CyVerse Documentation

CyVerse

Sep 18, 2020

Contents

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Learning Center Home

CHAPTER 1

Goal

This draft tutorial will introduce some of the features of the and tools for RNA-Sequencing of bulk and single-cell samples.

Warning: This tutorial is still in its draft form. These datasets are not yet available on the CyVerse Data Store, but are available on an Amazon AMI and docker container. These will later be migrated to . Additionally, these materials are part of a workshop collection and not yet designed for independent use. These should not be relied on for analysis of your own data - they are merely useful examples that can inform your own analysis.

CHAPTER 2

Prerequisites

2.1 Downloads, access, and services

In order to complete this tutorial you will need access to the following services/software

Prerequisite	Preparation/Notes	Link/Download
CyVerse account	You will need a CyVerse account to complete this exercise	
Docker	You must have access to Docker to run this tutorial	
Amazon AWS Account	You can run this tutorial from this AMI:	ami-042909f3c5b9bf6ed

2.2 Platform(s)

We will use the following CyVerse platform(s):

Platform	Interface	Link	Platform Documentation	Quick Start
Data Store	GUI/Command line			
Discovery Environment	Web/Point-and-click			
VICE	A flexible environment for using Jupyterlab, RStudio, and RShiny			

2.3 Important links for this workshop

2.3.1 Workshop logistics

Resource/Description	Link
Gitter channel - we will have live chat and share through this channel	
Opening poll	

2.3.2 Software resources

Resource/Description	Link
Bioconductor - resource for R-based bioinformatics tools	
Bioconda - Reproducible software installation	
CyVerse Learning Center - CyVerse learning materials	

2.3.3 Papers

Resource/Description	Link
A survey of best practices for RNA-seq data analysis	
Fast and accurate single-cell RNA-seq analysis by clustering of transcript-compatibility counts	
Differential analysis of RNA-seq incorporating quantification uncertainty	
Tackling the widespread and critical impact of batch effects in high-throughput data	
AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing	
Tutorial: guidelines for the experimental design of single-cell RNA sequencing studies	

2.3.4 Other learning resources

Resource/Description	Link
BioInfoSummer Workshop slides	
Hemberg single cell RNA-Seq wiki (very comprehensive)	
How to Use t-SNE Effectively	
Dana Pe'er: "Having fun with single-cell RNA-seq: imputation and manifolds"	
Lior Pachter: Differential analysis of count data in genomics	
Principal Component Analysis (PCA) clearly explained (2015)	
Single-cell RNA-Seq tools	
Seurat pipeline for SC RNA-Seq	

Fix or improve this documentation

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 Learning Center Home