

Chris Dean

PHD CANDIDATE

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Background

I am a bioinformatician with interdisciplinary training in computer science, epidemiology, microbiology and statistics. I am passionate about utilizing this diverse skillset to derive meaning from biological data sets originating in human and animal populations.

Education

Metro State University of Denver

BA PSYCHOLOGY

Denver, Colorado

2013

Colorado State University

BS COMPUTER SCIENCE

Fort Collins, Colorado

2015

University of Minnesota

PHD BIOINFORMATICS

Minneapolis, Minnesota

2022

Work Experience

Canomiks

RESEARCH SCIENTIST INTERN: UTILIZED COMPUTATIONAL AND STATISTICAL TOOLS TO COMPARE GENE EXPRESSION PROFILES BETWEEN HUMAN CELL CULTURES CHALLENGED WITH DIFFERENT FOOD AND BEVERAGE INGREDIENTS

Rochester, Minnesota

2021-2022

Norwegian University of Life Science

RESEARCH SCIENTIST INTERN: PARTICIPATED IN THE COLLECTION OF SEDIMENT FROM THE OCEAN FLOOR OF THE ATLANTIC FOR A METATRANSCRIPTOMIC STUDY. GAINED EXPOSURE TO THE AQUACULTURE INDUSTRY THROUGH CLASSES, CONFERENCES AND ON-SITE INDUSTRY VISITS

Ås, Norway

Fall 2019

IBM, Almaden Research Center

RESEARCH SCIENTIST INTERN: UTILIZED COMPUTATIONAL TOOLS TO TEST MY HYPOTHESIS THAT 16S rRNA GENE SEQUENCES WITHIN BACTERIAL POPULATIONS COULD BE HORIZONTALLY TRANSFERRED BETWEEN CLOSELY/DISTANTLY RELATED BACTERIA

San Jose, California

Summer 2019

Skills

- Sequencing Techniques: Whole genome, whole exome, microbiome, bulk rna
 - Illumina MiSeq, NextSeq and NovaSeq instruments
- Experimental Design: Cross-sectional, case-control and longitudinal designs
 - Confounding, effect modification, batch effects, negative and positive controls
- Statistical Methods: Linear models, mixed models, non-linear models, multivariate models
 - lme4, limma, mgcv, vegan
- Bioinformatic Methods: Alignment, annotation, assembly, classification, clustering
 - Bowtie2, BWA-MEM, DADA2, Decontam, Humann3, Kraken2, Metaphlan3, SAMtools, SPAdes
- Cloud and Programming: Mac, Linux, HPC
 - AWS EC2, S3, C/C++, Docker, Nextflow, Python, R

Publications

1. Dean, C. J., Peña-Mosca, F., Ray, T., Heins, B. J., Machado, V. S., Pinedo, P. J., Caixeta, L. S., & Noyes, N. R. (2022). Evaluation of Contamination in Milk Samples Pooled From Independently Collected Quarters Within a Laboratory Setting. *Frontiers in Veterinary Science*, 9. <https://www.frontiersin.org/articles/10.3389/fvets.2022.818778>
2. Ray, T., Gaire, T. N., Dean, C. J., Rowe, S., Godden, S. M., & Noyes, N. R. (2022). The microbiome of common bedding materials before and after use on commercial dairy farms. *Animal Microbiome*, 4(1), 18. <https://doi.org/10.1186/s42523-022-00171-2>

3. Weinroth, M. D., Belk, A. D., Dean, C., Noyes, N., Dittoe, D. K., Rothrock, M. J., Jr, Ricke, S. C., Myer, P. R., Henniger, M. T., Ramírez, G. A., Oakley, B. B., Summers, K. L., Miles, A. M., Ault-Seay, T. B., Yu, Z., Metcalf, J. L., & Wells, J. E. (2022). Considerations and best practices in animal science 16S ribosomal RNA gene sequencing microbiome studies. *Journal of Animal Science*, *100*(2), skab346. <https://doi.org/10.1093/jas/skab346>
4. Dean, C., Pena-Mosca, F., Ray, T., Heins, B., Pinedo, P., Machado, V., Caixeta, L., & Noyes, N. (2021). What is the Microbiome and Why is it Important for Organic Livestock Production? *eOrganic*. <https://doi.org/http://eorganic.org/node/34373>
5. Dean, C. J., Slizovskiy, I. B., Crone, K. K., Pfennig, A. X., Heins, B. J., Caixeta, L. S., & Noyes, N. R. (2021). Investigating the cow skin and teat canal microbiomes of the bovine udder using different sampling and sequencing approaches. *Journal of Dairy Science*, *104*(1), 644–661. <https://doi.org/10.3168/jds.2020-18277>
6. Slizovskiy, I. B., Mukherjee, K., Dean, C. J., Boucher, C., & Noyes, N. R. (2020). Mobilization of Antibiotic Resistance: Are Current Approaches for Colocalizing Resistomes and Mobilomes Useful? *Frontiers in Microbiology*, *11*. <https://doi.org/10.3389/fmicb.2020.01376>
7. Doster, E., Lakin, S. M., Dean, C. J., Wolfe, C., Young, J. G., Boucher, C., Belk, K. E., Noyes, N. R., & Morley, P. S. (2020). MEGARes 2.0: A database for classification of antimicrobial drug, biocide and metal resistance determinants in metagenomic sequence data. *Nucleic Acids Research*, *48*(D1), D561–D569. <https://doi.org/10.1093/nar/gkz1010>
8. Lakin, S. M., Kuhnle, A., Alipanahi, B., Noyes, N. R., Dean, C., Muggli, M., Raymond, R., Abdo, Z., Prosperi, M., Belk, K. E., Morley, P. S., & Boucher, C. (2019). Hierarchical Hidden Markov models enable accurate and diverse detection of antimicrobial resistance sequences. *Communications Biology*, *2*. <https://doi.org/10.1038/s42003-019-0545-9>
9. Doster, E., Rovira, P., Noyes, N. R., Burgess, B. A., Yang, X., Weinroth, M. D., Lakin, S. M., Dean, C. J., Linke, L., Magnuson, R., Jones, K. I., Boucher, C., Ruiz, J., Belk, K. E., & Morley, P. S. (2018). Investigating Effects of Tulathromycin Metaphylaxis on the Fecal Resistome and Microbiome of Commercial Feedlot Cattle Early in the Feeding Period. *Frontiers in Microbiology*, *9*. <https://doi.org/10.3389/fmicb.2018.01715>
10. Dean, C., Noyes, N., Lakin, S. M., Rovira-Sanz, P., Yang, X., Belk, K., Morley, P., Meinersmann, R., & Abdo, Z. (2018). Tychus: A whole genome sequencing pipeline for assembly, annotation and phylogenetics of bacterial genomes. *bioRxiv*, 283101. <https://doi.org/10.1101/283101>
11. Noyes, N. R., Weinroth, M. E., Parker, J. K., Dean, C. J., Lakin, S. M., Raymond, R. A., Rovira, P., Doster, E., Abdo, Z., Martin, J. N., Jones, K. L., Ruiz, J., Boucher, C. A., Belk, K. E., & Morley, P. S. (2017). Enrichment allows identification of diverse, rare elements in metagenomic resistome-virulome sequencing. *Microbiome*, *5*(1), 142. <https://doi.org/10.1186/s40168-017-0361-8>
12. Lakin, S. M., Dean, C., Noyes, N. R., Dettenwanger, A., Ross, A. S., Doster, E., Rovira, P., Abdo, Z., Jones, K. L., Ruiz, J., Belk, K. E., Morley, P. S., & Boucher, C. (2017). MEGARes: An antimicrobial resistance database for high throughput sequencing. *Nucleic Acids Research*, *45*(D1), D574–D580. <https://doi.org/10.1093/nar/gkw1009>