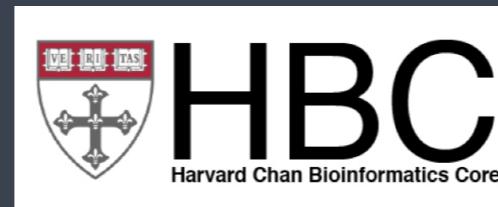


# Introduction to Single-cell RNA-seq analysis

Harvard Chan Bioinformatics Core



<http://tinyurl.com/hbc-scRNAseq-feb2024>

# Introductions!



Shannan Ho Sui  
*Director*



Meeta Mistry  
*Associate Director*



John Quackenbush  
*Faculty Advisor*



Emma Berdan



Heather Wick



Will Gammerdinger



Noor Sohail



James Billingsley



Zhu Zhuo



Maria Simoneau



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James Billingsley



Zhu Zhuo



Maria Simoneau

# Consulting

- Experimental design help
- RNA-seq analysis: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

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



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AND TRANSLATIONAL  
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# Training

A key component of the HBC's mission is its training initiative. Our dedicated training team holds workshop to help researchers at Harvard better understand analytical methods for NGS data.

HBC's training team is made up of four PhD-level scientists who devote substantial time to material development, training and community building/outreach. All members of the training team also participate in consultations on research projects to ensure they remain up-to-date on current best practices in NGS analysis.

Our hands-on workshops focus on **basic data skills** and **analysis of high-throughput sequencing data**, with an emphasis on **experimental design**, current **best practices** and **reproducibility**. Our workshops are designed for **wet-lab biologists** aiming to independently design sequencing-based experiments and analysing the resulting data.

We offer three types of workshops:

1. Short, 3-hour monthly workshops (*Current topics in bioinformatics*)
2. Basic Data Skills\*\*
3. Advanced Topics: Analysis of high-throughput sequencing (NGS) data\*\*

*\*\*The basic data skills workshops serve as the foundation for the advanced workshops.*

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

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

# Training

A key component of the HBC's mission is to provide training for researchers at Harvard and beyond.

HBC's training team is made up of experts in training and community based research projects to ensure that our trainees are well prepared for their future careers.

Our hands-on workshops focus on practical skills, with an emphasis on **experimental design** and **bioinformatics**, for **wet-lab biologists** and **computational biologists**.

We offer three types of workshops:

1. Short, 3-hour monthly workshops
2. Basic Data Skills\*\*
3. Advanced Topics: Analysis of high-throughput sequencing data

\*\*The basic data skills workshops are designed for wet-lab biologists and computational biologists.



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Our dedicated training team holds workshops to help researchers learn how to analyze high-throughput sequencing (NGS) data.

In addition to devote substantial time to material development, the training team also participate in consultations on best practices in NGS analysis.

The workshops focus on the analysis of high-throughput sequencing data, with an emphasis on **experimental design**, **bioinformatics**, and **reproducibility**. Our workshops are designed for wet-lab biologists and computational biologists, covering topics such as designing experiments and analysing the resulting data.

**bioinformatics**)

**bioinformatics (NGS) data**\*\*

and **bioinformatics for the advanced workshops**.

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

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

# Training

A key component of the HBC's mission is to support researchers at Harvard by providing training.

HBC's training team is made up of experts in training and community building who work on research projects to ensure our training is effective.

Our hands-on workshops focus on **bioinformatics**, with an emphasis on **experimental design** and **data analysis**. We also provide training for **wet-lab biologists** aiming to learn how to analyse their data.

We offer three types of workshops:

1. Short, 3-hour monthly workshops
2. Basic Data Skills\*\*
3. Advanced Topics: Analysis of high-throughput sequencing data

\*\*The basic data skills workshop is designed for researchers who have no prior experience with bioinformatics.



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Our dedicated training team holds workshops to help researchers learn how to analyse **high-throughput sequencing (NGS)** data.

The training team also devote substantial time to material development, and our training team also participate in consultations on best practices in NGS analysis.

Our workshops focus on the **analysis of high-throughput sequencing data**, with an emphasis on **experimental design**, **data quality**, and **reproducibility**. Our workshops are designed to help researchers understand how to perform sequencing-based experiments and analysing the resulting data.

**bioinformatics**)

**basic data skills** (e.g., **bioinformatics**)

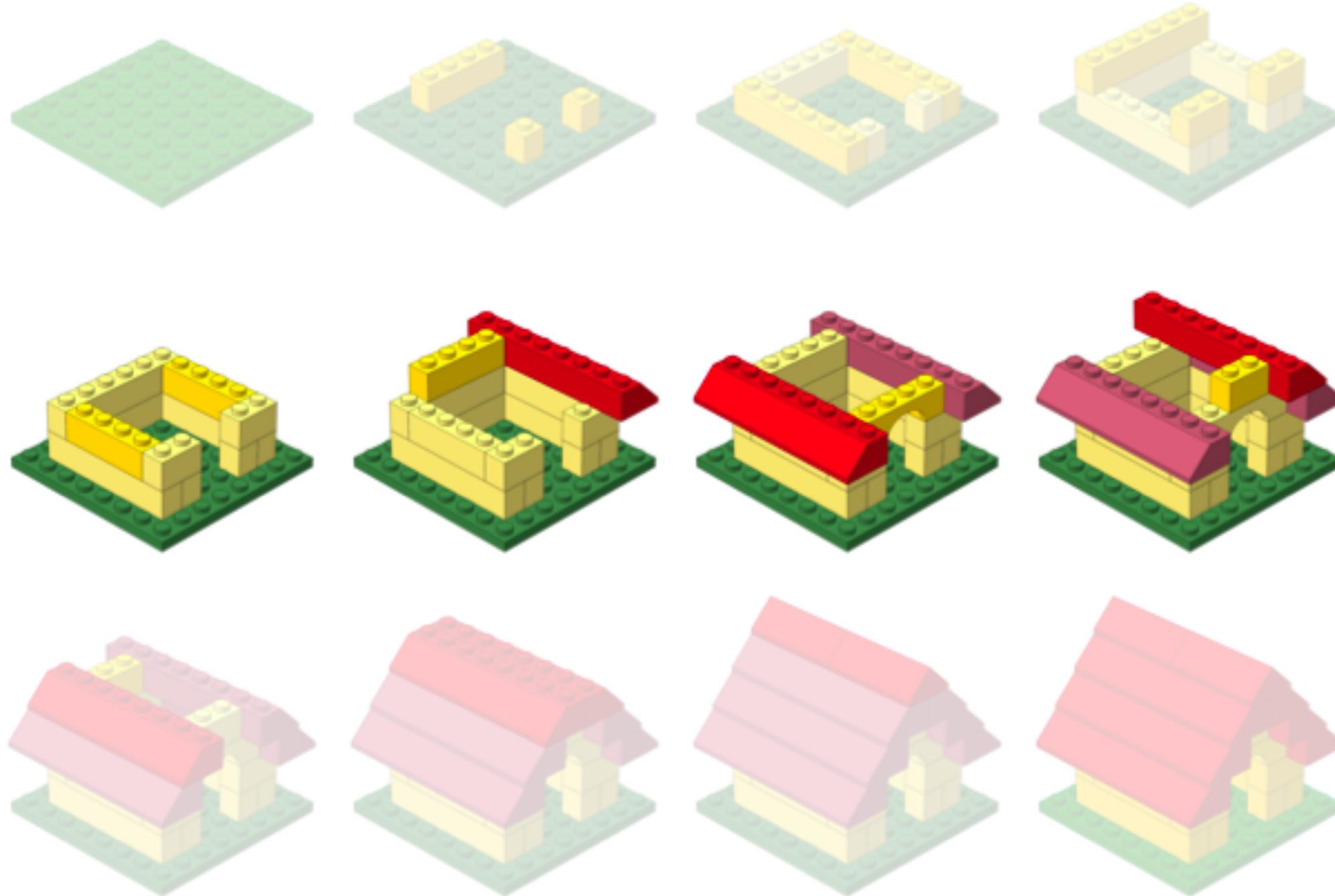
and **advanced topics** (e.g., **analysis of high-throughput sequencing (NGS)** data)\*\*

for the advanced workshops.

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

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

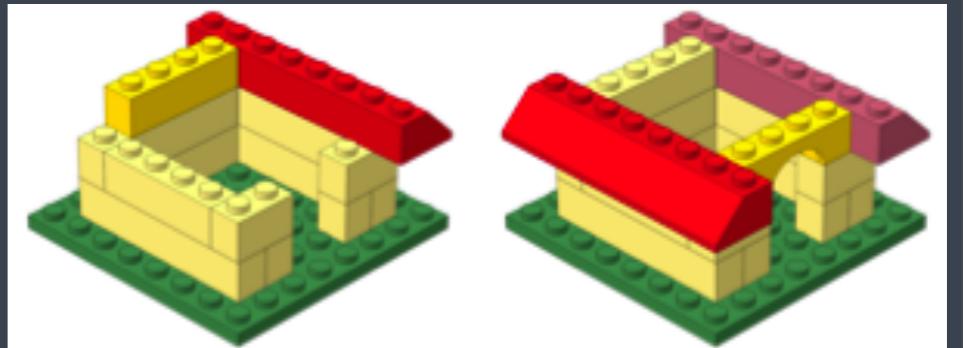
# Workshop scope



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

Bioinformatics data analysis

# Learning Objectives



- ✓ Describe best practices for designing a single-cell RNA-seq experiment
- ✓ Describe steps in a single-cell RNA-seq analysis workflow
- ✓ Use Seurat and associated tools to perform analysis of single-cell expression data, including data filtering, QC, integration, clustering, and marker identification
- ✓ Understand practical considerations for performing scRNA-seq, rather than in-depth exploration of algorithm theory

# Logistics

# Course webpage

<http://tinyurl.com/hbc-scRNAseq-feb2024>

# Course materials online

## Introduction to Single-cell RNA-seq

[View on GitHub](#)

Approximate time: 90 minutes

**Learning Objectives:**

- Understand how to bring in data from single-cell RNA-seq experiments
- Construct QC metrics and associated plots to visually explore the quality of the data
- Evaluate the QC metrics and set filters to remove low quality cells

**Single-cell RNA-seq: Quality control**

```
graph TD; A[Sequence reads] --> B[Generate count matrix]; B --> C["QC: Filter cells using quality metrics"]
```

# 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!



# Odds and Ends (1/3)

- ❖ Quit/minimize all applications that are not required for class
- ❖ Are you all set? We have provided sticky notes so you can let us know how you are doing with material during lectures
  - ▶ **green post-it** = "agree", "I'm all set"
  - ▶ **red post-it** = "disagree", "I need help"

# Odds and Ends (2/3)

- ❖ **Questions for the presenter?**

- Raise your hand! We love questions!!
- Put a **red post-it** on your computer

- ❖ **Need help troubleshooting an R/RStudio issue?**

- Signal to the co-teacher (the teacher not presenting) that you need help

# Odds and Ends (3/3)

- ❖ **The room we are in for class will change:**
  - February 09: Countway 403
  - February 13: Ballard 503
  - February 16: Countway 403
- ❖ **Please leave your nametags where you picked them up**
  - Do not take them home

# Bioinformatics Community Networking Breakfast!



- ***Free and open to the Harvard community***
- ***Food is first-come-first-served***
- ***No computers!***

More info: <http://bioinformatics.sph.harvard.edu/breakfast/>

# Contact us!

*Training team*  : [hbctraining@hsph.harvard.edu](mailto:hbctraining@hsph.harvard.edu)

*Consulting*  : [bioinformatics@hsph.harvard.edu](mailto:bioinformatics@hsph.harvard.edu)

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