

DDSOM (Data-driven Second Order Model) readme

◆ Setup

- Operating System: Windows XP or Windows 7

Step 1. Please download **DDSOM.rar**

(<http://www.stat.sinica.edu.tw/gshieh/ddsom/DDSOM.rar>) first, and unzip to "C:\", then DDSOM folder will be generated.

Step 2. Please copy the `cmath.dll` and `cstat.dll` from "C:\DDSOM\isml" to "C:\Windows\system".

◆ Execution

- Please execute `srs.exe` which is in "C:\DDSOM".
- The results are in "C:\DDSOM\output".

◆ Example: Application 2: Predicting AT/RT of 63 genes in yeast.

- Input:

Microarray gene expression data: `expr.txt`

Gene name: `genes.txt`

Note :

The last row of the input file can't be blank, otherwise the code cannot be executed.

- Output: the triplets sorted by 'Score' are outputted

`Predicted_output_tlag_full.txt`

- Need to manually match the output and GIs/TIs of interest.

Step 1. Suppose one pair in 132 AT/RTs is ROX1 \rightarrow CYC7.

TF	Targe	AT(+)/RT(-)
ROX1	CYC7	-

While the predicted triplets with $Score < 0.3$ include both $ROX1 \rightarrow CYC7$ and $ROX1 \rightarrow CYC7$ which are contradictory, thus are removed. For example,

A	R	T
ROX1	SWI5	CYC7
CLN2	ROX1	CYC7

Step 2. When there are more than one triplets having the same AT/RT, we select the triplet with the minimum $Score$. For example,

A	R	T	Score(A,R,T)
SWI5	YOX1	NDL1	0.170289
BAS1	YOX1	NDL1	0.214514
PHO11	YOX1	NDL1	0.215139
CLN3	YOX1	NDL1	0.221794

Result of Application 2: the ratio of correctly predicted TIs (the bold faced ones in the following table) over the intersection of the predicted and TRANSFAC = 6/14

TIs from TRANSFAC			The predicted		
TF	Target	AT(+)/RT(-)	A	R	T
ASH1	HO	-	ASH1	YGP1	HO
FKH2	RAX2	+	FKH2	CRH1	RAX2
GCN4	HIS4	+	MRH1	GCN4	HIS4
HAP1	CTT1	+	PCL9	HAP1	CTT1
HAP1	CYC7	+	CRH1	HAP1	CYC7
HAP1	HMG1	+	MRH1	HAP1	HMG1
HAP1	SOD2	+	CDC46	HAP1	SOD2
MSN4	CTT1	+	PCL9	MSN4	CTT1
ROX1	COX5B	-	ROX1	MRH1	COX5B
ROX1	HMG1	-	MRH1	ROX1	HMG1
SWI4	FKS1	+	SWI4	MRH1	FKS1
WHI5	PCL1	-	SWI5	WHI5	PCL1
YOX1	NDL1	-	SWI5	YOX1	NDL1
YOX1	YMR031C	-	MRH1	YOX1	YMR031C