

# Tutorial 7 – HTSeq & DESeq2

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30 OCTOBER 2020

MICB405

# Announcement

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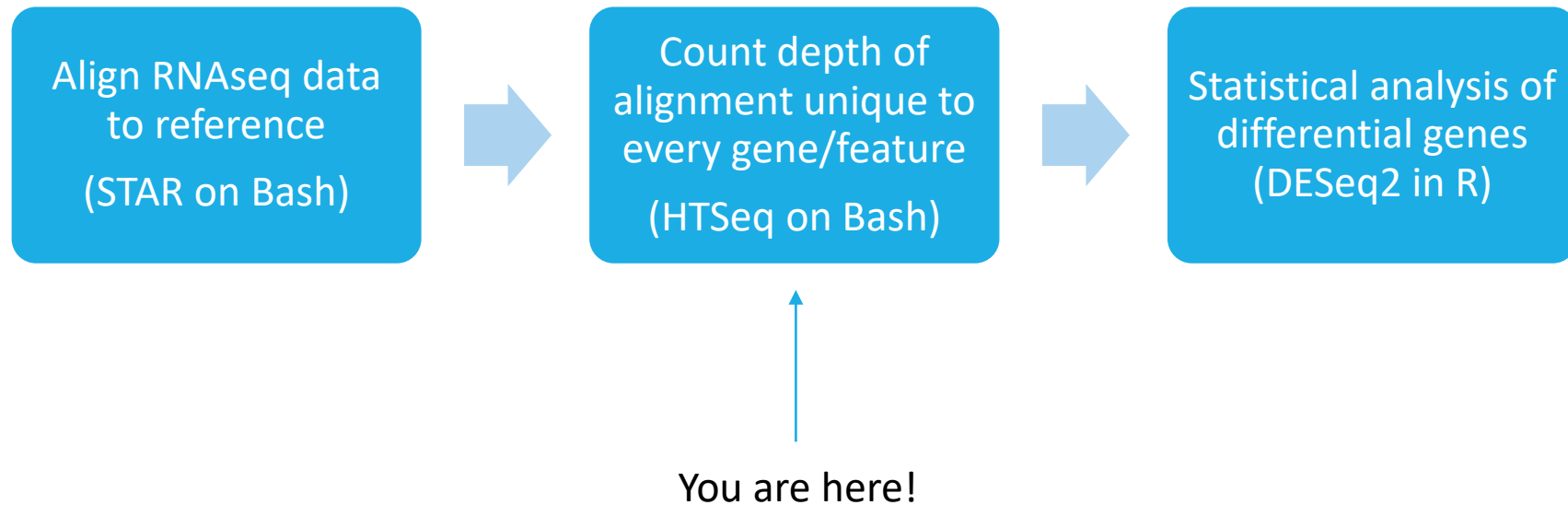
We are running out of disk space on the server!

- Please delete any large files such as SAM/BAM/etc

# Overview of HTSeq

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## Differential gene expression analysis workflow



# Overview of DESeq2

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Normalizes counts to account for differences in gene length and sequencing depth

Performs hypothesis testing to find genes that are differentially expressed

Calculates fold change of expression values between different treatment groups

Outputs a list of differentially expressed genes