sWriteData

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sWriteData   *Function to write out the best-matching hexagons and/or cluster bases in terms of data*

Description

sWriteData is supposed to write out the best-matching hexagons and/or cluster bases in terms of data.

Usage

```
sWriteData(sMap, data, sBase = NULL, filename = NULL, keep.data = F)
```

Arguments

sMap	an object of class "sMap" or a codebook matrix
data	a data frame or matrix of input data
sBase	an object of class "sBase"
filename	a character string naming a filename
keep.data	logical to indicate whether or not to also write out the input data. By default, it sets to false for not keeping it. It is highly expensive to keep the large data sets

Value

a data frame with following components:

- ID: ID for data. It inherits the rownames of data (if exists). Otherwise, it is sequential integer values starting with 1 and ending with dlen, the total number of rows of the input data
- Hexagon_index: the index for best-matching hexagons
- Cluster_base: optional, it is only appended when sBase is given. It stores the cluster memberships/bases
- data: optional, it is only appended when keep.data is true

Note

If "filename" is not NULL, a tab-delimited text file will be also written out. If "sBase" is not NULL and comes from the "sMap" partition, then cluster bases are also appended. if "keep.data" is true, the data will be part of output.

See Also

[sBMH](#)

Examples

```
# 1) generate an iid normal random matrix of 100x10
data <- matrix( rnorm(100*10,mean=0,sd=1), nrow=100, ncol=10)

# 2) get trained using by default setup
sMap <- sPipeline(data=data)

# 3) write data's BMH hitting the trained map
output <- sWriteData(sMap=sMap, data=data, filename="sData_output.txt")

# 4) partition the grid map into cluster bases
sBase <- sDmatCluster(sMap=sMap, which_neigh=1,
distMeasure="median", clusterLinkage="average")

# 5) write data's BMH and cluster bases
output <- sWriteData(sMap=sMap, data=data, sBase=sBase,
filename="sData_base_output.txt")
```