




# SERGIO RUIZ-CARMONA

I am currently a Research Officer at the Baker Institute<sup>1</sup>, under the supervision of professors Mike Inouye<sup>2</sup> and Agus Salim. My research interests are broad and involve mainly the relationship between genetic variants and their effect on protein structures. I carried out my MSc and PhD in Barcelona in the Barril Lab<sup>3</sup>, where I worked with different structure-based drug design methods with the aim to improve drug design for non-standard targets.






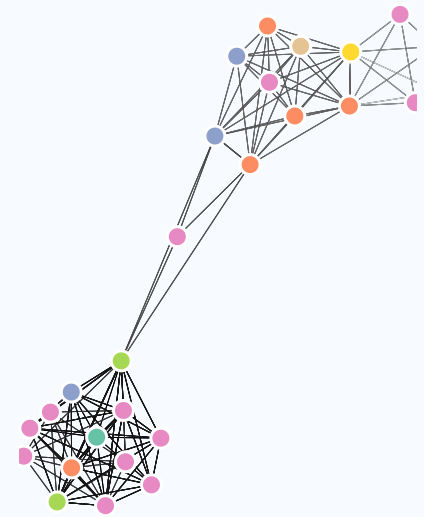
## EDUCATION

- 2017  
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2012
- PhD in Biomedicine**  
Universitat de Barcelona  Barcelona, ESP
    - Virtual Screening for novel MoA: Apps. and method developments
    - Development and application of structure-based drug discovery methods
    - Awards: Extraordinary prize for PhD Thesis and Ramon Margalef award for best publication
- 2012  
|  
2010
- MSc in Bioinformatics for Health Sciences**  
Universitat Pompeu Fabra  Barcelona, ESP
    - Expanding Druggable Genome: PP-Interfaces as a new target class
    - Study of novel rational approach to find PP interfacial binders
- 2010  
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2006
- BSc in Biotechnology**  
Universitat Autònoma de Barcelona  Barcelona, ESP








## RESEARCH EXPERIENCE

- current  
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2019
- Research Officer**  
Inouye Lab  Baker Heart and Diabetes Institute
    - Led development and implementation of interactive data visualizations to help users compare themselves to other demographics.
- 2018  
|  
2017
- Postdoctoral Researcher**  
Barril Lab  Universitat de Barcelona
    - Independently analyzed and constructed statistical models for large data sets pertaining to carbon decomposition rates.
- 2017  
|  
2012
- PhD Researcher**  
Barril Lab  Universitat de Barcelona
    - Independently analyzed and constructed statistical models for large data sets pertaining to carbon decomposition rates.

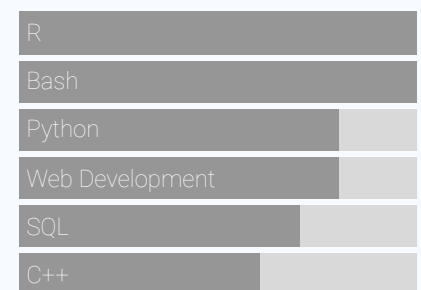


View this CV online with links at  
<https://www.ruizsergio.com/cv/>

## CONTACT

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## LANGUAGE SKILLS



The source code is available on  
[github.com/sruizcarmona/](https://github.com/sruizcarmona/).

Last updated on 2021-04-13.

2017  
|  
2017



### EMBO Short-Term Fellow

Andreas Bender Lab

📍 University of Cambridge

- Developed mathematical model to predict the transport of sulfur through the environment with applications in waste cleanup.

2017  
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2017



### MuTaLig COST Action Short-Term Fellow

Peter Kolb Lab

📍 Marburg University

- Analyzed and visualized data for CATOS fish tracking project.
- Head of data mining project to establish temporal trends in population densities of *Mysis diluviana* (Mysis).
- Ran project to mathematically model the migration patterns of Mysis (honors thesis project.)



## TEACHING EXPERIENCE

2020



### workshop

RStudio::conf 2020

- Served as TA for two day workshop on how to leverage Javascript in Shiny applications
- Lectured on using R2D3 package to build interactive visualizations.<sup>4</sup>

2018  
|  
2017



### R course baker

Vanderbilt Biostatistics Department

📍 Nashville, TN

- TA and lectured
- Topics covered from penalized regression to boosted trees and neural networks
- Highest level course offered in department

2017  
|  
2017



### pharmacy degree

Vanderbilt Biostatistics Department

📍 Nashville, TN

- TA and lectured
- Covered introduction to R language for statistics applications
- Graduate level class



## SELECTED DATA SCIENCE WRITING

2019



### small molecule param

LiveFreeOrDichotomize.com

- Story of parsing large amounts of genomics data.
- Provided advice for dealing with data much larger than disk.
- Reached top of HackerNews.

I am passionate about education. I believe that no topic is too complex if the teacher is empathetic and willing to think about new methods of approaching task.

I regularly blog about data science and visualization on my blog LiveFreeOrDichotomize.<sup>5</sup>

2018



## **rdock blogs**

RStudio Tensorflow Blog

- Walk through of training a convolutional neural network to achieve state of the art recognition of activities from accelerometer data.
- Contracted article.



## **SELECTED PRESS (ABOUT)**

2017

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2017



## **covid research**

Science

- Story of the app Papr<sup>6</sup> made with Jeff Leek and Lucy D'Agostino McGowan.



## **SELECTED PUBLICATIONS, POSTERS, AND TALKS**

2020



### **Building a software package in tandem with machine learning methods research can result in both more rigorous code and more rigorous research**

ENAR 2020

- Invited talk in Human Data Interaction section.
- How and why building an R package can benefit methodological research

2020



### **Stochastic Block Modeling in R, Statistically rigorous clustering with rigorous code<sup>7</sup>**

RStudio::conf 2020

- Invited talk about new sbmR package<sup>8</sup>.
- Focus on how software development and methodological research can improve both benefit when done in tandem.

2020



### **PheWAS-ME: A web-app for interactive exploration of multimorbidity patterns in PheWAS<sup>9</sup>**

Bioinformatics

- Manuscript detailing application for the exploration of multimorbidity patterns in PheWAS analyses
- See landing page<sup>10</sup> for more information.

2019

|

2019



### **Charge Reductions Associated with Shortening Time to Recovery in Septic Shock<sup>11</sup>**

Chest

- Authored with Wesley H. Self, MD MPH; Dandan Liu, PhD; Stephan Russ, MD, MPH; Michael J. Ward, MD, PhD, MBA; Nathan I. Shapiro, MD, MPH; Todd W. Rice, MD, MSc; Matthew W. Semler, MD, MSc.

- 2019  
|  
2019
- **Multimorbidity Explorer | A shiny app for exploring EHR and biobank data<sup>12</sup>**  
RStudio::conf 2019
    - Contributed Poster. Authored with Yaomin Xu.
- 2019  
|  
2019
- **Taking a network view of EHR and Biobank data to find explainable multivariate patterns<sup>13</sup>**  
Vanderbilt Biostatistics Seminar Series
    - University wide seminar series.
- 2019
- **Patient-specific risk factors independently influence survival in Myelodysplastic Syndromes in an unbiased review of EHR records**  
Under-Review (copy available upon request.)
    - Bayesian network analysis used to find novel subgroups of patients with Myelodysplastic Syndromes (MDS).
    - Analysis done using method built for my dissertation.
- 2019
- **Patient specific comorbidities impact overall survival in myelofibrosis**  
Under-Review (copy available upon request.)
    - Bayesian network analysis used to find robust novel subgroups of patients with given genetic mutations.
    - Analysis done using method built for my dissertation.
- 2018  
|  
2018
- **R timelineViz: Visualizing the distribution of study events in longitudinal studies**  
Under-Review (copy available upon request.)
    - Authored with Alex Sunderman of the Vanderbilt Department of Epidemiology.
- 2017  
|  
2017
- **Continuous Classification using Deep Neural Networks<sup>14</sup>**  
Vanderbilt Biostatistics Qualification Exam
    - Review of methods for classifying continuous data streams using neural networks
    - Successfully met qualifying examination standards
- 2015  
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2015
- **Asymmetric Linkage Disequilibrium: Tools for Dissecting Multiallelic LD**  
Journal of Human Immunology
    - Authored with Richard Single, Vanja Paunic, Mark Albrecht, and Martin Maier.
- 2015  
|  
2015
- **An Agent Based Model of Mysis Migration<sup>15</sup>**  
International Association of Great Lakes Research Conference
    - Authored with Brian O'Malley, Sture Hansson, and Jason Stockwell.
- 2015  
|  
2015
- **Declines of Mysis diluviana in the Great Lakes**  
Journal of Great Lakes Research
    - Authored with Peter Euclide and Jason Stockwell.



- 1: <https://www.baker.edu.au>
- 2: <https://www.inouyelab.com>
- 3: <https://www.ub.edu/bl>
- 4: [http://nickstrayer.me/js4shiny\\_r2d3/slides](http://nickstrayer.me/js4shiny_r2d3/slides)
- 5: <https://livefreeordichotomize.com/>
- 6: <https://jhubiostatistics.shinyapps.io/papr/>
- 7: [http://nickstrayer.me/rstudioconf\\_sbm](http://nickstrayer.me/rstudioconf_sbm)
- 8: <https://tbilab.github.io/sbmR/>
- 9: <https://academic.oup.com/bioinformatics/advance-article-abstract/doi/10.1093/bioinformatics/btaa870/5922817?redirectedFrom=fulltext>
- 10: [https://prod.tbilab.org/phewas\\_me\\_info/](https://prod.tbilab.org/phewas_me_info/)
- 11: <https://www.ncbi.nlm.nih.gov/pubmed/30419234>
- 12: [http://nickstrayer.me/rstudioconf19\\_me-poster/](http://nickstrayer.me/rstudioconf19_me-poster/)
- 13: [http://nickstrayer.me/biostat\\_seminar/](http://nickstrayer.me/biostat_seminar/)
- 14: [http://nickstrayer.me/qualifying\\_exam/](http://nickstrayer.me/qualifying_exam/)
- 15: <https://www.semanticscholar.org/paper/An-Agent-Based-Model-of-the-Diel-Vertical-Migration-Strayer-Stockwell/40493c78e8ecf22bd882d17ec99fd913ec4b9820>