Ted Laderas, PhD

Assistant Professor, Division of Bioinformatics and Computational Biology, Department of Medical Informatics and Clinical Epidemiology

Researcher, OHSU Knight Cancer Institute
Oregon Health & Science University
3181 SW Sam Jackson Park Road CR145
Portland, OR 97239
(503) 481-8470
laderast@ohsu.edu

EDUCATION

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

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 co-leader of BioData-Club, 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.

CURRENT ACADEMIC COURSES

- *BMI569/669 Data Analytics*, co-taught with Kaiser Permanente (Brian Sikora and Delilah Moore). Summer Quarter, 2015-Present.
- *NEUS640 Python Bootcamp for Neuroscientists.* Taught with Stephen David and Brad Buran. Winter Quarter, 2018.
- *BMI551/561 BCBII Statistical Methods in Computational Biology.* Co-instructor. Winter Quarter, 2014-Present.
- *HSMP/PHE410 Health Informatics.* Course Co-Director. Spring Quarter, 2018.
- *BMI 533/633 Data Harmonization and Standards for Translational Research.* Course to be taught Spring Quarter, 2019. Course is co-designed with Christina Zheng and Melissa Haendel.

COURSES WHICH I HAVE GUEST TAUGHT

- BMI523 Clinical Research Informatics (2017)
- BMI567 Network Science and Biology (2015, 2016, 2017)
- BMI535 Management and Processing of Large Scale Data (2017)
- CSE631 Data Visualization (2017, 2018)
- OHSU Data Science Institute (2017)
- BioData Club (2015-Present)

TEACHING MATERIALS AND COURSES

Lectures and Interactive Workshops are linked where possible.

1. A gRadual intRoduction to Data wRangling. Workshop for Cascadia R 2018. Ted Laderas and Chester Ismay.

2. A gRadual intRoduction to Data Visualization. Workshop for Cascadia R 2018. Chester Ismay and Ted Laderas.

3. Data Literacy. Based on DSIExplore (by myself and Jessica Minnier) and wmf-allhands18 by Mikhail Popov. GitHub repo (installable as a LearnR package).

4. *HMSP410: Health Informatics*. Course material for HMSP410 Health Informatics course at OHSU/PSU School of Public Health. Spring 2018.

5. *Exacloud Training Workshop*. Guest lecture for BMI535 Management and Processing of Large Scale Data. Winter 2018.

6. *A gRadual intRoduction to Shiny*. Workshop for Portland R user group. Winter 2018. Also given for CSE631, Data Visualization.

7. *How are Systems Science and Data Science Connected?*. Seminar for Portland State Systems Science Program. Winter 2018.

8. *NEUS640 Python Bootcamp For Neuroscientists*. Ted Laderas, Brad Buran, Daniela Sadieri, Charles Heller, Michael Mooney, Lisa Karstens, and Stephen David. 5 day in-person workshop for introductory Python using Neuroscience data. Winter 2018. Role: course coordinator.

9. *BMI 523: Actionable Gene Variants*. Guest Lecture for BMI 523 Clinical Research Informatics. November 2017. Role: Guest Lecturer

10. *Exploratory Data Analysis and Statistics*. Workshop with Jessica Minnier for OHSU Data Science Institute 2017. Role: instructor.

11. *R-Bootcamp (tidyverse version on DataCamp)*. Active exercises for learning introductory R using the tidyverse. Written with Jessica Minnier and Chester Ismay. 2017. Code and teaching material available at https://github.com/laderast/RBootcamp Role: course developer and instructor.

12. *A gRadual intRoduction to the `tidyverse`*. Workshop given with Chester Ismay for Cascadia-R 2017 introducing visualization and data cleaning using the `tidyverse`.

13. *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.

14. *An Intro to GitHub Pages*. Workshop given with Robin Champieux and Eric Leung on setting up a personal GitHub webpage. April 2017.

15. *An Intro To Data Carpentry*. Lecture given with Eric Leung about the tidyverse suite of packages for data wrangling and visualization. March 2017.

16. *The Magic of Markdown*. Updated for 2017, including examples of using Zotero as citation manager. March 2017. doi:10.5281/zenodo.495614

17. *Shiny Tutorial for CSE631*. Workshop on developing interactive visualizations using Shiny for CSE631 Data Visualization course. November 2016. DOI: 10.5281/zenodo.495621

18. *BMI569/669 Analytics*. New Course material in SQLite, Logistic Regression and Analysis. August 2016. doi:10.5281/zenodo.495623

19. *Exploring the DREAM Viral Respiratory Dataset using Shiny*. Tutorial in Exploratory Data Analysis (EDA) using *data.table* and *Shiny*. July 2016.

20. *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

21. *Introduction to Machine Learning using Markdown* - Interactive workshop using Markdown to explore machine learning algorithms for BD2K Advanced Skills Course. May 2016.

22. *Clustering Algorithms.* Lecture given for Statistical Methods class. February 2016.

23. *iGraph Tutorial.* Introductory lecture for the igraph package in R for network analysis course. November 2015. doi:10.5281/zenodo.495616

24. *The Magic of Markdown.* Introduction to Markdown in both R, GitHub pages, and Pandoc. BioDSP October 2015. doi:10.5281/zenodo.495614

25. *Pharmacogenomics* Lecture for Analytics Course, August 2015.

26. *Introduction to Clustering.* Interactive slides for understanding clustering. doi:10.5281/zenodo.495624

27. *Introduction to ggvis.* Lecture/Workshop given for OHSU Bioinformatics Discussion for Students and Postdocs, April 2015.

28. *Introduction to ggplot2.* Lecture/Workshop given for OHSU Bioinformatics Discussion for Students and Postdocs, March 2015. doi:10.5281/zenodo.495622

29. *Exacloud Tutorial* - A DIY tutorial to running jobs on Exacloud, OHSU's cluster computing environment. November 2015.

30. *Shiny Tutorial* - A do it yourself tutorial to try out Shiny, ggplot2, and dplyr for interactive graphics. September 2015. doi:10.5281/zenodo.495620

31. *Analytics Course.* Instructor. Hybrid Online/On-campus joint course with DMICE and Kaiser Permanente Analytics group. August 2015.

32. *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

33. *Your In-silico Lab Notebook: Best Practices 2015.* Lecture/Workshop given for OHSU BioDSP group, January 2015.

34. *Everything you wanted to know about bioinformatics but were afraid to ask.* Lecture/Workshop given for OHSU PhD/Postdoc Fellows meeting, October 2014.

35. *List Comprehensions in Python.* Lecture given for Bioinformatics Programming and Scripting Course, Fall 2012.

36. *Introduction to Unit Testing.* Lecture given for Bioinformatics Programming and Scripting Course, Fall 2012.

37. *Introduction to Numerical Python (NumPy).* Lecture given for Bioinformatics Programming and Scripting Course, Fall 2012.

38. *Introduction to SciPy.* Lectures given for Bioinformatics Programming and Scripting Course, Fall 2012.

39. *An Introduction to ODE Models.* Lecture given for Systems Biology Class, 2012.

40. *Integrating Data for Systems Biology.* Lecture given for Systems Biology Class, 2012.

41. *Work Smarter, Not Harder: Productivity Tools and You.* Lecture given for PhD/Postdoctoral meeting, 2011.

42. *Bayesian Networks.* Lecture given for Statistical Methods in Bioinformatics Class, 2011.

43. *Gibbs Samplers.* Lecture given for Statistical Methods in Bioinformatics Class, 2011. doi:10.6084/m9.figshare.4829530

44. *Workshop on Strings and Matrices in R*. Workshop given for Statistical Methods in Bioinformatics class. 2011.

45. *Introduction to R Workshop*. Workshop given for Statistical Methods in Bioinformatics class. 2011.

46. *Extended Dependency Analysis*. Presentation given for Information Theory Independent Study 2010.

47. *Conant's Laws of Information that Govern Systems*. Presentation given for Information Theory Independent Study, 2010.

48. *Ashby's Law of Requisite Variety and Conant's Information Transfer in Regulation*. Presentation given for Information Theory Independent Study, 2010.

49. *Lab: Using Consense-Cluster to explore the Bittner dataset.* Laboratory given as part of Microarray Analysis Course, OHSU, 2006.

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. *Teaching data science fundamentals through realistic synthetic clinical cardiovascular data.* **Ted Laderas**, Nicole Vasilevsky, Bjorn Pederson, Shannon McWeeney, Melissa Haendel, and David Dorr. Submitted to JAMIA. BioRxiv Link: https://www.biorxiv.org/content/early/2017/12/12/232611. 2017. Contribution: First author: helped conceive study, designed bayesian network, developed course material based on dataset.

2. *Integrated functional and mass spectrometry-based flow cytometric phenotyping to describe the immune microenvironment in acute myeloid leukemia.* Adam J Lamble, Matt Dietz, **Ted Laderas**, Shannon McWeeney, Evan F Lind. Journal of Immunological Methods. 2017. Contribution: developed informatics and visualization methodology.

3. *Probabilistic Graphical Models for Systems Biology.* **Ted Laderas**, Aurora Blucher, Guanming Wu and Shannon McWeeney. Awaiting submission. Contribution: first author and conception of manuscript.

4. *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.

5. *Mass Cytometry As a Modality to Identify Candidates for Immune Checkpoint Inhibitor Therapy within Acute Myeloid Leukemia.* Adam Lamble, Yoko Kosaka, Fei Huang, A Kate Sasser, Homer Adams III, Cristina E. Tognon, **Ted Laderas**, Shannon K. McWeeney, Marc M. Loriaux, Jeffrey W. Tyner, Brian J. Druker and Evan F. Lind. Blood, 2016. Contribution: contributed to panel development of CyTOF.

6. *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 Tabernero, 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.

7. *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

8. *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

9. *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

10. *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

11. *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

SOFTWARE DEVELOPMENT (Sole Developer unless specified)

1. `flowDashboard`. Visualization framework in R/Shiny and processing pipeline for CyTOF and flow cytometry data. https://doi.org/10.5281/zenodo.260421

2. `cvdRiskData`. Synthetic dataset for teaching fundamentals in data science. Available as an R package at: https://github.com/laderast/cvdRiskData.

3. `dataLiteracyTutorial`. `LearnR` package for teaching the fundamentals of graph literacy. Based on `DSIExplore` (written with Jessica Minnier) and `wmf-allhands18` (by Mikhail Popov).

4. `DSIExplore`. `LearnR` package for teaching Exploratory Data Analysis and Simple Statistics. Jessica Minnier and **Ted Laderas**.

5. *RBootcamp (tidyverse version)*. DataCamp active exercises for learning introductory R using the `tidyverse`. Jessica Minnier and **Ted Laderas**. Available for free at: https://www.datacamp.com/courses/rbootcamp https://doi.org/10.5281/zenodo.854727

6. `umapr`. R Wrapper package for python implementation. Malisa Smith, Angela Li, Ju Young Kim, **Ted Laderas**, and Sean Hughes. Contribution: documentation and visualization framework for results.

7. `infer`. Andrew Bray, Chester Ismay, Ben Baumer, Mine Cetinkaya-Rundel, **Ted Laderas**, Nick Solomon, Johanna Hardin, Albert Kim, Neal Fultz and Doug Friedman. Contribution: package testing.

8. *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.

9. *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

10. *Surrogate Mutation Explorer.* R/Shiny Interactive Application for exploring surrogate mutations. http://dx.doi.org/10.5281/zenodo.13757

11. *SurrogateMutation.* R Package for mapping mutations and copy number alterations to networks and associated statistics. http://dx.doi.org/10.5281/zenodo.17303

12. *Consense-Cluster.* R Package for comparing clustering output across algorithms. http://dx.doi.org/10.5281/zenodo.17304

13. *ExonModelStrain.* RPackage for detecting alternative exon usage between two strains of mice. http://dx.doi.org/10.5281/zenodo.17305

14. *TandTRAQ.* Perl Script for mapping iTRAQ protein quantitation to X!Tandem peptides.

RESEARCH PRESENTATIONS/LECTURES (Invited Lectures are Indicated)

1. *Mixing Active Learning and Lecturing: Using Interactive Visualization as a Teaching Tool.* Virtual Poster given for ECOTS 2018 (Electronic Conference On Teaching Statistics). May 2018. Jessica Minnier and **Ted Laderas**.

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

3. *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.

4. *Surrogate Mutations and Drug Sensitivity in Breast Cancer Cell Lines.* Plenary talk at NLM Training Conference, Pittsburgh, PA, June 2014.

5. *Connecting Genotypes to Drug Sensitivities in HER2 Positive Cancer Cell Lines.* Doctoral Defense, OHSU, March 2014.

6. *Understanding Expression Differences in RPPA Data: Implications for ODE Models.* Presentation at Integrative Cancer Biology Program retreat 2012.

7. *Connecting Genotypes to Drug Sensitivity in HER2+ Breast Cancer Cell Lines.* Lecture/Dissertation proposal given for PhD/Postdoc Meeting January 2012 and March 2012.

8. *Connecting Genotypes to Drug Sensitivity in Breast Cancer Cell Lines.* Invited presentation at Integrative Cancer Biology Program retreat, 2011.

9. *What are Models For? Making Sense of Systems Biology.* Predoctoral Symposium. 2010.

10. *Two kinds of Robustness.* Presentation given to Bioinformatics Development Group, 2010.

11. *Portland Alcohol Research Center Scientific Advisory Board Review: Bioinformatics & Statistics.* Presentation given to PARC SAB, OHSU, 2009.

12. *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.

13. *An introduction to Consensus Modules for Systems Biology.* Lecture given with Sophia Jeng to Bioinformatics Development Group, OHSU, 2008.

14. *An Introduction to Sloppy Systems Biology.* Lecture given to Bioinformatics Development Group, OHSU, 2008.

15. *Simulated and Synthetic Data for Benchmarking Algorithms.* Lecture given as part of Bioinformatics Methods class, OHSU, 2007.

16. *Introduction to QPACA Pathway Analysis Software and BioPAX.* Talk given at 2006 caBIG Annual Meeting, Washington DC.

17. *Consense: A software package for utilizing multiple clustering methods on Microarray Data.* Talk given at OHSU Student Research Forum, 2005.

RESEARCH POSTERS/ABSTRACTS

1. The `flowDashboard` package for doing comparative flow cytometry analysis. Ted Laderas, Gwendolyn Swarbrick, David Lewinsohn, Debbie Lewinsohn, Evan Lind, and Shannon McWeeney. BOSC2018. June 2018.

2. *Interactive Visualization as a Tool to Teach Mathematical Concepts to OHSU Data Science Institute Students.* Jessica Minnier and *Ted Laderas.* OHSU Symposium on Educational Excellence. April 2018.

3. *Getting your hands dirty with data.* **Ted Laderas**, Melissa Haendel, 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

4. *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

5. *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.

6. *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.

7. *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.

8. *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 Tabernero, 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.

9. *A Network-Based Model of Oncogenic Collaboration for Prediction of Drug Sensitivity.* **Ted Laderas**. RECOMB/ISCB Conference on Regulatory and Systems Genomics, November 2014.

10. *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

11. *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

12. *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.

13. *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 Darakijan, John Belknap, Robert Hitzemann, and Shannon McWeeney. Intelligent Systems in Molecular Biology conference, Toronto, July 2008.

14. *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.

15. *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.

16. *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.

17. *Consense-Cluster: a framework for comparing and benchmarking clustering algorithms.* **Ted Laderas** and Shannon McWeeney. Bioconductor Developer's Meeting, Seattle, Washington, August 2005.

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/APPOINTMENTS

1. Currently serving on DMICE Assessment Planning committee, DMICE BCB Division committee, and DMICE BMI Curriculum Committee.

2. Co-Founder of BioData Club group for students, postdocs, and staff at OHSU. Managed speakers, developed free workshops for students, and provided feedback for student presentations. BioData Club is currently at 109 members ranging from OHSU and PSU staff, faculty, students and postdocs, providing a unique opportunity to share information and provide peer mentoring to students across the organizations.

3. Co-organizer for Cascadia R Conference 2017 and 2018.

4. Contributor to instructor lesson materials to Software Carpentry.

5. Editor at Large for Radian Data.

6. Participant/Instructor for PDX Data Rescue/Open Data Day 2017.

7. Documentation support for Science Hack Day PDX 2017.

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

9. Reviewer for JAMIA, BMC Bioinformatics, and Neurocomputing, Bioinformatics, and AMIA Symposium.

10. My mentees include:

- Jason Li
- Eisa Mahyari
- Lawrence Hsu
- Gabrielle Choonoo (Thesis committee member)
- Connor Smith (Thesis Committee)
- Sean Babcock (Thesis Committee)

WORK EXPERIENCE

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

Ongoing Research Support

T15LM009461 (supplement) Hersh (PI) 7/01/1992-6/01/2018

Biomedical Informatics Research Training at Oregon Health & Science University. Supplement to develop Data Science Materials for T15 training grant. Role: educational developer and instructor.

1U24TR002306-01 Haendel (PI) 9/01/2017-9/01/2019

A National Center for Digital Health Informatics Innovation. We propose to create a national network for enabling digital health research, innovation, and continuous improvement. The goal is to use information science to impact the way that health care functions and the lives of those it serves. Role: education, software development, and data management advocate.

1U54CA224019-01 Tyner (PI) 10/01/2017-10/01/2022

Tumor intrinsic and microenvironmental mechanisms driving drug combination efficacy and resistance in AML. Most patients with acute myeloid leukemia (AML) eventually die when their disease becomes resistant to conventional or even newer treatments. Our proposed studies will shed light on the mechanisms of drug resistance, both within the tumor and in the surrounding environment. This knowledge will help identify more effective therapies — involving combinations of two drugs — that will avoid drug resistance and provide better outcomes for patients with AML. Role: Computational Biologist.

No # assigned Druker (PI) 5/1/2013-5/31/2018 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.

Completed Research Support

T15LM009461
Hersh (PI) 7/01/1992-6/30/2017 *Biomedical Informatics Research Training at Oregon Health & Science University.* Predoctoral and postdoctoral training grant in biomedical informatics. Role: Predoctoral Fellow (2009-14); Postdoctoral Fellow (2014-2015)

OPP1131709
Lewinsohn (PI) 10/26/2015-10/31/2017 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

BD2K Training Grant Dorr, D (Co-PI), Haendel, M (Co-PI), McWeeney, S (Co-PI) 2015-2017 *Big Data to Knowledge.* The goal of this project is to develop training materials in data science. Role: educational developer and instructor.

AWARDS

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