



Analysis of ChIP-seq peaks with ChIPseeker: an R package

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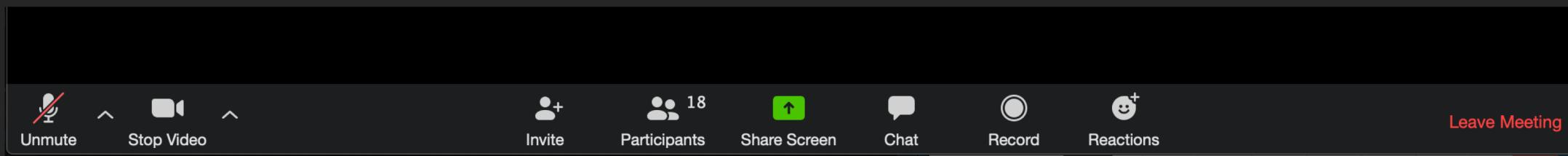
22nd April, 2020

Virtual class!!!

- Zoom orientation – Nur
- GitHub orientation - Sawyer
- Be respectful
 - Mute yourself (enjoy your drink, reduce ambient noises)
 - Video (depends on your comfort, share your screen if needed)
- Be flexible
- Relax
- Participate in the session
- We are there for continued support
- Take the survey at the end

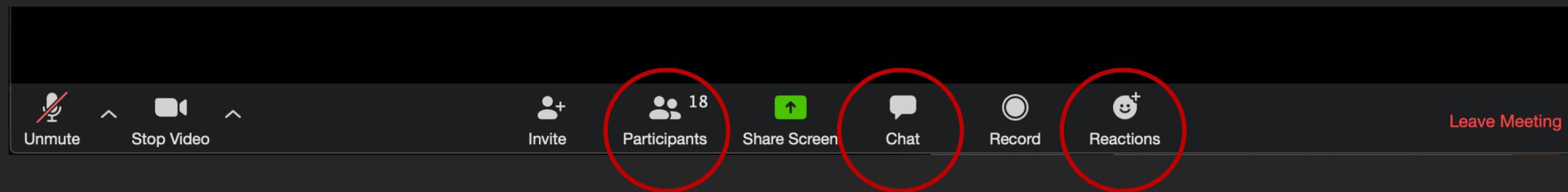
- Zoom orientation

At the bottom of your Zoom screen where
you see everyone



- Zoom orientation

At the bottom of your Zoom screen where
you see everyone





Zoom orientation

The screenshot shows a dark-themed Zoom interface. At the top right, a header reads "Participants (18)". Below it is a search bar with a magnifying glass icon. A list of participants is displayed, each with a small profile picture, initials, name, and status (video and audio icons). The first participant is Alyssa Grimsnaw (Guest). The control bar below the participants includes a red circle around the "raise hand" button (a blue hand icon), followed by "yes" (green checkmark), "no" (red X), "go slower" (left arrow), "go faster" (right arrow), and a "more" button (three dots). To the right of the control bar is an "Unmute Me" button. Below the control bar is a "Chat" section with a "To:" dropdown set to "Everyone" and a text input field placeholder "Type message here...".



Zoom orientation

The screenshot shows a Zoom video call interface. At the top right, it says "Participants (18)". Below that is a search bar. The participant list includes:

- Alyssa Grimsnaw (Guest) - video off, audio on
- Caitlin Meyer - video off, audio on
- Courtney Brombosz (Guest) - video off, audio on
- Janene Batten (Guest) - video off, audio on
- John Gallagher (Guest) - video off, audio off

Below the participant list is a control bar with the following options: raise hand, yes (circled in red), no, go slower, go faster, and more. There is also an "Unmute Me" button.

At the bottom left, there is a "Chat" section with a "To:" dropdown set to "Everyone" and a text input field "Type message here...".



Zoom orientation

The screenshot shows a dark-themed Zoom interface. At the top right, it says "Participants (18)". Below that is a search bar with a magnifying glass icon. A list of participants is shown, each with a small profile picture, their name, and their video and audio status. Below the participant list is a row of interactive icons: a blue hand icon labeled "raise hand", a green checkmark icon labeled "yes", a red circle with a white "X" icon labeled "no", a double-left arrow icon labeled "go slower", a double-right arrow icon labeled "go faster", and a three-dot ellipsis icon labeled "more". The "no" icon is circled in red. Below these icons is a button labeled "Unmute Me". Underneath the control bar is a section titled "Chat" with a "To:" dropdown set to "Everyone" and a text input field with placeholder text "Type message here...".



Zoom orientation

The screenshot shows a Zoom video call interface. At the top, a search bar contains the text "Search". Below it is a list of participants:

- Alyssa Grimsnaw (Guest) - Muted, Video Off
- Caitlin Meyer - Muted, Video Off
- Courtney Brombosz (Guest) - Muted, Video Off
- Janene Batten (Guest) - Muted, Video Off
- John Gallagher (Guest) - Muted, Video Off

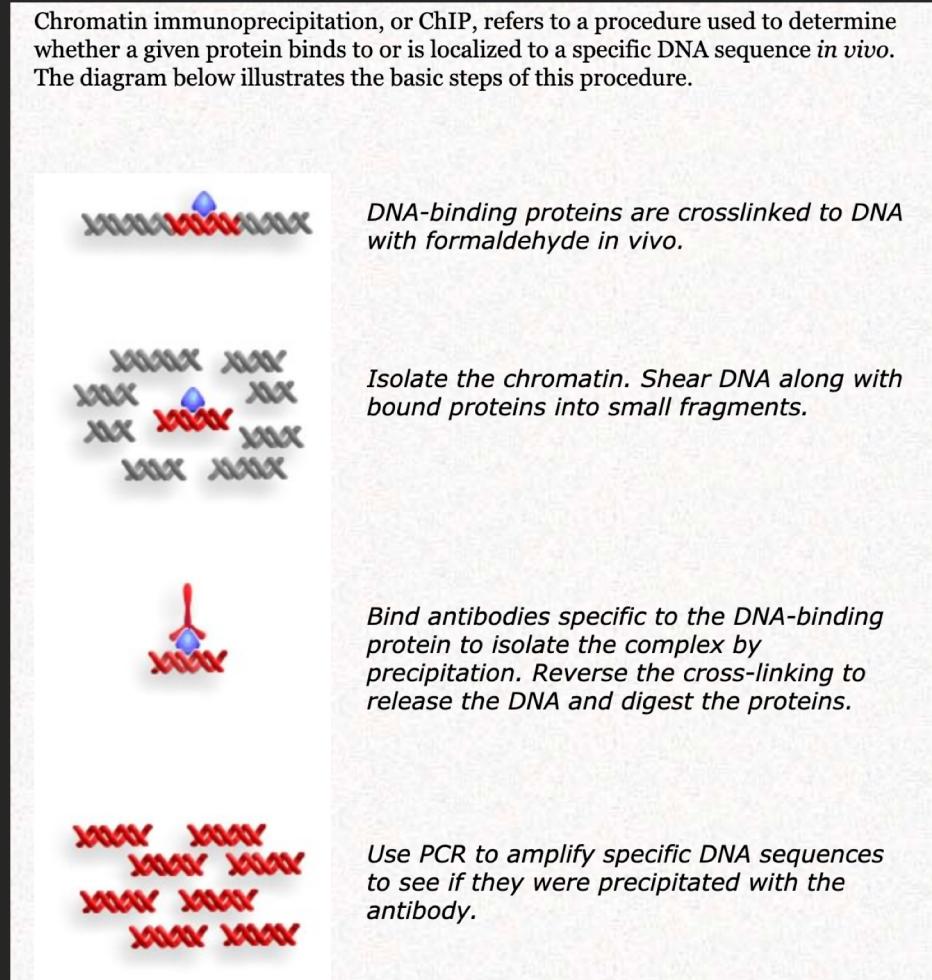
Below the participants are several control icons: raise hand, yes, no, go slower, go faster, and more. A large "Unmute Me" button is present. The interface includes a "Chat" section with a "To:" dropdown set to "Everyone" and a text input field "Type message here...". A large yellow arrow points from the left side of the slide towards the right side of the Zoom interface.

Why ChIPseeker?

- An updated (maintained) package that can nicely summarize ChIP-seq data
- After identifying genomic locations where transcription factors of interest are binding, understanding and annotating the peaks is the important/hardest part
- Not the only way to analyze ChIPseq “peaks,” there can be other tools, other platforms etc.

Brief overview of ChIP-seq and subsequent analysis

Chromatin immunoprecipitation, or ChIP, refers to a procedure used to determine whether a given protein binds to or is localized to a specific DNA sequence *in vivo*. The diagram below illustrates the basic steps of this procedure.



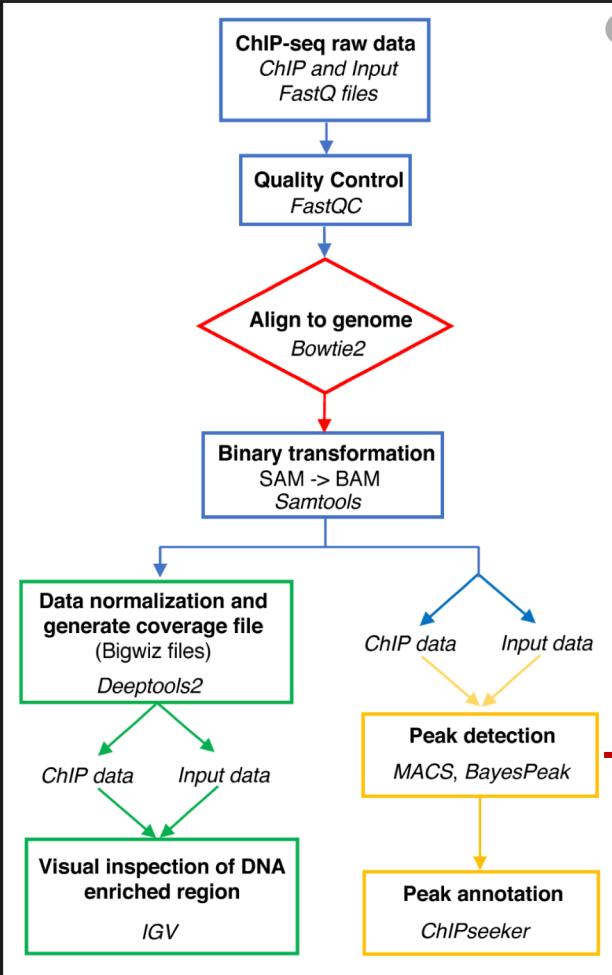
Library prep & prep for sequencing



Resources for the HiSeq 3000/HiSeq 4000...
illumina.com

Raw files (.fastq)

Brief overview of ChIP-seq and subsequent analysis



Giner-Lamia et al. (2018)
DOI: [10.21769/BioProtoc.2895](https://doi.org/10.21769/BioProtoc.2895)

What are “.bed” files?

Cannot be opened or read with any usual applications

Name	Date Modified	Size	Kind
GSM2891281_NY8_HNF1A_ChIP_1_peaks.bed	Apr 11, 2020 at 3:17 PM	4.2 MB	Document
GSM2891283_NY8_HNF1A_ChIP_2_peaks.bed	Apr 11, 2020 at 3:17 PM	836 KB	Document
GSM2891285_NY15_HNF1A_ChIP_1_peaks.bed	Apr 11, 2020 at 3:17 PM	321 KB	Document
GSM2891287_NY15_HNF1A_ChIP_2_peaks.bed	Apr 11, 2020 at 3:18 PM	550 KB	Document

Viewed on UNIX/Linux

```
[(base) MWC02YX0HTLVDV:ChIPseeker_2020_nr267$ cd peak_files_bed/
[(base) MWC02YX0HTLVDV:peak_files_bed_nr267$ ls
GSM2891281_NY8_HNF1A_ChIP_1_peaks.bed  GSM2891285_NY15_HNF1A_ChIP_1_peaks.bed
GSM2891283_NY8_HNF1A_ChIP_2_peaks.bed  GSM2891287_NY15_HNF1A_ChIP_2_peaks.bed
[(base) MWC02YX0HTLVDV:peak_files_bed_nr267$ head GSM2891281_NY8_HNF1A_ChIP_1_peaks.bed
chr1 2755383 2755614 NY8_HNF1A_ChIP_1_MACS_peak_1 72.59
chr1 2873845 2874608 NY8_HNF1A_ChIP_1_MACS_peak_2 58.82
chr1 2875156 2875685 NY8_HNF1A_ChIP_1_MACS_peak_3 168.61
chr1 2884922 2885088 NY8_HNF1A_ChIP_1_MACS_peak_4 61.19
chr1 2908209 2908427 NY8_HNF1A_ChIP_1_MACS_peak_5 55.17
chr1 2909480 2909654 NY8_HNF1A_ChIP_1_MACS_peak_6 52.43
chr1 2912552 2912800 NY8_HNF1A_ChIP_1_MACS_peak_7 72.15
chr1 2921117 2921291 NY8_HNF1A_ChIP_1_MACS_peak_8 55.14
chr1 3135865 3136206 NY8_HNF1A_ChIP_1_MACS_peak_9 99.48
chr1 4002889 4003112 NY8_HNF1A_ChIP_1_MACS_peak_10 67.65
(base) MWC02YX0HTLVDV:peak_files_bed_nr267$
```

Fun Fact!

".bed" → ".txt" → ".xls" (Excel file)

- Easier to do on a MacOS
- Can be done on Windows OS using “Unix simulator” like Cygwin
- Let me know in the survey if you want a short video tutorial



Let's start!

Brief overview of dataset

Feedback Time!



bit.ly/cwml-nur