

# Introduction to the command-line interface (shell)

Harvard Chan Bioinformatics Core  
in collaboration with  
HMS Research Computing

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



Shannan Ho Sui  
*Director*



John Hutchinson  
*Associate Director*



Brad Chapman



Meeta Mistry



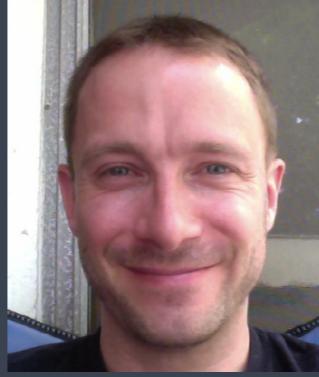
Radhika Khetani  
*Training Director*



Mary Piper



Victor Barrera



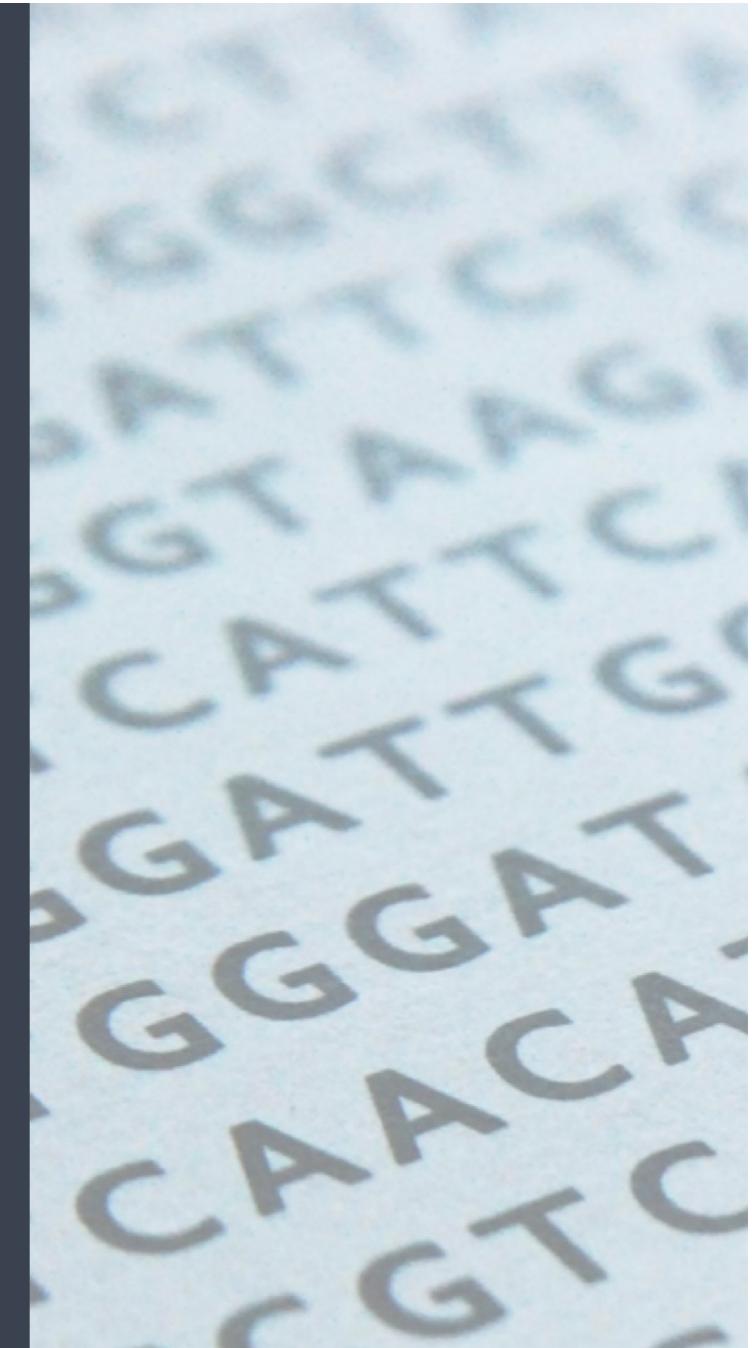
Rory Kirchner



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

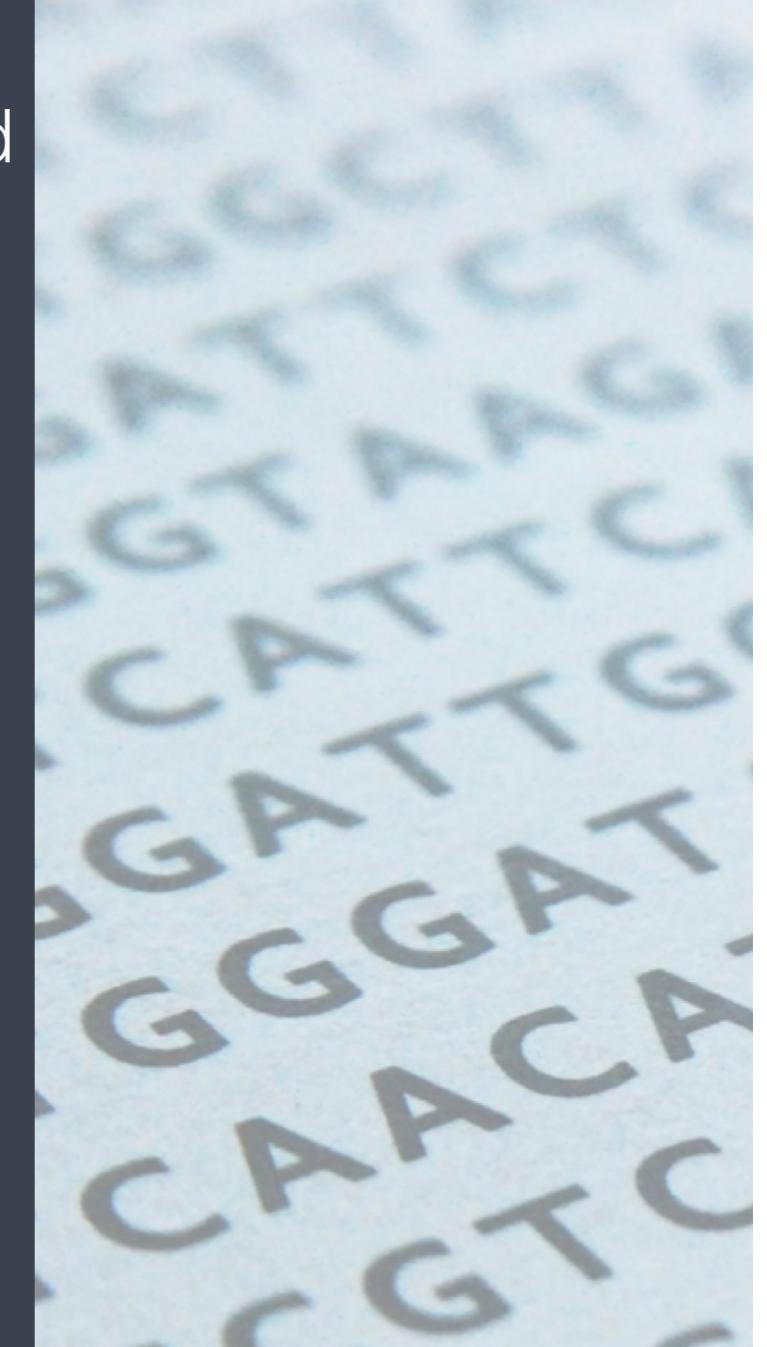


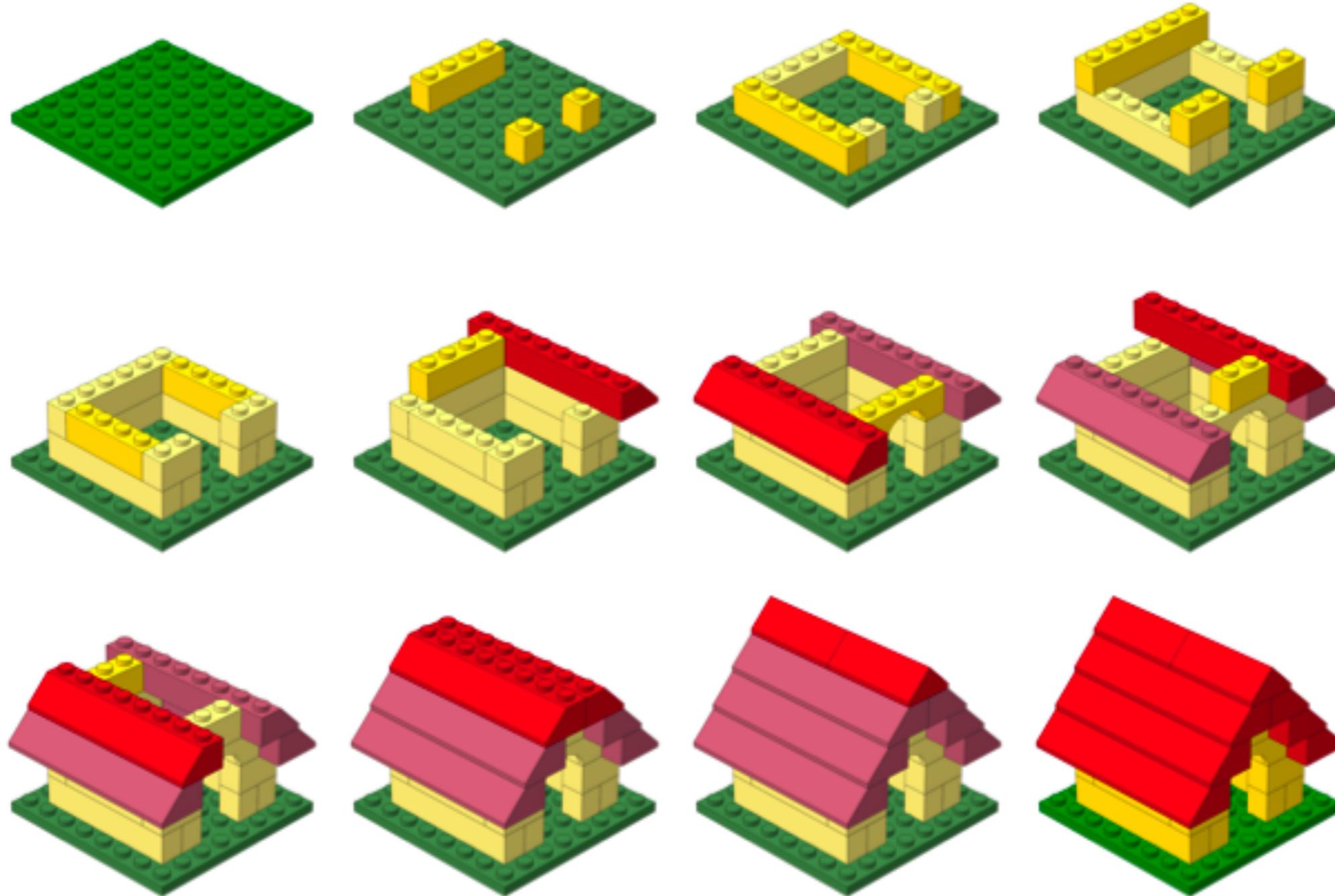
# Training

- Short workshops on introductory, intermediate and advanced topics related to NGS data analysis

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

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

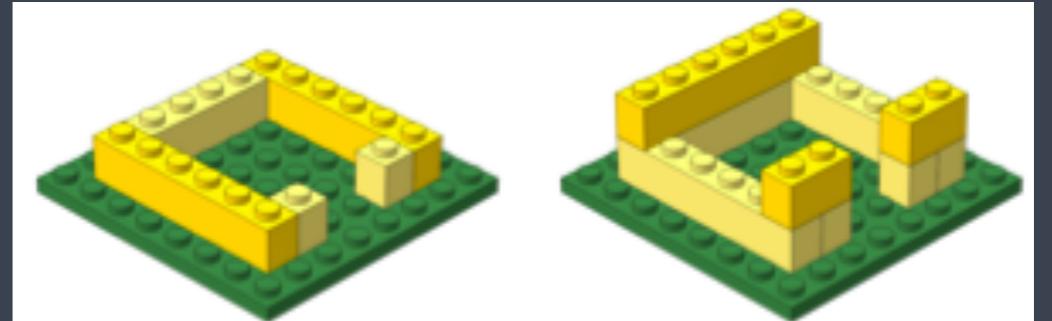




<http://anoved.net/tag/lego/page/3/>

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

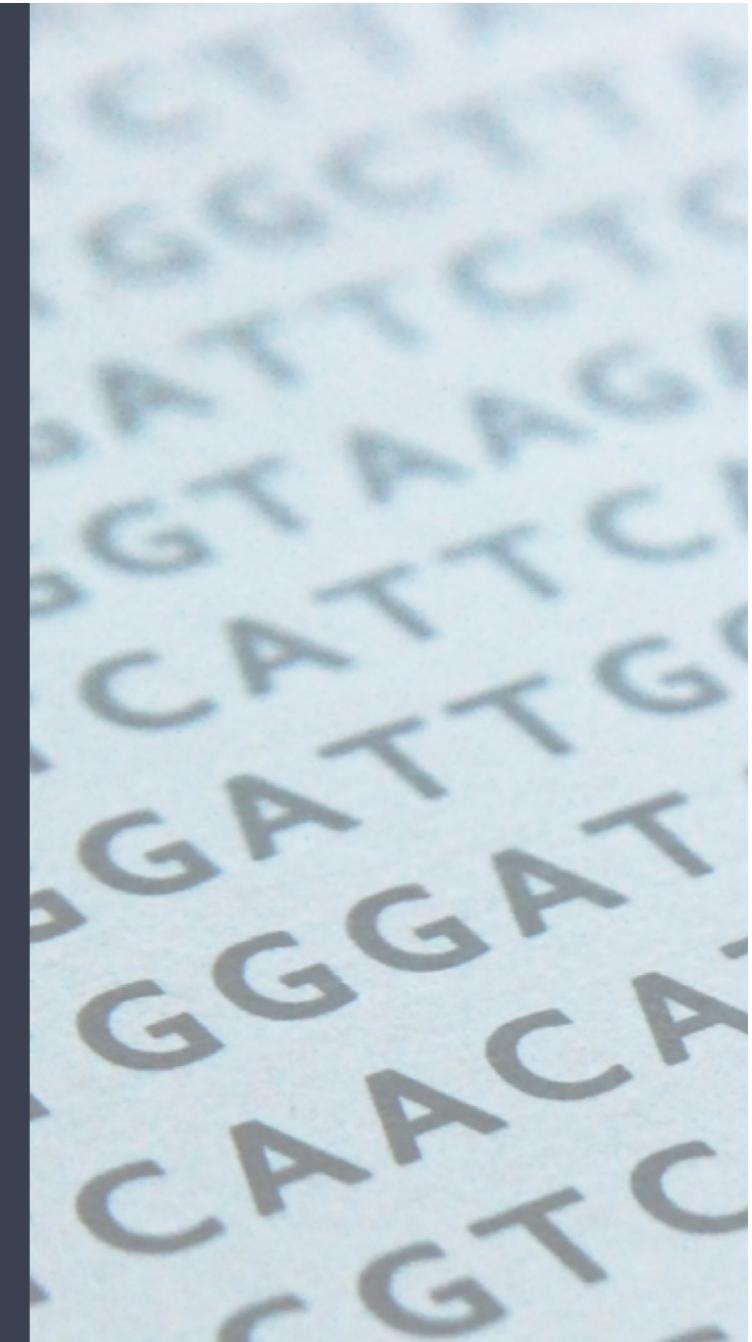
# Training

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](https://hbctraining.github.io/main/training_spring2019.html)

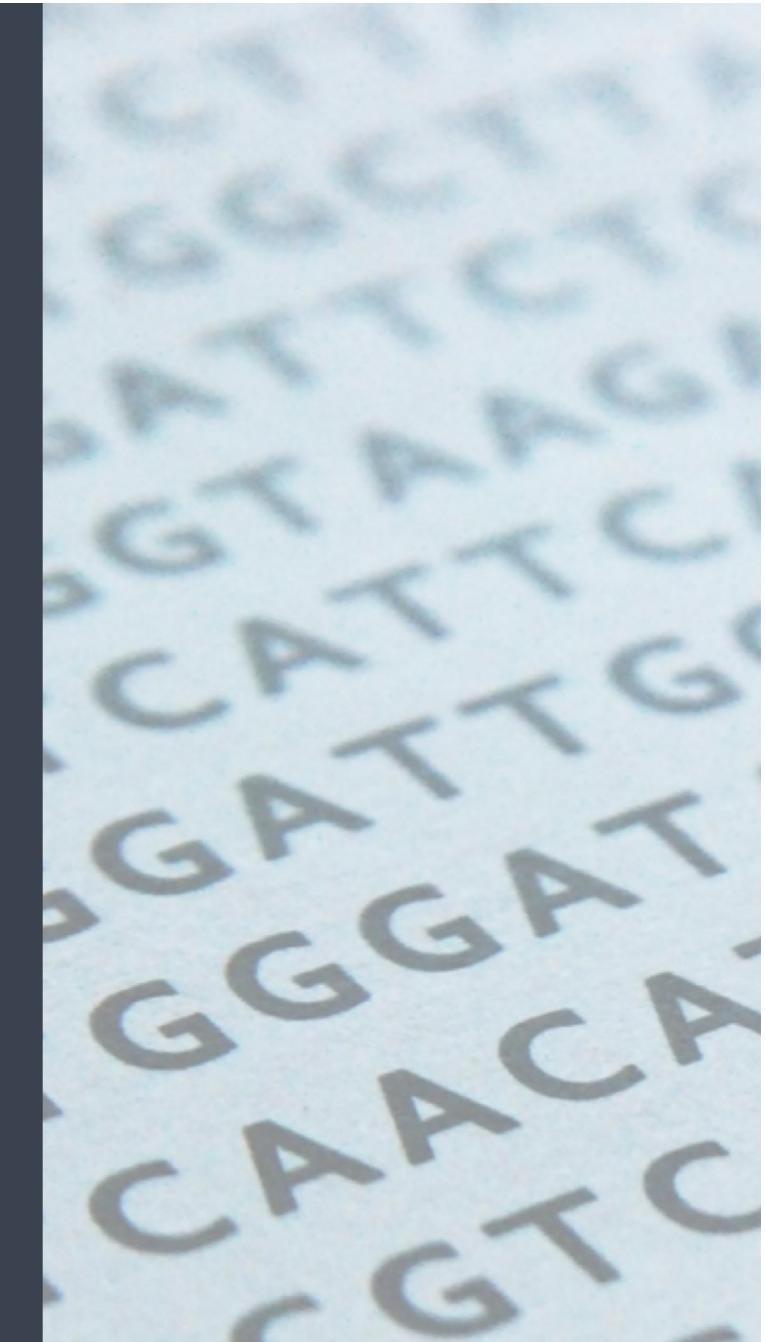


# Training

## Spring 2019 Schedule

We are structuring the training schedule such that it gives interested researchers several opportunities to take the basic workshops.

| Topic  | Category | Date                | Duration | Prerequisites      |
|--|----------|---------------------|----------|--------------------|
| Introduction to the command-line interface (shell)                   | Basic    | January 17th        | 1 day    | None               |
| Introduction to R  | Basic    | January 28th & 29th | 1.5 days | None               |
| Introduction to the command-line interface (shell)                   | Basic    | February 13th       | 1 day    | None               |
| Introduction to (bulk) RNA-seq                                       | Advanced | Late February       | 2 days   | Intro to shell     |
| Introduction to R  | Basic    | Early March         | 1.5 days | None               |
| Introduction to differential gene expression analysis (bulk RNA-seq) | Advanced | Late March          | 2 days   | Intro to R         |
| Introduction to the command-line interface (shell)                   | Basic    | Early April         | 1 day    | None               |
| Introduction to ChIP-seq analysis                                    | Advanced | Late April          | 2 days   | Intro to R + shell |

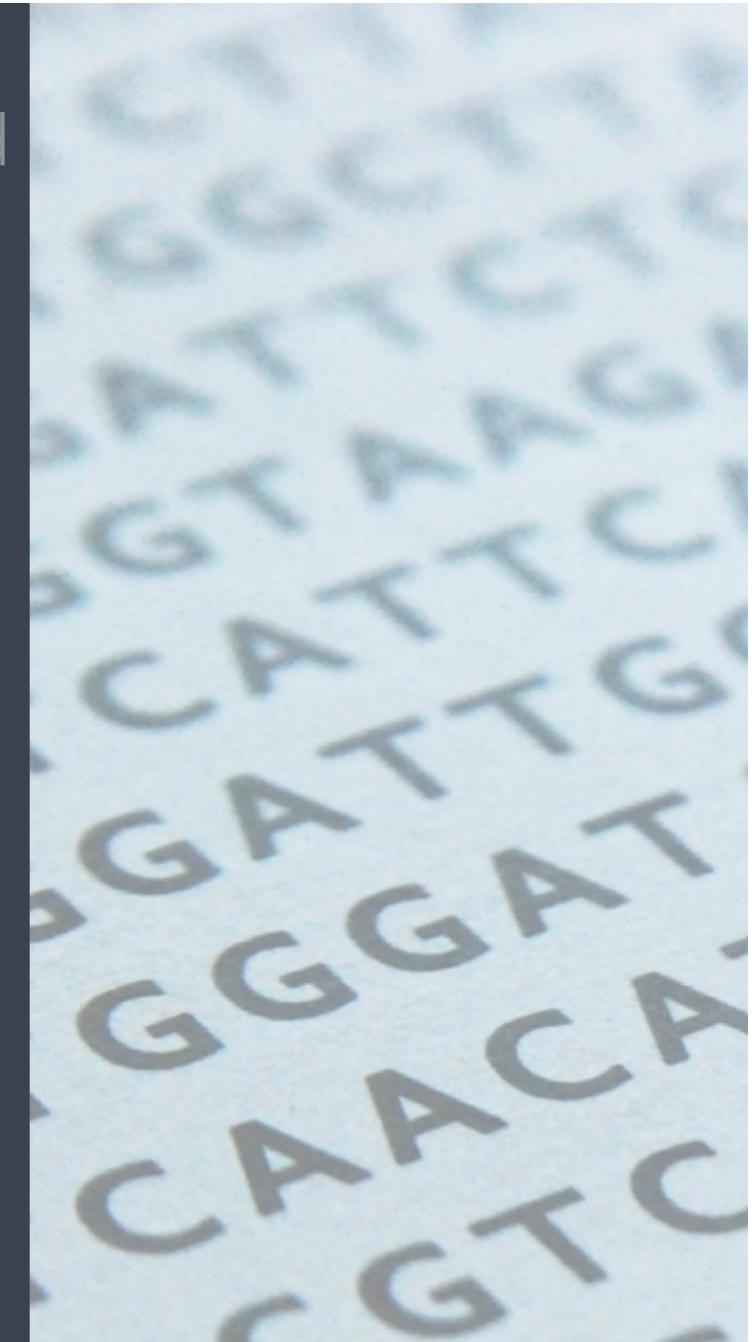


# Training

- Short workshops on introductory, intermediate and advanced topics related to NGS data analysis
- Monthly, 2-3 hour, hands-on and free workshops on “Current Topics in Bioinformatics”

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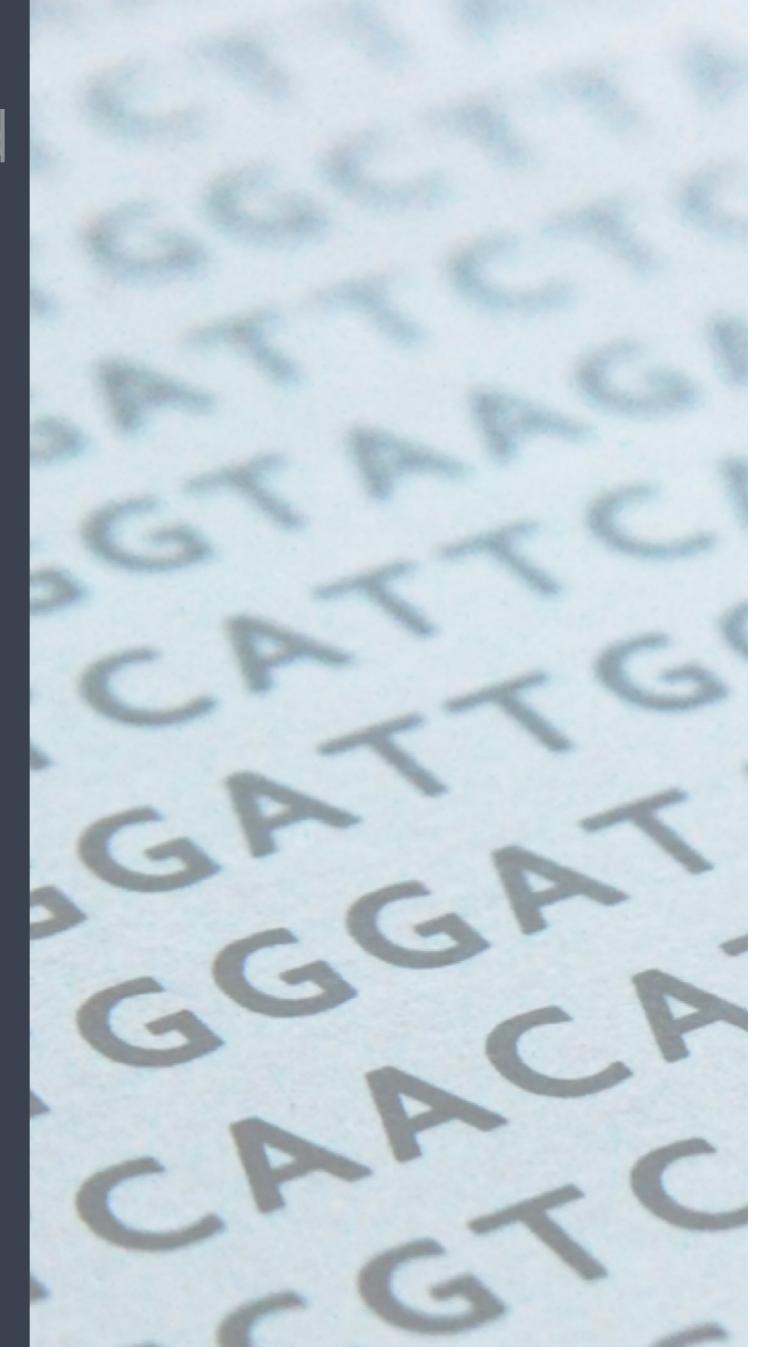


# Training

- Short workshops on introductory, intermediate and advanced topics related to NGS data analysis
- Monthly, 2-3 hour, hands-on and free workshops on “Current Topics in Bioinformatics”
- In-depth courses (8- or 12-day formats)

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# Introductions!



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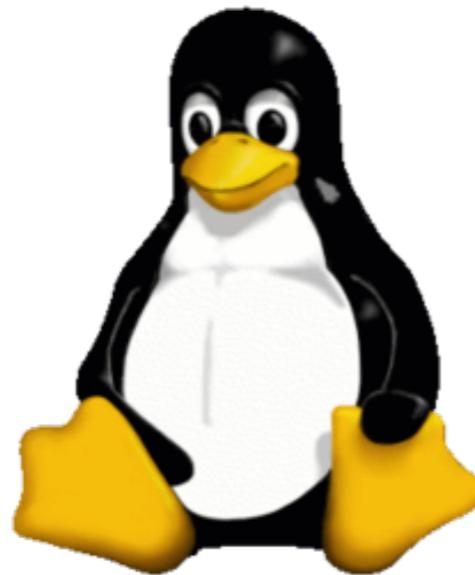


Rory Kirchner



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# Workshop scope



```
rkhetani — rsk27@clarinet002-072: ~ — ssh — 75x51
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:~$
```

*“Unix is user-friendly.*

*It's just very selective about who its friends are.”*

# The Unix command-line interface

- ◆ Unix is a stable, efficient and powerful operating system
- ◆ It can easily coordinate the use and sharing of a computer's (or a system's) resources, i.e. built to allow multi-user functionality
- ◆ Can easily handle complex and repetitive tasks easily on large and small datasets
- ◆ Usually, written commands are used to work with this OS, instead of the pointing and clicking used with operating systems like Windows and OSX

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## *Bioinformatics:*

- ◆ A lot of NGS-analysis tools are created for the Unix OS
- ◆ High-performance compute clusters which are necessary to analyze large datasets require a working knowledge of Unix

# Linux

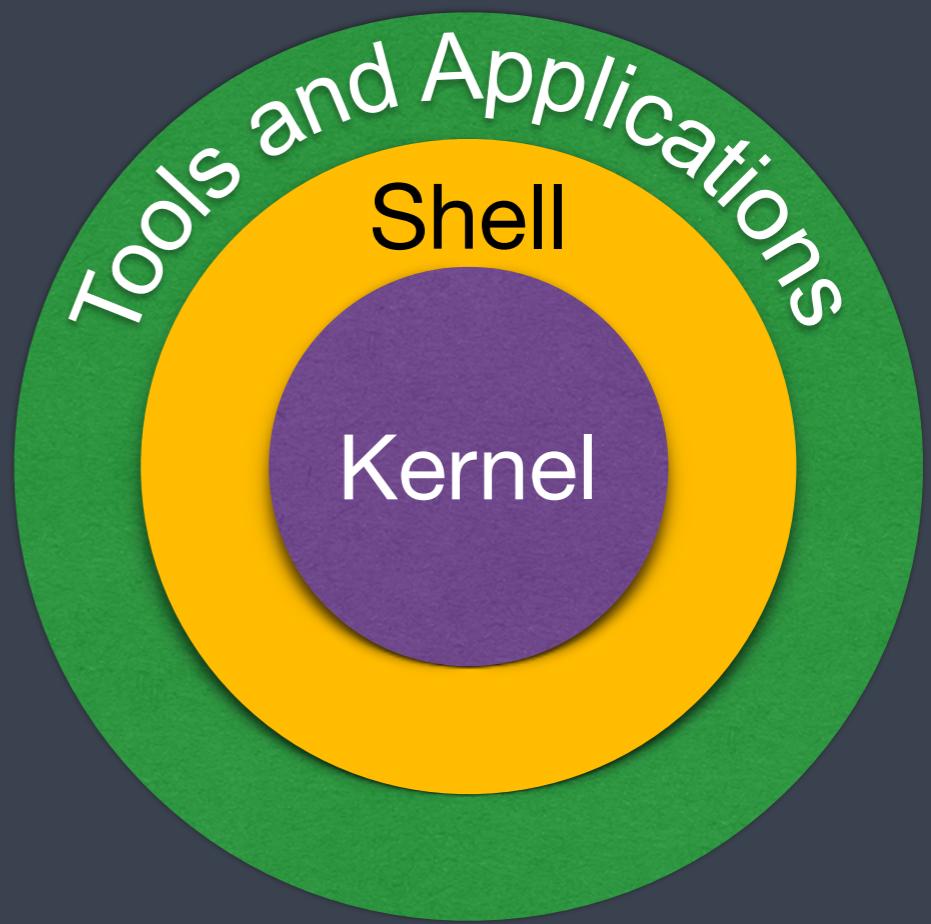
- ❖ Linux is a free, open-source operating system based on Unix
- ❖ It has the same components as the original, but the open source community is involved in active development of various distinct distributions of Linux



# Components

The Unix/Linux system is functionally organized at 3 levels:

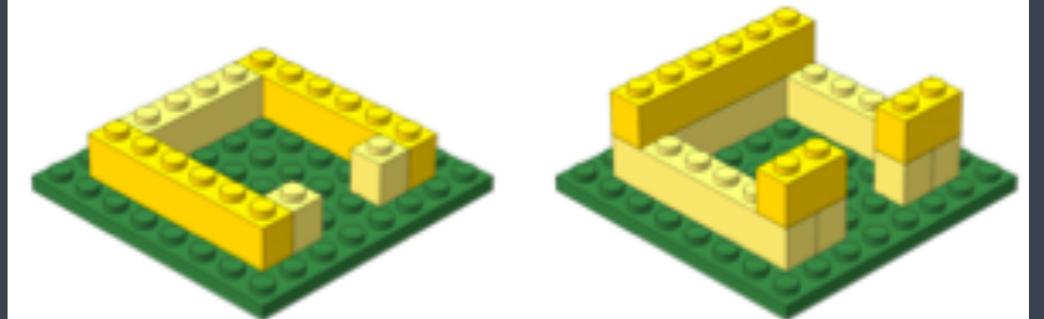
- ◆ **The kernel**, which schedules tasks and manages storage: *the brain of the system*
- ◆ **The shell**, *an interpreter* that helps interprets our input for the kernel
- ◆ **Utilities, tools and applications**, which use the shell to communicate with the kernel



# The “shell”

- ◆ The shell is **an interpreter**
- ◆ It is independent of the operating system
- ◆ Dozens of shells have been developed throughout UNIX history, and a lot of them are still in use
- ◆ The most commonly used shell is **bash**

# Learning Objectives



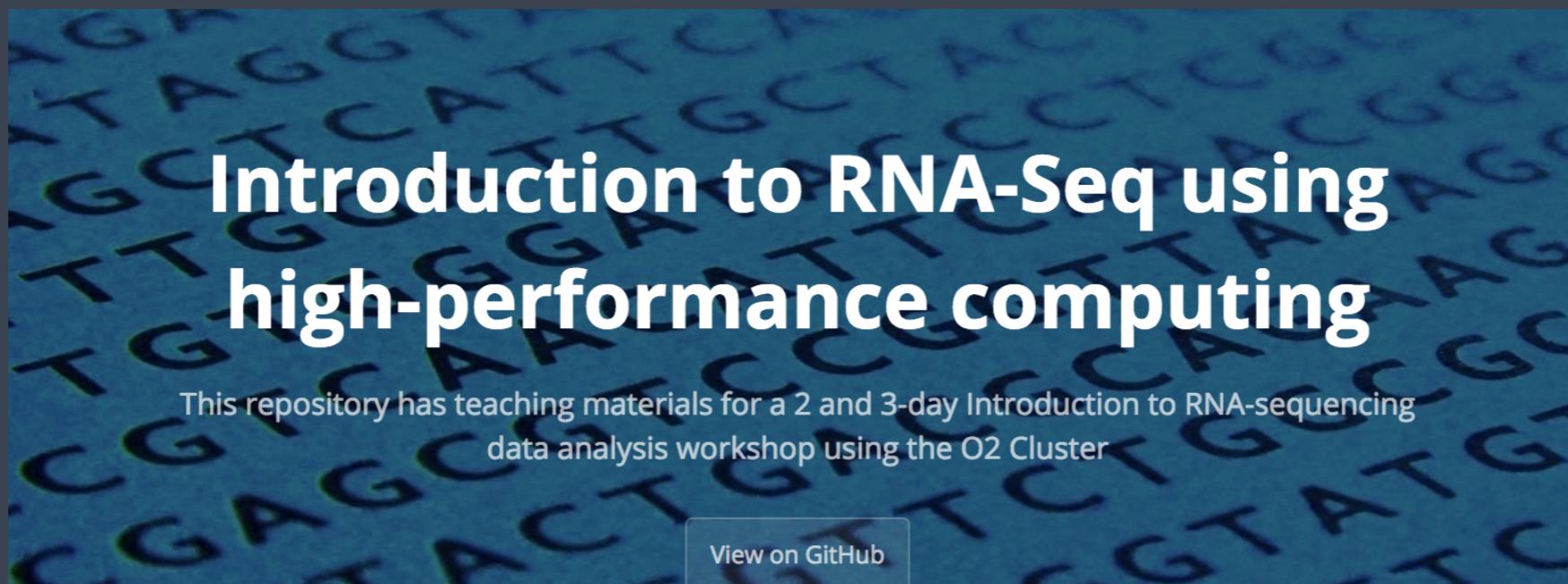
- ✓ Learn what a “shell” is and become comfortable with the command-line interface
  - Find your way around a filesystem using written commands
  - Work with small and large data files
  - Become more efficient when performing repetitive tasks
- ✓ Understand what a computational cluster is and why we need it

# Logistics

# Course webpage (wiki)

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

# Course materials online

A blue-tinted background image showing a dense grid of DNA sequence data, specifically ACGT nucleotide bases, arranged in a repeating pattern.

**Introduction to RNA-Seq using high-performance computing**

This repository has teaching materials for a 2 and 3-day Introduction to RNA-sequencing data analysis workshop using the O2 Cluster

[View on GitHub](#)

## Learning Objectives

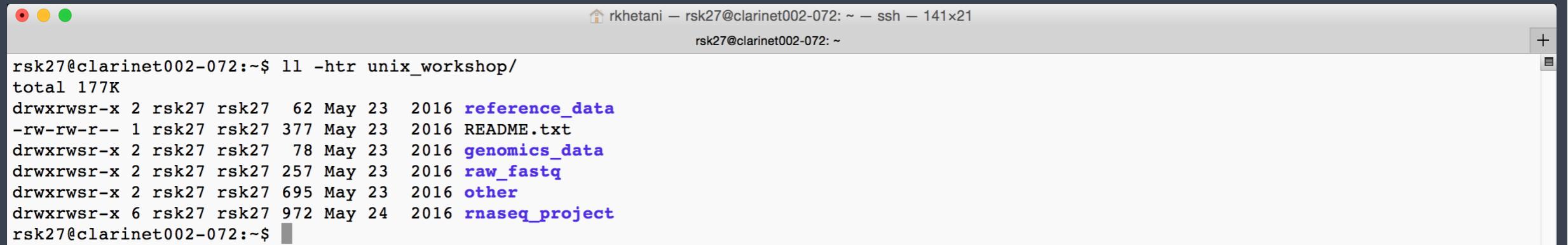
- How do you access the shell?
- How do you use it?
  - Getting around the Unix file system
  - looking at files
  - manipulating files
  - automating tasks
- What is it good for?

## 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...



```
rsk27@clarinet002-072:~$ ls -l unix_workshop/
total 177K
drwxrwsr-x 2 rsk27 rsk27 62 May 23 2016 reference_data
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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!

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

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# Contact us!

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