# Quick Start

TIGER*i*

**T** FA
**I** LLUSTRATOR FOR
**G** LOBAL
**E** XPLANATION OF
**R** EGULATORY
***i*** NTERACTIONS

## 1. Prerequisites

### Installing MATLAB Compiler

- Verify the MATLAB Compiler Runtime (MCR) is installed and ensure you have installed version 7.15.

- If the MCR is not installed, run MCRInstaller, located in:

**<*download location of TIGERi*>\Installation Prerequisites\MCRInstaller.exe**

### For more information on the MCR Installer, see the MATLAB Compiler website:

http://www.mathworks.co.uk/help/toolbox/compiler/f12-999353.html

NOTE: YOU WILL NEED ADMINISTRATOR RIGHT TO RUN MCRINSTALLER.

# 2. Files in TIGER*i* Package

## Files for Stand-alone Executable Software

**- TIGERi_WIN32.exe / TIGERi_WIN64.exe**

- is a stand-alone executable file for running TIGERi software.

**- MCRInstaller.exe**

- need to be installed, only if MatLab has not been installed on your computer.

## Files for Quick Start

**-Sample data files**

- can be useful if you want to have a quick start. This is a sample dataset, so your customised dataset should be in the same format.

# 3. Input files

## Gene ID list

This file should contain gene IDs that are the identifiers of gene expression data (microarray). The acceptable types of IDs are Official gene symbol, RefSeq ID, and Ensembl ID.

## Control Expression Data

This file should contain normalised logged gene expression of control (wild-type) sample. TIGERi allows multiple replicates.

NOTE: MUST BE IN SAME GENE ORDER AS IN "GENE LIST" FILE.

## Treatment Expression Data

This file should contain normalised logged gene expression of treatment (mutant) sample. TIGERi allows multiple replicates.

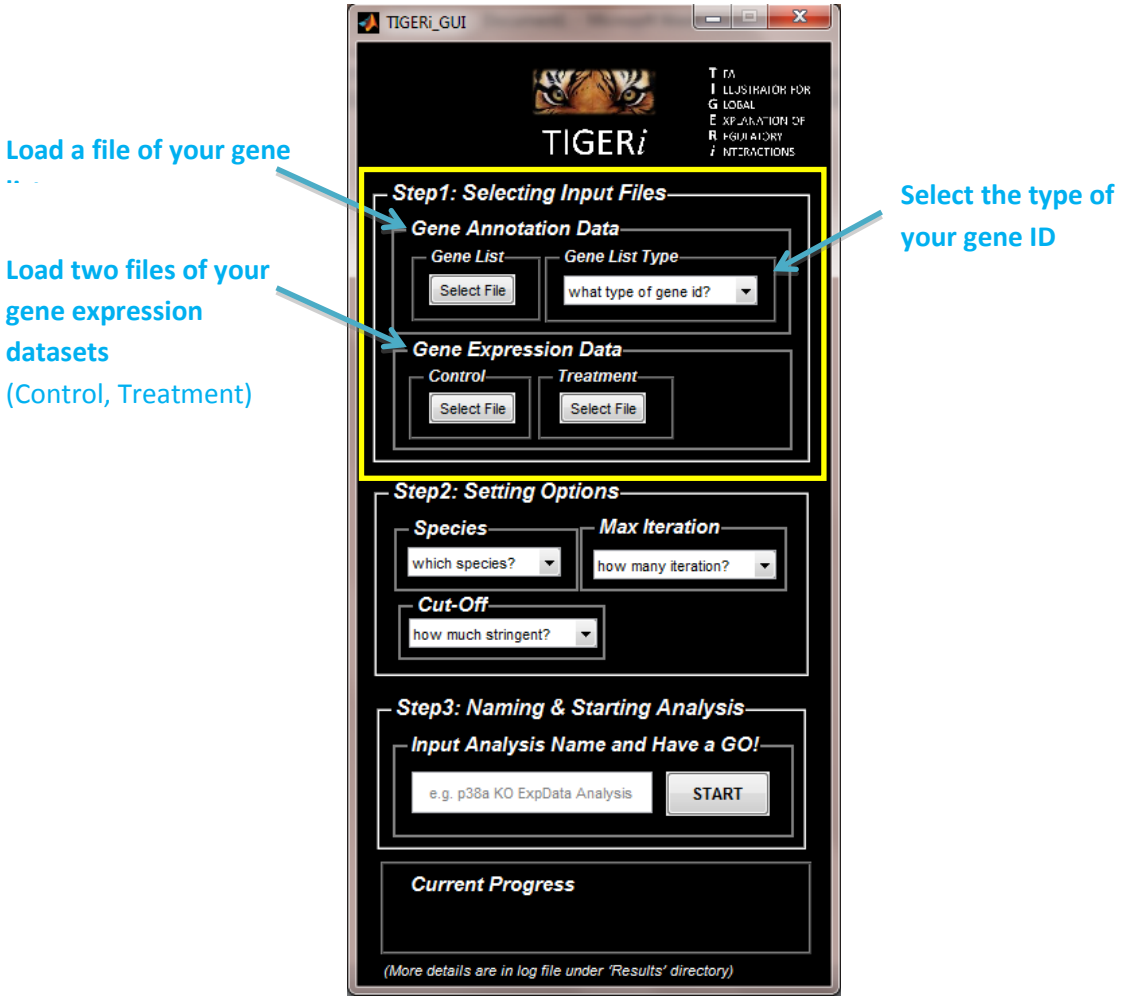
NOTE: MUST BE IN SAME GENE ORDER AS IN "GENE LIST" FILE.

# 4. Using the Software

## STEP1: Selecting Input Files

- Load three files: gene ID list, control gene expression data, and treatment gene expression data

- Select the type of gene ID



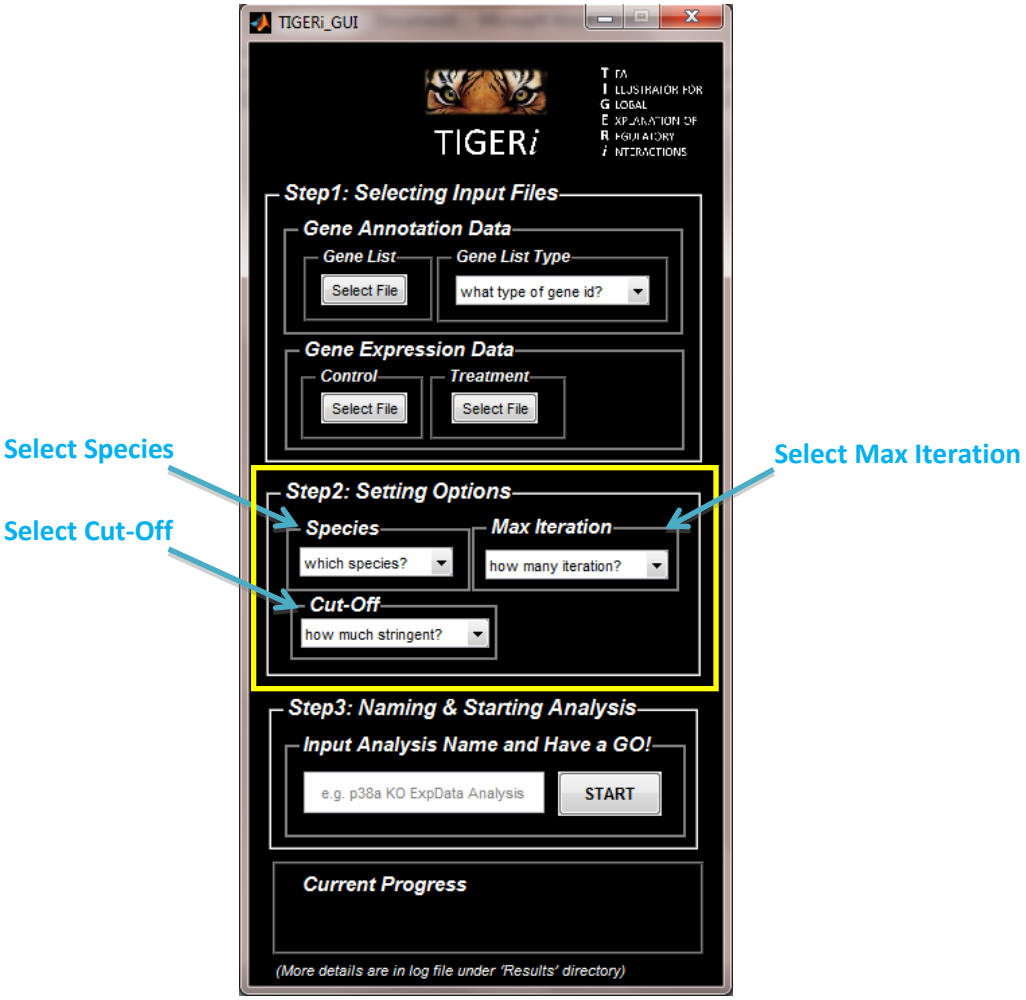
## STEP2: Selecting Options

- Select the species, max iteration, and cut-off

- **Species**: the species of your genes

- **Max Iteration**: the maximum iteration number of inference modelling procedure

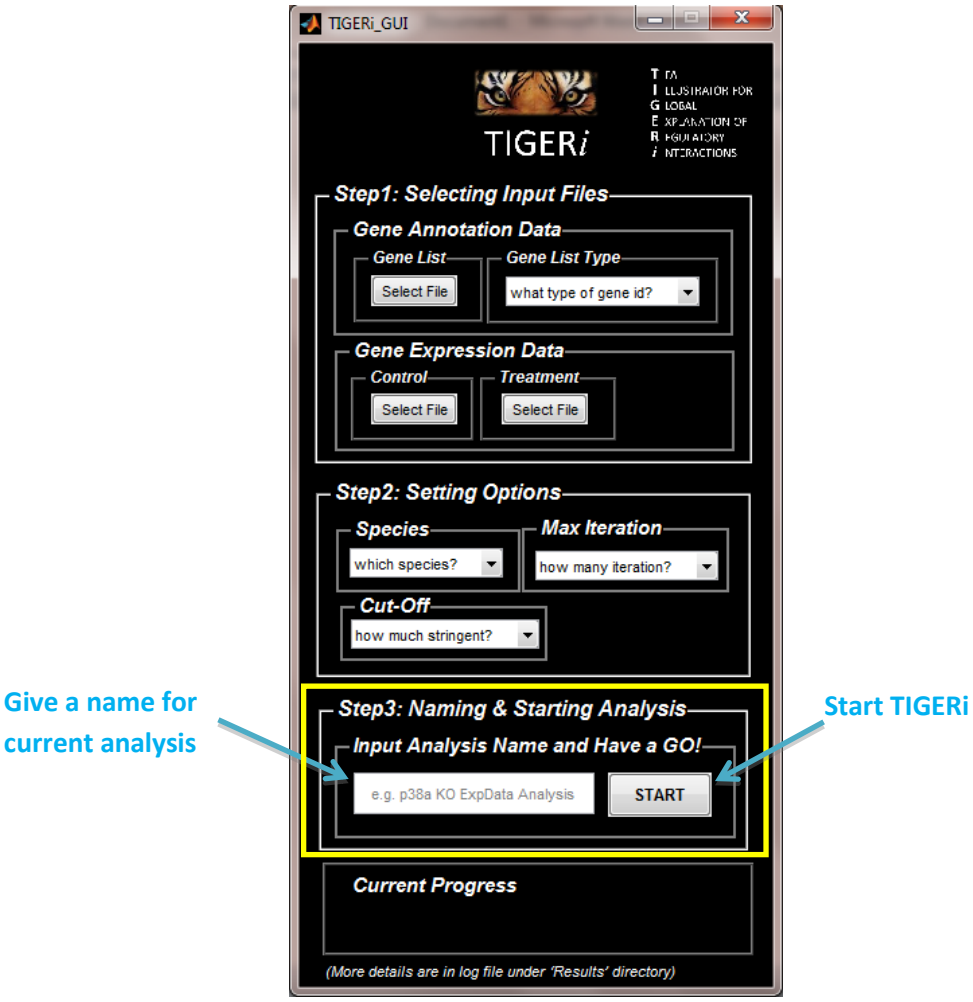
- **Cut-Off**: the threshold value to identify statistically significant differences between control expression data and treatment expression data



## STEP3: Naming & Starting Analysis

- Give a name for current analysis and start TIGERi

- **Name**: the name of current analysis that will be also used for saving results of current analysis
  (e.g., If you type the name as “p38a KO ExpData Analysis”, then the results of current analysis will be saved under the folder named “p38a KO ExpData Analysis”.)



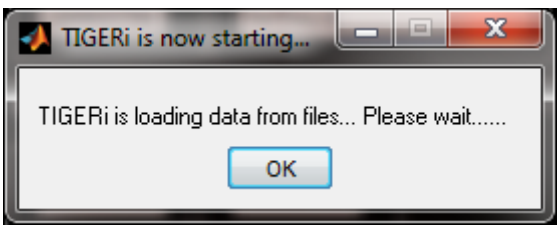
## Displaying Current Progress & Warning/Error Messages

- Current progress will be displayed at the bottom of TIGERi GUI window.

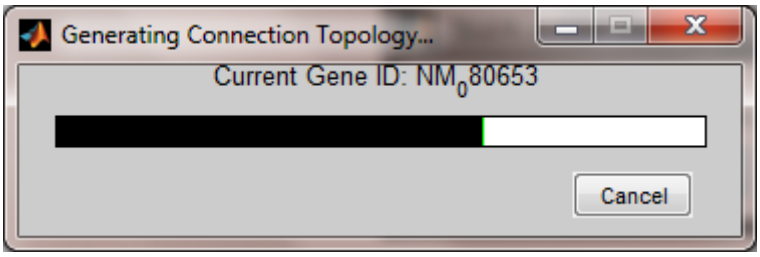
- Progress bar will be pop up, if the current procedure may require long computation time.

- Warning or Error messages will pop up, if any warning or error is occurred.

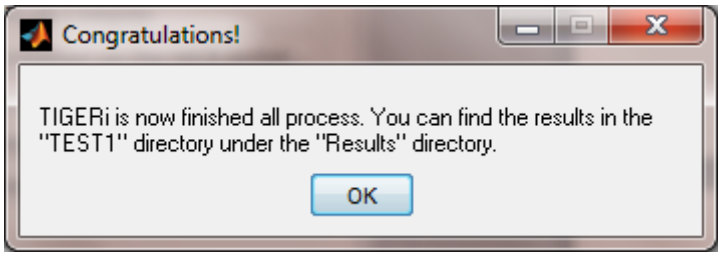

*Pop-up message (Starting)*



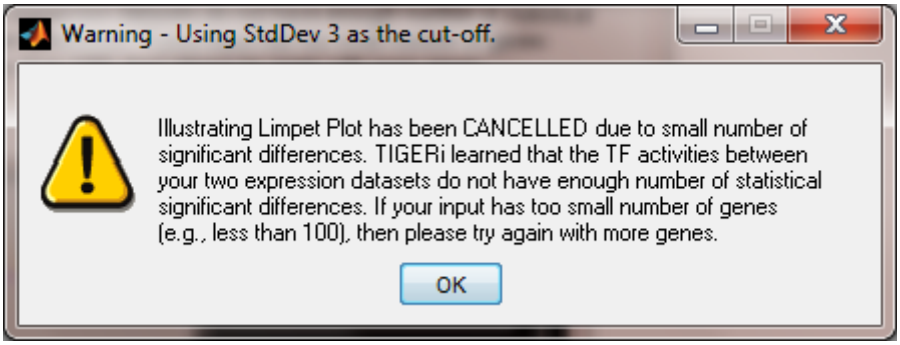
### *Progress bar*



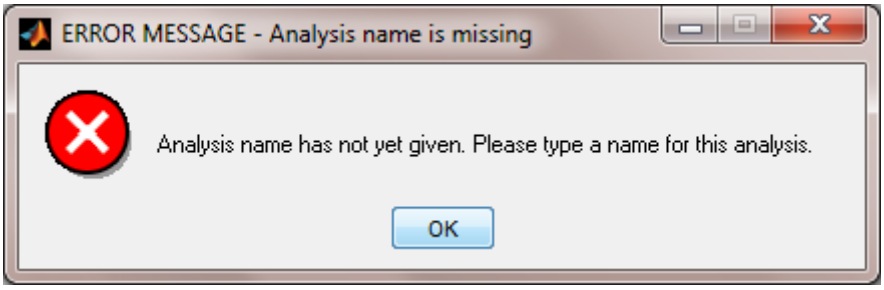

### *Pop-up message (Completed)*




### *Warning message*




### *Error message*



## Log File

- Detailed information of completed TIGERi analysis procedures are recorded in the log file that is also saved in the Result folder.

NOTE: NOTEPAD, WINDOWS EMBEDDED TEXT EDITOR, MAY NOT BE OPTIMISED TO DISPLAY THE LOG FILE. ANOTHER EMBEDDED PROGRAMME, CALLED WORDPAD, COULD BE THE ALTERNATIVE.

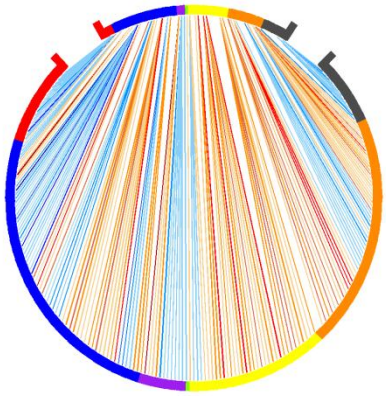
# 5. Results of TIGER*i*

All results are saved in the folder that has same name as you typed when TIGERi started.

## Figures

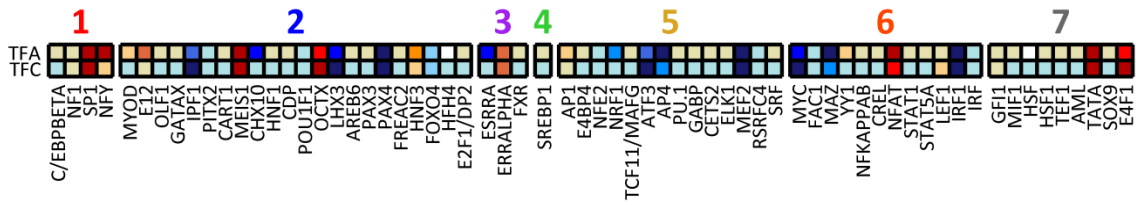
- TIGERi generates limpet-like plots, dot plot, and scatter plot.

- **Limpet-like plots**



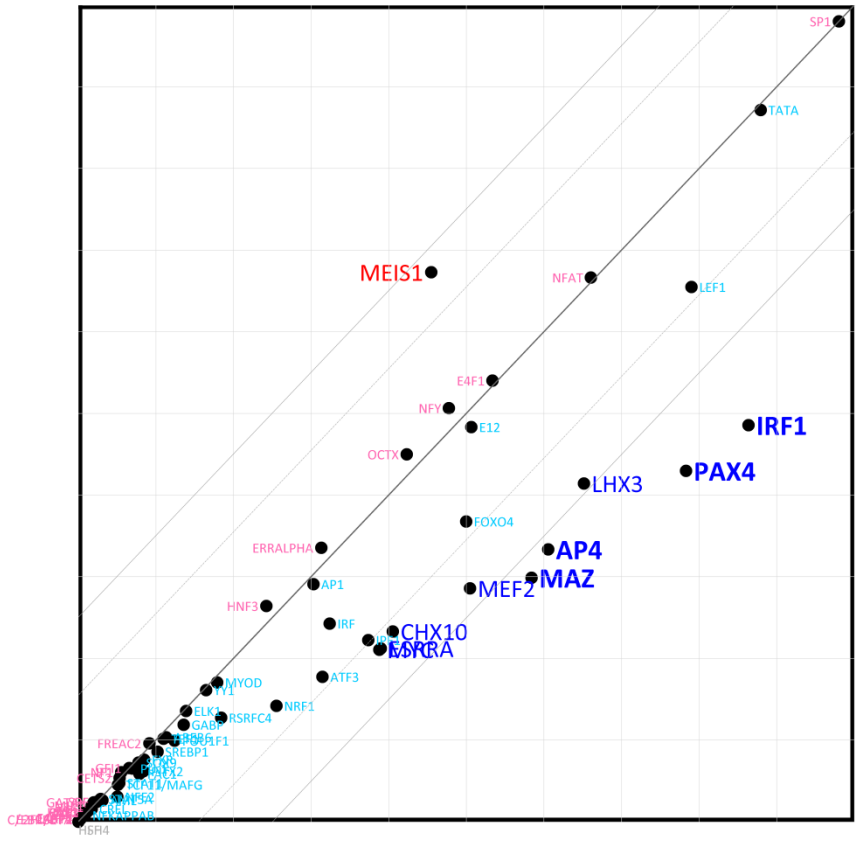
The significant differences in TF activities in the limpet-like plots. In the upper part of the limpet plots, the TFs are placed in order of functional group. Genes that have at least one significant change are located in the bottom of the plots. A line presents how much the TF activity of a certain gene is changed between the control data and treat data. The difference is displayed in blue indicating that the TF-gene pair has significantly higher TF activation in the control data; while, it is displayed in red indicating that the pair has significantly higher TF activation in the treatment data.

- **Dot plot**




TF activities and associated TF concentration levels of the 65 TFs showing results of the systematic analysis and classification of the functional TF groups. A square represents a significant difference in TF activities and associated TF concentration levels of 65 TFs.

- **Scatter plot**




Global view of TF activities in both control data and treatment data is illustrated in the scatter plot. The plot clearly shows not only which TFs have strong activity levels but also which TFs have significant differences in their activity pattern. The dot lines indicate the standard deviations centred on median value of the straight lines.

- All figures are saved in “Fig” folder under the result folder.

NOTE: IF TIGERI DOES NOT IDENTIFY ENOUGH SIGNIFICANT DIFFERENCES BETWEEN CONTROL DATA AND TREAT DATA, THEN THE LIMPET-LIKE PLOTS WILL NOT BE CREATED.

## Tables

- TIGERi generates two tables of genes that have statistically significant differences between control data and treatment data.

- **Classified_SigDiff_per_TF**: TF-perspective gene list

| TF Name | Labels for Graph | Sum of SigDiff | Sig UP in Treat | Sig UP in Control | Average of Sig Diff | Number of Genes per TF | Number of Up-regulated Genes in Control | Number of Up-regulated Genes in Treat |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |

- **SigDiff_Gene_List**: Gene-perspective gene list

| Serial Number | Gene Symbol | Gene Description | Ensembl ID | RefSeq ID | TF Name | Sig Diff | TF Activity in Control | TF Activity in Treat | Expression Control | Expression Treat | TF Concentration in Control | TF Concentration in Treat | Connectivity |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | |

- All tables are saved in the Cut-Off folders under the result folder.

NOTE: THE TABLES ARE BEST VIEWED IN MICROSOFT OFFICE EXCEL OR SIMILAR PROGRAMMES

# 6. Contact

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