Tutorial 7 – HTSeq & DESeq2

MICB405 – BIOINFORMATICS – 2021W-T1

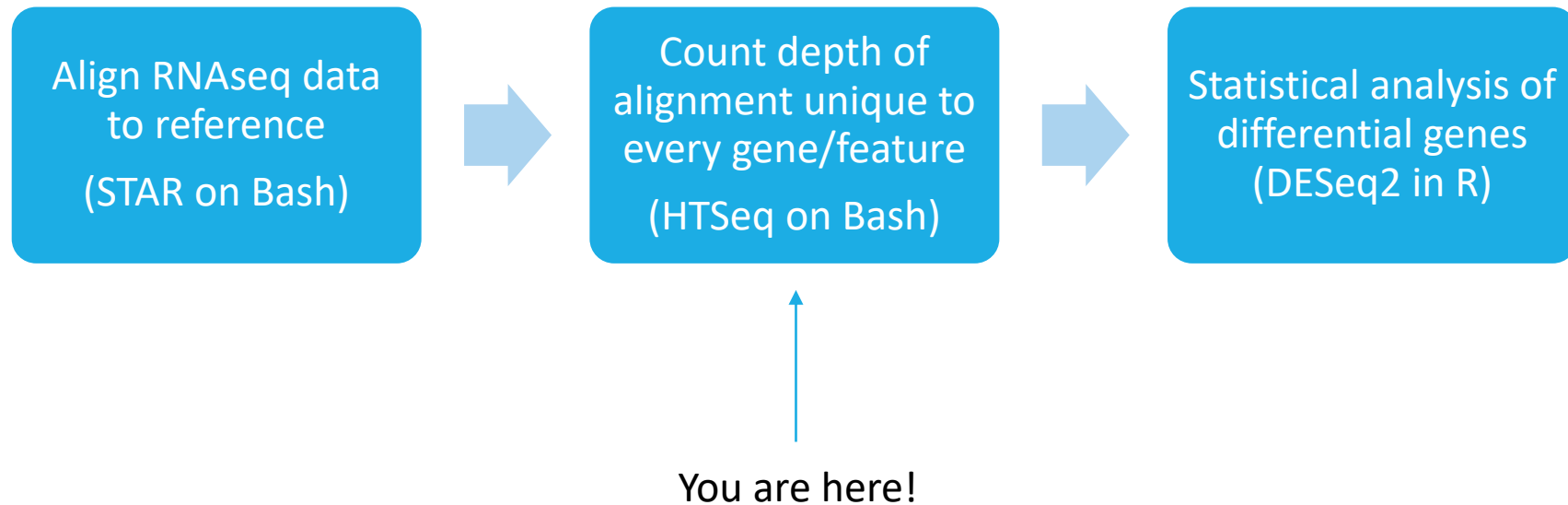29 OCTOBER 2021

AXEL HAUDUC

Overview of HTSeq

Differential gene expression analysis workflow

Align RNAseq data to reference

(STAR on Bash)

→

Count depth of alignment unique to every gene/feature

(HTSeq on Bash)

→

Statistical analysis of differential genes

(DESeq2 in R)

You are here!

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