**Introduction:**

* Biological Origins of the data

- Prior work in time series analysis

* How was the data analyzed
  + Phase 1 align reads to genome HISAT2
  + Phase 2 count reads associated with genomic features HTSeq\_Count
  + Phase 3 apply EdgeR’s CPM normalization to address library size
  + Phase 4 Evaluation of samples without batch adjustment
    - Sample clustering without batch correction
      * External Measures: Matching / F-Statistic
    - Genewise clustering separately, by Lab
      * Internal Measures:
  + Phase 5 Evaluation of batch corrected data
* What key observations were made

**Prior work in Time series analysis**

* what clustering methods have been used previously
* what types of results were observed
* how did I choose my clustering methods.

**Data Analysis:**

* Raw reads were aligned to the genome using HISAT2, and features were counted using HTSeq.
  + Add MultiQC Figures – Sequence Alignment Quality Metrics,
  + Feature Counts MultiQC
* Count data was normalized using edgeR’s TMM normalization method which calculates scaling factors based on library size and relative expression levels of invariant genes.
* Evaluation of Sample Variation Before Batch Correction
  + Principle Components on to 10, 50, 100 genes ranked by variance
    - Pair of plots colored by: Time point and by Batch
  + Sample Clusters before batch correction
    - Heirarchical, on top 10, 50, 100 genes by variance
      * Distance methods Euclidean and manhattan
      * Linkage methods, average, complete, single
      * Number of k 1 – 9
      * Measures: number of genes, Rand Index vs Ground Truth, silhouette coefficient(s) min, max, average
* Evaluation of Sample Variation After Batch Correction
  + Principle Components on 10, 50 and 100 genes ranked by variance
    - Pair of Plots colored by Time point and by Batch
* Within Batch Differential Expression Analysis.
  + Table: Number of Genes Differentially for each contrast
  + Venn Diagrams
    - Overlap of
* What were the results from the alignment and Quality Control phases