
Implementation of algorithm for 'Integrative Data Analysis
of Multi-platform Cancer Data
with a Multimodal Deep Learning Approach'

November 23, 2014

INSTALLATION

Put all the MATLAB script files in your MATLAB path.

USAGE

Directly run the m-file ** example.m ** in the directory to do an example.

Construct a gaussian-binary rbm by running ** rbm.m **

[W,a,b,hs,h,d,d1] = rbm(data,nh,nCD,nstep,nbat,maxepoch,lamda1,lamda2)

INPUT

In the example, we use the data in S. Zhang, C.-C. Liu, W. Li, H. Shen, P. W. Laird, and X. J. Zhou, "Discovery of multi-dimensional modules by integrative analysis of cancer genomic data," Nucleic Acids Research, vol. 40, no. 19, pp. 9379-9391, 2012.
We download from http://nar.oxfordjournals.org/content/40/19/9379/suppl/DC1

nh	the number of the hidden variables
nCD	parameter in CD-n algorithm
nstep	setting iteration for each batch
nbat	the size of each batch to train
maxepoch	setting iteration for all data
lambda1	parameter to prevent overfitting
lambda2	parameter to prevent overfitting

OUTPUT

W	weights between layers
a	bias for visible layer
b	bias for hidden layer
hs	a realization for hidden layer
h	expectation for hidden layer

d norm of difference in weights after each update
d1 norm of weights after each update

Construct a Binary-binary rbm by running ** rbmtop.m **

[errsum,poshidprobs,vishid,visbiases,hidbiases]=rbmtop(batchdata,numhid,maxepoch,restart)

Code provided by Geoff Hinton and Ruslan Salakhutdinov
Version 1.0.0

Instructions on input and output. Please refer to the following the ** rbm.m ** on website http://www.cs.toronto.edu/~hinton/MatlabForSciencePaper.html

NOTES

This software was developed and tested on MATLAB R2014a and Windows operating systems.

PROBLEMS

If you encounter any problem, please do not hesitate to contact us.

CITATION

Muxuan Liang, Zhizhong Li, Ting Chen and Jianyang Zeng
Integrative Data Analysis of Multi-platform Cancer Data with a Multimodal Deep Learning Approach

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Comments and bug-reports are higly appreciated.

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