



# 3000788 Intro to Comp Molec Biol

Week 6: RNA sequencing analysis demo

Fall 2024



**Sira Sriswasdi, PhD**

- Research Affairs
- Center of Excellence in Computational Molecular Biology (CMB)
- Center for Artificial Intelligence in Medicine (CU-AIM)

# Today's activity




- Process RNA-seq data from FASTQ using *kallisto*
- Perform differential expression analysis in *sleuth* R package
- Perform functional enrichment analysis on *WebGestalt*
- <https://www.webgestalt.org/>

# Preparations

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- Get the FASTQ data and yeast reference transcriptome
- [https://figshare.com/articles/dataset/Yeast\\_RNA-seq\\_data\\_and\\_transcriptome\\_for\\_kallisto-sleuth\\_demo\\_session/24182520](https://figshare.com/articles/dataset/Yeast_RNA-seq_data_and_transcriptome_for_kallisto-sleuth_demo_session/24182520)
- Install *R* & *RStudio*
- Install *sleuth* (see next slide)
- Get *run\_sleuth.R* from course website's *demo* folder
- Download *kallisto* (version 0.46.1, select your OS)
- <https://pachterlab.github.io/kallisto/download>

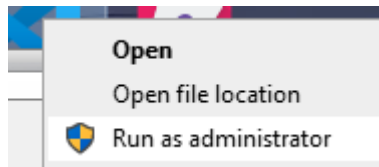


aerobic\_r1\_1.fq.gz  
aerobic\_r1\_2.fq.gz  
aerobic\_r2\_1.fq.gz  
aerobic\_r2\_2.fq.gz  
anaerobic\_r1\_1.fq.gz  
anaerobic\_r1\_2.fq.gz  
anaerobic\_r2\_1.fq.gz  
anaerobic\_r2\_2.fq.gz  
GCF\_000146045.2\_R64\_rna.fna.gz

# Preparations

## - Install *sleuth*

- You may have to run RStudio as administration
- In the command area, type
  - `install.packages("BiocManager")`
  - `BiocManager::install("rhdf5")`
  - `install.packages("devtools")`
  - `devtools::install_github("pachterlab/sleuth")`
- To test that you were successful, type
  - `library(sleuth)`
- If the program asks: `Update all/some/none? [a/s/n]`, it is safe to choose "n".



```
R 4.0.2 . ~/
```

R version 4.0.2 (2020-06-22) -- "Taking Off Again"  
Copyright (C) 2020 The R Foundation for Statistical Computing  
Platform: x86\_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.

```
> install.packages("BiocManager")
```

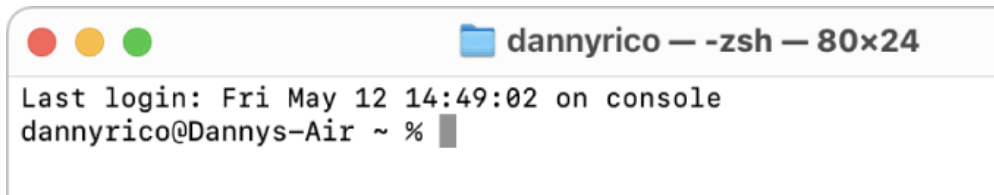


# Command line interface

# Terminal and Command Prompt



Command Prompt  
System



- Open
- Run as administrator
- Open file location
- Unpin from Start
- Pin to taskbar

```
C:\Users\Sira\Downloads\yeast_data>kallisto index -i yeast_rna GCF_000146045.2_R64_rna.fna.gz  
[build] loading fasta file GCF_000146045.2_R64_rna.fna.gz  
[build] k-mer length: 31  
[build] counting k-mers ... done.  
[build] building target de Bruijn graph ... done  
[build] creating equivalence classes ... done  
[build] target de Bruijn graph has 11192 contigs and contains 8200305 k-mers
```

# How to run script in command line?



```
kallisto 0.50.0
```

```
Usage: kallisto <CMD> [arguments] ..
```

```
Where <CMD> can be one of:
```

index	Builds a kallisto index
quant	Runs the quantification algorithm
quant-tcc	Runs quantification on transcript-compatibility counts
bus	Generate BUS files for single-cell data
h5dump	Converts HDF5-formatted results to plaintext
inspect	Inspects and gives information about an index
version	Prints version information
cite	Prints citation information

```
Running kallisto <CMD> without arguments prints usage information for <CMD>
```

# Let's index the yeast reference transcriptome



```
kallisto 0.50.0
Builds a kallisto index

Usage: kallisto index [arguments] FASTA-files

Required argument:
-i, --index=STRING      Filename for the kallisto index to be constructed

Optional argument:
-k, --kmer-size=INT      k-mer (odd) length (default: 31, max value: 31)
-d, --d-list=STRING      Path to a FASTA-file containing sequences to mask from quantification
    --make-unique         Replace repeated target names with unique names
    --aa                  Generate index from a FASTA-file containing amino acid sequences
    --distinguish         Generate index where sequences are distinguished by the sequence name
-t, --threads=INT        Number of threads to use (default: 1)
```

kallisto index -i yeast\_transcriptome GCF\_000146045.2\_R64\_rna.tna.gz



# kallisto quant



Bootstrap estimates  
technical variances

More CPUs = faster



Usage: kallisto quant [arguments] FASTQ-files

## Required arguments:

<code>-i, --index=STRING</code>	Filename for the kallisto index to be used for quantification
<code>-o, --output-dir=STRING</code>	Directory to write output to

One output folder per sample

## Optional arguments:

<code>-b, --bootstrap-samples=INT</code>	Number of bootstrap samples (default: 0)
<code>--seed=INT</code>	Seed for the bootstrap sampling (default: 42)
<code>--plaintext</code>	Output plaintext instead of HDF5
<code>--single</code>	Quantify single-end reads
<code>--single-overhang</code>	Include reads where unobserved rest of fragment is predicted to lie outside a transcript
<code>--fr-stranded</code>	Strand specific reads, first read forward
<code>--rf-stranded</code>	Strand specific reads, first read reverse
<code>-l, --fragment-length=DOUBLE</code>	Estimated average fragment length
<code>-s, --sd=DOUBLE</code>	Estimated standard deviation of fragment length (default: -l, -s values are estimated from paired end data, but are required when using --single)
<code>-t, --threads=INT</code>	Number of threads to use (default: 1)



# Differential expression

# Output from kallisto quant



- Four output folders (= number of samples)
- Look for abundance.h5 and abundance.tsv
  - abundance.h5 contains bootstrapping results

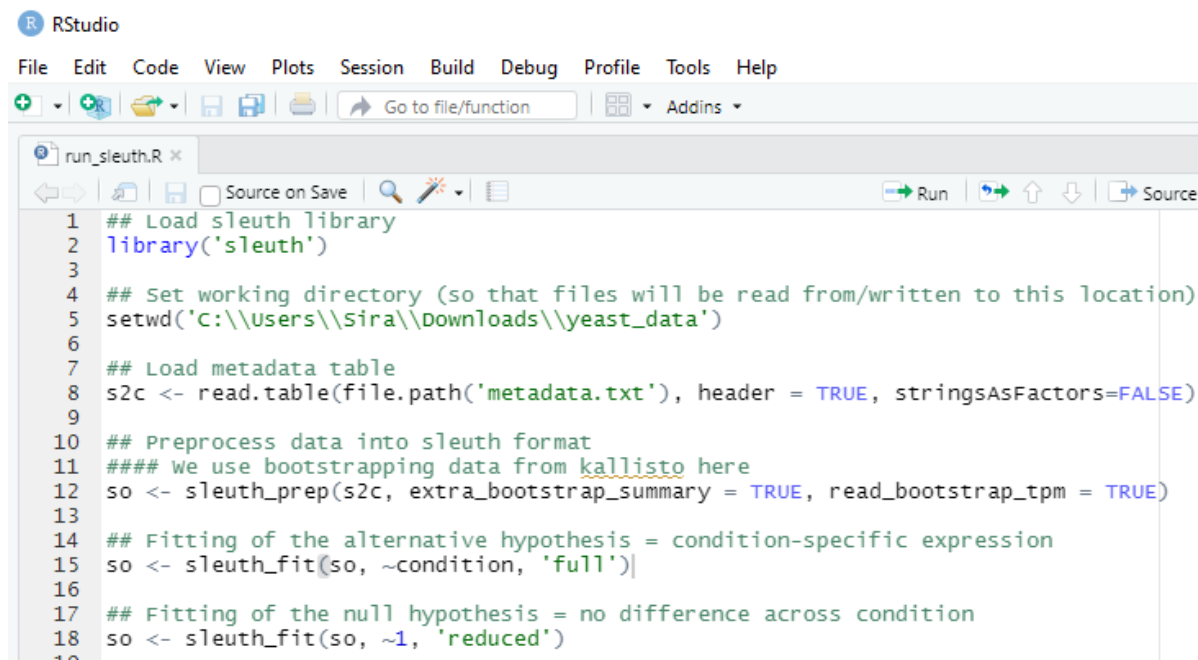


# Building a metadata table for *sleuth*

- Two required columns: sample and path
  - sample = name of each sample
  - path = directory to *kallisto* output
- condition will be used as an experimental design factor

	A	B	C
1	sample	condition	path
2	aerobic1	aerobic	C:\Users\Sira\Downloads\yeast_data\aerobic1
3	aerobic2	aerobic	C:\Users\Sira\Downloads\yeast_data\aerobic2
4	anaerobic1	anaerobic	C:\Users\Sira\Downloads\yeast_data\anaerobic1
5	anaerobic2	anaerobic	C:\Users\Sira\Downloads\yeast_data\anaerobic2

# Editing and running R script



The screenshot shows the RStudio application window. The title bar reads "RStudio". The menu bar includes "File", "Edit", "Code", "View", "Plots", "Session", "Build", "Debug", "Profile", "Tools", and "Help". The toolbar contains icons for file operations (new, open, save, print) and a search bar labeled "Go to file/function". Below the toolbar, the script editor shows a file named "run\_sleuth.R". The script content is as follows:

```
1 ## Load sleuth library
2 library('sleuth')
3
4 ## Set working directory (so that files will be read from/written to this location)
5 setwd('C:\\Users\\Sira\\Downloads\\yeast_data')
6
7 ## Load metadata table
8 s2c <- read.table(file.path('metadata.txt'), header = TRUE, stringsAsFactors=FALSE)
9
10 ## Preprocess data into sleuth format
11 ##### we use bootstrapping data from kallisto here
12 so <- sleuth_prep(s2c, extra_bootstrap_summary = TRUE, read_bootstrap_tpm = TRUE)
13
14 ## Fitting of the alternative hypothesis = condition-specific expression
15 so <- sleuth_fit(so, ~condition, 'full')
16
17 ## Fitting of the null hypothesis = no difference across condition
18 so <- sleuth_fit(so, ~1, 'reduced')
```

# Outputs from *sleuth*

- Table of transcript and p-value (and q-value)

A	B	C	D	E	F	G	H	I
	target_id	pval	qval	test_stat	rss	degrees_free	mean_obs	var_obs
1	NM_001181124.1	2.59E-10	1.27E-06	39.96539563	15.36339695	1	8.417310722	5.121132316
2	NR_132186.1	6.55E-10	1.27E-06	38.14979375	3.640905722	1	9.879766586	1.213635241
3	NR_132187.1	6.55E-10	1.27E-06	38.14979375	3.640905722	1	9.879766586	1.213635241
4	NM_001178902.1	4.30E-09	1.45E-06	34.48167964	6.678866411	1	8.185847672	2.226288804
5	NM_001179305.1	6.06E-09	1.45E-06	33.81376634	0.431345958	1	11.06920134	0.143781986
6	NM_001179347.3	6.59E-09	1.45E-06	33.65244067	14.28124796	1	8.201656196	4.760415988
7	NM_001180385.3	5.58E-09	1.45E-06	33.97442784	1.862161499	1	9.003896352	0.6207205
8	NM_001180810.3	6.39E-09	1.45E-06	33.71281635	2.818466062	1	8.519619279	0.939488687

- Table of expression level (in TPM)

A	B	C	D	E
	aerobic1	aerobic2	anaerobic1	anaerobic2
NM_001178148.1	9.924504945	9.865041182	10.84427431	9.033759097
NM_001178149.1	9.138502413	8.571050881	9.582161084	10.74528304
NM_001178150.1	1171.672132	1170.681103	2148.017091	2154.089911
NM_001178151.1	190.2430374	196.6867042	89.27467731	91.84976857
NM_001178152.1	167.4525834	167.4358872	120.3110809	118.6026502
NM_001178153.1	31.80449311	40.69292227	28.71252687	33.11786185



# Functional enrichment

# WebGestalt

- Provide all 3 methods
  - Overrepresentation
  - GSEA
  - Network-based
- Choices of organisms and functional databases
- Recognize some ID formats



## WEB-based GENE SeT Analysis Toolkit

*Translating gene lists into biological insights...*

[Manual](#) | [API](#) | [Citation](#) | [User Forum](#) |

**Basic parameters**

**Method of Interest** ? Over-Representation Analysis Gene Set Enrichment Analysis Network Topology-based Analysis

**Organism of Interest** ? Homo sapiens ▼  
Common Organisms: Homo sapiens Mus musculus Rattus norvegicus

**Functional Database** ? geneontology ▼  
+ Biological Process noRedundant ▼

List 1 ✎ Add List +

**Analyte Type** ? Gene/Protein Metabolite PTM Other

**Upload ID List** ? Click to upload Reset

**Input ID List** OR



# Gene/transcript ID converter

**g:GOST**  
Functional profiling

**g:Convert**  
Gene ID conversion

**g:Orth**  
Orthology search

**g:SNPense**  
SNP id to gene name

Query ?  

Run query

Options

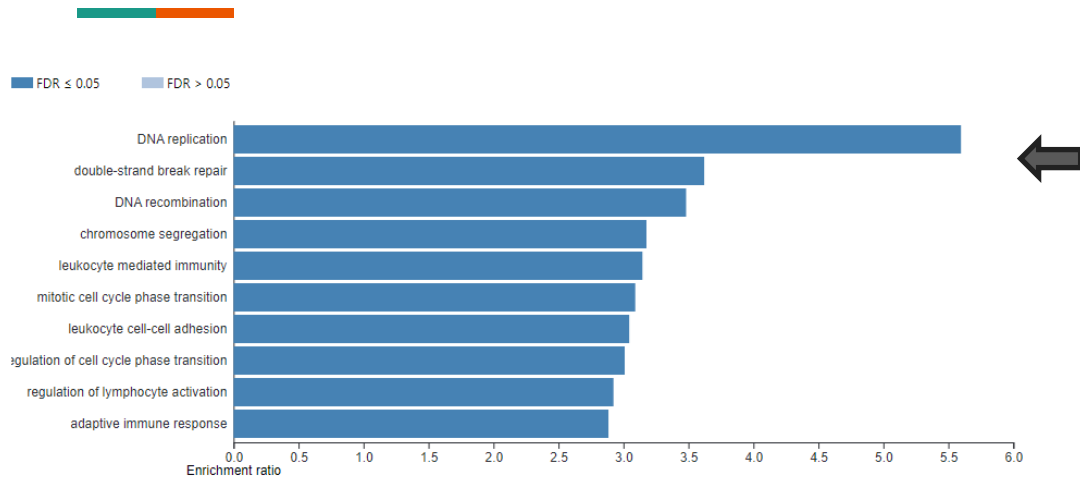
Organism: ?  
Homo sapiens (Human) ▼

Target namespace  
ENSG ▼

Numeric IDs treated as  
ENTREZGENE\_ACC ▼

<https://biit.cs.ut.ee/gprofiler/convert>

# WebGestalt output



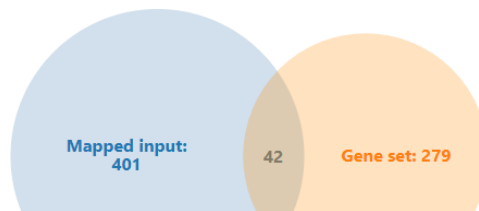
Enriched pathways or biological functions

Select an enriched analyte set...

GO:0006260: DNA replication

Analyte set: [GO:0006260](#)

DNA replication



Number of genes involved

# Any question?

