Package ‘GROAN’

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License GPL-3 | file LICENSE
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addRegressor

Add an extra regressor to a Workbench

Description
This function adds a regressor to an existing GROAN.Workbench object.

Usage
addRegressor(wb, regressor, regressor.name = regressor, ...)

Arguments
wb the GROAN.Workbench instance to be updated
regressor regressor function
regressor.name string that will be used in reports. Keep in mind that when deciding names.
... extra parameters are passed to the regressor function

Value
an updated instance of the original GROAN.Workbench

See Also
createWorkbench GROAN.run
Examples

```r
# creating a Workbench with all default arguments
wb = createWorkbench()

# adding a second regressor
wb = addRegressor(wb, regressor = phenoRegressor.dummy, regressor.name = 'dummy')

## Not run:
# trying to add again a regressor with the same name would result in a naming conflict error
wb = addRegressor(wb, regressor = phenoRegressor.dummy, regressor.name = 'dummy')

## End(Not run)
```

---

**are.compatible**

Check two GROAN.NoisyDataSet for dimension compatibility

Description

This function verifies that the two passed GROAN.NoisyDataSet objects have the same dimensions and can thus be used in the same experiment (typically training models on one and testing on the other). The function returns a TRUE/FALSE. In verbose mode the function also prints messages detailing the comparisons.

Usage

```r
are.compatible(nds1, nds2, verbose = FALSE)
```

Arguments

- **nds1**: the first GROAN.NoisyDataSet to be tested
- **nds2**: the second GROAN.NoisyDataSet to be tested
- **verbose**: boolean, if TRUE the function prints messages detailing the comparison.

Value

TRUE if the passed GROAN.NoisyDataSet are dimensionally compatible, FALSE otherwise

---

**createNoisyDataset**

Noisy Data Set Constructor

Description

This function creates a GROAN.NoisyDataset object (or fails trying). The class will contain all noisy data set components: genotypes and/or covariance matrix, phenotypes, strata (optional), a noise injector function and its parameters.

You can have a general description of the created object using the overridden `print.GROAN.NoisyDataset` function.
Usage

createNoisyDataset(
  name, 
  genotypes = NULL, 
  covariance = NULL, 
  phenotypes, 
  strata = NULL, 
  extraCovariates = NULL, 
  ploidy = 2, 
  noiseInjector = noiseInjector.dummy, 
  ...
)

Arguments

name A string defining the dataset name, used later do identify this particular instance in reports and result files. It is advisable for it to be it somewhat meaningful (to you, GROAN simply reports it as it is)
genotypes Matrix or dataframe containing SNP genotypes, one row per sample (N), one column per marker (M), 0/1/2 format (for diploids) or 0/1/2.../ploidy in case of polyploids
covariance matrix of covariances between samples of this dataset. It is usually a square (NxN) matrix, but rectangular matrices (NxW) are accepted to incapsulate covariances between samples in this set and samples of other sets. Please note that some regression models expect the covariance to be square and will fail on rectangular ones
phenotypes numeric array, N slots
strata array of M slots, describing the strata each data point belongs to. This is used for stratified crossvalidation (see createWorkbench)
extraCovariates dataframe of optional extra covariates (N lines, one column per extra covariate). Numeric ones will be normalized, string and categorical ones will be transformed in stub TRUE/FALSE variables (one per possible value, see model.matrix).
ploidy number of haploid sets in the cell. Defaults to 2 (diploid).
noiseInjector name of a noise injector function, defaults to noiseInjector.dummy
... further arguments are passed along to noiseInjector

Value

a GROAN.NoisyDataset object.

See Also

GROAN.run createWorkbench
createRunId

Examples

# For more complete examples see the package vignette
# creating a noisy dataset with normal noise
nds = createNoisyDataset(
    name = 'PEA, normal noise',
    genotypes = GROAN.KI$SNPs,
    phenotypes = GROAN.KI$yield,
    noiseInjector = noiseInjector.norm,
    mean = 0,
    sd = sd(GROAN.KI$yield) * 0.5
)

createRunId

Generate a random run id

Description

This function returns a partially random alphanumeric string that can be used to identify a single run.

Usage

createRunId()

Value

a partially random alphanumeric string

createWorkbench

Workbench constructor

Description

This function creates a GROAN.Workbench instance (or fails trying). The created object contains:
a) one regressor with its own specific configuration
b) the experiment parameters (number of repetitions, number of folds in case of crossvalidation, stratification...)
You can have a general description of the created object using the overridden print.GROAN.Workbench function.
It is possible to add other regressors to the created GROAN.Workbench object using addRegressor. Once the GROAN.Workbench is created it must be passed to GROAN.run to start the experiment.
createWorkbench

Usage

createWorkbench(
    folds = 10,
    reps = 5,
    stratified = FALSE,
    outfolder = NULL,
    saveHyperParms = FALSE,
    saveExtraData = FALSE,
    regressor = phenoRegressor.rrBLUP,
    regressor.name = "default regressor",
    ...
)

Arguments

folds number of folds for crossvalidation, defaults to 10. If NULL no crossvalidation happens and all training data will be used. In this case a second dataset, for test, is needed (see GROAN.run for details)
reps number of times the whole test must be repeated, defaults to 5
stratified boolean indicating whether GROAN should take into account data strata. This have two effects. First, the crossvalidation becomes stratified, meaning that folds will be split so that training and test sets will contain the same proportions of each data stratum. Second, prediction accuracy will be assessed (also) by strata. If no strata are present in the GROAN.NoisyDataSet object and stratified=TRUE all samples will be considered belonging to the same strata ("dummyStrata"). If stratified is FALSE (the default) GROAN will simply ignore the strata, even if present in the GROAN.NoisyDataSet.
outfolder folder where to save the data. If NULL (the default) nothing will be saved. File-names are standardized. If existing, accuracy and hyperparameter files will be updated, otherwise are created. ExtraData cannot be updated, so unique file-names will be generated using runId (see GROAN.run)
saveHyperParms boolean indicating if the hyperparameters from regressor training should be saved in outfolder. Defaults to FALSE.
saveExtraData boolean indicating if extradata from regressor training should be saved in outfolder as R objects (using the save function). Defaults to FALSE.
regressor regressor function. Defaults to phenoRegressor.rrBLUP
regressor.name string that will be used in reports. Keep that in mind when deciding names. Defaults to "default regressor"
...
extra parameter are passed to regressor function

Value

An instance of GROAN.Workbench

See Also

addRegressor GROAN.run createNoisyDataset
getNoisyPhenotype

Examples

#creating a Workbench with all default arguments
wb1 = createWorkbench()
#another Workbench, with different crossvalidation
wb2 = createWorkbench(folds=5, reps=20)
#a third one, with a different regressor and extra parameters passed to regressor function
wb3 = createWorkbench(regressor=phenoRegressor.BGLR, regressor.name='Bayesian Lasso', type='BL')

getNoisyPhenotype (Generate an instance of noisy phenotypes)

Description

Given a Noisy Dataset object, this function applies the noise injector to the data and returns a noisy version of it. It is useful for inspecting the noisy injector effects.

Usage

getNoisyPhenotype(nds)

Arguments

nds a Noisy Dataset object

Value

the phenotypes contained in nds with added noise.

GROAN.AI (Example data for pea AI lines)

Description

This list contains all data required to run GROAN examples. It refers to a pea experiment with 105 lines coming from a biparental Attika x Isard cross.

Usage

GROAN.AI
Format

A list with the following fields:

• “GROAN.AI$yield”: named array with 105 slots, containing data on grain yield [t/ha]
• “GROAN.AI$SNPs”: data frame with 105 rows and 647 variables. Each row is a pea AI line, each column a SNP marker. Values can either be 0, 1, or 2, representing the three possible genotypes (AA, Aa, and aa, respectively).
• “GROAN.AI$kinship”: square dataframe containing the realized kinships between all pairs of each of the 105 pea AI lines. Values were computed following the Astle & Balding metric. Higher values represent a higher degree of genetic similarity between lines. This metric mainly accounts for additive genetic contributions (as an alternative to dominant contributions).

Source

Annicchiarico et al., GBS-Based Genomic Selection for Pea Grain Yield under Severe Terminal Drought, The Plant Genome, Volume 10. doi: 10.3835/plantgenome2016.07.0072

Example data for pea KI lines

Description

This list contains all data required to run GROAN examples. It refers to a pea experiment with 103 lines coming from a biparental Kaspa x Isard cross.

Usage

GROAN.KI

Format

A list with the following fields:

• “GROAN.KI$yield”: named array with 103 slots, containing data on grain yield [t/ha]
• “GROAN.KI$SNPs”: data frame with 103 rows and 647 variables. Each row is a pea KI line, each column a SNP marker. Values can either be 0, 1, or 2, representing the three possible genotypes (AA, Aa, and aa, respectively).
• “GROAN.KI$kinship”: square dataframe containing the realized kinships between all pairs of each of the 103 pea KI lines. Values were computed following the Astle & Balding metric. Higher values represent a higher degree of genetic similarity between lines. This metric mainly accounts for additive genetic contributions (as an alternative to dominant contributions).

Source

Annicchiarico et al., GBS-Based Genomic Selection for Pea Grain Yield under Severe Terminal Drought, The Plant Genome, Volume 10. doi: 10.3835/plantgenome2016.07.0072
**GROAN.pea.kinship**

**Description**

This piece of data is deprecated and will be dismissed in next release. Please use GROAN.KI instead.

**Usage**

GROAN.pea.kinship

**Format**

A data frame with 103 rows and 103 variables. Row and column names are pea KI lines.

**Source**

Annicchiarico et al., *GBS-Based Genomic Selection for Pea Grain Yield under Severe Terminal Drought*, The Plant Genome, Volume 10. doi: 10.3835/plantgenome2016.07.0072

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**GROAN.pea.SNPs**

**Description**

This piece of data is deprecated and will be dismissed in next release. Please use GROAN.KI instead.

**Usage**

GROAN.pea.SNPs

**Format**

A data frame with 103 rows and 647 variables. Each row represent a pea KI line, each column a SNP marker.

**Source**

Annicchiarico et al., *GBS-Based Genomic Selection for Pea Grain Yield under Severe Terminal Drought*, The Plant Genome, Volume 10. doi: 10.3835/plantgenome2016.07.0072
**Description**

This piece of data is deprecated and will be dismissed in next release. Please use `GROAN.KI` instead.

**Usage**

`GROAN.pea.yield`

**Format**

A named array with 103 slots.

**Source**

Annicchiarico et al., *GBS-Based Genomic Selection for Pea Grain Yield under Severe Terminal Drought*, The Plant Genome, Volume 10. doi: 10.3835/plantgenome2016.07.0072

---

**GROAN.run**

*Compare Genomic Regressors on a Noisy Dataset*

**Description**

This function runs the experiment described in a `GROAN.Workbench` object, training regressor(s) on the data contained in a `GROAN.NoisyDataSet` object via parameter `nds`. The prediction accuracy is estimated either through crossvalidation or on separate test dataset supplied via parameter `nds.test`. It returns a `GROAN.Result` object, which have a `summary` function for quick inspection and can be fed to `plotResult` for visual comparisons. In case of crossvalidation the test dataset in the result object will report the `[CV]` suffix.

The experiment statistics are computed via `measurePredictionPerformance`.

Each time this function is invoked it will refer to a `runId` - an alphanumeric string identifying each specific run. The `runId` is usually generated internally, but it is possible to pass it if the intention is to join results from different runs for analysis purposes.

**Usage**

`GROAN.run(nds, wb, nds.test = NULL, run.id = createRunId())`
**Arguments**

- **nds**: a GROAN.NoisyDataSet object, containing the data (genotypes, phenotypes and so forth) plus a noiseInjector function.
- **wb**: a GROAN.Workbench object, containing the regressors to be tested together with the description of the experiment.
- **nds.test**: either a GROAN.NoisyDataSet or a list of GROAN.NoisyDataSet. The regression model(s) trained on nds will be tested on nds.test.
- **run.id**: an alphanumeric string identifying this specific run. If not passed it is generated using createRunId.

**Value**

A GROAN.Result object.

**See Also**

measurePredictionPerformance

**Examples**

```r
## Not run:
# Complete examples are found in the vignette
target = 'GROAN.vignette', package='GROAN')

# Minimal example
# 1) creating a noisy dataset with normal noise
nds = createNoisyDataset(
    name = 'PEA KI, normal noise',
    genotypes = GROAN.KI$SNPs,
    phenotypes = GROAN.KI$yield,
    noiseInjector = noiseInjector.norm,
    mean = 0,
    sd = sd(GROAN.KI$yield) * 0.5
)

# 2) creating a GROAN.WorkBench using default regressor and crossvalidation preset
wb = createWorkbench()

# 3) running the experiment
res = GROAN.run(nds, wb)

# 4) examining results
summary(res)
plotResult(res)

## End(Not run)
```
measurePredictionPerformance

*Measure Performance of a Prediction*

**Description**

This method returns several performance metrics for the passed predictions.

**Usage**

`measurePredictionPerformance(truevals, predvals)`

**Arguments**

- `truevals` true values
- `predvals` predicted values

**Value**

A named array with the following fields:

- `pearson` Pearson’s correlation
- `spearman` Spearman’s correlation (order based)
- `rmse` Root Mean Square Error
- `mae` Mean Absolute Error
- `coeff_det` Coefficient of determination

---

noiseInjector.dummy

*Noise Injector dummy function*

**Description**

This noise injector does not add any noise. Passed phenotypes are simply returned. This function is useful when comparing different regressors on the same dataset without the effect of extra injected noise.

**Usage**

`noiseInjector.dummy(phenotypes)`

**Arguments**

- `phenotypes` input phenotypes. This object will be returned without checks.
noiseInjector.norm

Value

the same passed phenotypes

See Also

Other noiseInjectors: noiseInjector.norm(), noiseInjector.swapper(), noiseInjector.unif()

Examples

```r
phenos = rnorm(10)
all(phenos == noiseInjector.dummy(phenos)) #TRUE
```

---

### noiseInjector.norm

**Inject Normal Noise**

**Description**

This function adds to the passed phenotypes array noise sampled from a normal distribution with
the specified mean and standard deviation.

The function can interest the totality of the passed phenotype array or a random subset of it (com-
manded by `subset` parameter).

**Usage**

```r
noiseInjector.norm(phenotypes, mean = 0, sd = 1, subset = 1)
```

**Arguments**

- **phenotypes**: an array of numbers.
- **mean**: mean of the normal distribution.
- **sd**: standard deviation of the normal distribution.
- **subset**: integer in [0,1], the proportion of original dataset to be injected

**Value**

An array, of the same size as phenotypes, where normal noise has been added to the original phe-
notype values.

**See Also**

Other noiseInjectors: noiseInjector.dummy(), noiseInjector.swapper(), noiseInjector.unif()
Examples

```r
# a sinusoid signal
phenos = sin(seq(0, 5, 0.1))
plot(phenos, type='p', pch=16, main='Original (black) vs. Injected (red), 100% affected')

# adding normal noise to all samples
phenos.noise = noiseInjector.norm(phenos, sd = 0.2)
points(phenos.noise, type='p', col='red')

# adding noise only to 30% of the samples
plot(phenos, type='p', pch=16, main='Original (black) vs. Injected (red), 30% affected')
phenos.noise.subset = noiseInjector.norm(phenos, sd = 0.2, subset = 0.3)
points(phenos.noise.subset, type='p', col='red')
```

Description

This function introduces swap noise, i.e. a number of couples of samples will have their phenotypes swapped. The number of couples is computed so that the total fraction of interested phenotypes approximates `subset`.

Usage

```r
noiseInjector.swapper(phenotypes, subset = 0.1)
```

Arguments

- `phenotypes`: an array of numbers
- `subset`: fraction of phenotypes to be interested by noise.

Value

the same passed phenotypes, but with some elements swapped

See Also

- Other noiseInjectors: `noiseInjector.dummy()`, `noiseInjector.norm()`, `noiseInjector.unif()`

Examples

```r
# a set of phenotypes
phenos = 1:10
# swapping two elements
phenos.sw2 = noiseInjector.swapper(phenos, 0.2)
# swapping four elements
```
noiseInjector.unif

phenos.sw4 = noiseInjector.swapper(phenos, 0.4)
# swapping four elements again, since 30% of 10 elements
# is rounded to 4 (two couples)
phenos.sw4.again = noiseInjector.swapper(phenos, 0.3)

---

**Inject Uniform Noise**

**Description**

This function adds to the passed phenotypes array noise sampled from a uniform distribution with the specified range. The function can interest the totality of the passed phenotype array or a random subset of it (commanded by subset parameter).

**Usage**

noiseInjector.unif(phenotypes, min = 0, max = 1, subset = 1)

**Arguments**

- **phenotypes** an array of numbers.
- **min, max** lower and upper limits of the distribution. Must be finite.
- **subset** integer in [0,1], the proportion of original dataset to be injected

**Value**

An array, of the same size as phenotypes, where uniform noise has been added to the original phenotype values.

**See Also**

Other noiseInjectors: `noiseInjector.dummy()`, `noiseInjector.norm()`, `noiseInjector.swapper()`

**Examples**

# a sinusoid signal
phenos = sin(seq(0, 5, 0.1))
plot(phenos, type='p', pch = 16, main='Original (black) vs. Injected (red), 100% affected')

# adding normal noise to all samples
phenos.noise = noiseInjector.unif(phenos, min=0.1, max=0.3)
points(phenos.noise, type='p', col='red')

# adding noise only to 30% of the samples
plot(phenos, type='p', pch = 16, main='Original (black) vs. Injected (red), 30% affected')
phenos.noise.subset = noiseInjector.unif(phenos, min=0.1, max=0.3, subset = 0.3)
points(phenos.noise.subset, type='p', col='red')
**Description**

This is a wrapper around BGLR. As such, it won’t work if BGLR package is not installed. Genotypes are modeled using the specified type. If type is 'RKHS' (and only in this case) the covariance/kinship matrix covariances is required, and it will be modeled as matrix K in BGLR terms. In all other cases genotypes and covariances are put in the model as X matrices. Extra covariates, if present, are modeled as FIXED effects.

**Usage**

```r
phenoRegressor.BGLR(
    phenotypes,
    genotypes,
    covariances,
    extraCovariates,
    type = c("FIXED", "BRR", "BL", "BayesA", "BayesB", "BayesC", "RKHS"),
    ...)
```

**Arguments**

- **phenotypes** : phenotypes, a numeric array (n x 1), missing values are predicted
- **genotypes** : SNP genotypes, one row per phenotype (n), one column per marker (m), values in 0/1/2 for diploids or 0/1/2/...ploidy for polyploids. Can be NULL if covariances is present.
- **covariances** : square matrix (n x n) of covariances. Can be NULL if genotypes is present.
- **extraCovariates** : extra covariates set, one row per phenotype (n), one column per covariate (w). If NULL no extra covariates are considered.
- **type** : character literal, one of the following: FIXED (Flat prior), BRR (Gaussian prior), BL (Double-Exponential prior), BayesA (scaled-t prior), BayesB (two component mixture prior with a point of mass at zero and a scaled-t slab), BayesC (two component mixture prior with a point of mass at zero and a Gaussian slab)

**Value**

The function returns a list with the following fields:

- **predictions** : an array of (n) predicted phenotypes, with NAs filled and all other positions repredicted (useful for calculating residuals)
- **hyperparams** : empty, returned for compatibility
- **extradata** : list with information on trained model, coming from BGLR
phenoRegressor.dummy

Regression dummy function

Description

This function is for development purposes. It returns, as "predictions", an array of random numbers. It accepts the standard inputs and produces a formally correct output. It is, obviously, quite fast.

Usage

phenoRegressor.dummy(phenotypes, genotypes, covariances, extraCovariates)
**Arguments**

- **phenotypes**: phenotypes, numeric array (n x 1), missing values are predicted.
- **genotypes**: SNP genotypes, one row per phenotype (n), one column per marker (m), values in 0/1/2 for diploids or 0/1/2/...ploidy for polyploids. Can be NULL if covariances is present.
- **covariances**: square matrix (n x n) of covariances. Can be NULL if genotypes is present.
- **extraCovariates**: extra covariates set, one row per phenotype (n), one column per covariate (w). If NULL no extra covariates are considered.

**Value**

The function should return a list with the following fields:

- **predictions**: an array of (k) predicted phenotypes
- **hyperparams**: named array of hyperparameters selected during training
- **extradata**: any extra information

**See Also**

Other phenoRegressors: `phenoRegressor.BGLR()`, `phenoRegressor.RFR()`, `phenoRegressor.SVR()`, `phenoRegressor.rrBLUP()`

**Examples**

```r
#genotypes are not really investigated. Only
#number of test phenotypes is used.
phenoRegressor.dummy(
  phenotypes = c(1:10, NA, NA, NA),
  genotypes = matrix(nrow = 13, ncol=30)
)
```

---

**Description**

This is a wrapper around `randomForest` and related functions. As such, this function will not work if randomForest package is not installed. There is no distinction between regular covariates (genotypes) and extra covariates (fixed effects) in random forest. If extra covariates are passed, they are put together with genotypes, side by side. Same thing happens with covariances matrix. This can bring to the scientifically questionable but technically correct situation of regressing on a big matrix made of SNP genotypes, covariances and other covariates, all collated side by side. The function makes no distinction, and it’s up to the user understand what is correct in each specific experiment.

**WARNING**: this function can be *very* slow, especially when called on thousands of SNPs.
Usage

phenoRegressor.RFR(
    phenotypes,
    genotypes,
    covariances,
    extraCovariates,
    ntree = ceiling(length(phenotypes)/5),
    ...
)

Arguments

phenotypes phenotypes, a numeric array (n x 1), missing values are predicted

genotypes SNP genotypes, one row per phenotype (n), one column per marker (m), values in 0/1/2 for diploids or 0/1/2/...ploidy for polyploids. Can be NULL if covariances is present.

covariances square matrix (n x n) of covariances. Can be NULL if genotypes is present.

extraCovariates extra covariates set, one row per phenotype (n), one column per covariate (w). If NULL no extra covariates are considered.

ntree number of trees to grow, defaults to a fifth of the number of samples (rounded up). As per randomForest documentation, it should not be set to too small a number, to ensure that every input row gets predicted at least a few times

... any extra parameter is passed to randomForest::randomForest()

Value

The function returns a list with the following fields:

- predictions : an array of (k) predicted phenotypes
- hyperparams : named vector with the following keys: ntree (number of grown trees) and mtry (number of variables randomly sampled as candidates at each split)
- extradata : the object returned by randomForest::randomForest(), containing the full trained forest and the used parameters

See Also

randomForest

Other phenoRegressors: phenoRegressor.BGLR(), phenoRegressor.SVR(), phenoRegressor.dummy(), phenoRegressor.rrBLUP()

Examples

## Not run:
# using the GROAN.KI dataset, we regress on the dataset and predict the first ten phenotypes
phenos = GROAN.KI$yield
phenos[1:10] = NA
# calling the regressor with random forest
results = phenoRegressor.RFR(
    phenotypes = phenos,
    genotypes = GROAN.KI$SNPs,
    covariances = NULL,
    extraCovariates = NULL,
    ntree = 20,
    mtry = 200 # randomForest-specific parameters
)

# examining the predictions
plot(GROAN.KI$yield, results$predictions,
     main = 'Train set (black) and test set (red) regressions',
     xlab = 'Original phenotypes', ylab = 'Predicted phenotypes')
points(GROAN.KI$yield[1:10], results$predictions[1:10], pch=16, col='red')

# printing correlations
test.set.correlation = cor(GROAN.KI$yield[1:10], results$predictions[1:10])
train.set.correlation = cor(GROAN.KI$yield[-(1:10)], results$predictions[-(1:10)])
writeLines(paste(
    'test-set correlation :', test.set.correlation,
    '\ntrain-set correlation:', train.set.correlation
))

## End(Not run)

---

**phenoRegressor.rrBLUP**  
*SNP-BLUP or G-BLUP using rrBLUP package*

**Description**

This is a wrapper around rrBLUP function `mixed.solve`. It can either work with genotypes (in form of a SNP matrix) or with kinships (in form of a covariance matrix). In the first case the function will implement a SNP-BLUP, in the second a G-BLUP. An error is returned if both SNPs and covariance matrix are passed.

In rrBLUP terms, genotypes are modeled as random effects (matrix Z), covariances as matrix K, and extra covariates, if present, as fixed effects (matrix X).

Please note that this function won’t work if rrBLUP package is not installed.

**Usage**

```r
phenoRegressor.rrBLUP(
    phenotypes,
    genotypes = NULL,
    covariances = NULL,
    extraCovariates = NULL,
    ...
)
```
Arguments

- **phenotypes**: a numeric array \((n \times 1)\), missing values are predicted
- **genotypes**: SNP genotypes, one row per phenotype \((n)\), one column per marker \((m)\), values in 0/1/2 for diploids or 0/1/2/...ploidy for polyploids. Can be NULL if covariances is present.
- **covariances**: square matrix \((n \times n)\) of covariances.
- **extraCovariates**: optional extra covariates set, one row per phenotype \((n)\), one column per covariate \((w)\). If NULL no extra covariates are considered.

... extra parameters are passed to rrBLUP::mixed.solve

Value

The function returns a list with the following fields:

- **predictions**: an array of \((k)\) predicted phenotypes
- **hyperparams**: named vector with the following keys: \(V_u, V_e, \beta, L_L\)
- **extradata**: list with information on trained model, coming from `mixed.solve`

See Also

- `mixed.solve`
- Other phenoRegressors: `phenoRegressor.BGLR()`, `phenoRegressor.RFR()`, `phenoRegressor.SVR()`, `phenoRegressor.dummy()`

Examples

```r
## Not run:
# using the GROAN.KI dataset, we regress on the dataset and predict the first ten phenotypes
phenos = GROAN.KI$yield
phenos[1:10] = NA

# calling the regressor with ridge regression BLUP on SNPs and kinship
results.SNP.BLUP = phenoRegressor.rrBLUP(
  phenotypes = phenos,
  genotypes = GROAN.KI$SNPs,
  SE = TRUE, return.Hinv = TRUE # rrBLUP-specific parameters
)
results.G.BLUP = phenoRegressor.rrBLUP(
  phenotypes = phenos,
  covariances = GROAN.KI$kinship,
  SE = TRUE, return.Hinv = TRUE # rrBLUP-specific parameters
)

# examining the predictions
plot(GROAN.KI$yield, results.SNP.BLUP$predictions,
     main = 'SNP-BLUP Train set (black) and test set (red) regressions',
     xlab = 'Original phenotypes', ylab = 'Predicted phenotypes')
abline(a=0, b=1)
```
points(GROAN.KI$yield[1:10], results.SNP.BLUP$predictions[1:10], pch=16, col='red')

plot(GROAN.KI$yield, results.G.BLUP$predictions, 
    main ='[G-BLUP] Train set (black) and test set (red) regressions', 
    xlab = 'Original phenotypes', ylab = 'Predicted phenotypes')
abline(a=0, b=1)
points(GROAN.KI$yield[1:10], results.G.BLUP$predictions[1:10], pch=16, col='red')

#printing correlations
correlations = data.frame(
    model = 'SNP-BLUP',
    test_set_correlations = cor(GROAN.KI$yield[1:10], results.SNP.BLUP$predictions[1:10]),
    train_set_correlations = cor(GROAN.KI$yield[-(1:10)], results.SNP.BLUP$predictions[-(1:10)])
)
correlations = rbind(correlations, data.frame(
    model = 'G-BLUP',
    test_set_correlations = cor(GROAN.KI$yield[1:10], results.G.BLUP$predictions[1:10]),
    train_set_correlations = cor(GROAN.KI$yield[-(1:10)], results.G.BLUP$predictions[-(1:10)])
))
print(correlations)

## End(Not run)

---

phenoRegressor.SVR  

**Support Vector Regression using package e1071**

**Description**

This is a wrapper around several functions from e1071 package (as such, it won’t work if e1071 package is not installed). This function implements Support Vector Regressions, meaning that the data points are projected in a transformed higher dimensional space where linear regression is possible.

phenoRegressor.SVR can operate in three modes: run, train and tune.

In **run** mode you need to pass the function an already tuned/trained SVR model, typically obtained either directly from e1071 functions (e.g. from svm, best.svm and so forth) or from a previous run of phenoRegressor.SVR in a different mode. The passed model is applied to the passed dataset and predictions are returned.

In **train** mode a SVR model will be trained on the passed dataset using the passed hyper parameters. The trained model will then be used for predictions.

In **tune** mode you need to pass one or more sets of hyperparameters. The best combination of hyperparameters will be selected through crossvalidation. The best performing SVR model will be used for final predictions. This mode can be very slow.

There is no distinction between regular covariates (genotypes) and extra covariates (fixed effects) in Support Vector Regression. If extra covariates are passed, they are put together with genotypes, side by side. Same thing happens with covariances matrix. This can bring to the scientifically questionable but technically correct situation of regressing on a big matrix made of SNP genotypes, covariances and other covariates, all collated side by side. The function makes no distinction, and
*phenoRegressor.SVR*

it's up to the user understand what is correct in each specific experiment.

**Usage**

```r
phenoRegressor.SVR(
  phenotypes, 
  genotypes, 
  covariances, 
  extraCovariates, 
  mode = c("tune", "train", "run"), 
  tuned.model = NULL, 
  scale.pheno = TRUE, 
  scale.geno = FALSE, 
  ...
)
```

**Arguments**

- **phenotypes**: phenotypes, a numeric array (n x 1), missing values are predicted
- **genotypes**: SNP genotypes, one row per phenotype (n), one column per marker (m), values in 0/1/2 for diploids or 0/1/2/...ploidy for polyploids. Can be NULL if covariances is present.
- **covariances**: square matrix (n x n) of covariances. Can be NULL if genotypes is present.
- **extraCovariates**: extra covariates set, one row per phenotype (n), one column per covariate (w). If NULL no extra covariates are considered.
- **mode**: this parameter decides what will happen with the passed dataset
  - `mode = "tune"`: hyperparameters will be tuned on a grid (you may want to specify its values using extra params) with a call to `e1071::tune.svm`. Use this option if you have no idea about the optimal choice of hyperparameters. This mode can be very slow.
  - `mode = "train"`: an SVR will be trained on the train dataset using the passed hyperparameters (if you know them). This more invokes `e1071::train`
  - `mode = "run"`: you already have a tuned and trained SVR (put it into tuned.model) and want to use it. The fastest mode.
- **tuned.model**: a tuned and trained SVR to be used for prediction. This object is only used if mode is equal to "run".
- **scale.pheno**: if TRUE (default) the phenotypes will be scaled and centered (before tuning or before applying the passed tuned model).
- **scale.geno**: if TRUE the genotypes will be scaled and centered (before tuning or before applying the passed tuned model). It is usually not a good idea, since it leads to worse results. Defaults to FALSE.
- **...**: all extra parameters are passed to `e1071::svm` or `e1071::tune.svm`
The function returns a list with the following fields:

- **predictions**: an array of (n) predicted phenotypes
- **hyperparams**: named vector with the following keys: gamma, cost, coef0, nu, epsilon. Some of the values may not make sense given the selected model, and will contain default values from e1071 library.
- **extradata**: depending on `mode` parameter, extradata will contain one of the following: 1) a SVM object returned by `e1071::tune.svm`, containing both the best performing model and the description of the training process 2) a newly trained SVR model 3) the same object passed as `tuned.model`

### See Also

- `svm`, `tune.svm`, `best.svm` from e1071 package

Other `phenoRegressors`: `phenoRegressor.BGLR()`, `phenoRegressor.RFR()`, `phenoRegressor.dummy()`, `phenoRegressor.rrBLUP()`

### Examples

```r
## Not run:
### WARNING ###
The '/quotesingle;Var tuning/quotesingle;' part of the example can take quite some time to run,
#depending on the computational power.

#using the GROAN.KI dataset, we regress on the dataset and predict the first ten phenotypes
phenos = GROAN.KI$yield
phenos[1:10] = NA

#-------- TUNE --------
#tuning the SVR on a grid of hyperparameters
results.tune = phenoRegressor.SVR(
  phenotypes = phenos,
  genotypes = GROAN.KI$SNPs,
  covariances = NULL,
  extraCovariates = NULL,
  mode = '/quotesingle;Var tune/quotesingle;',
  kernel = '/quotesingle;Var linear/quotesingle;',
  cost = 10^(-3:+3) #SVR-specific parameters
)

#examining the predictions
plot(GROAN.KI$yield, results.tune$predictions,
  main = 'Mode = Tuning\nTrain set (black) and test set (red) regressions',
  xlab = 'Original phenotypes', ylab = 'Predicted phenotypes')
points(GROAN.KI$yield[1:10], results.tune$predictions[1:10], pch=16, col='red')

# printing correlations

test.set.correlation = cor(GROAN.KI$yield[1:10], results.tune$predictions[1:10])
train.set.correlation = cor(GROAN.KI$yield[-(1:10)], results.tune$predictions[-(1:10)])
writeLines(paste(}
```
#--------- TRAIN ---------
# training the SVR, hyperparameters are given
results.train = phenoRegressor.SVR(
    phenotypes = phenos,
    genotypes = GROAN.KI$SNPs,
    covariances = NULL,
    extraCovariates = NULL,
    mode = 'train',
    kernel = 'linear', cost = 0.01 #SVR-specific parameters
)

# examining the predictions
plot(GROAN.KI$yield, results.train$predictions,
     main = 'Mode = TRAIN\nTrain set (black) and test set (red) regressions',
     xlab = 'Original phenotypes', ylab = 'Predicted phenotypes')
points(GROAN.KI$yield[1:10], results.train$predictions[1:10], pch=16, col='red')

# printing correlations
test.set.correlation = cor(GROAN.KI$yield[1:10], results.train$predictions[1:10])
train.set.correlation = cor(GROAN.KI$yield[-(1:10)], results.train$predictions[-(1:10)])
writelines(paste(
    'test-set correlation :', test.set.correlation,
    '\ntrain-set correlation: ', train.set.correlation
))

#--------- RUN ---------
# we recover the trained model from previous run, predictions will be exactly the same
results.run = phenoRegressor.SVR(
    phenotypes = phenos,
    genotypes = GROAN.KI$SNPs,
    covariances = NULL,
    extraCovariates = NULL,
    mode = 'run',
    tuned.model = results.train$extradata
)

# examining the predictions
plot(GROAN.KI$yield, results.run$predictions,
     main = 'Mode = RUN\nTrain set (black) and test set (red) regressions',
     xlab = 'Original phenotypes', ylab = 'Predicted phenotypes')
points(GROAN.KI$yield[1:10], results.run$predictions[1:10], pch=16, col='red')

# printing correlations
test.set.correlation = cor(GROAN.KI$yield[1:10], results.run$predictions[1:10])
train.set.correlation = cor(GROAN.KI$yield[-(1:10)], results.run$predictions[-(1:10)])
writelines(paste(
    'test-set correlation :', test.set.correlation,
    '\ntrain-set correlation: ', train.set.correlation
))
plotResult

Plot results of a run

Description

This function uses ggplot2 package (which must be installed) to graphically render the result of a run. The function receive as input the output of GROAN.run and returns a ggplot2 object (that can be further customized). Currently implemented types of plot are:

- **box**: boxplot, showing the distribution of repetitions. See `geom_boxplot`
- **bar**: barplot, showing the average over repetitions. See `stat_summary`
- **bar_conf95**: same as 'bar', but with 95% confidence intervals

Usage

```r
plotResult(
  res,
  variable = c("pearson", "spearman", "rmse", "time_per_fold", "coeff_det", "mae"),
  x.label = c("both", "train_only", "test_only"),
  plot.type = c("box", "bar", "bar_conf95"),
  strata = c("no_strata", "avg_strata", "single")
)
```

Arguments

- **res**: a result data frame containing the output of GROAN.run
- **variable**: name of the variable to be used as y values
- **x.label**: select what to put on x-axis between both train and test dataset (default), train dataset only or test dataset only
- **plot.type**: a string indicating the type of plot to be obtained
- **strata**: string determining behaviour toward strata. If 'no_strata' will plot accuracies not considering strata. If 'avg_strata' will average single strata accuracies. If 'single' each strata will be represented separately.

Value

a ggplot2 object
**print.GROAN.NoisyDataset**  
*Print a GROAN Noisy Dataset object*

**Description**
Short description for class GROAN.NoisyDataset, created with createNoisyDataset.

**Usage**
```r
## S3 method for class 'GROAN.NoisyDataset'
print(x, ...)
```

**Arguments**
- `x` object of class GROAN.NoisyDataset.
- `...` ignored, put here to match S3 function signature

**Value**
This function returns the original GROAN.NoisyDataset object invisibly (via invisible(x))

---

**print.GROAN.Workbench**  
*Print a GROAN Workbench object*

**Description**
Short description for class GROAN.Workbench, created with createWorkbench.

**Usage**
```r
## S3 method for class 'GROAN.Workbench'
print(x, ...)
```

**Arguments**
- `x` object of class GROAN.Workbench.
- `...` ignored, put here to match S3 function signature

**Value**
This function returns the original GROAN.Workbench object invisibly (via invisible(x))
Summary for GROAN Noisy Dataset object

Description

Returns a dataframe with some description of an object created with `createNoisyDataset`.

Usage

```r
## S3 method for class 'GROAN.NoisyDataset'
summary(object, ...)
```

Arguments

- `object`: instance of class `GROAN.NoisyDataset`.
- `...`: additional arguments ignored, added for compatibility to generic `summary` function.

Value

A data frame with `GROAN.NoisyDataset` stats.

Summary of GROAN.Result

Description

Performance metrics are averaged over repetitions, so that a data.frame is produced with one row per dataset/regressor/extra_covariates/strata/samples/markers/folds combination.

Usage

```r
## S3 method for class 'GROAN.Result'
summary(object, ...)
```

Arguments

- `object`: an object returned from `GROAN.run`.
- `...`: additional arguments ignored, added for compatibility to generic `summary` function.

Value

A data frame with averaged statistics.
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