

Package ‘BNN’

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Type Package

Title Bayesian Neural Network for High-Dimensional Nonlinear Variable Selection

Version 1.0.2

Date 2018-02-02

Depends R (>= 3.0.2)

Imports mvtnorm

Description Perform Bayesian variable selection for high-dimensional nonlinear systems and also can be used to test nonlinearity for a general regression problem. The computation can be accelerated using multiple CPUs. You can refer to <doi:10.1080/01621459.2017.1409122> for more detail.

License GPL-2

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BNN-package

Bayesian Neural Networks for High-Dimensional Nonlinear Variable Selection

Description

Perform Bayesian variable selection for high-dimensional nonlinear systems. The computation can be accelerated using multiple CPUs. The package can also be used to test nonlinearity for a general regression problem.

Details

Package: BNN
Type: Package
Version: 1.0.2
Date: 2018-02-02
License: GPL-2

The Bayesian neural network used in the package is a one-hidden layer feedforward neural network with shortcut connections. The first module of the package is to calculate the prior probabilities assigned to the class of linear models (i.e., those networks with only shortcut connections) and the class of nonlinear models; and the second module is to perform nonlinear variable selection and calculate the posterior probabilities of the classes of linear and nonlinear models.

Author(s)

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References

Liang, F., Li, Q., and Zhou, L. (2017). Bayesian Neural Networks for Selection of Drug Sensitive Genes. *Journal of the American Statistical Association*.

Xue, J. and Liang, F. (2017). Robust model-free feature screening for ultrahigh dimensional data. *Journal of Computational and Graphical Statistics*, in press.

Examples

```
library(BNN)
BNNprior(50, 1, hid_num = 3, lambda=0.025, total_iteration = 10000, popN = 10)
```

`BNNprior`*Prior Probability of Bayesian Neural Networks*

Description

Calculating the prior probability of linear and nonlinear classes of BNN models.

Usage

```
BNNprior(dimX, dimY, hid_num = 3, lambda=0.025, total_iteration=1000000, popN = 20)
```

Arguments

<code>dimX</code>	Dimension of the input data.
<code>dimY</code>	The dimension of reponse data. It is restricted to 1 in the current version of the package.
<code>hid_num</code>	Number of hidden units. The default setting is 3.
<code>lambda</code>	The prior probability for each connection of the neural network being selected for the final model. The default setting is 0.025.
<code>total_iteration</code>	Number of total iterations, default of 1000,000.
<code>popN</code>	Number of Markov Chains, default of 20.

Value

<code>prob</code>	Prior probability assigned to the class of linear models.
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Author(s)

Bochao Jia and Faming Liang

References

Liang, F., Li, Q., and Zhou, L. (2017). Bayesian Neural Networks for Selection of Drug Sensitive Genes. *Journal of the American Statistical Association*.

Examples

```
library(BNN)
BNNprior(50, 1, hid_num = 3, lambda=0.025, total_iteration = 10000, popN = 5)
```

 BNNsel

Bayesian Neural Network for Variable Selection

Description

Perform variable selection and calculate posterior probabilities for the classes of linear and nonlinear of models.

Usage

```
BNNsel(X,Y,train_num, hid_num=3, lambda=0.025, total_iteration=1000000
, popN=20, nCPUs=20)
```

Arguments

X	a $n \times p$ input data matrix.
Y	response vector.
train_num	Number of training samples, should be smaller or equal to n. The default setting is the first 80% rows of the input samples.
hid_num	Number of hidden units. The default setting is 3.
lambda	The prior probability for each connection of the neural network being selected for the final model. The default setting is 0.025.
total_iteration	Number of iterations, recommend to be larger than or equal to 10,000. The default setting is 1000,000.
popN	Number of Markov Chains in a parallel run, should be larger than or equal to 3. The default setting is 20.
nCPUs	Number of CPUs to be used in the simulation. The default setting is 20.

Value

A list of five elements:

net	Marginal inclusion probability of each connection of the neural network.
prob	Posterior probability of the class of linear models.
mar	Marginal inclusion probability of each input variable, which can be used for variable selection based on a multiple-hypothesis test or the median probability model criterion.
fit	Fitted value for the response vector of training data.
pred	Predicted value for the response vector of testing data.

Author(s)

Bochao Jia and Faming Liang

References

Liang, F., Li, Q., and Zhou, L. (2017). Bayesian Neural Networks for Selection of Drug Sensitive Genes. *Journal of the American Statistical Association*.

Examples

```
## simulate data ##
library(BNN)
library(mvtnorm)
n <- 200
p <- 50
X <- rmvnorm(n, mean = rep(1,p), sigma = diag(rep(1,p)))
eps <- rnorm(n,0,0.5)
Y <- X[,1]*X[,2]+3*sin(X[,3])-2*cos(X[,4])+X[,5]^2+eps

### fit BNN model ###
BNNsel(X,Y,hid_num = 3,lambda=0.025,total_iteration = 100000, popN = 10,nCPUs = 10)
```

Topotecan

Example dataset

Description

A subset drug response data extracted from the cancer cell line encyclopedia (CCLE) database for the drug topotecan.

Usage

```
data(Topotecan)
```

Format

X a $n \times p$ data matrix; $n=491$, $p=89$

Y response vector.

References

Liang, F., Li, Q., and Zhou, L. (2017). Bayesian Neural Networks for Selection of Drug Sensitive Genes. *Journal of the American Statistical Association*.

Xue, J. and Liang, F. (2017). Robust model-free feature screening for ultrahigh dimensional data. *Journal of Computational and Graphical Statistics*, in press.

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