

# Package ‘MiPP’

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**Title** Misclassification Penalized Posterior Classification

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**Depends** R (>= 2.4)

**Imports** Biobase, e1071, MASS, stats

**Description** This package finds optimal sets of genes that separate samples into two or more classes.

**License** GPL (>= 2)

**URL** <http://www.healthsystem.virginia.edu/internet/hes/biostat/bioinformatics/>

**biocViews** Microarray, Classification

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|       |                                              |
|-------|----------------------------------------------|
| colon | <i>Gene expression data for colon cancer</i> |
|-------|----------------------------------------------|

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**Description**

This data set consists of gene expression of colon cancer study.

**Usage**

data(colon)

**Format**

A matrix containing 2000 probe sets and 2 classes (T, F)

**Source**

Alon, U., Barkai, N., Notterman, D.A., Gish, K., Ybarra, S., Mack, D., Levine, A.J. (1999). Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues probed by Oligonucleotide Arrays, PNAS, 96(12), 6745–6750.

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|              |                                      |
|--------------|--------------------------------------|
| cv.mipp.rule | <i>Fitting cross-validation MiPP</i> |
|--------------|--------------------------------------|

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**Description**

Fits cross-validation MiPP

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|          |                        |
|----------|------------------------|
| get.mipp | <i>Choosing a rule</i> |
|----------|------------------------|

---

**Description**

Choose a rule to compute MiPP

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|              |                                    |
|--------------|------------------------------------|
| get.mipp.lda | <i>Fitting LDA to compute MiPP</i> |
|--------------|------------------------------------|

---

**Description**

Fits LDA to compute MiPP

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|                   |                                               |
|-------------------|-----------------------------------------------|
| get.mipp.logistic | <i>Fitting logistic model to compute MiPP</i> |
|-------------------|-----------------------------------------------|

---

**Description**

Fits logistic model to compute MiPP

---

|              |                                    |
|--------------|------------------------------------|
| get.mipp.qda | <i>Fitting QDA to compute MiPP</i> |
|--------------|------------------------------------|

---

**Description**

Fits QDA to compute MiPP

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|                     |                                             |
|---------------------|---------------------------------------------|
| get.mipp.svm.linear | <i>Fitting SVM (linear) to compute MiPP</i> |
|---------------------|---------------------------------------------|

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**Description**

Fits SVM (linear) to compute MiPP

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|                  |                                          |
|------------------|------------------------------------------|
| get.mipp.svm.rbf | <i>Fitting SVM (RBF) to compute MiPP</i> |
|------------------|------------------------------------------|

---

**Description**

Fits SVM (RBF) to compute MiPP

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|       |                                          |
|-------|------------------------------------------|
| leuk1 | <i>Gene expression data for leukemia</i> |
|-------|------------------------------------------|

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**Description**

This data set consists of gene expression of leukemia study.

**Usage**

```
data(leukemia)
```

**Format**

A matrix containing 6817 probe sets and 38 samples (2 classes: AML, ALL)

**Source**

Golub, T.R., Slonim, D.K., Tamayo, P., Huard, C., Gaasenbeek, M., Mesirov, P., Coller, H., Loh, M.L., Downing, J.R., Caliguri, M.A., Bloomfield, C.D., and Lander, E.S. (1999) Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science*, 286, 531-537.

---

|       |                                          |
|-------|------------------------------------------|
| leuk2 | <i>Gene expression data for leukemia</i> |
|-------|------------------------------------------|

---

**Description**

This data set consists of gene expression of leukemia study.

**Usage**

```
data(leukemia)
```

**Format**

A matrix containing 6817 probe sets and 34 samples (2 classes: AML, ALL)

**Source**

Golub, T.R., Slonim, D.K., Tamayo, P., Huard, C., Gaasenbeek, M., Mesirov, P., Coller, H., Loh, M.L., Downing, J.R., Caliguri, M.A., Bloomfield, C.D., and Lander, E.S. (1999) Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science*, 286, 531-537.

leukemia

*Gene expression data for leukemia***Description**

This data set consists of gene expression of leukemia study.

**Usage**

```
data(leukemia)
```

**Format**

A matrix containing 6817 probe sets and 2 classes (AML, ALL)

**Source**

Golub, T.R., Slonim, D.K., Tamayo, P., Huard, C., Gaasenbeek, M., Mesirov, P., Coller, H., Loh, M.L., Downing, J.R., Caliguri, M.A., Bloomfield, C.D., and Lander, E.S. (1999) Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science*, 286, 531-537.

```
linearkernel.decision.function
```

*SVM (linear) kernel to compute MiPP*

**Description**

SVM (linear) kernel to compute MiPP

mipp

*MiPP-based Classification***Description**

Finds optimal sets of genes for classification

**Usage**

```
mipp(x, y, x.test = NULL, y.test = NULL, probe.ID = NULL,
      rule = "lda", method.cut = "t.test", percent.cut = 0.01,
      model.sMiPP.margin = 0.01, min.sMiPP = 0.85, n.drops = 2,
      n.fold = 5, p.test = 1/3, n.split = 20,
      n.split.eval = 100)
```

**Arguments**

|                                 |                                                                                                                   |
|---------------------------------|-------------------------------------------------------------------------------------------------------------------|
| <code>x</code>                  | data matrix                                                                                                       |
| <code>y</code>                  | class vector                                                                                                      |
| <code>x.test</code>             | test data matrix if available                                                                                     |
| <code>y.test</code>             | test class vector if available                                                                                    |
| <code>probe.ID</code>           | probe set IDs; if NULL, row numbers are assigned.                                                                 |
| <code>rule</code>               | classification rule: "lda", "qda", "logistic", "svmlin", "svmrbf"; the default is "lda".                          |
| <code>method.cut</code>         | method for pre-selection; t-test is available.                                                                    |
| <code>percent.cut</code>        | proportion of pre-selected genes; the default is 0.01.                                                            |
| <code>model.sMiPP.margin</code> | smallest set of genes s.t. $sMiPP \leq (\max sMiPP - \text{model.sMiPP.margin})$ ; the default is 0.01.           |
| <code>min.sMiPP</code>          | Adding genes stops if max sMiPP is at least min.sMiPP; the default is 0.85.                                       |
| <code>n.drops</code>            | Adding genes stops if sMiPP decreases (n.drops) times, in addition to min.sMiPP criterion.; the default is 2.     |
| <code>n.fold</code>             | number of folds; default is 5.                                                                                    |
| <code>p.test</code>             | partition percent of train and test samples when test samples are not available; the default is 1/3 for test set. |
| <code>n.split</code>            | number of splits; the default is 20.                                                                              |
| <code>n.split.eval</code>       | numbr of splits for evalutation; the default is 100.                                                              |

**Value**

|                         |                                                                     |
|-------------------------|---------------------------------------------------------------------|
| <code>model</code>      | candiadate genes (for each split if no indep set is available)      |
| <code>model.eval</code> | Optimal sets of genes for each split when no indep set is available |

**Author(s)**

Soukup M, Cho H, and Lee JK

**References**

Soukup M, Cho H, and Lee JK (2005). Robust classification modeling on microarray data using misclassification penalized posterior, *Bioinformatics*, 21 (Suppl): i423-i430.

Soukup M and Lee JK (2004). Developing optimal prediction models for cancer classification using gene expression data, *Journal of Bioinformatics and Computational Biology*, 1(4) 681-694

**Examples**

```
#####
#Example 1: When an independent test set is available

data(leukemia)

#Normalize combined data
leukemia <- cbind(leuk1, leuk2)
leukemia <- mipp.preproc(leukemia, data.type="MAS4")

#Train set
```

```

x.train <- leukemia[,1:38]
y.train <- factor(c(rep("ALL",27),rep("AML",11)))

#Test set
x.test <- leukemia[,39:72]
y.test <- factor(c(rep("ALL",20),rep("AML",14)))

#Compute MiPP
out <- mipp(x=x.train, y=y.train, x.test=x.test, y.test=y.test, probe.ID = 1:nrow(x.train), n.fold=5, percent.

#Print candidate models
out$model

#####
#Example 2: When an independent test set is not available

data(colon)

#Normalize data
x <- mipp.preproc(colon)
y <- factor(c("T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
              "T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
              "T", "N", "T", "N", "T", "T", "T", "T", "T", "T",
              "T", "T", "T", "T", "T", "T", "T", "T", "N", "T",
              "T", "N", "N", "T", "T", "T", "T", "N", "T", "N",
              "N", "T", "T", "N", "N", "T", "T", "T", "T", "N",
              "T", "N"))

#Deleting contaminated chips
x <- x[,-c(51,55,45,49,56)]
y <- y[ -c(51,55,45,49,56)]

#Compute MiPP
out <- mipp(x=x, y=y, probe.ID = 1:nrow(x), n.fold=5, p.test=1/3, n.split=5, n.split.eval=100,
percent.cut= 0.1, rule="lda")

#Print candidate models for each split
out$model

#Print optimal models and independent evaluation for each split
out$model.eval

```

---

mipp.preproc

Preprocessing

---

## Description

Performs IQR normalization, thesholding, and log2-transformation

Usage

```
mipp.preproc(x, data.type = "MAS5")
```

Arguments

|           |                                   |
|-----------|-----------------------------------|
| x         | data                              |
| data.type | data type is MAS5, MAS4, or dChip |

See Also

[mipp](#)

Examples

```
library(MiPP)

data(colon)
colon.nor <- mipp.preproc(colon)
```

---

|           |                       |
|-----------|-----------------------|
| mipp.rule | <i>Computing MiPP</i> |
|-----------|-----------------------|

---

Description

Computes MiPP

---

|          |                                  |
|----------|----------------------------------|
| mipp.seq | <i>MiPP-based Classification</i> |
|----------|----------------------------------|

---

Description

sequentially finds optimal sets of genes for classification

Usage

```
mipp.seq(x, y, x.test = NULL, y.test = NULL, probe.ID = NULL,
rule = "lda", method.cut = "t.test", percent.cut = 0.01,
model.sMiPP.margin = 0.01, min.sMiPP = 0.85, n.drops = 2,
n.fold = 5, p.test = 1/3, n.split = 20, n.split.eval = 100,
n.seq=3, cutoff.sMiPP=0.7, remove.gene.each.model="all")
```



**Arguments**

|                                     |                                                                                                                               |
|-------------------------------------|-------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>                      | data matrix                                                                                                                   |
| <code>y</code>                      | class vector                                                                                                                  |
| <code>x.test</code>                 | test data matrix if available                                                                                                 |
| <code>y.test</code>                 | test class vector if available                                                                                                |
| <code>probe.ID</code>               | probe set IDs; if NULL, row numbers are assigned.                                                                             |
| <code>rule</code>                   | classification rule: "lda", "qda", "logistic", "svmlin", "svmrbf"; the default is "lda".                                      |
| <code>method.cut</code>             | method for pre-selection; t-test is available.                                                                                |
| <code>percent.cut</code>            | proportion of pre-selected genes; the default is 0.01.                                                                        |
| <code>model.sMiPP.margin</code>     | smallest set of genes s.t. $sMiPP \leq (\max sMiPP - model.sMiPP.margin)$ ; the default is 0.01.                              |
| <code>min.sMiPP</code>              | Adding genes stops if max sMiPP is at least min.sMiPP; the default is 0.85.                                                   |
| <code>n.drops</code>                | Adding genes stops if sMiPP decreases (n.drops) times, in addition to min.sMiPP criterion.; the default is 2.                 |
| <code>n.fold</code>                 | number of folds; default is 5.                                                                                                |
| <code>p.test</code>                 | partition percent of train and test samples when test samples are not available; the default is 1/3 for test set.             |
| <code>n.split</code>                | number of splits; the default is 20.                                                                                          |
| <code>n.split.eval</code>           | numbr of splits for evaluation; the default is 100.                                                                           |
| <code>n.seq</code>                  | Number of sequential gene model selection; the default is 3.                                                                  |
| <code>cutoff.sMiPP</code>           | Cutoff point of 5 percent sMiPP to select gene models                                                                         |
| <code>remove.gene.each.model</code> | Re-run after removing all genes in the selected models if "all" and the first gene for each of the selected models if "first" |

**Value**

|                             |                                                                     |
|-----------------------------|---------------------------------------------------------------------|
| <code>model</code>          | candiadate genes (for each split if no indep set is available)      |
| <code>model.eval</code>     | Optimal sets of genes for each split when no indep set is available |
| <code>genes.selected</code> | a list of genes selected by sequential selection                    |

**Author(s)**

Soukup M, Cho H, and Lee JK

**References**

- Soukup M, Cho H, and Lee JK (2005). Robust classification modeling on microarray data using misclassification penalized posterior, *Bioinformatics*, 21 (Suppl): i423-i430.
- Soukup M and Lee JK (2004). Developing optimal prediction models for cancer classification using gene expression data, *Journal of Bioinformatics and Computational Biology*, 1(4) 681-694

## Examples

```
#####
#Example 1: When an independent test set is available

data(leukemia)

#Normalize combined data
leukemia <- cbind(leuk1, leuk2)
leukemia <- mipp.preproc(leukemia, data.type="MAS4")

#Train set
x.train <- leukemia[,1:38]
y.train <- factor(c(rep("ALL",27),rep("AML",11)))

#Test set
x.test <- leukemia[,39:72]
y.test <- factor(c(rep("ALL",20),rep("AML",14)))

#Compute MiPP
out <- mipp.seq(x=x.train, y=y.train, x.test=x.test, y.test=y.test, n.fold=5, percent.cut=0.01, rule="lda", n

#Print candidate models
out$model

#Print the genes selected
out$genes.selected

#####
#Example 2: When an independent test set is not available

data(colon)

#Normalize data
x <- mipp.preproc(colon)
y <- factor(c("T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
              "T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
              "T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
              "T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
              "T", "N", "T", "N", "T", "N", "T", "N", "T", "N",
              "T", "N"))

#Deleting contaminated chips
x <- x[,-c(51,55,45,49,56)]
y <- y[ -c(51,55,45,49,56)]

#Compute MiPP
out <- mipp.seq(x=x, y=y, n.fold=5, p.test=1/3, n.split=5, n.split.eval=100,
percent.cut= 0.05, rule="lda", n.seq=2)

#Print candidate models for each split
out$model
```

```
#Print optimal models and independent evaluation for each split
out$model.eval
```

```
#Print the genes selected
out$genes.selected
```

---

|            |                      |
|------------|----------------------|
| pre.select | <i>Pre-selection</i> |
|------------|----------------------|

---

### Description

Pre-select genes

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|              |                               |
|--------------|-------------------------------|
| quant.normal | <i>Quantile normalization</i> |
|--------------|-------------------------------|

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### Description

Performs quantile normalization

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|               |                               |
|---------------|-------------------------------|
| quant.normal2 | <i>Quantile normalization</i> |
|---------------|-------------------------------|

---

### Description

Performs quantile normalization

---

|                             |                                         |
|-----------------------------|-----------------------------------------|
| rbfkernel.decision.function | <i>SVM (RBF) kernel to compute MiPP</i> |
|-----------------------------|-----------------------------------------|

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### Description

SVM (RBF) kernel to compute MiPP

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