

Introduction to RNA Seq Course 2014

Day 1: Introduction to RNA-Seq and Read Mapping

- Part 1: [Introduction to RNA-Seq](#)
- Part 2: Unix and TACC Refresher
 - [The Quickest Unix Refresher ever 2014](#)
 - [TACC Overview 2014](#)
 - [Using The Lonestar cluster](#)
 - [Lonestar directory structure](#)
 - [Submitting jobs to Lonestar](#)
 - [TACC/Unix Exercise](#)
- Part 3: Read Mapping
 - [The Big Picture](#)
 - [Evaluating your raw data 2014](#)
 - [Introduction to read mapping](#)
 - [Mapping with BWA 2014](#)
 - [Mapping with Tophat 2014](#)
 - [Assessing mapping results \(and more\)](#)

Day 2: Quantification and Differential Expression Analysis

- [Logistics](#)
- Wrapping up mapping
 - [Day 1 take aways](#)
 - [Assessing mapping results](#)
 - [Mapping with Tophat 2014](#)
- Part 1: [Gene counting](#)
- Part 2: [Testing for differential expression 2014](#)

Day 3: Splice Variant Analysis, Novel Transcripts and Non-Traditional RNA-Seq

- [Day 2 take aways](#)
- Part 1: Tuxedo suite for finding novel transcripts
 - [Lecture](#)
 - [Results](#)
- [Day 3-Part I take aways](#)
- Part 2: RIP-Seq
 - [Theoretical and Experimental Background](#)
 - [Software Overview](#)
 - [Exercise #1: RIP-Seq](#)
 - [Exercise #2: CLIP-Seq](#)

Day 4: Downstream Analysis of Differentially Expressed Genes

- [Logistics](#)
- [The Big Picture](#)
- Part 1: [Visualization using CummeRbund 2014](#)
- Part 2: [Visualization using Integrated Genome Viewer \(IGV\) 2014](#)
- Part 3: [Go Enrichment analysis using goseq 2014](#)
- Part 4: [Clustering using WGCNA](#)
- [Day 4 take aways](#)
- [Resources](#)
- Part 5: [Exercise time!](#)

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