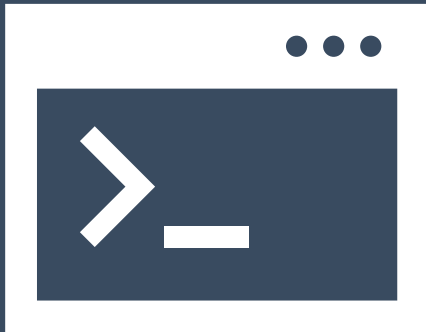# Peak Analysis

https://tinyurl.com/Peak-analysis

Harvard Chan Bioinformatics Core

Introductions!

Shannan Ho Sui
Director

Meeta Mistry
Associate Director

Lorena Pantano
Director of Bioinformatics Platform

John Quackenbush
*Faculty Advisor*

Upen Bhattarai

Heather Wick

Will Gammerdinger

Noor Sohail

Elizabeth Partan

Alex Bartlett

Emma Berdan

James Billingsley

Zhu Zhuo

Maria Simoneau

Shannan Ho Sui
Director

Meeta Mistry
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John Quackenbush
Faculty Advisor

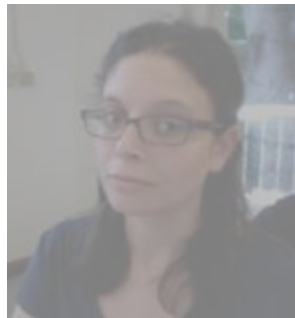Upen Bhattarai

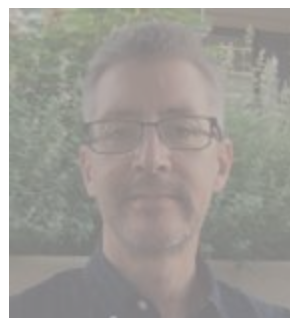Heather Wick

Will Gammerdinger

Noor Sohail

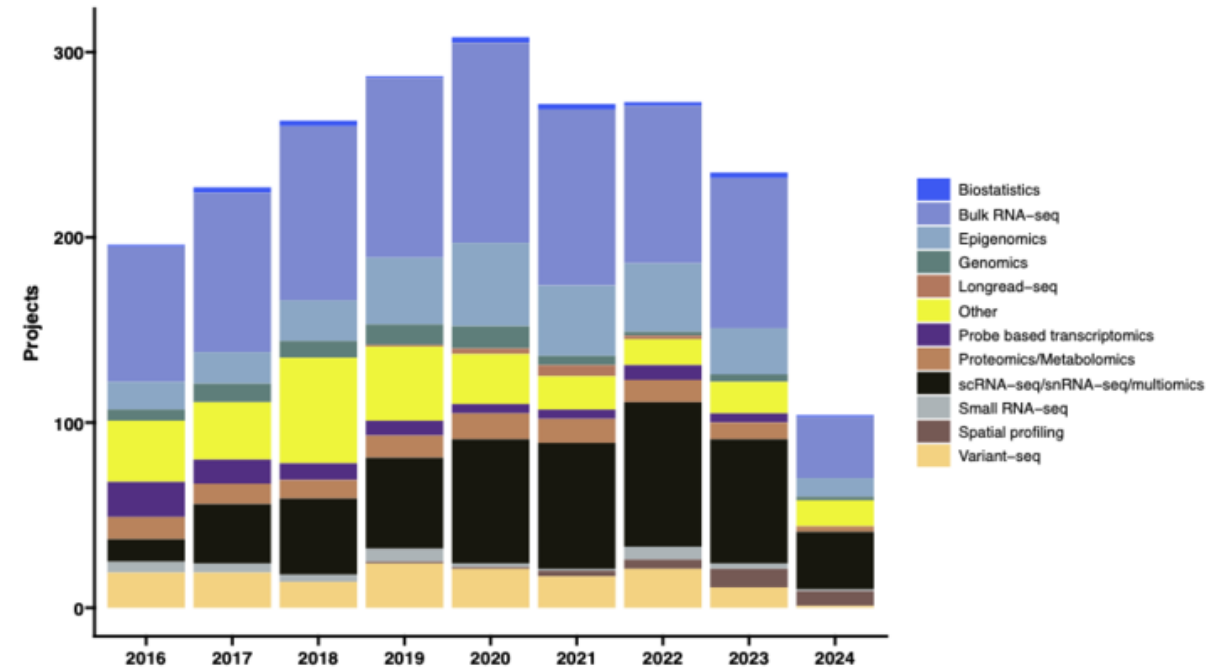Elizabeth Partan
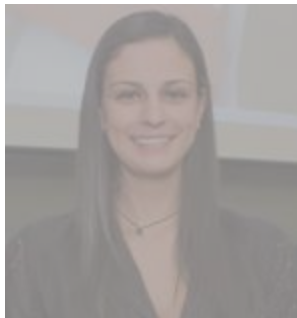
Alex Bartlett

Emma Berdan

James Billingsley

Zhu Zhuo

Maria Simoneau

Consulting

❖ Transcriptomics: Bulk, single cell, small RNA

❖ Epigenomics: ChIP-seq, CUT&RUN, ATAC-seq, DNA methylation

❖ Variant discovery: WGS, resequencing, exome-seq and CNV

❖ Multiomics integration

❖ Spatial biology

❖ Experimental design and grant support

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NIEHS

Training

❖ Hands-on workshops design to reflect best practices, reproducibility and an emphasis on experimental design

   ❖Basic Data Skills

      ❖ Shell

      ❖ R

   ❖Advanced Topics: Analysis of high-throughput sequencing data

      ❖ Chromatin Biology & Peak Analysis

      ❖ Bulk RNA-seq

      ❖ Differential Gene Expression (Bulk & scRNA)

      ❖ scRNA-seq

      ❖ Variant Calling

   ❖Current Topics in Bioinformatics

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

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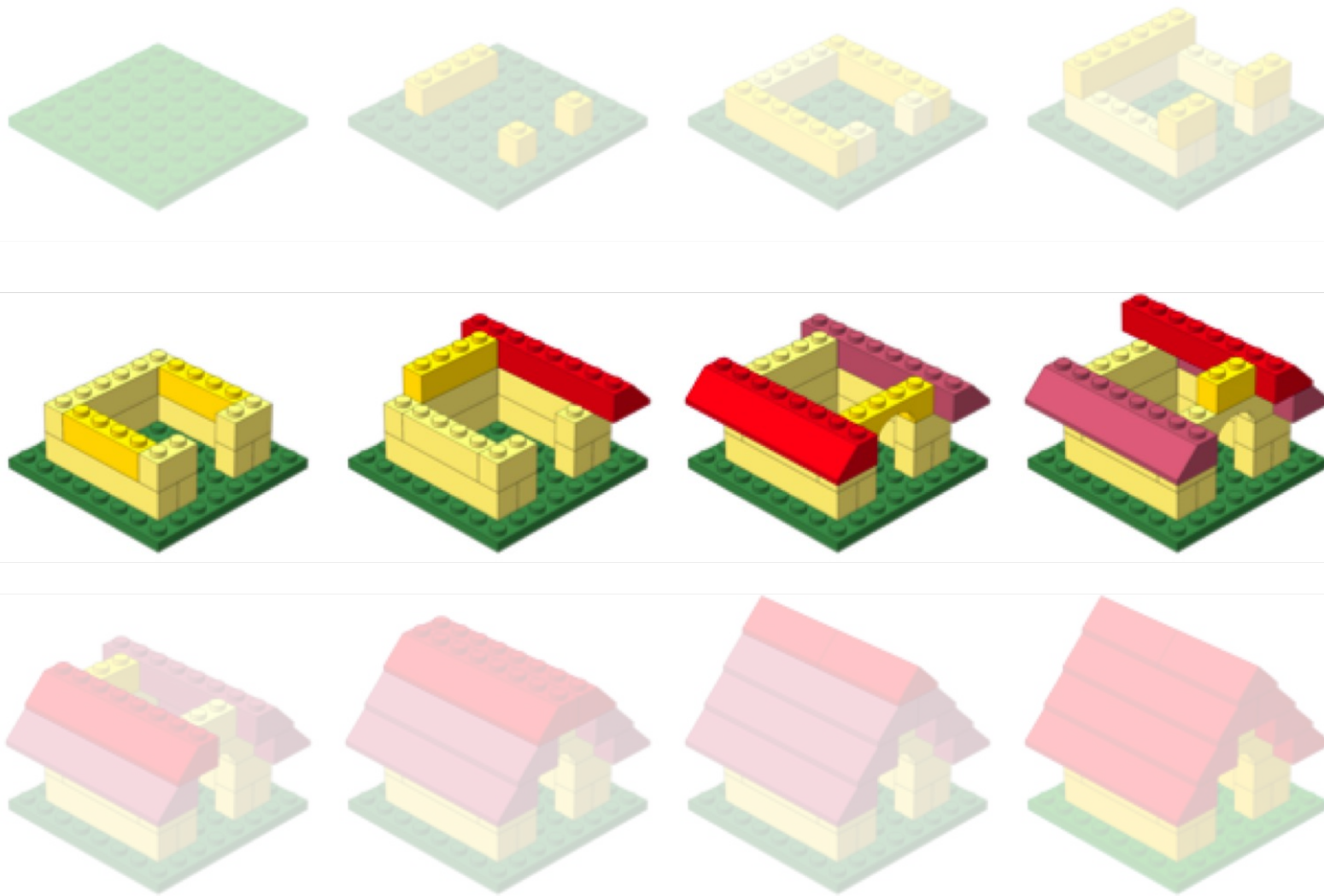
Workshop scope

Bioinformatic Data Analysis

Workshop Scope
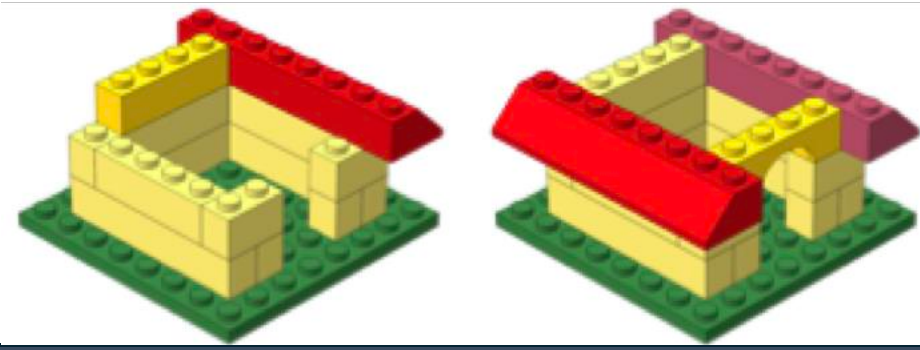
- ❖ Describe peak data and different file formats generated from peak calling algorithms

- ❖ Assess various metrics used to assess the quality of peak calls

- ❖ Compare peak calls across samples within a dataset

- ❖ Create visualizations to evaluate peak annotations

- ❖ Evaluate differentially enriched regions between two sample groups

Logistics

Course schedule

Day 1

Time	Topic	Instructor
09:30 - 09:45	Workshop Introduction	Meeta
09:45 - 10:15	Pre-reading discussion	Meeta
10:15 - 11:00	Understanding peaks and peak file formats	Meeta
11:00- 11:05	Break	
11:05 - 12:00	Assessing peak quality metrics	Will

Before the next class:

I. Please **study the contents** and **work through all the code** within the following lessons:

1. Assessing sample similarity and identifying potential outliers
   Click here for a preview of this lesson
2. Concordance across replicates using peak overlaps
   Click here for a preview of this lesson
3. **Complete the exercises**:
   - Each lesson above contains exercises; please go through each of them.
   - Copy over your solutions into the Google Forms the **day before the next class**.

https://tinyurl.com/Peak-analysis

Course materials

Intro to dataset and peak call file formats

An introduction to various methods/approaches for the analysis of peaks generated from ChIP-seq / CUT&RUN / ATAC-seq

View on GitHub

Contributors: Heather Wick, Upendra Bhattarai, Meeta Mistry, Will Gammerdinger

Approximate time: 40 minutes

Learning Objectives

In this lesson, we will:

- Explain the dataset and the biological context
- Define peaks as genomic coordinate data
- Describe file formats for peak data

Introduction to the dataset

For this workshop we will be working with ChIP-seq data from a publication in Neuron by *Baizabal et al., 2018* 1.

❖ We continuously update our materials to reflect changes in the field/software

https://tinyurl.com/Peak-analysis

Single Screen & 3 Windows

Single Screen & 3 Windows

Zoom

Our Recommendation

Single Screen & 3 Windows

Web Browser

Our Recommendation

Single Screen & 3 Windows

Our Recommendation

R Studio

Single Screen & 3 Windows

Zoom

Web Browser

R Studio

Our Recommendation

Course participation

❖ Mandatory review of self-learning lessons and assignments

❖ Attendance required for all classes

❖ Your questions and active participation drive learning

❖ **We look forward to all of your questions!**

Course participation

❖ At-home lessons and exercises after each session

❖ Cover material not previously discussed

❖ Provides us feedback to help pace the course appropriately

❖ 3-5 hours to complete

Using AI for Assignments

❖ Do

    ❖ Try to resolve error messages with it

    ❖ Test code written by AI on a dataset where you have expected results

    ❖ Take the time to review the generated code line-by-line

❖ Don't

    ❖ Implement it in replacement to learning

    ❖ Write code that you don't understand

    ❖ Assume the output from an AI process is correct
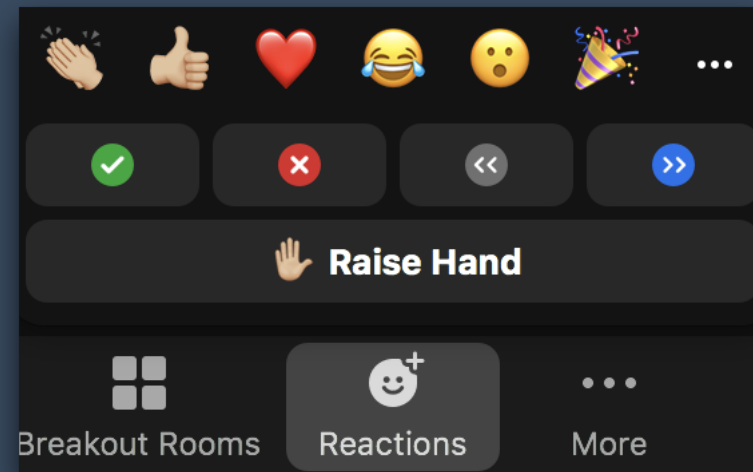
Odds & Ends

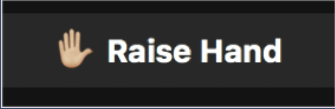❖ Quit/minimize all applications that are not required for class

❖ Are you all set?

　❖ ✅ = "agree", "I'm all set"

　❖ ❌ = "disagree", "I need help"

Odds & Ends

❖ Questions for the presenter?

  ❖ Post the question in the Chat window OR

  ❖ **✋ Raise Hand** when the presenter asks for questions

  ❖ Let the Moderator know

Odds & Ends

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    ❖ Let the Moderator know

❖ Technical difficulties with software?

    ❖ Start a private chat with the Troubleshooter with a description of the problem

Contact Us

- ❖ *HBC training team:* hbctraining@hsph.harvard.edu

- ❖ *HBC consulting:* bioinformatics@hsph.harvard.edu