

Mallory A Freeberg, Ph.D.

CONTACT INFORMATION

Wellcome Trust Genome Campus
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EDUCATION

University of Michigan, Ann Arbor, MI USA
Department of Computational Medicine and Bioinformatics
Ph.D. Bioinformatics, May 2015
Dissertation: Computational analysis of the post-transcriptional gene regulatory network

Saint Vincent College, Latrobe, PA USA
Herbert M. Boyer School of Natural Science, Mathematics, and Computing
B.S. Bioinformatics, May 2009
Dissertation: Functional annotation of non-coding elements in the *Amphioxus* genome

RESEARCH AND WORK EXPERIENCE

EMBL European Bioinformatics Institute, Hinxton, Cambridgeshire UK
Project Lead, European Genome-phenome Archive Aug 2019 - present
Coordinating archive and distribution of 500,000 UK Biobank whole genome sequences

Senior Bioinformatician, Human Cell Atlas Data Coordination Platform Oct 2018 - Jul 2019
Developed metadata standards for cellular-resolution genomics data and managed data ingestion

Bioinformatician, Human Cell Atlas Data Coordination Platform Oct 2017 - Sep 2018
Developed metadata standards for cellular-resolution genomics data and performed data ingestion

Johns Hopkins University, Baltimore, MD USA
Team Member, The Galaxy Project Jan 2017 - Sep 2017
Developed workflows, training materials, and best practices for transcriptomics & genomics research

Postdoctoral Research Fellow, Department of Biology Jun 2015 - Sep 2017
Investigated post-transcriptional gene regulatory networks and developed nanopore direct RNA sequencing protocols

PUBLICATIONS

Füllgrabe A, George N, Green M, Nejad P, Aronow B, Clarke L, Fexova SK, Fischer C, **Freeberg MA**, Huerta L, Morrison N, Scheuermann RH, Taylor D, Vasilevsky N, Gehlenborg N, Marioni J, Teichmann S, Brazma A, Papatheodorou I. (2019) Guidelines for reporting single-cell RNA-Seq experiments. *arXiv* (preprint) 1910.14623v1.

Fuller GG, Han T, **Freeberg MA**, Moresco JJ, Niaki AG, Roach NP, Yates III JR, Myong S, Kim JK. (2020) RNA promotes phase separation of glycolysis enzymes into yeast G bodies in hypoxia. *eLife* 2020;9:e48480. DOI:10.7554/eLife.48480 (*bioRxiv* preprint DOI:10.1101/638650)

Batut B, Hiltemann S, Bagnacani A, Baker D, Bhardwaj V, Blank C, Bretaudeau A, Brillet-Guéguen L, Cech M, Chilton J, Clements D, Doppelt-Azeroual O, Erxleben A, **Freeberg MA**, *et al.* (2018) Community-Driven Data Analysis Training for Biology. *Cell Syst* 6(6):752-758. DOI:10.1016/j.cels.2018.05.012 (*bioRxiv* preprint DOI:10.1101/225680)

Lariviere D, Mei H, **Freeberg MA**, Taylor J, Nekrutenko A. (2018) Understanding trivial challenges of microbial genomics: An assembly example. *bioRxiv* (preprint) 347625. DOI:10.1101/347625

Gruning B, Dale R, Sjodin A, Chapman BA, Rowe J, Tomkins-Tinch CH, Valieris R, Koster

- J, **The Bioconda Team**. (2018) Bioconda: sustainable and comprehensive software distribution for the life sciences. *Nat Meth* 15:475-6. DOI:10.1038/s41592-018-0046-7 (*bioRxiv* preprint DOI:10.1101/207092)
- Malhotra S, **Freeberg MA**, Winans SJ, Taylor J, Beemon KL. (2018) A Novel Long Non-Coding RNA in the *hTERT* Promoter Region Regulates *hTERT* Expression. *Non-Coding RNA* 4(1). DOI:10.3390/ncrna4010001
- Hong S, **Freeberg MA***, Han T*, Kamath A*, Yao Y, Fukuda T, Suzuki T, Kim JK, and Inoki K. (2017) LARP-1 functions as a molecular switch for mTORC1-mediated translation of an essential class of mRNAs. *eLife* 6:e25237. DOI:10.7554/eLife.25237
- Jin M*, Fuller GG*, Han T*, Yao Y, Alessi AF, **Freeberg MA**, Roach NP, Moresco JJ, Karnovsky A, Baba M, Yates JR III, Gitler AD, Inoki K, Klionsky DJ, Kim JK. (2017) Glycolytic Enzymes Coalesce in G Bodies Under Hypoxic Stress. *Cell Reports* 20(4):895-908. DOI:10.1016/j.celrep.2017.06.082
- Weiser NE, Yang DX, Feng S, Kalinava N, Brown KC, Khanikar J, **Freeberg MA**, Snyder MJ, Csankovszki G, Chan RC, Gu SG, Montgomery TA, Jacobsen SE, and Kim JK. (2017) MORC-1 Integrates Nuclear RNAi and Transgenerational Chromatin Architecture to Promote Germline Immortality. *Dev Cell* 41(4):408-23. DOI:10.1016/j.devcel.2017.04.023
- Turaga N, **Freeberg MA**, Baker D, Chilton J, The Galaxy Team, Nekrutenko A, and Taylor J. (2016) A guide and best practices for R/Bioconductor tool integration in Galaxy [version 1; referees: 1 approved, 1 approved with reservations]. *F1000Research* 5:2757. DOI:10.12688/f1000research.9821.1
- Freeberg MA** and Kim JK. (2016) Mapping the Transcriptome-Wide Landscape of RBP Binding Sites using gPAR-CLIP-seq: Bioinformatic Analysis. Invited chapter in *Methods in Mol Biol* 1361(6):91-104. DOI:10.1007/978-1-4939-3079-1
- Alessi AF*, Khivansara V*, Han T*, **Freeberg MA**, Moresco JJ, Tu PG, Montoye E, Yates JR III, Karp X, and Kim JK. (2015) Casein kinase II promotes target silencing by miRISC through direct phosphorylation of the DEAD-box RNA helicase CGH-1. *PNAS* 112(49):E6789. DOI:10.1073/pnas.1509499112
- Jin M, He D, Backues SK, **Freeberg MA**, Liu X, Kim JK, and Klionsky DJ. (2014) Transcriptional regulation by Pho23 modulates the frequency of autophagosome formation. *Curr Biol* 24(12):1314-22. DOI:10.1016/j.cub.2014.04.048
- Freeberg MA***, Han T*, Moresco JJ, Kong A, Yang Y, Lu Z, Yates JR III, and Kim JK. (2013) Pervasive and dynamic protein binding sites on the mRNA transcriptome in *Saccharomyces cerevisiae*. *Gen Biol* 14(2):R13. DOI:10.1186/gb-2013-14-2-r13
- Billi AC*, **Freeberg MA***, Day AM, Chun SY, Khivansara V, and Kim JK. (2013) A conserved upstream motif drives autonomous, germline-enriched expression of *Caenorhabditis elegans* piRNAs. *PLoS Genet* 9(3):e1003392. DOI:10.1371/journal.pgen.1003392
- Billi AC, **Freeberg MA**, and Kim JK. (2012) piRNAs and siRNAs collaborate in *Caenorhabditis elegans* genome defense. *Gen Biol* 13(7):164. DOI:10.1186/gb-2012-13-7-164
- Billi AC, Alessi AF, Khivansara V, Han T, **Freeberg M**, Mitani S, and Kim JK. (2012) The *Caenorhabditis elegans* HEN1 ortholog, HENN-1, methylates and stabilizes select subclasses of germline small RNAs. *PLoS Genet* 8(4):e1002617. DOI:10.1371/journal.pgen.1002617

*equal contribution

INVITED TALKS

Freeberg MA, Yordanova G, and Tickle T. How to engage with the Data Coordination Platform. Human Cell Atlas General Meeting; May 2019; Toyko, Japan

Clarke L, **Freeberg MA**, and Yordonova G. Human Cell Atlas Data Coordination Platform. Pilot Projects for a Human Cell Atlas Europe Retreat; Aug 2018; Stockholm, Sweden

Clarke L, **Freeberg MA**, O'Connor B, Osborn K, and Tickle T. Human Cell Atlas Data Coordination Platform: Status Update. Human Cell Atlas General Meeting; Mar 2018; Hinxton, UK

Freeberg MA. Single molecule RNA sequencing of the *C. elegans* transcriptome. Molecular Biosystems Conference on Eukaryotic Gene Regulation and Functional Genomics; Sep 2017; Puerto Varas, Chile. Sponsored by Oxford Nanopore Technologies

Freeberg MA. From high school to postdoc: lessons from a decade of bioinformatics education. Great Lakes Bioinformatics Conference; May 2017; University of Illinois at Chicago, Chicago, IL. DOI:10.7490/f1000research.1114161.1

Freeberg MA. A novel pipeline for identifying transcriptome-wide binding sites of RNA-binding proteins from PAR-CLIP sequencing data. NCIBI Tools and Technology Seminar Series; May 2013; University of Michigan, Ann Arbor, MI

CONFERENCE TALKS AND WORKSHOPS

Freeberg MA. The Data Coordination Platform: Making the Human Cell Atlas data easily accessible. The Biology of Genomes; May 2018; Cold Spring Harbor, NY (Poster)

Freeberg MA and Taylor J. Approaches for small RNA-seq in Galaxy [version 1; not peer reviewed]. Galaxy Community Conference; Jun 2017; Montpellier, France (Talk) *F1000Research* 6:1137. DOI:10.7490/f1000research.1114423.1

Freeberg MA and Heydarian M. RNAseq analysis in Galaxy. Galaxy Community Conference; Jun 2017; Montpellier, France (Workshop)

Freeberg MA and Heydarian M. Introduction to Genomic Data Analysis with Galaxy. U. S. Food and Drug Administration; Mar 2017; Silver Spring, MD, USA (Workshop)

Freeberg MA and Heydarian M. Galaxy to Genomics using NGS Data. 13th KOGO Winter Symposium; Feb 2017; Hongcheon, South Korea (Workshop)

Freeberg MA and Turaga N. Bioinformagic: Marrying Bioconductor and Galaxy. Galaxy Community Conference; Jun 2016; Bloomington, IN, USA (Workshop)

Freeberg MA. Transcriptome sequencing in nematodes. Oxford Nanopore Technologies London Calling; May 2016; London, UK (Poster)

Freeberg MA and Taylor J. Probabilistic modeling of protein:RNA interaction data identifies functional Transcript States. CSHL Genome Informatics; Oct 2015; Cold Spring Harbor, NY (Poster)

Freeberg MA. Identification and characterization of the mRNA-binding proteome *in vivo* in *Saccharomyces cerevisiae*. CSHL Systems Biology: Global Regulation of Gene Expression; Mar 2014; Cold Spring Harbor, NY (Talk)

Freeberg MA, Billi AC, and Kim JK. Germline expression, inheritance, and genomic characteristics of *Caenorhabditis elegans* 21U-RNAs. 18th International *C. elegans* Meeting; Jun 2011; Los Angeles, CA (Poster)

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| FUNDING AND AWARDS | XSEDE Educational Computational Resource Allocation (2017) | |
| | XSEDE Startup Computational Resource Allocation (2017) | |
| | Rackham Predoctoral Fellowship (2013-2014) | |
| | NSF Open Data IGERT Fellowship (2010-2013) | |
| | Rackham Graduate Student Research Grant (2010, 2012) | |
| | NIH Bioinformatics Training Grant (2009-2010) | |
| COMPUTING AND DATA ANALYSIS SKILLS | Operating Systems: MacOS X, Linux/Unix | |
| | Languages: Python, Perl, SQL, Unix shell | |
| | Statistical Packages: R, Bioconductor | |
| | Applications: JSON/XML, GitHub, L ^A T _E X, Galaxy, NGS analysis tools and methodologies | |
| TEACHING AND MENTORING EXPERIENCE | Open Life Science , Cambridge, UK | Aug 2020 - Dec 2020 |
| | Mentor for 16-week personal mentorship and cohort-based training program | |
| | Responsibilities: Mentoring two OLS-2 cohort participants on open practices | |
| | STEM Ambassador , Cambridge, UK | Jan 2018 - Present |
| | Ambassador for STEM-related volunteer program | |
| | Responsibilities: Supporting various public engagement activities including giving talks, demonstrating science experiments, providing career guidance | |
| | Johns Hopkins University , Baltimore, MD USA | Jan 2017 - May 2017 |
| | Instructor for Advanced Academic Program online course: <i>Bioinformatics: Tools for Genome Analysis</i> | |
| | Responsibilities: Created course materials, held office hours, graded assignments | |
| | Sisters Circle , Baltimore, MD USA | May 2015 - Sep 2017 |
| | Mentor/tutor for middle school girls | |
| | Responsibilities: Co-led weekly after-school sessions, tutored math, did 1-on-1 mentoring | |
| | University of Michigan , Ann Arbor, MI USA | Jul 2014 - Aug 2014 |
| | Mentor for high school student | |
| | Responsibilities: Designed bioinformatics/genomics research project, taught shell/perl programming | |