

# Package ‘phemd’

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**Type** Package

**Title** Phenotypic EMD for comparison of single-cell samples

**Version** 1.14.1

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**Description** Package for comparing and generating a low-dimensional embedding of multiple single-cell samples.

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.5), monocle, Seurat

**Imports** SingleCellExperiment, RColorBrewer, igraph, transport, pracma, cluster, Rtsne, destiny, RANN, ggplot2, maptree, pheatmap, scatterplot3d, VGAM, methods, grDevices, graphics, stats, utils, cowplot, S4Vectors, BiocGenerics, SummarizedExperiment, Biobase, phateR, reticulate

**Config/reticulate** list( packages = list( list(package = ` ` phate") ) )

**Suggests** knitr

**VignetteBuilder** knitr

**biocViews** Clustering, ComparativeGenomics, Proteomics, Transcriptomics, Sequencing, DimensionReduction, SingleCell, DataRepresentation, Visualization, MultipleComparison

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---

aggregateSamples	<i>Aggregate expression data from all samples</i>
------------------	---

---

## Description

Takes initial Phemd object and returns object with additional data frame in slot @data\_aggregate containing cells aggregated from all samples (to be used for further analyses e.g. Monocle 2 trajectory building / pseudotime mapping / cell clustering)

## Usage

```
aggregateSamples(obj, max_cells = 12000)
```

## Arguments

obj	'Phemd' object containing raw expression data and associated metadata
max_cells	Maximum number of cells across all samples to be included in final matrix on which Monocle 2 will be run

## Details

Subsamples cells as necessary based on max\_cells. If subsampling is performed, an equal number of cells are subsampled from each sample

## Value

Same as input 'Phemd' object with additional slot 'data\_aggregate' containing aggregated expression data (num\_markers x num\_cells)

## Examples

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
```

---

all_expn_data	<i>Single-cell RNA-seq expression data for melanoma samples</i>
---------------	---

---

**Description**

This dataset contains normalized single-cell RNA-seq expression data for 19 melanoma samples (immune cells).

**Usage**

```
data(all_expn_data)
```

**Format**

A list of length 19 with each element representing a distinct sample. Each list element (sample) is a matrix with dimension num\_genes x num\_cells.

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE72056>

**References**

Tirosh, I. et al. Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. *Science* 352, 189–196 (2016)

---

all_genes	<i>All genes included in (subsampling) melanoma single-cell RNA-seq expression data</i>
-----------	---

---

**Description**

This object contains 100 genes measured in melanoma single-cell RNA-seq expression data.

**Usage**

```
data(all_genes)
```

**Format**

Vector of length 100 representing row names of each matrix in melanoma expression dataset

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE72056>

## References

Tirosh, I. et al. Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. *Science* 352, 189–196 (2016)

---

assignCellClusterNearestNode

*Assign cells to a reference cell subtype*

---

## Description

Assigns each cell in `cur_cells` to a cluster based on nearest cell in Monocle 2 tree

## Usage

```
assignCellClusterNearestNode(  
  cur_cells,  
  ref_cells,  
  ref_cell_labels,  
  cell_model = c("monocle2", "seurat", "phate")  
)
```

## Arguments

<code>cur_cells</code>	Matrix of cells to be assigned to clusters (Dim: <i>num_cells</i> x <i>num_markers</i> )
<code>ref_cells</code>	Matrix of cells used to build reference Monocle 2 tree (Dim: <i>num_monocle_cells</i> x <i>num_markers</i> )
<code>ref_cell_labels</code>	Vector of length <i>num_monocle_cells</i> containing Monocle 2 cell branch assignments
<code>cell_model</code>	Either "monocle2", "seurat", or "phate" depending on method used to model cell state space

## Details

Private method (not exported in namespace). Uses RANN package for fast knn search

## Value

Vector of length *num\_cells* representing cluster assignments for each cell in *cur\_cells*

## Examples

```
## Not run:  
cur_cells_cluster_labels <- assignCellClusterNearestNode(cur_cells_expn_data,  
  clustered_cells_expn_data, clustered_cells_cluster_labels, cell_model='monocle2')  
  
## End(Not run)
```

---

batchIDs	<i>Accessor function for batch ID for each sample</i>
----------	---

---

**Description**

Accessor function for batch ID for each sample

**Usage**

```
batchIDs(obj)
```

**Arguments**

obj                      Phemd object

**Value**

Vector of length num\_samples representing the experiment (batch) in which the sample was profiled

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
batch_metadata <- batchIDs(phemdObj)
```

---

bindSeuratObj	<i>Attach 'Seurat' object to 'Phemd' object</i>
---------------	---

---

**Description**

Allows user to attach batch-normalized reference cell data from Seurat into 'Phemd' object containing raw expression data and metadata

**Usage**

```
bindSeuratObj(phemd_obj, seurat_obj, batch.colname = "plt")
```

**Arguments**

phemd\_obj              Phemd object initialized using createDataObj  
seurat\_obj              S4 'seurat' object containing batch-normalized reference cell data  
batch.colname          Name of column in Seurat object that denotes batch ID

**Value**

'Phemd' object containing with attached Seurat object

**Examples**

```

my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_seuratObj <- Seurat::CreateSeuratObject(counts = t(all_expn_data[[1]]), project = "A")
my_seuratObj <- Seurat::FindVariableFeatures(object = my_seuratObj)
my_seuratObj <- Seurat::ScaleData(object = my_seuratObj, do.scale=FALSE, do.center=FALSE)
my_seuratObj <- Seurat::RunPCA(object = my_seuratObj, pc.genes = colnames(all_expn_data[[1]]), do.print = FALSE)
my_seuratObj <- Seurat::FindNeighbors(my_seuratObj, reduction = "pca", dims.use = 1:10)
my_seuratObj <- Seurat::FindClusters(my_seuratObj, resolution = 0.6, print.output = 0, save.SNN = TRUE)
my_phemdObj <- bindSeuratObj(my_phemdObj, my_seuratObj)

```

---

celltypeFreqs

*Accessor function for cell subtype distribution for each sample*


---

**Description**

Accessor function for cell subtype distribution for each sample

**Usage**

```
celltypeFreqs(obj)
```

**Arguments**

obj                      Phemd object

**Value**

Matrix representing cell subtype relative frequencies for each sample (num\_samples x num\_genes)

**Examples**

```

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
celltype_weights <- celltypeFreqs(phemdObj)

```

---

clusterIndividualSamples

*Computes cell subtype abundances for each sample*


---

**Description**

Takes as input a Phemd object with all single-cell expression data of all single-cell samples in @data slot and cell-state embedding generated by embedCells. Returns updated object with cell subtype frequencies of each sample that may be retrieved by the 'celltypeFreqs' accessor function.

**Usage**

```
clusterIndividualSamples(
  obj,
  verbose = FALSE,
  cell_model = c("monocle2", "seurat", "phate")
)
```

**Arguments**

obj	'Phemd' object containing single-cell expression data of all samples in @data slot and cell-state embedding object generated and stored using the embedCells function.
verbose	Boolean that determines whether progress (sequential processing of samples) should be printed. FALSE by default
cell_model	Either "monocle2", "seurat", or "phate" depending on method used to model cell state space

**Details**

embedCells (and orderCellsMonocle if using the Monocle2 embedding technique) needs to be called before calling this function.

**Value**

'Phemd' object with cell subtype frequencies of each sample that can be retrieved using the 'cell-typeFreqs' accessor function

**Examples**

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
```

---

compareSamples	<i>Computes EMD distance matrix representing pairwise dissimilarity between samples</i>
----------------	---

---

**Description**

Takes as input a Phemd object with cell subtype relative frequencies for each sample in @data\_cluster\_weights slot and ground distance matrix (representing cell subtype pairwise dissimilarity) in @emd\_dist\_mat slot. Returns distance matrix representing pairwise dissimilarity between samples



**Usage**

```
compareSamples(obj)
```

**Arguments**

`obj` 'Phemd' object containing cell subtype relative frequencies for each sample in `@data_cluster_weights` slot and ground distance matrix (representing cell subtype dissimilarity) in `@emd_dist_mat` slot

**Details**

Requires 'transport' and 'pracma' packages

**Value**

Distance matrix of dimension `num_samples` x `num_samples` representing pairwise dissimilarity between samples

**Examples**

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
my_phemdObj_final <- generateGDM(my_phemdObj_final)
my_EMD_mat <- compareSamples(my_phemdObj_final)
```

---

createDataObj	<i>Create 'Phemd' object</i>
---------------	------------------------------

---

**Description**

Wrapper function to create 'Phemd' object containing raw expression data and metadata

**Usage**

```
createDataObj(data, markers, snames, datatype = "list", valtype = "counts")
```

**Arguments**

`data` List of length `num_samples` containing expression data; each element is of size `num_cells` x `num_markers`. Alternately a `SingleCellExperiment` object.

`markers` Vector containing marker names (i.e. column names of `all_data`)

`snames` Vector containing sample names (i.e. names of samples contained in `all_data`)

datatype	Either "list" or "sce" (SingleCellExperiment with genes x cells)
valtype	Type of assay data (i.e. "counts", "normcounts", "logcounts", "tpm", "cpm") if datatype is "sce"

**Details**

Note that each element in list can have different number of rows (i.e. number of cells in each sample can vary).

**Value**

'Phemd' object containing raw multi-sample expression data and associated metadata

**Examples**

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
```

---

drawColnames45	<i>Rotates heatmap marker labels 45 degrees</i>
----------------	---

---

**Description**

Overwrites default draw\_colnames in the pheatmap package

**Usage**

```
drawColnames45(coln, gaps, ...)
```

**Arguments**

coln	Column names
gaps	Spacing of labels
...	Additional parameters to be passed to gpar

**Details**

To be used with pheatmap plotting function; not to be called directly. Thanks to Josh O'Brien at <http://stackoverflow.com/questions/15505607>

**Value**

Formatted marker labels in heatmap

**Examples**

```
#Not to be called directly
```

---

embedCells	<i>Generate cell-state embedding</i>
------------	--------------------------------------

---

### Description

Takes as input a Phemd object with aggregated data and returns updated object containing cell-state embedding

### Usage

```
embedCells(
  obj,
  cell_model = c("monocle2", "seurat", "phate"),
  data_model = "negbinomial_sz",
  phate_ncluster = 8,
  phate_cluster_seed = NULL,
  ...
)
```

### Arguments

obj	'Phemd' object containing aggregated data
cell_model	Method to use to generate cell-state embedding. Currently supports "phate" and "monocle2". If using the Seurat to model the cell-state space, please identify cell subtypes as outlined in the Seurat software package and then use the bindSeuratObj function.
data_model	Only relevant if cell_model = "monocle2". One of the following: 'negbinomial_sz', 'negbinomial', 'tobit', 'uninormal', 'gaussianff'. See "Family Function" table at the following link for more details on selecting the proper one. <a href="http://cole-trapnell-lab.github.io/monocle-release/docs/#getting-started-with-monocle">http://cole-trapnell-lab.github.io/monocle-release/docs/#getting-started-with-monocle</a>
phate_ncluster	Only relevant if cell_model = "phate". Number of cell state clusters to return when using PHATE
phate_cluster_seed	Only relevant if cell_model = "phate". Seed to use when performing cell state clustering (optional)
...	Additional parameters to be passed to reduceDimension function for Monocle or phate function for PHATE

### Details

aggregateSamples needs to be called before running this function.

### Value

Same as input 'Phemd' object containing additional cell-state embedding object

**Examples**

```

my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_lg <- embedCells(my_phemdObj_lg, cell_model='monocle2', data_model = 'gaussianff', sigma=0.02, maxIter=100)

```

---

gaussianffLocal	<i>Models expression data using generalized linear model with Gaussian error</i>
-----------------	--

---

**Description**

Useful for modeling pre-normalized single-cell expression data.

**Usage**

```
gaussianffLocal(dispersion = 0, parallel = FALSE, zero = NULL)
```

**Arguments**

dispersion	Dispersion parameter. If 0, then estimate as described in VGAM 1.0-5 documentation.
parallel	A logical or formula. If a formula, the response of the formula should be a logical and the terms of the formula indicates whether or not those terms are parallel.
zero	An integer-valued vector specifying which linear/additive predictors are modelled as intercepts only. The values must be from the set 1...M where M is the number of columns of the matrix response.

**Details**

Private method (not to be called by user directly). Requires VGAM package. Obtained from VGAM v1.0-5 (<https://www.rdocumentation.org/packages/VGAM/versions/1.0-5/topics/gaussianff>)

**Value**

Generalized linear model with Gaussian error

---

GDM	<i>Accessor function for EMD ground distance matrix</i>
-----	---

---

**Description**

Accessor function for EMD ground distance matrix

**Usage**

```
GDM(obj)
```

**Arguments**

obj                    A Phemd object

**Value**

Sqaure matrix representing pairwise distances between cell subtypes

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
gdm <- GDM(phemdObj)
```

---

generateGDM	<i>Computes ground distance matrix based on cell embedding</i>
-------------	--

---

**Description**

Takes as input a Phemd object containing cell-state embedding object. Returns updated object with ground distance matrix representing pairwise distances between distinct cell subtypes based on cell state embedding.

**Usage**

```
generateGDM(
  obj,
  cell_model = c("monocle2", "seurat", "phate"),
  expn_type = "reduced",
  ndim = 8
)
```

**Arguments**

obj	'Phemd' object containing cell-state embedding object
cell_model	Method by which cell state was modeled (either "monocle2", "seurat", or "phate")
expn_type	Data type to use to determine cell-type dissimilarities
ndim	Number of embedding dimensions to be used for computing cell-type dissimilarity (optional)

**Details**

embedCells and orderCellsMonocle need to be called before calling this function. Requires 'igraph' package

**Value**

Phemd object with ground distance matrix (to be used in EMD computation) in @data\_cluster\_weights slot

**Examples**

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
my_phemdObj_final <- generateGDM(my_phemdObj_final)
```

---

getArithmeticCentroids

*Get arithmetic centroids (coordinates)*

---

**Description**

Takes initial list and returns a matrix with row  $i$  representing the arithmetic centroid of cluster  $i$

**Usage**

```
getArithmeticCentroids(ref_clusters)
```

**Arguments**

ref_clusters	list containing each cluster of interest (each list element is a matrix of dimension num_cells x num_markers)
--------------	---

**Details**

Private method (not exported in namespace)

**Value**

Matrix of dimension num\_cluster x num\_markers; row  $i$  representing the arithmetic centroid of cluster  $i$

**Examples**

```
## Not run:
cluster_centroids <- getArithmeticCentroids(ref_clusters)

## End(Not run)
```

---

getCellYield	<i>Gets cell yield of each sample as a table</i>
--------------	--

---

**Description**

Gets cell yield (number of viable cells) of each single-cell sample in decreasing order

**Usage**

```
getCellYield(myobj, cluster_assignments = NULL)
```

**Arguments**

myobj                    phemdObj object containing expression data for each sample in 'data' slot  
cluster\_assignments      Vector of cluster assignments to be included as additional column in output table  
                          (optional)

**Value**

Data frame representing cell yield of each sample

**Examples**

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
my_phemdObj_final <- generateGDM(my_phemdObj_final)
my_EMD_mat <- compareSamples(my_phemdObj_final)
cluster_assignments <- groupSamples(my_EMD_mat, distfun = 'hclust', ncluster=4)
getCellYield(my_phemdObj_final, cluster_assignments)
```

---

`getSampleCelltypeFreqs`*Returns cell subtype distribution for each sample as a table*

---

### Description

Returns cell subtype distribution for each single-cell sample along with (optional) final inhibitor cluster assignment

### Usage

```
getSampleCelltypeFreqs(myobj, cluster_assignments = NULL)
```

### Arguments

`myobj`                    phemdObj object containing expression data for each sample in 'data' slot

`cluster_assignments`        Vector of cluster assignments to be included as additional column in output table (optional)

### Value

Data frame representing relative frequencies of each cell subtype along with (optional) final inhibitor cluster assignment for each single-cell sample

### Examples

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
my_phemdObj_final <- generateGDM(my_phemdObj_final)
my_EMD_mat <- compareSamples(my_phemdObj_final)
cluster_assignments <- groupSamples(my_EMD_mat, distfun = 'hclust', ncluster=4)
getSampleCelltypeFreqs(my_phemdObj_final, cluster_assignments)
```



---

```
getSampleHistsByCluster
```

*Gets cell subtype frequency histograms for each sample by cluster ID*

---

### Description

Gets relative frequency ("weights") of cell subtypes ("bins" or "signatures") in each single-cell sample

### Usage

```
getSampleHistsByCluster(
  myobj,
  cluster_assignments,
  cell_model = c("monocle2", "seurat")
)
```

### Arguments

myobj	phemdObj object containing cell subtype relative frequency in @data_cluster_weights slot
cluster_assignments	Vector containing group assignments for each sample in myobj
cell_model	Method by which cell state was modeled (either "monocle2" or "seurat")

### Details

groupSamples must be called before calling this function. Saves plots in directory called "individual\_inhibs"

### Value

List of lists, with outer list representing sample cluster ID and inner list representing cell subtype frequencies of given sample

### Examples

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
my_phemdObj_final <- generateGDM(my_phemdObj_final)
my_EMD_mat <- compareSamples(my_phemdObj_final)
cluster_assignments <- groupSamples(my_EMD_mat, distfun = 'hclust', ncluster=4)
weights_by_cluster <- getSampleHistsByCluster(my_phemdObj_final, cluster_assignments)
```

getSampleSizes      *Retrieve single-cell sample sizes*

---

**Description**

Takes initial list of single-cell samples and returns vector containing number of cells in each sample.

**Usage**

```
getSampleSizes(data_list)
```

**Arguments**

data\_list      List of length num\_samples (each element has dimension num\_cells x num\_markers)

**Details**

Private method (not exported in namespace)

**Value**

Vector of length num\_samples representing number of cells in each sample

**Examples**

```
## Not run:  
sample_sizes <- getSampleSizes(all_expn_data)  
  
## End(Not run)
```

---

groupSamples      *Performs community detection on sample-sample distance matrix to identify groups of similar samples*

---

**Description**

Takes sample-sample distance matrix as input and returns group assignments for each sample

**Usage**

```
groupSamples(  
  distmat,  
  distfun = "hclust",  
  ncluster = NULL,  
  method = "complete",  
  ...  
)
```

**Arguments**

distmat	A distance matrix of dimension num_samples x num_samples representing pairwise dissimilarity between samples
distfun	Method of partitioning network of samples (currently either 'hclust' or 'pam')
ncluster	Optional parameter specifying total number of sample groups
method	Optional parameter for hierarchical clustering (see "hclust" documentation)
...	Optional additional parameters to be passed to diffusionKmeans method

**Details**

By default, uses 'kgs' (Kelley-Gardner-Sutcliffe) method for determining optimal number of groups. Alternatively, can take user-specified number of groups). Requires 'cluster' and 'maptree' packages.

**Value**

Vector containing group assignments for each sample (same order as row-order of distmat) based on user-specified partitioning method (e.g. hierarchical clustering)

**Examples**

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, cell_model = 'monocle2', data_model = 'gaussianff', sigma=0.02,
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
my_phemdObj_final <- generateGDM(my_phemdObj_final)
my_EMD_mat <- compareSamples(my_phemdObj_final)
cluster_assignments <- groupSamples(my_EMD_mat, distfun = 'hclust', ncluster=4)
```

---

heatmap_genes	<i>Genes to be used when plotting heatmap for melanoma single-cell RNA-seq expression data</i>
---------------	--

---

**Description**

This object contains genes to be used when plotting heatmap for melanoma single-cell RNA-seq expression data.

**Usage**

```
data(heatmap_genes)
```

**Format**

Vector of length 42 representing selected genes for plotting heatmap.

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE72056>

**References**

Tirosh, I. et al. Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. *Science* 352, 189–196 (2016)

---

identifyCentroids	<i>Identify cluster centroids (cell names)</i>
-------------------	--

---

**Description**

Takes initial list and returns list of cell names representing centroid of cluster

**Usage**

```
identifyCentroids(ref_clusters)
```

**Arguments**

ref\_clusters    list containing each cluster of interest (each list element is a matrix of dimension num\_cells x num\_markers)

**Details**

Private method (not exported in namespace)

**Value**

List of names; element  $i$  represents the name of the cell in cluster  $i$  that is closest to the centroid (arithmetic mean) of cluster  $i$

**Examples**

```
## Not run:  
centroid_names <- identifyCentroids(ref_clusters)  
  
## End(Not run)
```

---

monocleInfo	<i>Accessor function for stored Monocle object</i>
-------------	--

---

**Description**

Accessor function for stored Monocle object

**Usage**

```
monocleInfo(obj)
```

**Arguments**

obj                    A Phemd object.

**Value**

An object of class 'CellDataSet' (from Monocle)

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
monocle_obj <- monocleInfo(phemdObj)
```

---

orderCellsMonocle	<i>Compute Monocle2 cell state and pseudotime assignments</i>
-------------------	---

---

**Description**

Takes as input a Phemd object with Monocle2 object and returns updated object with Monocle2 object containing cell state and pseudotime assignments

**Usage**

```
orderCellsMonocle(obj, ...)
```

**Arguments**

obj                    'Phemd' object containing Monocle2 object initialized using embedCells  
 ...                    Additional parameters to be passed into orderCells function

**Details**

Wrapper function for orderCells in Monocle 2 package. embedCells needs to be called before calling this function.

**Value**

Same as input 'Phemd' object with updated cell-state embedding object containing cell state assignments

**Examples**

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, cell_model='monocle2', data_model='gaussianff', sigma=0.02, ma
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
```

---

phateInfo

*Accessor function for stored phate object*

---

**Description**

Accessor function for stored phate object

**Usage**

```
phateInfo(obj)
```

**Arguments**

obj                    A Phemd object.

**Value**

An object of class 'phate' (from phateR)

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
phateobj <- phateInfo(phemdObj)
```

---

Phemd	<i>Phemd class</i>
-------	--------------------

---

### Description

The main PhEMD class to store single-cell expression data.

### Fields

**data** List of matrices, each of which represents a single-cell sample (num\_cells x num\_genes)  
**markers** Column names (e.g. genes) for each element (i.e. data matrix) in "data"  
**snames** Sample ID for each element in "data"  
**data\_aggregate** Numeric matrix representing expression data for cells from all experimental conditions (rows = markers, cols = cells)  
**data\_subsample\_idx** List of vectors each representing the indices of elements in "data" that were subsampled and combined to form "data\_aggregate"  
**subsampled\_bool** Boolean represent whether or not subsampling was performed in the data aggregation process  
**monocle\_obj** Data object of type "CellDataSet" that is the core Monocle data structure  
**data\_cluster\_weights** Matrix representing cell subtype relative frequencies for each sample (num\_samples x num\_genes)  
**emd\_dist\_mat** Matrix representing pairwise distances between each pair of cell subtypes  
**seurat\_obj** Object of class "Seurat" that is the core Seurat data structure  
**phate\_obj** Object of class "phate" that is the core PHATE data structure  
**experiment\_ids** Vector of length num\_samples representing the experiment (batch) in which the sample was profiled

---

Phemd-methods	<i>Setter function for protein / gene markers</i>
---------------	---

---

### Description

Setter function for protein / gene markers  
 Setter function for stored expression data  
 Setter function for single-cell expression data aggregated from multiple samples  
 Setter function for indices of cells subsampled from each sample during aggregation  
 Setter function for boolean denoting whether cells were subsampled from each sample during aggregation  
 Setter function for Monocle2 CellDataSet object for experiment  
 Setter function for Seurat object for experiment

Setter function for phate object for experiment  
Setter function for cell subtype frequencies of each single-cell sample  
Setter function for batch IDs of each single-cell sample  
Setter function for EMD ground distance matrix

### Usage

```
selectMarkers(obj) <- value

## S4 replacement method for signature 'Phemd'
selectMarkers(obj) <- value

rawExpn(obj) <- value

## S4 replacement method for signature 'Phemd'
rawExpn(obj) <- value

pooledCells(obj) <- value

## S4 replacement method for signature 'Phemd'
pooledCells(obj) <- value

subsampledIdx(obj) <- value

## S4 replacement method for signature 'Phemd'
subsampledIdx(obj) <- value

subsampledBool(obj) <- value

## S4 replacement method for signature 'Phemd'
subsampledBool(obj) <- value

monocleInfo(obj) <- value

## S4 replacement method for signature 'Phemd'
monocleInfo(obj) <- value

seuratInfo(obj) <- value

## S4 replacement method for signature 'Phemd'
seuratInfo(obj) <- value

phateInfo(obj) <- value

## S4 replacement method for signature 'Phemd'
phateInfo(obj) <- value

celltypeFreqs(obj) <- value
```



```

## S4 replacement method for signature 'Phemd'
celltypeFreqs(obj) <- value

batchIDs(obj) <- value

## S4 replacement method for signature 'Phemd'
batchIDs(obj) <- value

GDM(obj) <- value

## S4 replacement method for signature 'Phemd'
GDM(obj) <- value

```

### Arguments

obj	A Phemd object
value	Assignment object

### Value

Updated Phemd object  
 Updated Phemd object  
 Updated Phemd object  
 Updated Phemd object  
 Updated Phemd object  
 Updated Phemd object containing Seurat object  
 Updated Phemd object containing phate object  
 Updated Phemd object  
 Updated Phemd object  
 Updated Phemd object

### Examples

```

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
new_genes <- all_genes
new_genes[1] <- 'IL2R'
selectMarkers(phemdObj) <- new_genes

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
new_expn_data <- all_expn_data
new_expn_data <- lapply(new_expn_data, function(x) {log2(x+1)})
rawExpn(phemdObj) <- new_expn_data

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
aggregated_data <- t(do.call(rbind,all_expn_data))
pooledCells(phemdObj) <- aggregated_data

```

```

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
subsampldIdxList<- rep(list(1:10), length(all_expn_data)) #subsampld cells 1-10 from each sample
subsampldIdx(phemdObj) <- subsampldIdxList

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
subsampldBool(phemdObj) <- TRUE

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
mydata <- pooledCells(phemdObj)
myCellDataSet <- newCellDataSet(mydata, phenoData=NULL, expressionFamily=VGAM::negbinomial.size())
monocleInfo(phemdObj) <- myCellDataSet

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_seuratObj <- Seurat::CreateSeuratObject(counts = t(all_expn_data[[1]]), project = "A")
seuratInfo(phemdObj) <- my_seuratObj

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
#my_phateObj <- phateR::phate(all_expn_data[[1]])
phateInfo(phemdObj) <- list()

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
myCellTypeFreqs <- matrix(rexp(length(all_expn_data)*10, rate=.1), ncol=10)
myCellTypeFreqs <- apply(myCellTypeFreqs, 1, function(x) {x / sum(x)})
celltypeFreqs(phemdObj) <- myCellTypeFreqs

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_seuratObj <- Seurat::CreateSeuratObject(counts = t(all_expn_data[[1]]), project = "A")
seuratInfo(phemdObj) <- my_seuratObj
batchIDs(phemdObj) <- rep('A', length(all_expn_data))

phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
cluster_locs <- 1:10
myGDM <- as.matrix(dist(cluster_locs))
GDM(phemdObj) <- myGDM

```

---

plotCellYield

*Plot cell yield of each sample as bar plot*


---

### Description

Plots cell yield (number of viable cells) of each single-cell sample in decreasing order as horizontal bar plot

### Usage

```
plotCellYield(myobj, labels = NULL, cmap = NULL, font_sz = 0.6, w = 8, h = 9.5)
```

**Arguments**

myobj	Phmed object containing expression data for each sample in 'data' slot
labels	Vector containing group labels for samples (optional). If not provided, bars will be of uniform color (blue)
cmap	Vector containing colors by which histogram bars should be colored (optional)
font_sz	Scaling factor for font size of sample names in barplot
w	Width of plot in inches
h	Height of plot in inches

**Value**

None

**Examples**

```
my_phemdObj <- createDataObj(all_exprn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
my_phemdObj_final <- generateGDM(my_phemdObj_final)
my_EMD_mat <- compareSamples(my_phemdObj_final)
cluster_assignments <- groupSamples(my_EMD_mat, distfun = 'hclust', ncluster=4)
plotCellYield(my_phemdObj_final, labels=cluster_assignments, font_sz = 0.8)
```

---

plotEmbeddings

*Plots Monocle2 cell embedding plots*

---

**Description**

Takes as input a Phemd object containing either a Monocle2 object or Seurat object (already embedded and ordered) and plots cell embedding plots side by side. Optionally saves to specified folder.

**Usage**

```
plotEmbeddings(
  obj,
  cell_model = c("monocle2", "seurat", "phate"),
  cmap = NULL,
  w = 4,
  h = 5,
  pt_sz = 1,
  ndims = NULL
)
```

**Arguments**

obj	'Phemd' object containing Monocle 2 object
cell_model	Method by which cell state was modeled (either "monocle2", "seurat", or "phate)
cmap	User-specified colormap to use to color cell state embedding (optional)
w	Width of plot in inches
h	Height of plot in inches
pt_sz	Scalar factor for point size
ndims	Number of dimensions to use for dimensionality reduction in case it hasn't been performed yet (only relevant when using Seurat data as input)

**Details**

embedCells and orderCellsMonocle need to be called before calling this function. Required additional packages: 'RColorBrewer', 'cowplot'

**Value**

Colormap (vector of colors) used to color Monocle2 cell state embedding

**Examples**

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model='gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
cmap <- plotEmbeddings(my_phemdObj_monocle)
```

---

plotGroupedSamplesDmap

*Plot diffusion map embedding of samples based on distance matrix*

---

**Description**

Visualizes diffusion map for network of samples based on square distance matrix (sample-sample pairwise dissimilarity)

**Usage**

```
plotGroupedSamplesDmap(
  my_distmat,
  cluster_assignments = NULL,
  pt_sz = 1,
  n_dim = 3,
  pt_label = NULL,
  cmap = NULL,
```

```

    w = 8,
    h = 5,
    scale.y = 1,
    angle = 40,
    autosave = FALSE,
    ...
)

```

### Arguments

my_distmat	phemdObj object containing sample names in @snames slot
cluster_assignments	Vector containing group assignments for each sample
pt_sz	Size of points representing samples in plot (scaling factor)
n_dim	Number of dimensions for embedding (either 2 or 3)
pt_label	Vector of sample names corresponding to each point (same order as samples in my_distmat and cluster_assignments)
cmap	Vector containing colors by which points should be colored (corresponding to cluster_assignments)
w	Width of plot in inches
h	Height of plot in inches
scale.y	Scaling factor for diffusion map y-axis
angle	Rotation factor for diffusion map plot
autosave	Boolean denoting whether or not to save output diffusion map
...	Additional parameters to be passed to DiffusionMap function

### Details

Requires 'destiny' package

### Value

DiffusionMap object containing biological sample embedding and associated metadata

### Examples

```

my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
my_phemdObj_final <- generateGDM(my_phemdObj_final)
my_EMD_mat <- compareSamples(my_phemdObj_final)
cluster_assignments <- groupSamples(my_EMD_mat, distfun = 'hclust', ncluster=4)
printClusterAssignments(cluster_assignments, my_phemdObj_final, '.', overwrite=TRUE)
dm <- plotGroupedSamplesDmap(my_EMD_mat, cluster_assignments, pt_sz=2)

```

---

plotHeatmaps

*Plot heatmap of cell subtypes*


---

### Description

Takes as input a Phemd object containing either a Monocle2, Seurat, or PHATE object (already embedded and clustered) and plots heatmap characterizing cell subtypes

### Usage

```
plotHeatmaps(
  obj,
  cell_model = c("monocle2", "seurat", "phate"),
  selected_genes = NULL,
  w = 8,
  h = 5,
  ...
)
```

### Arguments

obj	'Phemd' object containing cell-state embedding object
cell_model	Method by which cell state was modeled ("monocle2", "seurat", or "phate")
selected_genes	Vector containing gene names to include in heatmap (optional)
w	Width of plot in inches
h	Height of plot in inches
...	Additional parameters to be passed on to pheatmap function

### Details

embedCells (and orderCellsMonocle if using Monocle2) need to be called before calling this function. Required additional package: 'pheatmap'

### Value

Heatmap containing expression values for each cell subtype. If cell\_model is 'seurat', then returns a list of heatmaps (1 for each batch) that may be subsequently plotted individually

### Examples

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_lg <- selectFeatures(my_phemdObj_lg, selected_genes)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff',
  pseudo_expr=0, sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
```

```
myheatmap <- plotHeatmaps(my_phemdObj_monocle, cell_model='monocle2')
```

---

plotSummaryHistograms *Plots cell subtype frequency histograms summarizing each group of samples*

---

### Description

Visualizes plots of relative frequency ("weights") of cell subtypes ("bins" or "signatures") summarizing each group of single-cell samples. Each summary histogram is computed by taking the bin-wise mean of all samples in the group

### Usage

```
plotSummaryHistograms(
  myobj,
  cluster_assignments,
  cell_model = c("monocle2", "seurat", "phate"),
  cmap = NULL,
  ncol.plot = 4,
  ax.lab.sz = 2.5,
  title.sz = 3
)
```

### Arguments

myobj	Phemd object containing cell subtype relative frequency in @data_cluster_weights slot
cluster_assignments	Vector containing group assignments for each sample in myobj
cell_model	Method by which cell state was modeled (either "monocle2", "seurat", or "phate")
cmap	Vector containing colors by which histogram bars should be colored (optional)
ncol.plot	Number of columns to use to plot multi-panel histogram plot
ax.lab.sz	Scaling factor for axis labels (default 2.5)
title.sz	Scaling factor for plot title (default 3)

### Details

groupSamples must be called before calling this function. Saves plots in directory called "summary\_inhibs"

### Value

None

---

pooledCells	<i>Accessor function for aggregated cells used for cell subtype definition</i>
-------------	--

---

**Description**

Accessor function for aggregated cells used for cell subtype definition

**Usage**

```
pooledCells(obj)
```

**Arguments**

obj	Phemd object
-----	--------------

**Value**

Numeric matrix representing expression data for cells from all experimental conditions (rows = markers, cols = cells)

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
cells_aggregated <- pooledCells(phemdObj)
```

---

printClusterAssignments	<i>Writes samples to file based on community detection group assignments</i>
-------------------------	--

---

**Description**

Takes vector of cluster assignments and phemdObj containing sample names and writes sample groups to file

**Usage**

```
printClusterAssignments(cluster_assignments, obj, dest, overwrite = FALSE)
```

**Arguments**

cluster_assignments	Vector containing group assignments for each sample
obj	phemdObj object containing sample names in @snames slot
dest	Path to existing directory where output should be saved
overwrite	Boolean representing whether or not to overwrite contents of "dest" with output of printClusterAssignments



**Details**

Order of samples in `obj@snames` is assumed to be the same as the order of group assignments in `cluster_assignments`

**Value**

None

**Examples**

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_monocle <- embedCells(my_phemdObj_lg, data_model = 'gaussianff', sigma=0.02, maxIter=2)
my_phemdObj_monocle <- orderCellsMonocle(my_phemdObj_monocle)
my_phemdObj_final <- clusterIndividualSamples(my_phemdObj_monocle)
my_phemdObj_final <- generateGDM(my_phemdObj_final)
my_EMD_mat <- compareSamples(my_phemdObj_final)
cluster_assignments <- groupSamples(my_EMD_mat, distfun = 'hclust', ncluster=4)
printClusterAssignments(cluster_assignments, my_phemdObj_final, '.', overwrite=TRUE)
```

---

rawExpn

*Accessor function for stored multi-sample raw expression data*


---

**Description**

Accessor function for stored multi-sample raw expression data

**Usage**

```
rawExpn(obj)
```

**Arguments**

`obj`                    A Phemd object.

**Value**

List of matrices, each of which represents a single-cell sample

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
raw_expn_data <- rawExpn(phemdObj)
```

---

removeTinySamples      *Remove samples with too few cells*

---

### Description

Removes samples from Phemd that have fewer cells than `min_sz`

### Usage

```
removeTinySamples(obj, min_sz = 20)
```

### Arguments

`obj`                    'Phemd' object containing raw expression data and associated metadata  
`min_sz`                Minimum number of cells in each sample to be retained

### Details

Note: If used, this function must be called before (and not after) the `aggregateSamples` function is called

### Value

'Phemd' object containing raw multi-sample expression data and associated metadata (same as input minus removed samples)

### Examples

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10) #removes samples with fewer than 10 cells
```

---

retrieveRefClusters      *Retrieve reference cell clusters*

---

### Description

Takes initial Phemd struct and returns cell clusters as assigned by clustering algorithm (e.g. PHATE or Monocle2)

### Usage

```
retrieveRefClusters(
  obj,
  cell_model = c("monocle2", "seurat", "phate"),
  expn_type = "reduced",
  ndim = 10
)
```

**Arguments**

obj	Phemd struct containing cell-state embedding object and underlying expression data
cell_model	String representing data model for cell-state space ("seurat", "monocle2", or "phate")
expn_type	String representing whether to return raw expression values or coordinates in dimensionality-reduced feature space
ndim	Number of dimensions in reduced dimensionality space (e.g. PHATE / CCA) to use (only relevant in reduced dimensionality space)

**Details**

Private method (not exported in namespace)

**Value**

List of data matrices; each list element is of size num\_cells\_in\_cluster x num\_markers and represents a distinct cell cluster

**Examples**

```
## Not run:
cluster_expression_data <- retrieveRefClusters(my_phemdObj)

## End(Not run)
```

---

selected_genes	<i>Genes to be used when performing clustering and trajectory analyses on melanoma single-cell RNA-seq expression data</i>
----------------	--

---

**Description**

This object contains genes to be used when performing clustering and trajectory analyses on melanoma single-cell RNA-seq expression data.

**Usage**

```
data(selected_genes)
```

**Format**

Vector of length 44 representing selected genes for performing computational analyses such as generating cell embeddings and clustering cell subtypes.

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE72056>

## References

Tirosh, I. et al. Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. *Science* 352, 189–196 (2016)

---

selectFeatures	<i>Perform feature selection on aggregated data</i>
----------------	---

---

## Description

Takes as input a Phemd object with aggregated data and returns updated object after performing feature selection on aggregated data

## Usage

```
selectFeatures(obj, selected_genes)
```

## Arguments

`obj` 'Phemd' object containing aggregated data  
`selected_genes` Vector containing names of genes to use for downstream analyses

## Details

`aggregateSamples` needs to be called before running this function

## Value

Same as input 'Phemd' object after performing feature-selection based dimensionality reduction on aggregated expression data

## Examples

```
my_phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
my_phemdObj_lg <- removeTinySamples(my_phemdObj, 10)
my_phemdObj_lg <- aggregateSamples(my_phemdObj_lg, max_cells=1000)
my_phemdObj_lg <- selectFeatures(my_phemdObj_lg, selected_genes=c('TP53',
'EGFR', 'KRAS', 'FOXP3', 'LAG3'))
```

---

selectMarkers	<i>Accessor function for gene/protein markers measured in experiment</i>
---------------	--

---

**Description**

Accessor function for gene/protein markers measured in experiment

**Usage**

```
selectMarkers(obj)
```

**Arguments**

obj                    Phemd object

**Value**

Vector representing gene/protein markers corresponding to expression matrices

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
genes <- selectMarkers(phemdObj)
```

---

seuratInfo	<i>Accessor function for stored Seurat object within Phemd object</i>
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**Description**

Accessor function for stored Seurat object within Phemd object

**Usage**

```
seuratInfo(obj)
```

**Arguments**

obj                    A Phemd object.

**Value**

An object of class 'Seurat'

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
seurat_obj <- seuratInfo(phemdObj)
```

---

sNames	<i>Accessor function for identifiers of all single-cell samples in experiment</i>
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**Description**

Accessor function for identifiers of all single-cell samples in experiment

**Usage**

```
sNames(obj)
```

**Arguments**

obj                    Phemd object

**Value**

Vector representing sample names corresponding to expression matrices

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
sampleIDs <- sNames(phemdObj)
```

---

snames_data	<i>Sample names for melanoma single-cell RNA-seq expression data</i>
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---

**Description**

This object contains sample names corresponding to samples contained in melanoma expression data.

**Usage**

```
data("snames_data")
```

**Format**

Vector of length 19 representing sample names corresponding to order of samples in all\_expn\_data in melanomaData dataset.

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE72056>

**References**

Tirosch, I. et al. Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. *Science* 352, 189–196 (2016)

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subsampledBool	<i>Accessor function for whether or not cells were subsampled when aggregated for cell subtype analysis</i>
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---

**Description**

Accessor function for whether or not cells were subsampled when aggregated for cell subtype analysis

**Usage**

```
subsampledBool(obj)
```

**Arguments**

obj                      PheMd object

**Value**

Boolean represent whether or not subsampling was performed in the data aggregation process

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
subsampled <- subsampledBool(phemdObj)
```

---

subsampledIdx	<i>Accessor function for aggregated cells used for cell subtype definition</i>
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**Description**

Accessor function for aggregated cells used for cell subtype definition

**Usage**

```
subsampledIdx(obj)
```

**Arguments**

obj                      PheMd object

**Value**

List of vectors each representing the indices of elements in `rawExpn(obj)` that were subsampled and combined to form "data\_aggregate"

**Examples**

```
phemdObj <- createDataObj(all_expn_data, all_genes, as.character(snames_data))
subsampling_idx_list <- subsamplingIdx(phemdObj)
```



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