

Ted Laderas, PhD

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EDUCATION

B.A., Chemistry, Reed College, Portland, OR 1998.
M.S. Biomedical Informatics, Oregon Health & Science University, 2004.
PhD, Biomedical Informatics, Oregon Health & Science University, 2014.

RESEARCH STATEMENT

My research interests are complex diseases, precision medicine, applications of systems science (including network analysis and modeling), and applying data integration to difficult and high-impact translational research questions. These questions include immune system profiling in both infectious disease (tuberculosis) and Acute Myeloid Leukemia, understanding drug sensitivity in the context of multiple cancer types (AML, Colorectal, Breast and Head and Neck Cancer), and quantifying expression differences in alcoholic preference. I have worked with a large number of datatypes (high-throughput immunophenotyping, proteomics, expression, genomic, and functional drug screen data) and have focused on methods and frameworks integrating these datatypes within the biological and clinical context of these translational research questions. My training in biomedical informatics as a master's student in Biomedical Informatics, as an NLM Predoctoral Fellow, and as a NLM Postdoctoral fellow has enabled me to communicate with a wide variety of collaborators by giving me a strong background in Cancer Biology, Software Development, and Clinical Systems. Additionally, I am a strong advocate for Open Science initiatives, most notably the effort for reproducibility in scientific analysis. To this end, I have developed multiple novel software pipelines that transparently process data from raw data to through the final stages of analysis.

SELECTED RESEARCH PUBLICATIONS

1. *Probabilistic Graphical Models for Systems Biology*. **Ted Laderas**, Aurora Blucher, Guanming Wu and Shannon McWeeney. Awaiting submission. Contribution: first author and conception of manuscript.
2. *A Network-Based Model of Oncogenic Collaboration to Predict Drug Sensitivity*. **Ted Laderas**, Laura Heiser and Kemal Sonmez. Featured article in *Frontiers in Genetics*. 2015. Contribution: First author, developer of methodology and visualization framework.
3. *The Consensus Molecular Subtypes of Colorectal Cancer*. 123 citations, Impact Factor 30.36. Justin Guinney, Rodrigo Dienstmann, Xin Wang, Aurélien de Reyniès, Andreas Schlicker, Charlotte Soneson, Laetitia Marisa, Paul Roepman, Gift Nyamundanda, Paolo Angelino, Brian M. Bot, Jeffrey S. Morris, Iris Simon, Sarah Gerster, Evelyn Fessler, Felipe de Sousa e Melo, Edoardo Missiaglia, Hena Ramay, David Barras, Krisztian Homicsko, Dipen Maru, Ganiraju C. Manyam, Bradley Broom, Valerie Boige, **Ted Laderas**, Ramon Salazar, Joe W. Gray, Douglas Hanahan, Josep Taberner, Rene Bernards, Stephen H. Friend, Pierre Laurent-Puig, Jan P. Medema, Anguraj Sadanandam, Lodewyk Wessels, Mauro Delorenzi, Scott Kopetz, Louis Vermeulen, and Sabine Tejpar. *Nature Medicine*. 2015. Contribution: mapped and analyzed OMICs data to consensus cancer subtypes.
4. *Between Pathways and Networks lies Context*. Impact Factor: 1.76. **Ted Laderas**, Guanming Wu, and Shannon McWeeney. *Science Progress*. 2015. Contribution: first author, conceptualized and wrote manuscript. doi:10.3184/003685015X14368898634462

5. *Computational detection of alternative exon usage*. 8 citations, Impact Factor: 3.398. **Ted Laderas**, Nicole A Walter, Michael Mooney, Kristina Vartanian, Priscila Darakjian, Kari Buck, Chris Harrington, John Belknap, Robert Hitzemann, and Shannon McWeeney. *Frontiers in Neurogenomics*. 2011. Article 69. PMID 21625610. Contribution: First author, developer of methodology. doi:10.3389/fnins.2011.00069
6. *High throughput sequencing in mice: a platform comparison identifies a preponderance of cryptic SNPs*. 19 Citations, Impact Factor 3.87. Nicole A Walter, Daniel Bottomly, **Ted Laderas**, Michael Mooney, Priscila Darakjian, Robert P Searles, Christina Harrington, Shannon K McWeeney, Robert Hitzemann, Kari J Buck. *BMC Genomics*. 2009 Aug 17;10:379. Contribution: helped develop methodology of manuscript, conceptualization. doi:10.1186/1471-2164-10-379
7. *TandTRAQ: An open-source tool for integrated protein identification and quantitation*. 14 citations, Impact Factor 5.766. **Ted Laderas**, Cory Bystrom, Debra McMillen, Guang Fan and Shannon McWeeney. *Bioinformatics*. 2007. Contribution: first author, designed software framework. doi:10.1093/bioinformatics/btm467
8. *A consensus framework for exploring microarray data using multiple clustering methods*. 16 citations. **Ted Laderas** and Shannon McWeeney. *OMICS: A Journal of Integrative Biology*. *OMICS: A Journal of Integrative Biology*. 2007. 116-128. Contribution: first author, developed methodology for comparison analysis. doi:10.1089/omi.2006.0008

RESEARCH SOFTWARE (Sole Developer unless specified)

1. *RBootcamp (tidyverse version)*. DataCamp active exercises for learning introductory R using the **tidyverse**. With Jessica Minnier and Chester Ismay. Available for free at: <https://www.datacamp.com/courses/rbootcamp> <https://doi.org/10.5281/zenodo.854727>
2. *flowDashboard*. Visualization framework in R/Shiny and processing pipeline for CyTOF and flow cytometry data. Currently under embargo, waiting publication and submission. <https://doi.org/10.5281/zenodo.260421>
3. *Surrogate Network Explorer for Head and Neck Cancer*. Interactive visualization framework for understanding network effects in Head and Neck cancer. Awaiting validation, publication, and submission.
4. *R-Bootcamp: Introduction to R*. Script-based introductory MOOC to R. With contributions from Eric Leung, Dian Chase, Tracy Edinger, Clint Olson, and Gabrielle Chonoo. <http://dx.doi.org/10.5281/zenodo.13756>
5. *Surrogate Mutation Explorer*. R/Shiny Interactive Application for exploring surrogate mutations. <http://dx.doi.org/10.5281/zenodo.13757>
6. *SurrogateMutation*. R Package for mapping mutations and copy number alterations to networks and associated statistics. <http://dx.doi.org/10.5281/zenodo.17303>
7. *Consense-Cluster*. R Package for comparing clustering output across algorithms. <http://dx.doi.org/10.5281/zenodo.17304>
8. *ExonModelStrain*. RPackage for detecting alternative exon usage between two strains of mice. <http://dx.doi.org/10.5281/zenodo.17305>
9. *TandTRAQ*. Perl Script for mapping iTRAQ protein quantitation to X!Tandem peptides.

RESEARCH PRESENTATIONS/LECTURES (Invited Lectures are Indicated)

1. *Data Science for Basic Scientists*. Invited talk for OHSU Symposium on Educational Excellence. April 2017. doi:10.6084/m9.figshare.4876811.v3

2. *Moving From Big Data to Knowledge: Implications for the Health Care and Biomedical Sciences*. Invited Lecture given for BioCatalyst Advanced Training workshop at Oregon Bioscience Association. June 2015.
3. *Surrogate Mutations and Drug Sensitivity in Breast Cancer Cell Lines*. Plenary talk at NLM Training Conference, Pittsburgh, PA, June 2014.
4. *Connecting Genotypes to Drug Sensitivities in HER2 Positive Cancer Cell Lines*. Doctoral Defense, OHSU, March 2014.
5. *Understanding Expression Differences in RPPA Data: Implications for ODE Models*. Presentation at Integrative Cancer Biology Program retreat 2012.
6. *Connecting Genotypes to Drug Sensitivity in HER2+ Breast Cancer Cell Lines*. Lecture/Dissertation proposal given for PhD/Postdoc Meeting January 2012 and March 2012.
7. *Connecting Genotypes to Drug Sensitivity in Breast Cancer Cell Lines*. Invited presentation at Integrative Cancer Biology Program retreat, 2011.
8. *What are Models For? Making Sense of Systems Biology*. Predoctoral Symposium. 2010.
9. *Two kinds of Robustness*. Presentation given to Bioinformatics Development Group, 2010.
10. *Portland Alcohol Research Center Scientific Advisory Board Review: Bioinformatics & Statistics*. Presentation given to PARC SAB, OHSU, 2009.
11. *An introduction to trend analysis and consensus modules for systems biology*. Presentation given with Sophia Jeng to Mathematical Modeling Core for Systems Virology, OHSU 2009.
12. *An introduction to Consensus Modules for Systems Biology*. Lecture given with Sophia Jeng to Bioinformatics Development Group, OHSU, 2008.
13. *An Introduction to Sloppy Systems Biology*. Lecture given to Bioinformatics Development Group, OHSU, 2008.
14. *Simulated and Synthetic Data for Benchmarking Algorithms*. Lecture given as part of Bioinformatics Methods class, OHSU, 2007.
15. *Introduction to QPACA Pathway Analysis Software and BioPAX*. Talk given at 2006 caBIG Annual Meeting, Washington DC.
16. *Consense: A software package for utilizing multiple clustering methods on Microarray Data*. Talk given at OHSU Student Research Forum, 2005.

RESEARCH POSTERS/ABSTRACTS

1. *Getting your hands dirty with data*. **Ted Laderas**, Melissa Hanedel, Bjorn Pederson, Jackie Wirz, William Hersh, David A. Dorr, Shannon McWeeney. Big Data to Knowledge (BD2K) All Hands meeting, November 2016. doi:10.6084/m9.figshare.4235594.v1
2. *Get Real: A synthetic dataset illustrating clinical and genetic covariates*. **Ted Laderas**, Nicole Vasilevsky, Melissa Haendel, Shannon McWeeney and David A. Dorr. BD2K All Hands meeting, November 2016. doi:10.6084/m9.figshare.4239959.v1
3. *Mass Cytometry as a Modality to Identify Candidates for Immune Checkpoint Inhibitor Therapy within Acute Myeloid Leukemia*. Adam Lamble, Fei Huang, Kate Sasser, Homer Adams III, Cristina E. Tognon, **Ted Laderas**, Shannon McWeeney, Marc Loriaux, Jeffery W. Tyner, Brian J. Druker, and Evan F. Lind. American Society for Hematology, December 2016.
4. *Enhanced VISTA Expression in a Subset of Patients with Acute Myeloid Leukemia*. Adam Lamble, Yoko Kosaka, Fei Huang, Kate Sasser, Homer Adams III, Cristina E. Tognon, **Ted Laderas**, Shannon McWeeney, Marc Loriaux, Jeffery W. Tyner, Brian J. Druker, and Evan F. Lind. American Society for Hematology, December 2016.

5. *Improving Knowledge Discovery Through Development of Big Data to Knowledge Skills Courses and Open Educational Resources*. Nicole Vasilevsky, Shannon McWeeney, William Hersh, David A. Dorr, **Ted Laderas**, Jackie Wirz, Bjorn Pederson and Melissa Haendel. Poster for BICC Building 25th Anniversary.
6. *Consensus molecular subtyping through a community of experts advances unsupervised gene expression-based disease classification and facilitates clinical translation*. Justin Guinney, Rodrigo Dienstmann, Xin Wang, Aurelien de Reynies, Andreas Schlicker, Charlotte Soneson, Laetitia Marisa, Paul Roepman, Gift Nyamundanda, Paolo Angelino, Brian Bot, Jeffrey S. Morris, Iris Simon, Sarah Gerster, Evelyn Fessler, Felipe de Sousa e Melo, Edoardo Missiaglia, Hena Ramay, David Barras, Krisztian Homicsko, Dipen Maru, Ganiraju Manyam, Bradley Broom, Valerie Boige, **Ted Laderas**, Ramon Salazar, Joe W. Gray, Josep Taberner, Rene Bernards, Stephen Friend, Pierre Laurent-Puig, Jan P. Medema, Anguraj Sadanandam, Lodewyk Wessels, Mauro Delorenzi, Scott Kopetz, Louis Vermeulen and Sabine Tejpar. American Association for Cancer Research Conference, August 2015.
7. *A Network-Based Model of Oncogenic Collaboration for Prediction of Drug Sensitivity*. **Ted Laderas**. RECOMB/ISCB Conference on Regulatory and Systems Genomics, November 2014.
8. *Integrating proteomics and genomic data to illuminate the effects of Lapatinib in HER2+ Cells*. **Ted Laderas** and Kemal Sonmez. National Library of Medicine Training Conference, Utah, 2013. doi:10.6084/m9.figshare.4829749.v1
9. *Integrating to Interact: Using Reconstructability Analysis to Integrate Genomic and Proteomic Data to Predict Drug Sensitivity*. **Ted Laderas** and Kemal Sonmez. Intelligent Systems in Molecular Biology conference, 2012. doi:10.6084/m9.figshare.4830007.v1
10. *Tales from the Cryptic Snp: High Throughput Sequencing of DBA/2J and C57BL/6J mouse chromosome 1 reveals an abundance of polymorphisms*. Kari J. Buck, Nicole A.R. Walter, Daniel Bottomly, **Ted Laderas**, Michael Mooney, Priscila Darakjian, Shannon McWeeney, Robert Hitzemann. Research Society on Alcoholism Annual Meeting. 2009.
11. *A computational framework for the detection of alternative exon usage using Affymetrix Exon arrays*. **Ted Laderas**, Michael Mooney, Nikki Walter, Kristina Vartanian, Christina Harrington, Priscila Darakjian, John Belknap, Robert Hitzemann, and Shannon McWeeney. Intelligent Systems in Molecular Biology conference, Toronto, July 2008.
12. *Cerebrospinal fluid (CSF) proteomics in children with acute lymphoblastic leukemia (ALL)*. Robert C Trueworthy, Linda C Stork, Yanping Zhong, Sharon Pine, Yousif Matloub, **Ted Laderas**, Shannon McWeeney, and Guang Fan. Poster 2006.
13. *A metrics-based low-level preprocessing framework for proteomics data*. **Ted Laderas**, Solange Mongoue-Tchokote, Veena Rajaraman, Kimberly Sellers, Cory Bystrom and Shannon McWeeney. Bioconductor Developer's Meeting, Seattle, Washington, August 2006.
14. *A diagnostic test suite for the RProteomics statistical routines*. **Ted Laderas**, Solange Mongoue-Tchokote, Veena Rajaraman, Kimberly Sellers and Shannon McWeeney. caBIG annual meeting, Washington DC, April 2006.
15. *Consense-Cluster: a framework for comparing and benchmarking clustering algorithms*. **Ted Laderas** and Shannon McWeeney. Bioconductor Developer's Meeting, Seattle, Washington, August 2005.

TEACHING STATEMENT

Effective communication, hands-on learning, and mentoring are core to my teaching philosophy. I am a strong believer in enabling students in self-directed learning through hands-on workshops including both practical skills in bioinformatics (software development, design, and data analysis and visualization) and social skills essential to collaboration (interpretation and communication). In terms of practical skills, I have developed and contributed to a number of courses (Analytics, RBootcamp, Network Analysis, and BD2K skills courses) and workshops in a large variety of software development and communication topics. These topics include software design, interactive visualization, exploratory data analysis, and presentation of results. In terms of

fostering social and collaborative skills in students, I am a founder and leader of BioDSP (Bioinformatics Discussion for Students and Postdocs), a collaborative forum for students and postdocs to share and teach each other practical skills for success in a research environment. Through BioDSP, I have informally mentored a number of students through feedback and collaboration on workshops and presentations. I believe that by “training the trainers”, we can more effectively educate students in these skills in Data Science and Analytics. In order to accomplish this training of trainers, my course materials are openly available for use and modification by other teachers. Because of my dedication to teaching and incorporation of student feedback, I have consistently high ratings from students in terms of teaching both long-form courses and short-term workshops.

TEACHING EXPERIENCE

Lectures and Interactive Workshops are linked where possible.

1. R-Bootcamp (tidyverse version on DataCamp). Active exercises for learning introductory R. Written with Jessica Minnier and Chester Ismay. Code available at <https://github.com/laderast/RBootcamp>
2. *A gRadual intRoduction to the tidyverse*. Workshop given with Chester Ismay for Cascadia-R 2017 introducing visualization and data cleaning using the `tidyverse`.
3. *Assessing Cardiovascular Risk*. 2 night Workshop for Portland State University Students teaching Exploratory Data Analysis and Machine Learning on a synthetic patient cohort. With David Dorr. May 2017.
4. *An Intro to GitHub Pages*. Workshop given with Robin Champieux and Eric Leung on setting up a personal GitHub webpage. April 2017.
5. *An Intro To Data Carpentry*. Lecture given with Eric Leung about the tidyverse suite of packages for data wrangling and visualization. March 2017.
6. *The Magic of Markdown*. Updated for 2017, including examples of using Zotero as citation manager. March 2017. doi:10.5281/zenodo.495614
7. *Shiny Tutorial for CSE631*. Workshop on developing interactive visualizations using Shiny for CSE631 Data Visualization course. November 2016. DOI: 10.5281/zenodo.495621
8. *Analytics Course*. New Course material in SQLite, Logistic Regression and Analysis. August 2016. doi:10.5281/zenodo.495623
9. *Exploring the DREAM Viral Respiratory Dataset using Shiny*. Tutorial in Exploratory Data Analysis (EDA) using `data.table` and `Shiny`. July 2016.
10. *Introduction to Exploratory Data Analysis using Shiny* - Interactive workshop in using a Shiny Dashboard to conduct EDA on a dataset for BD2K Advanced Skills Course. May 2016. doi:10.5281/zenodo.495618
11. *Introduction to Machine Learning using Markdown* - Interactive workshop using Markdown to explore machine learning algorithms for BD2K Advanced Skills Course. May 2016.
12. *Clustering Algorithms*. Lecture given for Statistical Methods class. February 2016.
13. *iGraph Tutorial*. Introductory lecture for the igraph package in R for network analysis. November 2015. doi:10.5281/zenodo.495616
14. *The Magic of Markdown*. Introduction to Markdown in both R, GitHub pages, and Pandoc. BioDSP October 2015. doi:10.5281/zenodo.495614
15. *Pharmacogenomics* Lecture for Analytics Course, August 2015.
16. *Introduction to Clustering*. Interactive slides for understanding clustering. doi:10.5281/zenodo.495624
17. *Introduction to ggvis*. Lecture/Workshop given for OHSU Bioinformatics Discussion for Students and Postdocs, April 2015.

18. *Introduction to ggplot2*. Lecture/Workshop given for OHSU Bioinformatics Discussion for Students and Postdocs, March 2015. doi:10.5281/zenodo.495622
19. *Exacloud Tutorial* - A DIY tutorial to running jobs on Exacloud, OHSU's cluster computing environment. November 2015.
20. *Shiny Tutorial* - A do it yourself tutorial to try out Shiny, ggplot2, and dplyr for interactive graphics. September 2015. doi:10.5281/zenodo.495620
21. *Analytics Course*. Instructor. Hybrid Online/On-campus joint course with DMICE and Kaiser Permanente Analytics group. August 2015.
22. *R-Bootcamp*. Massively Open Online Course available at: <http://dx.doi.org/10.5281/zenodo.13756>. With contributions from Eric Leung, Dian Chase, Tracy Edinger, Clint Olson, and Gabrielle Chonoo. 2014-Present
23. *Your In-silico Lab Notebook: Best Practices 2015*. Lecture/Workshop given for OHSU BioDSP group, January 2015.
24. *Everything you wanted to know about bioinformatics but were afraid to ask*. Lecture/Workshop given for OHSU PhD/Postdoc Fellows meeting, October 2014.
25. *List Comprehensions in Python*. Lecture given for Bioinformatics Programming and Scripting Course, Fall 2012.
26. *Introduction to Unit Testing*. Lecture given for Bioinformatics Programming and Scripting Course, Fall 2012.
27. *Introduction to Numerical Python (NumPy)*. Lecture given for Bioinformatics Programming and Scripting Course, Fall 2012.
28. *Introduction to SciPy*. Lectures given for Bioinformatics Programming and Scripting Course, Fall 2012.
29. *An Introduction to ODE Models*. Lecture given for Systems Biology Class, 2012.
30. *Integrating Data for Systems Biology*. Lecture given for Systems Biology Class, 2012.
31. *Work Smarter, Not Harder: Productivity Tools and You*. Lecture given for PhD/Postdoctoral meeting, 2011.
32. *Bayesian Networks*. Lecture given for Statistical Methods in Bioinformatics Class, 2011.
33. *Gibbs Samplers*. Lecture given for Statistical Methods in Bioinformatics Class, 2011. doi:10.6084/m9.figshare.4829530
34. *Workshop on Strings and Matrices in R*. Workshop given for Statistical Methods in Bioinformatics class. 2011.
35. *Introduction to R Workshop*. Workshop given for Statistical Methods in Bioinformatics class. 2011.
36. *Extended Dependency Analysis*. Presentation given for Information Theory Independent Study 2010.
37. *Conant's Laws of Information that Govern Systems*. Presentation given for Information Theory Independent Study, 2010.
38. *Ashby's Law of Requisite Variety and Conant's Information Transfer in Regulation*. Presentation given for Information Theory Independent Study, 2010.
39. *Lab: Using Consense-Cluster to explore the Bittner dataset*. Laboratory given as part of Microarray Analysis Course, OHSU, 2006.

SERVICE STATEMENT

I am a strong supporter of service at OHSU and beyond. I currently participate in the DMICE BCB (Bioinformatics and Computational Biology) Faculty Division meeting, the DMICE Mentoring committee, and have participated in the BCB Curriculum Retreat in order to plan upcoming coursework at DMICE.

As a Pacific Islander, I have a unique viewpoint about diversity and I hope to enhance equal opportunity by participating in OHSU's Diversity Advisory Council (DAC). Beyond OHSU, I believe that we need to increase public engagement of science and increase outreach and mentoring of next-generation science students, especially from disadvantaged populations will enable these students to succeed in STEM-based careers. As a former student of Saturday Academy's scientific mentoring program, I want to contribute back to this community and engage potential STEM students through student outreach and mentoring. I am also involved in outreach through the development of course material for the Biocatalyst training program through Oregon Bioscience Association, which provides bioscience training for unemployed or under-employed professionals.

SERVICE ACCOMPLISHMENTS

Co-organizer for Cascadia R Conference.

Participant/Instructor for PDX Data Rescue/Open Data Day.

Co-Founder of BioData Club group for students and postdocs. Managed speakers, developed free workshops for students, and provided feedback for student presentations. BioData Club is currently at 100 members ranging from OHSU staff, faculty, students and postdocs, providing a unique opportunity to share information and provide mentoring to students.

Developed coursework for unemployed or underemployed IT workers in both biosciences and healthcare for Oregon Bioscience Association.

Reviewer for AMIA, BMC Bioinformatics, and Neurocomputing.

My mentees include Jason Li and Eisa Mahyari, both PhD candidates in DMICE.

Contributor to instructor lesson materials to Software Carpentry.

WORK EXPERIENCE

Assistant Professor, Department of Medical Informatics and Clinical Epidemiology, OHSU, 2017-present.
Postdoctoral Researcher, OHSU Knight Cancer Institute, 2014-2017.

Current Research Support:

Dorr, D (Co-PI), Haendel, M (Co-PI), McWeeney, S (Co-PI) 2015-Present BD2K Training Grant Big Data to Knowledge

No # assigned

Druker (PI)

5/1/2013-4/30/2016

The Leukemia & Lymphoma Society

Beat AML: Precision Medicine for AML Based on Functional Genomics

The major goals of this project is to transform our approach to AML treatment through a deeper understanding of the diversity of the underlying molecular causes of disease and to bring targeted therapies to AML patients through 1) understanding the spectrum of genetic lesions and molecular drivers, 2) functionally annotating drug sensitivity, and 3) Initiating clinical trials with combinations of drugs in refractory patients. Role: Computational Biologist

OPP1131709

Lewinsohn, DM (PI)

10/26/2015-10/31/2018

Bill & Melinda Gates Foundation

Targeting MAIT cells for TB vaccines

This proposal is designed to establish whether or not a vaccine targeting Mucosal Associated Invariant (MAIT) can be used to prevent tuberculosis (TB). Role: Computational Biologist

Instructor, Department of Medical Informatics and Clinical Epidemiology. 2015-Present.
NLM Postdoctoral Fellow, Oregon Health & Science University. 2014-2015.
Visiting Scientist, Sage Bionetworks, Seattle Washington. 2014-2015.
NLM Predoctoral Fellow, Medical Informatics and Clinical Epidemiology, Oregon Health & Science University. 2009–2014.
Bioinformatics Developer/Project Manager, OHSU Knight Cancer Institute, Oregon Health & Science University. 2003-2009. *Teaching Assistant/Computer Programmer/Server Admin*, Department of Medical Informatics & Clinical Epidemiology, Oregon Health & Science University. 2001-2002.
Research Assistant/Computer Programmer, Department of Molecular Medicine, Oregon Health & Science University. 1999-2001.
Research Assistant/Teaching Assistant, Department of Chemistry, Reed College. 1998

AWARDS

NLM Predoctoral Fellowship. 2009-2013.
NLM Postdoctoral Fellowship. 2014-2015.