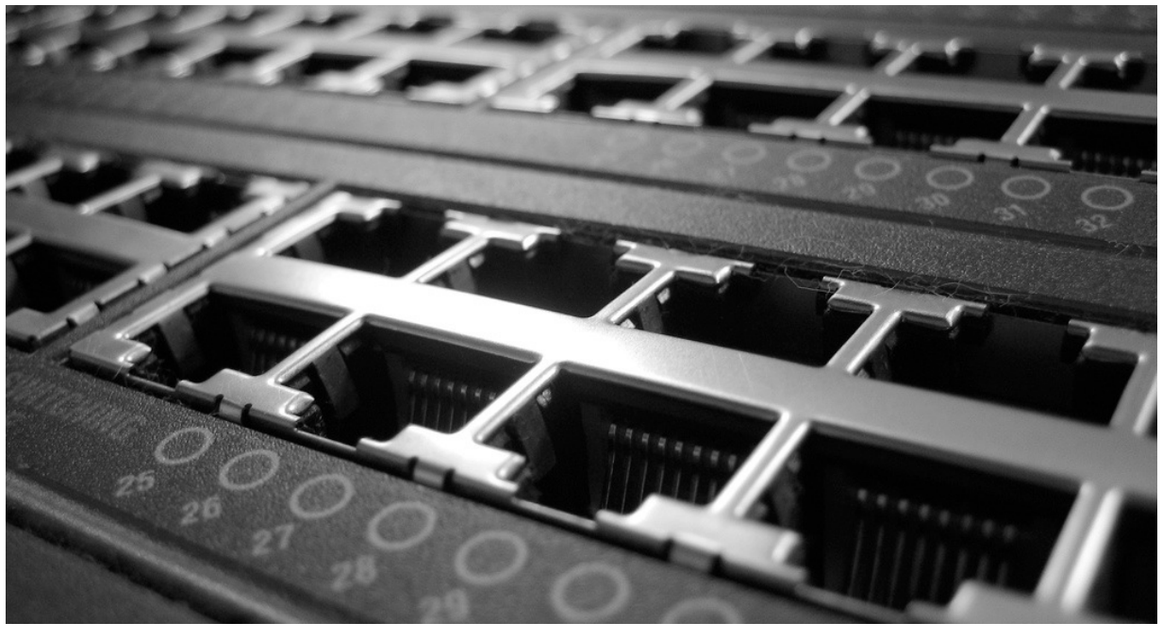


Introduction to RNA-seq using High-Performance Computing (HPC)

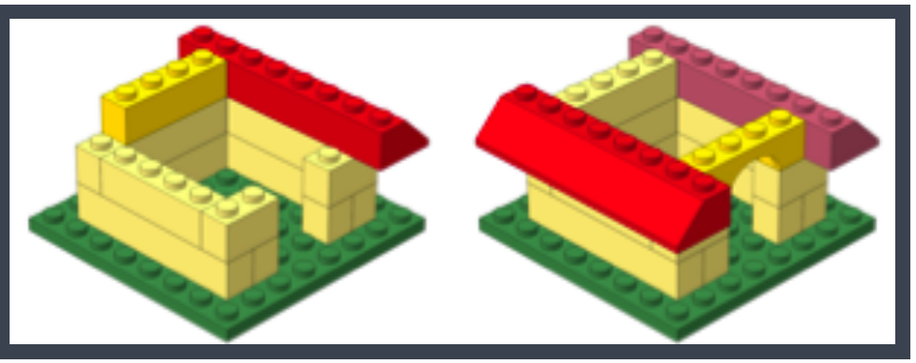
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

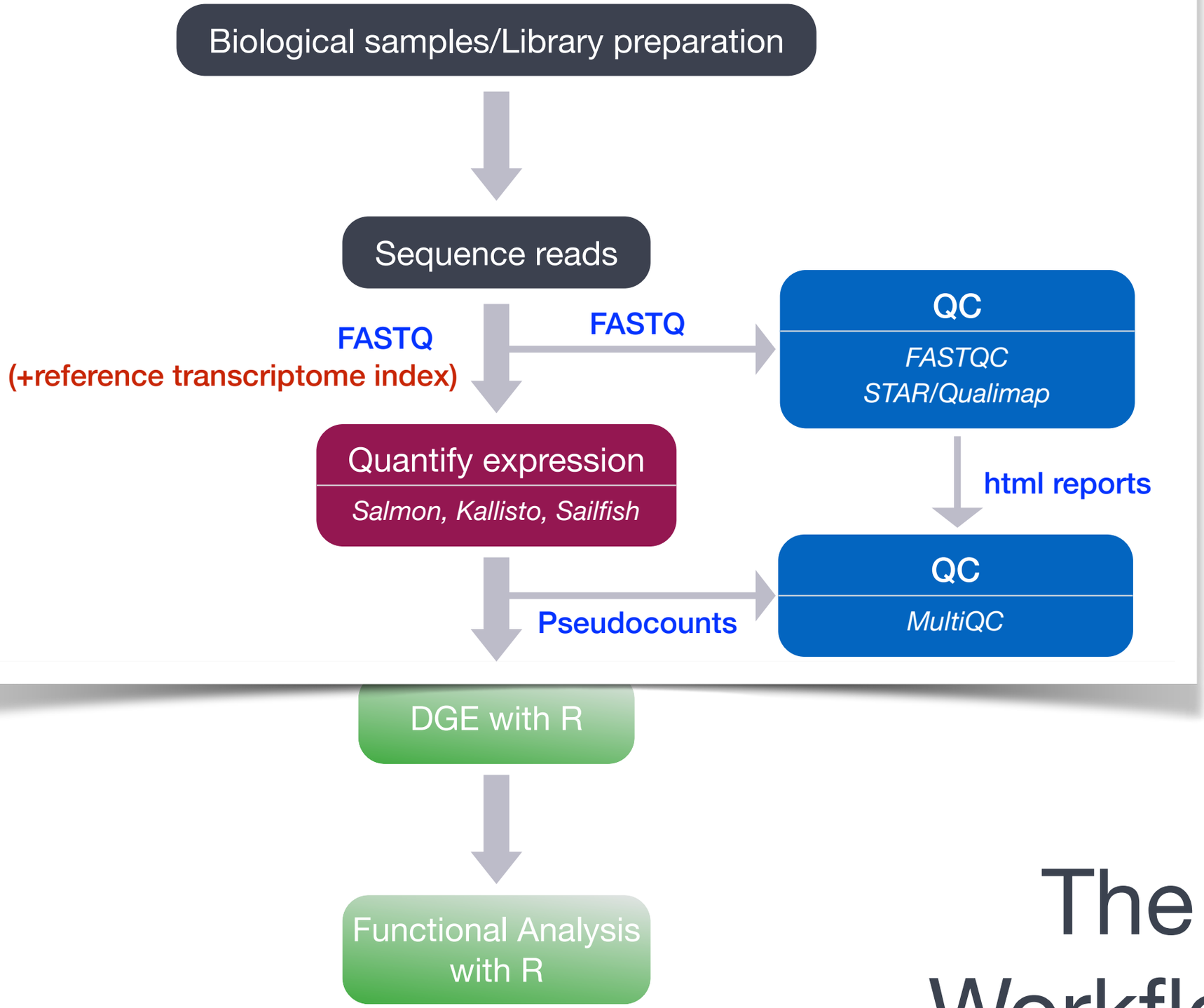
https://tinyurl.com/hbc-rnaseq

Learning Objectives



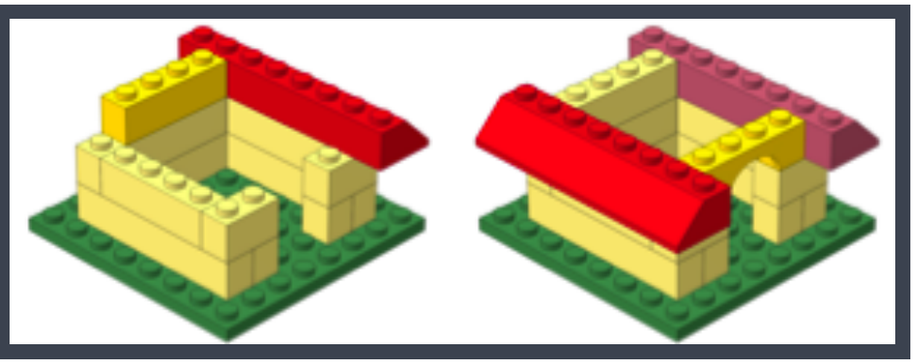
- ✓ Describe best practices for designing a bulk RNA-seq experiment
- ✓ Describe steps in an RNA-seq analysis workflow (from sequence data to expression quantification).
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps.

We won't be covering how to perform differential gene expression (DGE) analysis on count data in this workshop. A DGE workshop will be held on April 1st/2nd and the pre-requisite for it is a working knowledge of R (March 12th/13th).



The Workflow

Learning Objectives



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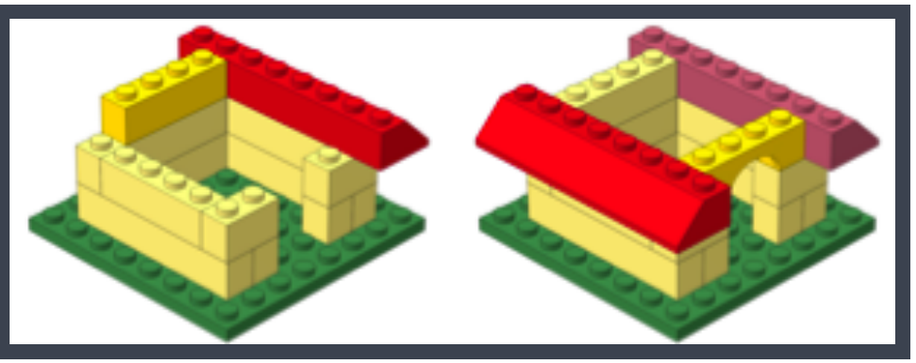
Survey



https://tinyurl.com/hbc-hsph-rnaseq-exit

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https://bioinformatics.sph.harvard.edu/current-bioinformatics-topics-workshops

Thanks!

- Daniel Caunt and Maggie McFee from FAS-RC
- Data Carpentry

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