

# Package ‘PSEA’

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**Title** Population-Specific Expression Analysis.

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**Imports** Biobase, MASS

**Suggests** BiocStyle

**Description** Deconvolution of gene expression data by  
Population-Specific Expression Analysis (PSEA).

**biocViews** Software

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## R topics documented:

coefmat . . . . .	2
crplot . . . . .	3
em_quantvg . . . . .	5
expression . . . . .	7
expression_GSE19380 . . . . .	8
fmm . . . . .	8
groups . . . . .	9
information . . . . .	10
lmfitst . . . . .	10
marker . . . . .	13
pvalmat . . . . .	14

slt . . . . .	16
swlm . . . . .	17

<b>Index</b>	<b>19</b>
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coefmat	<i>Extracts fitted coefficients.</i>
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## Description

Takes a list of fitted models (lm objects) and returns coefficients in matrix format.

## Usage

```
coefmat(lst, regressors)
```

## Arguments

lst	list of lm objects.
regressors	character vector. Names of the coefficients to extract.

## Details

Simple wrapper function that returns fitted coefficients.

The names of the coefficient to extract are matched in `names(lst[[i]]$coef)`.

The column in the matrix of extracted coefficients are named by prepending "coef." to the regressor names.

## Value

coefm	numeric matrix. Matrix of extracted coefficients with one row for each model in the list and one column for each targeted coefficient.
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## Author(s)

Alexandre Kuhn <alexandre.m.kuhn@gmail.com>

## See Also

[pvalmat](#).

**Examples**

```
## Load example expression data (variable "expression")
## and phenotype data (variable "groups")
data("example")

## Four cell population-specific reference signals
neuron_probesets <- list(c("221805_at", "221801_x_at", "221916_at"),
                        "201313_at", "210040_at", "205737_at", "210432_s_at")
neuron_reference <- marker(expression, neuron_probesets)

astro_probesets <- list("203540_at",c("210068_s_at", "210906_x_at"),
                        "201667_at")
astro_reference <- marker(expression, astro_probesets)

oligo_probesets <- list(c("211836_s_at", "214650_x_at"), "216617_s_at",
                        "207659_s_at", c("207323_s_at", "209072_at"))
oligo_reference <- marker(expression, oligo_probesets)

micro_probesets <- list("204192_at", "203416_at")
micro_reference <- marker(expression, micro_probesets)

## Stepwise model selection for 2 transcripts (202429_s_at and
## 200850_s_at) and focusing on control samples (i.e. groups == 0)
lmlist <- swlm(expression[c("202429_s_at", "200850_s_at"),],
              subset = which(groups == 0),
              upper = formula(~neuron_reference + astro_reference +
                              oligo_reference + micro_reference))

coefmat(lmlist, c("(Intercept)", "neuron_reference", "astro_reference",
                 "oligo_reference", "micro_reference"))
```

---

crplot

*Component-plus-residual (CR) plot*


---

**Description**

Component-plus-residual (CR) plot for quantitative variables and group-specific effects.

**Usage**

```
crplot(lm, quantv, g=NULL, newplot=TRUE, col=c(1, 2, 4), xlab=NULL, ylab='CR', ...)
```

**Arguments**

lm	object of class "lm". Fitted model.
quantv	character. Name of the quantitative independent variable ("component" to be plotted).
g	character vector. Interaction regressors coding for group-specific effects in the model.

newplot	logical. If TRUE (default) a new plot (graphics device) is opened.
col	integer vector. Colors of groups. Defaults to 1 (black), 2 (red) and 4 (blue) for group 1, 2 and 3, respectively.
xlab	character. x-axis label. Absent by default.
ylab	character. y-axis label. "CR" by default.
...	Further arguments passed to plot()

### Details

In the fitted model (lm), group-specific effects are specified by interaction regressors. In this case, an interaction regressor is a quantitative variable multiplied by a binary variable (i.e. where 0s represent samples of group 1 and 1s represent samples of group 2).

Predicted components are not centered and the intercept of the CR is 0 by definition. This function thus differs from cr.plot in the car package.

### Value

NULL This function is used for plotting.

### Author(s)

Alexandre Kuhn <alexandre.m.kuhn@gmail.com>

### References

Kuhn A, Thu D, Waldvogel HJ, Faull RL, Luthi-Carter R. Population-specific expression analysis (PSEA) reveals molecular changes in diseased brain. Nat Methods 2011, 8(11):945-7

### Examples

```
## Load example expression data (variable "expression")
## for 23 transcripts and 41 samples, and associated
## phenotype (i.e. group) information (variable "groups")
data("example")

## The group data is encoded as a binary vector where
## 0s represent control samples (first 29 samples) and
## 1s represent disease samples (last 12 samples)
groups

## Neuronal reference signals (i.e. quantitative variable)
## and group-specific change in neuronal expression
## (i.e. interaction regressor)
neuron_probesets <- list(c("221805_at", "221801_x_at", "221916_at"),
                        "201313_at", "210040_at", "205737_at", "210432_s_at")
neuron_reference <- marker(expression, neuron_probesets)
neuron_difference <- groups * neuron_reference

## Fit an expression model containing neuronal expression and
## neuron-specific change in expression between control and
```

```
## disease samples
model <- lm(expression["202429_s_at",] ~ neuron_reference +
neuron_difference)

## Visualize the dependence on the neuronal reference signal and
## the group-specific effect (decreased neuronal expression in
## disease samples). Black and red dots represent control and
## disease samples, respectively.
crplot(model, "neuron_reference", g="neuron_difference")
```

---

em\_quantvg

*Specifies particular models useful for gene expression modeling*


---

## Description

Enumerates sets of integer that specify variables to include in each model of the family.

## Usage

```
em_quantvg(vi, tnv=NULL, ng=1, sk=NULL, mnr=NULL, int=TRUE)
```

## Arguments

vi	integer vector. Indices of the quantitative variables in the full model matrix.
tnv	integer. Total number of quantitative variables (excluding the intercept) in the full model matrix (if (int=TRUE) tnv>=(max(vi)-1). If (int=FALSE) tnv>=max(vi)). By default: tnv=(max(vi)-1) if (int=TRUE) and tnv=max(vi) if (int=FALSE).
ng	integer. Number of samples groups: 1 (default), 2 or 3.
sk	character. Indicates if the models with group-specific regressors defining group 2 ("skip2") should be eliminated or if models containing group-specific regressors for groups 2 and 3 (simultaneously) should be prohibited ("skip23"). These apply only if ng=3.
mnr	integer. Maximal total number of regressors (including the intercept if "int" is TRUE) in the enumerated models.
int	logical. If TRUE (default) the first column of the full model matrix is assumed to be an intercept.

## Details

We specify a family of linear models corresponding to a (multiple) regression on selected quantitative variables and up to 3 different treatment groups. The function enumerates all subset models with up to 1 (i.e. 0 or 1) group-specific change in any of selected the quantitative variables. Regressors coding for a group-specific change in a given quantitative variable are only allowed if the corresponding quantitative variable is present in the model.

The function returns sets of integers that define models by specifying indices to the columns of a full model matrix. The full model matrix can contain more quantitative variables than those selected for building the enumeration.

The full model matrix (with columns as regressors) is assumed to contain all quantitative variables first, followed by the interaction regressors coding for differences between sample group 1 and 2, possibly followed by the interaction regressors coding for differences between group 1 and 3. The maximal number of sample groups is 3. The order of interaction regressors for a given group is assumed to be the same as for the quantitative variables.

The first column of the full model matrix is assumed to be an intercept. If the full model matrix does not contain an intercept, the argument "int" should be set to FALSE (and the returned models will not include an intercept).

### Value

mi list of integer vectors. Each vector defines a model by specifying column indices in the full model matrix.

### Author(s)

Alexandre Kuhn <alexandre.m.kuhn@gmail.com>

### References

Kuhn A, Thu D, Waldvogel HJ, Faull RL, Luthi-Carter R. Population-specific expression analysis (PSEA) reveals molecular changes in diseased brain. Nat Methods 2011, 8(11):945-7

### See Also

[fmm](#).

### Examples

```
## Load example expression data (variable "expression")
## for 23 transcripts and 41 samples, and associated
## phenotype (i.e. group) information (variable "groups")
data("example")

## The group data is encoded as a binary vector where
## 0s represent control samples (first 29 samples) and
## 1s represent disease samples (last 12 samples)
groups

## Four cell population-specific reference signals
## (i.e. quantitative variable)
neuron_probesets <- list(c("221805_at", "221801_x_at", "221916_at"),
                        "201313_at", "210040_at", "205737_at", "210432_s_at")
neuron_reference <- marker(expression, neuron_probesets)

astro_probesets <- list("203540_at",c("210068_s_at", "210906_x_at"),
                       "201667_at")
astro_reference <- marker(expression, astro_probesets)

oligo_probesets <- list(c("211836_s_at", "214650_x_at"), "216617_s_at",
                       "207659_s_at", c("207323_s_at", "209072_at"))
```

```
oligo_reference <- marker(expression, oligo_probesets)

micro_probesets <- list("204192_at", "203416_at")
micro_reference <- marker(expression, micro_probesets)

## Full model matrix with an intercept, 4 quantitative variables and
## group-specific (disease vs control) differences for the
## 4 quantitative variables
model_matrix <- fmm(cbind(neuron_reference,astro_reference,
oligo_reference, micro_reference), groups)

## Enumerate all possible models with any subset of the 4 reference signals
## (quantitative variables) and at most 1 group-specific effect
## (interaction regressor)
model_subset <- em_quantvg(c(2,3,4,5), tnv=4, ng=2)

## There are 48 models
length(model_subset)

## For instance the 17th model in the list contains an intercept (column 1 in model_matrix), the neuronal reference s
model_subset[[17]]
```

---

expression

*Expression data.*

---

## Description

Numeric matrix containing expression data for 23 transcripts (rows) and 41 samples (columns).

The data correspond to samples 1, 101, 11, 126, 14, 15, 17, 2, 20, 21, 52, 64, 8, H104, H109, H113, H115, H117, H118, H120, H121, H124, H126, H128, H129, H131, H132, H137, H85, 12, 13, 3, 7, HC103, HC105, HC53, HC55, HC74, HC81, HC83, HC86 for which expression data has been deposited as GSE3790 at Gene Expression Omnibus <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3790>. Column names in the expression data matrix contain the corresponding CEL file names.

The first 29 samples are control samples and the next 12 samples are disease samples.

## Format

Numeric matrix with 23 rows and 41 columns.

## Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3790>

---

expression\_GSE19380    *Expression data for GSE19380 (RNA mixture experiment)*

---

### Description

Numeric matrix containing normalized expression data for 31099 transcripts (rows) and 26 samples (columns).

### Format

Numeric matrix with 31099 rows and 26 columns.

---

fmm                      *Full model matrix*

---

### Description

Generates a model matrix containing (quantitative) independent variables and interaction regressors coding for group-specific effects for each of the quantitative variable.

### Usage

```
fmm(v,d,int=TRUE)
```

### Arguments

v	n-by-m numeric matrix. Matrix containing m quantitative variables as columns (i.e. n is the number of samples).
d	n-by-o numeric matrix. Matrix containing o binary regressors (encoding o group-specific differences) as columns. n is the number of samples.
int	logical. If TRUE (default) an intercept is included as the first column of the full model matrix.

### Details

Quantitative variables are specified via the argument "v". Sample groups are specified using binary (i.e. 0,1) variables (argument "d"). The returned model matrix represents a linear model with "m" quantitative variables and "o" group effects (corresponding to "o"+1 sample groups).

Specifically, the columns of the full model matrix contain (in this order): an intercept (if "int" is TRUE), the quantitative variables in the same order as they are provided in the input, group-specific effects for each quantitative variable (encoded as interaction regressors and in the same order as the quantitative variable are provided in the input).

An interaction regressor corresponds a quantitative variable multiplied by a (group-specific) binary variable. It encodes the difference (for the particular variable) between a specific group and the reference group.



**Value**

fmm                    numeric matrix. The full model matrix. Its dimension is n-by-(m\*(o+1)+1) if int is TRUE and n-by-(m\*(o+1)) if int is FALSE.

**Author(s)**

Alexandre Kuhn <alexandre.m.kuhn@gmail.com>

**Examples**

```
## Load example expression data (variable "expression")
## for 23 transcripts and 41 samples, and associated
## phenotype (i.e. group) information (variable "groups")
data("example")

## The group data is encoded as a binary vector where
## 0s represent control samples (first 29 samples) and
## 1s represent disease samples (last 12 samples)
groups

## Four cell population-specific reference signals
## (i.e. quantitative variable)
neuron_probesets <- list(c("221805_at", "221801_x_at", "221916_at"),
                        "201313_at", "210040_at", "205737_at", "210432_s_at")
neuron_reference <- marker(expression, neuron_probesets)

astro_probesets <- list("203540_at",c("210068_s_at", "210906_x_at"),
                       "201667_at")
astro_reference <- marker(expression, astro_probesets)

oligo_probesets <- list(c("211836_s_at", "214650_x_at"), "216617_s_at",
                       "207659_s_at", c("207323_s_at", "209072_at"))
oligo_reference <- marker(expression, oligo_probesets)

micro_probesets <- list("204192_at", "203416_at")
micro_reference <- marker(expression, micro_probesets)

## Full model matrix with an intercept, 4 quantitative variables and
## group-specific (disease vs control) differences for the
## 4 quantitative variables
fmm(cbind(neuron_reference, astro_reference, oligo_reference,
micro_reference), groups)
```

---

groups

*Binary vector encoding sample group information.*

---

**Description**

Numeric vector of length 41 containing 0s and 1s. 0s and 1s represent samples belonging to sample group 1 and 2, respectively.

This vector actually correspond to samples 1, 101, 11, 126, 14, 15, 17, 2, 20, 21, 52, 64, 8, H104, H109, H113, H115, H117, H118, H120, H121, H124, H126, H128, H129, H131, H132, H137, H85, 12, 13, 3, 7, HC103, HC105, HC53, HC55, HC74, HC81, HC83, HC86 for which expression data has been deposited as GSE3790 at Gene Expression Omnibus <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3790>. 0s are control samples and 1s are disease samples.

**Format**

Numeric vector of length 41.

**Source**

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3790>

---

information

*Sample information for GSE19380 (RNA mixture experiment)*

---

**Description**

data.frame

**Format**

Data.frame with 26 rows and 33 columns.

---

l`m`fitst

*Fits a set of models and performs model selection.*

---

**Description**

For each response (dependent variable), the function fits a set of models and identify the best models based on AIC.

**Usage**

```
lmfitst(y, fmdlm, st, subset=NULL, d=2, lm=TRUE)
```

**Arguments**

<code>y</code>	numeric matrix or ExpressionSet. Matrix with response (dependent) variable as columns. If an ExpressionSet is provided the response matrix is extracted with the function <code>exprs</code> and transposed.
<code>fmdl</code>	numeric matrix. Full model matrix with regressors as columns.
<code>st</code>	list of integer vectors. Each vector defines a model by specifying column indices in <code>fmdl</code> .
<code>subset</code>	Integer vector. Subset of samples to be used for fitting. By default all samples are used.
<code>d</code>	numeric. Maximal distance (in AIC units) to the model with smallest AIC (defaults to 2). Models with an AIC difference less than or equal to <code>d</code> are returned.
<code>lm</code>	logical. If TRUE (default) the function also returns the fit (as returned by the function <code>lm</code> ) obtained for the best model obtained for each response. If FALSE, the function only returns the indices (in <code>st</code> ) corresponding to the selected models.

**Details**

This function is useful for performing model selection. It fits all possible models of a given set (instead of heuristically searching for the best one for instance) and compares them using Akaike Information Criterion (AIC).

For each response, all specified models are tested and all models obtaining an AIC within "d" AIC units of the model with smallest AIC are identified. These models are ordered by increasing number of regressors. Models with the same number of regressors are ordered by increasing AIC. The first model in this ordered list is considered the best model. Optionally the full fit (as returned by the function `lm`) of the best model is returned.

The formula for AIC follows the implementation of the function `extractAIC` and is:  $n * \log(\text{RSS} / n) + 2 * \text{edf}$ , where `n` is the number of observations, `RSS` is the residual sum of squares and `edf` the number of free parameters.

Model fitting is implemented with `lm.fit` and NAs are not allowable in the response matrix `y`.

**Value**

<code>wcrt</code>	list of integer vector (of length equal to the number of responses). Each integer vector represents the models (identified as indices into <code>st</code> ) within <code>d</code> AIC units of the model with smallest AIC.
<code>ft</code>	list of <code>lm</code> objects. Each <code>lm</code> object contains the fit for the best model (defined as the model with the smallest number of regressors within <code>d</code> AIC units of the model with smallest AIC). Only returned if <code>lm</code> is TRUE (default).

**Author(s)**

Alexandre Kuhn <alexandre.m.kuhn@gmail.com>

**References**

Kuhn A, Thu D, Waldvogel HJ, Faull RL, Luthi-Carter R. Population-specific expression analysis (PSEA) reveals molecular changes in diseased brain. *Nat Methods* 2011, 8(11):945-7

**See Also**

[marker,swlm](#).

**Examples**

```
## Load example expression data (variable "expression")
## for 23 transcripts and 41 samples, and associated
## phenotype (i.e. group) information (variable "groups")
data("example")

## The group data is encoded as a binary vector where
## 0s represent control samples (first 29 samples) and
## 1s represent disease samples (last 12 samples)
groups

## Four cell population-specific reference signals
## (i.e. quantitative variable)
neuron_probesets <- list(c("221805_at", "221801_x_at", "221916_at"),
                        "201313_at", "210040_at", "205737_at", "210432_s_at")
neuron_reference <- marker(expression, neuron_probesets)

astro_probesets <- list("203540_at",c("210068_s_at", "210906_x_at"),
                       "201667_at")
astro_reference <- marker(expression, astro_probesets)

oligo_probesets <- list(c("211836_s_at", "214650_x_at", "216617_s_at",
                        "207659_s_at", c("207323_s_at", "209072_at"))
oligo_reference <- marker(expression, oligo_probesets)

micro_probesets <- list("204192_at", "203416_at")
micro_reference <- marker(expression, micro_probesets)

## Full model matrix with an intercept, 4 quantitative variables and
## group-specific (disease vs control) differences for the
## 4 quantitative variables
model_matrix <- fmm(cbind(neuron_reference, astro_reference,
oligo_reference, micro_reference), groups)

## Enumerate all possible models with any subset of the 4 reference signals
## (quantitative variables) and at most 1 group-specific effect
## (interaction regressor)
model_subset <- em_quantvg(c(2,3,4,5), tnv=4, ng=2)

## AIC-based model selection for 2 transcripts of interest
## (202429_s_at and 200850_s_at). For the first one, the selected
## model contains an intercept, the neuronal reference signal and
## a neuron-specific change (i.e. model 17 in model_subset
## corresponding to columns 1, 2 and 6 in model_matrix). For the
## second transcript, the selected model contains an intercept and
## the astrocytic reference signal (i.e. model 3 in model_subset
## corresponding to columns 1 and 3 in model_matrix)
lmfitst(t(expression[c("202429_s_at", "200850_s_at"),]),
```

```
model_matrix, model_subset)
```

---

marker	<i>Reference signal</i>
--------	-------------------------

---

## Description

Generates a population-specific reference signal.

## Usage

```
marker(expr, id, sampleSubset=NULL, targetMean=1)
```

## Arguments

expr	Numeric matrix or ExpressionSet. The matrix contains the expression data with transcripts (i.e. for a microarray, probes) as rows and samples as columns. Row names should be defined and are used to determine the transcripts used to generate the reference signal (specified with the argument id). If an ExpressionSet is provided the expression data is extracted with the function exprs.
id	List of strings. Names of the transcripts to use to generate the reference signal. Names correspond to row names in expr if it is a matrix or row names in exprs(expr) if it is an ExpressionSet.
sampleSubset	Integer vector. Represents a subset of samples (specified as column indices in expr) to use to normalize the reference signal (see Details). By default all samples are used.
targetMean	Numeric. Mean of the reference signal (defaults to 1).

## Details

A reference signal for a given population is generated by averaging the expression of multiple transcripts that are expressed in a cell population-specific manner.

The reference signal is scaled to have an average value determined by targetMean (1 by default). The argument sampleSubset restricts the samples to take into account for normalization (i.e. the average of the reference signal over sampleSubset will be the value specified by targetMean, but the reference signal will still be of length equal to the number of columns in expr).

The expression value of each transcript is normalized before averaging over multiple transcripts so that they have same weight in the final reference signal (i.e to avoid that highly expressed transcripts dominate the reference signal).

The names of transcripts to be used are specified as items of a list (id). If the expression matrix contains multiple measures of the same transcript (for instance several probes of a microarray measuring the same transcript) they can be averaged before taking the average over different transcripts. Thereby every transcript has the same weight in the final reference signal, independently of the number of probes used to measure it. Multiple measures of the same transcript are specified as a vector in the list.

**Value**

refSignal        Numeric vector of the same length as the number of columns in expr (or in exprs(expr) if expr is provided as an ExpressionSet). Reference signal (see Details).

**Author(s)**

Alexandre Kuhn <alexandre.m.kuhn@gmail.com>

**References**

Kuhn A, Thu D, Waldvogel HJ, Faull RL, Luthi-Carter R. Population-specific expression analysis (PSEA) reveals molecular changes in diseased brain. Nat Methods 2011, 8(11):945-7

**Examples**

```
## Load example expression data
data("example")

## List of probes corresponding to neuronal genes:
## 221805_at, 221801_x_at, 221916_at all measure NEFL expression.
## 201313_at, 210040_at, 205737_at, 210432_s_at measure
## ENO2, SLC12A5, KCNQ2 and SCN3A expression, respectively.
neuron_probesets <- list(c("221805_at", "221801_x_at", "221916_at"),
"201313_at", "210040_at", "205737_at", "210432_s_at")

## Neuronal reference signal
neuron_reference <- marker(expression, neuron_probesets)
```

---

pvalmat

*Extracts p-values*

---

**Description**

Takes a list of fitted models (lm objects) and obtains the p-values associated with each fit.

**Usage**

```
pvalmat(lst, regressors)
```

**Arguments**

lst                list of lm objects.

regressors        character vector. Names of the coefficients for which p-values are extracted.

**Details**

Simple wrapper function that returns p-values extracted from `summary(lm)`.

The coefficient names corresponding to the p-values to be extracted are matched based on their names in `rownames(summary(lst[[i]])$coef)`.

**Value**

`pvalm` numeric matrix. Matrix of extracted p-values with one row for each model in the list and one column for each targeted coefficient.

**Author(s)**

Alexandre Kuhn <alexandre.m.kuhn@gmail.com>

**See Also**

[coefmat](#).

**Examples**

```
## Load example expression data (variable "expression")
## and phenotype data (variable "groups")
data("example")

## Four cell population-specific reference signals
neuron_probesets <- list(c("221805_at", "221801_x_at", "221916_at"),
"201313_at", "210040_at", "205737_at", "210432_s_at")
neuron_reference <- marker(expression, neuron_probesets)

astro_probesets <- list("203540_at",c("210068_s_at", "210906_x_at"),
"201667_at")
astro_reference <- marker(expression, astro_probesets)

oligo_probesets <- list(c("211836_s_at", "214650_x_at"), "216617_s_at",
"207659_s_at", c("207323_s_at", "209072_at"))
oligo_reference <- marker(expression, oligo_probesets)

micro_probesets <- list("204192_at", "203416_at")
micro_reference <- marker(expression, micro_probesets)

## Stepwise model selection for 2 transcripts (202429_s_at and
## 200850_s_at) and focusing on control samples (i.e. groups == 0)
lmlist <- swlm(expression[c("202429_s_at", "200850_s_at"),],
subset = which(groups == 0),
upper = formula(~neuron_reference + astro_reference +
oligo_reference + micro_reference))

pvalmat(lmlist, c("(Intercept)", "neuron_reference", "astro_reference",
"oligo_reference", "micro_reference"))
```

---

`slt`*Extracts from a list of objects*

---

**Description**

Simple wrapper to extract a particular slot for each object in a list.

**Usage**

```
slt(ls,slot,index=NULL)
```

**Arguments**

<code>ls</code>	list of objects.
<code>slot</code>	character. Name of the slot to extract.
<code>index</code>	integer vector. Optional index vector to extract only a subset of the elements contained in the slot.

**Details**

The slot to be extracted is defined by matching "slot" against slot names of the first object in the list.

Slot extraction is done with `sapply` and the format of the output will depend on the content of the slots (see the value returned by `sapply` for details).

**Value**

`sc` vector or matrix.

**Author(s)**

Alexandre Kuhn <alexandre.m.kuhn@gmail.com>

**Examples**

```
## Two arbitrary regression summaries in a list
x<-1:10
y1 <- x + rnorm(10,sd=1)
y2 <- x + rnorm(10,sd=5)

slm<-list()
slm[[1]] <- summary(lm(y1 ~ x))
slm[[2]] <- summary(lm(y2 ~ x))

## Extract R-squared from the list of summary.lm objects
slt(slm, "adj.r.squared")
```



---

**swlm** *Stepwise model selection*

---

**Description**

Simple wrapper around `stepAIC()` (package MASS) to repeatedly perform stepwise model selection by AIC on several dependent variables (or responses, taken as rows of a matrix).

**Usage**

```
swlm(y, subset=NULL, upper, lower=formula(~1), direction='both', trace=FALSE, keep=NULL, verbose=FALSE)
```

**Arguments**

<code>y</code>	Numeric matrix (with responses as rows and samples as columns) or <code>ExpressionSet</code> . Typically the expression data with transcripts (i.e. for a microarray, probes) as rows and samples as columns. If an <code>ExpressionSet</code> is provided the expression data is extracted with the function <code>exprs</code> .
<code>subset</code>	Integer vector. Represents a subset of samples (specified as column indices in <code>y</code> ) to use for model fitting. By default all samples are used.
<code>verbose</code>	logical. If TRUE (default) the response number being fitted is printed.
<code>upper</code>	see <code>?stepAIC</code>
<code>lower</code>	see <code>?stepAIC</code>
<code>direction</code>	see <code>?stepAIC</code>
<code>trace</code>	see <code>?stepAIC</code>
<code>keep</code>	see <code>?stepAIC</code>

**Details**

The initial model for the stepwise approach only contains an intercept term.

**Value**

`swft` List of stepwise-selected models (see `?stepAIC`)

**Author(s)**

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**References**

Kuhn A, Kumar A, Beilina A, Dillman A, Cookson MR, Singleton AB. Cell population-specific expression analysis of human cerebellum. *BMC Genomics* 2012, 13:610.

**See Also**

[marker.lmfitst](#).

**Examples**

```
## Load example expression data (variable "expression")
## and phenotype data (variable "groups")
data("example")

## Four cell population-specific reference signals
neuron_probesets <- list(c("221805_at", "221801_x_at", "221916_at"),
"201313_at", "210040_at", "205737_at", "210432_s_at")
neuron_reference <- marker(expression, neuron_probesets)

astro_probesets <- list("203540_at",c("210068_s_at", "210906_x_at"),
"201667_at")
astro_reference <- marker(expression, astro_probesets)

oligo_probesets <- list(c("211836_s_at", "214650_x_at"), "216617_s_at",
"207659_s_at", c("207323_s_at", "209072_at"))
oligo_reference <- marker(expression, oligo_probesets)

micro_probesets <- list("204192_at", "203416_at")
micro_reference <- marker(expression, micro_probesets)

## Stepwise model selection for 2 transcripts (202429_s_at and 200850_s_at)
## and focusing on control samples (i.e. groups == 0)
swlm(expression[c("202429_s_at", "200850_s_at"),],
subset = which(groups == 0),
upper = formula(~neuron_reference + astro_reference +
oligo_reference + micro_reference))
```

# Index

## \* datasets

- expression, [7](#)
- expression\_GSE19380, [8](#)
- groups, [9](#)
- information, [10](#)

## \* models

- coefmat, [2](#)
- crplot, [3](#)
- lmfitst, [10](#)
- pvalmat, [14](#)
- swlm, [17](#)

coefmat, [2](#), [15](#)  
crplot, [3](#)

em\_quantvg, [5](#)  
expression, [7](#)  
expression\_GSE19380, [8](#)

fmm, [6](#), [8](#)

groups, [9](#)

information, [10](#)

lmfitst, [10](#), [17](#)

marker, [12](#), [13](#), [17](#)

pvalmat, [2](#), [14](#)

slt, [16](#)  
swlm, [12](#), [17](#)