

# Package ‘SubCellBarCode’

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**Type** Package

**Title** SubCellBarCode: Integrated workflow for robust mapping and visualizing whole human spatial proteome

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**Description** Mass-Spectrometry based spatial proteomics have enabled the proteome-wide mapping of protein subcellular localization (Orre et al. 2019, Molecular Cell). SubCellBarCode R package robustly classifies proteins into corresponding subcellular localization.

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## R topics documented:

<code>applyThresholdCompartment</code> . . . . .	2
<code>applyThresholdNeighborhood</code> . . . . .	3
<code>calculateCoveredProtein</code> . . . . .	4
<code>calRowMean</code> . . . . .	5
<code>candidateRelocatedProteins</code> . . . . .	5

compareCls . . . . .	6
computeThresholdCompartment . . . . .	8
computeThresholdNeighborhood . . . . .	9
convert2symbol . . . . .	9
hcc827Ctrl . . . . .	10
hcc827CtrlPSMCount . . . . .	11
hcc827exon . . . . .	11
hcc827GEF . . . . .	12
hcc827GEFClass . . . . .	12
hcc827GefPSMCount . . . . .	13
loadData . . . . .	13
markerProteins . . . . .	14
markerQualityControl . . . . .	14
mergeCls . . . . .	15
mergeProbability . . . . .	16
plotBarcode . . . . .	17
plotMultipleProtein . . . . .	18
replacePrediction . . . . .	19
sankeyPlot . . . . .	20
sumProbability . . . . .	20
svmClassification . . . . .	21
svmExternalData . . . . .	22
tsneVisualization . . . . .	23
<b>Index</b>	<b>24</b>

---

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	<i>Compute the means of replicates</i>
------------	--

---

**Description**

Duplicated fractions A and B are summarized by taking their mean for each protein. After taking the mean, the data log<sub>2</sub> 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	<i>Identify candidate relocated proteins</i>
----------------------------	--

---

**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**

sampleCls1	data.frame; merged classification, combination of compartment and neighborhood classification.
s1PSM	data.frame; minimum PSM count table across ten TMT channel
s1Quant	data.frame; fractionation quantification data
sampleCls2	data.frame; merged classification, combination of compartment and neighborhood classification.
s2PSM	data.frame; minimum PSM count table across ten TMT channel
s2Quant	data.frame; fractionation quantification data
annotation	boolean; labeling the selected proteins
min.psm	numeric; minimum psm, peptide spectra matching value
pearson.cor	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"),
                        Secretary = 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"),
                        Secretary = 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

*HCC827 Control Cell Line*

---

**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(hcc827CtrlPSMCount)  
}
```

---

hcc827exon	<i>HCC827 Control Exon Cell Line</i>
------------	--------------------------------------

---

**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(hcc827GEFClass)  
}
```

---

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      *Marker Proteins Source*

---

### 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      *Evaluate the quality of the marker proteins*

---

### 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	<i>Replace compartment predictions to neighborhood predictions</i>
-------------------	--

---

### 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	<i>Sankey plot for condition-dependent protein relocation</i>
------------	---

---

**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***Protein subcellular localization classification*

---

**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, 500)
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))
}

```

# Index

## \* datasets

- [hcc827Ctrl](#), [10](#)
- [hcc827CtrlPSMCount](#), [11](#)
- [hcc827exon](#), [11](#)
- [hcc827GEF](#), [12](#)
- [hcc827GEFClass](#), [12](#)
- [hcc827GefPSMCount](#), [13](#)
- [markerProteins](#), [14](#)

- [applyThresholdCompartment](#), [2](#)
- [applyThresholdNeighborhood](#), [3](#)

- [calculateCoveredProtein](#), [4](#)
- [calRowMean](#), [5](#)
- [candidateRelocatedProteins](#), [5](#)
- [compareCls](#), [6](#)
- [computeThresholdCompartment](#), [8](#)
- [computeThresholdNeighborhood](#), [9](#)
- [convert2symbol](#), [9](#)

- [hcc827Ctrl](#), [10](#)
- [hcc827CtrlPSMCount](#), [11](#)
- [hcc827exon](#), [11](#)
- [hcc827GEF](#), [12](#)
- [hcc827GEFClass](#), [12](#)
- [hcc827GefPSMCount](#), [13](#)

- [loadData](#), [13](#)

- [markerProteins](#), [14](#)
- [markerQualityControl](#), [14](#)
- [mergeCls](#), [15](#)
- [mergeProbability](#), [16](#)

- [plotBarcode](#), [17](#)
- [plotMultipleProtein](#), [18](#)

- [replacePrediction](#), [19](#)

- [sankeyPlot](#), [20](#)
- [sumProbability](#), [20](#)
- [svmClassification](#), [21](#)
- [svmExternalData](#), [22](#)

- [tsneVisualization](#), [23](#)