Chase Clark

Postdoctoral Research Associate

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Curriculum Vitae
September 2021

Skills

- Bioinformatics
- Metabolomics
- Genomics/Metagenomics
- Natural product isolation and drug discovery

Current Bioinformatic Tools

- Advanced: R, Rmarkdown, Shiny, Neo4j, Nextflow
- Intermediate: Python, Flask, HTML
- Familiar: JavaScript

Education

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

2020-Current	**Postdoctoral Research Associate** School of Pharmacy, Pharmaceutical Sciences Division	University of Wisconsin-Madison
2021-Current	**Computation and Informatics in Biology and Medicine (CIBM) Trainee**	National Library of Medicine
2019-2020	**F31 Fellow** National Center for Complementary and Integrative Health	U.S. National Institutes of Health (NIH)
2015-2019	**Ph.D. Student** Medicinal Chemistry and Pharmacognosy	University of Illinois at Chicago
2013-2015	**Research and Development Technician** R&D, Method Development	Deerland Enzymes
2008-2012	**Bonner Scholar**	Bonner Foundation

Recent Solo Projects

2021	**socialgene** Repository-scale genome search platform	Python, Flask app, 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
2018	**IDBac** MALDI protein and small molecule bioinformatics platform	R, Shiny, Electron

Recent Team Projects

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

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

Talks

2020-06-01	**IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization** St. Jude National Graduate Student Symposium (cancelled due to Covid19)
2020-05-08	**Protein MS isn't the only MS… Programming in R for Metabolomics Mass Spectrometry** May Institute 2020: Future developers meeting
2020-02-25	**IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization** Gordon Research Conference on Marine Natural Products
2020-02-23	**IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization** Marine Natural Products Gordon Research Seminar (GRS)
2019-08-23	**Your Missing Step in Reproducible R Programming: Continuous Deployment** R/Pharma, Harvard University
2019-04-27	**Bioinformatics in R** satRdays Chicago
2019-01-23	**Single Function Lightning Talks: "lengths(), not length()"** Chicago R User Group
2018-08-15	**IDBac: A New Paradigm in Developing Microbial Libraries for Drug Discovery** R/Pharma, Harvard University
2018-01-27	**IDBac: A Shiny App to Analyze Bacterial Fingerprints and Aid in the Discovery of Potential New Antibiotics** Chicago R User Group
2017-03-09	**IDBac: A proteomic & chemometric pipeline for rapid bacterial characterization** Center for Biomolecular Sciences, UIC
2016-11-03	**Rational design of bacterial strain libraries for drug discovery** UIC Specialized Metabolite Community
2016-07-22	**Use of MALDI-MS to Create 'Smart' Libraries for Drug-Lead Discovery** Chicago Mass Spec Day
2015-04-15	**HPLC-DAD Method for Trace Detection of Benzoic and Sorbic Acids in High Protein Matrices** SSAOAC Annual Meeting

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: 34*. 10.1073/pnas.1801247115