BIOGRAPHICAL SKETCH

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NAME: Nathan C. Sheffield, PhD

eRA COMMONS USER NAME (credential, e.g., agency login): NSHEFF

POSITION TITLE: Assistant professor

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
Stanford University, Stanford, CA	Postdoc	08/2016	Computational Epigenomics
Center for Molecular Medicine, Vienna, Austria	Postdoc	12/2015	Computational Epigenomics
Duke University, Durham, NC	PhD	05/2013	Bioinformatics and Computational Biology
Brigham Young University, Provo, UT	BS	04/2008	Bioinformatics

A. Personal Statement

I am an assistant professor leading a group in computational biology. My research consists of applying molecular and computational methods to generate and analyze large-scale epigenomic data. In this process, I develop novel analytical approaches and implement open-source computational tools focused on specific biological questions. The general biological goal of my work is to understand the basic biology of gene regulation and epigenetics. I am interested in how DNA encodes regulatory networks to enable cellular differentiation, and how these regulatory systems break down in disease. To better understand normal and diseased gene regulation, I collect high-throughput genome-scale data in single cells and cell populations, and then harness the power of supercomputing, machine learning, and software engineering to answer questions about biological systems.

Publications to highlight:

Lawson JT, Smith JP, Bekiranov S, Garrett-Bakelman FE, and Sheffield NC. COCOA: coordinate covariation analysis of epigenetic heterogeneity. **2020**. *Genome Biology* 21. DOI: 10.1186/s13059-020-02139-4.

Sheffield NC, Pierron G, Klughammer J, Datlinger P, Schönegger A, Schuster M, Hadler J, Surdez D, Guillemot D, Lapouble E, Freneaux P, Champigneulle J, Bouvier R, Walder D, Ambros IM, Hutter C, Sorz E, Amaral AT, de Alava E, Schallmoser K, Strunk D, Rinner B, Liegl-Atzwanger B, Huppertz B, Leithner A, de Pinieux G, Terrier P, Laurence V, Michon J, Ladenstein R, Holter W, Windhager R, Dirksen U, Ambros PF, Delattre O, Kovar H, Bock C, and Tomazou EM. DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma. **2017**. *Nature Medicine* 23:386–395. PMCID:PMC5951283 DOI: 10.1038/nm.4273.

Tomazou EM, *Sheffield NC, Schmidl C, Schuster M, Schonegger A, Datlinger P, Kubicek S, Bock C, and Kovar H. Epigenome mapping reveals distinct modes of gene regulation and widespread enhancer reprogramming by the oncogenic fusion protein EWS-FLI1. **2015**. *Cell Reports* 10:1082–1095. PMCID:PMC4542316 DOI: 10.1016/j.celrep.2015.01.042. *co-first author.

B. Positions, Scientific Appointments, and Honors

Positions and Employment

2020-pres Assistant Professor of Data Science, University of Virginia, Charlottesville, VA
2016-pres Affiliated Faculty Member, Cancer Center, University of Virginia, Charlottesville, VA
2016-pres Affiliated Faculty Member, Child Health Research Center, University of Virginia, Charlottesville, VA
2016-pres Assistant Professor of Biomedical Engineering, Public Health Sciences, and Biochemistry and Molecular Genetics, University of Virginia, Charlottesville, VA
2016-pres Assistant Professor, Center for Public Health Genomics, University of Virginia, Charlottesville, VA

Honors and Awards

2014 HFSP Long-term Postdoctoral Fellowship, Human Frontier Science Program
2014 EMBO Long-term Postdoctoral Fellowship, European Molecular Biology Organization
2011 Nordic Research Opportunity Award, NSF and Research Council of Norway ($15,000)
2010 NSF Graduate Research Fellowship ($121,000)
2010 Duke Graduate School Teaching Mini-grant (for Scientific Writing Resource) ($2,000)
2010 Duke Primate Genomics Initiative Summer Fellowship ($10,000)
2008 James B. Duke Graduate Fellowship, Duke University ($19,000)
2008 Undergraduate Research ORCA Grant, BYU Office of Research and Creative Activities ($1,800)
2002 Heritage Scholarship, Brigham Young University (4 years full tuition)

C. Contributions to Science

H-index: 25. ORCID: 0000-0001-5643-4068.

1. Profiling and analyzing cancer epigenomes

One of my major contributions has been in cancer epigenomics. In my first major study in Ewing sarcoma, I led the computational analysis of a multi-omic dataset profiling 7 histone marks, RNA-seq, DNA methylation, and ATAC-seq of Ewing sarcoma (Epigenome mapping reveals distinct modes of gene regulation and widespread enhancer reprogramming by the oncogenic fusion protein EWS-FLI1). I also led a follow-up study of DNA methylation in a large cohort of Ewing sarcoma patient samples (DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma). Finally, I have contributed to other projects in other cancers, including Glioblastoma, breast cancer (COCOA: coordinate covariation analysis of epigenetic heterogeneity) and cell-to-cell cancer heterogeneity. As I have started my own group, I have extended these general analytical approaches to other cancers, including development of new approaches to assess breast cancer.

Lawson JT, Smith JP, Bekiranov S, Garrett-Bakelman FE, and Sheffield NC. COCOA: coordinate covariation analysis of epigenetic heterogeneity. **2020**. *Genome Biology* 21. DOI: 10.1186/s13059-020-02139-4.

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