

程序代写代做 CS编程辅导



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Assignment Project Exam Help

This is using yeast data to understand how to analyze non-human RNA-seq samples

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Background

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Status

Public on Oct 12

Title

Sequencing of mutants with or without phosphate depletion

Organism

[Saccharomyces cerevisiae](#)

Experiment type

Expression profiling by high throughput sequencing

Summary

Targeting of yeast with genetic mutant perturbation to assess mitochondrial membrane potential and its regulation.

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Overall design

RNA-seq (3 replicates of WT, prototrophic WT, pho85, rpo41, or rpo41/pho85 deletion in yeast, and bar1 deletion in W303 yeast) in samples with or without depletion of phosphate, nitrogen, and/or uracil.

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE212790>

Data

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- Experiments:

grow with **no phosphate** for 4hr



grow with **phosphate** for 4hr

- Data

https://ncbi.nlm.nih.gov/Traces/study/?acc=SRP395898&o=acc_s%3Aa&s=SRR21445048,SRR21445049,SRR21445050,SRR21445042,SRR21445043,SRR21445044

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<input checked="" type="checkbox"/>	19	SRR21445042	SAMN30693178	6.57 G	1.94 Gb	SRX17448893	wild-type	GSM6552448	GSM6552448	Saccharomyces cerevisiae (BY)	grow with no phosphate for 4hr
<input checked="" type="checkbox"/>	20	SRR21445043	SAMN30693179	7.81 G	2.31 Gb	SRX17448892	wild-type	GSM6552447	GSM6552447	Saccharomyces cerevisiae (BY)	grow with no phosphate for 4hr
<input checked="" type="checkbox"/>	21	SRR21445044	SAMN30693180	6.69 G	1.96 Gb	SRX17448891	wild-type	GSM6552446	GSM6552446	Saccharomyces cerevisiae (BY)	grow with no phosphate for 4hr
<input type="checkbox"/>	22	SRR21445045	SAMN30693181	6.49 G	1.92 Gb	SRX17448890	wild-type	GSM6552445	GSM6552445	Saccharomyces cerevisiae (BY)	no treatment (ctrl for no ura)
<input type="checkbox"/>	23	SRR21445046	SAMN30693182	7.89 G	2.31 Gb	SRX17448889	wild-type	GSM6552444	GSM6552444	Saccharomyces cerevisiae (BY)	no treatment (ctrl for no ura)
<input type="checkbox"/>	24	SRR21445047	SAMN30693183	6.08 G	1.81 Gb	SRX17448888	wild-type	GSM6552443	GSM6552443	Saccharomyces cerevisiae (BY)	no treatment (ctrl for no ura)
<input checked="" type="checkbox"/>	25	SRR21445048	SAMN30693184	6.70 G	2.01 Gb	SRX17448887	wild-type	GSM6552442	GSM6552442	Saccharomyces cerevisiae (BY)	grow with phosphate for 4hr
<input checked="" type="checkbox"/>	26	SRR21445049	SAMN30693185	7.06 G	2.06 Gb	SRX17448886	wild-type	GSM6552441	GSM6552441	Saccharomyces cerevisiae (BY)	grow with phosphate for 4hr
<input checked="" type="checkbox"/>	27	SRR21445050	SAMN30693186	10.38 G	3.03 Gb	SRX17448885	wild-type	GSM6552440	GSM6552440	Saccharomyces cerevisiae (BY)	grow with phosphate for 4hr

Objectives

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1. Quality control (Galaxy 'FastQC' on raw reads (<https://usegalaxy.org/>)).
2. Mapping RNA-seq reads to *sacCer3* (Galaxy 'STAR', use **Galaxy Version 2.7.8a** for this analysis, use '**sacCer3.ensGene.gtf**' as the GTF file, be aware that the RNA-seq data is **paired-end**).
3. Differential gene expression analysis (DE-analysis) between two conditions (with and without phosphate) (Use 'DESeq2' in R, **prefiltering out lowly expressed genes** before the DE-analysis)
4. Functional analysis (both GSEA and GSEA) using KEGG pathways, GO_BP (biological process), and GO_MF (molecular function) gene sets in Gene Ontology ('ClusterProfiler' in R)
5. **Questions to answer in your report:**
 - a) What do you think about the quality of the sequencing reads based on FastQC reports?
 - b) Compared to samples without, how many up-regulated genes and down-regulated genes did you find, respectively (cutoff: BH-adjusted p-value < 0.05 and |log2 fold change| > 1)?
 - c) Based on the literature review and the functional analysis result, discuss the altered biological functions in response to the depletion of phosphate.

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example

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It produces 24 outputs:

- 643: FastQC on data 629: Webpage
- 644: FastQC on data 629: RawData
- 645: FastQC on data 630: Webpage
- 646: FastQC on data 630: RawData
- 647: FastQC on data 631: Webpage
- 648: FastQC on data 631: RawData
- 649: FastQC on data 632: Webpage
- 650: FastQC on data 632: RawData
- 651: FastQC on data 633: Webpage
- 652: FastQC on data 633: RawData
- 653: FastQC on data 634: Webpage
- 654: FastQC on data 634: RawData
- 655: FastQC on data 635: Webpage
- 656: FastQC on data 635: RawData
- 657: FastQC on data 636: Webpage
- 658: FastQC on data 636: RawData
- 659: FastQC on data 637: Webpage
- 660: FastQC on data 637: RawData
- 661: FastQC on data 638: Webpage
- 662: FastQC on data 638: RawData
- 663: FastQC on data 639: Webpage
- 664: FastQC on data 639: RawData
- 665: FastQC on data 640: Webpage
- 666: FastQC on data 640: RawData

You can check the status of queued jobs and view the resulting data by refreshing the History panel. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

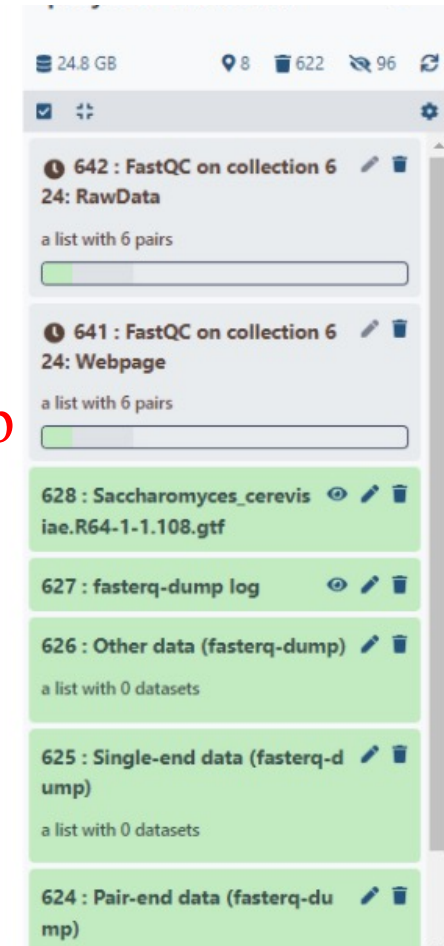
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It produces 24 outputs:

- 671: RNA STAR on data 628, data 630, and data 629: log
- 672: RNA STAR on data 628, data 630, and data 629: splice junctions.bed
- 673: RNA STAR on data 628, data 630, and data 629: mapped.bam
- 674: RNA STAR on data 628, data 630, and data 629: reads per gene
- 675: RNA STAR on data 628, data 632, and data 631: log
- 676: RNA STAR on data 628, data 632, and data 631: splice junctions.bed
- 677: RNA STAR on data 628, data 632, and data 631: mapped.bam
- 678: RNA STAR on data 628, data 632, and data 631: reads per gene
- 679: RNA STAR on data 628, data 634, and data 633: log
- 680: RNA STAR on data 628, data 634, and data 633: splice junctions.bed
- 681: RNA STAR on data 628, data 634, and data 633: mapped.bam
- 682: RNA STAR on data 628, data 634, and data 633: reads per gene
- 683: RNA STAR on data 628, data 636, and data 635: log
- 684: RNA STAR on data 628, data 636, and data 635: splice junctions.bed
- 685: RNA STAR on data 628, data 636, and data 635: mapped.bam
- 686: RNA STAR on data 628, data 636, and data 635: reads per gene
- 687: RNA STAR on data 628, data 638, and data 637: log
- 688: RNA STAR on data 628, data 638, and data 637: splice junctions.bed
- 689: RNA STAR on data 628, data 638, and data 637: mapped.bam
- 690: RNA STAR on data 628, data 638, and data 637: reads per gene

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STAR-Fusion detect fusion genes in RNA-Seq data

RNA STAR Gapped-read mapper for RNA-seq data

MiRDeep2 Quantifier fast quantitation of reads mapping to known miRBase precursors

RNA STARSolo mapping, demultiplexing and gene quantification for single cell RNA-seq

/Search clustering

QualiMap RNA-Seq QC

Q-TREE Phylogenomic / evolutionary tree construction from multiple sequences

staramr Scans genome assemblies against the ResFinder, PlasmidFinder,

24.9 GB 12 622 120

670 : RNA STAR on collection 624: reads per gene

a list with 6 datasets

669 : RNA STAR on collection 624: mapped.bam

a list with 6 datasets

668 : RNA STAR on collection 624: splice junctions.bed

a list with 6 datasets

667 : RNA STAR on collection

Submission

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1. FastQC reports in '.html' format for each sample (Objective 1). Take a screenshot of your analyses on Galaxy as well, save into jpg format (Objective 1).
2. The STAR mapping results in Galaxy in '.tabular' format (Objective 2).
3. A table summarizing the results of differential gene expression analysis phosphate depleted culture and control samples in '.csv' format (Objective 3).
4. Tables summarizing GSOA and GSEA results, and save into '.csv' format (Objective 4).
5. Enrichment maps for GSOA and GSEA and save into '.pdf' format (Objective 4).
6. Programming code in R script or R Markdown format and/or Galaxy snapshots (for every step on Galaxy).

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Report

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1. A Word file summarizing your answers to the questions in Objective 5, with proper figures and proper citation.
2. This report has to be at least one page excluding the reference page.

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