Bulk RNA-seq Analysis Part II

Differential Gene Expression

Harvard Chan Bioinformatics Core

https://tinyurl.com/hbc-dge-online

Workshop Scope
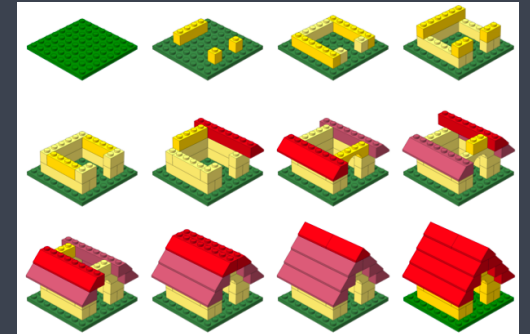
Differential Gene Expression analysis

✓ Understand the considerations for performing statistical analysis on RNA-seq data

✓ Start with gene counts (after alignment and counting)

✓ Perform QC on count data

✓ Use DESeq2 to perform differential expression analysis on the count data and obtain a list of significantly different genes

✓ Visualize results of the analysis

✓ Perform functional analysis on the lists of differentially expressed genes
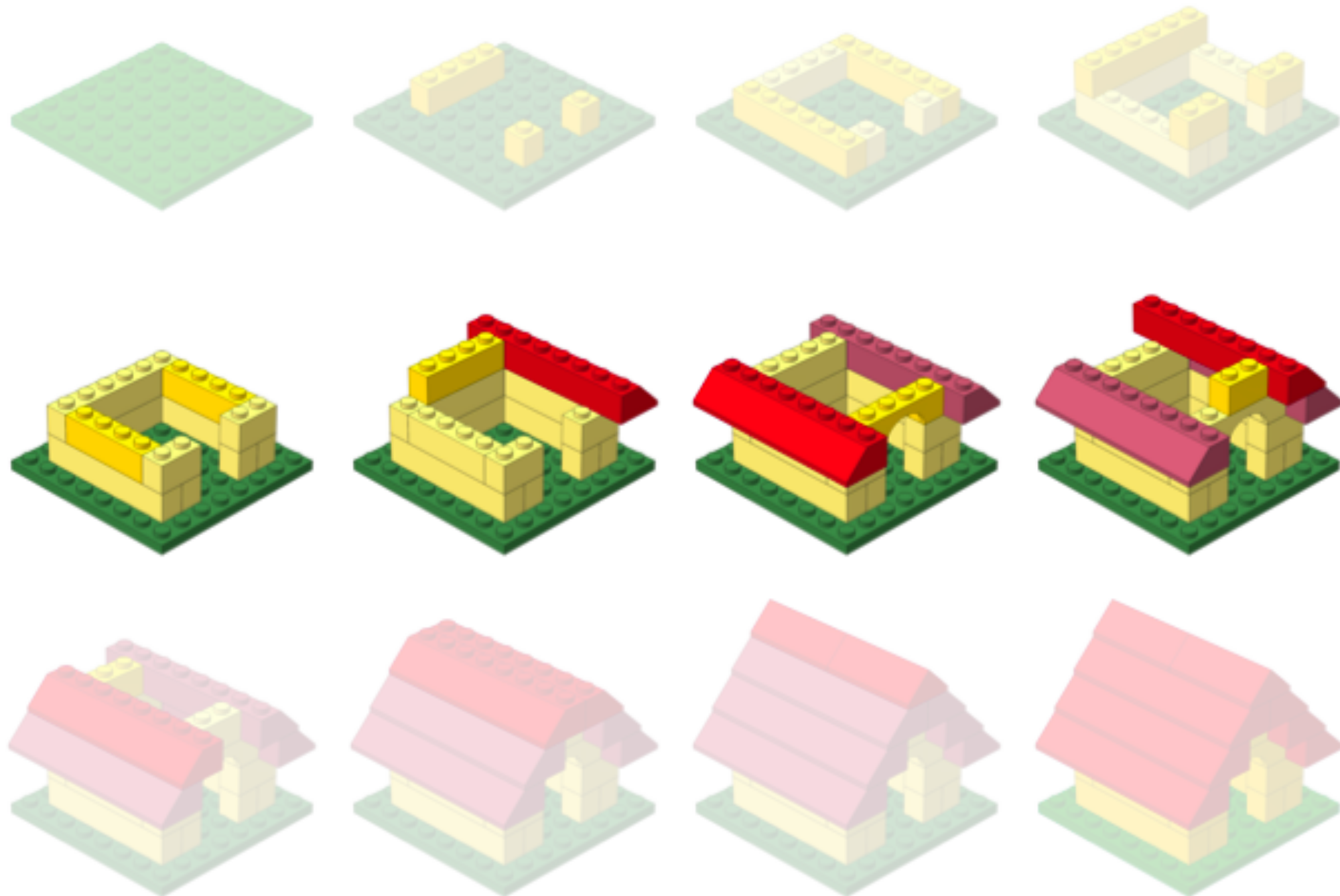
Bioinformatics data analysis

Exit survey

https://tinyurl.com/DGE-exit-survey

Office hours

- 30 minute office hours for trainees

- Every other Wednesday at 11 AM or 11:30 AM

- Sign up form will be emailed to you

Interested in additional training?

All workshop materials available at:

https://hbctraining.github.io/main

Next workshops

- scRNA-seq (Starting on Feb 11th, 2022)

- Intro to shell and O2 (Starting on Feb 25th, 2022)

Current topics in Bioinformatics

Single cell analysis tools

1PM - Dr. Cliff Meyer and Allen Lynch - MIRA:
   Joint regulatory modeling of multimodal expression and chromatin
   accessibility in single cells

2PM - Dr. Jill Lundell and Dr. Kelly Street - cytofQC
   Where did my tumor cells go? A better way to clean CyTOF data using
   'cytofQC'.

Tomorrow, Dec 15th

Get (stay) in touch with us!

Sign up for our mailing list:

https://tinyurl.com/hbc-training-mailing-list

Training email: hbctraining@hsph.harvard.edu

Consulting email: bioinformatics@hsph.harvard.edu

Twitter: @bioinfocore