Package 'primePCA'

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Type Package

Title Projected Refinement for Imputation of Missing Entries in PCA

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Description Implements the primePCA algorithm, developed and analysed in Zhu, Z., Wang, T. and Samworth, R. J. (2019) High-dimensional principal component analysis with heterogeneous missingness. <arXiv:1906.12125>.

Imports softImpute, Matrix, MASS, methods

RoxygenNote 7.1.1

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R topics documented:

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col_scale	*Center and/or normalize each column of a matrix*

Description

Center and/or normalize each column of a matrix

Usage

```
col_scale(X, center = T, normalize = F)
```

Arguments

X	a numeric matrix with NAs or "Incomplete" matrix object (see softImpute package)
center	center each column of X if center == TRUE. The default value is TRUE.
normalize	normalize each column of X such that its sample variance is 1 if normalize == TRUE. The default value is False.

Value

a centered and/or normalized matrix of the same dimension as X.

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inverse_prob_method	*Inverse probability weighted method for estimating the top K eigenspaces*

Description

Inverse probability weighted method for estimating the top K eigenspaces

Usage

```
inverse_prob_method(X, K, trace.it = F, center = T, normalize = F)
```

Arguments

X	a numeric matrix with NAs or "Incomplete" matrix object (see softImpute package)
K	the number of principal components of interest
trace.it	report the progress if trace.it == TRUE
center	center each column of X if center == TRUE. The default value is TRUE.
normalize	normalize each column of X such that its sample variance is 1 if normalize == TRUE. The default value is False.

Value

Columnwise centered matrix of the same dimension as X.

Examples

```
X <- matrix(1:30 + .1 * rnorm(30), 10, 3)
X[1, 1] <- NA
X[2, 3] <- NA
v_hat <- inverse_prob_method(X, 1)
```

---

primePCA	*primePCA algorithm*

Description

primePCA algorithm

Usage

```
primePCA(
  X,
  K,
  V_init = NULL,
  thresh_sigma = 10,
  max_iter = 1000,
  thresh_convergence = 1e-05,
  thresh_als = 1e-10,
  trace.it = F,
  prob = 1,
  save_file = "",
  center = T,
  normalize = F
)
```

Arguments

X	an n-by-d data matrix with NA values
K	the number of the principal components of interest
V_init	an initial estimate of the top K eigenspaces of the covariance matrix of X. By default, primePCA will be initialized by the inverse probability method.
thresh_sigma	used to select the "good" rows of X to update the principal eigenspaces σ_* in the paper).
max_iter	maximum number of iterations of refinement
thresh_convergence	
	The algorithm is halted if the Frobenius-norm sine-theta distance between the two consecutive iterates

thresh_als	This is fed into thresh in svd.als of softImpute. is less than thresh_convergence.
trace.it	report the progress if trace.it = TRUE
prob	probability of reserving the "good" rows. prob == 1 means to reserve all the "good" rows.
save_file	the location that saves the intermediate results, including V_cur, step_cur and loss_all, which are introduced in the section of returned values. The algorithm will not save any intermediate result if save_file == "".
center	center each column of X if center == TRUE. The default value is TRUE.
normalize	normalize each column of X such that its sample variance is 1 if normalize == TRUE. The default value is False.

Value

a list is returned, with components V_cur, step_cur and loss_all. V_cur is a d-by-K matrix of the top K eigenvectors. step_cur is the number of iterations. loss_all is an array of the trajectory of MSE.

Examples

```
X <- matrix(1:30 + .1 * rnorm(30), 10, 3)
X[1, 1] <- NA
X[2, 3] <- NA
v_tilde <- primePCA(X, 1)$V_cur
```

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sin_theta_distance   *Frobenius norm sin theta distance between two column spaces*

Description

Frobenius norm sin theta distance between two column spaces

Usage

```
sin_theta_distance(V1, V2)
```

Arguments

| V1 | a matrix with orthonormal columns |
| V2 | a matrix of the same dimension as V1 with orthonormal columns |

Value

the Frobenius norm sin theta distance between two V1 and V2

Index