

Tutorial 8 – HTSeq & DESeq2

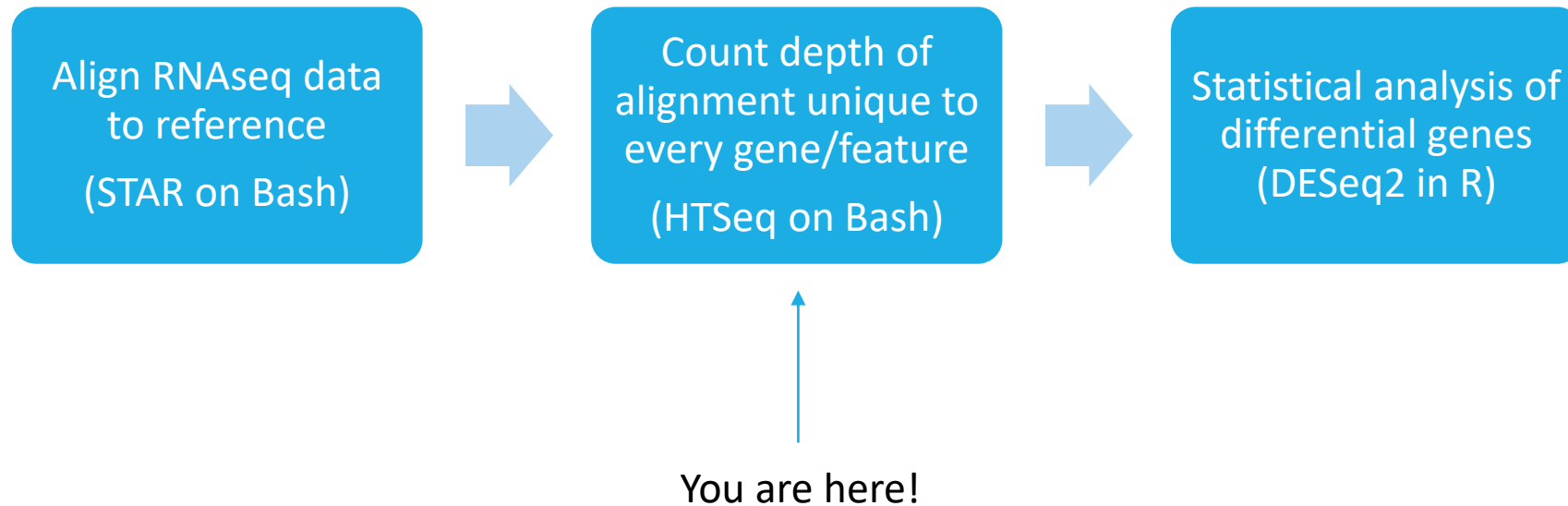
MICB405 – BIOINFORMATICS – 2021W-T1

29 OCTOBER 2021

AXEL HAUDUC

Overview of HTSeq

Differential gene expression analysis workflow



Overview of DESeq2

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