Mallory A Freeberg, Ph.D.

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PROFESSIONAL EXPERIENCE

EMBL European Bioinformatics Institute, Hinxton, UK

Coordinator, European Genome-phenome Archive   Jun 2021 - present
- Manage day-to-day team operations to provide high-quality production services
- Engage with external partners and stakeholders to ensure data submission, discovery, and distribution services align with community standards
- Contribute expertise to help establish the Federated EGA network for transnational discovery of and access to sensitive human data

UK Biobank Project Lead, European Genome-phenome Archive   Aug 2019 - May 2021
- Coordinated data flow to archive 500,000 whole human genomes (12PB of data)
- Led distribution of 4PB of data to cloud-based analysis platform

Senior Bioinformatician, Human Cell Atlas Data Coordination Platform   Oct 2018 - Jul 2019
- Managed data wrangling tasks and priorities for six-person team across two institutions
- Represented HCA DCP by presenting at three international HCA meetings

Bioinformatician, Human Cell Atlas Data Coordination Platform   Oct 2017 - Sep 2018
- Performed curation and ingestion of three flagship HCA datasets
- Developed HCA metadata standard for cellular-resolution transcriptomics data (publication)

Johns Hopkins University, Baltimore, MD USA

Trainer, Galaxy Training Network, The Galaxy Project   Jan 2017 - Sep 2017
- Designed and delivered seven Galaxy training workshops in three countries (publication)
- Created training materials and computational workflows to support reproducible transcriptomics research (contributions)

Postdoctoral Research Fellow, Department of Biology   Jun 2015 - Sep 2017
- Investigated post-transcriptional gene regulatory networks using neural networks
- Piloted Oxford Nanopore direct RNA sequencing protocols to catalog transcriptomes

EDUCATION

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

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

TRAINING COURSES

EMBL-EBI Storytelling Workshop	Jul 2021
EMBL-EBI Managing Managers Course	Apr 2021
EMBL-EBI Moving into Management Course	Sep 2020 - Oct 2020
Talented Women's Impact Programme	Sep 2019 - Jan 2020
EICAT Complementary Scientific Skills Training - Scientific Project Management	Sep 2019
Handling Conflict and Difficult Conversations	Sep 2018

SELECTED INVITED TALKS	**Freeberg MA**. FAIR principles and promoting openness in the life sciences. *NIHR Statistics Group Workshop*; Feb 2022; Virtual
	Freeberg MA. The EGA Metadata Model. *GHGA Workshop on Metadata in Biomedical Genome Research*; Jun 2021; Virtual
	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
SELECTED PUBLICATIONS	**Freeberg MA**, Fromont L., D'Altri T, Romero AF, Ciges JI, Jene A, Kerry G, Moldes M, Ariosa R, Bahena S, *et al.* (2021) The European Genome-phenome Archive in 2021. *Nucleic Acids Res*, 2021. DOI:10.1093/nar/gkab1059
	Rehm HL, Page AJH, Smith L, Adams JB, Alterovitz G, Babb LJ, Barkley MP, Baudis M, Beauvais MJS, Beck T, *et al.* (2021) GA4GH: International policies and standards for data sharing across genomic research and healthcare. *Cell Genomics* 1. DOI:10.1016/j.xgen.2021.100029
	Lawson J, Cabili MN, Kerry G, Boughtwood T, Thorogood A, Alper P, Bowers SR, Boyles RR, Brookes AJ, Brush M, *et al.* (2021) The Data Use Ontology to streamline responsible access to human biomedical datasets. *Cell Genomics* 1. DOI:10.1016/j.xgen.2021.100028
	Füllgrabe A, George N, Green M, Nejad P, Aronow B, Fexova SK, Fischer C, **Freeberg MA**, Huerta L, Morrison N, Scheuermann RH, Taylor D, Vasilevsky N, Clarke L, Gehlenborg N, Kent J, Marioni J, Teichmann S, Brazma A, Papatheodorou I. (2020) Guidelines for reporting single-cell RNA-seq experiments. *Nat Biotechnol* 38:1384-6. DOI:10.1038/s41587-020-00744-z (*arXiv* preprint DOI:1910.14623v1)
	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)
TEACHING AND MENTORING EXPERIENCE	**Open Life Science**, Cambridge, UK Jul 2020 - Present Mentor, 16-week personal mentorship and cohort-based training program Responsibilities: Mentoring participants on open science practices
	STEM Ambassador, Cambridge, UK Jan 2018 - Present Ambassador, STEM-related public engagment program Responsibilities: Giving talks, demonstrating science experiments, providing career guidance
	Johns Hopkins University, Baltimore, MD USA Jan 2017 - May 2017 Instructor, Advanced Academic Program online course: *Bioinformatics: Tools for Genome Analysis* Responsibilities: Created course materials, held office hours, graded assignments
CONFERENCES AND WORKSHOPS	Bacon W, Morgan S, Welter D, and **Freeberg MA**. Managing single cell transcriptomics data. EMBL Course; Jul 2019; Cambridge, UK (Workshop)

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. 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 (Talk)

Freeberg MA and Taylor J. Approaches for small RNA-seq in Galaxy. Galaxy Community Conference; Jun 2017; Montpellier, France (Talk) 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)

OTHER PUBLICATIONS

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)

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)

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

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 Coa-

lesce 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

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