

## ***Pipeline for model systems***

1. Map to an existing reference genome (e.g. **Tophat2**)

2. Filter and clean data, as appropriate

3. Count reads with **HTSeq-count**

3. Test for differential expression (e.g., **DESeq, EdgeR**, etc.)

## ***Pipeline for non-model systems***

1. Transcriptome assembly and annotation (*de novo* or reference guided)

2. Filter and clean data, as appropriate

1. Map to transcriptome (e.g. **Tophat2**)

3. Test for differential expression (e.g., **DESeq, EdgeR**, etc.)