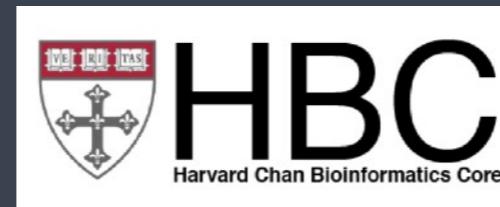


Introduction to Single-cell RNA-seq analysis

Harvard Chan Bioinformatics Core



<https://tinyurl.com/hbc-scrnaseq-online>



Shannan Ho Sui
Director



Victor Barrera



James Billingsley



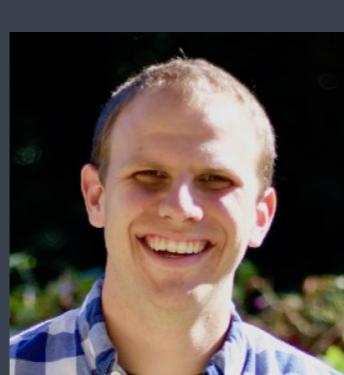
Zhu Zhuo



Meeta Mistry
*Interim Director
of Education*



Heather Wick



Will Gammerdinger



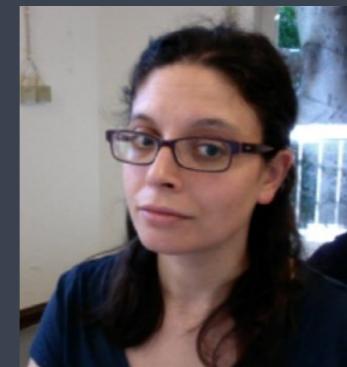
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Consulting

- 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

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



NIEHS



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 train researchers at Harvard and beyond.

HBC's training team is made up of scientists, educators, and community based organizations who work on research projects to ensure the best training for our students.

Our hands-on workshops are designed to provide an emphasis on **experimental design** and **informatics** for **wet-lab biologists** and **bioinformaticians** alike.

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 those new to bioinformatics.



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Our dedicated training team holds workshops to help researchers learn how to analyze and interpret 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**, **informatics**, and **reproducibility**. Our workshops are designed to provide an emphasis on performing wet-lab experiments and analysing the resulting sequencing data.

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 train researchers at Harvard and beyond.

HBC's training team is made up of scientists, educators, and community based organizations involved in research projects to ensure that our training is relevant and effective.

Our hands-on workshops are designed to provide an emphasis on **experimental design** and **informatics**, as well as training for **wet-lab biologists** and **bioinformaticians** to work with NGS 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 NGS data analysis.



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

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

informatics)

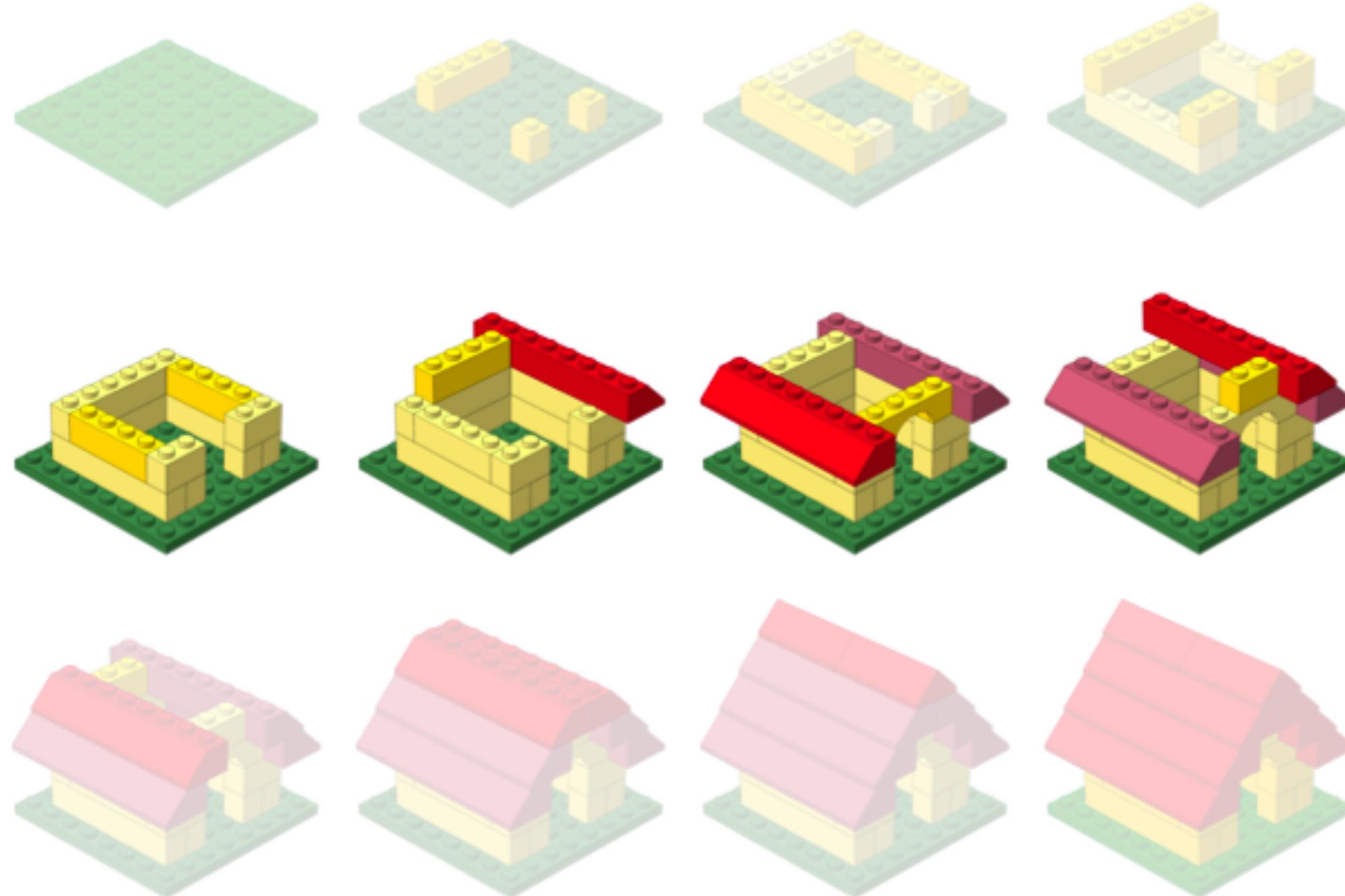
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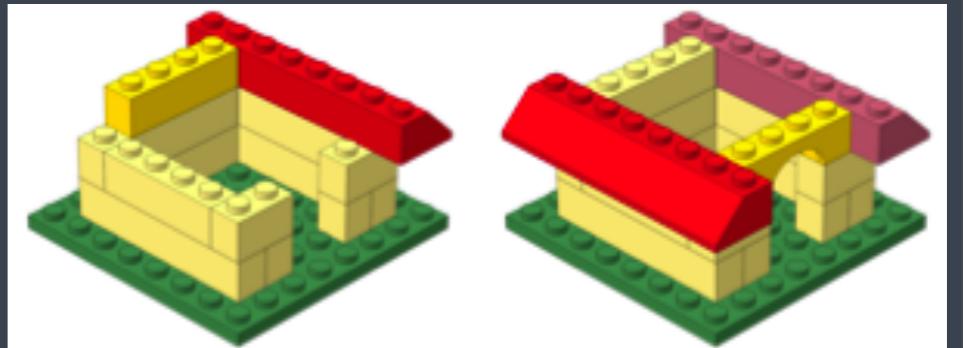
Workshop scope



<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

<https://tinyurl.com/hbc-scrnaseq-online>

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

- ▶ Please keep your videos on, we would love to see your faces!
- ▶ 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!



Homework and Expectations

- ❖ 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

Odds and Ends

- ❖ Name tags
- ❖ Post-its
 - green - I am all set
 - red - I need time/help
- ❖ Quit/minimize all applications that are not required for class
- ❖ Phones on vibrate/silent
- ❖ Bathrooms

Contact us!

Training team  : hbctraining@hsph.harvard.edu

Consulting  : bioinformatics@hsph.harvard.edu

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