

Package ‘FSDAM’

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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 CRAN

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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) Non-linear 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

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