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**Day 2**Date and Time: Monday October 20th 1PM-3PM

**Workshop Lead: Alejandro Mejia Garcia**  
**Facilitator: Ryan Huang**  
**Registration link:**   
**Approximate duration: 2 hours**

**Prerequisites:**

1. Basic understanding of bash
2. A gmail account

**Summary: (2-3 sentences summarizing the workshop)**

This workshop introduces participants to the fundamentals of RNA-seq, from raw sequencing data to raw count matrices ready for analysis. We will cover quality control of sequencing data, alignment and read counting.

**Learning Outcomes: (List 3-5 learning outcomes participants will learn upon completion of this workshop)**

1. RNA-seq technologies knowledge: Students will be able to differentiate between expression microarrays and RNA-seq, and what types of RNAs they can capture with different kits.
2. Quality control, alignment and read counting: Students will understand quality control of raw sequencing data, how to align to human reference genome and generate read counts for their data.

**Content**

1. **Module 1: Overview of RNA-seq (55 minutes)**
   1. Overview of RNA-seq technologies
      1. Comparison with expression microarrays
      2. RNA-seq kits (Poly A, total RNA, etc).
   2. Bioinformatics pipeline
      1. Quality control
      2. Adapter removing and low-quality bases trimming
      3. Alignment to human genome
      4. Generating count matrix
2. **Break (5 mins)**
3. **Module 2: practice session on google collab (60 mins)**
   1. Quality control with FASTQC
      1. Running FASTQC on short read FASTQ files
   2. Trimming and post-trimming QC with Trimmomatic
      1. Adapter removal
      2. Trimming of low-quality bases from reads
      3. Running FASTQC on trimmed fastq file
   3. Alignment to human genome
      1. Splicing-aware alignment using STAR
   4. Post-alignment QC
      1. Sorting, indexing and removing low-quality mapped reads
   5. Generating read count matrix
      1. Running FeatureCounts to generate a count matrix