Package 'FSDAM'

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LazyLoad yes

LazyData yes

Version 2020.11-18

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 CRAN

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R topics documented:

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.

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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	
x	fsdam object
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.

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)
```

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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.

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