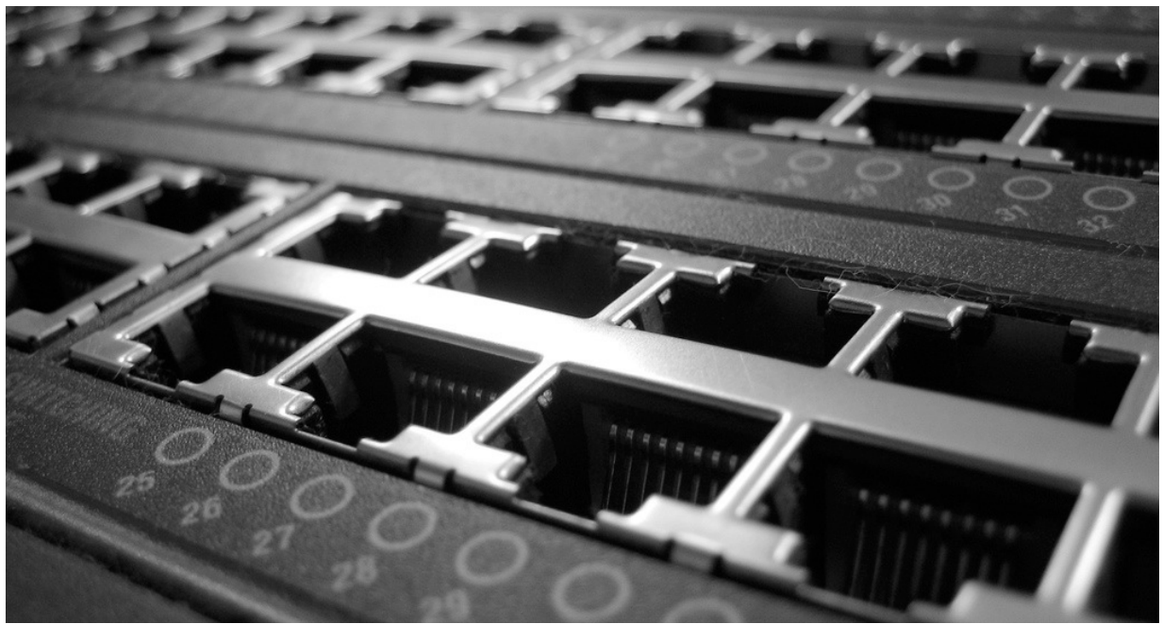


Introduction to ChIP-seq using High-Performance Computing (HPC)

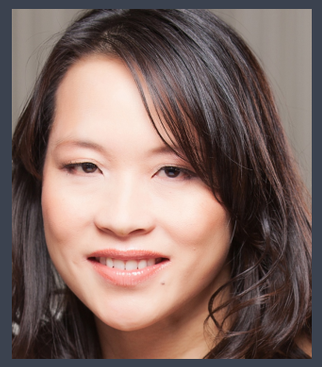
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

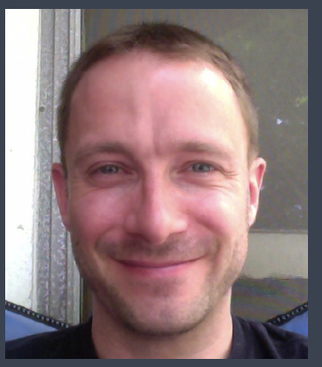
March 21-23, 2018

https://tinyurl.com/hbc-intro-to-chipseq


Shannan Ho Sui


John Hutchinson


Brad Chapman


Rory Kirchner


Meeta Mistry

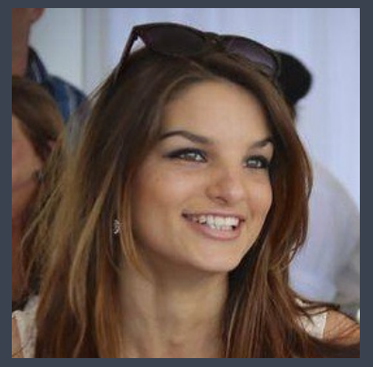

Radhika Khetani


Mary Piper


Lorena Pantano


Michael Steinbaugh


Victor Barrera


Kayleigh Rutherford


Peter Kraft

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

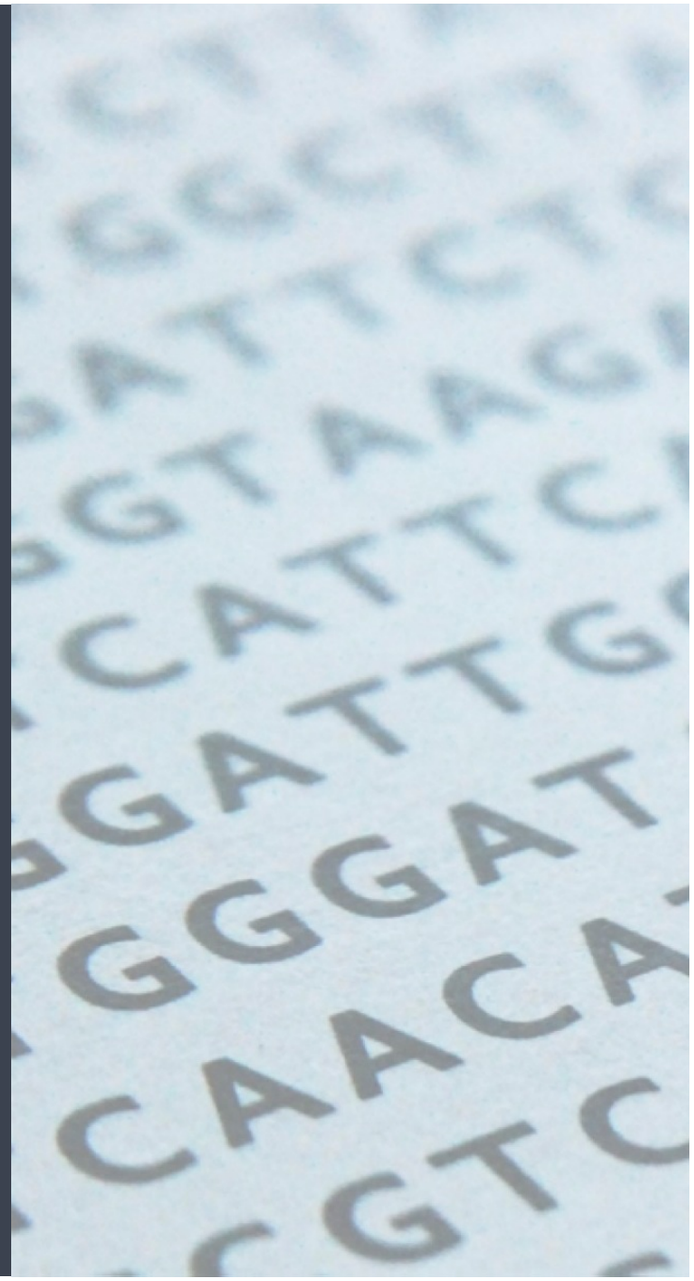
Harvard Catalyst Bioinformatics Consulting

HMS Tools & Technology

Harvard NeuroDiscovery Center

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

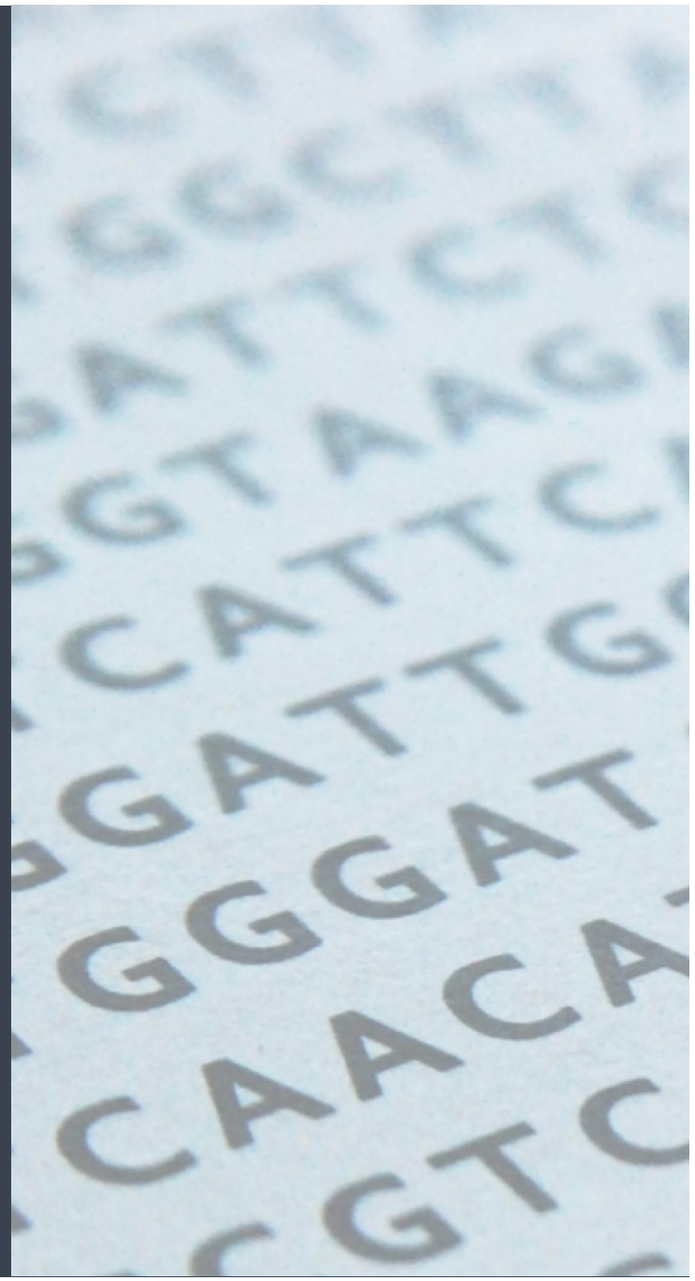


Training

- Short workshops on introductory, intermediate and advanced topics related to NGS data analysis
- Monthly, 2-3 hour, hands-on and free workshops on “Current Topics in Bioinformatics”
- In-depth courses (8- or 12-day formats) [Fall 2018]

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

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



HARVARD T.H. CHAN SCHOOL OF PUBLIC HEALTH

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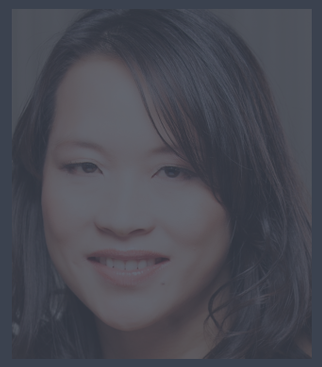
Introductions!



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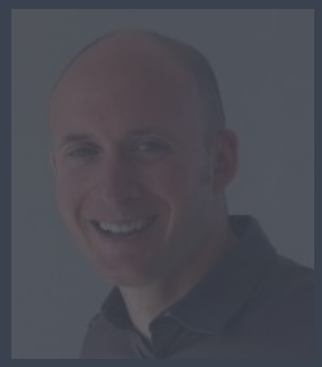
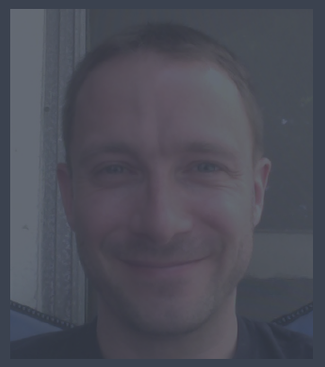


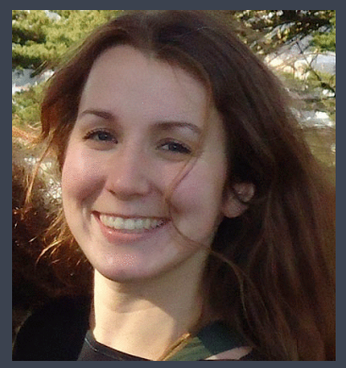
Brad Chapman



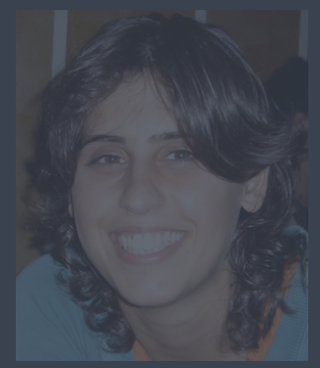
Rory Kirchner

Meeta Mistry

Radhika Khetani



Mary Piper



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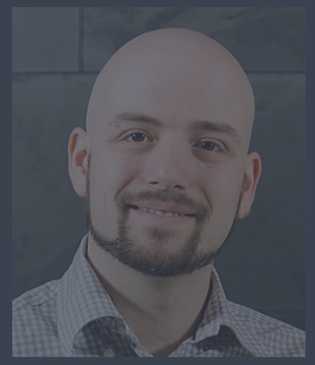
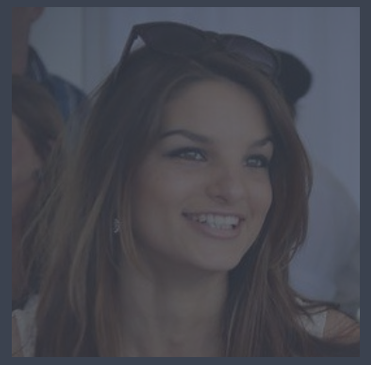
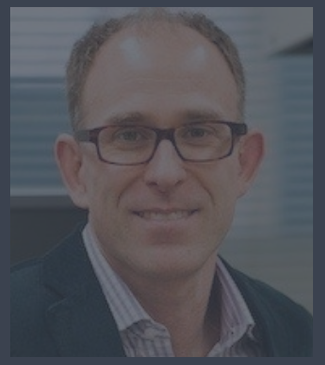


Victor Barrera

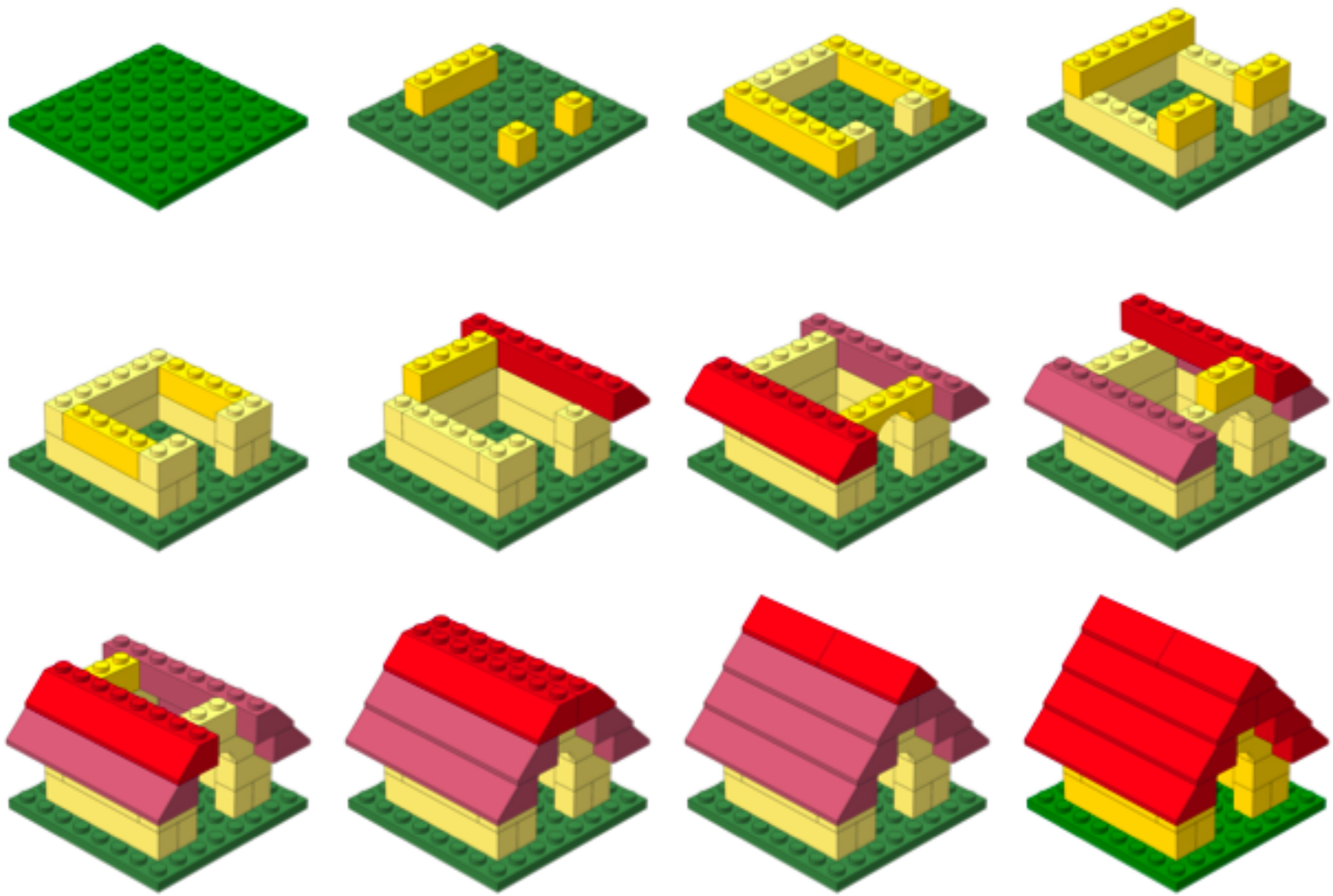


Kayleigh Rutherford



Peter Kraft

Workshop scope



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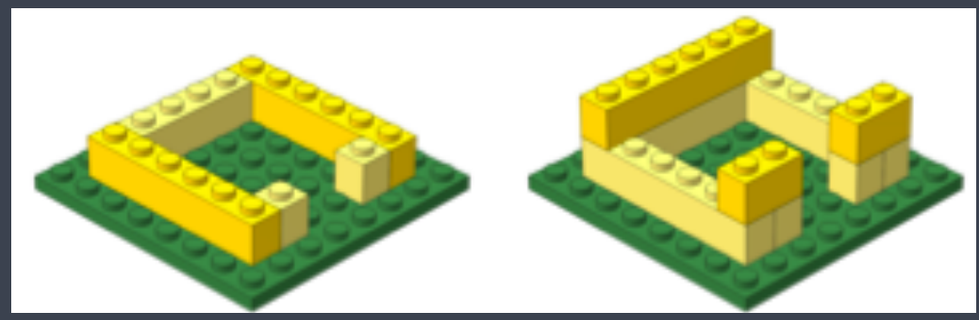
Bioinformatics data analysis

Base components



- ✓ Introduction to the UNIX shell
  - Dealing with large data files
  - Using bioinformatics tools
  - Accessing and using compute clusters
- ✓ R *(outside the scope of today's workshop)*
  - Parsing and working with smaller results text files
  - Statistical analysis, e.g. differential expression analysis
  - Generating figures from complex data

```
rkhetani — rsk27@clarinet002-072: ~ — ssh — 75×51
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:~$
```

“UNIX is user-friendly.

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

http://en.wikipedia.org/wiki/Unix, http://en.wikipedia.org/wiki/Tux

Why UNIX?

- 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

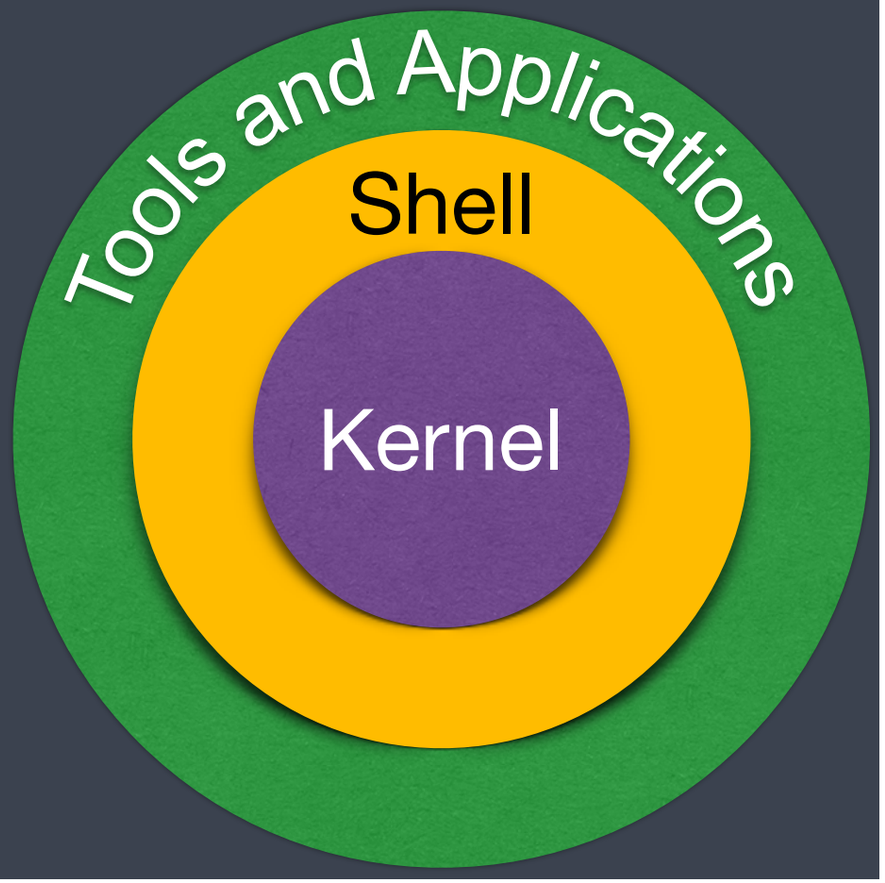
Linux

- 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:

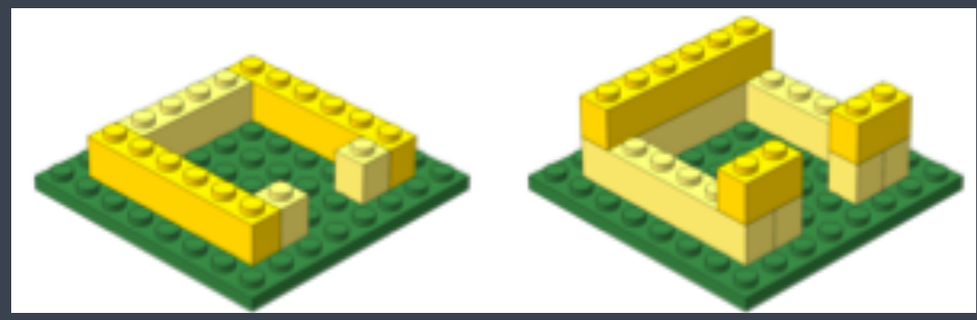
- The kernel, which schedules tasks and manages storage: ***the brain of the system***
- The shell, ***an interpreter*** that helps interprets our input for the kernel
- Utilities, tools and applications, which use the shell to communicate with the kernel



The “shell”

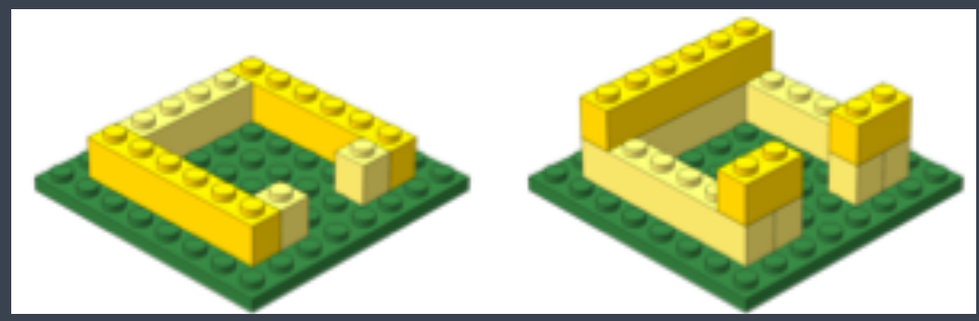
- The shell is **an interpreter**
- It is independent of the operating system
- Dozens of shells have been developed throughout UNIX history, and a lot of them are still in use
- The most commonly used shell is **bash**

Learning Objectives



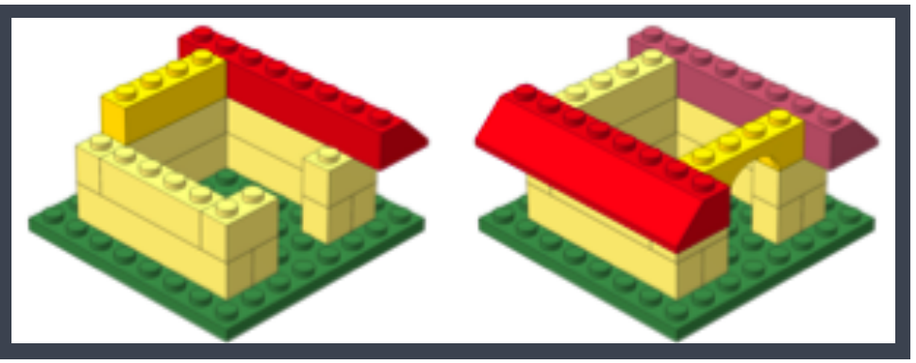
- ✓ Learn what a “shell” is and become comfortable with the command line interface
  - Find your way around a filesystem using the command line
  - Work with small and large data files
  - Become more efficient when performing repetitive tasks

Learning Objectives



- ✓ Learn what a “shell” is and become comfortable with the command line interface
  - Find your way around a filesystem using the command line
  - 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
  - Independently access the O2 cluster
  - Perform analysis using the cluster (run programs, pipelines, etc.)

Learning Objectives



- ✓ Describe best practices for designing an ChIP-seq experiment
- ✓ Describe steps in a typical ChIP-seq analysis workflow
- ✓ Use HMS-RC's O2 compute cluster to efficiently run the ChIP-seq workflow from sequence reads to peak calls, including QC and visualization.

Some steps in the ChIP-seq workflow require a working knowledge of R, and we won't be covering these in much detail.

Logistics

Course schedule

https://tinyurl.com/hbc-intro-to-chipseq

Course materials online

Workshop Schedule

Day 1

Time	Topic	Instructor
9:00 - 9:40	Workshop Introduction	Radhika
9:40 - 10:30	Introduction to the Shell	Radhika
10:30 - 10:45	Break	
10:45 - 11:35	Introduction to the Shell (cont.)	Meeta

The 2 Window problem…

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

rsk27@clarinet002-072: ~

```
rsk27@clarinet002-072:~$ ll -htr unix_workshop/
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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
- Wi-Fi: **HMS Public**
- Lunch locations
- Bathrooms
- Water Fountain
- Phones on vibrate/silent!

Thanks!

- Shannan Ho Sui (HBC)
- Andy Bergman (HMS-RC)
- Kristina Holton (HMS-RC)
- Data Carpentry

Contact us!

HBC training team: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

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

Twitter

HBC: @bioinfocore

HMS-RC: @hms_rc