**Instructions for using MAGENTA**

**Installation:**

1. Download MAGENTA files and add the folder to the MATLAB path



1. Download dependencies – the Random Forest toolbox for MATLAB

<https://code.google.com/p/randomforest-matlab/downloads/list>

**Data description:**

* MAGENTA\_supplementary\_dataset.xlsx –this file contains the drug interaction training and validation data
* MAGENTA\_tutorial.m – this file reproduces all the results in the manuscript
* MAGENTA\_supplementary\_dataset.xlsx – the sheet ‘triplet predictions' contains the experimental drug interaction validation data for 56 three-way combinations
* MAGENTA\_supplementary\_dataset.xlsx – the sheet 'media predictions' contains the experimental drug interaction training data for MAGENTA
* MAGENTA\_supplementary\_dataset.xlsx – the sheet 'media predictions test' contains the experimental drug interaction validation data for 55 two-way combinations measured in glycerol media
* MAGENTA\_supplementary\_dataset.xlsx – the sheet 'acinetobacter' contains the experimental drug interaction validation data for 15 two-way combinations in three conditions – LB, glucose and glycerol for *A. baumannii*
* ecoli\_phenotype\_data\_cell.xlsx – has the chemogenomic data taken from the supplementary information of Nichols et al, 2011.
* process\_chemgen\_v2 –This function takes in the chemo-genomics data and identifies significant interactions using the z-score threshold provided as input.
* 'ecoli\_fulldata\_MSB\_2016.xlsx' – has the drug interaction data taken from Chandrasekaran et al, 2016. It contains 171 pairwise combinations of 19 drugs. This data will be used for training MAGENTA
* MAGENTA\_train - MAGENTA takes in drug interaction scores and chemogenomic data to train the random forest model. The trained model can be used to predict new drug interactions using the function MAGENTA\_predict.
* ecoli\_acinetobacter\_orthologs.xlsx – this file contains the list of orthologs between *E. coli* and *A. baumannii*
* identifiers\_match.xlsx – It matches the drug identifiers used in the drug interaction data with the chemogenomic data.