Chase Clark

University of Wisconsin-Madison, School of Pharmacy, VCRGE/BIOTECH/GENOMICS

chasemc ChasingMicrobes chasingmicrobes@gmail.com hirechase chasemc.github.io

Employment

2020	**PhD Pharmacognosy** Chicago, IL	University of Illinois at Chicago
2012	**BS Biochemistry** Mount Berry, GA	Berry College
2010	**Principia Consortium Study Abroad** Glasgow, Glasgow	University of Glasgow

Experience

Jun 2021 - present **Computation and Informatics in Biology and Medicine (CIBM) Postdoctoral Trainee**
Remote, Chicago, IL

- Training grant funded through the National Library of Medicine
- Developing genomic and metagenomic bioinformatics software
- Currently developing a repository scale analysis platform (synthesizing tens of billions of data points)

Sep 2020 - present **Postdoctoral Research Associate** University of Wisconsin-Madison
Remote, Chicago, IL

May 2019 - Aug 2020 **F31 Fellow** U.S. National Institutes of Health (NIH)
Chicago, IL, US

Aug 2015 - Aug 2020 **Ph.D. Student** University of Illinois at Chicago
Chicago, IL, US

- Natural product drug dicovery, specifically bacterial-derived antibiotics
- Conceived, learned to code, and built a bioinformatics program (R Shiny app) for rapid bacterial metabolomics analyses
- Isolated and cultured 1000's of bacterial isolates and performed natural product isolation and structure elucidation
- First or co-first author on four studies/manuscripts
- Mentored undergradaute and graduate students leading to publishable studies

Mar 2013 - Aug 2015 **Research and Development Technician** Deerland Probiotics & Enzymes
Kennesaw, GA, US

- Assisted in the design and results analysis of three clinical studies
- Presented monthly projects to CEO, VP Sales and VP Science & Technology
- Head of method development and identification of raw materials to meet CFR 21, FDA requirements.
- Developed identifications for over 140 materials, from enzymes and botanicals to minerals and additives.
- Overhauled the Method Development Department establishing inter-departmental responsibilities, improving and creating new SOPs, streamlining identification requests by establishing a formal request process and interactive database
- Strengthened and created new relationships with third-party vendors, labs, and universities.
- Controlled budget of method development for purchase of standards, consumables, equipment and third-party testing.
- Mentored interns from Kennesaw Mountain High School magnet program

Aug 2008 - May 2012 **Bonner Scholar** Bonner Foundation
Rome, GA, US

- Four-year community service scholarship requiring weekly and summer commitments.

Skills

Bioinformatics: metabomics • genomics • metagenomics
Cloud Computing: remote server computing (ssh, etc) • high-performance and high-throughput computing (Open science grid, HTCondor)
Communication: presentations (public speaking, technical writing,peer-reviewed publications, SOPs) • writing (customer-facing documents, peer-reviewed publications, SOPs) • full-stack design (Shiny, Flask,Django) • reports (Rmarkdown, Jupyter) • visualization (Base R, ggplot2, plotly, leaflet, cytoscape, networkx, gephi, etc)
Programming: general (R, Python) • database (Neo4j, SQL) • automation (Nextflow, Make) • containers (Docker) • pipeline (Nextflow, Make)
Software Development: source control (Git) • CI/CD (Github, Travis, Azure, DevOps, etc.) • automated testing (testthat, pytest, etc)
Statistics: machine learning • data analysis • cluster analysis • factor analysis • principal components analysis • cross-validation • experimental design

Select Individual Software Projects

2021	**socialgene** Repository-scale genome pattern search platform	Python, Django, Nextflow, High-throughput computing
2019	**electricShine** Shiny packaging with Electron	R, Javascript, Node/Electron
2019	**mzEasy** Shiny app for converting and visualizing mass spectrometry data	R, Shiny
2019	**mzPlotter** Automated summary of of LC-MS/MS data with interactive Rmarkdown reports	R, Rmarkdown
2019	**mzFromImage** Predict a mass spectrum's values from a static image file	R, Shiny
2019	**mgfparse** Low-dependency R package for quickly and efficiently parsing mgf files into R	R
2018	**IDBac** MALDI protein and small molecule bioinformatics platform	R, Shiny, Electron

Select Team Software Projects

2021	**Autometa** Automated binning pipeline for single metagenomes	Python, Nextflow
2021	**metaBenchmarks** Benchmark metagenomic profiling/binning software	Nextflow

Talks

2020-06-01 **St. Jude National Graduate Student Symposium (cancelled due to Covid19)**
- IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization

2020-05-08 **May Institute 2020: Future developers meeting**
- Protein MS isn't the only MS… Programming in R for Metabolomics Mass Spectrometry

2020-02-25 **Gordon Research Conference on Marine Natural Products**
- IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization

2020-02-23 **Marine Natural Products Gordon Research Seminar (GRS)**
- IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization

2019-08-23 **R/Pharma, Harvard University**
- Your Missing Step in Reproducible R Programming: Continuous Deployment

2019-04-27 **satRdays Chicago**
- Bioinformatics in R

2019-01-23 **Chicago R User Group**
- Single Function Lightning Talks: “lengths(), not length()”

2018-08-15 **R/Pharma, Harvard University**
- IDBac: A New Paradigm in Developing Microbial Libraries for Drug Discovery

2018-01-27 **Chicago R User Group**
- IDBac: A Shiny App to Analyze Bacterial Fingerprints and Aid in the Discovery of Potential New Antibiotics

2017-03-09 **Center for Biomolecular Sciences, UIC**
- IDBac: A proteomic & chemometric pipeline for rapid bacterial characterization

2016-11-03 **UIC Specialized Metabolite Community**
- Rational design of bacterial strain libraries for drug discovery

2016-07-22 **Chicago Mass Spec Day**
- Use of MALDI-MS to Create ‘Smart’ Libraries for Drug-Lead Discovery

2015-04-15 **SSAOAC Annual Meeting**
- HPLC-DAD Method for Trace Detection of Benzoic and Sorbic Acids in High Protein Matrices

Awards

2017 **American Society of Pharmacognosy Student Travel Award**
$600

2017 **University of Illinois at Chicago Provost Deiss Award**
$2,500

2019-2020 **NIH Predoctoral Individual National Research Service Award (F31)**
$90,000.00

2021-2023 **Computation and Informatics in Biology and Medicine (CIBM) training**
$100,000.00

Workshops

Sep 2021 **Artificial Intelligence for Natural Product Drug Discovery (Lorentz Center)**

Aug 2019 **Integration of Metabolomics and Genomics (University of Chicago)**

Dec 2016 **PATRIC/RAST Workshop (Argonne National Laboratory)**

Publications

1. Leao, T. F., Clark, C. M., Bauermeister, A., Elijah, E. O., Gentry, E. C., Husband, M., Oliveira, M. F., Bandeira, N., Wang, M., & Dorrestein, P. C. (2021). Quick-start infrastructure for untargeted metabolomics analysis in GNPS. *Citations: 0.* 10.1038/s42255-021-00429-0
2. Clark, C. M., Murphy, B. T., & Sanchez, L. M. (2020). A call to action: The need for standardization in developing open-source mass spectrometry-based methods for microbial subspecies discrimination. *Citations: 2.* 10.1128/msystems.00813-19
3. Clark, C. M., Costa, M. S., Conley, E., Li, E., Sanchez, L. M., & Murphy, B. T. (2019). Using the open-source MALDI TOF-MS IDBac pipeline for analysis of microbial protein and specialized metabolite data. *Citations: 7.* 10.3791/59219
4. Braesel, J., Clark, C. M., Kunstman, K. J., Green, S. J., Maienschein-Cline, M., Murphy, B. T., & Eustáquio, A. S. (2019). Genome sequence of marine-derived streptomyces sp. Strain F001, a producer of akashin a and diazaquinomycins. *Citations: 0.* 10.1128/mra.00165-19

5. Costa, M. S., Clark, C. M., Ómarsdóttir, S., Sanchez, L. M., & Murphy, B. T. (2019). Minimizing taxonomic and natural product redundancy in microbial libraries using MALDI-TOF MS and the bioinformatics pipeline IDBac. *Citations: 7*. 10.1021/acs.jnatprod.9b00168
6. Clark, C. M., Costa, M. S., Sanchez, L. M., & Murphy, B. T. (2018). Coupling MALDI-TOF mass spectrometry protein and specialized metabolite analyses to rapidly discriminate bacterial function. *Citations: 36*. 10.1073/pnas.1801247115