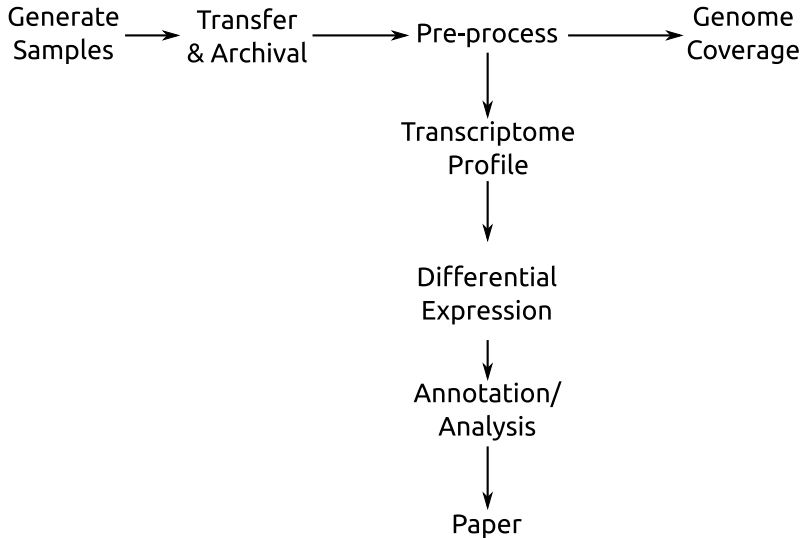


# Practical Bioinformatics

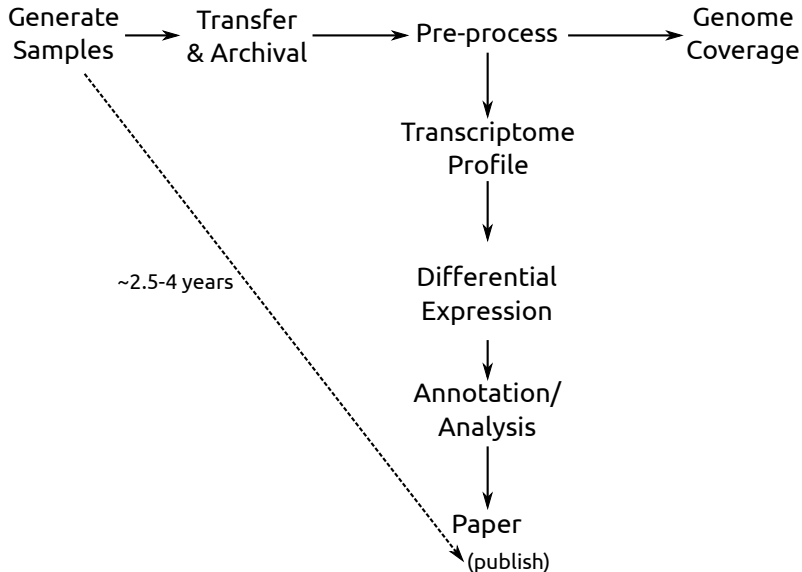
Mark Voorhies

5/29/2019

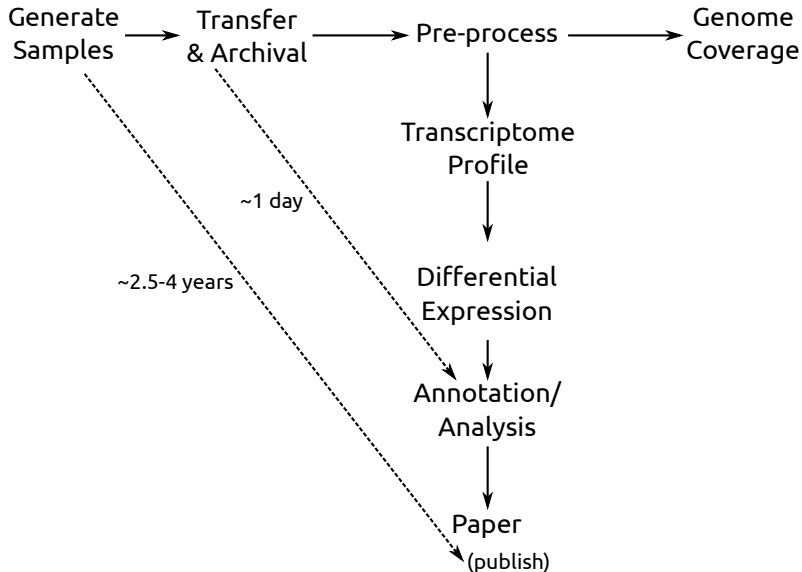
# Example Pipeline: Overview



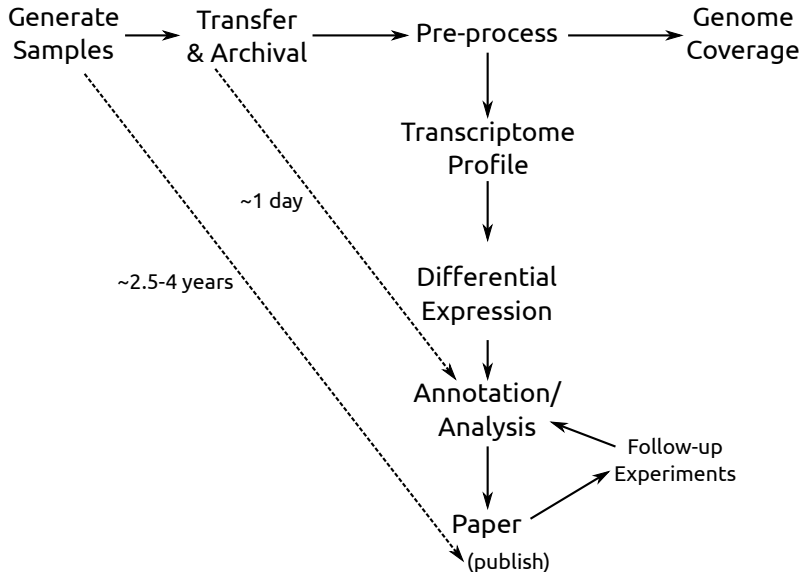
# Example Pipeline: Overview



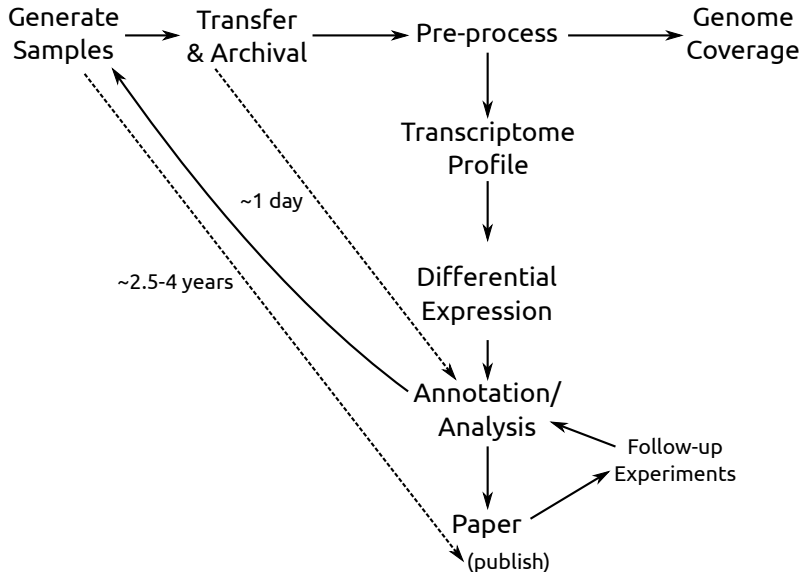
# Example Pipeline: Overview



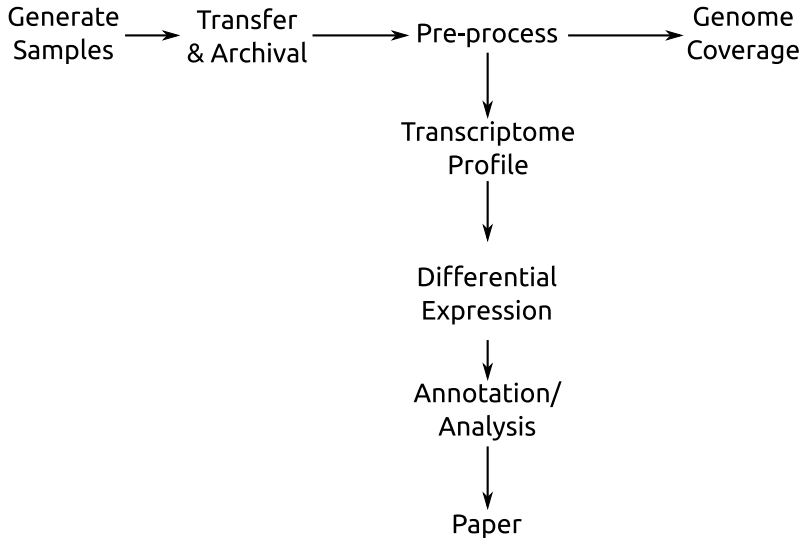
# Example Pipeline: Overview



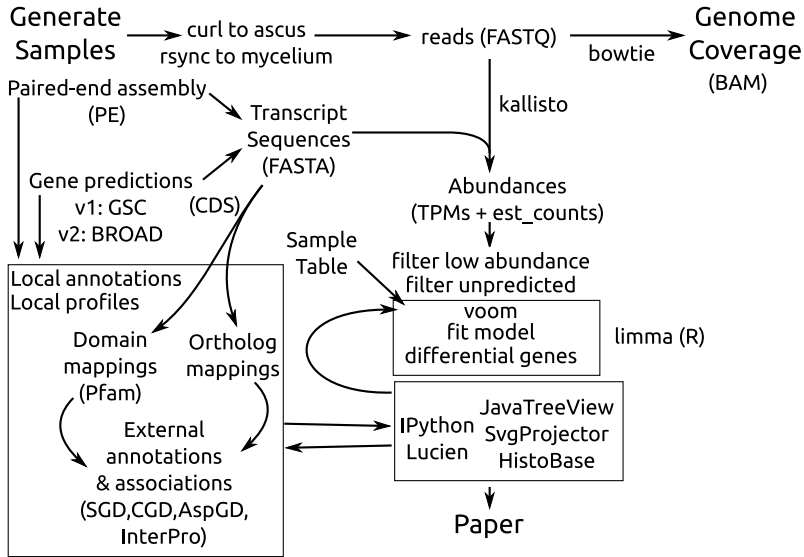
# Example Pipeline: Overview



# Example Pipeline: Overview

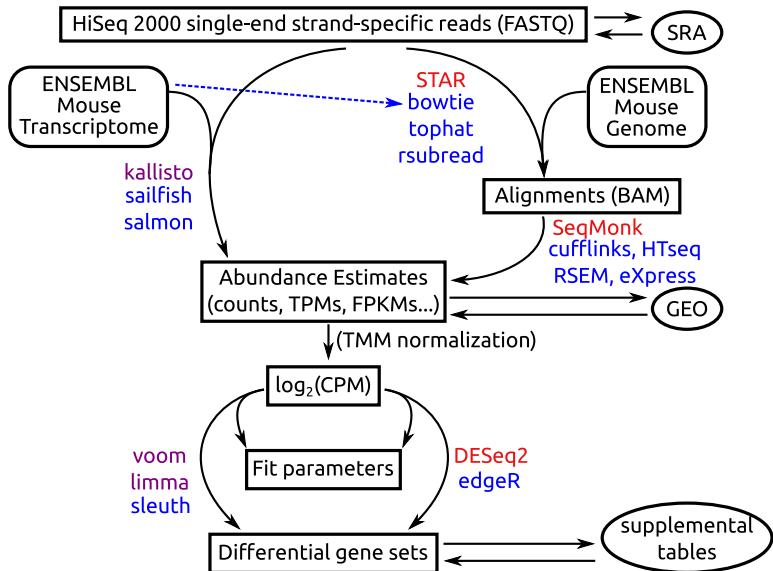


# Example Pipeline: Details





# GSE88801 Pipelines

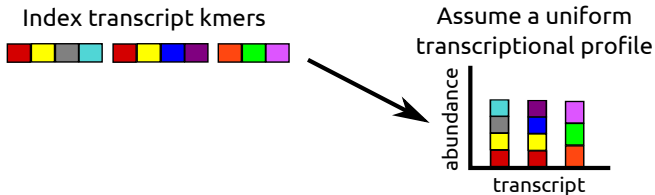


# Abundance estimation with kallisto

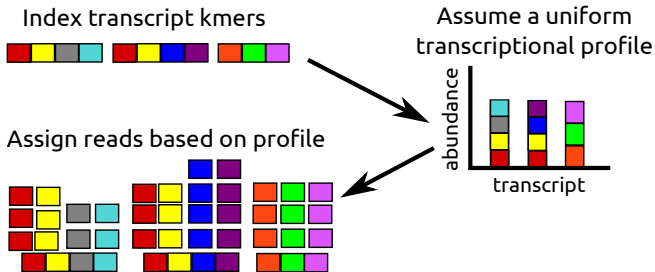
Index transcript kmers



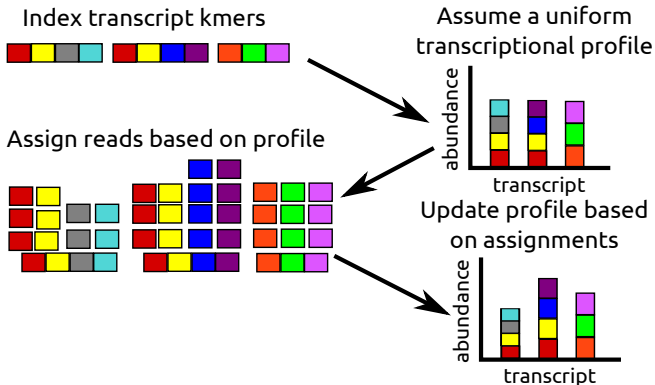
# Abundance estimation with kallisto



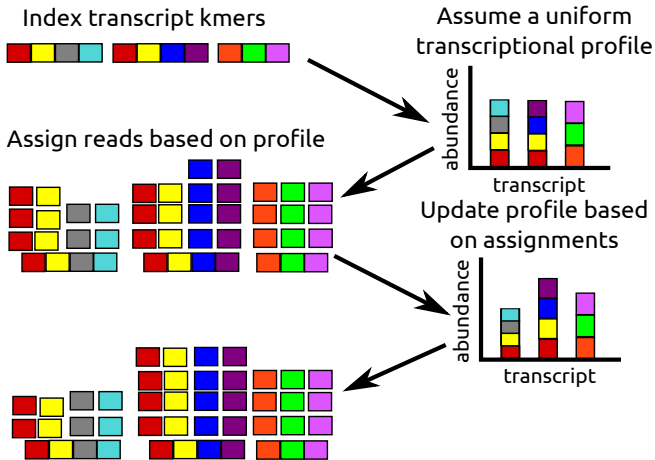
# Abundance estimation with kallisto



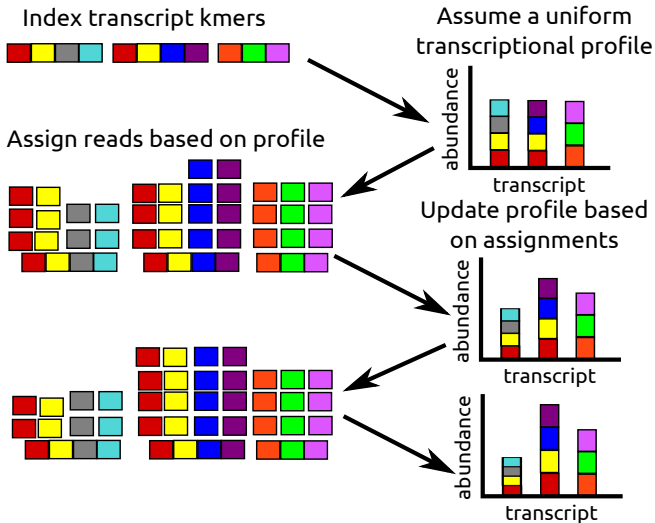
# Abundance estimation with kallisto



# Abundance estimation with kallisto



# Abundance estimation with kallisto



# Abundance estimation with kallisto

```
export transcriptome="GRCm38_all_mRNA"  
while read i; do  
  export jobname="${i}.${transcriptome}.fr"  
  kallisto quant -i "${transcriptome}.idx" \  
    -t 4 --single --fr-stranded -l 250 -s 50  
    -o "${jobname}" "${i}_1.fastq.gz" \  
    > "${jobname}.log" \  
    2> "${jobname}.err"  
done < sample_names.txt
```