R documentation

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R topics documented:

`downsample` *Downsample an image.*

Description

Downsample an image.

Usage

```
downsample(img, subFactor = 1, method = c("FLIRT", "SUBSAMP2"),
  bin = FALSE, thresh = 0.9)
```

Arguments

`img`	An image of class `nifti`.
`subFactor`	Downsampling factor.
`method`	Downsampling method.
`bin`	`logical`. Set to `TRUE` for downsampling of binary images or masks.
`thresh`	Treshhold for re-binarisation of downsampled binary images and masks. A threshold near 1 (say 0.9) is conservative according to FLIRT FAQ.

Value

A downsampled image.

`getSNPfdr` *Get False Discovery Rates.*

Description

Get False Discovery Rates.

Usage

```
getSNPfdr(p.value, eff.no.tests)
```

Arguments

`p.value`	A vector of raw p-values.
`eff.no.tests`	Efficient number of performed tests.

Value

A summary of FDR q-values.

`getSNPresults` *Get vGWAS results for selected SNPs.*

Description

Get vGWAS results for selected SNPs.

Usage

```
getSNPresults(meh, sel.snps)
```

Arguments

`meh`	vGWAS results.
`sel.snps`	`character` vector of SNP names.

Value

A named list of results for each SNP.

performVGWAS *Perform voxelwise genome-wide association study.*

Description

Loads and prepares the data, runs preliminary (if necessary) and full analyses. Then visualises the results.

Usage

```
performVGWAS(genePath, niiFiles, niiIDs, ref.imgPath, maskPath, subFactor,
  covar = character(), errorCovariance = numeric(),
  out.subFactor = subFactor, matPath = NULL, outPath = NULL,
  force.snps = NULL, useModel = MatrixEQTL::modelLINEAR, top.thresh = 5,
  log.cutoff = 4, eff.no.tests = 275575, sampleSize = NULL,
  randomSample = FALSE, visualise = TRUE, mockPath.flatROIs = NULL,
  mockPath.pre = NULL)
```

Arguments

genePath	Path to a directory containing plink files with genomic data.
niiFiles	Paths to files containing imaging data.
niiIDs	Subject IDs for each image. Shuffle for permutation tests.
ref.imgPath	Path to a referance image.
maskPath	Path to an image mask.
subFactor	Downsampling factor.
covar	Covariates matrix with subject IDs as column names.
errorCovariance	Covariance matrix for the error term. Set to `numeric()` for multiple of identity (default, most cases).
out.subFactor	Output images downsampling factor. Default: equal to `subFactor`.
matPath	Path to convolution matrix for coregistration of results to the reference image. Set to `NULL` if in the same space.
outPath	Path to output directory.
force.snps	`character` vector of SNPs forced to be analysed even if not passing the quality control.
useModel	Regression model to use.
top.thresh	Number of top SNPs to be analysed and visualised.
log.cutoff	Negative log p-value cutoff value for results visualisation.
eff.no.tests	Effective number of tests (SNPs) for p-value correction.
sampleSize	Subject sample size.
randomSample	`logical`. Set to `TRUE` for subject sample randomisation.
visualise	`logical`. Set to `FALSE` to disable results visualisation for bigger analyses.

`mockPath.flatROIs`
: Path to input file with saved flatROIs object for vGWAS mocking. Mock parameters should match original parameters. Useful for registering results to different standard spaces and resolutions, selecting alternative SNPs for the full analysys, of using different genetic models.

`mockPath.pre`
: Path to input file with saved preliminary analysis results object for vGWAS mocking. Mock parameters should match original parameters. Useful for registering results to different standard spaces and resolutions, selecting alternative SNPs for the full analysys, of using different genetic models. `NULL` for real analyses.

Value

A list containing all the resulting statistical parametric maps.

`readFlatROIs` *Read flattened ROIs from a list of NIfTI files using a cluster of choice.*

Description

Read flattened ROIs from a list of NIfTI files using a cluster of choice.

Usage

```
readFlatROIs(paths, ids, subFactor = 0, mask = NULL, method = c("FLIRT",
  "SUBSAMP2"), nCores = getOption("mc.cores", detectCores(logical = FALSE)),
  clType = "PSOCK", makeCluster = TRUE, userCluster = NULL)
```

Arguments

`paths`	A list of paths to the NIfTI files.
`ids`	A list of subject IDs.
`subFactor`	Downsampling factor.
`mask`	Image mask (a `nifti` object or an array).
`method`	Downsampling method.
`nCores`	number of cores to use. Default: all physical cores available
`clType`	cluster type. Default: `PSOCK`
`makeCluster`	`logical`. `TRUE` if a cluster should be made (default).
`userCluster`	Cluster to use specified by the user. If `NULL` and makeCluster is `FALSE`, a default cluster will be used.

Value

Array of chosen voxel intensities for all the subjects.

`readSNPs` *Read SNPs performing genome quality control.*

Description

Read SNPs performing genome quality control.

Usage

```
readSNPs(plinkFiles, call.rate.cutoff = 0.95, maf.cutoff = 0.1,
  hwe.pval = 5.7e-07, force.snps = NULL, forcedOnly = FALSE,
  outPath = NULL)
```

Arguments

`plinkFiles`	Paths to the plink files
`call.rate.cutoff`	Call rate cutoff value
`maf.cutoff`	Minor allele frequency cutoff value
`hwe.pval`	Hardy-Weinberg equilibrium p-value cutoff value
`force.snps`	`character` vector of SNPs forced to be analysed even if not passing the quality control.
`forcedOnly`	`logical`. If `TRUE`, only the SNPs of interest will be analysed, regardless of their data quality.
`outPath`	A character string giving the base filenamefor optional output of QC-ed data. The extensions .bed, .bim, and .fam are appended to this string to give the filenames of the three output files.

Value

`SnpMatrix` of SNPs passing the quality control

`RImaGen` *RImaGen: An R package for voxelwise genome-wide association studies.*

Description

This package allows you to perform vGWAS analyses as described in Stein et al., 2010, but faster.

selectSNPs *Select SNPs by name from a SlicedData object.*

Description

Select SNPs by name from a SlicedData object.

Usage

```
selectSNPs(sel.snps, snpData)
```

Arguments

sel.snps	character vector of SNP names.
snpData	SlicedData object containing SNP data.

Value

Array containing selected SNP data.

vGWAS *Perform voxelwise genome-wide association analysis.*

Description

Checks for associations prepared SlicedData objects containing flattened image ROIs, genomic data and covariates. Wrapper for Matrix_eQTL_engine.

Usage

```
vGWAS(snpData, voxelData, cvrt, useModel, prescan,
  errorCovariance = numeric(), pvalue.hist = FALSE)
```

Arguments

snpData	SlicedData object containing selected SNPs.
voxelData	SlicedData object containing flat voxel ROIs.
cvrt	SlicedData object containing covariates.
useModel	Regression model to use.
prescan	logical. TRUE for preliminary analysis allowing "winning SNP" ranking.
errorCovariance	numeric. The error covariance matrix. Use numeric() for homoskedastic independent errors.
pvalue.hist	logical, numeric or "qq-plot". Defines whether and how the distribution of p-values is recorded in the returned object. Set to FALSE for a faster analysis. To record information for a histogram set to the number of bins. To record information for a qq-plot, set to qq-plot. Use plot on the returned object.

Value

vGWAS results.

`visualiseSNP` *Visualise by-voxel statistics for a chosen SNP, e.g that SNP's p-value per voxel.*

Description

Visualise by-voxel statistics for a chosen SNP, e.g that SNP's p-value per voxel.

Usage

```
visualiseSNP(snp.name, results, mask, ref.img, pv.range = NULL,
  log.cutoff = 0, plot = TRUE, title = snp.name, titleSize = 2,
  beforeTitle = "-log10 p-values by\n", afterTitle = "", outPath = NULL,
  matPath = NULL)
```

Arguments

`snp.name`	Chosen SNP name.
`results`	A named list of results for each SNP.
`mask`	Image mask (a `nifti` object or an array).
`ref.img`	Reference image.
`pv.range`	P-value range for scale.
`log.cutoff`	Negative log p-value cutoff value.
`plot`	`logical`. Set to `TRUE` for automated plotting of the results.
`title`	Plot title.
`titleSize`	Title font size.
`beforeTitle`	Text to print before the title.
`afterTitle`	Text to print after the title.
`outPath`	Output path. If `NULL` (default) no plot files will be saved.
`matPath`	Path to convolution matrix for coregistration of results to the reference image. Set to `NULL` if in the same space.

Value

Results visualisation image.

visualiseVox *Visualise by-voxel statistics for each voxel, e.g winning SNP p-value per voxel.*

Description

Visualise by-voxel statistics for each voxel, e.g winning SNP p-value per voxel.

Usage

```
visualiseVox(result, mask, ref.img, pv.range = NULL, log.cutoff = 0,
  plot = TRUE, title = "winning SNP", titleSize = 2,
  beforeTitle = "-log10 p-values by\n", afterTitle = "", outPath = NULL,
  matPath = NULL)
```

Arguments

result	Vector of target statistics.
mask	Image mask.
ref.img	Reference image.
pv.range	P-value range for scale.
log.cutoff	Negative log p-value cutoff value.
plot	logical. Set to TRUE for automated plotting of the results.
title	Plot title.
titleSize	Title font size.
beforeTitle	Text to print before the title.
afterTitle	Text to print after the title.#'
outPath	Output path. If NULL (default) no plot files will be saved.
matPath	Path to convolution matrix for coregistration of results to the reference image. Set to NULL if in the same space.

Value

Results visualisation image.

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