

Package ‘SubCellBarCode’

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Type Package

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License GPL-2

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applyThresholdCompartment

Apply thresholds to compartments

Description

Apply thresholds for all predictions to increase the true positive rate and remove poor classification.

Usage

```
applyThresholdCompartment(all.repA, all.repB, threshold.df)
```

Arguments

all.repA data.frame; all predictions and probability vectors for each protein in replicate A
all.repB data.frame; all predictions and probability vectors for each protein in replicate B
threshold.df data.frame; collection of precision and recall values for each compartment

Value

c.cls.df

Examples

```
{  
  df <- loadData(SubCellBarCode::hcc827Ctrl)  
  c.prots <- calculateCoveredProtein(rownames(df), markerProteins[,1])  
  set.seed(7)  
  c.prots <- sample(c.prots, 550)  
  cls <- svmClassification(c.prots, df, markerProteins)  
  test.A <- cls[[1]]$svm.test.prob.out  
  test.B <- cls[[2]]$svm.test.prob.out  
  t.c.df <- computeThresholdCompartment(test.A, test.B)  
  all.A <- cls[[1]]$all.prot.pred  
  all.B <- cls[[2]]$all.prot.pred  
  c.cls.df <- applyThresholdCompartment(all.A, all.B, t.c.df)  
}
```

applyThresholdNeighborhood

Apply thresholds to neighborhood classification

Description

Apply thresholds for all predictions at the neighborhood level to increase the true positive rate and remove poor classification.

Usage

```
applyThresholdNeighborhood(all.repA, all.repB, threshold.df)
```

Arguments

all.repA data.frame; all predictions and probability vectors for each protein in replicate A
 all.repB data.frame; all predictions and probability vectors for each protein in replicate B
 threshold.df data.frame; collection of precision and recall values for each neighborhood

Value

n.cls.df

Examples

```
{
df <- loadData(SubCellBarCode::hcc827Ctrl)

c.prots <- calculateCoveredProtein(rownames(df), markerProteins[,1])

set.seed(7)
c.prots <- sample(c.prots, 600)
cls <- svmClassification(c.prots, df, markerProteins)

test.A <- cls[[1]]$svm.test.prob.out
test.B <- cls[[2]]$svm.test.prob.out

t.n.df <- computeThresholdNeighborhood(test.A, test.B)

all.A <- cls[[1]]$all.prot.pred
all.B <- cls[[2]]$all.prot.pred

n.cls.df <- applyThresholdNeighborhood(all.A, all.B, t.n.df)
}
```

calculateCoveredProtein

Evaluate marker protein coverage

Description

Given the proteomics data, number of overlapped marker proteins is calculated. Bar plot for each compartment is plotted.

Usage

```
calculateCoveredProtein(proteinIDs, markerproteins)
```

Arguments

proteinIDs character; gene symbol id
 markerproteins character; 3365 proteins gene symbol ids

Value

covered.proteins

Examples

```
{  
df <- loadData(SubCellBarCode::hcc827Ctrl)  
  
c.prots <- calculateCoveredProtein(rownames(df), markerProteins[,1])  
}
```

calRowMean

Compute the means of replicates

Description

Duplicated fractions A and B are summarized by taking their mean for each protein. After taking the mean, the data log2 transformed. Further, the 5 main fractions are used to check correlation between input datas. It is a helper function.

Usage

```
calRowMean(d.df)
```

Arguments

d.df data.frame; A data frame of 10 fraction profiles consisting of replicate A and B.

Value

r.df

Examples

```
{  
  
r.df <- calRowMean(SubCellBarCode::hcc827Ctrl)  
  
}
```

`candidateRelocatedProteins`*Identify candidate relocated proteins*

Description

Identify candidate condition-dependent relocated proteins by comparing neighborhood classifications with respect to protein-protein pearson correlation and mininum PSM, peptide spectrum matching, count.

Usage

```
candidateRelocatedProteins(  
  sampleCls1,  
  s1PSM,  
  s1Quant,  
  sampleCls2,  
  s2PSM,  
  s2Quant,  
  annotation = FALSE,  
  min.psm = 2,  
  pearson.cor = 0.8  
)
```

Arguments

| | |
|--------------------------|--|
| <code>sampleCls1</code> | data.frame; merged classification, combination of compartment and neighborhood classification. |
| <code>s1PSM</code> | data.frame; minimum PSM count table across ten TMT channel |
| <code>s1Quant</code> | data.frame; fractionation quantification data |
| <code>sampleCls2</code> | data.frame; merged classification, combination of compartment and neighborhood classification. |
| <code>s2PSM</code> | data.frame; minimum PSM count table across ten TMT channel |
| <code>s2Quant</code> | data.frame; fractionation quantification data |
| <code>annotation</code> | boolean; labeling the selected proteins |
| <code>min.psm</code> | numeric; minimum psm, peptide spectra matching value |
| <code>pearson.cor</code> | numeric; pearson correlation threshold |

Value`candidate.df`

Examples

```
{
  candidate.df <- candidateRelocatedProteins(hcc827GEFClass, hcc827GefPSMCount,
  hcc827GEF, hcc827GEFClass, hcc827GefPSMCount, hcc827GEF,
  annotation = FALSE)
}
```

 compareCls

Compare exon and gene centric classifications

Description

Comparison of the gene centric and exon centric classification. Additionally, correlation analysis is performed using quantification data.

Usage

```
compareCls(geneCls, exonCls)
```

Arguments

| | |
|---------|---|
| geneCls | data frame gene centric classification output |
| exonCls | data frame exon centric classification output |

Value

```
c.df
```

Examples

```
{
  exon.cls <- data.frame(Protein = c("ENSE00000331854",
  "ENSE00000331855",
  "ENSE00000331859"),
  NeighborhoodCls = c("Cytosol",
  "Cytosol",
  "Cytosol"),
  CompartmentCls = c("C1", "C1", "C1"),
  Secretory = c(0.1, 0.1, 0.1),
  Nuclear = c(0.2, 0.2, 0.2),
  Cytosol = c(0.2, 0.2, 0.2),
  Mitochondria = c(0.2, 0.2, 0.2),
  S1 = c(0.2, 0.2, 0.2),
  S2 = c(0.2, 0.2, 0.2),
  S3 = c(0.2, 0.2, 0.2),
```

```

S4 = c(0.2, 0.2, 0.2),
N1 = c(0.2, 0.2, 0.2),
N2 = c(0.2, 0.2, 0.2),
N3 = c(0.2, 0.2, 0.2),
N4 = c(0.2, 0.2, 0.2),
C1 = c(0.2, 0.2, 0.2),
C2 = c(0.2, 0.2, 0.2),
C3 = c(0.2, 0.2, 0.2),
C4 = c(0.2, 0.2, 0.2),
C5 = c(0.2, 0.2, 0.2),
M1 = c(0.2, 0.2, 0.2),
M2 = c(0.2, 0.2, 0.2),
GeneSymbol = c("COPB1", "COPB1", "COPB1"),
PeptideCount = c(2, 4, 7))

gene.cls <- data.frame(Protein = c("COPB1"),
  NeighborhoodCls = c("Cytosol"),
  CompartmentCls = c("C1"),
  Secretory = c(0.1),
  Nuclear = c(0.2),
  Cytosol = c(0.2),
  Mitochondria = c(0.2),
  S1 = c(0.2),
  S2 = c(0.2),
  S3 = c(0.2),
  S4 = c(0.2),
  N1 = c(0.2),
  N2 = c(0.2),
  N3 = c(0.2),
  N4 = c(0.2),
  C1 = c(0.2),
  C2 = c(0.2),
  C3 = c(0.2),
  C4 = c(0.2),
  C5 = c(0.2),
  M1 = c(0.2),
  M2 = c(0.2))

comp.df <- compareCls(gene.cls, exon.cls)

}

```

```
computeThresholdCompartment
```

Probability threshold for compartment classification

Description

Thresholds for each compartment are decided to get confident predictions.

Usage

```
computeThresholdCompartment(test.repA, test.repB)
```

Arguments

| | |
|-----------|---|
| test.repA | data.frame; test predictions, observation and probability vectors for each protein in replicate A |
| test.repB | data.frame; test predictions, observation and probability vectors for each protein in replicate B |

Value

```
threshold.compartment.df
```

Examples

```
{  
  df <- loadData(SubCellBarCode::hcc827Ctrl)  
  
  c.prots <- calculateCoveredProtein(rownames(df), markerProteins[,1])  
  
  set.seed(7)  
  c.prots <- sample(c.prots, 550)  
  cls <- svmClassification(c.prots, df, markerProteins)  
  
  test.A <- cls[[1]]$svm.test.prob.out  
  test.B <- cls[[2]]$svm.test.prob.out  
  
  t.c.df <- computeThresholdCompartment(test.A, test.B)  
}
```

```
computeThresholdNeighborhood
```

Probability threshold for neighborhood classification

Description

Thresholds for each neighborhood are decided to get confident predictions.

Usage

```
computeThresholdNeighborhood(test.repA, test.repB)
```

Arguments

| | |
|-----------|---|
| test.repA | data.frame; test predictions, observation and probability vectors for each protein in replicate A |
| test.repB | data.frame; test predictions, observation and probability vectors for each protein in replicate B |

Value

threshold.neighborhood.df

Examples

```
{  
df <- loadData(SubCellBarCode::hcc827Ctrl)  
  
c.prots <- calculateCoveredProtein(rownames(df), markerProteins[,1])  
  
set.seed(7)  
c.prots <- sample(c.prots, 600)  
cls <- svmClassification(c.prots, df, markerProteins)  
  
test.A <- cls[[1]]$svm.test.prob.out  
test.B <- cls[[2]]$svm.test.prob.out  
  
t.n.df <- computeThresholdNeighborhood(test.A, test.B)  
}
```

convert2symbol

Convert identifier to gene symbol

Description

Identifier for each feature should be converted into gene symbols unless they are not gene symbols

Usage

```
convert2symbol(df, id = "UNIPROT")
```

Arguments

| | |
|----|--|
| df | data.frame; fractionated proteomics data where data contains 10 columns of duplicated 5 fractionations and rownames must be identifier e.g. UNIPROT, Entrez ID |
| id | caharacter; identifier id for each protein |

Value

df

Examples

```
{  
  
df <- data.frame(Uniprot = c("A4D0S4", "A8TX70", "000305", "000337"),  
Organism = rep("Homo Sap.", 4))  
  
rownames(df) <- df$Uniprot  
}
```

| | |
|------------|---------------------------------|
| hcc827Ctrl | <i>HCC827 Control Cell Line</i> |
|------------|---------------------------------|

Description

Subcellular fractionated cell line.

Usage

```
hcc827Ctrl
```

Format

A data frame where 10480 protein gene-centric ids and 5 replicated subcellular fractions.

References

Orre et al. 2019 Cell 73, 1-17

Examples

```
{  
head(hcc827Ctrl)  
}
```

| | |
|--------------------|---|
| hcc827CtrlPSMCount | <i>Minimum PSM Count in HCC827Ctrl Cell Line.</i> |
|--------------------|---|

Description

Minimum PSM, Peptide Sequence Match, Count table for HCC827Ctrl Cell Line.

Usage

```
hcc827CtrlPSMCount
```

Format

A data frame where 10480 protein gene-centric ids minimum PSM count.

References

Orre et al. 2019 Cell 73, 1-17

Examples

```
{  
head(hcc827Ctr1PSMCount)  
}
```

hcc827exon

HCC827 Control Exon Cell Line

Description

Exon-centric sub data of hcc827 fractionated data.

Usage

hcc827exon

Format

A data frame where 500 exon-centric ensemble identifiers, corresponding gene symbols, 5 replicated subcellular fractions and number of unique peptides matched to associated exon.

References

Orre et al. 2019 Cell 73, 1-17

Examples

```
{  
head(hcc827exon)  
}
```

`hcc827GEF`*Gefitinib treated HCC827 Cell Line*

Description

HCC827 cell line was treated with Gefitinib which is EGFR inhibition.

Usage`hcc827GEF`**Format**

A data frame where 10398 protein gene-centric ids and 5 replicated subcellular fractions with duplicates.

References

Orre et al. 2019 Cell 73, 1-17

Examples

```
{  
  head(hcc827GEF)  
}
```

`hcc827GEFClass`*Gefitinib treated HCC827 Cell Line Classification*

Description

Gefitinib treated HCC827 cell line classification contains both neighborhood and compartment level. The data will be used for the relocalization analysis.

Usage`hcc827GEFClass`**Format**

A data frame where 10398 protein gene-centric ids and corresponding compartment and neighborhood classification along with classification probabilities.

References

Orre et al. 2019 Cell 73, 1-17

Examples

```
{  
  head(hcc827GEFC1ass)  
}
```

| | |
|-------------------|---|
| hcc827GefPSMCount | <i>Minimum PSM Count in HCC827 Gefitinib Cell Line.</i> |
|-------------------|---|

Description

Minimum PSM, Peptide Sequence Match, Count table for HCC827 Gefitinib Cell Line.

Usage

```
hcc827GefPSMCount
```

Format

A data frame where 10398 protein gene-centric ids minimum PSM count.

References

Orre et al. 2019 Cell 73, 1-17

Examples

```
{  
  head(hcc827GefPSMCount)  
}
```

| | |
|----------|--|
| loadData | <i>Load the fractionated proteomics data</i> |
|----------|--|

Description

Sampled median normalized TMT ratios are checked if there is any "NA" value. If any, the corresponding row is filtered out. Later, the data is normalized by taking log2.

Usage

```
loadData(protein.data)
```

Arguments

protein.data data.frame; fractionated proteomics data where data contains 10 columns of duplicated 5 fractionations and rownames must be gene-centric protein names

Value

protein.data.df

Examples

```
{  
df <- loadData(SubCellBarCode::hcc827Ctrl[1:20,])  
}
```

| | |
|----------------|-------------------------------|
| markerProteins | <i>Marker Proteins Source</i> |
|----------------|-------------------------------|

Description

Data for the proteins whose localizations were well characterized. It also contains color codes for each compartment and median fractionation profiles for 5 fractions which are Cyto., Nsol., Nucl., Horg., Lorg., with replicates A and B. These fractionation profiles will be used for the marker protein quality control.

Usage

markerProteins

Format

A data frame of 3365 proteins as rows and 13 columns headers.

References

Orre et al. 2019 Cell 73, 1-17

| | |
|----------------------|--|
| markerQualityControl | <i>Evaluate the quality of the marker proteins</i> |
|----------------------|--|

Description

Given the proteomics data, quality of the overlapped marker proteins are evaluated by correlating replicates of fractions.

Usage

markerQualityControl(coveredProteins, protein.data)

Arguments

`coveredProteins` character; list of marker proteins, gene symbols, that are covered in 3365 marker proteins.

`protein.data` data.frame; fractionated proteomics data, rownames are gene symbols associated protein.

Value

`robustMarkers`

Examples

```
{
df <- loadData(SubCellBarCode::hcc827Ctrl)
c.prots <- calculateCoveredProtein(rownames(df), markerProteins[,1])
r.markers <- markerQualityControl(c.prots[1:5], df)
}
```

`mergeCls`

Merge compartment and neighborhood classification

Description

Compartment and neighborhood classifications are merged for the single output.

Usage

```
mergeCls(compartmentCls, neighborhoodCls)
```

Arguments

`compartmentCls` data.frame; all predictions, including unclassified as well, and probability vectors for each protein in compartment classification

`neighborhoodCls` data.frame; all predictions, including unclassified as well, and probability vectors for each protein in neighborhood classification

Value

`cls.df`

Examples

```
{  
  
  #create mock data  
  com.df <- data.frame(Proteins = "TP53",  
    svm.pred = "N1",  
    S1 = as.numeric(0.02),  
    S2 = as.numeric(0.02),  
    S3 = as.numeric(0.02),  
    S4 = as.numeric(0.02),  
    N1 = as.numeric(0.72),  
    N2 = as.numeric(0.02),  
    N3 = as.numeric(0.02),  
    N4 = as.numeric(0.02),  
    C1 = as.numeric(0.02),  
    C2 = as.numeric(0.02),  
    C3 = as.numeric(0.02),  
    C4 = as.numeric(0.02),  
    C5 = as.numeric(0.02),  
    M1 = as.numeric(0.02),  
    M2 = as.numeric(0.02))  
  
  rownames(com.df) <- "TP53"  
  
  neig.df <- data.frame(Proteins = "TP53",  
    svm.pred.all = "Nuclear",  
    Secretary = as.numeric(0.01),  
    Nuclear = as.numeric(0.95),  
    Cytosol = as.numeric(0.02),  
    Mitochondria = as.numeric(0.02))  
  
  rownames(neig.df) <- "TP53"  
  
  cls.df <- mergeCls(com.df, neig.df)  
  
}
```

mergeProbability*Merge compartment probabilities to neighborhood probabilities*

Description

Compartment levels classifications are summed up to associated neighborhood levels. It is a helper function.

Usage

```
mergeProbability(df)
```

Arguments

df data.frame; all predictions at the neighborhood level and probability vectors for each protein

Value

merged.df

Examples

```
{  
  
#create mock data  
df <- data.frame(Protein = "TP53",  
S1 = as.numeric(0.02),  
S2 = as.numeric(0.02),  
S3 = as.numeric(0.02),  
S4 = as.numeric(0.02),  
N1 = as.numeric(0.72),  
N2 = as.numeric(0.02),  
N3 = as.numeric(0.02),  
N4 = as.numeric(0.02),  
C1 = as.numeric(0.02),  
C2 = as.numeric(0.02),  
C3 = as.numeric(0.02),  
C4 = as.numeric(0.02),  
C5 = as.numeric(0.02),  
M1 = as.numeric(0.02),  
M2 = as.numeric(0.02))  
  
rownames(df) <- "TP53"  
  
merged.df <- mergeProbability(df)  
  
}
```

plotBarcode

Visualize the SubCellBarCode

Description

Stacked bar plot are plotted for compartment and neighborhood level with respect to classification probabilities.

Usage

```
plotBarcode(sampleClassification, protein, s1PSM)
```

Arguments

| | |
|----------------------|--|
| sampleClassification | data.frame; merged classification, combination of compartment and neighborhood classification. |
| protein | character; protein gene symbol name |
| s1PSM | data.frame; minimum PSM count table. Row names should be gene centric protein id. |

Value

proteinPlot

Examples

```
{
#create mock data
plot.df <- data.frame(Protein = "TP53",
NeighborhoodCls = "Nuclear",
CompartmentCls = "N1",
Secretory = as.numeric(0.01),
Nuclear = as.numeric(0.95),
Cytosol = as.numeric(0.02),
Mitochondria = as.numeric(0.02),
S1 = as.numeric(0.02),
S2 = as.numeric(0.02),
S3 = as.numeric(0.02),
S4 = as.numeric(0.02),
N1 = as.numeric(0.72),
N2 = as.numeric(0.02),
N3 = as.numeric(0.02),
N4 = as.numeric(0.02),
C1 = as.numeric(0.02),
C2 = as.numeric(0.02),
C3 = as.numeric(0.02),
C4 = as.numeric(0.02),
C5 = as.numeric(0.02),
M1 = as.numeric(0.02),
M2 = as.numeric(0.02))

rownames(plot.df) <- "TP53"

psm.df <- data.frame(Protein = "TP53",
PSMs.for.quant = as.numeric(31))

rownames(psm.df) <- "TP53"

proteinPlot <- plotBarcode(plot.df, "TP53", psm.df)
}
```

plotMultipleProtein *Visualization of multiple protein localizations*

Description

Distributions of subcellular localizations of multiple proteins both at the compartment and neighborhood level are plotted.

Usage

```
plotMultipleProtein(sampleClassification, proteinList)
```

Arguments

sampleClassification data.frame; merged classification, combination of compartment and neighborhood classifications per protein.

proteinList vector; protein gene symbol names.

Value

multipleProt.df

Examples

```
{
  proteasome26s <- c("PSMA7", "PSMC3", "PSMB1", "PSMA1", "PSMA3", "PSMA4",
    "PSMA5", "PSMB4", "PSMB6", "PSMB5", "PSMC2", "PSMC4", "PSMB3", "PSMB2",
    "PSMD4", "PSMA6", "PSMC1", "PSMC5", "PSMC6", "PSMB7", "PSMD13")

  exp.cls.df <- SubCellBarCode::hcc827GEFCClass

  multipleProt.df <- plotMultipleProtein(exp.cls.df, proteasome26s )
}
```

replacePrediction *Replace compartment predictions to neighborhood predictions*

Description

Compartment level classifications are replaced with neighborhood level assignment. It is a helper function.

Usage

```
replacePrediction(df, column = c("svm.pred.all", "Observation", "svm.pred"))
```

Arguments

`df` data.frame; all predictions at the compartment level and probability vectors for each protein

`column` character; selected column in the data frame, `df`

Value

replaced.df

Examples

```
{
#define mock data frame
df <- data.frame(svm.pred.all = c("S1","S2","S3","S4",
"N1","N2","N3","N4",
"C1","C2","C3","C4","C5",
"M1","M2"))

df$svm.pred.all <- as.character(df$svm.pred.all)
df$Prob <- "1"

df <- replacePrediction(df, column = "svm.pred.all")
}
```

sankeyPlot

Sankey plot for condition-dependent protein relocation

Description

Identify candidate condition-dependent relocated proteins by comparing neighborhood classifications.

Usage

```
sankeyPlot(sampleCls1, sampleCls2)
```

Arguments

`sampleCls1` data.frame; merged classification, combination of compartment and neighborhood classification.

`sampleCls2` data.frame; merged classification, combination of compartment and neighborhood classification.

Value

label.link.df

Examples

```
{  
  exp.cls.df <- SubCellBarCode::hcc827GEFCClass  
  sankeyData <- sankeyPlot(exp.cls.df, exp.cls.df)  
}
```

| | |
|----------------|--|
| sumProbability | <i>Sum compartment test data probabilities to neighborhood probabilities</i> |
|----------------|--|

Description

Compartment levels classifications on the test data are summed up to associated neighborhood levels. It is a helper function.

Usage

```
sumProbability(df)
```

Arguments

df data.frame; test data classifications at the neighborhood level and probability vectors for each protein.

Value

summed.df

Examples

```
{  
  
  #create mock data  
  df <- data.frame(Protein = "TP53",  
    svm.pred = "N1",  
    S1 = as.numeric(0.02),  
    S2 = as.numeric(0.02),  
    S3 = as.numeric(0.02),  
    S4 = as.numeric(0.02),  
    N1 = as.numeric(0.72),  
    N2 = as.numeric(0.02),  
    N3 = as.numeric(0.02),
```

```
N4 = as.numeric(0.02),
C1 = as.numeric(0.02),
C2 = as.numeric(0.02),
C3 = as.numeric(0.02),
C4 = as.numeric(0.02),
C5 = as.numeric(0.02),
M1 = as.numeric(0.02),
M2 = as.numeric(0.02))

rownames(df) <- "TP53"

sum.df <- sumProbability(df)

}
```

| | |
|-------------------|--|
| svmClassification | <i>Protein subcellular localization classification</i> |
|-------------------|--|

Description

Support Vector Machine classifier is trained and used for prediction of protein subcellular localization

Usage

```
svmClassification(markerProteins, protein.data, markerprot.df)
```

Arguments

markerProteins character; robust marker proteins along with subcellular localization that are present in the given data.

protein.data data.frame; fractionated proteomics data

markerprot.df data.frame; collection of marker proteins along with corresponding subcellular localization

Value

all.classifications

Examples

```
{

df <- loadData(SubCellBarCode::hcc827Ctrl)

c.prots <- calculateCoveredProtein(rownames(df), markerProteins[,1])

set.seed(7)
c.prots <- sample(c.prots, 500)
```

```
cls <- svmClassification(c.prots, df, markerProteins)
}
```

svmExternalData

Peptide/exon/transcript centric or PTM enriched classification

Description

Peptide/exon/transcript centric or PTM enriched classification is applied to predict localization of them.

Usage

```
svmExternalData(df, modelA, modelB)
```

Arguments

| | |
|--------|--|
| df | data frame fractionated additional data |
| modelA | model for the replicate A classification |
| modelB | model for the replicate B classification |

Value

c.cls.df

Examples

```
{
df <- loadData(SubCellBarCode::hcc827Ctrl)

c.prots <- calculateCoveredProtein(rownames(df), markerProteins[,1])

set.seed(7)
c.prots <- sample(c.prots, 550)
cls <- svmClassification(c.prots, df, markerProteins)
modelA <- cls[[1]]$model
modelB <- cls[[2]]$model

exon.cls <- svmExternalData(SubCellBarCode::hcc827exon,
modelA = modelA, modelB = modelB)
}
```

| | |
|-------------------|--|
| tsneVisualization | <i>Visualization of marker proteins by t-SNE map</i> |
|-------------------|--|

Description

The marker proteins are visualized in 3D t-SNE map to see the distributions of the marker proteins.

Usage

```
tsneVisualization(protein.data, markerProteins, dims, theta, perplexity)
```

Arguments

| | |
|----------------|--|
| protein.data | data.frame; fractionated proteomics data |
| markerProteins | character; robust marker proteins, gene symbols, that are present in the given data and overlapped with package's marker protein list. |
| dims | integer; dimensionality |
| theta | numeric; Speed/accuracy trade-off ,increase for less accuracy |
| perplexity | integer; Perplexity parameter |

Value

tsneMap.df

Examples

```
{  
  
df <- loadData(SubCellBarCode::hcc827Ctrl)  
  
c.prots <- calculateCoveredProtein(rownames(df), markerProteins[,1])  
  
set.seed(21)  
tsneMap.df <- tsneVisualization(protein.data = df,  
markerProteins = c.prots[1:20],  
dims = 2, theta = c(0.4), perplexity = c(5))  
}
```

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