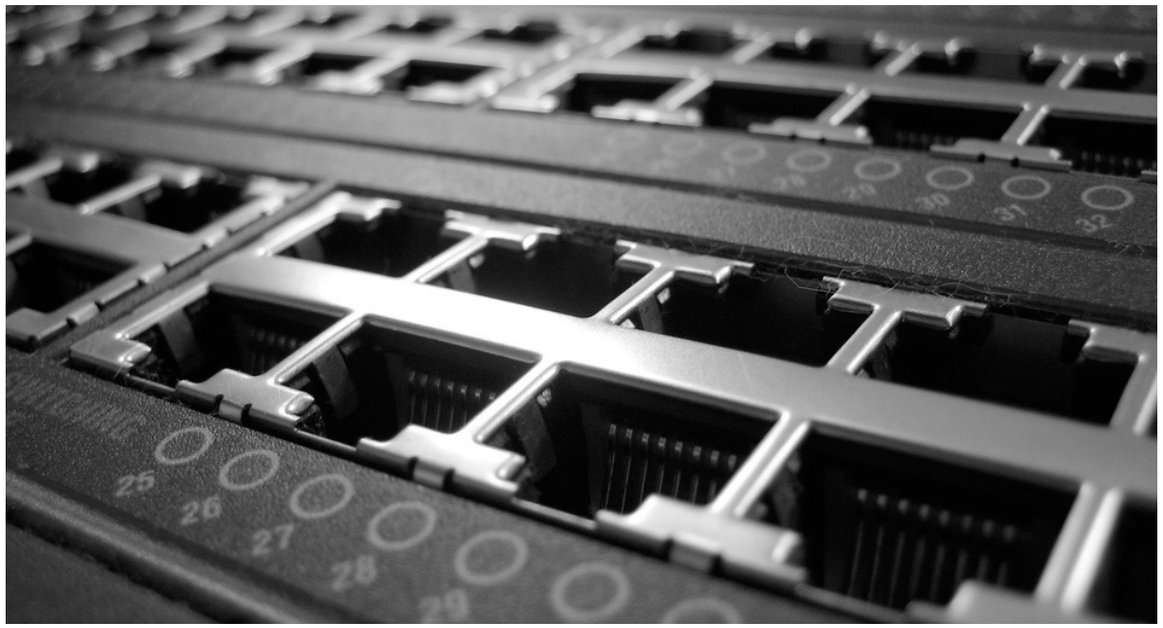


Introduction to RNA-seq using High-Performance Computing (HPC)

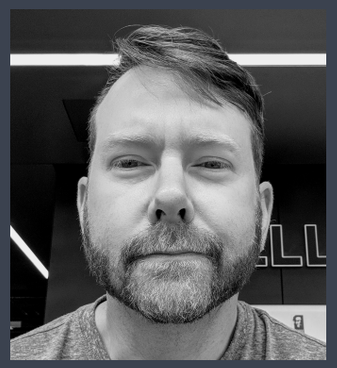
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

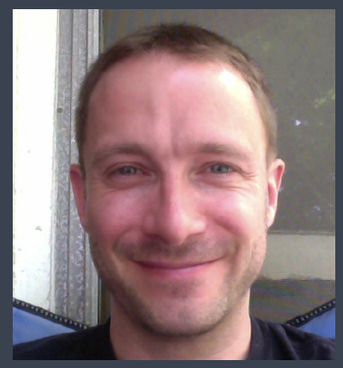
https://tinyurl.com/intro-to-rnaseq-adv

Shannan Ho Sui
Director



John Hutchinson
Associate Director

Victor Barrera



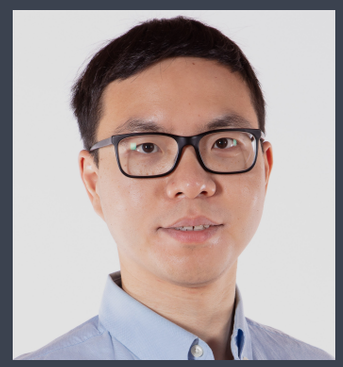
Rory Kirchner

Zhu Zhuo

Preetida Bhetariya

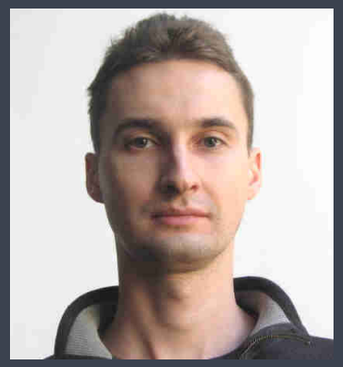
Meeta Mistry

Mary Piper



Jihe Liu

Radhika Khetani
Training Director



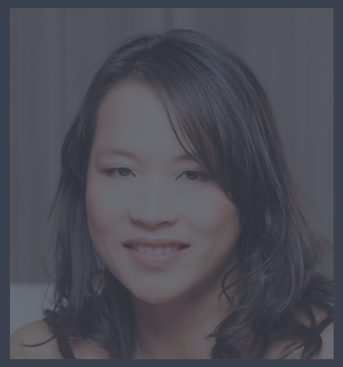
Ilya Sytchev

James Billingsley

Sergey Naumenko

Joon Yoon

Peter Kraft
Faculty Advisor



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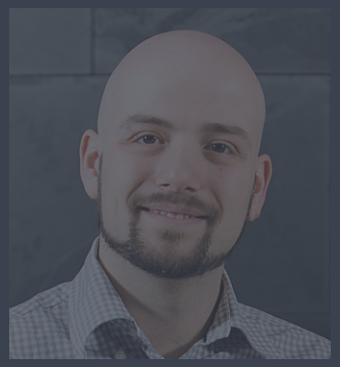

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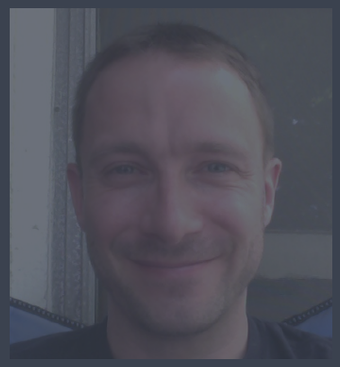

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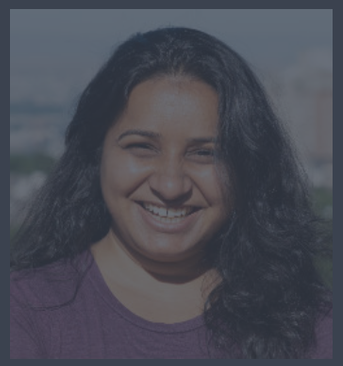

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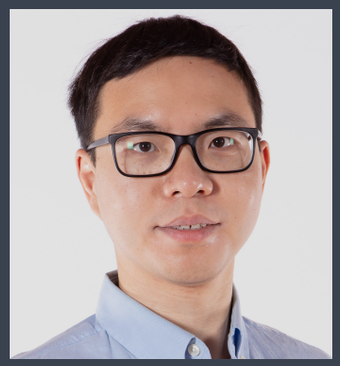

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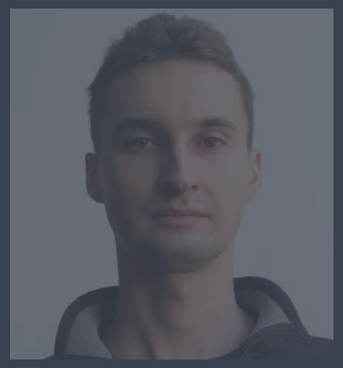

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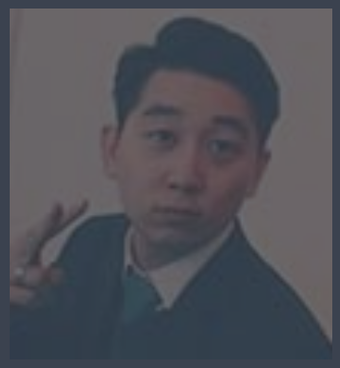
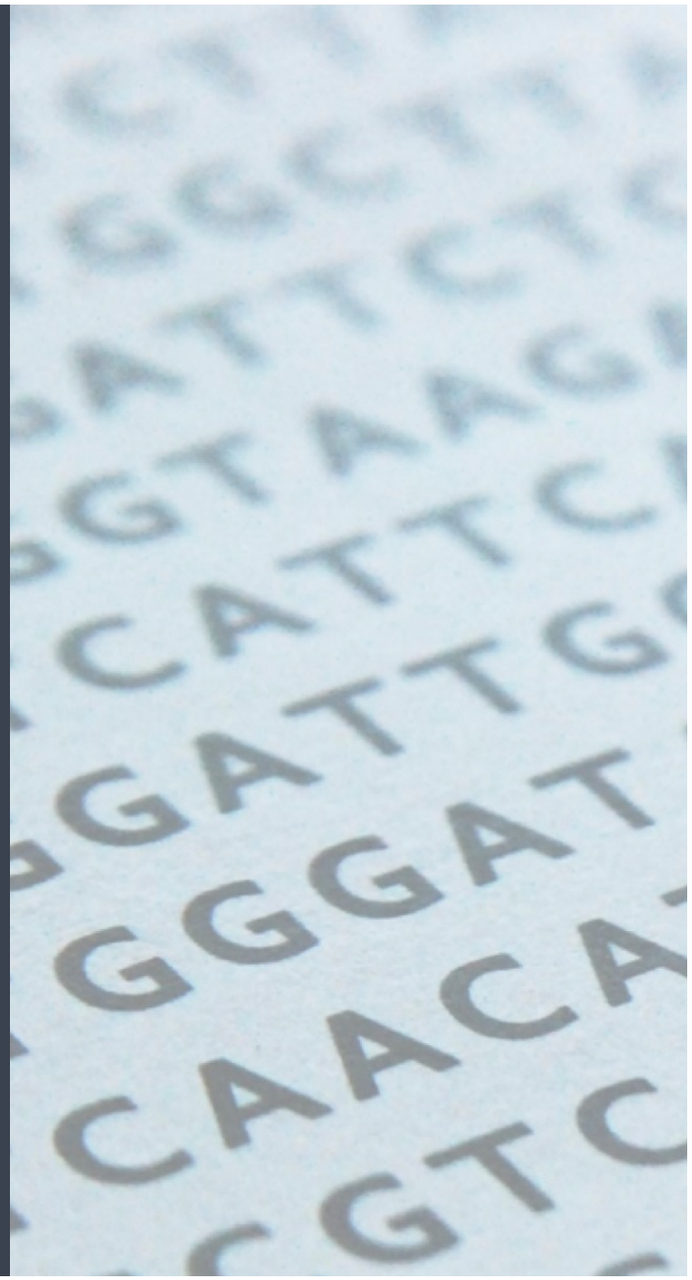


Joon Yoon

Peter Kraft
Faculty Advisor

Consulting

- RNA-seq, small RNA-seq and ChIP-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- Quality assurance and analysis of gene expression arrays
- Functional enrichment analysis
- Grant support



HARVARD T.H. CHAN SCHOOL OF PUBLIC HEALTH

HSCI HARVARD STEM CELL INSTITUTE

HARVARD CATALYST THE HARVARD CLINICAL AND TRANSLATIONAL SCIENCE CENTER

HARVARD MEDICAL SCHOOL

NIEHS / CFAR Bioinformatics Core

Center for Stem Cell Bioinformatics

Harvard Catalyst Bioinformatics Consulting

HMS Tools & Technology

Training

We have divided our short workshops into 2 categories:

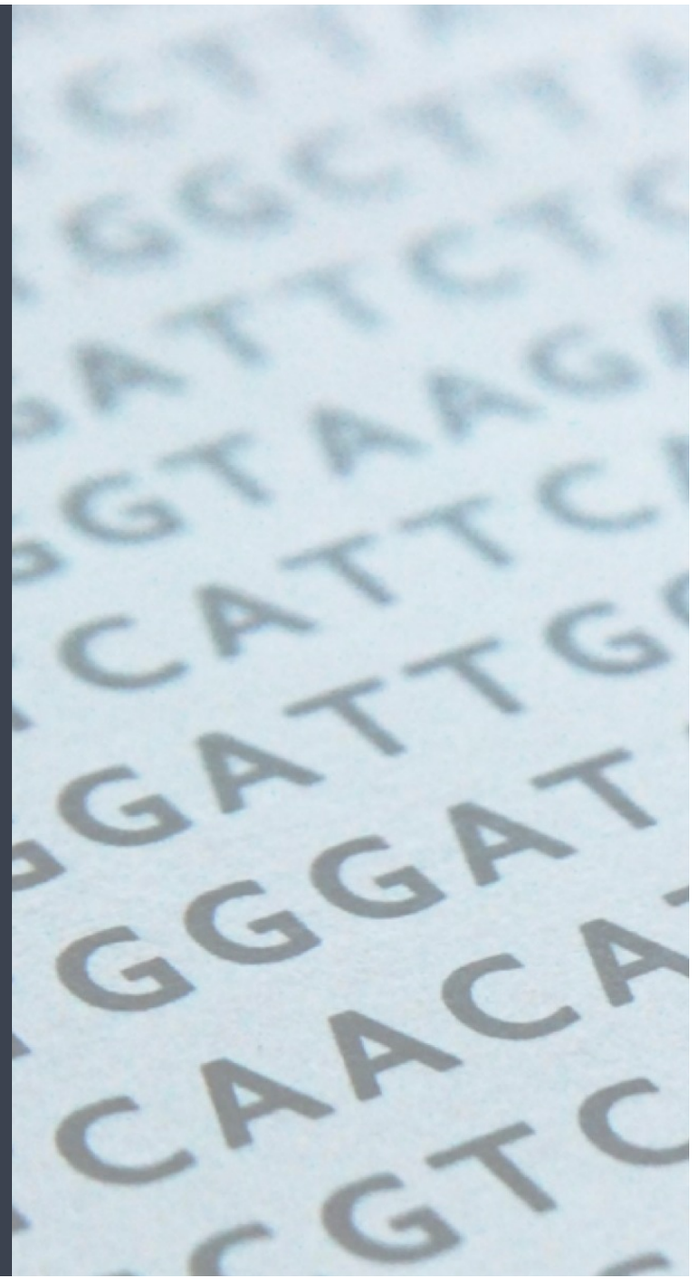
1. **Basic Data Skills** - No prior programming knowledge needed (no prerequisites)
2. **Advanced Topics: Analysis of high-throughput sequencing (NGS) data** - Certain “Basic” workshops required as prerequisites.

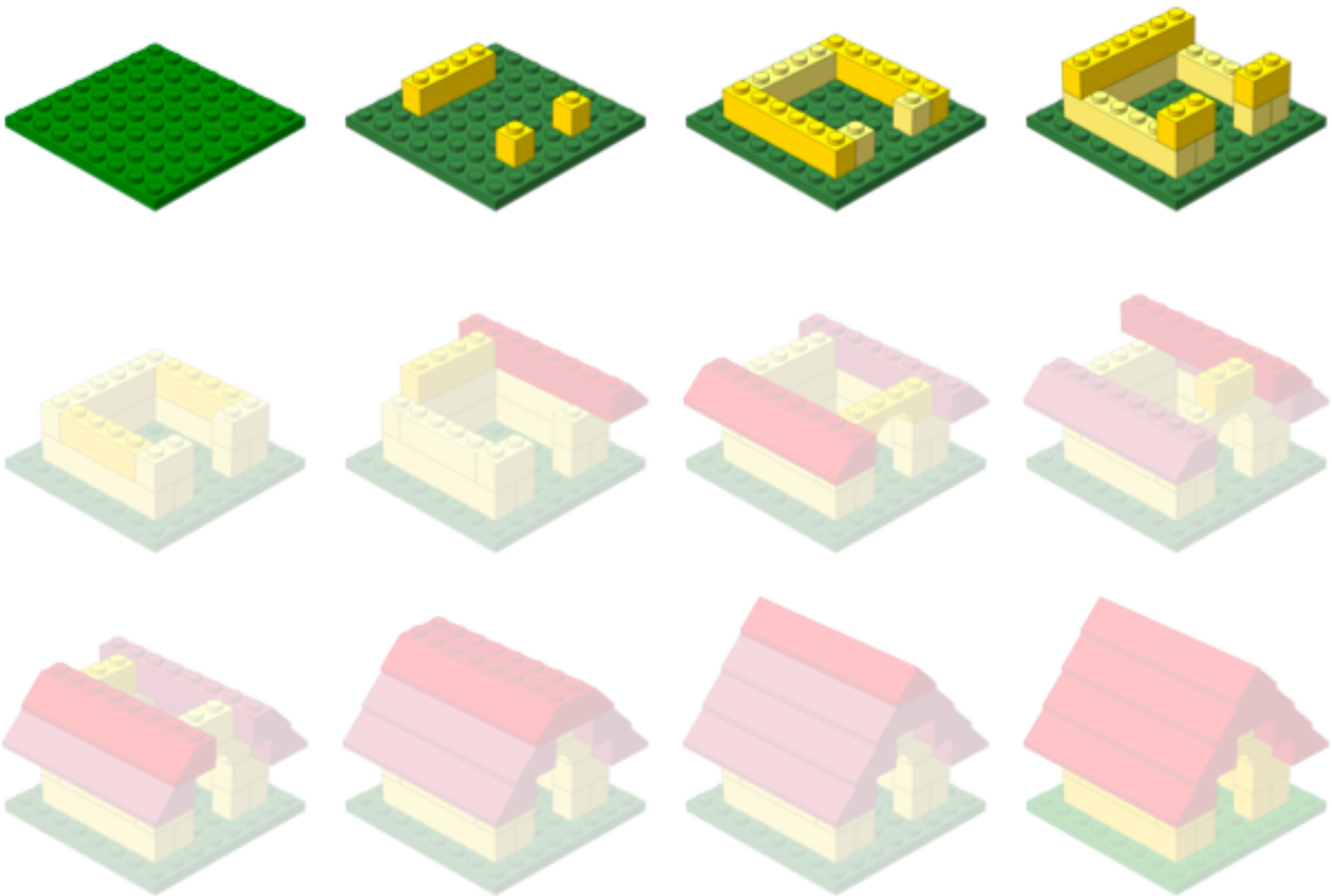
Any participants wanting to take an advanced workshop will have to have taken the appropriate basic workshop(s) within the past 6 months.

https://hbctraining.github.io/main/training_spring2019.html

http://bioinformatics.sph.harvard.edu/training/

https://hbctraining.github.io/main/

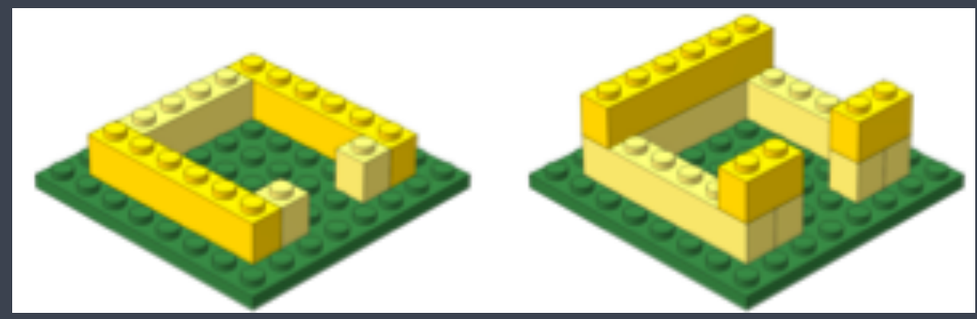




http://anoved.net/tag/lego/page/3/

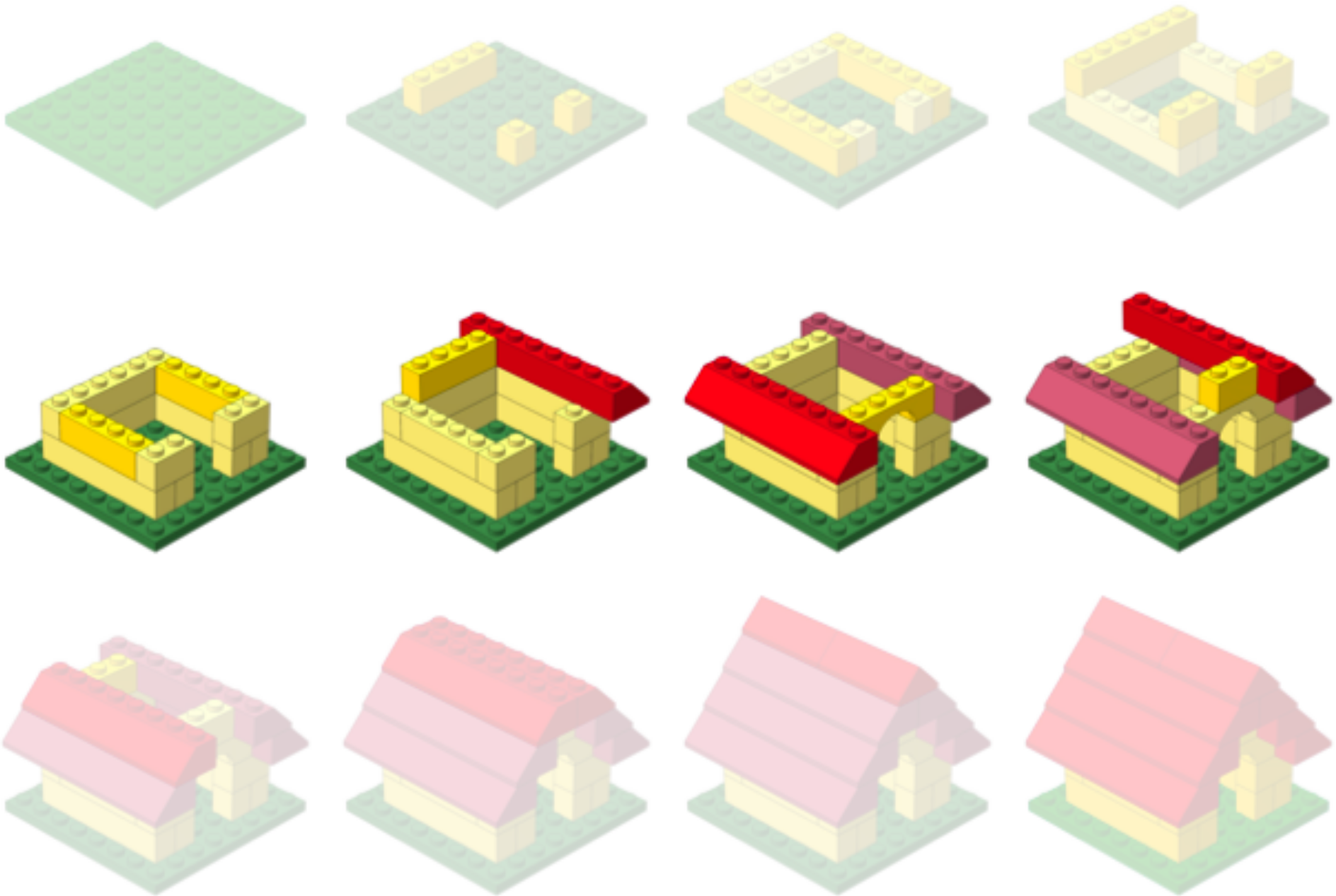
Setting up to perform Bioinformatics analysis

Setting up…



- ✓ Introduction to the command-line interface (shell, Unix, Linux)
  - Dealing with large data files
  - Performing bioinformatics analysis
  - Using tools
  - Accessing and using compute clusters
- ✓ R
  - Parsing and working with smaller results text files
  - Statistical analysis, e.g. differential expression analysis
  - Generating figures from complex data

Workshop scope



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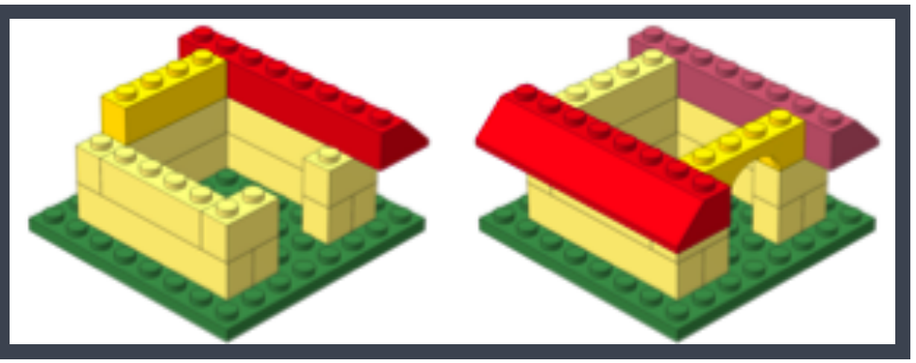
Bioinformatics data analysis

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.

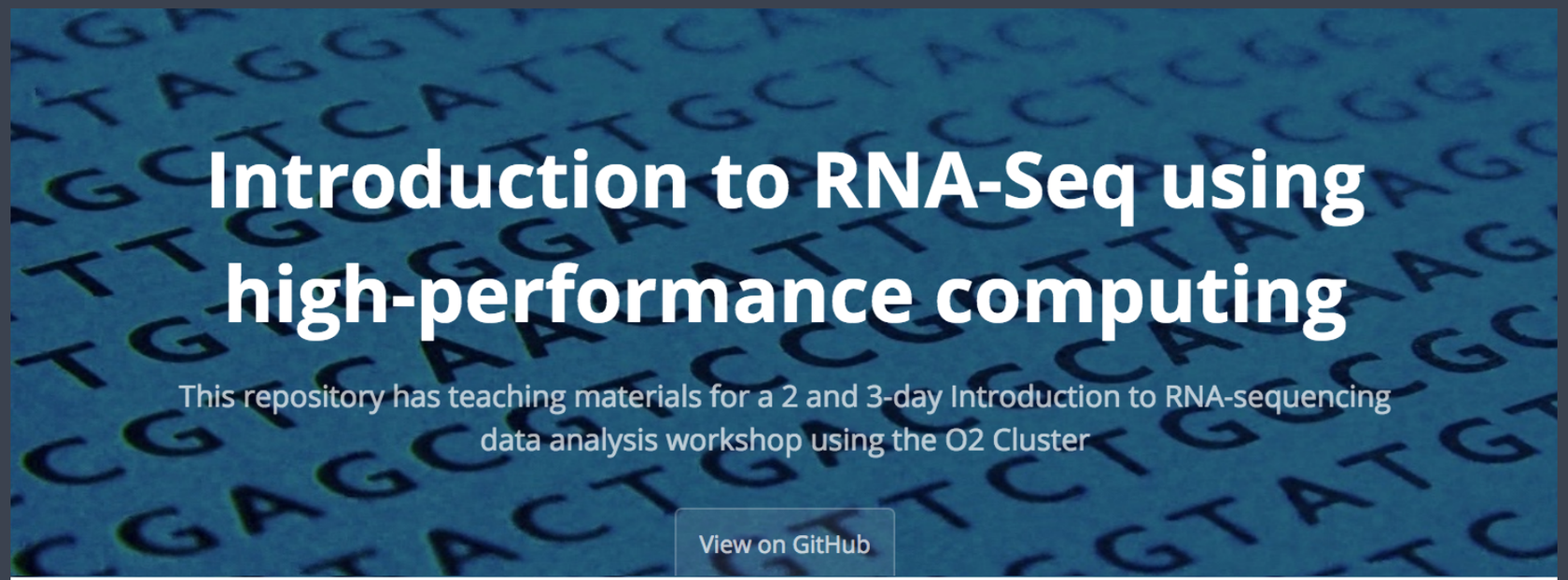
We won't be covering how to perform differential gene expression (DGE) analysis on count data in this workshop. A DGE workshop will be held on October 21st/ 22nd and the pre-requisite for it is a working knowledge of R (October 3rd/4th).

Logistics

Course webpage (wiki)

https://tinyurl.com/intro-to-rnaseq-adv

Course materials online



Learning Objectives

- How do you access the shell?
- How do you use it?
  - Getting around the Unix file system
  - looking at files
  - manipulating files
  - automating tasks
- What is it good for?

Setting up

We will spend most of our time learning about the basics of the shell by exploring experimental data.

Since we are going to be working with this data on our remote server, **Orchestra 2 (O2)**, we first need to log onto the server. After we're logged on, we will each make our own copy of the example data folder.

The 2 Window problem…

rkhetani — rsk27@clarinet002-072: ~ — ssh — 141×21

rsk27@clarinet002-072: ~

```
rsk27@clarinet002-072:~$ ll -htr unix_workshop/
total 177K
drwxrwsr-x 2 rsk27 rsk27  62 May 23  2016 reference_data
-rw-rw-r-- 1 rsk27 rsk27 377 May 23  2016 README.txt
drwxrwsr-x 2 rsk27 rsk27  78 May 23  2016 genomics_data
drwxrwsr-x 2 rsk27 rsk27 257 May 23  2016 raw_fastq
drwxrwsr-x 2 rsk27 rsk27 695 May 23  2016 other
drwxrwsr-x 6 rsk27 rsk27 972 May 24  2016 rnaseq_project
rsk27@clarinet002-072:~$
```

Starting with the shell

We have each created our own copy of the example data folder into our home directory, **unix_workshop**. Let's go into the data folder and explore the data using the shell.

```
$ cd unix_workshop
```

> 'cd' stands for 'change directory'

Let's see what is in here. Type:

```
$ ls
```

Odds and Ends

- Name tags: Tent Cards
- Post-its
- Phones on vibrate/silent!

Thanks!

- Andy Bergman & Kathleen Keating from HMS-RC
- Data Carpentry

These materials have been developed by members of the teaching team at the Harvard Chan Bioinformatics Core (HBC). These are open access materials distributed under the terms of the Creative Commons Attribution license (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

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Twitter

HBC: @bioinfocore

HMS-RC: @hms_rc