Marc G. Chevrette

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Education

University of Wisconsin-Madison, Madison, WI **In progress**
Doctor of Philosophy (Ph.D.), Genetics
Advisor: Cameron Currie, Ph.D.

Harvard University Extension, Cambridge, MA **03/2015**
Master of Liberal Arts (ALM), Biotechnology – Bioengineering & Nanotechnology
Advisor: Tomás Maira-Litrán, Pharm.D., Ph.D.

Rensselaer Polytechnic Institute, Troy, NY **12/2010**
Bachelor of Science, Molecular Biology & Bioinformatics

Experience

Currie Lab, University of Wisconsin-Madison **08/2015–present**
Graduate Research Assistant *Madison, WI*

- Built genomics-driven computational and analytical pipelines to uncover novel therapeutics and biosynthesis in free-living and host-associated actinomycetes.

Johnson Biosignatures Lab, Harvard & Georgetown Universities **10/2013–10/2015**
Lead Computational Biologist *Washington, DC (remote)*

- Performed whole genome sequencing and metagenomic analysis of environmental samples from sulfur-rich, extreme environments with implications in microbial ecology, biogeochemistry, and exobiology.
- Characterized biosynthetic potential of metagenomic data.

Warp Drive Bio **04/2013–08/2015**
Head of Experimental Genomics, (04/2014–08/2015) *Cambridge, MA*
Research Associate, Experimental Genomics & Computational Biology, (04/2013–03/2014)

- Executed genomic-directed natural products drug discovery, high throughput Next Generation Sequencing (htNGS), computational biology, and molecular biology of actinomycetes and fungi.
- Designed and implemented genomic searches of business development and internal interest.
- Developed and curated computational pipelines and databases for assembly, annotation, and custom analysis of public and internal htNGS data (1.6×10^5 bacterial genomes, >150 closed and complete genomes) for analysis of novel polyketide, non-ribosomal peptide, and other natural product classes.
- Handled processing and management of sequence data, predictions, and analyses supporting multiple projects across discovery, molecular biology, engineering, and synthetic biology.
- Executed elucidation and prediction of novel chemical products of bacterial biosynthetic gene clusters and metabolic pathways (e.g. beta-lactams, aminoglycosides, rapamycin analogues, etc.).
- Developed internal pipelines for applied phylogenomic annotations and prioritizations of multiple data types to inform discovery and engineering efforts.
- Oversaw all lab and experimental support of actinomycete and fungal sequencing efforts for Illumina, Pacific Biosciences, and Oxford-Nanopore platforms.
- Bioinformatics software development to support molecular and synthetic biology efforts.
- Direct written and verbal communication of findings to senior leadership and business partners.
- Database management and delivery of sequence information to molecular biology, microbiology, and chemistry groups to aid drug discovery, strain engineering, and generation of expression constructs.

Maira-Litrán Infectious Disease Lab, Brigham & Women's Hospital **03/2013–08/2015**
Research Assistant, Microbiology & Computational Biology *Boston, MA*

- Investigated *in vivo* fitness of many virulent pathogens through microbiology, computational, and genomic techniques.
- Developed and optimized genetic tools to enable examinations of pathogen fitness, invasion, and virulence using high-throughput transposon-directed insertion site sequencing of infections in mice.

Broad Institute of MIT & Harvard **01/2011–03/2013**
Research Associate II, Molecular Biology Process Development *Cambridge, MA*

- Independently designed development initiatives including supporting htNGS, microfluidics, and automation goals.
- Oversaw production and up-scaling of microbial mate-pair library construction (LC), integrated internal development with vendor technologies, and managed sample-tracking via internal LIMS.
- Increased throughput of microbial LC Platform 4-fold by automation and protocol development.
- Worked extensively with mate-pair NGS LC, sequence analysis tools, genomic databases, statistical software, and programming/operating lab robotics.

Rutledge Molecular Genetics Lab, Rensselaer Polytechnic Institute **05/2010–12/2010**
Research Associate, Molecular Genetics *Troy, NY*

BCR Biotech **09/2009–12/2009**
Research Assistant, Microbiology *Jamestown, RI*

Publications

P2: Lewin, GR, C Carlos, **MG Chevrette**, HA Horn, BR McDonald, RJ Stankey, BG Fox, CR Currie. *In press*. "Ecology and Evolution of Actinobacteria and their Bioenergy Applications."

P1: Johnson, SS, **MG Chevrette**, BL Ehlmann, KC Benison. 2015. "Insights from the Metagenome of an Acid Salt Lake: the Role of Biology in an Extreme Depositional Environment." *PLOS ONE*. 2015 Apr; **10**(4):e0122869.

Service & Outreach

Co-chair **01/2016–present**
Computational Biology, Ecology, & Evolution (ComBEE) – UW-Madison

- Coordinated and scheduled speakers, discussions, workshops, and meetings focused on molecular microbial ecology and evolution, computational biology, and data science.

Co-organizer **10/2015–11/2015**
Discovery Niche – Wisconsin Institutes for Discovery

- Planned, built, and maintained interactive public exhibits showcasing natural products drug discovery and bioenergy research for local Madison, Wisconsin community.

Volunteer **10/2015**
Wisconsin Science Festival

Open Genomics Advisor **04/2014–10/2015**
Long Now Foundation – Revive & Restore

- Advised projects with Revive and Restore and Cofactor Genomics seeking to understand the genomics of the endangered and extremely bottlenecked black footed ferret and the extinct heath hen in an effort to reintroduce genetic diversity and aid in restoration of healthy wild populations.

Environmental, Health, and Safety Representative **01/2011–03/2013**
Broad Institute of MIT & Harvard