

# Package ‘muHVT’

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**Type** Package

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**Title** Constructing Hierarchical Voronoi Tessellations and Overlay  
Heatmap for Data Analysis

**Version** 3.0.0

**Description** The muHVT package is a collection of R functions to facilitate building topology preserving maps for rich multivariate data. See <[https://en.wikipedia.org/wiki/Voronoi\\_diagram](https://en.wikipedia.org/wiki/Voronoi_diagram)> for more information. Credits to Mu Sigma for their continuous support throughout the development of the package.

**License** Apache License 2.0

**Encoding** UTF-8

**Imports** MASS, deldir, grDevices, splancs, sp, conf.design, Hmisc,  
stats, dplyr, purrr, magrittr, polyclip, rgeos, ggplot2, tidy,  
scales, cluster, reshape2, plyr

**Depends** R (>= 3.6.0)

**BugReports** <https://github.com/Mu-Sigma/muHVT/issues>

**URL** <https://github.com/Mu-Sigma/muHVT>

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data.table

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**NeedsCompilation** no

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exploded_hmap	<i>Function to construct an interactive 3D heatmap overlay for each HVT Level</i>
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### Description

Function to construct an interactive 3D heatmap overlay for each HVT Level

### Usage

```
exploded_hmap(
  hvt.results,
  child.level = NULL,
  hmap.cols = NULL,
  n_cells.hmap = NULL,
  separation_width = 7,
  layer_opacity = c(0.5, 0.75, 0.99),
  dim_size = 1000,
  ...
)
```

**Arguments**

<code>hvt.results</code>	List. A list of <code>hvt.results</code> obtained from the HVT function.
<code>child.level</code>	Numeric. Indicating the level for which the heat map is to be plotted.
<code>hmap.cols</code>	Numeric or Character. The column number of column name from the dataset indicating the variables for which the heat map is to be plotted.
<code>n_cells.hmap</code>	Numeric. An integer indicating the number of clusters per hierarchy (level)
<code>sepration_width</code>	Numeric. An integer indicating the width between two Levels
<code>layer_opacity</code>	Numeric. A vector indicating the opacity of each layer/ level
<code>dim_size</code>	Numeric. An integer indicating the dimension size used to create the matrix for the plot
<code>...</code>	<code>color.vec</code> and <code>line.width</code> can be passed from here

**Author(s)**

Shubhra Prakash <shubhra.prakash@mu-sigma.com>

---

get\_cell\_id

*Function to generate cell ID based on 1D sammons projection*

---

**Description**

To generate cell id for the multivariate data, the data is being projected from n-dimensions to 1-dimension and the cell id is being assigned by ordering these values and finding the corresponding indexes. The output CellID gets appended to the HVT model.

**Usage**

```
get_cell_id(hvt.results)
```

**Arguments**

<code>hvt.results</code>	List. A list of <code>hvt.results</code> obtained from the HVT function.
--------------------------	--

**Details**

Cell ID

**Author(s)**

Shubhra Prakash <shubhra.prakash@mu-sigma.com>

**Examples**

```

data(USArrests)
hvt.results <- list()
hvt.results <- HVT(USArrests, n_cells = 15, depth = 1, quant.err = 0.2,
                  distance_metric = "L1_Norm", error_metric = "mean",
                  projection.scale = 10, normalize = TRUE,
                  quant_method="kmeans",diagnose=TRUE)
plotHVT(hvt.results, line.width = c(0.8), color.vec = c('#141B41'),
        maxDepth = 1)
get_cell_id (hvt.results)

```

HVT

*Constructing Hierarchical Voronoi Tessellations***Description**

Main function to construct hierarchical voronoi tessellations.

**Usage**

```

HVT(
  dataset,
  min_compression_perc = NA,
  n_cells = NA,
  depth = 1,
  quant.err = 0.2,
  projection.scale = 10,
  normalize = FALSE,
  distance_metric = c("L1_Norm", "L2_Norm"),
  error_metric = c("mean", "max"),
  quant_method = c("kmeans", "kmedoids"),
  scale_summary = NA,
  diagnose = FALSE,
  hvt_validation = FALSE,
  train_validation_split_ratio = 0.8
)

```

**Arguments**

dataset	Data frame. A data frame with different columns is given as input.
min_compression_perc	Numeric. An integer indicating the minimum percent compression rate to be achieved for the dataset
n_cells	Numeric. An integer indicating the number of cells per hierarchy (level)
depth	Numeric. An integer indicating the number of levels. (1 = No hierarchy, 2 = 2 levels, etc ...)

quant.err	Numeric. A number indicating the quantization error treshold.
projection.scale	Numeric. A number indicating the scale factor for the tessellations so as to visualize the sub-tessellations well enough.
normalize	Logical. A logical value indicating if the columns in your dataset should be normalized. Default value is TRUE.
distance_metric	character. The distance metric can be "L1_Norm" or "Manhattan". L1_Norm is selected by default.
error_metric	character. The error metric can be "mean" or "max". mean is selected by default
quant_method	character. The quant_method can be "kmeans" or "kmedoids". kmeans is selected by default
scale_summary	List. A list with mean and standard deviation values for all the features in the dataset. Pass the scale summary when the input dataset is already scaled or normalize is set to False.
diagnose	Logical. A logical value indicating if the diagnose is required. Default value is TRUE.
hvt_validation	Logical. A logical value indicating if the MAD values are to tested for validation set. Default value is FALSE.
train_validation_split_ratio	Numeric. A numeric value indicating the train and validation split ratio.

## Details

This is the main function to construct hierarchical voronoi tessellations. The hvq function is called from this function. The output of the hvq function is hierarchical clustered data which will be the input for constructing tessellations. The data is then represented in 2d coordinates and the tessellations are plotted using these coordinates as centroids. For subsequent levels, transformation is performed on the 2d coordinates to get all the points within its parent tile. Tessellations are plotted using these transformed points as centroids. The lines in the tessellations are chopped in places so that they do not protrude outside the parent polygon. This is done for all the subsequent levels.

## Value

A list that contains the hierarchical tessellation information. This list has to be given as input argument to plot the tessellations.

[[1]]	List. Information about the tessellation co-ordinates - level wise
[[2]]	List. Information about the polygon co-ordinates - level wise
[[3]]	List. Information about the hierarchical vector quantized data - level wise
[[4]]	List. Information about the model diagnosis- selected level
[[5]]	List. Information about the MAD values and percentage anomalies for validation dataset

## Author(s)

Shubhra Prakash <shubhra.prakash@mu-sigma.com>, Sangeet Moy Das <sangeet.das@mu-sigma.com>, Shantanu Vaidya <shantanu.vaidya@mu-sigma.com>

**See Also**

[plotHVT](#)  
[hvtHmap](#)

**Examples**

```
data(USArrests)
hvt.results <- list()
hvt.results <- HVT(USArrests, min_compression_perc = 70, quant.err = 0.2,
  distance_metric = "L1_Norm", error_metric = "mean",
  projection.scale = 10, normalize = TRUE,
  quant_method="kmeans")
plotHVT(hvt.results, line.width = c(0.8), color.vec = c('#141B41'),
  maxDepth = 1)

hvt.results <- list()
hvt.results <- HVT(USArrests, n_cells = 15, depth = 3, quant.err = 0.2,
  distance_metric = "L1_Norm", error_metric = "mean",
  projection.scale = 10, normalize = TRUE,
  quant_method="kmeans")
plotHVT(hvt.results, line.width = c(1.2,0.8,0.4), color.vec = c('#141B41', '#0582CA', '#8BA0B4'),
  maxDepth = 3)
```

---

hvtHmap

*Heat Map over Hierarchical Voronoi Tessellations*


---

**Description**

Main function to construct heatmap overlay for hierarchical voronoi tessellations.

**Usage**

```
hvtHmap(
  hvt.results,
  dataset,
  child.level,
  hmap.cols,
  color.vec = NULL,
  line.width = NULL,
  centroid.size = 3,
  pch = 21,
  palette.color = 6,
  previous_level_heatmap = T,
  show.points = F,
  asp = 1,
  ask = T,
  tess.label = NULL,
  quant.error.hmap = NULL,
```

```

    n_cells.hmap = NULL,
    label.size = 0.5,
    ...
)

```

### Arguments

<code>hvt.results</code>	List. A list of <code>hvt.results</code> obtained from the HVT function.
<code>dataset</code>	Data frame. The input data set.
<code>child.level</code>	Numeric. Indicating the level for which the heat map is to be plotted.
<code>hmap.cols</code>	Numeric or Character. The column number of column name from the dataset indicating the variables for which the heat map is to be plotted.
<code>color.vec</code>	Vector. A color vector such that <code>length(color.vec) = (child.level - 1)</code> . (default = NULL)
<code>line.width</code>	Vector. A line width vector such that <code>length(line.width) = (child.level - 1)</code> . (default = NULL)
<code>centroid.size</code>	Numeric. Indicating the centroid size of the first level. (default = 3)
<code>pch</code>	Numeric. Indicating the centroid's symbol type. (default = 21)
<code>palette.color</code>	Numeric. Indicating the heat map color palette. 1 - rainbow, 2 - heat.colors, 3 - terrain.colors, 4 - topo.colors, 5 - cm.colors, 6 - seas color. (default = 6)
<code>previous_level_heatmap</code>	Logical. If TRUE, the heatmap of previous level will be overlayed on the heatmap of selected level. If # FALSE, the heatmap of only selected level will be plotted
<code>show.points</code>	Logical. Indicating if the centroids should be plotted on the tessellations. (default = FALSE)
<code>asp</code>	Numeric. Indicating the aspect ratio type. For flexible aspect ratio set, <code>asp = NA</code> . (default = 1)
<code>ask</code>	Logical. If TRUE (and the R session is interactive) the user is asked for input, before a new figure is drawn. (default = TRUE)
<code>tess.label</code>	Vector. A vector for labelling the tessellations. (default = NULL)
<code>quant.error.hmap</code>	Numeric. A number indicating the quantization error threshold.
<code>n_cells.hmap</code>	Numeric. An integer indicating the number of cells/clusters per hierarchy (level)
<code>label.size</code>	Numeric. The size by which the tessellation labels should be scaled. (default = 0.5)
<code>...</code>	The ellipsis is passed to it as additional argument. (Used internally)

### Details

The output of the HVT function has all the required information about the HVT. Now a heat map is overlayed over this HVT. The user defines the level and also those variables of the data for which the heat map is to be plotted. Now for each variable a separate heat map is plotted. The plot area is divided into 2 screens where the first screen is relatively large and will have the heat

map. The second screen is small and contains the gradient scale. To plot the heat map, the data is first normalized. The gradient scale is divided into 'n' regions(500 is the set default). Using the normalized data, the different regions into which the data items fall are found. Each data item is now having a region on the gradient scale. This color is filled in the tile corresponding to the data item. This procedure is done for all the tiles for that level to get the complete heat map. Once the heat map is ready, the higher level tessellations are plotted to represent the hierarchies. The size of the centroids, the thickness of the lines and the color of the tessellation lines can be given as input by the user. Appropriate values for these parameters should be given to identify the hierarchies properly. In the second screen the gradient scale is plotted. The heat maps and hierarchical tessellations are obtained for all the desired variables.

### Author(s)

Shubhra Prakash <shubhra.prakash@mu-sigma.com>, Sangeet Moy Das <sangeet.das@mu-sigma.com>

### See Also

[plotHVT](#)

### Examples

```
data(USArrests)
hvt.results <- list()
hvt.results <- HVT(USArrests, n_cells = 15, depth = 1, quant.err = 0.2,
  distance_metric = "L1_Norm", error_metric = "mean",
  projection.scale = 10, normalize = TRUE,
  quant_method="kmeans",diagnose=TRUE)
hvtHmap(hvt.results, USArrests, child.level = 1,hmap.cols = 'Murder',
  line.width = c(0.2), color.vec = c('#141B41'),palette.color = 6,
  quant.error.hmap = 0.2, n_cells.hmap = 6)
```

---

mlayerHVT

*Predict which cell and what level each point in the test dataset belongs to*

---

### Description

Predict which cell and what level each point in the test dataset belongs to

### Usage

```
mlayerHVT(
  data,
  hvt_mapA,
  hvt_mapB,
  hvt_mapC,
  mad.threshold = 0.2,
  normalize = T,
```



```

distance_metric = "L1_Norm",
error_metric = "max",
child.level = 1,
line.width = c(0.6, 0.4, 0.2),
color.vec = c("#141B41", "#6369D1", "#D8D2E1"),
yVar = NULL,
...
)

```

### Arguments

data	Data Frame. A dataframe containing test dataset. The dataframe should have atleast one variable used while training. The variables from this dataset can also be used to overlay as heatmap
hvt_mapA	A list of hvt.results.model obtained from HVT function while performing hierarchical vector quantization on train data
hvt_mapB	A list of removed outlier rows using removedOutliers function
hvt_mapC	A list of hvt.results.model obtained from HVT function while performing hierarchical vector quantization on train data without outlier(s)
mad.threshold	A numeric values indicating the permissible Mean Absolute Deviation
normalize	Logical. A logical value indicating if the columns in your dataset should be normalized. Default value is TRUE.
distance_metric	character. The distance metric can be 'Euclidean' or 'Manhattan'. Euclidean is selected by default.
error_metric	character. The error metric can be "mean" or "max". mean is selected by default
child.level	A number indicating the level for which the heat map is to be plotted.(Only used if hmap.cols is not NULL)
line.width	Vector. A line width vector
color.vec	Vector. A color vector
yVar	character. Name of the dependent variable(s)
...	color.vec and line.width can be passed from here

### Author(s)

Shubhra Prakash <shubhra.prakash@mu-sigma.com>, Sangeet Moy Das <sangeet.das@mu-sigma.com>, Shantanu Vaidya <shantanu.vaidya@mu-sigma.com>

### See Also

[HVT](#)  
[hvtHmap](#)

**Examples**

```

data(USArrests)

#Split in train and test
train <- USArrests[1:40,]
test <- USArrests[41:50,]

hvt_mapA <- list()
hvt_mapA <- HVT(train, min_compression_perc = 70, quant.err = 0.2,
               distance_metric = "L1_Norm", error_metric = "mean",
               projection.scale = 10, normalize = TRUE,
               quant_method="kmeans")

identified_outlier_cells <- c(2, 10)
output_list <- removeOutliers(identified_outlier_cells, hvt_mapA)
hvt_mapB <- output_list[[1]]
dataset_without_outliers <- output_list[[2]]

mapA_scale_summary = hvt_mapA[[3]]$scale_summary
hvt_mapC <- list()
hvt_mapC <- HVT(dataset_without_outliers, n_cells = 15,
               depth = 2, quant.err = 0.2, distance_metric = "L1_Norm",
               error_metric = "max", quant_method = "kmeans",
               projection.scale = 10, normalize = FALSE, scale_summary = mapA_scale_summary)

predictions <- list()
predictions <- mlayerHVT(test, hvt_mapA, hvt_mapB, hvt_mapC)

```

---

multiNormalDist

*Multivariate normal distribution*


---

**Description**

Function to generate multivariate normal distribution where each variable has a standard normal distribution  $N(0,1)$

**Usage**

```
multiNormalDist(sample.size = 2500, ncol = 5)
```

**Arguments**

sample.size	Numeric. Indicating the sample size for distribution
ncol	Numeric. Indicating the number of columns

**Details**

The multivariate normal distribution, multivariate Gaussian distribution, or joint normal distribution is a generalization of the one-dimensional (univariate) normal distribution to higher dimensions. It is a vector in multiple normally distributed variables, such that any linear combination of the variables is also normally distributed.

**Author(s)**

Shubhra Prakash <shubhra.prakash@mu-sigma.com>

**Examples**

```
multiNormalDist(2500,2)
x=multiNormalDist(2500,2)
hist(x[,1])
```

---

plotCells	<i>Plot the identified outlier cell(s) in the voronoi tessellations map. Plotting function to construct hierarchical voronoi tessellations and highlight the cells using the compressed HVT map.</i>
-----------	--

---

**Description**

Plot the identified outlier cell(s) in the voronoi tessellations map.

Plotting function to construct hierarchical voronoi tessellations and highlight the cells using the compressed HVT map.

**Usage**

```
plotCells(
  plot.cells,
  hvt.map,
  line.width = c(0.6),
  color.vec = c("#141B41"),
  pch1 = 21,
  centroid.size = 0.5,
  title = NULL,
  maxDepth = 1
)
```

**Arguments**

plot.cells	Vector. A vector indicating the cells to be highlighted in the map
hvt.map	List. A list containing the output of HVT function which has the details of the tessellations to be plotted.
line.width	Numeric Vector. A vector indicating the line widths of the tessellation boundaries for each level.

color.vec	Vector. A vector indicating the colors of the boundaries of the tessellations at each level.
pch1	Numeric. Symbol type of the centroids of the tessellations (parent levels). Refer <a href="#">points</a> . (default = 21)
centroid.size	Numeric. Size of centroids of first level tessellations. (default = 3)
title	String. Set a title for the plot. (default = NULL)
maxDepth	Numeric. An integer indicating the number of levels. (default = NULL)

**Author(s)**

Shantanu Vaidya <shantanu.vaidya@mu-sigma.com>

**See Also**

[HVT](#)  
[hvtHmap](#)

---

plotDiag

*Make the diagnostic plots for hierarchical voronoi tessellations model.*

---

**Description**

Make the diagnostic plots for hierarchical voronoi tessellations model.

**Usage**

```
plotDiag(model_obj)
```

**Arguments**

model\_obj      List. A list of model\_obj obtained from the HVT function or prediction object

**Author(s)**

Shubhra Prakash <shubhra.prakash@mu-sigma.com>

**See Also**

[plotHVT](#)

---

plotHVT	<i>Plot the hierarchical tessellations. Main plotting function to construct hierarchical voronoi tessellations.</i>
---------	---

---

**Description**

Plot the hierarchical tessellations.

Main plotting function to construct hierarchical voronoi tessellations.

**Arguments**

<code>hvt.results</code>	List. A list containing the output of HVT function which has the details of the tessellations to be plotted.
<code>line.width</code>	Numeric Vector. A vector indicating the line widths of the tessellation boundaries for each level.
<code>color.vec</code>	Vector. A vector indicating the colors of the boundaries of the tessellations at each level.
<code>pch1</code>	Numeric. Symbol type of the centroids of the tessellations (parent levels). Refer <a href="#">points</a> . (default = 21)
<code>centroid.size</code>	Numeric. Size of centroids of first level tessellations. (default = 3)
<code>title</code>	String. Set a title for the plot. (default = NULL)
<code>maxDepth</code>	Numeric. An integer indicating the number of levels. (default = NULL)

**Author(s)**

Shubhra Prakash <shubhra.prakash@mu-sigma.com>, Sangeet Moy Das <sangeet.das@mu-sigma.com>

**See Also**

[HVT](#)  
[hvtHmap](#)

**Examples**

```
data("USArrests", package="datasets")

hvt.results <- list()
hvt.results <- HVT(USArrests, n_cells = 15, depth = 1, quant.err = 0.2,
                  distance_metric = "L1_Norm", error_metric = "mean",
                  projection.scale = 10, normalize = TRUE,
                  quant_method="kmeans", diagnose=TRUE)
plotHVT(hvt.results, line.width = c(0.8), color.vec = c('#141B41'),
        maxDepth = 1)
```

---

predictHVT	<i>Predict which cell and what level each point in the test dataset belongs to</i>
------------	--

---

### Description

Predict which cell and what level each point in the test dataset belongs to

### Usage

```
predictHVT(
  data,
  hvt.results.model,
  child.level = 1,
  mad.threshold = 0.2,
  line.width = c(0.6, 0.4, 0.2),
  color.vec = c("#141B41", "#6369D1", "#D8D2E1"),
  normalize = T,
  distance_metric = "L1_Norm",
  error_metric = "max",
  yVar = NULL,
  ...
)
```

### Arguments

data	List. A dataframe containing test dataset. The dataframe should have atleast one variable used while training. The variables from this dataset can also be used to overlay as heatmap
hvt.results.model	A list of hvt.results.model obtained from HVT function while performing hierarchical vector quantization on train data
child.level	A number indicating the level for which the heat map is to be plotted.(Only used if hmap.cols is not NULL)
mad.threshold	A numeric values indicating the permissible Mean Absolute Deviation
line.width	Vector. A line width vector
color.vec	Vector. A color vector
normalize	Logical. A logical value indicating if the columns in your dataset should be normalized. Default value is TRUE.
distance_metric	character. The distance metric can be 'Euclidean' or 'Manhattan'. Euclidean is selected by default.
error_metric	character. The error metric can be "mean" or "max". mean is selected by default
yVar	character. Name of the dependent variable(s)
...	color.vec and line.width can be passed from here

**Author(s)**

Shubhra Prakash <shubhra.prakash@mu-sigma.com>, Sangeet Moy Das <sangeet.das@mu-sigma.com>

**See Also**

[HVT](#)  
[hvtHmap](#)

**Examples**

```
data(USArrests)
#Split in train and test

train <- USArrests[1:40,]
test <- USArrests[41:50,]

hvt.results <- list()
hvt.results <- HVT(train, n_cells = 15, depth = 1, quant.err = 0.2,
                  distance_metric = "L1_Norm", error_metric = "mean",
                  projection.scale = 10, normalize = TRUE,
                  quant_method="kmeans",diagnose=TRUE)

predictions <- predictHVT(test,hvt.results, child.level=2, mad.threshold = 0.2)
print(predictions$scoredPredictedData)
```

---

qeHistPlot

*plotDiag Make the diagnostic plots for hierarchical voronoi tessellations model.*

---

**Description**

plotDiag

Make the diagnostic plots for hierarchical voronoi tessellations model.

**Usage**

```
qeHistPlot(hvt.results, hvt.predictions)
```

**Arguments**

hvt.results      List. A list of hvt.results obtained from the HVT function.  
hvt.predictions      List. A list of hvt.predictions obtained from the Predict function.

**Author(s)**

Shubhra Prakash <shubhra.prakash@mu-sigma.com>

**See Also**[plotHVT](#)

---

removeOutliers	<i>removeOutliers</i>
----------------	-----------------------

---

**Description**

Remove identified outlier cell(s) from the dataset

**Usage**

```
removeOutliers(outlier_cells, hvt_results)
```

**Arguments**

`outlier_cells` Vector. A vector with the cell number of the identified outliers  
`hvt_results` List. A list having the results of the compressed map i.e. output of HVT function

**Details**

This function is used to remove the identified outlier cell(s) from the dataset. It is recommended to run the HVT function before running this function. It takes input in the form of cell number of the outlier cell(s) identified using the output of the HVT function and the compressed map (`hvt_mapA`) generated using the HVT function. The output of this function is a list of two items: a new map having the data of removed outlier cell(s) and the subset of dataset without outliers.

**Value**

A list of two items: a map having the data of removed outlier cells and the subset of the dataset without outlier(s) which has to be passed as input argument to HVT function to generate another map

[[1]]            Dataframe. Information about the removed outlier cell(s)  
[[2]]            Dataframe. Subset of dataset without the outlier cell(s)

**Author(s)**

Shantanu Vaidya <shantanu.vaidya@mu-sigma.com>

**See Also**

[HVT](#)  
[m1ayerHVT](#)



**Examples**

```
data(USArrests)
hvt_mapA <- list()
hvt_mapA <- HVT(USArrests, min_compression_perc = 70, quant.err = 0.2,
               distance_metric = "L1_Norm", error_metric = "mean",
               projection.scale = 10, normalize = TRUE,
               quant_method="kmeans")
plotHVT(hvt_mapA, line.width = c(0.8), color.vec = c('#141B41'),
        maxDepth = 1)

identified_outlier_cells <- c(2, 10)
output_list <- removeOutliers(identified_outlier_cells, hvt_mapA)
hvt_mapB <- output_list[[1]]
dataset_without_outliers <- output_list[[2]]
```

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