Package ‘vcpen’

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### kernel_linear

**Variance Component Linear Kernel Matrix**

**Description**

Variance component Linear kernel matrix from genotype dosage

**Usage**

```r
kernel_linear(dose, method = "linear")
```

**Arguments**

- `dose`: data.frame or matrix with
- `method`: type of kernel; currently only linear kernel implemented

**Value**

square symmetric kernel matrix for subject similarity by genotype dosage

**Author(s)**

JP Sinnwell, DJ Schaid

**See Also**

vcpen

**Examples**

```r
data(vcexample)
Kern1 <- kernel_linear(dose[,which(doseinfo[,1]==1)], method="linear")
Kern1[1:5,1:5]
```

### minque

**MINQUE estimation of variance components**

**Description**

Estimate variance components by MINQUE method, allowing multiple iterations

**Usage**

```r
minque(y, X, Kerns, n.iter = 1, eps = 0.001)
```
Arguments

y Numeric vector of traits. Only continuous trait currently allowed.
X Matrix of covariates (columns) for subjects (rows), matching subjects in the trait (y) vector.
Kerns List of kernel matrices: a kernel matrix for each variance component. The last kernel matrix in the list (an identity matrix) is for the residual variance component.
n.iter Number of minque iterations
eps Default small positive value for non-positive vc estimates within iterations.

Value

List with estimates of variance components (vc), covariate regression coefficients (beta), and residuals of model fit.

Author(s)

JP Sinnwell, DJ Schaid

Examples

data(vcexample)
nvc <- 1+length(unique(doseinfo[,2]))
id <- 1:nrow(dose)
## vc for genetic kernel matrices
Kerns <- vector("list", length=nvc)
for(i in 1:(nvc-1)){
  Kerns[[i]] <- kernel_linear(dose[,grep(i, doseinfo[,2])])
  rownames(Kerns[[i]]) <- id
  colnames(Kerns[[i]]) <- id
}
## vc for residual variance
Kerns[[nvc]] <- diag(nrow(dose))
rownames(Kerns[[nvc]]) <- id
colnames(Kerns[[nvc]]) <- id
prefit <- minque(response, covmat, Kerns, n.iter=2)
prefit[1]
prefit[2]
fit <- vcpen(response, covmat, Kerns, vc_init = prefit$vc)

vcexample

Example data for Penalized Variance Component method

Description

Datasets for an example run of vcpen with 4 variance components calculated as kernel matrices from genotype dosage (dose) on 100 subjects with two covariates (covmat), and a continuous response.
Format

The example contains three data.frames and a response vector for 100 subjects at 70 SNPs accross 4 variance components:

- `covmat` two arbitrary covariates (columns) for 100 subjects (rows)
- `dose` genotype dosage at 70 SNPs (columns) and 100 subjects (rows)
- `doseinfo` 2-column matrix with indices for grouping SNPs into variance components (for Kernel Matrix)
- `response` continuous response vector for 100 subjects

Examples

```r
data(vcexample)
dim(dose)
dim(doseinfo)
dim(covmat)
length(response)
```

---

vcpen

**Penalized Variance Components**

Description

Penalized Variance Component analysis

Usage

```r
vcpen(
    y,
    X,
    Kerns,
    frac1 = 0.8,
    lambda_factor = NULL,
    lambda_grid = NULL,
    maxiter = 1000,
    vc_init = NULL,
    print_iter = FALSE
)
```

## S3 method for class 'vcpen'

```r
summary(object, ..., digits = 4)
```
Arguments

\(y\) Numeric vector of traits. Only continuous trait currently allowed.

\(X\) Matrix of covariates (columns) for subjects (rows), matching subjects in the trait (y) vector.

Kerns List of kernel matrices: a kernel matrix for each variance component. The last kernel matrix in the list (an identity matrix) is for the residual variance component.

frac1 Fraction of penalty imposed on L1 penalty, between 0 and 1 (0 for only L2; 1 for only L1 penalty).

lambda_factor Weight for each vc (values between 0 and 1) for how much it should be penalized: 0 means no penalty. Default value of NULL implies weight of 1 for all vc’s.

lambda_grid Vector of lambda penalties for fitting the penalized model. Best to order values from largest to smallest so parameter estimates from a large penalty can be used as initial values for the next smaller penalty. Default value of NULL implies initial values of seq(from=.10, to=0, by=-0.01).

maxiter Maximum number of iterations allowed during penalized fitting.

vc_init Numeric vector of initial values for variance components. Default value of NULL implies initial values determined by 2 iterations of minque estimation.

print_iter Logical: if TRUE, print the iteration results (mainly for refined checks)

object Fitted vcpen object (used in summary method)

... Optional arguments for summary method

digits Significant digits for summary method

Value

object with S3 class vcpen

Author(s)

JP Sinnwell, DJ Schaid

Examples

data(vcexample)
nvc <- 1+length(unique(doseinfo[,2]))
id <- 1:nrow(dose)
## vcs for genetic kernel matrices
Kerns <- vector("list", length=nvc)
for(i in 1:(nvc-1)){
  Kerns[[i]] <- kernel_linear(dose[,grep(i, doseinfo[,2])])
  rownames(Kerns[[i]]) <- id
  colnames(Kerns[[i]]) <- id
}
## vc for residual variance
Kerns[[nvc]] <- diag(nrow(dose))
rownames(Kerns[[nvc]]) <- id
colnames(Kerns[[nvc]]) <- id
fit <- vcpen(response, covmat, Kerns, frac1 = .6)
summary(fit)
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