

Introduction to R

Harvard Chan Bioinformatics Core

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

Sponsored by DF/HCC and HMS Foundry



Shannan Ho Sui
Director



Victor Barrera



Amelie Jule



Zhu Zhuo



James Billingsley



Radhika Khetani
Director of Education



Meeta Mistry



Jihe Liu



Will Gammerdinger



Emma Berdan
(Starts Nov 2022)



Sergey Naumenko



Maria Simoneau



We are hiring!
Email bioinformatics@hsph.harvard.edu
for more information



Peter Kraft
Faculty Advisor

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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NIEHS



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AND TRANSLATIONAL
SCIENCE CENTER



HARVARD
MEDICAL SCHOOL

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/>

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**The basic data skills



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or the advanced workshops.

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Training

A key component of the Harvard Bioinformatics Center's mission is to train researchers at Harvard and beyond.

[HBC's training team](#) is made up of experts in training and community building. We support research projects to ensure high-quality data.

Our hands-on workshops place an emphasis on **experimentation** for **wet-lab biologists** and **bioinformaticians** alike. We focus on generating high-quality data.

We offer three types of workshops:

1. [Short, 3-hour monthly](#)
2. [Basic Data Skills](#)**
3. [Advanced Topics: Analyzing](#)

**The basic data skills workshop is required for the advanced workshops.



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HARVARD
MEDICAL SCHOOL

Our dedicated training team holds workshops to help researchers analyze and interpret their NGS data.

We do not devote substantial time to material development, but our training team also participate in consultations on best practices in NGS analysis.

We focus on the **analysis of high-throughput sequencing data**, with an emphasis on **reproducibility**. Our workshops are designed to help researchers design and analyze sequencing-based experiments and analyzing the resulting data.

(Bioinformatics)

(NGS) data**

for the advanced workshops.

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

Introductions!



Shannan Ho Sui
Director



Victor Barrera



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Will Gammerdinger



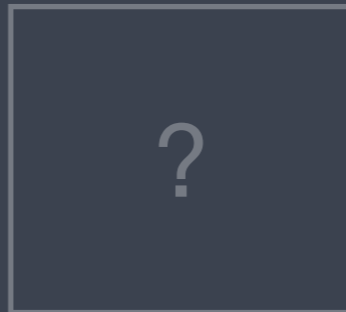
Emma Berdan
(Starts Nov 2022)



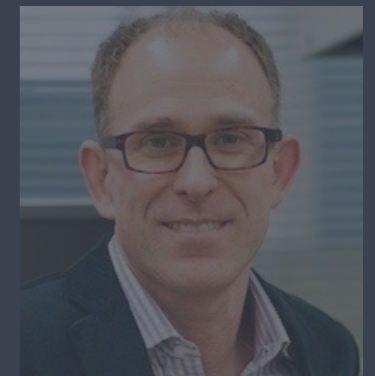
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Maria Simoneau

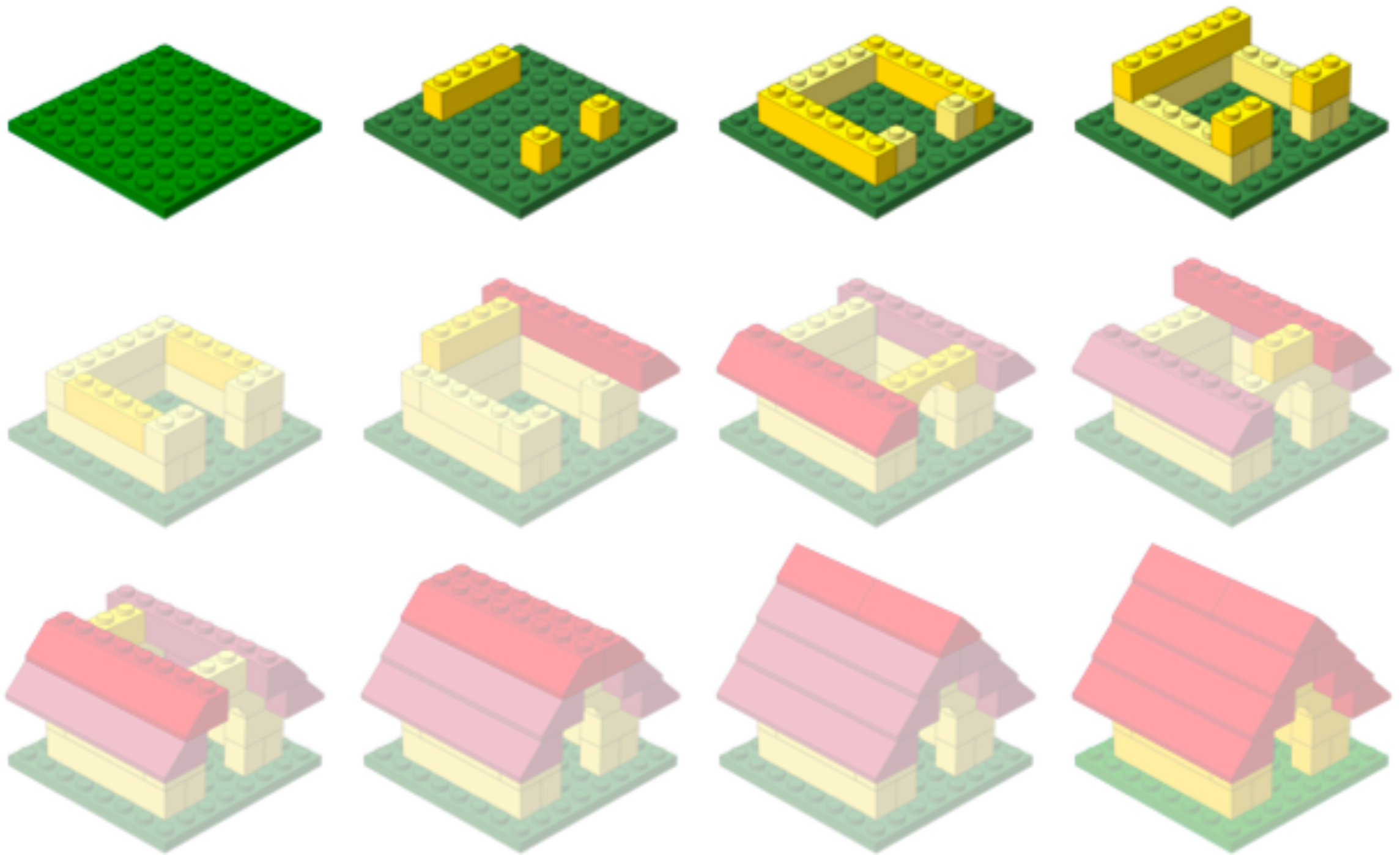


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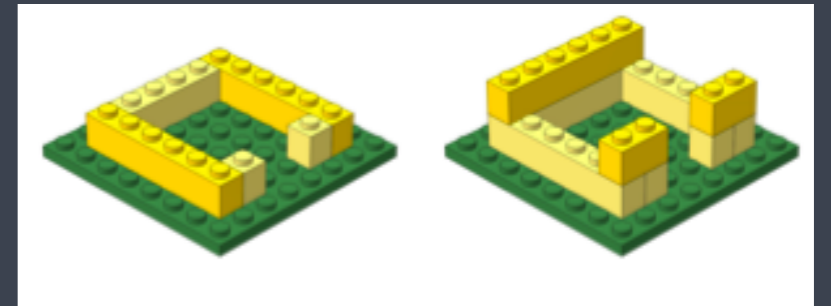
Peter Kraft
Faculty Advisor

Workshop Scope...



Learning R

Workshop Scope



- ✓ Comfortably use RStudio (a graphical interface for R)
- ✓ Fluently interact with R using RStudio
- ✓ Become familiar with R syntax
- ✓ Understand data structures in R
- ✓ Inspect and manipulate data structures
- ✓ Install packages and use functions in R

CRAN

(Comprehensive R Archive Network)



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[Mirrors](#)
[What's new?](#)
[Task Views](#)
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[R Homepage](#)
[The R Journal](#)

[A3](#)
[abbyyR](#)
[abc](#)
[ABCanalysis](#)
[abc.data](#)
[abcdeFBA](#)
[ABCOptim](#)
[ABCp2](#)
[abcrf](#)

Available CRAN Packages By Name

[A](#)[B](#)[C](#)[D](#)[E](#)[F](#)[G](#)[H](#)[I](#)[J](#)[K](#)[L](#)[M](#)[N](#)[O](#)[P](#)[Q](#)[R](#)[S](#)[T](#)[U](#)[V](#)[W](#)[X](#)[Y](#)[Z](#)

Accurate, Adaptable, and Accessible Error Metrics for Predictive Models
Access to Abbyy Optical Character Recognition (OCR) API
Tools for Approximate Bayesian Computation (ABC)
Computed ABC Analysis
Data Only: Tools for Approximate Bayesian Computation (ABC)
ABCDE_FBA: A-Biologist-Can-Do-Everything of Flux Balance Analysis with this package
Implementation of Artificial Bee Colony (ABC) Optimization
Approximate Bayesian Computational Model for Estimating P2
Approximate Bayesian Computation via Random Forests

- The main repository for R packages
- Easy to install

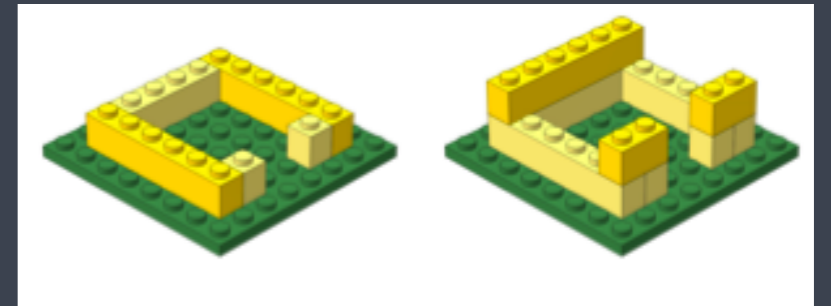
<https://cran.r-project.org/>



- An alternative package repository; “..provides tools for the analysis and comprehension of *high-throughput genomic data*.”
- Includes (but is not limited to) tools for:
 - ✦ performing statistical analysis
 - ✦ accessing public datasets
- Open source and open development
- Free

www.bioconductor.org

Workshop Scope



- Comfortably use RStudio (a graphical interface for R)
- Fluently interact with R using RStudio
- Become familiar with R syntax
- Understand data structures in R
- Inspect and manipulate data structures
- Install packages and use functions in R
- ✓ Visualize data using *ggplot2*
- ✓ Utilize pipes, tibbles and functions from the Tidyverse package suite

Logistics

Course webpage

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

Course schedule online

Workshop Schedule

Day 1

Time	Topic	Instructor
10:00 - 10:30	Workshop Introduction	Jihe
10:30 - 11:45	Introduction to R and RStudio	Radhika
11:45 - 12:00	Overview of self-learning materials and homework submission	Mary

Before the next class:

1. Please **study the contents** and **work through all the code** within the following lessons:
 - [R Syntax and Data Structure](#)
 - [Functions and Arguments](#)
 - [Reading in and inspecting data](#)
2. **Complete the exercises:**
 - Each lesson above contain exercises; please go through each of them.
 - **Copy over** your code from the exercises into a text file.
 - **Upload the saved text file** to [Dropbox](#) the **day before the next class**.

Course materials online

Introduction to R

[View on GitHub](#)

Approximate time: 70 min

Learning Objectives

- Employ variables in R.
- Describe the various data types used in R.
- Construct data structures to store data.

The R syntax

Now that we know how to talk with R via the script editor or the console, we want to use R for something more than adding numbers. To do this, we need to know more about the R syntax.

Below is an example script highlighting the many different “parts of speech” for R (syntax):

- the **comments** `#` and how they are used to document function and its content
- **variables** and **functions**
- the **assignment operator** `<-`

Single screen & 3 windows?

The image shows a Zoom meeting interface with three participants: Mary Piper (Co-host), Jihe Liu (Host), and Troubleshooter (Radhika) (Co-host). The shared screen displays RStudio with three windows:

- Code Editor:** Contains R code for assignment operators, functions, and rounding functions.
- Console:** Shows the execution of the code, including the output of the `round` function.
- Documentation:** Displays the R documentation for the `round` function, including a description and usage examples.

```
1 # Assignment operator
2 x <- 3
3
4 # Functions
5 getwd()
6
7 sqrt(81)
8
9 round(3.14159)
10 ?round
11 |
```

```
> x <- 3
> # Functions
> getwd()
[1] "/Users/marypiper/Desktop/R-testing"
> sqrt(81)
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[1] 3
> ?round
> |
```

Environment History Connections
Global Environment

Values

Variable	Value
x	3

Files Plots Packages Help Viewer

R: Rounding of Numbers - Find in Topic

Round (base) R Documentation

Rounding of Numbers

Description

`ceiling` takes a single numeric argument `x` and returns a numeric vector containing the smallest integers not less than the corresponding elements of `x`.

`floor` takes a single numeric argument `x` and returns a numeric vector containing the largest integers not greater than the corresponding elements of `x`.

`trunc` takes a single numeric argument `x` and returns a numeric vector containing the integers formed by truncating the values in `x` toward 0.

`round` rounds the values in its first argument to the specified number of decimal places (default 0). See 'Details' about "round to even" when rounding off a 5.

`signif` rounds the values in its first argument to the specified number of significant digits.

Usage

```
ceiling(x)
floor(x)
trunc(x, ...)
```

Single screen & 3 windows?

ZOOM

Our recommendation

```
483  
484  
485 getwd()  
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Single screen & 3 windows?

Web browser

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*Our
recommendation*

Single screen & 3 windows?

The image is a composite of three windows. The top window is a Zoom meeting interface showing three participants: Mary Piper (Co-host, me), Troubleshooter (Radhika) (Co-host), and Jihe Liu (Host). The middle window is an RStudio IDE showing a script with R code and its execution output in the console. The bottom window is an R documentation page for the 'Rounding of Numbers' section.

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RStudio

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ZOOM

Our recommendation

RStudio

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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
- ❖ Homework load is heavier in the beginning of this workshop series and tapers off



Odds and Ends (1/2)

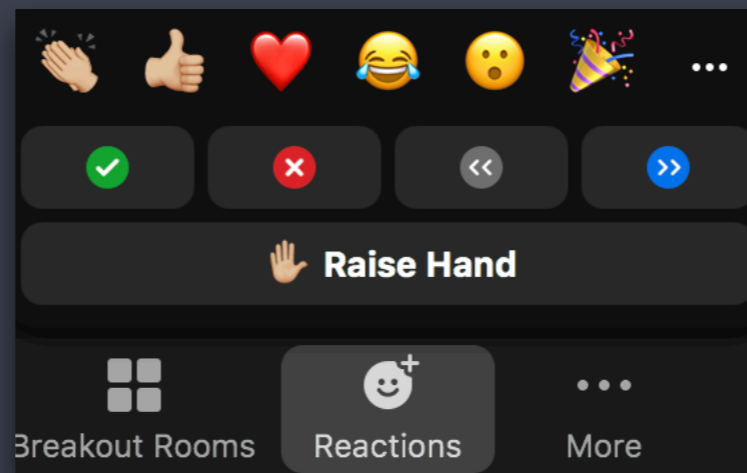
- ❖ Quit/minimize all applications that are not required for class

Odds and Ends (1/2)

- ❖ Quit/minimize all applications that are not required for class
- ❖ Captioning is available upon request

Odds and Ends (1/2)

- ❖ Quit/minimize all applications that are not required for class
- ❖ Captioning is available upon request
- ❖ Are you all set?
 - ▶  = "agree", "I'm all set" (equivalent to a **green post-it**)
 - ▶  = "disagree", "I need help" (equivalent to a **red post-it**)



Odds and Ends (2/2)

❖ Questions for the presenter?

- Post the question in the Chat window OR



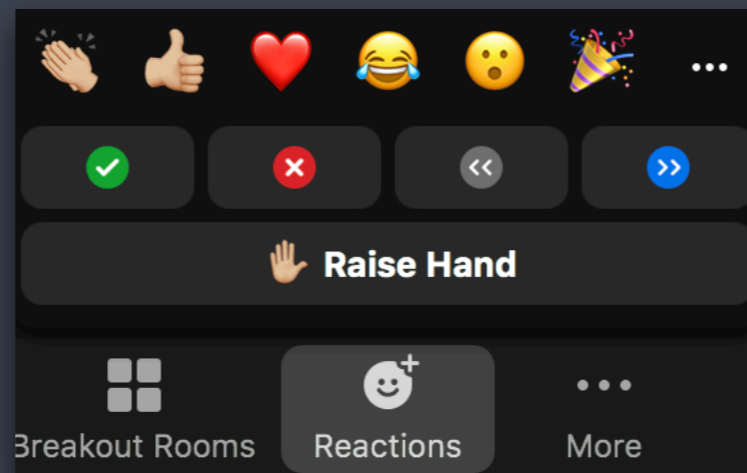
Raise Hand

when the presenter asks for questions

- 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

Twitter

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