

# Package: vcpen (via r-universe)

October 23, 2024

**Type** Package

**Title** Penalized Variance Components Analysis

**Version** 1.9

**Date** 2022-01-02

**Description** Method to perform penalized variance component analysis.

**License** GPL (>= 3)

**Suggests** rmarkdown, testthat

**Depends** R (>= 4.0.0), methods

**Imports** knitr, Rcpp (>= 1.0.0), RcppArmadillo (>= 0.8.0)

**LinkingTo** Rcpp, RcppArmadillo

**NeedsCompilation** yes

**RoxygenNote** 7.1.2

**VignetteBuilder** knitr

**URL** <https://cran.r-project.org/package=vcpen>

**Author** Jason Sinnwell [aut, cre]

(<https://orcid.org/0000-0003-1964-5522>), Daniel Schaid [aut]

(<https://orcid.org/0000-0003-1457-6433>)

**Maintainer** Jason Sinnwell <[sinnwell.jason@mayo.edu](mailto:sinnwell.jason@mayo.edu)>

**Repository** CRAN

**Date/Publication** 2022-01-03 16:40:02 UTC

## Contents

kernel_linear . . . . .	2
minque . . . . .	2
vcexample . . . . .	3
vcpen . . . . .	4

<b>Index</b>	<b>7</b>
--------------	----------

---

kernel_linear	<i>Variance Component Linear Kernel Matrix</i>
---------------	--

---

**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	<i>MINQUE estimation of variance components</i>
--------	---

---

**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)
```

---

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 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**

<code>y</code>	Numeric vector of traits. Only continuous trait currently allowed.
<code>X</code>	Matrix of covariates (columns) for subjects (rows), matching subjects in the trait ( <code>y</code> ) vector.
<code>Kerns</code>	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.
<code>frac1</code>	Fraction of penalty imposed on L1 penalty, between 0 and 1 (0 for only L2; 1 for only L1 penalty).
<code>lambda_factor</code>	Weight for each <code>vc</code> (values between 0 and 1) for how much it should be penalized: 0 means no penalty. Default value of <code>NULL</code> implies weight of 1 for all <code>vc</code> 's.
<code>lambda_grid</code>	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 <code>NULL</code> implies initial values of <code>seq(from=.10, to=0, by=-0.01)</code> .
<code>maxiter</code>	Maximum number of iterations allowed during penalized fitting.
<code>vc_init</code>	Numeric vector of initial values for variance components. Default value of <code>NULL</code> implies initial values determined by 2 iterations of minque estimation.
<code>print_iter</code>	Logical: if <code>TRUE</code> , print the iteration results (mainly for refined checks)
<code>object</code>	Fitted <code>vcpen</code> object (used in summary method)
<code>...</code>	Optional arguments for summary method
<code>digits</code>	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)
```

# Index

`covmat (vcexample)`, 3  
`dose (vcexample)`, 3  
`doseinfo (vcexample)`, 3  
`kernel_linear`, 2  
`minque`, 2  
`response (vcexample)`, 3  
`summary.vcpen (vcpen)`, 4  
`vcexample`, 3  
`vcpen`, 2, 4