

# 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

My research focus is on the Systems Biology of Complex Diseases. I use integrative modeling approaches across OMICs types to achieve this.

I am also passionate about teaching students to think about data, and have taught Data Science to a variety of groups, including graduate students, post-docs, staff, and clinicians. I am also an RStudio Certified Trainer in both the tidyverse and Shiny.



## EDUCATION

- |                   |  |
|-------------------|--|
| 2014<br> <br>2009 | <ul style="list-style-type: none"><li>● <b>PhD, Biomedical Informatics</b><br/>Oregon Health &amp; Science University <span style="float: right;">📍 Portland, OR</span><ul style="list-style-type: none"><li>• Dissertation: Connecting Genotypes to Drug Sensitivities in HER2 Positive Cancer Cell Lines<sup>1</sup></li></ul></li></ul> |
| 2004<br> <br>2002 | <ul style="list-style-type: none"><li>● <b>M.S., Biomedical Informatics</b><br/>Oregon Health &amp; Science University <span style="float: right;">📍 Portland, OR</span><ul style="list-style-type: none"><li>• Thesis: Developing and validating a tool for microarray cluster analysis<sup>2</sup></li></ul></li></ul>                   |
| 1998<br> <br>1994 | <ul style="list-style-type: none"><li>● <b>B.A., Chemistry</b><br/>Reed College <span style="float: right;">📍 Portland, OR</span><ul style="list-style-type: none"><li>• Thesis: Resonance-Raman Spectroscopy, Chromium Hexacarbonyl, and Me: A Tale of Intrigue</li></ul></li></ul>   |

View this CV online with links at [laderast.github.io/cv](https://laderast.github.io/cv)

## CONTACT

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- 📞 503-481-8470

## LANGUAGE SKILLS



## TEACHING

### ● **Teaching Statement**

I believe in democratizing data science. To this end, I have been involved with several national educational efforts: Big Data to Knowledge, National Library of Medicine's efforts with data science. My workshops, lectures and lessons have been utilized at multiple schools, and by multiple audiences, including clinicians, bioinformaticians, undergraduates.

I utilize evidence-based pedagogical techniques in my teaching, specifically active learning and psychological safety. I am a firm believer in making students feel psychologically safe and giving them space to be curious. As a result, my work has been recognized as being accessible to a wide audience.

I believe that we must give graduate students more transferrable skills, and so I have co-founded BioData Club, a group at OHSU and beyond that focuses on teaching and learning data science skills. I am dedicated to my students, and courses and workshops show consistently high ratings and evaluations.

In my educational work, I have focused on Exploratory Data Analysis (EDA) as a way to be curious and to not be afraid of your data, Predictive Modeling and Data Analytics, and the importance of interdisciplinary collaboration.

## COURSES

Current  
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2015

### ● **BMI569: Data Analytics<sup>3</sup>**

Biomedical Informatics, Oregon Health & Science University  
 Portland, OR

- Course co-director. Hybrid course co-taught with Kaiser Permanente Insight group.
- Winner of the Sakai Torchbearer Award 2020. Multiple nominations from students.
- Audience is both clinicians and bioinformaticians.

Current  
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2020

### ● **HIP 523 Computerized Data Management**

Human Investigations Program, Oregon Health & Science University  
 Portland, OR

- Course instructor. Taught two active lab sessions in exploratory data analysis and predictive modeling.

Current  
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2020

### ● **BMI535/635: Management and Processing of Large Scale Data**

Biomedical Informatics, Oregon Health & Science University  
 Portland, OR

- Course co-director. A course that focuses on UNIX scripting, parallel computing, and large scale databases.

Current  
|  
2020

- **BMI507: Ready for R<sup>4</sup>**  
Biomedical Informatics, Oregon Health & Science University  
 Portland, OR
  - Course Director. A gentle introduction to visualization, data transformation, and statistics using R and the tidyverse.
  - Course is open to anyone at <https://ready4r.netlify.app/mailing>
  - Currently over 1000 external students have enrolled.
- **NEUS643: Stats for Neuroscientists<sup>5</sup>**  
Neuroscience Graduate Program, Oregon Health & Science University  
 Portland, OR
  - Course Director. An introduction to image processing, statistics, and machine learning focusing on confocal microscopy data.
  - Lecture/Active Learning Labs using RStudio.cloud.
- **BMI551/651 Bioinformatics and Computational Biology II: Statistical Methods**  
Biomedical Informatics, Oregon Health & Science University  
 Portland, OR
  - Course co-instructor. Provided drop-in sessions for R/Bioconductor programming and general tutoring.
- **HMSP410/PHE427: Introduction to Health Informatics<sup>6</sup>**  
Health Systems Management/Public Health Education, Portland State University  
 Portland, OR
  - Course co-director. A gentle introduction to relevant data science and informatics concepts for undergraduate students.
  - Includes sections on data literacy, genomics, and metadata
- **NEUS642: Python Bootcamp for Neuroscientists<sup>7</sup>**  
Neuroscience Graduate Program, Oregon Health & Science University  
 Portland, OR
  - Course director. Week long introduction to Python for non-computational neuroscientists.
  - With Daniela Saderi, Lucille Moore, Brad Buran, Charles Heller, Zack Swartz, Lisa Karstens, Stephen David, Michael Mooney.

2019  
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2015

2018  
|  
2017

2018



## EDUCATIONAL RESOURCES

Current  
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2015

- **RBootcamp<sup>8</sup>**  
Online Course
  - Online Interactive Introduction to the Tidyverse. Currently available as a free course to everyone.
  - Written with Jessica Minnier. Taken by incoming Bioinformatics students.

Current  
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2017

- **Clinical Data Wrangling<sup>9</sup>**  
NLM T15 Data Science Workshop
  - Multi-day workshop on understanding clinical data quality issues through both didactic lecturing and active data exploration.
  - Written with Eilis Boudreau and Nicole Weiskopf.
  - Given as an intro to both our incoming clinical and bioinformatics students.

Current  
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2015

- **Introduction to iGraph<sup>10</sup>**  
Interactive Lecture
  - Workshop introducing the basics of network analysis using the `igraph` package.
  - Given for the last 4 years in Guanming Wu's Network Analysis course

2019  
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2017

- **A gRadual Introduction to Shiny<sup>11</sup>**  
Workshop
  - Workshop introducing basic interactive visualization and dashboard building using the Shiny framework for R
  - Written with Jessica Minnier
  - Given for PDX R User Group and WNAR 2019. Used by multiple colleges, including Reed College and Lehmann College

2019

- **NHANES Data Scavenger Hunt<sup>12</sup>**  
BioData Club Workshop
  - An introduction to Exploratory Data Analysis using the burro app to explore outcomes using the NHANES (National Health and Nutrition Examination Survey) dataset.
  - Written with Jessica Minnier and Thomas Frohwein

2019

- **How to make a reproducible paper<sup>13</sup>**  
BioData Club Workshop
  - Workshop introducing best practices in data management and code management to make an analysis reproducible.
  - Written with Aurora Blucher. Given for BioData Club.

- 2019
- **Data Storytelling Workshop<sup>14</sup>**  
BioData Club Workshop
    - You are making a figure for your paper and want it to be the best it can be. Come and learn techniques for communicating your findings clearly. Learn about the role of color, annotations, and simplifying your figures to communicate effectively.
    - Workshop given for BioData Club. RStudio materials can be freely accessed online.
- 2018
- **cvdRiskData Prediction Workshop<sup>15</sup>**  
Big Data to Knowledge (BD2K) workshop
    - A workshop given for Portland State University students exploring the difficulties of predicting cardiovascular risk using shiny for exploratory data analysis and caret for machine learning. Part 1 and Part 2.
    - Written with David Dorr
- 2018  
|  
2017
- **Data Literacy Tutorial<sup>16</sup>**  
Interactive Tutorial
    - Interactive tutorial introducing the basic concepts of visualization and data literacy
    - Used in both HMSP410 and PHE427 courses.
- 2018
- **Academic Site Workshop Using GitHub Pages<sup>17</sup>**  
BioData Club Workshop
    - Workshop for setting up a personal academic website using GitHub Pages
    - 115 students, faculty, and staff have used this workshop, many at external institutions



## SOFTWARE

- Current  
|  
2018
- **burro<sup>18</sup>**  
R Package
    - R Package for exploring data. Used in multiple courses
- Current  
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2017
- **flowDashboard<sup>19</sup>**  
R Package
    - Visualization framework in R/Shiny and processing pipeline for CyTOF and high dimensionality flow cytometry data.

Current 2017	● <b>DSIExplore<sup>20</sup></b> R Package <ul style="list-style-type: none"><li>• LearnR interactive tutorial explaining the basic behind exploratory data analysis for categorial and continuous data</li><li>• Written with Jessica Minnier</li></ul>
2019	● <b>decampr</b> R Package <ul style="list-style-type: none"><li>• R Package for editing interactive lessons using the course-R-starter framework by Ines Montani</li><li>• Written with Jessica Minnier</li></ul>
2014	● <b>surrogateMutation<sup>21</sup></b> R Package <ul style="list-style-type: none"><li>• R Package for mapping mutations and copy number alterations to networks and associated statistics. <a href="http://dx.doi.org/10.5281/zenodo.17303">http://dx.doi.org/10.5281/zenodo.17303<sup>22</sup></a></li></ul>
2011	● <b>ExonModelStrain<sup>23</sup></b> R Package <ul style="list-style-type: none"><li>• R Package for detecting alternative exon usage in the Affymetrix Exon Array.</li></ul>
2004	● <b>Consense-Cluster<sup>24</sup></b> R Package <ul style="list-style-type: none"><li>• R Package for comparing multiple clustering methods</li></ul>

## RESEARCH

### ● 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 PUBLICATIONS, POSTERS, AND TALKS

2020

### ● Reversible suppression of T cell function in the bone marrow microenvironment of acute myeloid leukemia<sup>25</sup>

PNAS <https://doi.org/10.1073/pnas.1916206117>

• Adam J Lamble, Yoko Kosaka, **Ted Laderas**, Allie Maffit, Andy Kaempf, Lauren K Brady, Weiwei Wang, Nicola Long, Jennifer N Saultz, Motomi Mori, David Soong, Clare V LeFave, Fei Huang, Homer Adams, Marc M Loriaux, Cristina E Tognon, Pierrette Lo, Jeffrey W Tyner, Guang Fan, Shannon K McWeeney, Brian J Druker, Evan F Lind

2019

### ● Illuminating Biological Pathways for Drug Targeting in Head and Neck Squamous Cell Carcinoma<sup>26</sup>

PLOS One <https://doi.org/10.1371/journal.pone.0223639>

• Gabrielle Choonoo, Aurora S. Blucher, Samuel Higgins, Mitzi Boardman, Sophia Jeng, Christina Zheng, James Jacobs, Ashley Anderson, Steven Chamberlin, Nathaniel Evans, Myles Vigoda, Benjamin Cordier, Jeffrey W. Tyner, Molly Kulesz-Martin, Shannon K. McWeeney, and **Ted Laderas**.  
• Senior Author. Did code review of entire workflow and published the workflow as an RMarkdown Notebook at mybinder.org

- 2019 ● **CSF1R inhibitors exhibit anti-tumor activity in acute myeloid leukemia by blocking paracrine signals from support cells<sup>27</sup>**  
Blood <https://doi.org/10.1182/blood-2018-03-838946>  
• David K Edwards, Kevin Watanabe-Smith, Angela Rofelty, Alisa Dammersawad, **Ted Laderas**, Adam Lamble, Evan F Lind, Andy Kaempf, Motomi Mori, Mara Rosenberg, Amanda d'Almeida, Nicola Long, Anupriya Agarwal, David Tyler Sweeney, Marc Loriaux, Shannon K McWeeney, Jeffrey W Tyner.
- 2019 ● **Immune checkpoint inhibitors reverse T-cell functional suppression in the bone marrow of a subset of AML patients**  
The Journal of Immunology  
• Evan F Lind, Adam J Lamble, Yoko Kosaka, **Ted Laderas**, Lauren Brady, Fei Huang, Brian J Druker, Jeffrey W Tyner, Shannon McWeeney
- 2019 ● **Conversations about Sleep: Clinical Data Wrangling**  
AMIA Informatics Educators Conference  
• **Ted Laderas**, Nicole Weiskopf, and Eilis Boudreau. Talk given for American Medical Informatics Association's Informatics Educator's Conference
- 2019 ● **Clinical Data Wrangling: Active/Didactic Learning.**  
Symposium on Data Science and Statistics  
• **Ted Laderas**, Nicole Weiskopf, and Eilis Boudreau. Talk given for Symposium on Data Science and Statistics.
- 2019 ● **Data Scavenger Hunts: Learning about datasets together<sup>28</sup>**  
CSV Conference <https://doi.org/10.6084/m9.figshare.12654140.v1>  
• Talk given for CSV Conference
- 2019 ● **Teaching Bioinformatics Students about Clinical Data<sup>29</sup>**  
OSU Center for Genome Research and Computing Spring Conference <https://doi.org/10.6084/m9.figshare.12654152.v1>  
• Invited talk.
- 2019 ● **Democratizing Data Science Using LearnR and Shiny<sup>30</sup>**  
RStudio Conference  
• Poster on interactive visualization and pedagogy.  
• Written with Jessica Minnier
- 2018 ● **Immunogenomic Exploration of the Acute Myeloid Leukemia Microenvironment Identifies Determinants of T-Cell Fitness.<sup>31</sup>**  
Blood <https://doi.org/10.1182/blood-2018-99-118424>  
• Lauren K Brady, David Soong, Evan F Lind, Yoko Kosaka, Adam J Lamble, Michael Schaffer, Brendan P Hodgkinson, Clare Lefave, **Ted Laderas**, Shannon K McWeeney, Homer Adams, Yann Abraham, Pegah Safabakhsh, Jeffrey W Tyner, Brian J Druker, Fei Huang.

- 2018
- **Integrated functional and mass spectrometry-based flow cytometric phenotyping to describe the immune microenvironment in acute myeloid leukemia<sup>32</sup>**  
Journal of immunological methods  
<https://doi.org/10.1016/j.jim.2017.11.010>
- 2018
- **How are Data Science and Systems Science Connected?<sup>33</sup>**  
Systems Science Program, Portland State University
    - Talk given about the relationship between machine learning and systems science
- 2017
- **Training future biocurators through data science trainings and open educational resources.**  
F1000 Research
    - Nicole Vasilevsky, **Ted Laderas**, Jackie Wirz, Bjorn Pederson, David A Dorr, William Hersh, Shannon McWeeney, Melissa Haendel.
- 2017
- **Teaching data science fundamentals through realistic synthetic clinical cardiovascular data<sup>34</sup>**  
Biorkv
    - **Ted Laderas**, Nicole Vasilevsky, Bjorn Pederson, Shannon McWeeney, Melissa Haendel, and David Dorr.
    - Contribution: First author: helped conceive study, designed bayesian network, developed course material based on dataset.
- 2017
- **Data Science for Basic Scientists<sup>35</sup>**  
OHSU Symposium on Educational Excellence  
<https://doi.org/10.6084/m9.figshare.12654158.v1>
    - Invited talk.
- 2016
- **Comprehensive characterization of VISTA expression in patients with acute myeloid leukemia<sup>36</sup>**  
Journal of Clinical Oncology  
[https://doi.org/10.1200/JCO.2016.34.15\\_suppl.e14546](https://doi.org/10.1200/JCO.2016.34.15_suppl.e14546)
    - Adam Lamble, Yoko Kosaka, Fei Huang, Kate Sasser, Cristina Tognon, **Ted Laderas**, Shannon McWeeney, Marc Loriaux, Brian J Druker, Jeffrey Tyner, Evan Lind

- 2015 ● **The Consensus Molecular Subtypes of Colorectal Cancer<sup>37</sup>**  
Nature Medicine <https://doi.org/10.1038/nm.3967>  
· 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 Missaglia, 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.  
· Contribution: mapped and analyzed OMICs data to consensus cancer subtypes.
- 2015 ● **Between Pathways and Networks lies Context<sup>38</sup>**  
Science Progress <https://doi.org/10.3184/003685015x14368898634462>  
· **Ted Laderas**, Guanming Wu, and Shannon McWeeney.
- 2015 ● **A network-based model of oncogenic collaboration for prediction of drug sensitivity<sup>39</sup>**  
Frontiers in Genetics <https://dx.doi.org/10.3389%2Ffgene.2015.00341>  
· **Ted G Laderas**, Laura M Heiser, Kemal Sönmez
- 2011 ● **Computational detection of alternative exon usage<sup>40</sup>**  
Frontiers in Neuroscience <https://doi.org/10.3389/fnins.2011.00069>  
· **Ted G Laderas**, Nicole AR Walter, Michael Mooney, Kristina Vartanian, Priscila Darakjian, Kari Buck, Christina A Harrington, John Belknap, Robert Hitzemann, Shannon K McWeeney
- 2009 ● **High throughput sequencing in mice: a platform comparison identifies a preponderance of cryptic SNPs<sup>41</sup>**  
BMC genomics <https://doi.org/10.1186/1471-2164-10-379>  
· Nicole AR Walter, Daniel Bottomly, **Ted Laderas**, Michael A Mooney, Priscila Darakjian, Robert P Searles, Christina A Harrington, Shannon K McWeeney, Robert Hitzemann, Kari J Buck
- 2007 ● **Consensus framework for exploring microarray data using multiple clustering methods<sup>42</sup>**  
OMICS <https://doi.org/10.1089/omi.2006.0008>  
· **Ted Laderas** and Shannon McWeeney
- 2007 ● **TandTRAQ: an open-source tool for integrated protein identification and quantitation<sup>43</sup>**  
Bioinformatics <https://doi.org/10.1093/bioinformatics/btm467>  
· **Ted Laderas**, Cory Bystrom, Debra McMillen, Guang Fan, Shannon McWeeney

## ↗ SELECTED DATA SCIENCE WRITING

- |      |   |
|------|---|
| 2020 | <ul style="list-style-type: none"><li>● <b>Rebuilding the RBootcamp and Generating R Tutorials<sup>45</sup></b><br/>RStudio Education Blog<ul style="list-style-type: none"><li>• Story about building our interactive RBootcamp using Ines Montani's interactive R/Python Framework.</li><li>• Written with Florencia D'Andrea and Jessica Minnier</li></ul></li></ul>         |
| 2019 | <ul style="list-style-type: none"><li>● <b>RStudioConf 2019: Education and Organizations<sup>46</sup></b><br/>Personal Blog<ul style="list-style-type: none"><li>• Story about presenting our poster about interactive data science education and educational resources/talks at RStudioConf 2019</li></ul></li></ul>   |
| 2019 | <ul style="list-style-type: none"><li>● <b>My Experience with RStudio Instructor Training<sup>47</sup></b><br/>RStudio Education Blog<ul style="list-style-type: none"><li>• Story about becoming an RStudio Certified Instructor in the Tidyverse and Shiny</li></ul></li></ul>  |
| 2019 | <ul style="list-style-type: none"><li>● <b>Package Building: How <code>DESCRIPTION</code>, <code>NAMESPACE</code>, <code>roxygen</code>, and <code>devtools::document</code> work together<sup>48</sup></b><br/>Personal Blog<ul style="list-style-type: none"><li>• My notes on the bits about package building in R that are a little hard to understand.</li></ul></li></ul> |
| 2018 | <ul style="list-style-type: none"><li>● <b>What we learned teaching Python to Neuroscience Students<sup>49</sup></b><br/>Personal Blog<ul style="list-style-type: none"><li>• Notes on organizing an intro Python course for Neuroscience Students</li></ul></li></ul>  |
| 2018 | <ul style="list-style-type: none"><li>● <b>Things we learned teaching clinical data wrangling<sup>50</sup></b><br/><ul style="list-style-type: none"><li>• My notes on teaching the clinical data wrangling short course, and intro course introducing students to the critical thinking data process with the Sleep Heart Health Study dataset</li></ul></li></ul>             |
| 2018 | <ul style="list-style-type: none"><li>● <b>So You've Accidentally Checked a Large File Into Git<sup>51</sup></b><br/>Personal Blog<ul style="list-style-type: none"><li>• Notes on fixing your Git history using the BFG</li></ul></li></ul>  |
| 2017 | <ul style="list-style-type: none"><li>● <b>Some Lessons we Learned Running Cascadia R<sup>52</sup></b><br/>Personal Blog<ul style="list-style-type: none"><li>• Notes on organizing and running the first NW regional R Conference, Cascadia R</li></ul></li></ul>  |

## SERVICE

### ● 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 have dedicated myself to making classes and workshops psychologically safe.

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 HISTORY AND ACCOMPLISHMENTS

Current  
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2015

### ● BioData Club<sup>53</sup>

Oregon Health & Science University

- Co-founder. Data Science focused community of practice. We are students, postdocs, staff, and faculty focused on learning Data Science skills together
- Currently at 329 members spanning OHSU, PSU and beyond

Current  
|  
2019

### ● Portland R User Group<sup>54</sup>

- Co-organizer.

Current  
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2017

### ● DMICE Assessment and Planning Committee

Current  
|  
2017

### ● DMICE BCB Division Committee

Current  
|  
2017

### ● Biomedical Informatics Curriculum Committee

Current  
|  
2017

### ● DMICE BCB Admissions Committee

Oregon Health & Science University

- Current | 2019
- **OHSU Computational Forum**
    - Co-organizer
- 2019
- **Engaging Students in Statistics & Data Science**  
Symposium on Data Science and Statistics
    - Session Chair.
- 2019
- **Software Carpentry**
    - Contributor to instructor training materials.
- 2018 | 2017
- **Cascadia-R Conference<sup>55</sup>**  
Oregon Health & Science University
    - Co-founder. Regional Conference focused on sharing skills and projects using the R Statistical language. Responsible for logistics, talk selection, and scholarship selection
    - 254 Attendees in 2018.

## POSITIONS AND WORK EXPERIENCE

- Current | 2017
- **Assistant Professor, Division of Bioinformatics and Computational Biomedicine**  
Medical Informatics and Clinical Epidemiology, Oregon Health & Science University  Portland, OR
- 2017 | 2015
- **Postdoctoral Researcher, OHSU Knight Cancer Institute**  
Oregon Health & Science University  Portland, OR
- 2017 | 2014
- **Faculty Instructor**  
Medical Informatics and Clinical Epidemiology, Oregon Health & Science University  Portland, OR
- 2015 | 2014
- **NLM Postdoctoral Fellow, Division of Bioinformatics and Computational Biology**  
Medical Informatics and Clinical Epidemiology, Oregon Health & Science University  Portland, OR
- 2015 | 2014
- **Visiting Scientist**  
Sage Bionetworks  Seattle, WA
- 2014 | 2009
- **NLM Predoctoral Fellow, Division of Bioinformatics and Computational Biology**  
Medical Informatics and Clinical Epidemiology, Oregon Health & Science University  Portland, OR

- 2009 |  
2003
- **Bioinformatics Developer/Project Manager, OHSU Knight Cancer Institute**  
Oregon Health & Science University 📍 Portland, OR
- 2002 |  
2001
- **Teaching Assistant/Computer Programmer/Server Admin, Medical Informatics and Clinical Epidemiology**  
Oregon Health & Science University 📍 Portland, OR
- 2001 |  
1999
- **Research Assistant/Computer Programmer, Department of Molecular Medicine**  
Oregon Health & Science University 📍 Portland, OR
    - Developed and extended real time image processing pipeline using LabView. Conducted surface tension experiments using lung surfactant components
- 1998 |  
1996
- **Research Assistant/Teaching Assistant**  
Gerrity Lab 📍 Reed College
    - TA in Instrumentation Lab
    - Conducted research using resonance raman spectroscopy/
    - Programmed in LabView/Igor

## CURRENT SUPPORT

- 10/01/2022 |  
10/01/2017
- **Tumor intrinsic and microenvironmental mechanisms driving drug combination efficacy and resistance in AML (Current)**  
Tyner (PI) U54CA224019 📍 National Cancer Institute
    - 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
- 5/31/2022 |  
09/01/2018
- **The Gut Microbiome and HLA B27-associated Acute Anterior Uveitis (Current)**  
Rosenbaum (PI) 5R01EY029266-02 📍 National Eye Institute
    - Uveitis is a leading cause of blindness and acute anterior uveitis is the most common form of uveitis. Although a cell surface molecule known as HLA B27 markedly increases the risk to develop acute anterior uveitis, the mechanism is unknown. We have made novel observations about the effect of HLA B27 on the microbiome in the gut and in the joint in rats, and propose to extrapolate these studies to patients with acute anterior uveitis.
    - Role: Coinvestigator



## COMPLETED SUPPORT

- 06/01/2019 ● **Biomedical Informatics Research Training at Oregon Health & Science University**  
I 07/01/2017 Hersh (PI) 3T15LM007088026S1 National Library of Medicine
  - Supplement to develop data science materials for T15 training grant.
  - Role: Educational Developer and Instructor
- 6/30/2022 ● **A National Center for Digital Health Informatics Innovation (Completed)**  
I 09/01/2017 Haendel (PI) U24TR002306 National Center for Advancing Translational Sciences
  - 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 (2017-2019)
- 10/31/2018 ● **Targeting MAIT cells for TB vaccines (completed)**  
I 10/26/2015 Lewinsohn (PI) OPP1131709 Bill and Melinda Gates Foundation
  - 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
- 6/30/2022 ● **Biomedical Informatics Research Training at Oregon Health & Science University**  
I 07/01/1992 Hersh (PI) T15LM007088 National Library of Medicine
  - Predoctoral and postdoctoral training in biomedical informatics
  - Role: Predoctoral Fellow (2019-2014), Postdoctoral Fellow (2014-2015)
- 5/31/2017 ● **Beat AML: Precision Medicine for AML Based on Functional Genomics**  
I 5/1/2013 Druker (PI) (No # Assigned) Leukemia and Lymphoma Society
  - 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



## LINKS

- 1: <https://scholararchive.ohsu.edu/concern/etds/kk91fk708?locale=en>
- 2: <https://scholararchive.ohsu.edu/concern/etds/76537133j?locale=en>
- 3: <https://laderast.github.io/AnalyticsCourse>
- 4: <https://ready4r.netlify.app>
- 5: <https://stats4neuro.netlify.app>

- 6: <https://laderast.github.io/PHE427/>
- 7: [https://github.com/dasaderi/python\\_neurobootcamp](https://github.com/dasaderi/python_neurobootcamp)
- 8: <https://r-bootcamp.netlify.app>
- 9: [https://laderast.github.io/clinical\\_data\\_wrangling](https://laderast.github.io/clinical_data_wrangling)
- 10: <http://laderast.github.io/graphTutorial/>
- 11: [https://laderast.github.io/gradual\\_shiny](https://laderast.github.io/gradual_shiny)
- 12: [https://laderast.github.io/nhanes\\_explore](https://laderast.github.io/nhanes_explore)
- 13: [https://biodata-club.github.io/talks/repro\\_paper.pdf](https://biodata-club.github.io/talks/repro_paper.pdf)
- 14: [https://laderast.github.io/data\\_storytelling\\_bdc/#1](https://laderast.github.io/data_storytelling_bdc/#1)
- 15: <https://github.com/laderast/cvdRiskData>
- 16: <https://tladeras.shinyapps.io/dataLiteracyTutorial/>
- 17: [https://github.com/laderast/academic\\_site\\_workshop](https://github.com/laderast/academic_site_workshop)
- 18: <https://laderast.github.io/burro>
- 19: <https://github.com/laderast/flowDashboard>
- 20: <https://github.com/laderast/DSIExplore>
- 21: <https://github.com/laderast/surrogateMutation>
- 22: <http://dx.doi.org/10.5281/zenodo.17303>
- 23: <https://github.com/laderast/ExonModelStrain>
- 24: <https://github.com/laderast/consense>
- 25: <https://doi.org/10.1073/pnas.1916206117>
- 26: <https://doi.org/10.1371/journal.pone.0223639>
- 27: <https://doi.org/10.1182/blood-2018-03-838946>
- 28: <https://doi.org/10.6084/m9.figshare.12654140.v1>
- 29: <https://doi.org/10.6084/m9.figshare.12654152.v1>
- 30: [http://bit.ly/equal\\_vis](http://bit.ly/equal_vis)
- 31: <https://doi.org/10.1182/blood-2018-99-118424>
- 32: <https://doi.org/10.1016/j.jim.2017.11.010>
- 33: [https://laderast.github.io/sysc\\_data\\_sci/](https://laderast.github.io/sysc_data_sci/)
- 34: <https://www.biorxiv.org/content/early/2017/12/12/232611>
- 35: <https://doi.org/10.6084/m9.figshare.12654158.v1>
- 36: [https://doi.org/10.1200/JCO.2016.34.15\\_suppl.e14546](https://doi.org/10.1200/JCO.2016.34.15_suppl.e14546)
- 37: <https://doi.org/10.1038/nm.3967>
- 38: <https://doi.org/10.3184/003685015x14368898634462>
- 39: <https://dx.doi.org/10.3389%2Ffgene.2015.00341>
- 40: <https://doi.org/10.3389/fnins.2011.00069>
- 41: <https://doi.org/10.1186/1471-2164-10-379>
- 42: <https://doi.org/10.1089/omi.2006.0008>
- 43: <https://doi.org/10.1093/bioinformatics/btm467>
- 44: <https://laderast.github.io/blog/>
- 45: <https://education.rstudio.com/blog/2020/03/r-bootcamp/>
- 46: <http://laderast.github.io/2019/01/24/rstudio-conf-2019-education-and-organizations/>
- 47: <https://education.rstudio.com/blog/2019/11/my-experience-with-rstudio-instructor-training/>
- 48: <http://laderast.github.io/2019/02/12/package-building-description-namespace/>
- 49: <http://laderast.github.io/2018/01/17/what-we-learned-teaching-python-to-neuroscience-students/>
- 50: <http://laderast.github.io/2018/10/15/clinical-data-wrangling/>
- 51: <http://laderast.github.io/2018/01/05/so-you've-accidentally-checked-in-a-large-file-into-git/>
- 52: <http://laderast.github.io/2017/06/07/cascadiarnotes/>
- 53: <https://biodata-club.github.io>
- 54: <https://pdxrlang.org>

55: <https://cascadiarconf.com/>