



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

Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

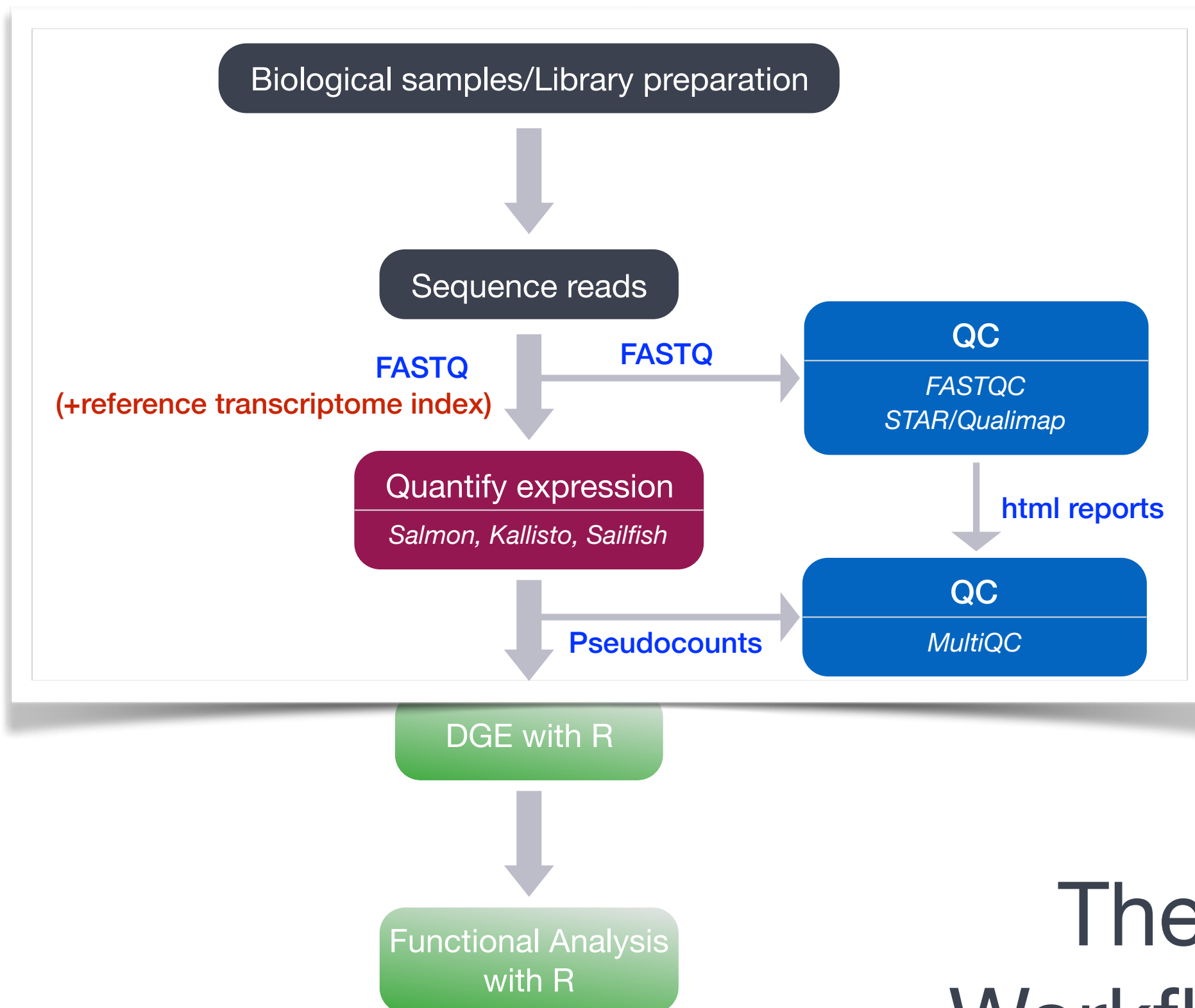
<https://tinyurl.com/hbc-rnaseq>

Learning Objectives



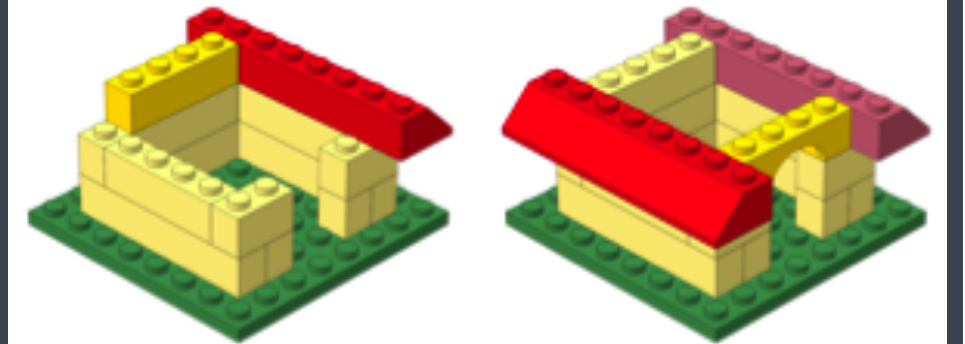
- ✓ Describe best practices for designing a bulk RNA-seq experiment
- ✓ Describe steps in an RNA-seq analysis workflow (from sequence data to expression quantification).
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps.

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

Survey



<https://tinyurl.com/hbc-rnaseq-exit>

Thanks!

- Kathleen Keating and Andy Bergman from HMS-RC
- [Data Carpentry](#)

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Contact us!

HBC training team: hbctraining@hsph.harvard.edu

O2 (HMS-RC): rchelp@hms.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

HBC: @bioinfocore

HMS-RC: @hms_rc