To reproduce results of whole-genome experiment on Spellman et al. (1998) S. cerevisiae dataset, run consecutively next files on MATLAB platform:

* BFN\_preprocess\_whole\_genome.m performs imputation of missing values and discretization
* Test1\_whole\_genome.m performs Test1 on whole genome data. The output is pairs of regulatory relations, their corresponding Boolean functions, time-delays and significance levels. File test1\_result\_whole\_genome.csv contains output and available within seconds. The result of Test1 can be used as preliminary GRN reconstruction.
* Test2\_whole\_genome.m performs Test2 on whole genome data. The output is pairs of regulatory relations, their corresponding Boolean functions, time-delays and significance levels. File test2\_result\_whole\_genome.csv contains output and available within hours. As this is the most time consuming part, there is possibility to divide it into parallel processes . Test2 is refinement of Test1 results and reduces number of false positive relations.
* Performance\_evaluation\_whole\_genome.m takes as input results of Test1 and Test2 (S1\_Table.xlsx) and compute ROC characteristics such as number of True Positives (TP), False Negatives (FN) etc. when using as ground truth the Golden-standard GRNs from Ma et al. (2014)

To reproduce results of 103 known cell cycle genes experiment which illustrates performance evaluation of BFN with SGD, run consecutively next files on MATLAB platform:

* BFN\_preprocess\_103\_cell\_cycle\_genes.m
* Test1\_103\_cell\_cycle\_genes.m
* Performance\_evaluation\_103\_cell\_cycle\_genes.m

To reproduce results of 103 known cell cycle genes phase succession experiment, run consecutively next files on MATLAB platform. This experiment, unlike the previous ones doesn’t use prior knowledge in form of list of Transcription Factors.

* BFN\_preprocess\_103\_cc\_phase\_exp.m
* Test1\_103\_cc\_phase\_exp.m
* Test2\_103\_cc\_phase\_exp.m