

# Understanding chromatin biology using high throughput sequencing methods

<https://tinyurl.com/hbc-chipseq>

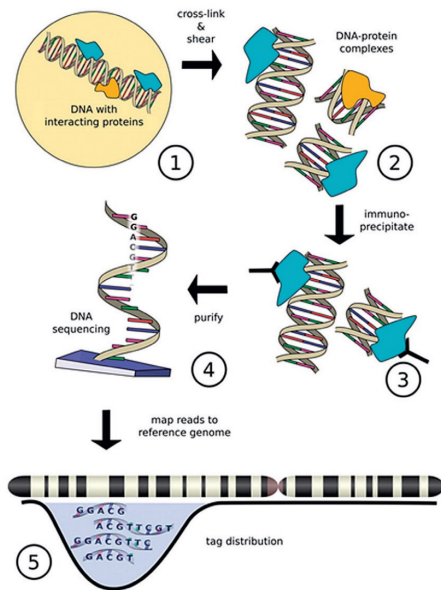


**Harvard Chan Bioinformatics Core**  
in collaboration with  
**HMS Research Computing**



# Genomic Methods for Profiling Chromatin

## ChIP-seq



## CUT&RUN

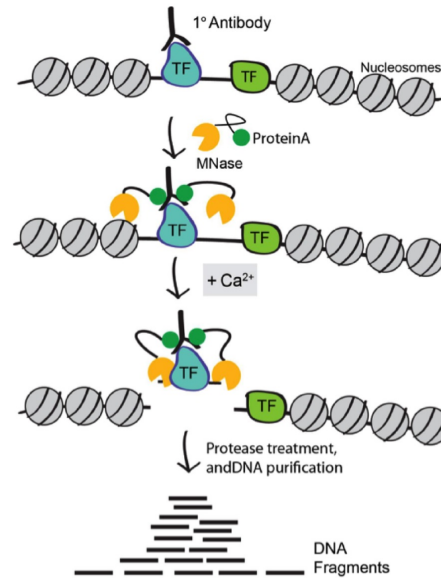
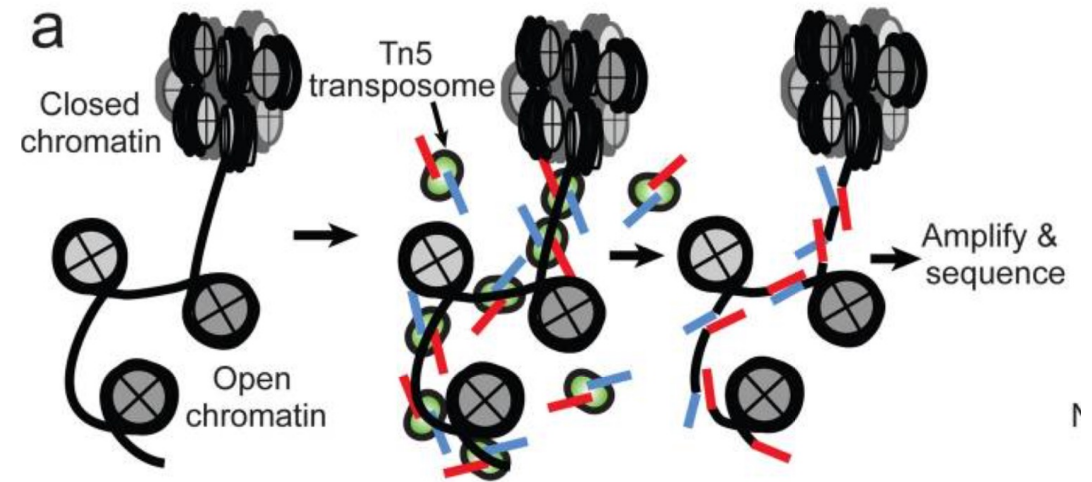
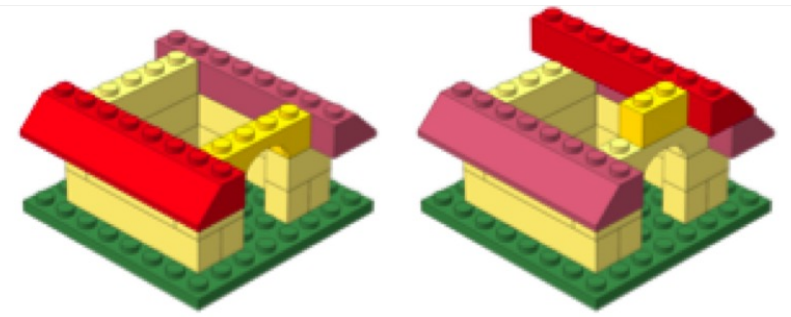


Figure 1. CUT&RUN schematic (see text for details).

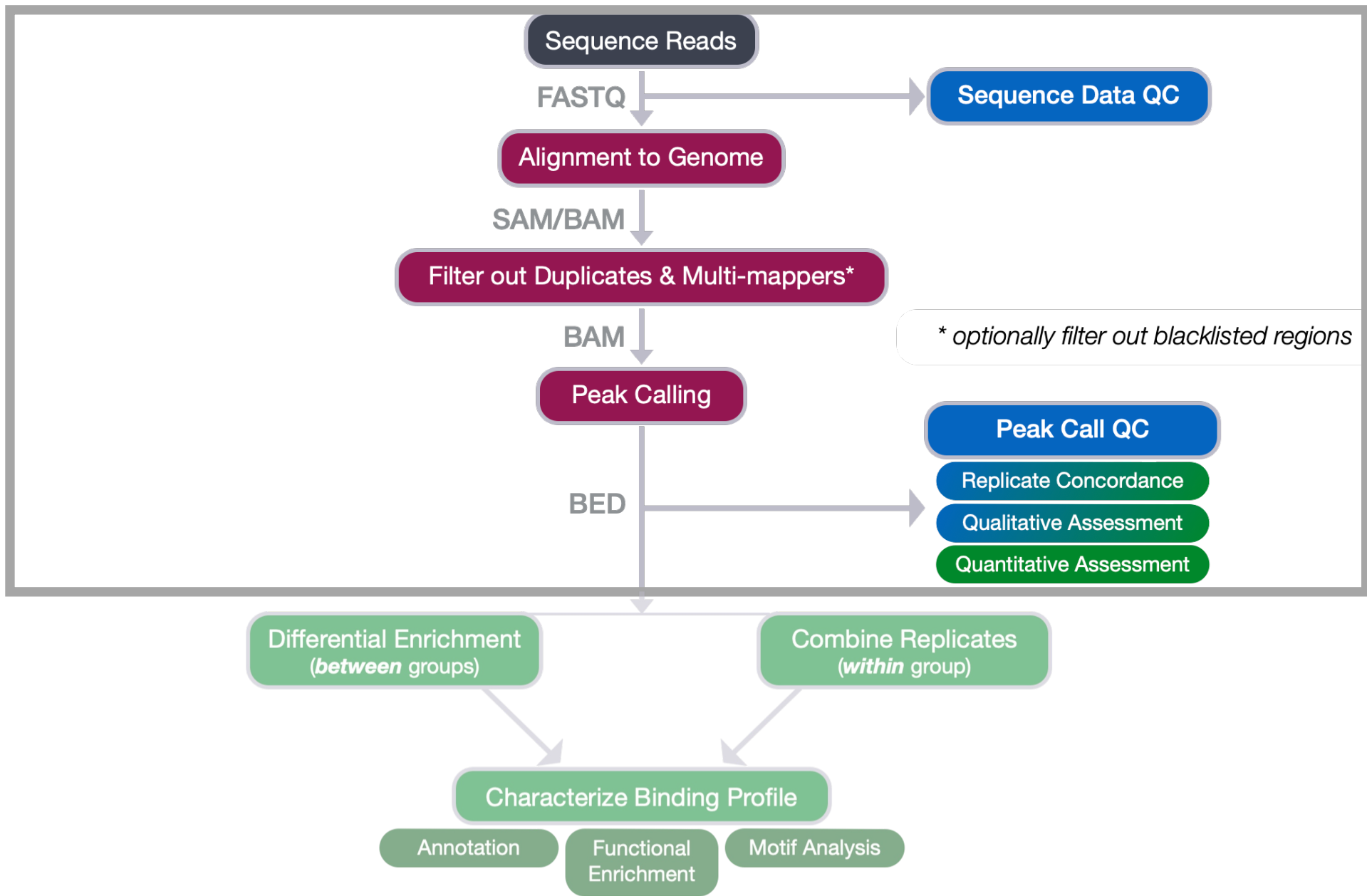
## ATAC-seq



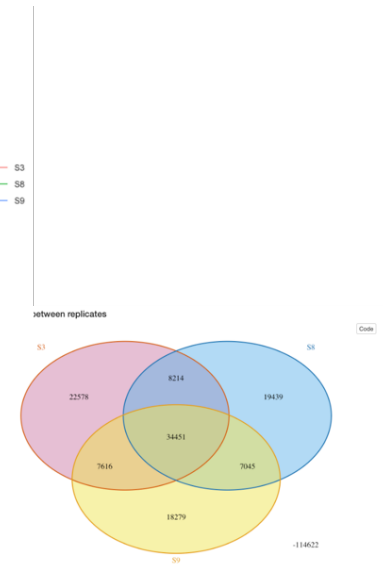
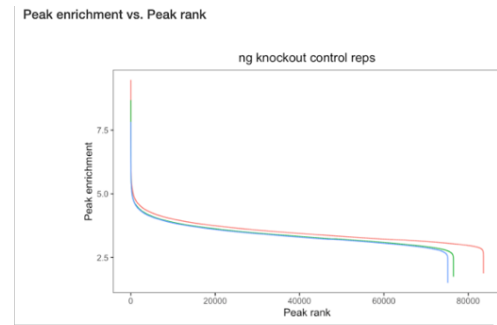
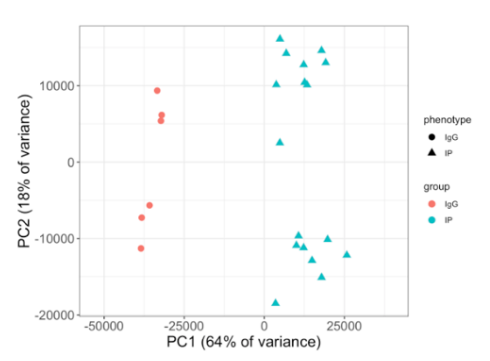
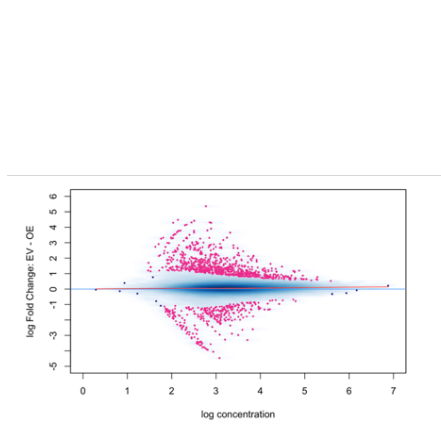
# Learning Objectives



- ❖ Describe important considerations for setting up a successful ChIP-seq, CUT&RUN or ATAC-seq experiment
- ❖ Describe the steps in an ChIP-seq analysis workflow (from sequence data to peak calls) and contrast any differences for CUT&RUN and ATAC-seq analyses
- ❖ Learn how to handle various file formats encountered when analyzing ChIP-seq and related data
- ❖ Implement shell scripts on a high-performance compute cluster to perform the above steps



Boxes in green represent parts of the workflow that will not be covered in this workshop



Differential Enrichment  
(between groups)

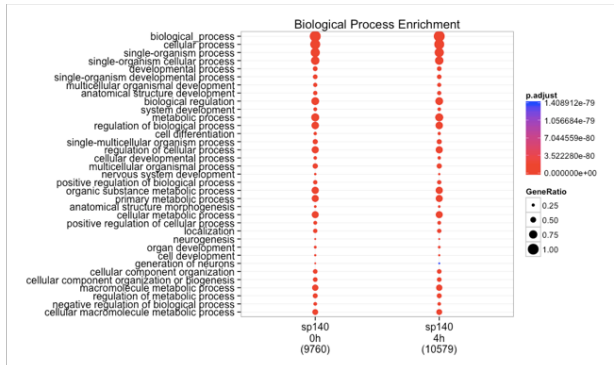
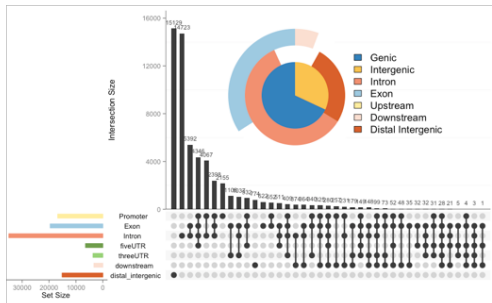
Combine Replicates  
(within group)

Characterize Binding Profile

Annotation

Functional Enrichment

Motif Analysis



**DREME**  
Discriminative Regular Expression Motif Elicitation

For further information on how to interpret these results or to get a copy of the MEME software please access <http://meme.nbcr.net>.  
If you use DREME in your research please cite the following paper:  
Timothy L. Bailey, "DREME: Motif discovery in transcription factor ChIP-seq data", *Bioinformatics*, 27(12):1653-1659, 2011. [\[full text\]](#)

DISCOVERED MOTIFS | INPUTS & SETTINGS | PROGRAM INFORMATION

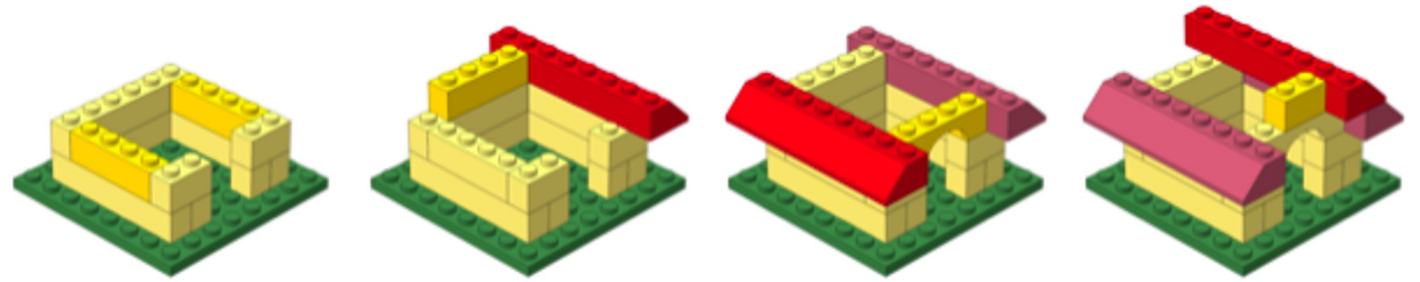
Motif	Logo	RC Logo	E-value	Unersered E-value	More	Submit/Download
1. CYWTTGTB			4.2e-299	4.2e-299	<a href="#">↓</a>	<a href="#">→</a>
2. AIGWAAAT			8.4e-179	1.1e-179	<a href="#">↓</a>	<a href="#">→</a>
3. CCMCDCCC			1.3e-130	1.1e-131	<a href="#">↓</a>	<a href="#">→</a>

# Downstream of Peak Calls

# Exit survey

<http://tinyurl.com/hbc-chromatin-bio-exitsurvey>

# Keep building!



Topic	Pre-requisites	Date/Time	Time	Registration
<a href="#">R basics</a>	None	6/26/24*	1 – 4pm	<a href="#">Register!</a>
Publication Perfect I	<a href="#">R basics</a>	7/17/24	1 – 4pm	Coming soon!
Publication Perfect II	<a href="#">R basics</a>	8/21/24	1 – 4pm	Coming soon!
RShiny	<a href="#">R basics</a>	9/18/24	1 – 4pm	Coming soon!

# Get an O2 account!

Home > Service Catalog

Search IT services and kn 

## O2 Cluster Account

### Description

What does it do?

Get an account on O2, the HMS High Performance Compute cluster

### Available To

Who is eligible?

Any HMS or HMS-affiliated researcher who has an HMS eCommons account.

### Cost

What does it cost?

There is no cost to labs whose PI has a primary or secondary faculty appointment in an HMS Quad department.

If the PI of your lab does not have a primary or secondary faculty appointment in an HMS Quad department, cluster usage will be charged for beginning later in 2021. Please see the following page for current details about rates: <https://it.hms.harvard.edu/rc/core/rates>.

### Support

Please fill out the [online help request form](#), or email [rchelp@hms.harvard.edu](mailto:rchelp@hms.harvard.edu).

### How to Access

How do I get it?

Two-factor authentication is required to request an account on O2, as well as for O2 logins once your account is created. Harvard University uses a mobile app called Duo that makes the process quick and easy. Even if you already use Duo for HarvardKey, you will still need to setup a Duo profile for HMS.

- [Setup HMS two-factor Authentication \(HMS Duo Mobile\)](#)
- [Reactivate or Reconnect HMS two-factor Authentication \(HMS Duo Mobile\)](#)

Once you have Duo set up, Click the "Get Service" link to login and complete the request form.

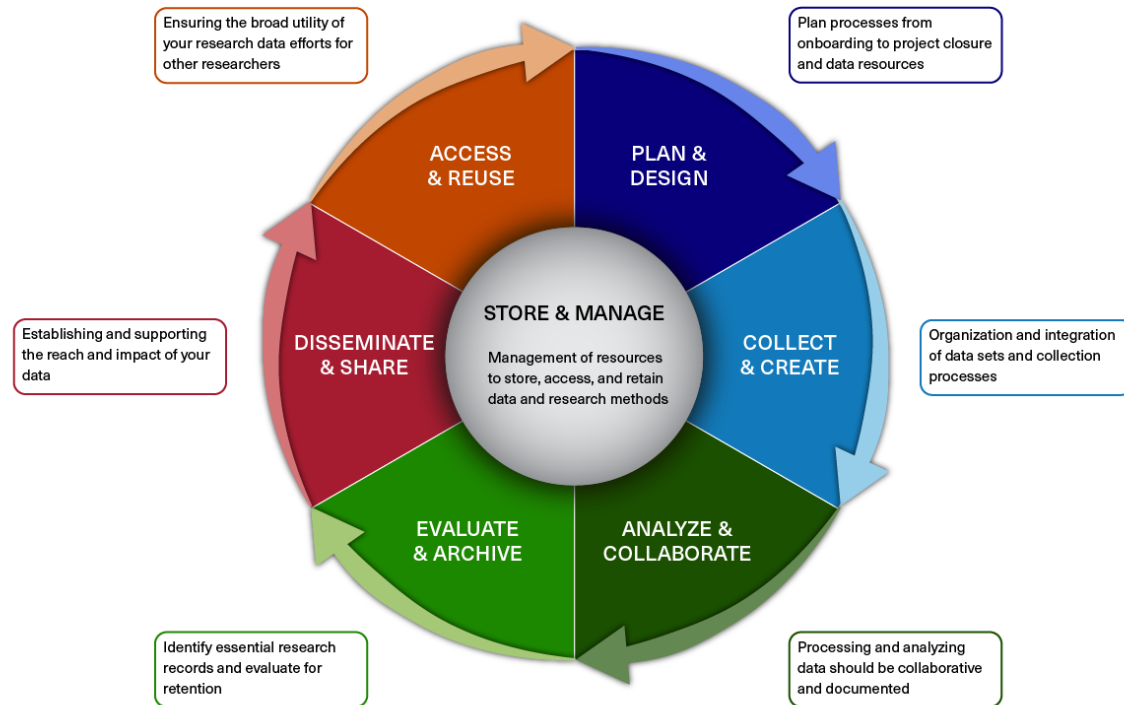
[Get this service](#) [Learn more](#)

Don't see what you're looking for?



# Research Data Management (RDM)

## BIOMEDICAL RESEARCH DATA LIFECYCLE



Date	Time	Event	Location
Jun 28	12pm	<b>Level Up Your GIS Skills: A Three-Part Series (Part 3)</b>	Countway Library Classroom L2-025
Jul 24	12pm	<b>Best Practices for Data Visualization</b>	Zoom
Jul 31	12pm	<b>Plotting like a Pro: Data Visualization with ggplot2</b>	Zoom

# Better RDM practice benefits you

- ❖ **HMS Data Management LMA**

- ❖ **Webpage:** <https://datamanagement.hms.harvard.edu>

- ❖ **Sign up** for quarterly email updates

- ❖ **Harvard-wide Research data Management**

- ❖ <https://researchdatamanagement.harvard.edu/>

# Join us for HBC Community Breakfast!

- ❖ An opportunity to get to know others in the community
- ❖ Free food and beverages
- ❖ Great conversations



**Thursday September 5<sup>th</sup>, 2024  
9:00 to 10:30am**

**More Info:**

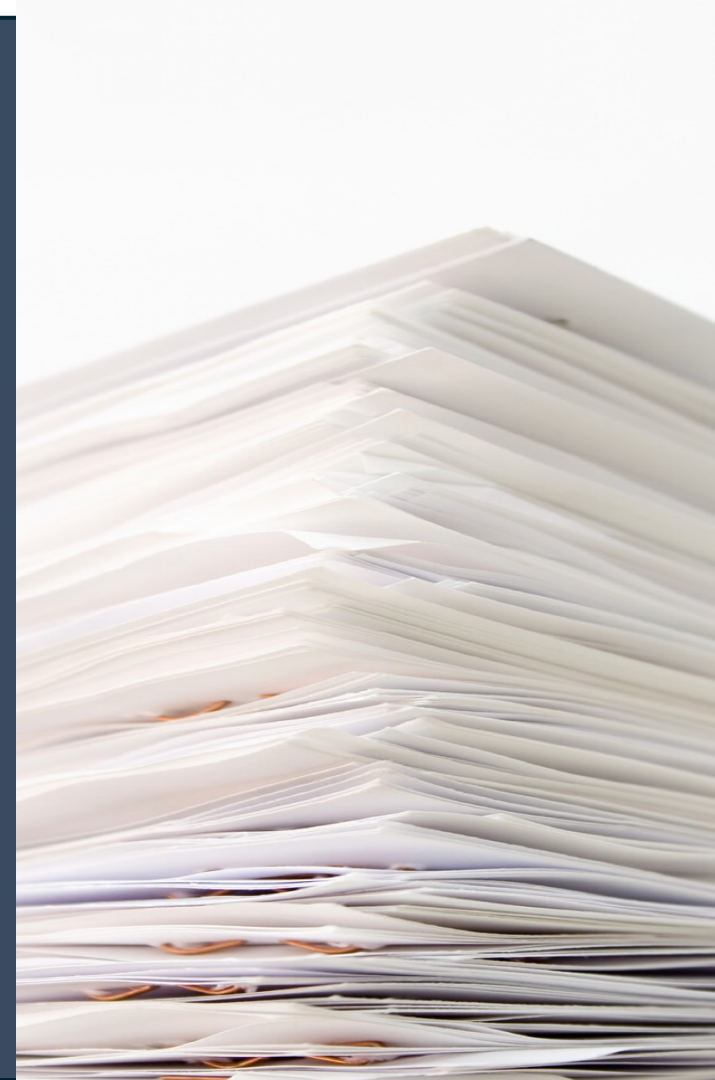
<http://bioinformatics.sph.harvard.edu/breakfast/>

# Contact Us

- ❖ *HBC training team:* [hbctraining@hsph.harvard.edu](mailto:hbctraining@hsph.harvard.edu)
- ❖ *HBC consulting:* [bioinformatics@hsph.harvard.edu](mailto:bioinformatics@hsph.harvard.edu)
- ❖ *O2 (HMS-RC):* [rchelp@hms.harvard.edu](mailto:rchelp@hms.harvard.edu)

# Talk to us early!

Involvement in study design to optimize experiments



# Thanks!

- ❖ Shannan Ho Sui
- ❖ Kathleen Chappell and Andy Bergman from HMS-RC
- ❖ Data Carpentry

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*These materials have been developed by members of the teaching team at the Harvard Chan Bioinformatics Core (HBC). These are open access materials distributed under the terms of the Creative Commons Attribution license (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.*

# More Information

- ❖ *HBC training materials: <https://hbctraining.github.io/main>*
- ❖ *HBC website: <http://bioinformatics.sph.harvard.edu>*
- ❖ *O2 Wiki (HMS-RC): <https://wiki.rc.hms.harvard.edu/display/O2>*