Package ‘vcpen’

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kernel_linear

Variance Component Linear Kernel Matrix

Description
Variance component Linear kernel matrix from genotype dosage

Usage
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
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
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)
## 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
prefit <- minque(response, covmat, Kerns, n.iter=2)
prefit[1]
prefit[2]
fit <- vcpen(response, covmat, Kerns, vc_init = prefit$vc)

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 across 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

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

vcpen

Penalized Variance Components

Description

Penalized Variance Component analysis

Usage

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'
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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