

# Package: capr (via r-universe)

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**Title** Covariate Assisted Principal Regression

**Version** 0.2.0

**Author** Xi Luo [aut, cre], Yi Zhao [aut], Brian Caffo [aut]

**Maintainer** Xi Luo <xi.rossi.luo@gmail.com>

**Description** Covariate Assisted Principal Regression (CAPR) for multiple covariance-matrix outcomes. The method identifies (principal) projection directions that maximize the log-likelihood of a log-linear regression model of the covariates. See Zhao et al. (2021), ``Covariate Assisted Principal Regression for Covariance Matrix Outcomes" <doi:10.1093/biostatistics/kxz057>.

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**Suggests** testthat, roxygen2

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capr	<i>Covariate Assisted Principal (CAP) Regression</i>
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### Description

Fits CAP components sequentially for principal direction vectors  $\gamma^{(k)}$  and regression coefficients  $\beta^{(k)}$ ,  $k = 1, \dots, K$ . Each component is estimated via a flip-flop algorithm with optional orthogonalization of successive directions.

### Usage

```
capr(
  S,
  X,
  K,
  B.init = NULL,
  Gamma.init = NULL,
  weight = NULL,
  max_iter = 200L,
  tol = 1e-06,
  orth = TRUE,
  n.init = 10L
)
```

### Arguments

S	Numeric 3D array of size $p \times p \times n$ (for example, a stack of covariance matrices).
X	Numeric matrix $n \times q$ (design matrix), created for example by <code>model.matrix()</code> .
K	Integer scalar; number of components ( $K \geq 1$ ).
B.init	Initial value of the coefficient array $B \in \mathbb{R}^{q \times n.init \times K}$ (default: zero 3D array).
Gamma.init	Initial value of the principal direction array $\Gamma \in \mathbb{R}^{p \times n.init \times K}$ (default: random Gaussian 3D array).

weight	Numeric vector of length $n$ (default <code>rep(1, n)</code> ); each element should be proportional to the sample size for the corresponding slice $S[:, i]$ .
max_iter	Integer scalar; maximum flip-flop iterations per component (default 200).
tol	Positive numeric scalar; convergence tolerance (default 1e-6).
orth	Logical scalar; if TRUE (default), enforce orthogonality of successive $\gamma^{(k)}$ . If FALSE, no orthogonalization is performed (which may yield identical components).
n.init	Integer scalar; number of random initializations (default 10). If <code>B.init</code> and <code>Gamma.init</code> are both supplied, <code>n.init</code> is ignored.

## Details

For component  $k$ , CAP solves

$$\min_{\beta^{(k)}, \gamma^{(k)}} \frac{1}{2} \sum_{i=1}^n (\mathbf{x}_i^\top \beta^{(k)}) T_i + \frac{1}{2} \sum_{i=1}^n \gamma^{(k)\top} S_i \gamma^{(k)} \exp(-\mathbf{x}_i^\top \beta^{(k)})$$

subject to

$$\gamma^{(k)\top} H \gamma^{(k)} = 1$$

and, for  $k > 1$ ,

$$\Gamma^{(k-1)\top} \gamma^{(k)} = \mathbf{0}.$$

Here  $T_i$  denotes the weight for slice  $i$ ,  $S_i$  is the  $i$ -th covariance slice, and  $H$  is the positive definite matrix used for the orthogonality constraint (see Zhao et al., 2021). The algorithm fits  $\gamma^{(k)}$  and  $\beta^{(k)}$  sequentially with multiple random initializations and returns the solution pair that minimizes the negative log-likelihood.

## Value

A list of class `capr` with:

B	numeric matrix $q \times K$ whose $k$ -th column stores $\beta^{(k)}$
Gamma	numeric matrix $p \times K$ whose $k$ -th column stores $\gamma^{(k)}$
loglike	negative log-likelihood, up to constant scaling and shift
S	3D array used for fitting
X	design matrix used for fitting
weight	weight values used for fitting

## References

Zhao, Y., Wang, B., Mostofsky, S. H., Caffo, B. S., & Luo, X. (2021). "Covariate assisted principal regression for covariance matrix outcomes." *Biostatistics*, 22(3), 629-645.

**Examples**

```

simu.data <- simu.capr(seed = 123L, n = 120L)
K <- 2L
fit <- capr(
  S = simu.data$S,
  X = simu.data$X,
  K = K
)
print(fit)

```

---

capr.boot

*Bootstrap confidence intervals for CAP coefficients*


---

**Description**

Generates bootstrap inference for the CAP regression coefficients while holding the fitted directions  $\Gamma$  fixed. Each replicate samples the covariance slices  $S[:, i]$  with replacement, projects them onto the fixed directions to obtain component-specific variances, and re-solves the  $\beta^{(k)}$  equations. Quantile-based confidence intervals are returned for every predictor/component pair.

**Usage**

```

capr.boot(
  fit,
  nboot = 1000L,
  level = 0.95,
  max_iter = 100L,
  tol = 1e-06,
  seed = NULL
)

```

**Arguments**

fit	A <a href="#">capr</a> fit containing components B and Gamma.
nboot	Integer; number of bootstrap replicates.
level	Confidence level for the returned intervals.
max_iter	Maximum Newton iterations for solving $\beta$ .
tol	Convergence tolerance for the Newton solver.
seed	Optional integer seed for reproducibility.

**Value**

A list of class `capr.boot` with:

beta	bootstrap average of $\beta$ with dimension $q \times K$
ci_lower, ci_upper	Matrices $q \times K$ with the lower/upper confidence limits.
level	The requested confidence level.

**Examples**

```
simu.data <- simu.capr(seed = 123L, n = 120L)
K <- 3L
fit <- capr(
  S = simu.data$S,
  X = simu.data$X,
  K = K
)
capr.boot(fit, nboot = 10L, level = 0.95, seed = 42L)
```

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cosine\_similarity      *Cosine similarity between numeric vectors*

---

**Description**

Computes the cosine of the angle between two numeric vectors. Both vectors must have equal length and non-zero Euclidean norms.

**Usage**

```
cosine_similarity(a, b, eps = 1e-12)
```

**Arguments**

a, b	Numeric vectors of equal length.
eps	Non-negative numeric tolerance used to guard against division by zero. Defaults to 1e-12.

**Value**

A scalar double value in  $[-1, 1]$  representing the cosine similarity between a and b.

**Examples**

```
cosine_similarity(c(1, 2, 3), c(1, 2, 3))
cosine_similarity(c(1, 0), c(0, 1))
cosine_similarity(c(1, 2), c(-1, -2))
```

**Description**

Implements the Flury & Gautschi (1986) (FG) iterative algorithm and a variant to estimate a common loading matrix across multiple covariance matrices. Each iteration cycles over all ordered pairs of variable indices and updates a (2 x 2) rotation so that the transformed matrices share diagonal structure.

**Usage**

```
FG(cov_array, p = NULL, m = NULL, maxit = 30L)
```

```
FG2(cov_array, p = NULL, m = NULL, maxit = 30L)
```

**Arguments**

<code>cov_array</code>	Numeric 3D array of shape $p \times p \times m$ containing covariance matrices in its $m$ slices.
<code>p</code>	Optional integer specifying the matrix dimension; defaults to <code>dim(cov_array)[1]</code> .
<code>m</code>	Optional integer specifying the number of matrices/slices; defaults to <code>dim(cov_array)[3]</code> .
<code>maxit</code>	Integer scalar; number of outer iterations of the algorithm.

**Details**

Two solvers are exported:

`FG()` The original FG algorithm.

`FG2()` An alternative algorithm by Eslami et al. (2013).

**Value**

A  $p \times p$  numeric matrix of estimated common loadings.

**References**

Flury, B. N. (1984). "Common Principal Components in k Groups." *Journal of the American Statistical Association*, 79, 892-898.

Flury, B. N., & Gautschi, W. (1986). "An Algorithm for Simultaneous Orthogonal Transformation of Several Positive Definite Symmetric Matrices to Nearly Diagonal Form." *SIAM Journal on Scientific and Statistical Computing*, 7(1), 169-184.

Eslami, A., Qannari, E. M., Kohler, A., & Bougeard, S. (2013). "General Overview of Methods of Analysis of Multi-Group Datasets." *Revue des Nouvelles Technologies de l'Information*, 25, 108-123.

**Examples**

```

set.seed(1)
p <- 3
m <- 4
mats <- replicate(m,
  {
    A <- matrix(rnorm(p * p), p, p)
    crossprod(A)
  },
  simplify = FALSE
)
cov_cube <- array(NA_real_, dim = c(p, p, m))
for (k in 1:m) cov_cube[, , k] <- mats[[k]]
FG(cov_cube, maxit = 5)
FG2(cov_cube, maxit = 5)

```

---

log\_deviation\_from\_diagonality

*Log deviation from diagonality*


---

**Description**

Evaluates the Flury-Gautschi log-deviation criterion for a collection of covariance matrices transformed by a loading matrix.

**Usage**

```
log_deviation_from_diagonality(S_cube, nval, B)
```

**Arguments**

S_cube	Numeric 3D array of shape $p \times p \times n$ containing covariance matrices in its slices.
nval	Numeric vector of length $n$ giving weights for each matrix.
B	Numeric $p \times p$ orthonormal matrix applied to the covariance slices.

**Value**

Numeric scalar value equal to  $\sum_i n_i (\log \det \text{diag}(B^\top S_i B) - \log \det(B^\top S_i B)) / (\sum_i n_i)$ .

**Examples**

```

covs <- array(diag(2), dim = c(2, 2, 1))
log_deviation_from_diagonality(covs, 1, diag(2))

```

plot.capr

*Plot deviation diagnostics by component count***Description**

For a fitted CAP regression, plots two diagnostics across the first  $K$  components: (1) the negative log-likelihood returned by `capr()` and (2) the log deviation-from-diagonality (DfD) for the loading matrix formed by the first  $k$  directions. Both curves help assess the gain from adding components.

**Usage**

```
## S3 method for class 'capr'
plot(x, ...)
```

**Arguments**

`x` A capr object returned by `capr()`.  
`...` Additional arguments passed to `graphics::plot()` and applied to both panels (for example, `pch`, `col`, or axis limits).

**Details**

The DfD criterion for the first  $k$  directions  $\Gamma^{(k)}$  is

$$\text{DfD}(\Gamma^{(k)}) = \left( \prod_{i=1}^n \nu \left( \Gamma^{(k)\top} S_i \Gamma^{(k)} / T_i \right)^{T_i} \right)^{1/\sum_i T_i},$$

where

$$\nu(A) = \frac{\det\{\text{diag}(A)\}}{\det(A)}$$

for a positive definite matrix  $A$ . The curve shows  $\log \text{DfD}(\Gamma^{(k)})$ . A common choice for  $k$  is the last point before a sudden jump in the negative log-likelihood or log-DfD curve.

**Value**

Invisibly returns the numeric vector of log deviation values (one per component).

**See Also**

[log\\_deviation\\_from\\_diagonality\(\)](#)

**Examples**

```
sim <- simu.capr(seed = 123L, n = 120L)
fit <- capr(S = sim$S, X = sim$X, K = 3L)
plot(fit)
```

---

print.capr                      *Print method for CAP regression fits*

---

### Description

Formats the coefficient matrix  $\hat{B}$  returned by `capr()` in a linear-regression style table, showing the estimate for each predictor and component.

### Usage

```
## S3 method for class 'capr'
print(x, digits = max(3L, getOption("digits") - 3L), ...)
```

### Arguments

`x`                      An object of class `capr`, typically the result of `capr()`.

`digits`                 Number of significant digits to show when printing numeric values.

`...`                    Additional arguments passed on to `print.data.frame()`.

### Value

The input object `x`, invisibly.

### Examples

```
simu.data <- simu.capr(seed = 123L, n = 120L)
K <- 2L
fit <- capr(
  S = simu.data$S,
  X = simu.data$X,
  K = K
)
print(fit)
```

---

print.capr.boot                 *Print method for capr.boot objects*

---

### Description

Displays bootstrap coefficient estimates and their confidence intervals component by component as compact tables.

### Usage

```
## S3 method for class 'capr.boot'
print(x, digits = max(4L, getOption("digits") - 4L), ...)
```

**Arguments**

<code>x</code>	An object of class <code>capr.boot</code> , typically produced by <code>capr.boot()</code> .
<code>digits</code>	Number of significant digits to show when printing numeric values.
<code>...</code>	Additional arguments passed on to <code>print.data.frame()</code> .

**Value**

The input object `x`, invisibly.

**Examples**

```
simu.data <- simu.capr(seed = 123L, n = 120L)
K <- 2L
fit <- capr(
  S = simu.data$S,
  X = simu.data$X,
  K = K
)
fit.boot <- capr.boot(
  fit = fit,
  nboot = 10L,
  max_iter = 20L,
  tol = 1e-6,
  seed = 123L
)
print(fit.boot)
```

---

`simu.capr`

*Simulate covariance matrices compatible with `capr()`*

---

**Description**

Generates a simple synthetic dataset for CAP regression consisting of a covariance cube, design matrix, and the latent orthogonal directions used to build the covariance slices.

**Usage**

```
simu.capr(seed = 123L, n = 120L)
```

**Arguments**

<code>seed</code>	Integer seed used for reproducibility.
<code>n</code>	Number of observations (slices) to generate.

**Value**

A list with components:

S	Array of dimension $p \times p \times n$ holding the simulated covariance matrices.
X	Design matrix of size $n \times 2$ with an intercept and a Bernoulli covariate.
Q	Orthogonal matrix whose columns are the latent directions.
BetaMat	True coefficient matrix used to form the eigenvalues.
H	Average covariance matrix $\frac{1}{n} \sum_i S_i$ .
p, n	The dimension and sample size supplied to the generator.

**Examples**

```
sim <- simu.capr(seed = 10, n = 50)
str(sim$S)
```

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