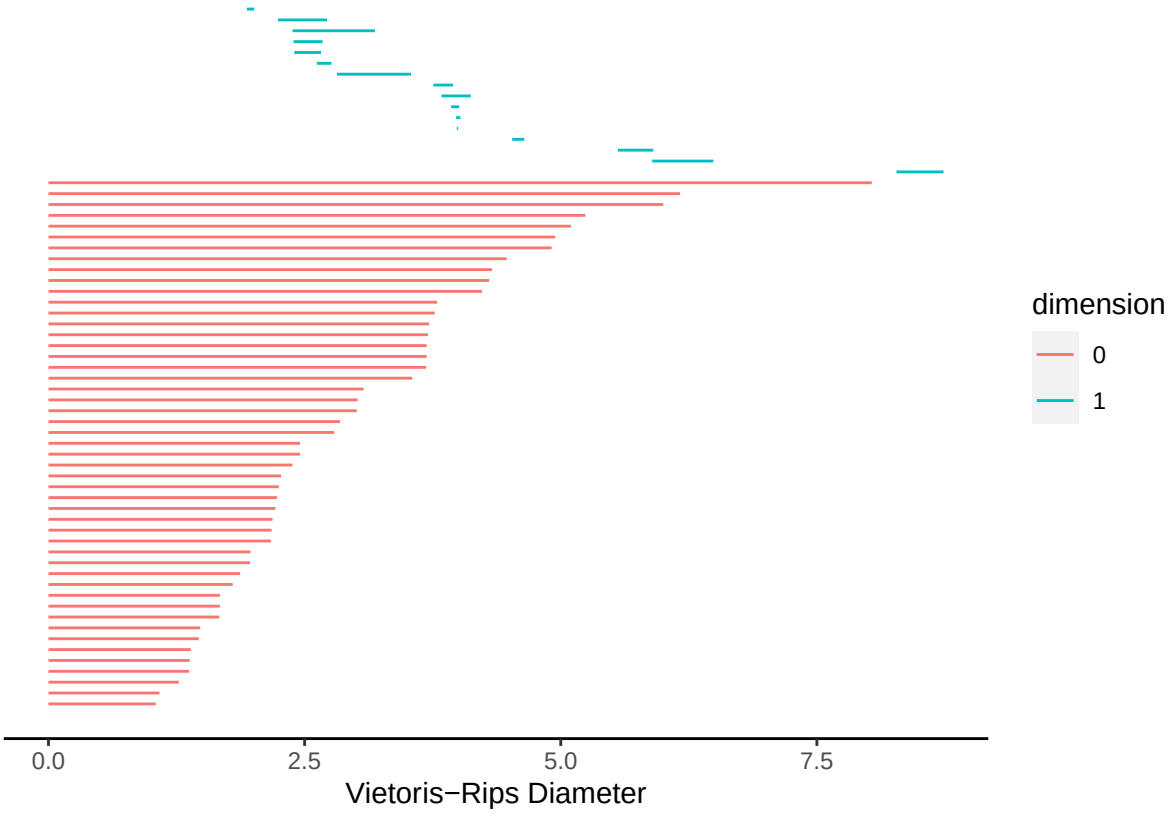



```
plot_persist(sam.phom)
```

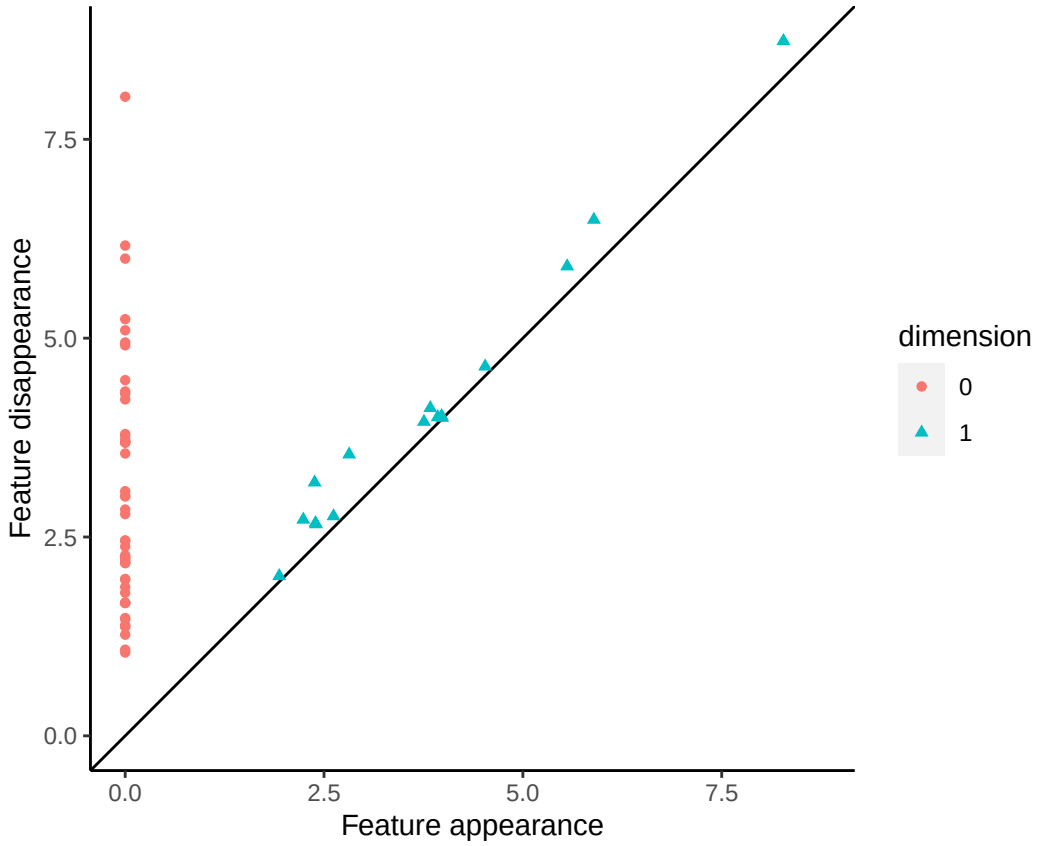


The persistence barcode and persistence diagram of Asia language syntactic structures

```
asia.phom <- calculate_homology(glottodist_asia)

par(mfrow=c(1,2))
plot_barcode(asia.phom)
```



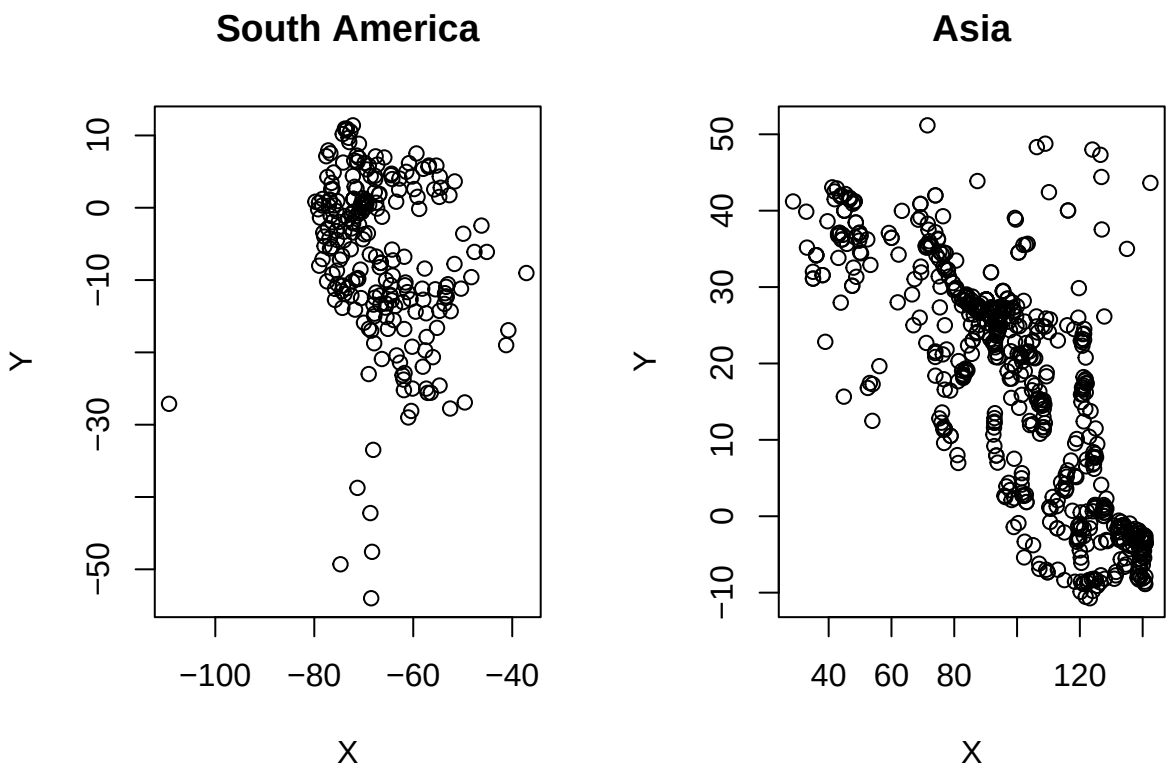

```
plot_persist(asia.phom)
```



2.3.2 The spatial data of South America and Asia

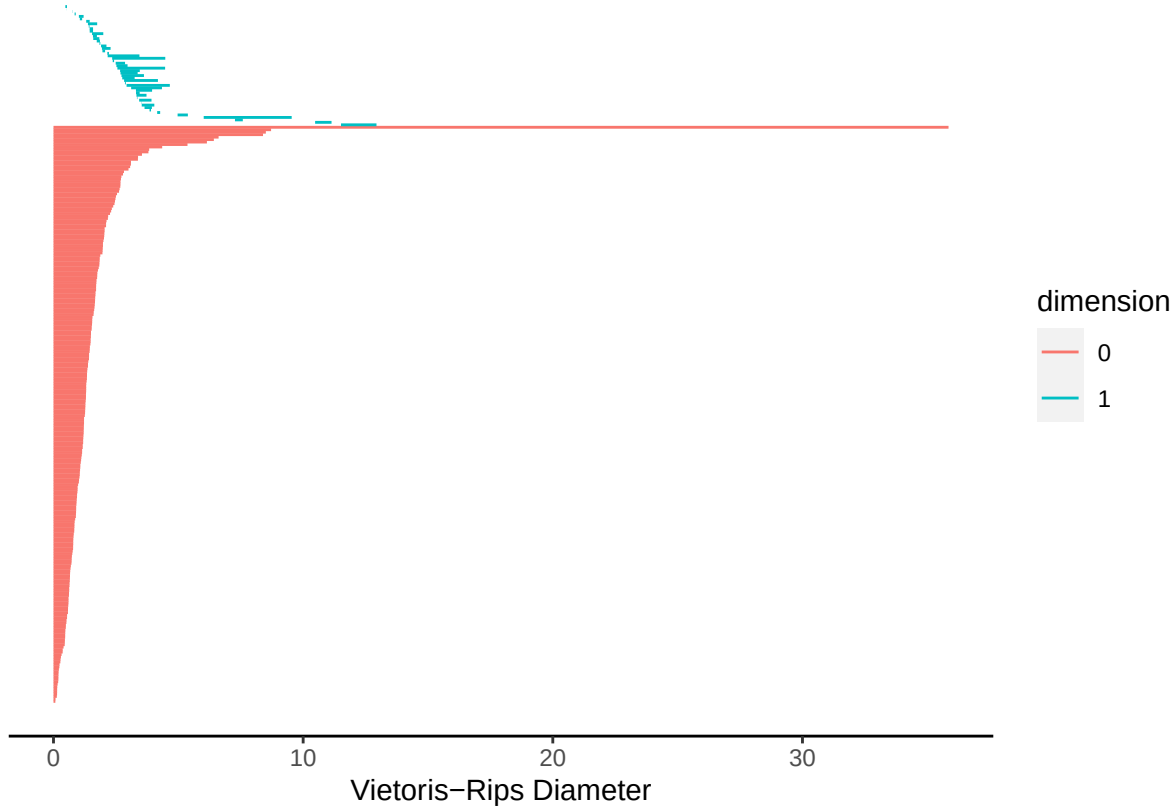
```
sam_coordinates <- st_coordinates(wals_sam)
asia_coordinates <- st_coordinates(wals_asia)

sam_geo_phm <- calculate_homology(sam_coordinates)
asia_geo_phm <- calculate_homology(asia_coordinates)
```

```
par(mfrow=c(1,2))
plot(sam_coordinates, main="South America")
plot(asia_coordinates, main="Asia")
```

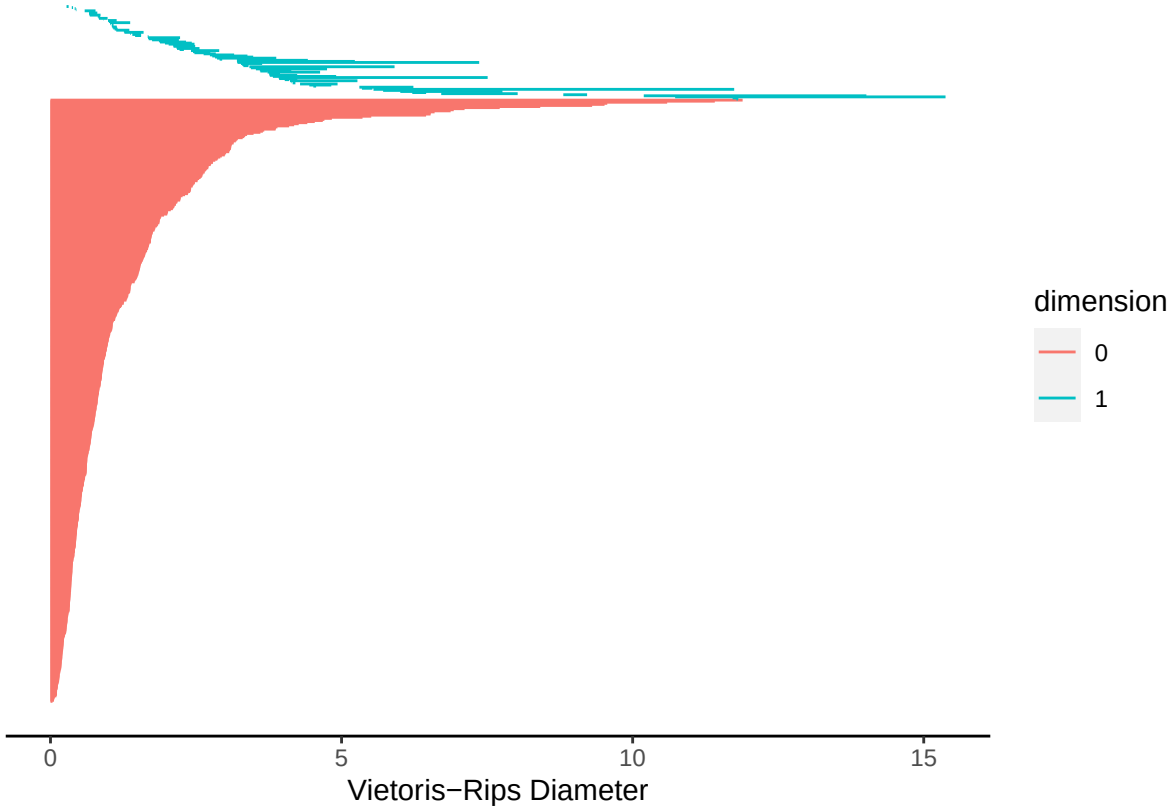


The persistence barcodes of spatial data of South America and Asia:

```
par(mfrow=c(1,2))
plot_barcode(sam_geo_phm)
```

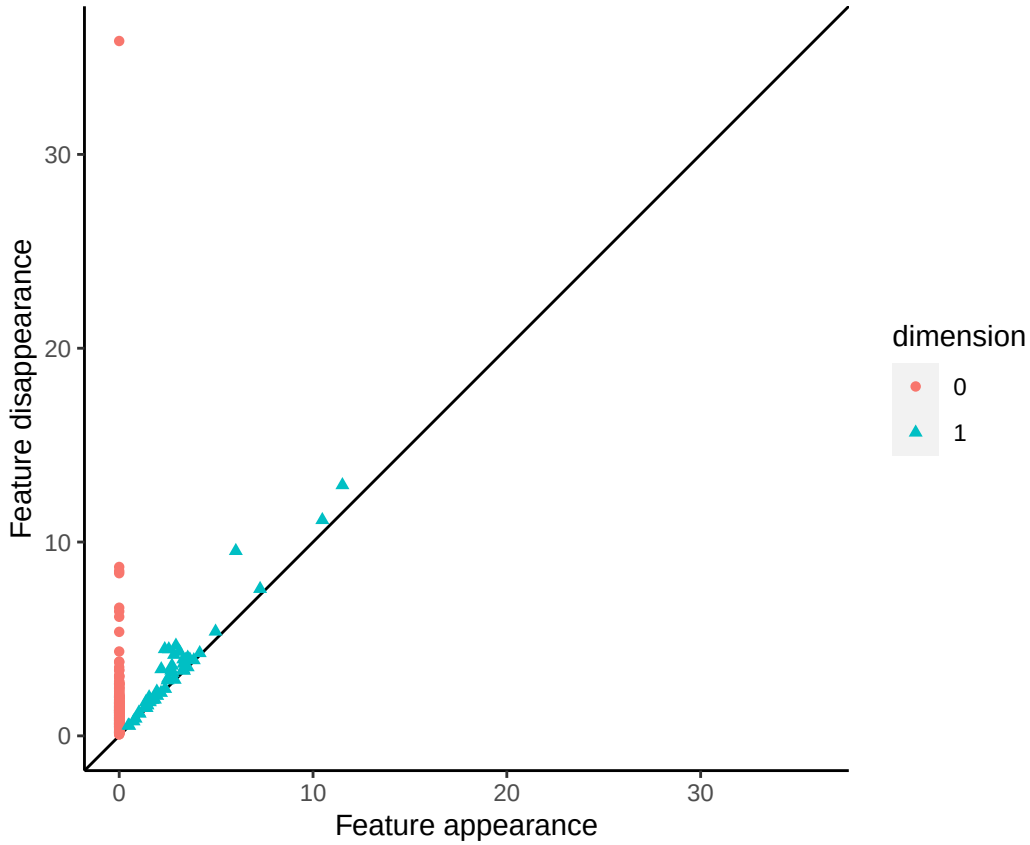


```
plot_barcode(asia_geo_phm)
```

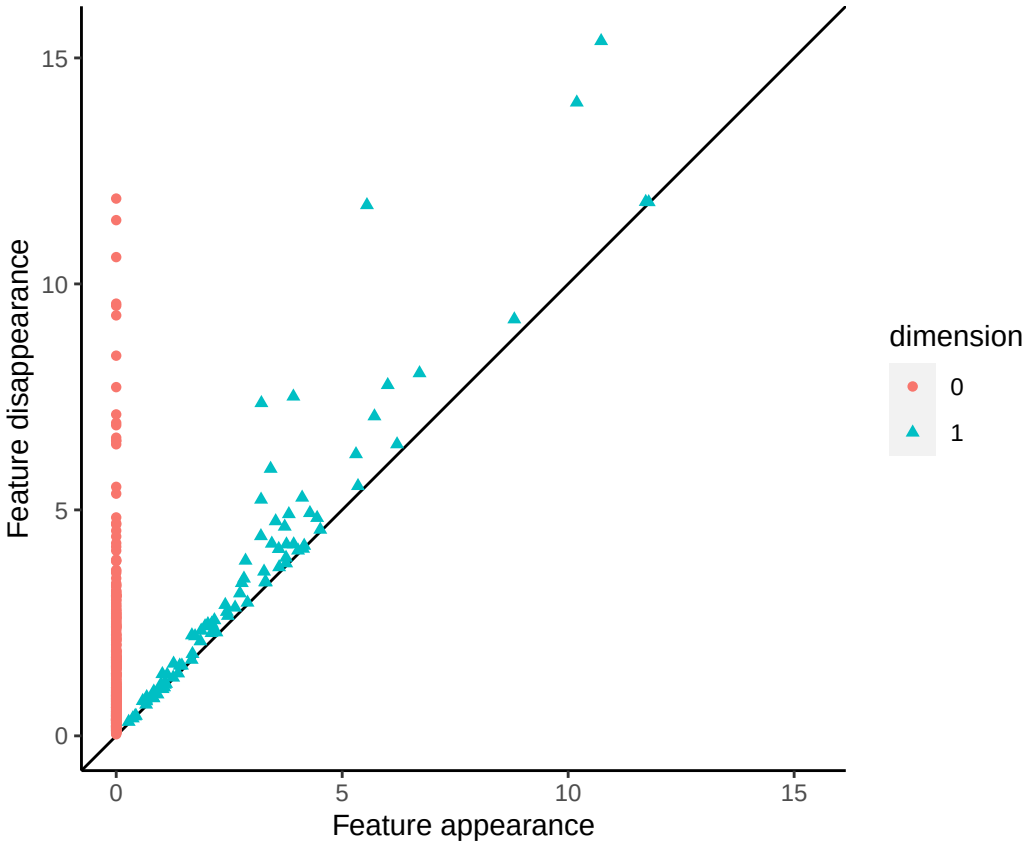


The persistence diagrams of spatial data of South America and Asia:

```
par(mfrow=c(1,2))
plot_persist(sam_geo_phm)
```




```
plot_persist(asia_geo_phm)
```



2.4 Futher codes

Codes about spectral graph theory methods and heat kernel analysis methods like described in [Ortegaray et al., 2021] in the future?

References

[Boriah et al., 2008] Boriah, S., Chandola, V., and Kumar, V. (2008). Similarity measures for categorical data: A comparative evaluation. In *SDM*.

[Feng et al., 2022] Feng, M., Hickok, A., and Porter, M. A. ([2022] ©2022). Topological data analysis of spatial systems. In *Higher-order systems*, Underst. Complex Syst., pages 389–399. Springer, Cham.

[Ortegaray et al., 2021] Ortegaray, A., Berwick, R. C., and Marcolli, M. (2021). Heat kernel analysis of syntactic structures. *Math. Comput. Sci.*, 15(4):643–660.

[Port et al., 2018] Port, A., Gheorghita, I., Guth, D., Clark, J. M., Liang, C., Dasu, S., and Marcolli, M. (2018). Persistent topology of syntax. *Math. Comput. Sci.*, 12(1):33–50.

[Port et al., 2022] Port, A., Karidi, T., and Marcolli, M. (2022). Topological analysis of syntactic structures. *Math. Comput. Sci.*, 16(1):Paper No. 2, 68.