Package: FSDAM (via r-universe)

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LazyLoad yes

LazyData yes

Version 2024.7-30

Title Forward Stepwise Deep Autoencoder-Based Monotone NLDR

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Depends R (>= 3.5.0)

Suggests R.rsp, RUnit

Imports kyotil, reticulate (>= 1.10)

VignetteBuilder R.rsp

Description FS-DAM performs feature extraction through latent variables identification. Implementation is based on autoencoders with monotonicity and orthogonality constraints.

License GPL (>= 2)

NeedsCompilation no

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Repository https://youyifong.r-universe.dev

RemoteUrl https://github.com/cran/FSDAM

RemoteRef HEAD

RemoteSha 1b0d1eeccd11682a118ac2054d0908baf0c8b679

Contents

cc.505 2
fsdam 3
hvtn505tier1 4

Index **6**

`cc.505` *Select Biomarkers from the HVTN 505 Correlates Analysis*

Description

See reference.

Usage

```
data("cc.505")
```

Format

A data frame with 189 observations on the following 27 variables.

`ptid`	a character vector
`trt`	a numeric vector
`case`	a numeric vector
`control`	a numeric vector
`perprot`	a numeric vector
`last_uninfec_immun_vst`	a numeric vector
`racefull`	a numeric vector
`racefulltxt`	a character vector
`bmi`	a numeric vector
`bmicat`	a numeric vector
`bmicattxt`	a character vector
`earliest_pos_vst`	a numeric vector
`level`	a character vector
`matchlevel`	a character vector
`samplingfraction`	a numeric vector
`vst9subcohort`	a numeric vector
`HIVwk28preunbl`	a numeric vector
`age`	a numeric vector
`racecc`	a character vector
`bhvrisk`	a numeric vector
`BMI`	a numeric vector
`stratuminds_vaccs`	a numeric vector
`stratuminds`	a numeric vector
`cd4.env.poly`	a numeric vector
`cd8.env.poly`	a numeric vector
`mfounders`	a numeric vector
`wei`	a numeric vector

References

Fong, Y, Xu, J. Multi-Stage Simultaneous Deep Autoencoder-based Monotone (MSS-DAM) Nonlinear Dimensionality Reduction Methods, Journal of Computational and Graphical Statistics, in press.

`fsdam` *FS-DAM NLDR*

Description

Forward stepwise deep autoencoder-based monotone nonlinear dimension reduction.

Usage

```
fsdam(dat, opt_numCode = ncol(dat), opt_seed = 1, opt_model = "n", opt_gpu = 0,
opt_k = 100, opt_nEpochs = 10000,
opt_constr = c("newpenalization", "constrained", "none"),
 opt_tuneParam = 10, opt_penfun = "mean", opt_ortho = 1, opt_earlystop = "no",
 verbose = FALSE)

## S3 method for class 'fsdam'
 plot(x, which=c("mse", "history", "decoder.func", "scatterplot"),
 k=NULL, dim.1=NULL, dim.2=NULL, col.predict=2, ...)
```

Arguments

`dat`	data frame.
`opt_numCode`	number of components to extract
`opt_seed`	seed for torch
`opt_model`	n for newpenalization
`opt_gpu`	zero-based index of gpu to be used among all gpus. If negative, then no gpu is used
`opt_k`	number of nodes in the coding/decoding layers
`opt_nEpochs`	number of epochs for training
`opt_constr`	constraint string
`opt_tuneParam`	tuning parameter for monotonicity penalty
`opt_penfun`	penalize sum or mean
`opt_ortho`	tuning parameter for orthogonality penalty
`opt_earlystop`	whether to stop early
`verbose`	verbose
`x`	fsdam object
`which`	which

`k`	the component to plot
`dim.1`	index of the first variable
`dim.2`	index of the second variable
`col.predict`	color of the predicted curve when which = scatterplot
`...`	plotting arguments

Details

If the torch python package is not available, this function will stop.

To make sure the right python installation is used, run reticulate::use_python("/app/easybuild/software/Python/3.7.4-foss-2016b/bin/python") in R before running this function for the first time.

It is recommended that dat is scaled before calling fsdam.

References

Fong, Y, Xu, J. Multi-Stage Simultaneous Deep Autoencoder-based Monotone (MSS-DAM) Non-linear Dimensionality Reduction Methods, Journal of Computational and Graphical Statistics, in press.

Examples

```
## Not run:

fit=fsdam(hvtn505tier1[1:100,-1], opt_numCode=2, verbose=TRUE)
fit
plot(fit,which="mse")
plot(fit,which="history")


## End(Not run)
```

`hvtn505tier1` *HVTN 505 Immune Correlates Tier 1 Dataset*

Description

Contains eight immune response variables from the vaccine arm of the HVTN 505 trial.

Usage

```
data("hvtn505tier1")
```

Format

A data frame with 150 observations on the following 9 variables.

`ptid`	a character vector
`CD8_ANYVRCENV_PolyfunctionalityScore_score`	a numeric vector
`IgGw28_env_mdw`	a numeric vector
`IgGw28_V1V2_mdw`	a numeric vector
`IgGw28_gp41_mdw`	a numeric vector
`ADCP1`	a numeric vector
`R2aConSgp140CFI`	a numeric vector
`IgAw28_env_mdw`	a numeric vector
`IgG3w28_env_mdw`	a numeric vector

References

Fong, Y, Xu, J. Multi-Stage Simultaneous Deep Autoencoder-based Monotone (MSS-DAM) Nonlinear Dimensionality Reduction Methods, Journal of Computational and Graphical Statistics, in press.

Janes, H.E., Cohen, K.W., Frahm, N., De Rosa, S.C., Sanchez, B., Hural, J. et al (2017), Higher T-cell responses induced by DNA/rAd5 HIV-1 preventive vaccine are associated with lower HIV-1 infection risk in an efficacy trial, The Journal of infectious diseases, 215, 1376-1385.

Fong, Y., Shen, X., Ashley, V.C., Deal, A., Seaton, K.E., Yu, C. et al (2018), Vaccine-induced antibody responses modify the association between T-cell immune responses and HIV-1 infection risk in HVTN 505, The Journal of Infectious Diseases, 217, 1280–1288.

Neidich, S.D., Fong, Y., Shen, X., Ashley, V.C., Deal, A., Seaton, K.E. et al (2019), Antibody Fc-effector Functions and IgG3 Associates with Decreased HIV-1 Acquisition Risk, The Journal of Infectious Diseases, 129, 4838-4849.

Index

cc.505, 2

FSDAM *(fsdam)*, 3
fsdam, 3

hvtn505tier1, 4

plot.fsdam *(fsdam)*, 3