



A bioinformatics approach to identify DNA-binding factors at a specific genomic locus

Casey A. Schmidt¹, Lauren J. Hodkinson¹, H. Skye Comstra¹, and Leila E. Rieder

Emory University, Biology Department, 1510 Clifton Rd, Atlanta, GA, 30322, USA

Abstract

Research experiences provide numerous benefits for undergraduates. However, many students struggle to find a space in laboratories already at capacity. To alleviate this issue, many scientists are turning to bioinformatics as a way to include more undergraduates in their research programs. Bioinformatics research offers an alternative to wet-lab experiments that is free, safe, compatible with remote learning, and may be more accessible for students with disabilities. In this workshop, I will present a bioinformatics project that leverages publicly available datasets to discover novel proteins that target a genomic locus of interest. This approach uses the free, user-friendly bioinformatics platform Galaxy to map ChIP-seq datasets to a genome, which removes the code-writing and computing burden from students. I will guide participants through the process of finding a dataset, importing it into Galaxy, aligning to a genome, visualizing the results, and drawing conclusions. Both faculty and students directly benefit from bioinformatic research. Students can perform a candidate screen for novel transcription factors that target a genomic locus, and the results can seed future wet-lab experiments in a faculty member's lab. In addition, students gain not only basic bioinformatics knowledge, but also transferable skills, including hypothesis formation, database navigation, and primary literature experience. This project is flexible and can be expanded to analyze different types of high-throughput data or to investigate different genomic loci in any species. Furthermore, it can be deployed as a standalone research project for individual students, or as a CURE in a classroom setting.

Keywords: ChIP-seq, Galaxy, bioinformatics, transcription factor

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Correspondence to: Casey Schmidt, casey.schmidt@emory.edu and Leila Rieder, lrieder@emory.edu

About the Authors

Casey Schmidt is an IRACDA postdoctoral fellow at Emory University in the Biology Department.

Lauren Hodkinson is a graduate student at Emory University in the Genetics and Molecular Biology program.

Skye Comstra is a faculty member at Emory University in the Biology Department.

Leila Rieder is a faculty member at Emory University in the Biology Department.

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