

Teaching with Galaxy in a High School Setting

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Labs can support projects for high school students

- The Fred Hutchinson Cancer Research Center's Science Education Partnership runs a program for high school students to work with researchers at the Hutch. This year it was **completely virtual**
 - Pathways to cancer research: <https://www.fredhutch.org/en/about/education-outreach/science-education-partnership/pathways-to-cancer-research.html>
 - Mentors can be group leaders, staff scientists, postdocs, grad students, and technicians.
 - The Pathways to Cancer Research High School program runs during the entire school year.
 - I meet with my two students one-on-one and in a group setting once a week and they meet with program leaders once per week.
 - Students spend ~6 hours per week reading and working on their analyses for their projects.



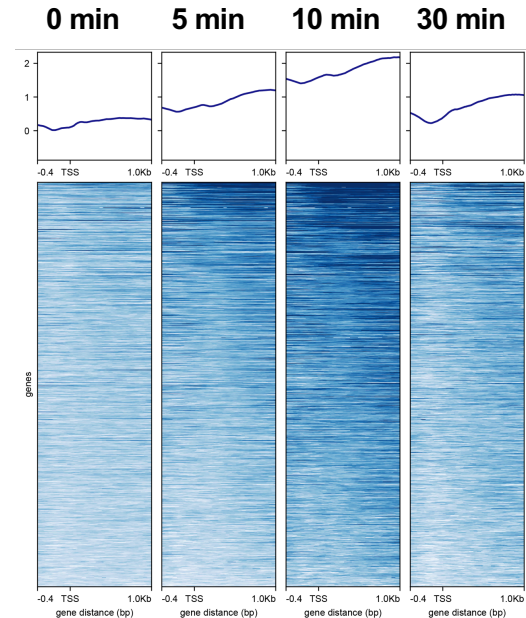
Designing a project for virtual research experiences for high school students

- Like many genomics labs, we have a lot of data to analyze, probably more than we can handle!
- This gives us a great opportunity to teach students about gene expression, give them a research experience, and gain new insights into data we already have.
- My research area focuses on understanding how cells re-activate from periods of dormancy.
 - Datasets we work with in the lab include: ChIP-seq, MNase-seq, and RNase-seq datasets.



Creating a project for high school students using existing datasets

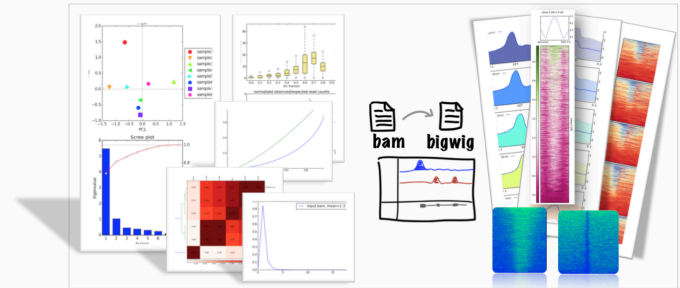
- With this project, students learn the central dogma of biology, how genes are transcribed, and how DNA is occluded or accessible to transcription factors
- At the beginning of the project, students were initially given .fastq files of Pol II ChIP-seq single-end datasets from an existing paper from the lab
- Students learned basics of high throughput sequencing and how to perform genome alignments using **Bowtie2** and used **DeepTools** for further processing



Identifying transcription factors regulating reactivation from dormancy

- Using Pol II ChIP-seq data, students performed clustering analysis to identify genes induced, not induced, etc. **Most analyses were contained in DeepTools**
- Here is a point where you can give students freedom to choose gene sets of interest and have them formulate their own hypotheses.
- Questions students can ask:
 - Which genes are induced?
 - Which genes never induce?
 - What is the chromatin state at selected genes?
 - What sequence motifs are present at genes of interest?

deepTools: tools for exploring deep sequencing data

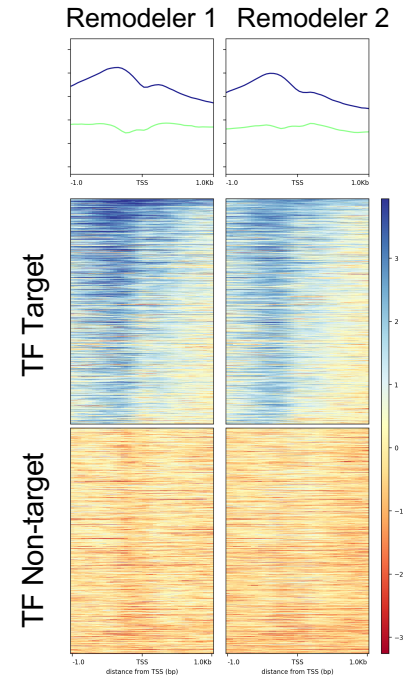


QUALITY CHECKS – FORMAT CONVERSION & NORMALIZATION – PLOTTING

<https://deeptools.readthedocs.io/en/develop/>

Identifying transcription factors regulating reactivation from dormancy

- One high school student, found ~800 activated genes with motifs for a yeast transcription factor (TF). This is 30-fold higher than what has been seen in normal growth conditions.
- He further analyzed paired-end MNase-seq data and found the chromatin architecture was likely being remodeled at these sites
- Our lab has a lot of chromatin factor data, so he then re-analyzed the data with his gene lists and saw striking co-localizations!
- In the lab **we are testing his hypothesis** that this transcription factor candidate targets remodeling factors
- Tip: give students projects where they can take ownership of the ideas!





Virtual mentoring programs & the power of Galaxy in creating research experiences for all

- With Galaxy being so accessible and system agnostic, there are many opportunities for mentoring virtual research projects!
- No need to acquire university access to computing centers (sometimes this process can be difficult at places)
- Can get projects up and running quickly, important for short-term programs or courses
- A couple online mentoring programs include:
 - **Undergraduate Level:** National summer undergraduate research program (NSURP): <https://nsurp.org/>
 - **High School Level:** Athena women in STEM program: <https://www.athenabywistem.org/>