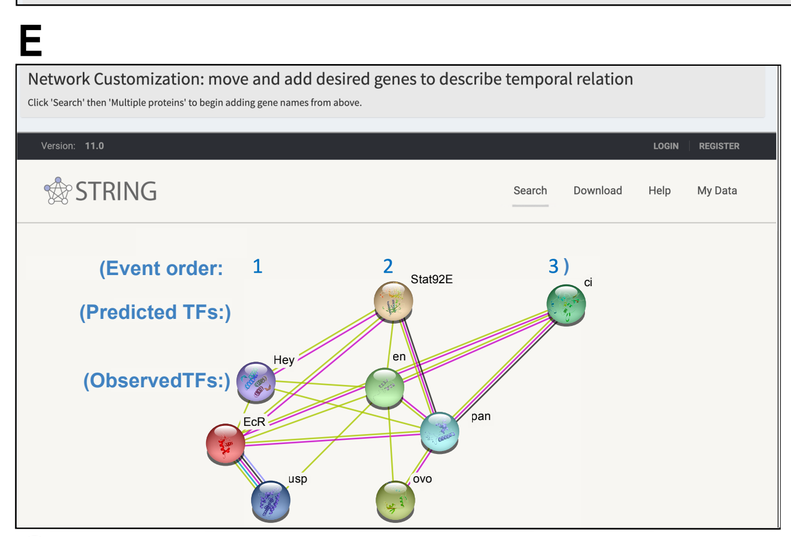
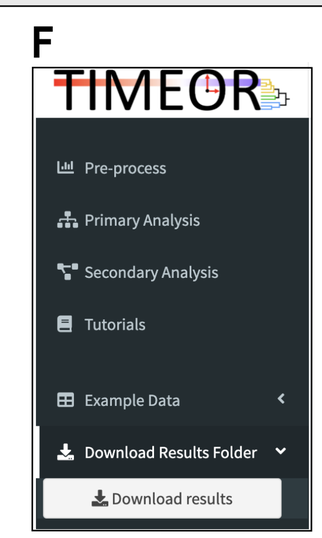
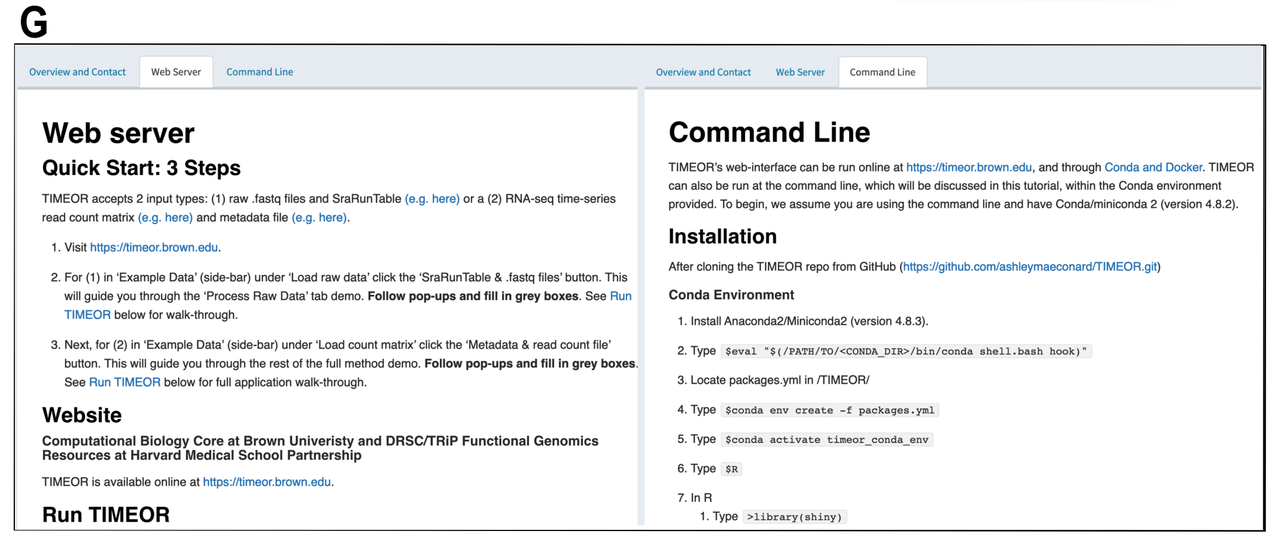
A
Enrichment
Factor Binding
Temporal Relations
Gene Expression Trajectory Clusters
Select a gene trajectory cluster to analyze:
3
Clustermap of simulated DEGs Across Time
Genes
Stages
X1
X2
X3
X4
Chosen Cluster Gene Set
"ptc', 'lncRNA:CR46077', 'Smurf', 'Su(fu)', 'hh', 'fu', 'boi', 'rdx', 'Pka-C1', 'lncRNA:CR46076', 'CR40354', 'Bin1', 'slmb', 'Cul3', 'ihog', 'Roc1a', 'disp', 'Shc', 'csw', 'msn', 'Usp8', 'Cul4', 'Gug', 'shf', 'krz', 'Gprk2', 'Pka-R1', 'dlp', 'dally', 'dco', 'flw', 'cos', 'rasp', 'Sos"
ON
Analyze
Pathway
NOTCH SIGNALING PATHWAY
Network
Protein-protein interaction enrichment p-value:
Molecular Function
signaling receptor binding
enzyme binding
ubiquitin protein ligase binding
ubiquitin-like protein ligase binding
G protein-coupled receptor binding
transcription factor binding
protein serine/threonine kinase activity
protein kinase binding
protein tyrosine kinase binding
phosphoprotein binding
GeneRatio
Motif Analysis
Download MEME interactive results.
Top de novo motif:
bits

C
Top Predicted Transcription Factors by Orthology
Clusters
obs. TF
pred.TF 1
pred.TF 2
pred.TF 3
pred.TF 4
Top Predicted TFs by Orthology Per Method
pred. TF1
pred. TF2
pred. TF3
pred. TF4
method 1
method 2
method 3
% concordance
Top Predicted Transcription Factors by Motif Similarity
Top Predicted TFs by Motif Similarity Per Method
D
Enrichment
Factor Binding
Temporal Relations
Gene Expression Trajectory Clusters
Clustermap of simulated DEGs Across Time
Observed and Top Predicted Transcription Factors
observed_TFs
top_TF_1
top_TF_2
top_TF_3
top_TF_4
ENCODE_accession_num_TF_1
usp|EcR|Hey
ovo|en|pan
Showing 1 to 3 of 3 entries
Transcription Factor Network
Protein-protein interaction enrichment p-value:
Legend
Temporal Relations Between Observed and Predicted Transcription Factors
timepoint
regulator
regulated
regulation_type
edge_type
Showing 1 to 6 of 15 entries
Network Customization: move and add desired genes to describe temporal relation

B
Enrichment
Factor Binding
Temporal Relations
Gene Expression Trajectory Clusters
Clustermap of simulated DEGs Across Time
Genes
Stages
Observed and Top Predicted Transcription Factors
At least 40% of methods must agree on top predicted transcription factors, otherwise cell is left blank. Row names are clusters.
observed_TFs
top_TF_1
top_TF_2
top_TF_3
top_TF_4
usp|EcR|Hey
ovo|en|pan
Showing 1 to 3 of 3 entries
Details about individual method predicted transcription factors
logo
geneSet
motif
NES
AUC
cluster
transfac_pro__M01139
transfac_pro__M05700
transfac_pro__M03796
transfac_pro__M02856
Average Profiles Across Each Gene Expression Trajectory Cluster
Upload .bigWig Files
(e.g. ChIP-seq or CUT&RUN)
1. Go to ENCODE .
2. Choose ENCODE data from provided ENCODE ID or TF name.
3. Download .bigWig file.
4. Upload to TIMEOR to visualize.
Note : each cluster is the same color as in clustermap.
ID: identifier, TF: transcription factor
TF name:
pho
Upload .bigWig
Browse...
ENCFF609FCZ.bigWig
Upload complete
Go
No file selected
(Heatmap sits underneath distribution plot)


E
Network Customization: move and add desired genes to describe temporal relation
Click 'Search' then 'Multiple proteins' to begin adding gene names from above.
Version: 11.0
LOGIN
REGISTER
STRING
Search
Download
Help
My Data
(Event order:
(Predicted TFs:)
(ObservedTFs:)
1
2
3)
Stat92E
ci
Hey
en
EcR
pan
usp
ovo


F
TIMEOR
Pre-process
Primary Analysis
Secondary Analysis
Tutorials
Example Data
Download Results Folder
Download results


G
Overview and Contact
Web Server
Command Line
Web server
Quick Start: 3 Steps
TIMEOR accepts 2 input types: (1) raw .fastq files and SraRunTable (e.g. here) or a (2) RNA-seq time-series read count matrix (e.g. here) and metadata file (e.g. here).
1. Visit https://timeor.brown.edu.
2. For (1) in 'Example Data' (side-bar) under 'Load raw data' click the 'SraRunTable & .fastq files' button. This will guide you through the 'Process Raw Data' tab demo. Follow pop-ups and fill in grey boxes. See Run TIMEOR below for walk-through.
3. Next, for (2) in 'Example Data' (side-bar) under 'Load count matrix' click the 'Metadata & read count file' button. This will guide you through the rest of the full method demo. Follow pop-ups and fill in grey boxes. See Run TIMEOR below for full application walk-through.
Website
Computational Biology Core at Brown Univeristy and DRSC/TRiP Functional Genomics Resources at Harvard Medical School Partnership
TIMEOR is available online at https://timeor.brown.edu.
Run TIMEOR
Command Line
TIMEOR's web-interface can be run online at https://timeor.brown.edu, and through Conda and Docker. TIMEOR can also be run at the command line, which will be discussed in this tutorial, within the Conda environment provided. To begin, we assume you are using the command line and have Conda/miniconda 2 (version 4.8.2).
Installation
After cloning the TIMEOR repo from GitHub (https://github.com/ashleymaeconard/TIMEOR.git)
Conda Environment
1. Install Anaconda2/Miniconda2 (version 4.8.3).
2. Type $eval "$(/PATH/TO/<CONDA_DIR>/bin/conda shell.bash hook)"
3. Locate packages.yml in /TIMEOR/
4. Type $conda env create -f packages.yml
5. Type $conda activate timeor_conda_env
6. Type $R
7. In R
1. Type >library(shiny)