

# Package ‘joinet’

November 13, 2019

**Version** 0.0.3

**Title** Multivariate Elastic Net Regression

**Description** Implements high-dimensional multivariate regression by stacked generalisation (Wolpert 1992 <doi:10.1016/S0893-6080(05)80023-1>). For positively correlated outcomes, a single multivariate regression is typically more predictive than multiple univariate regressions. Includes functions for model fitting, extracting coefficients, outcome prediction, and performance measurement.

**Depends** R (>= 3.0.0)

**Imports** glmnet, palasso, cornet

**Suggests** knitr, testthat, MASS

**Enhances** spls, SiER, MRCE

**VignetteBuilder** knitr

**License** GPL-3

**LazyData** true

**Language** en-GB

**RoxygenNote** 6.1.1

**URL** <https://github.com/rauschenberger/joinet>

**BugReports** <https://github.com/rauschenberger/joinet/issues>

**NeedsCompilation** no

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**joinet-package***Multivariate Elastic Net Regression*

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**Description**

The R package **joinet** implements multivariate ridge and lasso regression using stacked generalisation. This multivariate regression typically outperforms univariate regression at predicting correlated outcomes. It provides predictive and interpretable models in high-dimensional settings.

**Details**

Use function **joinet** for model fitting. Type `library(joinet)` and then `?joinet` or `help("joinet")` to open its help file.

See the vignette for further examples. Type `vignette("joinet")` or `browseVignettes("joinet")` to open the vignette.

**References**

Armin Rauschenberger and Enrico Glaab (2019). "joinet: predicting correlated outcomes jointly to improve clinical prognosis". *Manuscript in preparation*.

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**Examples**

```

#--- data simulation ---
n <- 50; p <- 100; q <- 3
X <- matrix(rnorm(n*p),nrow=n,ncol=p)
Y <- replicate(n=q,expr=rnorm(n=n,mean=rowSums(X[,1:5])))
# n samples, p inputs, q outputs

#--- model fitting ---
object <- joinet(Y=Y,X=X)
# slot "base": univariate
# slot "meta": multivariate

#--- make predictions ---
y_hat <- predict(object,newx=X)
# n x q matrix "base": univariate
# n x q matrix "meta": multivariate

#--- extract coefficients ---
coef <- coef(object)
# effects of inputs on outputs

```

```
# q vector "alpha": intercepts
# p x q matrix "beta": slopes

#--- model comparison ---
loss <- cv.joinet(Y=Y,X=X)
# cross-validated loss
# row "base": univariate
# row "meta": multivariate
```

**coef.joinet***Extract Coefficients***Description**

Extracts pooled coefficients. (The meta learners linearly combines the coefficients from the base learners.)

**Usage**

```
## S3 method for class 'joinet'
coef(object, ...)
```

**Arguments**

<code>object</code>	<code>joinet</code> object
<code>...</code>	further arguments (not applicable)

**Value**

This function returns the pooled coefficients. The slot alpha contains the intercepts in a vector of length  $q$ , and the slot beta contains the slopes in a matrix with  $p$  rows (inputs) and  $q$  columns.

**Examples**

```
n <- 50; p <- 100; q <- 3
X <- matrix(rnorm(n*p),nrow=n,ncol=p)
Y <- replicate(n=q,expr=rnorm(n=n,mean=rowSums(X[,1:5])))
object <- joinet(Y=Y,X=X)
coef <- coef(object)
```

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`cv.joinet`*Model comparison*

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## Description

Compares univariate and multivariate regression.

## Usage

```
cv.joinet(Y, X, family = "gaussian", nfolds.ext = 5, nfolds.int = 10,
          foldid.ext = NULL, foldid.int = NULL, type.measure = "deviance",
          alpha.base = 1, alpha.meta = 0, mnorm = FALSE, spls = FALSE,
          sier = FALSE, mrce = FALSE, cvpred = FALSE, ...)
```

## Arguments

<code>Y</code>	outputs: numeric matrix with $n$ rows (samples) and $q$ columns (variables), with positive correlation (see details)
<code>X</code>	inputs: numeric matrix with $n$ rows (samples) and $p$ columns (variables)
<code>family</code>	distribution: vector of length 1 or $q$ with entries "gaussian", "binomial" or "poisson"
<code>nfolds.ext</code>	number of external folds
<code>nfolds.int</code>	number of internal folds
<code>foldid.ext</code>	external fold identifiers: vector of length $n$ with entries between 1 and <code>nfolds.ext</code> ; or <code>NULL</code>
<code>foldid.int</code>	internal fold identifiers: vector of length $n$ with entries between 1 and <code>nfolds.int</code> ; or <code>NULL</code>
<code>type.measure</code>	loss function: vector of length 1 or $q$ with entries "deviance", "class", "mse" or "mae" (see <a href="#">cv.glmnet</a> )
<code>alpha.base</code>	elastic net mixing parameter for base learners: numeric between 0 (ridge) and 1 (lasso)
<code>alpha.meta</code>	elastic net mixing parameter for meta learner: numeric between 0 (ridge) and 1 (lasso)
<code>mnorm, spls, sier, mrce</code>	experimental arguments: logical (requires packages <code>spls</code> , <code>SiER</code> , or <code>MRCE</code> )
<code>cvpred</code>	return cross-validated prediction: logical
<code>...</code>	further arguments passed to <a href="#">glmnet</a> and <a href="#">cv.glmnet</a>

## Value

This function returns a matrix with  $q$  columns, including the cross-validated loss from the univariate models (base), the multivariate models (meta), and the intercept-only models (none).

## Examples

```

n <- 50; p <- 100; q <- 3
X <- matrix(rnorm(n*p), nrow=n, ncol=p)
Y <- replicate(n=q, expr=rnorm(n=n, mean=rowSums(X[, 1:5])))
cv.joinet(Y=Y, X=X)

## Not run:
# correlated features
n <- 50; p <- 100; q <- 3
mu <- rep(0, times=p)
Sigma <- 0.90^abs(col(diag(p))-row(diag(p)))
X <- MASS::mvrnorm(n=n, mu=mu, Sigma=Sigma)
mu <- rowSums(X[, sample(seq_len(p), size=5)])
Y <- replicate(n=q, expr=rnorm(n=n, mean=mu))
#Y <- t(MASS::mvrnorm(n=q, mu=mu, Sigma=diag(n)))
cv.joinet(Y=Y, X=X)
## End(Not run)

## Not run:
# other distributions
n <- 50; p <- 100; q <- 3
X <- matrix(rnorm(n*p), nrow=n, ncol=p)
eta <- rowSums(X[, 1:5])
Y <- replicate(n=q, expr=rbinom(n=n, size=1, prob=1/(1+exp(-eta))))
cv.joinet(Y=Y, X=X, family="binomial")
Y <- replicate(n=q, expr=rpois(n=n, lambda=exp(scale(eta))))
cv.joinet(Y=Y, X=X, family="poisson")
## End(Not run)

## Not run:
# uncorrelated outcomes
n <- 50; p <- 100; q <- 3
X <- matrix(rnorm(n*p), nrow=n, ncol=p)
y <- rnorm(n=n, mean=rowSums(X[, 1:5]))
Y <- cbind(y, matrix(rnorm(n*(q-1)), nrow=n, ncol=q-1))
cv.joinet(Y=Y, X=X)
## End(Not run)

## Not run:
# sparse and dense models
n <- 50; p <- 100; q <- 3
X <- matrix(rnorm(n*p), nrow=n, ncol=p)
Y <- replicate(n=q, expr=rnorm(n=n, mean=rowSums(X[, 1:5])))
set.seed(1) # fix folds
cv.joinet(Y=Y, X=X, alpha.base=1) # lasso
set.seed(1)
cv.joinet(Y=Y, X=X, alpha.base=0) # ridge
## End(Not run)

```

joinet

*Multivariate Elastic Net Regression*

## Description

Implements multivariate elastic net regression.

## Usage

```
joinet(Y, X, family = "gaussian", nfolds = 10, foldid = NULL,
       type.measure = "deviance", alpha.base = 1, alpha.meta = 0, ...)
```

## Arguments

Y	outputs: numeric matrix with $n$ rows (samples) and $q$ columns (variables), with positive correlation (see details)
X	inputs: numeric matrix with $n$ rows (samples) and $p$ columns (variables)
family	distribution: vector of length 1 or $q$ with entries "gaussian", "binomial" or "poisson"
nfolds	number of folds
foldid	fold identifiers: vector of length $n$ with entries between 1 and nfolds; or NULL (balance)
type.measure	loss function: vector of length 1 or $q$ with entries "deviance", "class", "mse" or "mae" (see <a href="#">cv.glmnet</a> )
alpha.base	elastic net mixing parameter for base learners: numeric between 0 (ridge) and 1 (lasso)
alpha.meta	elastic net mixing parameter for meta learner: numeric between 0 (ridge) and 1 (lasso)
...	further arguments passed to <a href="#">glmnet</a>

## Details

**correlation:** The  $q$  outcomes should be positively correlated. Avoid negative correlations by changing the sign of the variable.

**elastic net:** alpha.base controls input-output effects, alpha.meta controls output-output effects; lasso renders sparse models (alpha= 1), ridge renders dense models (alpha= 0)

## Value

This function returns an object of class joinet. Available methods include [predict](#), [coef](#), and [weights](#). The slots base and meta each contain  $q$  [cv.glmnet](#)-like objects.

## References

Armin Rauschenberger, Enrico Glaab (2019) "joinet: predicting correlated outcomes jointly to improve clinical prognosis" *Manuscript in preparation*.

**See Also**

[cv.jointet](#), vignette

**Examples**

```
n <- 50; p <- 100; q <- 3
X <- matrix(rnorm(n*p), nrow=n, ncol=p)
Y <- replicate(n=q, expr=rnorm(n=n, mean=rowSums(X[, 1:5])))
object <- jointet(Y=Y, X=X)

## Not run:
browseVignettes("jointet") # further examples
## End(Not run)
```

**predict.jointet** *Make Predictions*

**Description**

Predicts outcome from features with stacked model.

**Usage**

```
## S3 method for class 'jointet'
predict(object, newx, type = "response", ...)
```

**Arguments**

object	<a href="#">jointet</a> object
newx	covariates: numeric matrix with $n$ rows (samples) and $p$ columns (variables)
type	character "link" or "response"
...	further arguments (not applicable)

**Value**

This function returns predictions from base and meta learners. The slots `base` and `meta` each contain a matrix with  $n$  rows (samples) and  $q$  columns (variables).

**Examples**

```
n <- 50; p <- 100; q <- 3
X <- matrix(rnorm(n*p), nrow=n, ncol=p)
Y <- replicate(n=q, expr=rnorm(n=n, mean=rowSums(X[, 1:5])))
Y[, 1] <- 1*(Y[, 1]>median(Y[, 1]))
object <- jointet(Y=Y, X=X, family=c("binomial", "gaussian", "gaussian"))
predict(object, newx=X)
```

**weights.joinet**      *Extract Weights*

## Description

Extracts coefficients from the meta learner, i.e. the weights for the base learners.

## Usage

```
## S3 method for class 'joinet'
weights(object, ...)
```

## Arguments

object	<b>joinet</b> object
...	further arguments (not applicable)

## Value

This function returns a matrix with  $1 + q$  rows and  $q$  columns. The first row contains the intercepts, and the other rows contain the slopes, which are the effects of the outcomes in the row on the outcomes in the column.

## Examples

```
n <- 50; p <- 100; q <- 3
X <- matrix(rnorm(n*p), nrow=n, ncol=p)
Y <- replicate(n=q, expr=rnorm(n=n, mean=rowSums(X[, 1:p])))
object <- joinet(Y=Y, X=X)
weights(object)
```

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