BIOGRAPHICAL SKETCH
DO NOT EXCEED FIVE PAGES.

NAME: Berg, Jordan

eRA COMMONS USER NAME (credential, e.g., agency login): [redacted]

POSITION TITLE: Graduate Research Assistant

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
Brigham Young University, Provo, UT	B.S.	06/2010	05/2016	Molecular Biology
University of Utah, Salt Lake City, UT	Ph.D.	08/2016	05/2022	Biochemistry

A. Personal Statement

While human metabolism has been elementally understood and appreciated since at least the time of Aristotle's "Parts of Animals", and vigorously dissected over the past two centuries, a holistic, systematic understanding of metabolism is incomplete. Currently, much of metabolism research takes a reductionist stance by removing a gene or protein in a pathway to determine its effect. But even in these scenarios, the systematic consequences are difficult to parse out from the noise. In order to improve our understanding in this realm, my aims are two-fold. 1) Develop automated, robust tools for performing complex interrogations system-wide in metabolism, and 2) Use these tools to address questions related to the complex and dispersed regulation of cancer metabolism that without such tools would be impossible to answer. With these tools, the pace of scientific discovery can modernize and accelerate, expanding the reach of our insights into the complex pathology of cancer that can then be used to offer novel therapeutic avenues.

During my training as a scientist, I have become entranced by "big data" methodology and its inherent capability to answer difficult questions in complex systems. As such, I have focused my training efforts to fill my toolkit with the mathematical and statistical methods necessary to allow me to ask and answer these complex questions. I chose to work with Dr. Rutter due to his expertise in metabolism and his enthusiasm to leverage computational methods to ask new and difficult questions in cancer metabolism. After my graduate training, I will find a position as a postdoctoral research fellow in a lab focusing on network biology and machine learning that will allow me to continue to expand this toolkit, particularly in relationship to metabolism research. My driving goal behind all of these career stages is to run my own computational metabolism lab where we will develop the tools necessary to deconvolute noisy and complex datasets to provide a more holistic view of metabolism. I will use these tools and approaches to research our own hypotheses of complex metabolism regulation.

B. Positions and Honors

Positions and Employment

2014 iGEM Project Leader, 2014 iGEM Team, Brigham Young University
2013-2016 Undergraduate Research Assistant, Julianne Grose Lab, Brigham Young University
2014-2016 Teaching Assistant, Freshman Research 1&2/HHMI SEAPHAGES Program, Brigham Young University
2018 Teaching Assistant, Lit. & Problem Solving, University of Utah
2016-current Graduate Student, Molecular Biology Program, University of Utah
2017-current Graduate Research Assistant, Jared Rutter Lab, University of Utah

Other Experience and Professional Memberships

2015 Member, American Society for Microbiology
2014-2016 Youth Mentor, Provo Youth Mentoring
2018 Lead Recruitment Host, Molecular Biology Graduate Program, University of Utah
2018 Volunteer, Adventure Scientists
2017-current Reviewer, Journal of Emerging Investigators
2018-current SACNAS Webmaster/Social Media Outreach Officer

Academic and Professional Honors

2014 iGEM World Jamboree, Silver Medal
2016 Outstanding Research Award, Department of Microbiology and Molecular Biology, Brigham Young University
2018-2020 T32 Training Grant in Computational Approaches to Diabetes and Metabolism

C. Contributions to Science

***Brevibacillus/Paenibacillus* Bacteriophage/Host Evolution (Undergraduate)**

During my undergraduate degree, my research focus centered around the isolation, genomic characterization, and evolutionary analysis of bacteriophage infecting the bee probiotic *Brevibacillus laterosporus* and the bee pathogen *Paenibacillus larvae*. Through the isolation and characterization of these phages, I was the first author of two published peer-reviewed papers. I mentored 22 undergraduate research assistants and students, 16 of whom contributed as co-authors on published papers and/or primary authors on posters presented at external conferences. Additionally, I co-authored 13 phage genome annotations published in NCBI's Genbank (Accession #s: MG727695, MG727697, MG727696, MG727701, MG727702, MG727699, MG727698, MG727700, KT151958, KT151959, KT151957, KT151956, KT151955). I was also involved the isolation, genomic characterization, and evolutionary analysis of bacteriophages infecting the tree pathogen *Erwinia amylovora*. I published 11 complete and annotated Erwinia phage genomes on Genbank as first author (Accession #: NC_031127, NC_031120, NC_031043, NC_031010, NC_031007, NC_031126, NC_031107, KX397373, KX397371, KX397370, KX098389) and was a co-author on 5 additional phage genomes (Accession #: KU886222, KU886224, KU886223, KX098391, KX098390). I was invited to give an oral presentation on my *Erwinia* phage research at 2015 Tri-Branch American Society for Microbiology (ASM) conference and presented several posters on these research topics. In collaboration with the U.S. Environmental Protection Agency (EPA), I developed phage cocktails for treating *Erwinia amylovora* infections in apple and pear orchards.

1. **Berg JA**, Merrill BD, Breakwell DP, Grose JH, Hope S. A PCR-based method for distinguishing between two common beehive bacteria, *Paenibacillus larvae* and *Brevibacillus laterosporus*. (2018) **Journal of Appl Environ Microbiol**. 84:e01886-18. DOI: 10:1128/AEM.01886-18.
2. Sharma R, **Berg JA**, Beatty NJ, Choi MC, Cowger AE, Duncan SG, Fajardo C, Ferguson HP, Galbraith T, Herring JA, Hoj TR, Hughes J, Hyde JR, Jensen GL, Ke K, Keele BR, Killpack S, Lawrence EEK, Nwosu I, Roark BJ, Thompson DW, Tueller JA, Ward MEH, Webb CJ, Wood ME, Wynne H, Yeates EL, Baltrus D, Breakwell DP, Hope S, Grose JH. Genome Sequences of 10 *Erwinia amylovora* Bacteriophages. (2018) **Microbiol Resour Announc**. 7(14):e00944-18. DOI: 10.1128/MRA.00944-18.
3. Walker JK, Merrill BD, **Berg JA**, Dhalai A, Dingman DW, Fajardo CP, Graves K, Hill HL, Hilton JA, Imahara C, Knabe BK, Mangohig J, Monk J, Mun H, Payne AM, Salisbury A, Stamereilers C, Velez K, Ward AT, Breakwell DP, Grose JH, Hope S, Tsourkas PK. Complete Genome Sequences of *Paenibacillus larvae* Phages BN12, Dragolir, Kiel007, Leyra, Likha, Pagassa, PBL1c, and Tadhana. (2018) **Genome Announc.** 6(24):e01602-17. DOI: 10.1128/genomeA.01602-17.
4. Esplin IND, **Berg JA**, Sharma R, et. al. Genome sequences of 19 novel *Erwinia amylovora* bacteriophages. (2017) **Genome Announc.** 5(46):e00931-17. DOI: 10.1128/genomeA.00931-17.
5. **Berg JA**, Merrill BD, Crockett JT, Esplin KP, Evans MR, Heaton KE, Hilton JA, Hyde JR, McBride MS, Schouten JT, Simister AR, Thurgood TL, Ward AT, Breakwell DP, Burnett SH, Grose JH. Characterization of five novel *Brevibacillus* bacteriophages and genomic comparison of *Brevibacillus* phages. (2016) **PLoSONE** 11(6): e0156838. DOI: 10.1371/journal.pone.0156838.
6. Merrill BD, **Berg JA**, Graves KA, Ward AT, Hilton JA, Wake BN, Grose JH, Breakwell DP, Burnett SH. Genome sequences of five additional *Brevibacillus laterosporus* bacteriophages. (2015) **Genome Announc.** 3(5):e01146-15. DOI: 10.1128/genomeA.01146-15.

Computational Approaches to Deconvoluting Complex Metabolism (Graduate)
In order to enable the curation and analysis of the massive amounts of data needed to investigate network metabolism, we developed the toolkit, XPRESSyourself, for standardizing and automating ribosome profiling and RNA-Seq data analysis. With Drs. Bei Wang, James Cox, and others, we are building upon this first toolkit to create Metaboverse, which will standardize and contextualize proteomics and metabolomics data, with the help of RNA-Seq and ribosome profiling data. We also recently completed a work investigating key considerations when analyzing and visualizing metabolic networks, which will serve as a foundation for contextualizing metabolism. These projects feed into one of my primary objectives, namely developing novel computational tools for analyzing large datasets to leverage their use in understanding complex metabolic networks and their regulation. These tools will be essential in future projects with Dr. Jared Rutter in more finely dissecting signal from noise in metabolic data to discover new regulatory mechanisms within metabolism.

1. **Berg JA[&]**, Belyeu JR, Morgan JT, Ouyang Y, Bott AJ, Quinlan AR, Gertz J, Rutter J[&]. XPRESSyourself: Enhancing, Standardizing, and Automating Ribosome Profiling Computational Analyses Yields Improved Insight into Data. (2019) **bioRxiv**. 704320. DOI: 10.1101/704320. Under review.
2. Hughes CE, Coody TK, Jeong M, **Berg JA**, Winge DR, Hughes AL. Amino acid toxicity drives age-related mitochondrial decline by altering iron metabolism. Under review.
3. Bensard CL*, Wisidigama DR*, Olsen KA, **Berg JA**, Krah NM, Schell JC, Nowinski SM, Fogarty S, Bott AJ, Wei P, Dove KK, Tanner JM, Panic V, Cluntun A, Lettlova S, Earl CS, Namnath DF, Vázquez-Arregun K, Villanueva CJ, Tantin D, Murtaugh LC, Evason KJ, Ducker GS, Thummel CS, Rutter J. Regulation of Tumor Initiation by the Mitochondrial Pyruvate Carrier. **In Press at Cell Metabolism**.
4. Waller TC[&], **Berg JA**, Lex A, Chapman BE, Rutter J[&]. Compartment and Hub Definitions Tune Metabolic Networks for Metabolic Interpretations. **In Press at GigaScience**.
5. Van Vranken JG, Nowinski SM, Clowers KJ, Jeong M, Ouyang Y, **Berg JA**, Gygi J, Gygi SP, Winge DR, Rutter J. Mitochondrial fatty acid synthesis couples acetyl-CoA sensing with electron transport chain biogenesis. (2018) **Mol Cell.** 71(4):567-580.e4. DOI: 10.1016/j.mocel.2018.06.039.

([&] denotes co-corresponding authors, * denotes equal contributions)

D. Scholastic Performance

Brigham Young University

YEAR	SCIENCE COURSE TITLE	GRADE
2010		B+
2013		B
2013		A
2013		B+
2013		A
2013		A
2013		A-
2013		A
2014		A
2014		B
2014		A-
2014		A
2014		A
2014		A
2014		A-
2014		A
2014		C+
2014		B+
2014		A
2014		A

YEAR	SCIENCE COURSE TITLE	GRADE
2014	[redacted]	B-
2015		B
2015		C-
2015		B-
2015		C+
2015		B
2015		E
2015		C+
2015		P
2016		B+
2016		B-
2016		A

YEAR	OTHER COURSE TITLE	GRADE
2010	[redacted]	A-
2010		A
2010		B+
2010		B
2010		A
2010		A
2010		A-
2013		A
2013		A-
2013		B+
2013		A
2013		B
2013		B
2014		A
2015		B+
2015		B-
2016		E

Cumulative Undergraduate GPA=3.23
*Undergraduate grades based on an A-E scale, E equaling a failing grade; or reported as Pass (P), Fail (F)

University of Utah

YEAR	SCIENCE COURSE TITLE	GRADE
2016	[redacted]	P
2016		B+
2016		B
2016		A-
2016		P
2016		P
2017		P
2017		P
2017		P
2017		C+
2017		P
2017		P
2017		P

YEAR	SCIENCE COURSE TITLE	GRADE
2017	[redacted]	A
2018		P
2018		P
2018		P
2018		A
2018		A
2019		A
2019		P
2019		P

Cumulative Graduate GPA=3.807
*Graduate grades based on an A-D, F scale or reported as Pass (P), Fail (F)