

Chase Clark

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

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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 Fellow Remote, Chicago, IL <ul style="list-style-type: none">• 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 Remote, Chicago, IL	University of Wisconsin-Madison
May 2019 - Aug 2020	F31 Fellow Chicago, IL, US	U.S. National Institutes of Health (NIH)
Aug 2015 - Aug 2020	Ph.D. Student Chicago, IL, US <ul style="list-style-type: none">• Natural product drug discovery, 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 undergraduate and graduate students leading to publishable studies	University of Illinois at Chicago
Mar 2013 - Aug 2015	Research and Development Technician Kennesaw, GA, US <ul style="list-style-type: none">• 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	Deerland Probiotics & Enzymes
Aug 2008 - May 2012	Bonner Scholar Rome, GA, US <ul style="list-style-type: none">• Four-year community service scholarship requiring weekly and summer commitments.	Bonner Foundation

Data Science Skills

Bioinformatics: metabonomics () • 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 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

2022-03-09	Gordon Research Conference on Marine Natural Products • Towards near-instant, repository-scale searching for homologous BGCs with Social-gene (Selected alternate speaker, didn't present)
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 **Gordon Research Seminar (GRS) on Marine Natural Products**
 - 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

- 2021-2023 **Computation and Informatics in Biology and Medicine (CIBM) training**
\$100,000.00
- 2019-2020 **NIH Predoctoral Individual National Research Service Award (F31)**
\$90,000.00
- 2017 **American Society of Pharmacognosy Student Travel Award**
\$600
- 2017 **University of Illinois at Chicago Provost Deiss Award**
\$2,500

Publications

1. Clark, C. M., Hernandez, A., Mallowney, M. W., Fitz-Henley, J., Li, E., Romanowski, S. B., Pronzato, R., Manconi, R., Sanchez, L. M., & Murphy, B. T. (2022). Relationship between bacterial phylotype and specialized metabolite production in the culturable microbiome of two freshwater sponges. *ISME Communications*. Citations: 0. 10.1038/s43705-022-00105-8
2. 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. *Nature Metabolism*. Citations: 1. 10.1038/s42255-021-00429-0
3. 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. *mSystems*. Citations: 2. 10.1128/msystems.00813-19
4. 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. *Journal of Visualized Experiments*. Citations: 9. 10.3791/59219
5. 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. *Microbiology Resource Announcements*. Citations: 0. 10.1128/mra.00165-19

6. 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. *Journal of Natural Products*. Citations: 11. 10.1021/acs.jnatprod.9b00168
7. 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. *Proceedings of the National Academy of Sciences*. Citations: 45. 10.1073/pnas.1801247115