

Korin Eckstrom

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Experience

Genentech, Remote — *Bioinformatics Programmer/Analyst, Scientific Insights Engineering*

January 2022 – Present

Bioinformatics analyst/Data Engineer within the Early Research & Development arm of Genentech in the Computational Workflows team. Developed and maintained production bioinformatics workflows for analysis of clinical trial, preclinical, and safety assessment data, from sample registration to final deliverable. Involved in cloud migration efforts & strategy, benchmarking of new tools and workflows, and development of visualization applications for company-wide use.

- Maintained and developed new features for genomics workflows of various NGS types at scale, including WES, cf/ctDNA, and bulk-RNASeq
- Developed R package and accompanying tools for interacting with variant calling data, improving data accessibility and standardization for stakeholders.
- Benchmarked new tools and workflows including copy number alterations, ctDNA assays, and single-cell RNAseq to evaluate performance and utility to research teams
- Led technical documentation efforts and provided trainings for cross-functional teams on bioinformatics best practices and usage of high-dimensional omics outputs
- Developed data class & metadata standards shared across the organization for multi-omic data storage and analysis
- Developed and maintained Nextflow, WDL, and Snakemake workflows for HPC + AWS deployment, including versioned containers (Docker/Singularity)
- Contributed to codebase and documentation in GitLab & GitHub for data usage, RShiny applications, and more
- Led team Jira project and improved processes through API-based automation, streamlining tasks and issue resolution for decreased time from data ingestion to final data products

Skills include:

- R, Bash, Git, Python
- Nextflow, WDL, Snakemake
- AWS suite including Omics, Batch, ECR, Step & Lambda functions
- Jira
- Docker & Singularity
- CI/CD, FAIR Data Standards, Regulatory Documentation

University of Vermont, Burlington, VT — *Researcher/Analyst: Bioinformatics*

September 2018 - January 2022

Bioinformatics analyst in the Bioinformatics Shared Resource branch of VIGR and Colgate Labs within the Larner College of Medicine, serving stakeholders in colleges across the university at large. Responsible for assisting in design, data management & delivery, and analysis for customers of the VIGR core facility, partners at numerous medical centers, and Vermont state entities. Projects include metagenomics, both single-cell and bulk RNAseq, targeted amplicon analysis, long-read sequencing applications, genome assembly, and more. Assistant instructor in courses taught by VIGR faculty, including MMG 231 and 232.

- Developed and implemented pipelines for metagenomics & metatranscriptomics, single cell RNAseq, structural variant detection, and more leading to an increase in revenue year-over-year
- Lead bioinformatician on multi-cohort trials focused on the gut microbiome associated with bacterial infections and vaccination
- Led development of bioinformatics analysis of Oxford Nanopore data within the core
- Managed data & analysis for clinical applications, including COVID-19 sequence analysis for the Vermont Department of Health and the University of Vermont Medical Center
- Experience analyzing sequencing data from a variety of platforms including Illumina, Oxford Nanopore, and PacBio
- Oversee trainee education (15+ students and faculty members) and analyses as part of both VIGR and as an instructor in the Microbiology & Molecular Genetics department
- Host webinars for users on new equipment, methodologies, and data management standards

University of Vermont, Burlington, VT — *Bioinformatician/Lab Technician*

March 2018 - September 2018

Responsible for the bioinformatic & statistical analysis for a variety of projects with the Wargo Lab, including transcriptomics, whole genome assembly & annotation, and modeling of complex microbial interactions.

- Created and managed in-house bioinformatic analyses for lab members and collaborators
- Trained interns and researchers in bioinformatic analyses and statistical modeling
- Produced genomic resources for novel bacterial species from culturing to genome assemblies

Education

University of Vermont, Burlington, VT — *MSc Animal and Veterinary Sciences*

Focused on using cutting edge sequencing technologies and modeling to address issues in agriculture, such as animal health and consumer product safety. Managed and created NGS pipelines for the lab including MHC Class 1 genotyping and shotgun metagenomic analyses. Experience in a wide variety of bench skills including cell culture, DNA extraction, PCR, immunologic assays such as ELISA/ELISpot, large and small animal handling, and more. Thesis: Evaluating The Resistome And Microbial Composition During Food Waste Feeding And Composting On A Vermont Poultry Farm

University of Vermont, Burlington, VT — *BSc Animal and Veterinary Sciences*

Concentration in Pre-Veterinary Medicine and dual-graduate of the Honors College. Thesis: Next-generation Sequencing in the Identification of Bovine Major Histocompatibility Complex (MHC) Class I Molecules: A Comparison of Platforms

Awards

NERLSCD/MAD SSCI Travel Award 2019

UVM CALS Mini Grant 2017

Northeast SARE Research Grant 2016-2017

GNE16-117 Table to Farm: Using Shotgun Metagenomics to Quantify Antibiotic Resistance on Farms Feeding Food Scraps to Laying Hens

NOFA Winter Conference Scholarship 2016

Distinguished Undergraduate Research Award 2015

Publications

1. Lactobacillaceae differentially impact butyrate-producing gut microbiota to drive CNS autoimmunity. Theresa Montgomery, Eamonn Heney, **Korin Eckstrom**, and Dmitry Kremmentsov. Gut Microbes, 2024. Jan-Dec;16(1):2418415. doi: 10.1080/19490976.2024.2418415
2. Hybrid Illumina-Nanopore assembly improves identification of multilocus sequence types and antimicrobial resistance genes of Staphylococcus aureus isolated from Vermont dairy farms: comparison to Illumina-only and R9.4.1 nanopore-only assemblies. Ashma Chakrawarti, **Korin Eckstrom**, Pheobe Laaguiby and John W. Barlow. Access Microbiology, Vol. 6 Issue 3, March 2024. <https://doi.org/10.1099/acmi.0.000766.v3>
3. Determining the impact of vaccination on SARS-CoV-2 RT-PCR cycle threshold values and infectious viral titers. Katherine L Peterson, Julia P Snyder, Hannah W Despres, Madaline M Schmidt, **Korin M Eckstrom**, Allison L Unger, Marya P Carmolli, Joseph L Sevigny, David J Shirley, Julie A Dragon, W. Kelley Thomas, Emily A Bruce, Jessica W Crothers. Access Microbiology, 2023 <https://doi.org/10.1099/acmi.0.000597.v1>
4. Small regulatory RNAs are mediators of the Streptococcus mutans SloR regulon Drummond I, DePaolo A, Krieger M, Driscoll H, **Eckstrom K**, Spatafora G. Journal of Bacteriology Vol. 205, No. 9 2023. <https://doi.org/10.1128/jb.00172-23>
5. Human alveolar hydrogels promote morphological and transcriptional differentiation in iPSC-derived alveolar type 2 epithelial cells. Hoffman ET, Uriarte JJ, Uhl FE, **Eckstrom K**, Tanneberger AE, Becker C, Moulin C, Asarian L, Ikonomou L, Kotton DN, Weiss DJ. Scientific Reports 13, 12057 (2023). <https://doi.org/10.1038/s41598-023-37685-x>
6. Creatine utilization as a sole nitrogen source in Pseudomonas putida KT2440 is transcriptionally regulated by CahR. Lauren A. Hinkel, Graham G. Willsey, Sean M. Lenahan, **Korin Eckstrom**, Kristin C. Schutz, Matthew J. Wargo. bioRxiv doi:10.1101/2021.11.02.466972

7. Molecular Characterization of Increased Amplicon Length in SARS-CoV-2 Reverse Transcription Loop-Mediated Isothermal Amplification Assays. Tighe SW, Hayden AF, Kuentzel ML, **Eckstrom KM**, Foox J, Vellone DL, Finstaad KH, Laaguiby PK, Hoffman JJ, Chittur SV. *Journal of Biomolecular Techniques*;00:1-7 2022. doi: 10.7171/jbt.21-3203-015
8. The Kidney-Associated Microbiome of Wild-Caught *Artibeus* spp. in Grenada, West Indies. Ramos-Nino ME, Fitzpatrick DM, **Eckstrom KM**, Tighe S, Dragon JA, Cheetham S. *Animals (Basel)*. 2021 May 27;11(6):1571. doi: 10.3390/ani11061571. PMID: 34072244
9. Immunotranscriptomic profiling the acute and clearance phases of a human challenge dengue virus serotype 2 infection model. Hanley JP, Tu HA, Dragon JA, Dickson DM, Rio-Guerra RD, Tighe SW, **Eckstrom KM**, Selig N, Scarpino SV, Whitehead SS, Durbin AP, Pierce KK, Kirkpatrick BD, Rizzo DM, Fietze S, Diehl SA. *Nat Commun*. 2021 May 24;12(1):3054. doi: 10.1038/s41467-021-22930-6. PMID: 34031380
10. Facility-dependent metabolic phenotype and gut bacterial composition in CD-1 mice from a single vendor: A brief report. Unger AL, **Eckstrom K**, Jetton TL, Kraft J. *PLoS One*. 2020 Sep 21;15(9):e0238893. doi: 10.1371/journal.pone.0238893. eCollection 2020. PMID: 32956361
11. Ramos-Nino ME, Fitzpatrick DM, **Eckstrom KM**, Tighe S, Hattaway LM, Hsueh AN, Stone DM, Dragon JA, Cheetham S. Metagenomic analysis of *Aedes aegypti* and *Culex quinquefasciatus* mosquitoes from Grenada, West Indies. *PLoS One*. 2020;15(4):e0231047. doi: 10.1371/journal.pone.0231047. eCollection 2020. PubMed PMID: 32282857; PubMed Central PMCID: PMC7153883.
12. Ramos-Nino ME, Fitzpatrick DM, Tighe S, **Eckstrom KM**, Hattaway LM, Hsueh AN, Stone DM, Dragon J, Cheetham S. High prevalence of Phasi Charoen-like virus from wild-caught *Aedes aegypti* in Grenada, W.I. as revealed by metagenomic analysis. *PLoS One*. 2020;15(1):e0227998. doi: 10.1371/journal.pone.0227998. eCollection 2020. PubMed PMID: 32004323; PubMed Central PMCID: PMC6993974.
13. Thompson AF, English EL, Nock AM, Willsey GG, **Eckstrom K**, Cairns B, Bavelock M, Tighe SW, Foote A, Shulman H, Pericleous A, Gupta S, Kadouri DE, Wargo MJ. Characterizing species interactions that contribute to biofilm formation in a multispecies model of a potable water bacterial community. *Microbiology*. 2020 Jan;166(1):34-43. doi: 10.1099/mic.0.000849. Epub 2019 Oct 4. PubMed PMID: 31585061; PubMed Central PMCID: PMC7137775.
14. Unger AL, **Eckstrom K**, Jetton TL, Kraft J. Colonic bacterial composition is sex-specific in aged CD-1 mice fed diets varying in fat quality. *PLoS One*. 2019;14(12):e0226635. doi: 10.1371/journal.pone.0226635. eCollection 2019. PubMed PMID: 31851713; PubMed Central PMCID: PMC6919604.
15. **Eckstrom K**, Barlow JW. Resistome metagenomics from plate to farm: The resistome and microbial composition during food waste feeding and composting on a Vermont poultry farm. *PLoS One*. 2019;14(11):e0219807. doi: 10.1371/journal.pone.0219807. eCollection 2019. PubMed PMID: 31751342; PubMed Central PMCID: PMC6874062.
16. Sitt T, Kenney M, Barrera J, Pandya M, **Eckstrom K**, Warner M, Pacheco JM, LaRocco M, Palarea-Albaladejo J, Brake D, Rieder E, Arzt J, Barlow JW, Golde WT. Duration of protection and humoral immunity induced by an adenovirus-vectored subunit vaccine for foot-and-mouth disease (FMD) in Holstein steers. *Vaccine*. 2019 Sep 30;37(42):6221-6231. doi: 10.1016/j.vaccine.2019.08.017. Epub 2019 Sep 5. PubMed PMID: 31493951.
17. Willsey GG, **Eckstrom K**, LaBauve AE, Hinkel LA, Schutz K, Meagher RJ, LiPuma JJ, Wargo MJ. *Stenotrophomonas maltophilia* Differential Gene Expression in Synthetic Cystic Fibrosis Sputum Reveals Shared and Cystic Fibrosis Strain-Specific Responses to the Sputum Environment. *J*

Bacteriol. 2019 Aug 1;201(15). doi: 10.1128/JB.00074-19. Print 2019 Aug 1. PubMed PMID: 31109991; PubMed Central PMCID: PMC6620408.

18. GG Willsey, L Hinkel, **K Eckstrom**, J LiPuma, MJ Wargo. Conserved *Stenotrophomonas maltophilia* responses to artificial sputum and characterization of genes required for growth on mucin. 2018 53 (308-309) Pediatric Pulmonology, Wiley.
19. **Eckstrom K**, Willsey GG, LiPuma JJ, Wargo MJ. Draft Genome Sequences of Two Cystic Fibrosis Strains of *Stenotrophomonas maltophilia*, AU30115 and AU32848. Microbiol Resour Announc. 2018 Sep;7(11). doi: 10.1128/MRA.01137-18. eCollection 2018 Sep. PubMed PMID: 30533649; PubMed Central PMCID: PMC6256672.

Abstracts

1. Case report and genomic analysis of a virulent *P. wickerhamii* isolate causing cutaneous protothecosis in a patient using topical steroids: Unique presentation of a rare pathogen. Matthew S., Karamatullah Danyal, Sean Bullis, **Korin Eckstrom**, Anne Stowman, Jessica Crothers. College of American Pathologists 2021
2. Comparison of Whole Genome Sequencing with conventional methods for strain typing and antimicrobial resistance of *Staphylococcus aureus* isolated from cheese making dairy farms. Ashma Chakrawarti, **Korin Eckstrom**, Pheobe Laaguiby, Robert Mugabi, Ariela Burke, John W. Barlow. ASM World Microbe Forum 2021
3. Gut commensal *Lactobacillus reuteri* exacerbates CNS autoimmunity in a dietary tryptophan-dependent manner. Theresa L. Montgomery, **Korin Eckstrom**, Axel Künstner, Josephine J. Kennedy, Hauke Busch, Matthew J. Wargo, Dmitry N. Kremmentsov. AAI Immunology 2021
4. Analysis of midgut microbiome diversity and *Borrellia* presence within *Ixodes scapularis* ticks sampled from Vermont Farms. Sean T. Quigley and **Korin Eckstrom**. University of Vermont Student Research Conference 2019
5. Primary Dengue Serotype 2 Infection in Humans Imprints a Blood Transcriptomic Profile After Virus Clearance. Diehl, S. A., Hanley, J., **Eckstrom, K.**, Dickson, D. M., Selig, N., Whitehead, S. S., ... & Rizzo, D. Journal of Tropical Medicine and Hygiene 2019

Invited Talks

National

Introduction to Oxford Nanopore Bioinformatics

ABRF | 2020 | Virtual

A Table to Farm Approach to Food Safety: Resistome, microbiome, and virulence characterization of composted food scraps and agricultural products in a laying poultry operation

Soil Metagenomics Argonne National Laboratories | 2017 | Lemont, IL

Machine Learning Tools for Predicting Sequence Type using MLST Isolate Databases

ASM Microbe | 2017 | New Orleans, LA

Regional

Genomic Technologies: Best Practices for Core Centers

NERLSCD | 2019 | Philadelphia, PA

Presentations & Lectures

Analysis of Single Cell Data: Assays, Methods, and Requirements

VIGR Webinar Series | 2020

Oxford Nanopore Technologies with the GridION MK5: Long Read Sequencing Analysis

VIGR Webinar Series | 2020

New Paradigms of Campylobacter Persistence and Transmission in Young Children in Low-and Middle-Income Countries

Bill & Melinda Gates Foundation Campylobacter Convening | UVA | 2019

Bioinformatics & Bacteria

MMG Department Retreat | 2019

Molecular Diagnostics & Next Generation Techniques for Exploring the 'Dark Matter' of Disease

ASCI 192 | 2016

Evaluating the Use of Illumina MiSeq in Bovine MHC Class I Amplicon Sequencing

ASCI Departmental Seminar | 2016

Teaching Experience

2020 - 2021	Assistant Instructor	MMG 231 Bioinformatics & Data Analysis
2020	Assistant Instructor	MMG 232 Advanced Bioinformatics
2016 - 2017	Teaching Assistant	ASCI 141 Anatomy and Physiology
2016	Teaching Assistant	ASCI 110 Animal Nutrition, Metabolism, & Feeding
2015	Teaching Assistant	ASCI 001 Introduction to Animal Science
2014	Teaching Assistant	PSS 003 Coffee Ecologies & Livelihoods

Societies & Memberships

Association of Biomolecular Resource Facilities (ABRF)

2019-2022

Northern New England Clinical & Translational Research Network (NNE-CTR)

2019-2022

American Society for Microbiology

2017-2019