



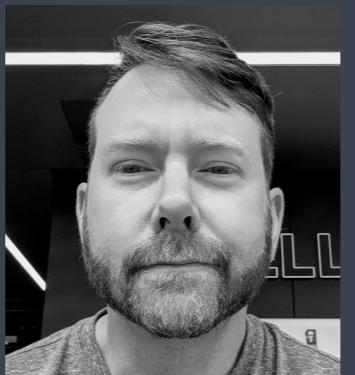
Introduction to Differential Gene Expression Analysis

Harvard Chan Bioinformatics Core

<http://tinyurl.com/hbc-intro-to-dge>



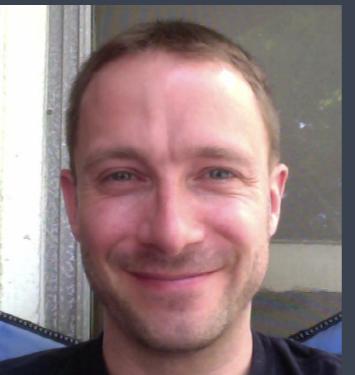
Shannan Ho Sui
Director



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



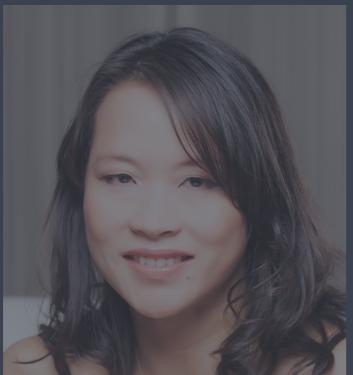
Sergey Naumenko



Joon Yoon



Peter Kraft
Faculty Advisor



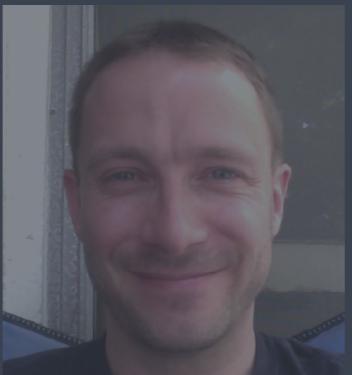
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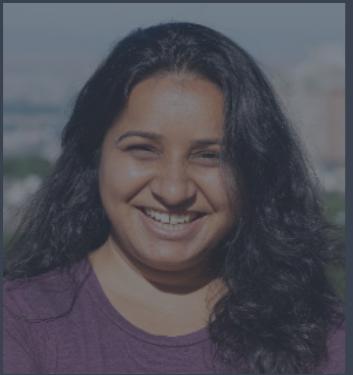
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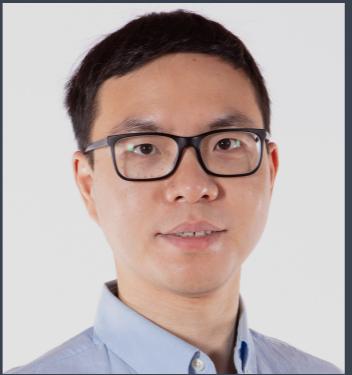
Preetida Bhetariya



Meeta Mistry



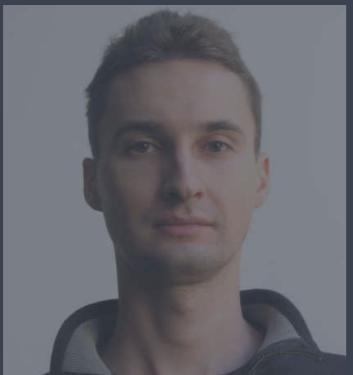
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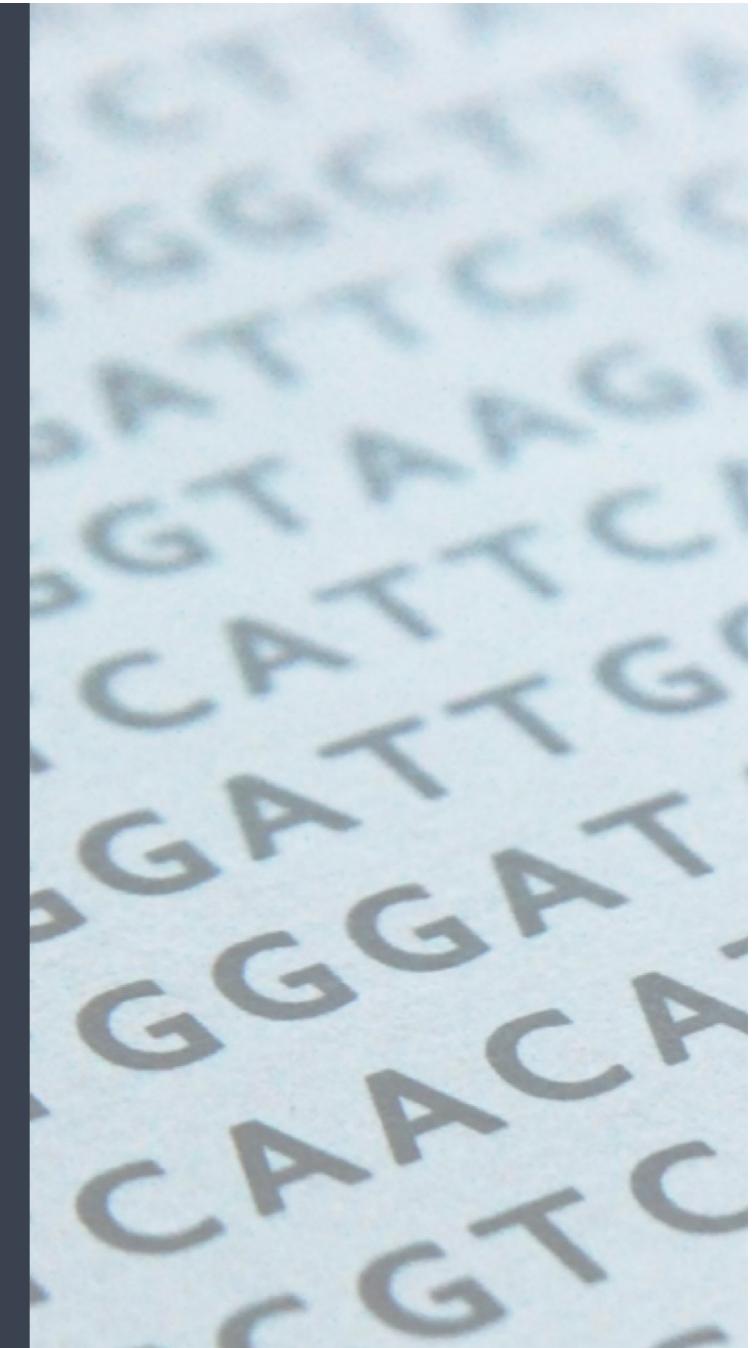
Joon Yoon



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
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SCHOOL OF PUBLIC HEALTH

NIEHS / CFAR
Bioinformatics
Core

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HARVARD STEM CELL
INSTITUTE

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Harvard
Catalyst
Bioinformatics
Consulting

HMS
Tools &
Technology

Training

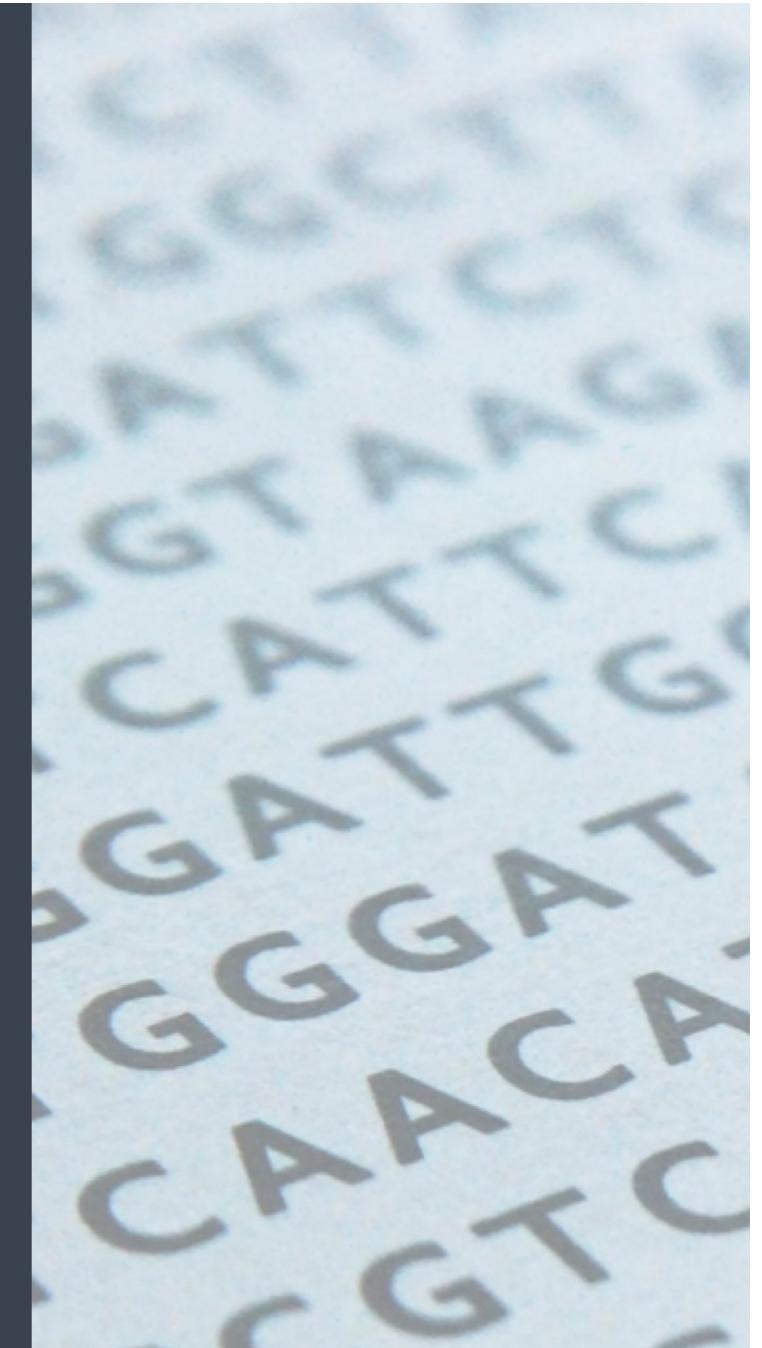
Our short workshops are divided into 2 categories:

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.

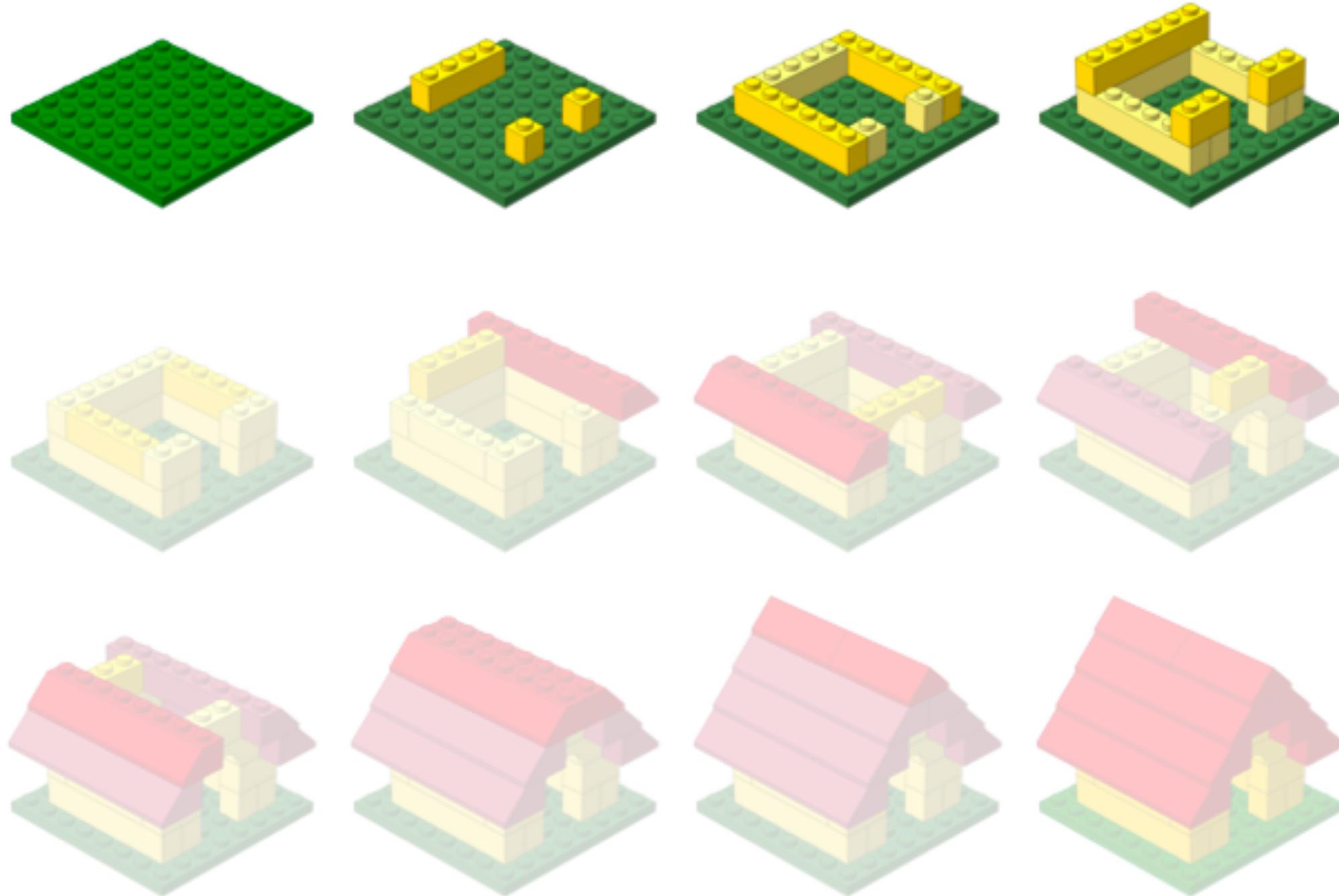
Any participants wanting to take an advanced workshop will have to have taken the appropriate basic workshop(s) within the past 6 months.

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

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



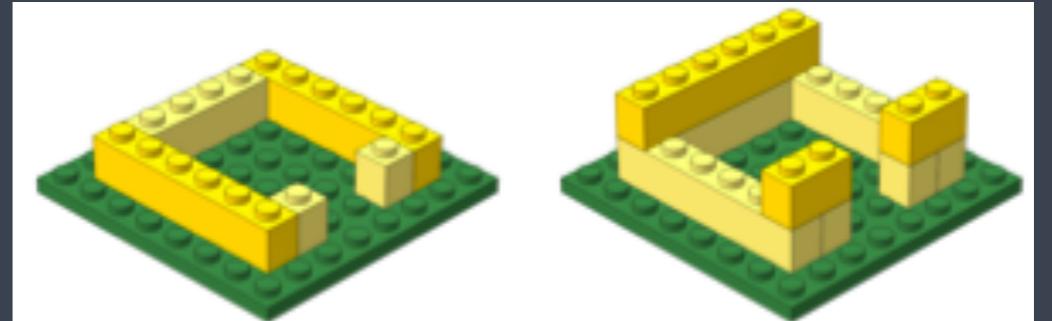
Workshop Scope...



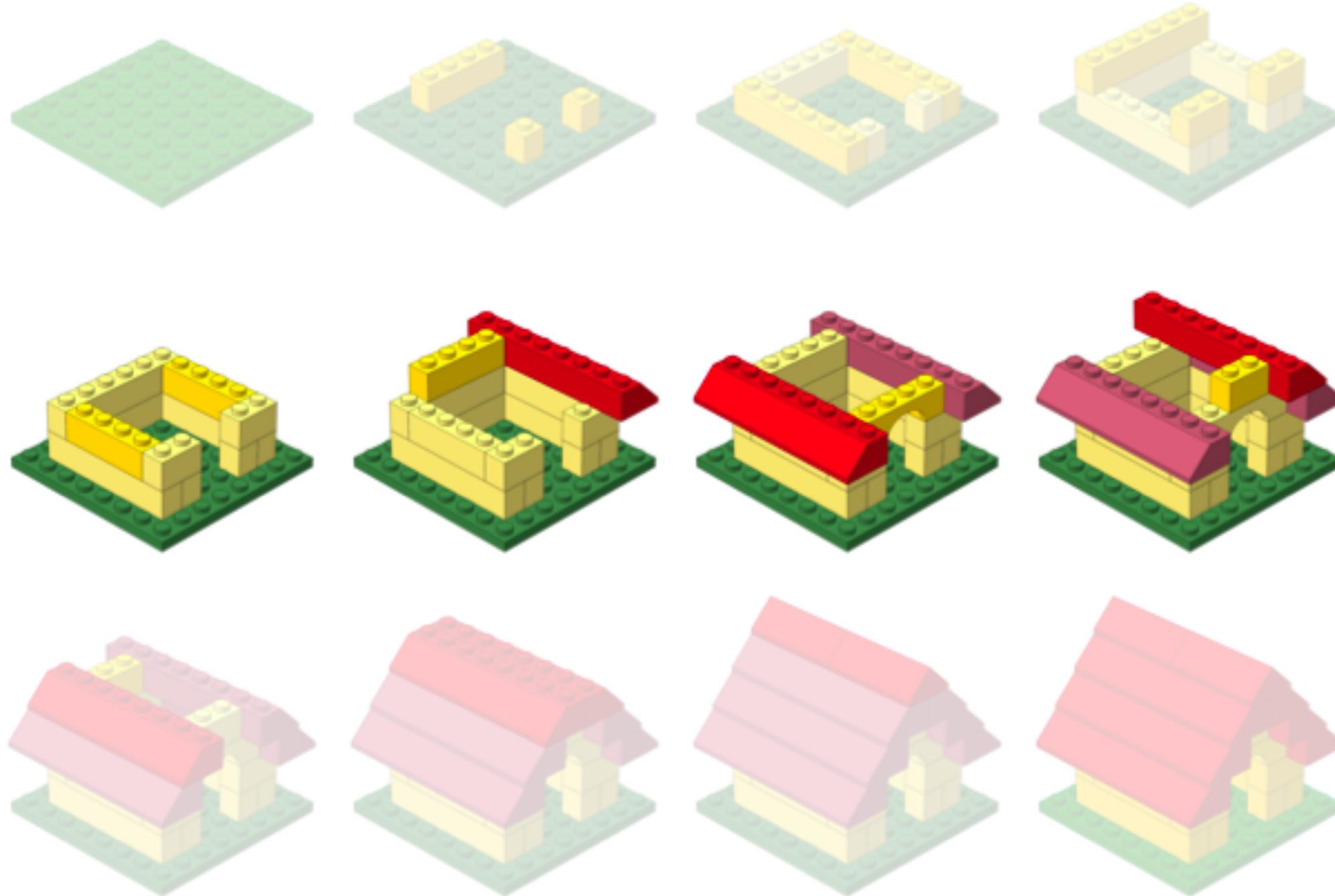
<http://anoved.net/tag/lego/page/3/>

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



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

Bioinformatics data analysis

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

Logistics

Course webpage

<http://tinyurl.com/hbc-intro-to-dge>

Course webpage

Introduction to DGE

[View on GitHub](#)

Approximate time: 60 minutes

Learning Objectives

- Explore different types of normalization methods
- Become familiar with the `DESeqDataSet` object
- Understand how to normalize counts using DESeq2

Normalization

The first step in the DE analysis workflow is count normalization, which is necessary to make accurate comparisons of gene expression between samples.

```
graph TD; A["Pseudocounts with  
Kallisto, Sailfish, Salmon"] --> B["Read counts  
associated with genes"]; B --> C["Normalization"]; C --> D["Unsupervised clustering analyses"]; C -.-> E["Quality control"]
```

The diagram illustrates the DE analysis workflow. It starts with 'Pseudocounts with Kallisto, Sailfish, Salmon', followed by 'Read counts associated with genes'. This leads to 'Normalization', which then leads to 'Unsupervised clustering analyses'. A bracket on the right side groups 'Normalization' and 'Unsupervised clustering analyses' under the heading 'Quality control'.

Odds and Ends

- ❖ Name tags: Tent Cards
- ❖ Post-its
- ❖ Wi-Fi: **HMS Public** or **HMS Secure**
- ❖ Lunch locations
- ❖ Bathrooms
- ❖ Water Fountain
- ❖ Phones on vibrate/silent!

Contact us!

HBC training team: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

[@bioinfocore](https://twitter.com/bioinfocore)