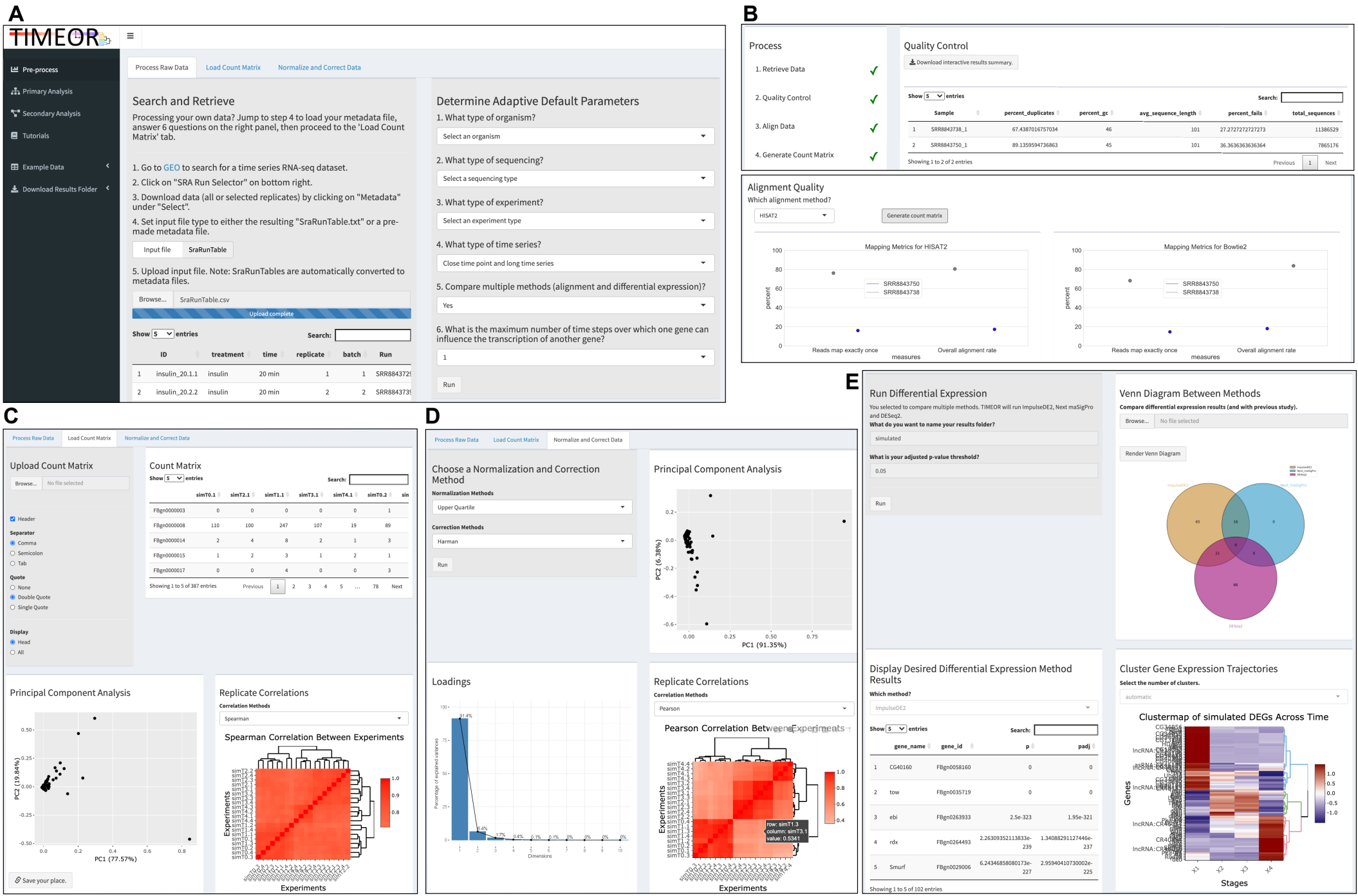
A
TIMEOR
Pre-process
Primary Analysis
Secondary Analysis
Tutorials
Example Data
Download Results Folder
Process Raw Data
Load Count Matrix
Normalize and Correct Data
Search and Retrieve
Processing your own data? Jump to step 4 to load your metadata file, answer 6 questions on the right panel, then proceed to the 'Load Count Matrix' tab.
1. Go to GEO to search for a time series RNA-seq dataset.
2. Click on "SRA Run Selector" on bottom right.
3. Download data (all or selected replicates) by clicking on "Metadata" under "Select".
4. Set input file type to either the resulting "SraRunTable.txt" or a pre-made metadata file.
Input file
SraRunTable
5. Upload input file. Note: SraRunTables are automatically converted to metadata files.
Browse...
SraRunTable.csv
Upload complete
Show 5 entries
Search:
ID
treatment
time
replicate
batch
Run
1 insulin_20.1.1 insulin 20 min 1 1 SRR8843725
2 insulin_20.2.2 insulin 20 min 2 2 SRR8843735
Determine Adaptive Default Parameters
1. What type of organism?
Select an organism
2. What type of sequencing?
Select a sequencing type
3. What type of experiment?
Select an experiment type
4. What type of time series?
Close time point and long time series
5. Compare multiple methods (alignment and differential expression)?
Yes
6. What is the maximum number of time steps over which one gene can influence the transcription of another gene?
1
Run
B
Process
1. Retrieve Data
2. Quality Control
3. Align Data
4. Generate Count Matrix
Quality Control
Download interactive results summary.
Show 5 entries
Search:
Sample
percent_duplicates
percent_gc
avg_sequence_length
percent_fails
total_sequences
1 SRR8843738_1 67.4387016757034 46 101 27.2727272727273 11386529
2 SRR8843750_1 89.1359594736863 45 101 36.3636363636364 7865176
Showing 1 to 2 of 2 entries
Previous
Next
Alignment Quality
Which alignment method?
HISAT2
Generate count matrix
Mapping Metrics for HISAT2
Mapping Metrics for Bowtie2
percent
SRR8843750
SRR8843738
Reads map exactly once
Overall alignment rate
measures
C
Process Raw Data
Load Count Matrix
Normalize and Correct Data
Upload Count Matrix
Browse...
No file selected
Header
Separator
Comma
Semicolon
Tab
Quote
None
Double Quote
Single Quote
Display
Head
All
Count Matrix
Show 5 entries
Search:
simT0.1
simT2.1
simT1.1
simT3.1
simT4.1
simT0.2
FBgn0000003 0 0 0 0 0 1
FBgn0000008 110 100 247 107 19 89
FBgn0000014 2 4 8 2 1 3
FBgn0000015 1 2 3 1 2 1
FBgn0000017 0 0 4 0 0 3
Showing 1 to 5 of 387 entries
Previous
Next
Principal Component Analysis
PC2 (19.84%)
PC1 (77.57%)
Save your place.
Replicate Correlations
Correlation Methods
Spearman
Spearman Correlation Between Experiments
Experiments
D
Process Raw Data
Load Count Matrix
Normalize and Correct Data
Choose a Normalization and Correction Method
Normalization Methods
Upper Quartile
Correction Methods
Harman
Run
Principal Component Analysis
PC2 (6.38%)
PC1 (91.35%)
Loadings
Percentage of explained variances
Dimensions
Replicate Correlations
Correlation Methods
Pearson
Pearson Correlation Between Experiments
row: simT1.3
column: simT3.1
value: 0.5341
Experiments
E
Run Differential Expression
You selected to compare multiple methods. TIMEOR will run ImpulseDE2, Next maSigPro and DESeq2.
What do you want to name your results folder?
simulated
What is your adjusted p-value threshold?
0.05
Run
Venn Diagram Between Methods
Compare differential expression results (and with previous study).
Browse...
No file selected
Render Venn Diagram
ImpulseDE2
Next_maSigPro
DESeq2
Display Desired Differential Expression Method Results
Which method?
ImpulseDE2
Show 5 entries
Search:
gene_name
gene_id
p
padj
1 CG40160 FBgn0058160 0 0
2 tow FBgn0035719 0 0
3 ebi FBgn0263933 2.5e-323 1.95e-321
4 rdx FBgn0264493 2.26309352113833e-239 1.34088291127446e-237
5 Smurf FBgn0029006 6.24346858080173e-227 2.95940410730002e-225
Showing 1 to 5 of 102 entries
Cluster Gene Expression Trajectories
Select the number of clusters.
automatic
Clustermap of simulated DEGs Across Time
Genes
Stages
X1
X2
X3
X4