



TIMEOR: a web-based tool to uncover temporal regulatory mechanisms from multi-omics data



Trajectory Inference and Mechanism Exploration with Omics in R

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Pre-processing Stage

Search and Retrieve

- 1) Upload (un)published time series RNA-seq data.
- 2) Answer 6 questions to set adaptive default analysis methods.

Getting the details

1. What type of sequencing?
2. What type of experiment?
3. What type of time course?
4. Compare multiple methods (alignment/mapping, and differential expression)?
5. What is the maximum putative number of time steps to determine influence of one gene on another?
6. What type of organism?

Correlate Samples

PCA After Correction

Compare Alignment Methods

Clustered Gene Trajectories

Primary Analysis

Run Differential Expression

What do you want to name your results folder?

What is your p-value threshold?

3) Set p-value threshold to choose from comparison of differential expression methods and a past study.

4) Cluster gene trajectories automatically or manually.

Venn Diagram Between Methods

Clustering

Secondary Analysis

Enrichment

Cluster Map

5) Explore GO, pathway, network, motif analysis for each gene trajectory cluster.

Molecular Function

Biological Process

Cellular Component

Pathway

Network

Motif Analysis de novo

Factor Binding

Transcription Factor Table

Cluster	Perturbed TF gene	Top TF likely bind cluster	Top 4 TFs likely bind cluster	Encode IDs
4	MYC	MYC	MYC, MAX, MNT, CLK	ENC...
3	pdp1	CWO	CWO, CLK, TGO, MONDO	ENC...
2	cwo	CYC	CYC, RFX, USF, CG9727	ENC...
5	DIF	DIF	DIF, DL, REL, PNT	ENC...
1	cg32772	HNF4	HNF4, SVP, FOXF, GRN	ENC...

Choose ChIP-seq .bigwig

1. Go to [encode](#).
2. Choose encode data from ENCODE ID or TF name.
3. Download .bigWig file.
4. Upload to TIMEOR to visualize.

Upload up to 4 .bigWigs

.bigwig 1 upload bar TF name: HNF4

.bigwig 2 upload bar TF name: CYC

.bigwig 3 upload bar TF name: CWO

.bigwig 4 upload bar TF name: MYC

Go

ChIP-seq average profiles

Temporal Relations

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1	cg32772	HNF4	HNF4, SVP, FOXF, GRN	ENC...

Temporal Relations Table

Cluster	Regulator	Regulated	Regulation type	Edge type
3	CWO	pdp1	activate	predicted
3	CWO	pdp1	activate	high_confidence
2	CYC	cwo	activate	predicted
1	CG32772	cwo	activate	high_confidence
1	HNF4	cg32772	repress	putative

6) Choose from inferred transcription factor ChIP-seq or CUT&RUN data.

7) Reconstruct transcription factor regulatory network.

Publicly available soon:



timeor.org

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