

# LEONARDO COLLADO-TORRES

At the Lieber Institute for Brain Development ([LIBD](#)), I lead the [R/Bioconductor-powered Team Data Science](#) group that works on understanding the roots and signatures of disease (particularly psychiatric disorders) by zooming in across dimensions of gene activity. We achieve this by studying gene expression at all expression feature levels (genes, exons, exon-exon junctions, and un-annotated regions) and by using different gene expression measurement technologies (bulk RNA-seq, single cell/nuclei RNA-seq, and spatial transcriptomics) that provide finer biological resolution and localization of gene expression. My group works closely with collaborators from LIBD as well as from Johns Hopkins University (JHU) which reflects the cross-disciplinary approach and diversity in expertise needed to further advance our understanding of high throughout biology. I am also interested in outreach activities as member of the [Bioconductor Community Advisory Board](#), the advisory board for [rOpenSci's Statistical Software Peer Review](#), and the board of the [Community of Bioinformatics Software Developers](#) in Mexico. In order to provide a supportive and stimulating research environment the team is involved in [career planning](#), [internal training opportunities](#), [Data Science guidance sessions](#), the [LIBD rstats club](#), among other initiatives.

As a quick background, I graduated from the [Undergraduate Program on Genomic Sciences](#) from the National Autonomous University of Mexico ([UNAM](#)) in 2009 and worked for two years at Winter Genomics analyzing high-throughput sequencing data. I then got a PhD in 2016 from the [Department of Biostatistics at Johns Hopkins Bloomberg School of Public Health](#) thanks to a CONACyT scholarship. There I worked with [Jeff Leek](#) and [Andrew Jaffe](#) in developing [derfinder](#) and [recount](#). I then worked ~ 4 years as a Staff Scientist and Research Scientist in Andrew Jaffe's lab on a variety of data analysis projects.

Every day I use [R](#) and [Bioconductor](#), and on some days I [write R packages](#). Occasionally I write [blog posts](#) about them and other tools. I'm a co-founder of the [LIBD rstats club](#) and the [CDSB community](#) of R and Bioconductor developers in Mexico and Latin America, just like we described at the [R Consortium website](#).

If you want to join my team, please check the [LIBD career opportunities!](#) ^\_^



[Download a PDF of this CV](#)

## CONTACT

- [lcolladotor@gmail.com](mailto:lcolladotor@gmail.com)
- [lcolladotor](#)
- [lcolladotor](#)
- [lcolladotor.github.io](#)
- [Team website](#)
- [Icollado](#)
- [ORCID](#)
- [Google Scholar](#)
- [Speaker Deck](#)
- [slideshare](#)
- [publons](#)
- [NIH Reporter](#)

## LANGUAGE SKILLS

R

Bash

Git/GitHub

Made with the R package [pagedown](#). The source code is available at [lcolladotor/cv](#) and is powered by [nstrayer/cv](#).

Last updated on 2022-05-01.



## TABLE OF CONTENTS

- Education
- Research Experience
- Industry Experience
- Funding Secured as (co-)PI
- Honors and Awards
- Publications
- Software
- Leadership and Service
- Mentoring Experience
- Teaching Experience
- Courses, Meetings, Talks, and Posters
- Languages



## EDUCATION

2016  
|  
2011

### PhD., Biostatistics

Johns Hopkins Bloomberg School of Public Health

Baltimore, MD, USA

- Advisors: [Jeffrey T. Leek](#) and [Andrew E. Jaffe](#)
- Thesis: Annotation-Agnostic Differential Expression and Binding Analyses.
- Description: The goal was to develop statistical methods and software that enable researchers to differentiate the sources of variation observed in RNA-seq while minimizing the dependence on known annotation. This allows researchers to correct for technological variation and study the biological variation driving their phenotype of interest. We applied these methods to further our understanding of neuropsychiatric disorders using the Lieber Institute for Brain Development human brains collection (> 1000 samples).

2009  
|  
2005

### B.S., Genomic Sciences

National Autonomous University of Mexico (UNAM)

Cuernavaca, Morelos, Mexico

- Grade 9.71/10
- Third generation at [LCG-UNAM](#)

2005  
|  
2002

### H.S.

ITESM Campus Cuernavaca

Cuernavaca, Morelos, Mexico

[Table of Contents](#)

- Grade 97.8/100
- Best high school average ( 200 students): awarded ITESM system 90% scholarship for college studies, declined to join LCG-UNAM.



## RESEARCH EXPERIENCE

2022  
|  
2020

### Investigator

Lieber Institute for Brain Development

Baltimore, MD, USA

- Leader of the [R/Bioconductor-powered Team Data Science](#) group at LIBD.
- Currently building a team, developing research ideas, and performing analyses for several grants.
- Applying for a formal JHU joint appointment.
- Implemented the [Data Science guidance sessions](#) system and taught internal [bootcamp courses](#).
- Working on research projects with LIBD collaborators such as Kristen R Maynard, Keri Martinowich, Joel Kleinman, and Thomas Hyde; JHU collaborators including Stephanie Hicks, Ben Langmead, Kasper Daniel Hansen, Steven Salzberg, Fernando Goes, and Peter Zandi; external collaborators such as Mina Ryten, Nicholas Clifton, Dana Hancock, and Andrew Jaffe.
- Led LIBD rstats club (ongoing) and CDSB Mexico (until 2021).

2020

### Research Scientist

Lieber Institute for Brain Development

Baltimore, MD, USA

- Affiliated to Andrew Jaffe's Data Science Team I.
- Official data science mentoring role at LIBD through: weekly LIBD rstats club sessions; individual 30 min guidance sessions; and occasional internal LIBD courses.
- Worked on research projects with LIBD collaborators such as Andrew E Jaffe, Kristen R Maynard, and Keri Martinowich, JHU collaborators including Stephanie Hicks, Ben Langmead, and Kasper Daniel Hansen, as well as external collaborators such as Mina Ryten and Nicholas Clifton.
- Developed recount3, biocthis, megadepth, and contributed to dasper that were included in the Bioconductor 3.12 release.
- Led LIBD rstats club and CDSB Mexico.

2020  
|  
2019

### Staff Scientist II at Andrew Jaffe's lab

Lieber Institute for Brain Development

Baltimore, MD, USA

- Innovation and research head at Andrew Jaffe's Data Science Team I.
- Last author for the recount-brain project.
- Senior role in a collaborative project with Mina Ryten.
- Co-first author in the spatialLIBD project along with Kristen R Maynard. Also established a collaboration with Stephanie Hicks and Lukas M Weber.
- Presented research findings at conferences such as ASHG.
- Created or contributed to the sgejobs, libdRSE, brainflowprobes, GenomicState and spatialLIBD R packages.
- Led the LIBD rstats club and CDSB Mexico.

2019  
|  
2016

### Staff Scientist I at Andrew Jaffe's lab

Lieber Institute for Brain Development

 Baltimore, MD, USA

- Lead or co-lead role in research projects such as BrainSEQ Phase II, recount, recountWorkflow and wgbsExprs, official mentor for two MPH students, informal mentor for members of Andrew Jaffe's team, co-author of several research projects including recount2 and wgbsExprs.
- JHBSPH MPH advisor for Ashkaun Razmara and Amy Peterson.
- Co-authored an RNA-seq processing pipeline with Emily Burke and oversaw a collaboration with Winter Genomics that we used to process thousands of samples.
- Presented research findings at conferences such as Biology of Genomes (CSHL).
- Created new collaborations such as those with Mina Ryten from UCL and Jesus Martínez from INSP-Mexico.
- Developed the jaffelab, shinycsv, LIBDpheno, wgbsExprs, recount, recount.bwtool R packages and shiny web applications.
- Co-founded the [LIBD rstats club](#).
- Taught at several workshops and presented research at conferences.
- Participated in several grant submissions.
- Co-founded [CDSB Mexico](#).

2016  
|  
2011

### Research Assistant at Jeff Leek's lab

Johns Hopkins Bloomberg School of Public Health

 Baltimore, MD, USA

- Worked with Jeff Leek and Andrew Jaffe on improving methods such as derfinder for studying the un-annotated transcriptome and applying these methods to study the human brain transcriptome.
- Worked with Marie Diener-West as a teaching assistant for the 140.621 series of Biostatistics courses (methods and statistics) as well as for the MPH capstone program.

2011  
|  
2009

### Bioinformatician at Enrique Morett's Lab

IBT-UNAM

 Cuernavaca, Morelos, Mexico

- Identified transcription start sites and transcription units in *Escherichia coli* and *Geobacter sulfurreducens* with RNA-seq data. Developed the [BacterialTranscription](#) R package.

2009  
|  
2007

### Undergrad research assistant at Guillermo Dávila's Lab

CCG-UNAM

 Cuernavaca, Morelos, Mexico

- Determined bacteriophage ecological groups by developing a method based on codon distribution of all phage sequenced genomes. Joint work with [Sur Herrera-Paredes](#).

2007  
|  
2006

### Undergrad research assistant at Roberto Kolter's lab

Harvard University

📍 Boston, MA, US

[Table of Contents](#)

- Supervisor: [Elizabeth Shank](#). Carried out screenings to identify bacteria that activate the production of exopolysaccharide through the activation of the gene tasA in *Bacillus subtilis*.

2011  
|  
2010

## Industry Experience

### Data Science Division Leader

Winter Genomics

📍 Cuernavaca, Morelos, Mexico

- Responsible for recruiting and hiring new personnel, overseeing and supervising bioinformaticians, training new employees, writing research reports, presenting reports to colleagues and clients, and organizing all scientific projects.
- Projects completed:
  - integrated analysis of more than 20 RNA-seq samples for determination of transcription initiation in *Escherichia coli* reported in Gama-Castro et al., [PMID 21051347](#),
  - de novo assembly of four *Escherichia coli* strains and lead to Aguilar et al., [PMID 22884033](#); Designed training material for new employees.

I typically like creating or joining R clubs, advocate in favor of version control, find some time to keep up with developments in R, and figure out how we can work together better: [from using google docs for writing papers to learning from our search history](#).

2010  
|  
2009

### Data Scientist

Winter Genomics

📍 Cuernavaca, Morelos, Mexico

- First scientific staff member at Winter Genomics. Developed analysis pipelines for de novo genome assembly among other uses of high-throughput sequencing data.
- Projects completed: - de novo genome assembly simulations,
  - assembly and annotation of the phiVC8 bacteriophage genome.

[Table of Contents](#)

2022  
|  
2020

## Funding Secured as (Co-)PI

### R21 MH120497 from the National Institutes of Health (NIH)

An expanded framework for RNA quality correction in expression analyses in the human brain

📍 Baltimore, MD, USA

- PI on [5R21MH120497-02](#) (\$233,250 USD) which is for year 2/2 of an R21 that [Andrew E Jaffe](#) secured and managed during year 1 as [1R21MH120497-01](#).

2021	<b>Code for Science and Society (CS&amp;S) Event Fund Award for CDSB</b>
	Cuernavaca, Morelos, Mexico
	<ul style="list-style-type: none"> <li>• PI on a \$18,963.40 USD grant from CS&amp;S for organizing mini-courses and the <a href="#">International Bioinformatics Meeting 2021</a> along with the <a href="#">RMB</a> and <a href="#">NNB-CCG-UNAM</a> teams as described on <a href="#">this blog post</a>.</li> </ul>
2021   2019	<b>R Consortium for CDSB</b>
	Cuernavaca, Morelos, Mexico
	<ul style="list-style-type: none"> <li>• Secured \$1,000 USD yearly for organizing the CDSB summer workshops from the R Consortium <a href="#">R User Small Conference Fund</a> support program.</li> </ul>
2020	<b>Bioconductor Foundation of NA support for CDSB</b>
	Cuernavaca, Morelos, Mexico
	<ul style="list-style-type: none"> <li>• Secured \$1,200 USD for organizing the CDSB2020 event.</li> </ul>
	<a href="#">Table of Contents</a>

## ❖ HONORS AND AWARDS

2021	<b>Bioconductor Award 2021</b>
	<a href="#">BiocAwards</a>
	<ul style="list-style-type: none"> <li>• <a href="#">Thank you Twitter thread</a></li> </ul>
2021   2018	<b>National Researcher level 1 announcement</b>
	CONACyT, Mexico
2019   2010	<b>Travel awards</b>
	<p><a href="#">BioC2019</a>, <a href="#">BioC2017</a>, <a href="#">BioC2014</a>, <a href="#">useR2013</a>, <a href="#">BioC2011</a>, From Functional Genomics to Systems Biology 2010 and <a href="#">BioCDevelEurope 2010</a>.</p> <ul style="list-style-type: none"> <li>• Taught a <a href="#">workshop on recount</a> at BioC2019 and <a href="#">BioC2017</a>. Gave a talk on <a href="#">BacterialTranscription</a> at BioCDevelEurope2010. BioC2019 <a href="#">scholarship application</a></li> <li>• BioC2019 <a href="#">scholarship application</a></li> </ul>
2019	<b>rstudio::conf 2019 diversity award recipient announcement</b>
	<ul style="list-style-type: none"> <li>• <a href="#">Scholarship application</a>.</li> </ul>
2019	<b>Early Career Clinical Research Symbiont Award</b>
	<a href="http://researchsymbionts.org">http://researchsymbionts.org</a>
	<ul style="list-style-type: none"> <li>• For our work on <a href="#">recount2</a>.</li> </ul>
2018	<b>rOpenSci Unconf 2018</b>
	<a href="#">unconf18 participants</a> and <a href="#">application</a>
	<ul style="list-style-type: none"> <li>• Worked on <a href="#">pkginspector</a>.</li> </ul>

2018

## Bioinformatics Peer Prize III

### announcement

- Competition website, and our winning entry.

[Table of Contents](#)

2022  
|  
2021

## PUBLICATIONS

### spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data

#### R/Bioconductor package

- Brenda Pardo, Abby Spangler, Lukas M. Weber, Stephanie C. Hicks, Andrew E. Jaffe, Keri Martinowich, Kristen R. Maynard, **Leonardo Collado-Torres** †. spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data. *bioRxiv* (2021) doi: [10.1101/2021.04.29.440149](https://doi.org/10.1101/2021.04.29.440149).
- Corresponding author
- [pre-print](#) [Twitter summary](#)

\* indicates equal contribution, † indicates corresponding author

2022

### Data-driven Identification of Total RNA Expression Genes (TREGs) for Estimation of RNA Abundance in Heterogeneous Cell Types

#### R/Bioconductor package

- Louise A. Huuki-Myers, Kelsey D. Montgomery, Sang Ho Kwon, Stephanie C. Page, Stephanie C. Hicks, Kristen R. Maynard †, **Leonardo Collado-Torres** †. Data-driven Identification of Total RNA Expression Genes (TREGs) for Estimation of RNA Abundance in Heterogeneous Cell Types. *bioRxiv* (2022) doi: [10.1101/2022.04.28.489923](https://doi.org/10.1101/2022.04.28.489923).
- Co-corresponding author
- [pre-print](#) [Twitter summary](#)

2022  
|  
2021

### SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor

#### R/Bioconductor package

- Dario Righelli \*, Lukas M. Weber \*, Helena L. Crowell \*, Brenda Pardo, **Leonardo Collado-Torres**, Shila Ghazanfar, Aaron T. L. Lun, Stephanie C. Hicks †, Davide Risso †. SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor. *Bioinformatics* (2022) doi:[[10.1093/bioinformatics/btac299](https://doi.org/10.1093/bioinformatics/btac299)] (<https://doi.org/10.1093/bioinformatics/btac299>) *bioRxiv* (2021) doi: [10.1101/2021.01.27.428431](https://doi.org/10.1101/2021.01.27.428431).
- Supporting role: provided feedback in the design of the package
- [Twitter summary](#) [pre-print](#) [Twitter summary](#)

2022

## **BiocMAP: A Bioconductor-friendly, GPU-Accelerated Pipeline for Bisulfite-Sequencing Data software, documentation, example use case**

- Nicholas J. Eagles, Richard Wilton, Andrew E. Jaffe, **Leonardo Collado-Torres** †. BiocMAP: A Bioconductor-friendly, GPU-Accelerated Pipeline for Bisulfite-Sequencing Data. *bioRxiv* (2022) doi: [10.1101/2022.04.20.488947](https://doi.org/10.1101/2022.04.20.488947).
- Corresponding author
- [pre-print Twitter summary](#)

2022

## **Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways**

- Peter P. Zandi, Andrew E. Jaffe, Fernando S. Goes, Emily E. Burke, **Leonardo Collado-Torres**, Louise Huuki-Myers, Arta Seyedian, Yian Lin, Fayaz Seifuddin, Mehdi Pirooznia, Christopher A. Ross, Joel E. Kleinman, Daniel R. Weinberger, Thomas M. Hyde †. Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways. *Nature Neuroscience* (2022) doi: [10.1038/s41593-022-01024-6](https://doi.org/10.1038/s41593-022-01024-6).
- Supporting and supervisor roles: data analysis and supervision
- [Twitter summary](#)

2022

## **Genetics and Brain Transcriptomics of Completed Suicide**

- Giovanna Punzi, Gianluca Ursini, Qiang Chen, Eugenia Radulescu, Ran Tao, Louise A. Huuki, Pasquale Di Carlo, **Leonardo Collado-Torres**, Joo Heon Shin, Roberto Catanesi, Andrew E. Jaffe, Thomas M. Hyde, Joel E. Kleinman, Trudy F.C. Mackay, Daniel R. Weinberger †. Genetics and Brain Transcriptomics of Completed Suicide. *American Journal of Psychiatry* (2022) doi: [10.1176/appi.ajp.2021.21030299](https://doi.org/10.1176/appi.ajp.2021.21030299).
- Supporting role: processed some data
- [Twitter summary](#)

2021

## **recount3: summaries and queries for large-scale RNA-seq expression and splicing**

### **R/Bioconductor package**

- Christopher Wilks, Shijie C. Zheng, Feng Yong Chen, Rone Charles, Brad Solomon, Jonathan P. Ling, Eddie Luidy Imada, David Zhang, Lance Joseph, Jeffrey T. Leek, Andrew E. Jaffe, Abhinav Nellore, **Leonardo Collado-Torres**, Kasper D. Hansen †, Ben Langmead †. recount3: summaries and queries for large-scale RNA-seq expression and splicing. *Genome Biology* (2021) doi: [10.1186/s13059-021-02533-6](https://doi.org/10.1186/s13059-021-02533-6) *bioRxiv* (2021) doi: [10.1101/2021.05.21.445138](https://doi.org/10.1101/2021.05.21.445138).
- Developed the recount3 Bioconductor package and the documentation website, and contributed to writing the paper
- [pre-print Twitter summary](#)

2021  
|  
2020

**Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain analysis code**

- Matthew N. Tran \*, Kristen R. Maynard \*, Abby Spangler, Louise A Huuki, Kelsey D Montgomery, Vijay Sadashivaiah, Madhavi Tippanni, Brianna K. Barry, Dana B. Hancock, Stephanie C. Hicks, Joel E. Kleinman, Thomas M. Hyde, **Leonardo Collado-Torres**, Andrew E. Jaffe †, Keri Martinowich †.  
Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. *Neuron* (2021) doi: [10.1016/j.neuron.2021.09.001](https://doi.org/10.1016/j.neuron.2021.09.001) *bioRxiv* (2020) doi: [10.1101/2020.10.07.329839](https://doi.org/10.1101/2020.10.07.329839).
- Supporting role: analysis
- [Twitter summary](#) [pre-print](#) [Twitter summary](#)

2021  
|  
2020

**Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk**

- Kira A. Perzel Mandell, Nicholas J. Eagles, Richard Wilton, Amanda J. Price, Stephen A. Semick, **Leonardo Collado-Torres**, William S. Ulrich, Ran Tao, Shizhong Han, Alexander S. Szalay, Thomas M. Hyde, Joel E. Kleinman, Daniel R. Weinberger†, Andrew E. Jaffe †. Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. *Nature Communications* (2021) doi: [10.1038/s41467-021-25517-3](https://doi.org/10.1038/s41467-021-25517-3). *bioRxiv* (2020) doi: [10.1101/2020.09.24.311878](https://doi.org/10.1101/2020.09.24.311878).
- Supporting role: data preparation
- [Twitter summary](#) [pre-print](#) [Twitter summary](#)

2021  
|  
2020

**SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/Bioconductor-powered RNA-seq analyses software, documentation, example use case**

- Nicholas J. Eagles, Emily E. Burke, Jacob Leonard, Brianna K. Barry, Joshua M. Stoltz, Louise Huuki, BaDoi N. Phan, Violeta Larios Serrato, Everardo Gutiérrez-Millán, Israel Aguilar-Ordoñez, Andrew E. Jaffe, **Leonardo Collado-Torres** †. SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/Bioconductor-powered RNA-seq analyses. *BMC Bioinformatics* (2021) doi: [10.1186/s12859-021-04142-3](https://doi.org/10.1186/s12859-021-04142-3). *bioRxiv* (2020) doi: [10.1101/2020.12.11.386789](https://doi.org/10.1101/2020.12.11.386789).
- Corresponding author
- [pre-print](#) [Twitter summary](#)

2021

## Detection of pathogenic splicing events from RNA-sequencing data using dasper

### R/Bioconductor package

- David Zhang, Regina H. Reynolds, Sonia Garcia-Ruiz, Emil K Gustavsson, Sid Sethi, Sara Aguti, Ines A. Barbosa, Jack J. Collier, Henry Houlden, Robert McFarland, Francesco Muntoni, Monika Oláhová, Joanna Poulton, Michael Simpson, Robert D.S. Pitceathly, Robert W. Taylor, Haiyan Zhou, Charu Deshpande, Juan A. Botia, **Leonardo Collado-Torres**, Mina Ryten †. Detection of pathogenic splicing events from RNA-sequencing data using dasper. *bioRxiv* (2021) doi: [2021.03.29.437534](https://doi.org/10.1101/2021.03.29.437534).
- Mentoring role: provided advice in the design of the dasper Bioconductor package
- [Twitter post](#)

2021

## Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity

- Nicholas E. Clifton, **Leonardo Collado-Torres**, Emily E. Burke, Antonio F. Pardiñas, Janet C. Harwood, Arianna Di Florio, James T. R. Walters, Michael J. Owen, Michael C. O'Donovan, Daniel R. Weinberger, Peter A. Holmans, Andrew E. Jaffe †, Jeremy Hall †. Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. *Biological Psychiatry* (2021) doi: [10.1016/j.biopsych.2021.03.009](https://doi.org/10.1016/j.biopsych.2021.03.009).
- Supporting role: data preparation and advice
- [Twitter summary](#)

2021  
|  
2020

## Megadepth: efficient coverage quantification for BigWigs and BAMs

### R/Bioconductor package

- Christopher Wilks, Omar Ahmed, Daniel N Baker, David Zhang, **Leonardo Collado-Torres**, Ben Langmead †. Megadepth: efficient coverage quantification for BigWigs and BAMs. *Oxford Bioinformatics* (2021) doi: [10.1093/bioinformatics/btab152](https://doi.org/10.1093/bioinformatics/btab152). *bioRxiv* (2020) doi: [10.1101/2020.12.17.423317](https://doi.org/10.1101/2020.12.17.423317).
- Supporting role: wrote the R/Bioconductor package with David Zhang.
- [pre-print Twitter summary](#)

2021  
|  
2020

## Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex

### shiny app, R/Bioconductor package, analysis code

- Kristen R Maynard \*, **Leonardo Collado-Torres** \*, Lukas M. Weber, Cedric Uytingco, Brianna K. Barry, Stephen R. Williams, Joseph L. Catallini II, Matthew N. Tran, Zachary Besich, Madhavi Tippani, Jennifer Chew, Yifeng Yin, Joel E. Kleinman, Thomas M. Hyde, Nikhil Rao, Stephanie C. Hicks, Keri Martinowich †, Andrew E Jaffe †. *Nature Neuroscience* (2021). doi: [10.1038/s41593-020-00787-0](https://doi.org/10.1038/s41593-020-00787-0). *bioRxiv* (2020). doi: [10.1101/2020.02.28.969931](https://doi.org/10.1101/2020.02.28.969931)
- Co-first author
- [Twitter summary](#) [pre-print Twitter summary](#)

2021  
|  
2020

## Genetic and environmental regulation of caudate nucleus transcriptome: insight into schizophrenia risk and the dopamine system

- Kynon JM Benjamin, Arthur S Feltrin, André Rocha Barbosa, Andrew E Jaffe, **Leonardo Collado-Torres**, Emily E Burke, Joo Heon Shin, William S Ulrich, Amy Deep-Soboslay, Ran Tao, the BrainSeq Consortium, Thomas M Hyde, Joel E Kleinman, Jennifer A Erwin, Daniel R Weinberger †, Apuã CM Paquola †. Genetic and environmental regulation of caudate nucleus transcriptome: insight into schizophrenia risk and the dopamine system. *medRxiv* (2021) doi: [10.1101/2020.11.18.20230540](https://doi.org/10.1101/2020.11.18.20230540).
- Supporting role: data preparation and advice
- [pre-print Twitter summary](#)

2020

## Programmatic access to bacterial regulatory networks with regutools R/Bioconductor package

- Joselyn Chávez \*, Carmina Barberena-Jonas \*, Jesus E Sotelo-Fonseca \*, José Alquicira-Hernández, Heladia Salgado, **Leonardo Collado-Torres** †, Alejandro Reyes †. Programmatic access to bacterial regulatory networks with regutools. *Oxford Bioinformatics* (2020). doi: [10.1093/bioinformatics/btaa575](https://doi.org/10.1093/bioinformatics/btaa575). *bioRxiv* (2020). doi: [10.1101/2020.04.29.068551](https://doi.org/10.1101/2020.04.29.068551)
- Co-corresponding author
- [Twitter summary](#)

2020

## SynGAP isoforms differentially regulate synaptic plasticity and dendritic development

- Yoichi Araki, Ingie Hong, Timothy R Gamache, Shaowen Ju, **Leonardo Collado-Torres**, Joo Heon Shin, Richard L Huganir. SynGAP isoforms differentially regulate synaptic plasticity and dendritic development. *eLife* (2020) doi: [10.7554/eLife.56273](https://doi.org/10.7554/eLife.56273). *bioRxiv* (2020). doi: [10.1101/2020.01.28.922013](https://doi.org/10.1101/2020.01.28.922013)
- Supporting role: analysis
- [Twitter summary](#)

2020

## Profiling gene expression in the human dentate gyrus granule cell layer reveals insights into schizophrenia and its genetic risk

- Andrew E Jaffe \* †, Daniel J Hoeppner \*, Takeshi Saito, Lou Blanpain, Joy Ukaigwe, Emily E Burke, **Leonardo Collado-Torres**, Ran Rato, Katsunori Tajinda, Kristen R Maynard, Matthew N Tran, Keri Martinowich, Amy Deep-Soboslay, Joo Heon Shin, Joel E Kleinman, Daniel R Weinberger, Mitsuyuki Matsumoto †, Thomas M Hyde †. Profiling gene expression in the human dentate gyrus granule cell layer reveals insights into schizophrenia and its genetic risk. *Nature Neuroscience* (2020). doi: [10.1038/s41593-020-0604-z](https://doi.org/10.1038/s41593-020-0604-z)
- Supporting role: analysis
- [Twitter summary](#)

2020  
|  
2019

## Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex

- Kira A Perzel Mandell\*, Amanda J Price, Richard Wilton, **Leonardo Collado-Torres**, Ran Tao, Nicholas J Eagles, Alexander S Szalay, Thomas M Hyde, Daniel R Weinberger, Joel E Kleinman, Andrew E Jaffe†.  
Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. *Epigenetics* (2020). doi: [10.1080/15592294.2020.1786304](https://doi.org/10.1080/15592294.2020.1786304). *bioRxiv* (2019). doi: [10.1101/823781](https://doi.org/10.1101/823781)
- Supporting role: analysis
- [pre-print Twitter summary](#)

2020  
|  
2019

## Recounting the FANTOM CAGE–Associated Transcriptome

[related code](#). Used data from [recount2](#) and code from [recount.bwtool](#)

- Eddie-Ludy Imada\*, Diego Fernando Sanchez\*, **Leonardo Collado-Torres**, Christopher Wilks, Tejasvi Matam, Wikum Dinalankara, Aleksey Stupnikov, Francisco Lobo-Pereira, Chi-Wai Yip, Kayoko Yasuzawa, Naoto Kondo, Masayoshi Itoh, Harukazu Suzuki, Takeya Kasukawa, Chung-Chau Hon, Michiel JL de Hoon, Jay W Shin, Piero Carninci, Andrew E Jaffe, Jeffrey T Leek, Alexander Favorov, Gloria R Franco, Benjamin Langmead†, Luigi Marchionni†. Recounting the FANTOM Cage Associated Transcriptome. *Genome Research* (2020) doi: [10.1101/gr.254656](https://doi.org/10.1101/gr.254656) *bioRxiv* (2019). doi: [10.1101/659490](https://doi.org/10.1101/659490)
- Supporting role: data preparation and advice
- [Twitter summary](#)

2020  
|  
2018

## Incomplete annotation has a disproportionate impact on our understanding of Mendelian and complex neurogenetic disorders

Used data from [recount2](#) and code from [recount.bwtool](#)

- David Zhang\*, Sebastian Guelfi\*, Sonia Garcia Ruiz, Beatrice Costa, Regina H Reynolds, Karishma D'Sa, Wenfei Liu, Thomas Courtin, Amy Peterson, Andrew E Jaffe, John Hardy, Juan Botia, **Leonardo Collado-Torres**, Mina Ryten. Incomplete annotation of OMIM genes is likely to be limiting the diagnostic yield of genetic testing, particularly for neurogenetic disorders. *Science Advances* (2020). doi: [10.1126/sciadv.aay8299](https://doi.org/10.1126/sciadv.aay8299). *bioRxiv* (2018). doi: [10.1101/499103](https://doi.org/10.1101/499103)
- Supervisor role, data generation, overall project advice
- [public endorsement tweet pre-print Twitter summary](#)

2020  
|  
2019

## Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information

Used data from [recount2](#) and code from [recount.bwtool](#)

- Sebastian Guelfi\*, Karishma D'Sa\*, Juan Botía\*, Jana Vandrovčová, Regina H. Reynolds, David Zhang, Daniah Trabzuni, **Leonardo Collado-Torres**, Andrew Thomason, Pedro Quijada Leyton, Sarah A. Gagliano, Mike A. Nalls, International Parkinson's Disease Genomics Consortium (IPDGC), UK Brain Expression Consortium, Kerrin S. Small, Colin Smith, Adaikalavan Ramasamy, John Hardy, Michael E. Weale†, Mina Ryten†. Regulatory sites for known and novel splicing in human basal ganglia are enriched for disease-relevant information. *Nature Communications* (2020) doi: [10.1038/s41467-020-14483-x](https://doi.org/10.1038/s41467-020-14483-x). *bioRxiv* (2019). doi: [10.1101/591156](https://doi.org/10.1101/591156)
- Supporting role: data preparation and advice
- [Twitter summary](#)

2020  
|  
2018

## Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs

[Web browser](#)

- Emily E Burke\*, Joshua G Chenoweth\*, Joo Heon Shin, **Leonardo Collado-Torres**, Suel Kee Kim, Nicola Micali, Yanhong Wang, Carlo Colantuoni, Richard E Straub, Daniel J Hoepfner, Huei-Ying Chen, Alana Sellers, Kamel Shabbani, Gregory R Hamersky, Marcelo Diaz Bustamante, BaDoi N Phan, William S Ulrich, Cristian Valencia, Amritha Jaishankar, Amanda J Price, Anandita Rajpurohit, Stephen A Semick, Roland Bürl, James C Barrow, Daniel J Hiler, Stephanie C Page, Keri Martinowich, Thomas M Hyde, Joel E Kleinman, Karen F Berman, José A Apud, Alan J Cross, Nick J Brandon, Daniel R Weinberger, Brady J Maher, Ronald DG McKay†, Andrew E Jaffe†. Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. *Nature Communications* (2020) doi: [10.1038/s41467-019-14266-z](https://doi.org/10.1038/s41467-019-14266-z) *bioRxiv* (2018). doi: [10.1101/380758](https://doi.org/10.1101/380758)
- Supporting role: analysis
- [Twitter summary](#)

2019

## *recount-brain*: a curated repository of human brain RNA-seq datasets metadata

[shiny app](#), [code](#)

- Ashkaun Razmara, Shannon E Ellis, Dustin J Sokolowski, Sean Davis, Michael D Wilson, Jeffrey T Leek, Andrew E Jaffe, **Leonardo Collado-Torres**†. *recount-brain*: a curated repository of human brain RNA-seq datasets metadata. *bioRxiv* (2019). doi: [10.1101/618025](https://doi.org/10.1101/618025)
- Corresponding author
- [pre-print Twitter summary](#)

2019  
|  
2018

**Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation.**

[shiny web application](#)

- Amanda J. Price\*, **Leonardo Collado-Torres\***, Nikolay A. Ivanov, Wei Xia, Emily E. Burke, Joo Heon Shin, Ran Tao, Liang Ma, Yankai Jia, Thomas M. Hyde, Joel E. Kleinman, Daniel R. Weinberger, Andrew E Jaffe†. Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. *Genome Biology* 2019. doi: [10.1186/s13059-019-1805-1](https://doi.org/10.1186/s13059-019-1805-1). *bioRxiv* (2018). doi: [10.1101/428391](https://doi.org/10.1101/428391)

• Co-first author

• [Twitter summary](#) and [summary numbertwo](#)

2019  
|  
2018

**Regional heterogeneity in gene expression, regulation, and coherence in the frontal cortex and hippocampus across development and schizophrenia**

[web browser](#)

- **Leonardo Collado-Torres**, Emily E Burke, Amy Peterson, JooHeon Shin, Richard E Straub, Anandita Rajpurohit, Stephen A Semick, William S Ulrich, BrainSeq Consortium, Amanda J Price, Cristian Valencia, Ran Tao, Amy Deep-Soboslay, Thomas M Hyde, Joel E Kleinman, Daniel R Weinberger†, Andrew E Jaffe†. Regional heterogeneity in gene expression, regulation, and coherence in the frontal cortex and hippocampus across development and schizophrenia. *Neuron* 2019. doi: [10.1016/j.neuron.2019.05.013](https://doi.org/10.1016/j.neuron.2019.05.013) *bioRxiv* (2018). doi: [10.1101/426213](https://doi.org/10.1101/426213)

• First-author

• [Twitter summary](#)

2019  
|  
2018

**Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods.**

- Carrie Wright\*, Anandita Rajpurohit\*, Emily E. Burke, Courtney Williams, **Leonardo Collado-Torres**, Martha Kimos, Nicholas J. Brandon, Alan J. Cross, Andrew E. Jaffe, Daniel R. Weinberger†, Joo Heon Shin† .Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods. *BMC Genomics* (2019). doi: [10.1186/s12864-019-5870-3](https://doi.org/10.1186/s12864-019-5870-3). *bioRxiv* (2018). doi: [10.1101/445437](https://doi.org/10.1101/445437)

• Supporting role

• [Twitter summary](#)

2019

### Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells.

Used data from [recount2](#).

- Anil K Madugundu, Chan Hyun Na, Raja Sekhar Nirujogi, Santosh Renuse, Kwang Pyo Kim, Kathleen H. Burns, Christopher Wilks, Ben Langmead, Shannon E. Ellis, **Leonardo Collado-Torres**, Marc K. Halushka, Min-Sik Kim, Akhilesh Pandey†. Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. *Proteomics* 2019. doi: [10.1002/pmic.201800315](https://doi.org/10.1002/pmic.201800315)
- Supporting role
- [Twitter summary](#)

2019  
|  
2018

### Integrated DNA methylation and gene expression profiling across multiple brain regions implicate novel genes in Alzheimer's disease.

- Stephen A Semick, Rahul A Bharadwaj, **Leonardo Collado-Torres**, Ran Tao, Joo Heon Shin, Amy Deep-Soboslay, James R. Weiss, Daniel R Weinberger, Thomas M Hyde, Joel E Kleinman, Andrew E Jaffe†, Venkata S Mattay†. Integrated DNA methylation and gene expression profiling across multiple brain regions implicate novel genes in Alzheimer's disease. *Acta Neuropathologica* 2019. doi: [10.1007/s00401-019-01966-5](https://doi.org/10.1007/s00401-019-01966-5). *bioRxiv* (2018). doi: [10.1101/430603](https://doi.org/10.1101/430603)
- Supporting role: analysis
- [Twitter summary](#)

2018

### RNA-seq transcript quantification from reduced-representation data in [recount2](#)

Data available from [recount2](#).

- Fu J, Kammers K, Nellore A, **Collado-Torres L**, Leek JT, Taub MA. RNA-seq transcript quantification from reduced-representation data in [recount2](#). *bioRxiv* (2018). doi: [10.1101/247346](https://doi.org/10.1101/247346)
- Supporting role
- [pre-print Twitter summary](#)

2018

### Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses.

- Helena Kuri-Magaña, **Leonardo Collado-Torres**, Andrew E Jaffe, Humberto Valdovinos-Torres, Marbella Ovilla-Muñoz, Juan M Téllez-Sosa, Laura C Bonifaz-Alfonzo, Jesús Martínez-Barnetche. Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses. *Frontiers in Immunology* 2018. doi: [10.3389/fimmu.2018.02679](https://doi.org/10.3389/fimmu.2018.02679) *bioRxiv* (2018). doi: [10.1101/384172](https://doi.org/10.1101/384172)
- Supporting role: data preparation and advice
- [Twitter summary](#)

2018  
|  
2017

## Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome.

- Semick SA, Collado-Torres L, Markunas CA, Shin JH, Deep-Soboslay A, Tao R, Huestis MA, Bierut LJ, Maher BS, Johnson EO, Hyde TM, Weinberger DR, Hancock DB, Kleinman JE†, Jaffe AE†. Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. *Molecular Psychiatry* 2018. doi: [10.1038/s41380-018-0223-1](https://doi.org/10.1038/s41380-018-0223-1). *bioRxiv* (2017). doi: [10.1101/236968](https://doi.org/10.1101/236968)
- Supporting role: analysis
- [Twitter summary](#)

2018  
|  
2017

## Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis.

- Jaffe AE, Straub R, Shin JH, Tao R, Gao Y, Collado-Torres L, Kam-Thong T, Xi HS, Quan J, Chen Q, Colantuoni C, Ulrich WS, Maher BJ, Deep-Soboslay A, The BrainSeq Consortium, Cross AJ, Brandon NJ, Leek JT, Hyde TM, Kleinman JE, Weinberger DR. Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis. *Nat. Neurosci.* 2018. doi: [10.1038/s41593-018-0197-y](https://doi.org/10.1038/s41593-018-0197-y). *bioRxiv* (2017). doi: [10.1101/145656](https://doi.org/10.1101/145656)
- Supporting role: analysis
- [Twitter summary](#)

2018  
|  
2017

## Improving the value of public RNA-seq expression data by phenotype prediction.

- Ellis SE, Collado-Torres L, Jaffe AE, Leek JT. Improving the value of public RNA-seq expression data by phenotype prediction. *Nucl. Acids Res.* 2018. doi: [10.1093/nar/gky102](https://doi.org/10.1093/nar/gky102) *bioRxiv* (2017). doi: [10.1101/145656](https://doi.org/10.1101/145656)
- Supporting role: data preparation and advice
- [Twitter summary](#) and [this tweet](#)

2017

## Accessing over 70,000 human RNA-seq samples with Bioconductor

- Collado-Torres L†, Nellore A, Jaffe AE. recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor [version 1; referees: 1 approved, 2 approved with reservations]. *F1000Research* (2017). doi: [10.12688/f1000research.12223.1](https://doi.org/10.12688/f1000research.12223.1). Winning entry for the [Bioinformatics Peer Prize III](#).
- First and corresponding author
- [Twitter summary](#)

2017

## Altered expression of histamine signaling genes in autism spectrum disorder

- Wright C, Shin JH, Rajpurohit A, Deep-Soboslay A, **Collado-Torres L**, Brandon NJ, Hyde TM, Kleinman JE, Jaffe AE, Cross AJ, Weinberger DR. Altered expression of histamine signaling genes in autism spectrum disorder. *Translational Psychiatry* 2017. doi: [10.1038/tp.2017.87](https://doi.org/10.1038/tp.2017.87)
- Supporting role: visualization
- [Twitter summary](#)

2017

|

2016

## Reproducible RNA-seq analysis using *recount2*

- **Collado-Torres L\***, Nellore A\*, Kammers K, Ellis SE, Taub MA, Hansen KD, Jaffe AE, Langmead B, Leek JT. Reproducible RNA-seq analysis using *recount2*. *Nature Biotechnology* 2017. doi: [10.1038/nbt.3838](https://doi.org/10.1038/nbt.3838) *bioRxiv* (2016). doi: [10.1101/068478](https://doi.org/10.1101/068478)
- Co-first author
- [Twitter summary](#)

2016

## Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive.

- Nellore A, Jaffe AE, Fortin JP, Alquicira-Hernández J, **Collado-Torres L**, Wang S, Phillips RA, Karbhari N, Hansen KD, Langmead B, Leek JT. Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. *Genome Biology* 2016. doi: [10.1186/s13059-016-1118-6](https://doi.org/10.1186/s13059-016-1118-6). *bioRxiv* (2016). doi: [10.1101/038224](https://doi.org/10.1101/038224)
- Supporting role: analysis
- [bioRxiv tweet](#)

2016

## Flexible expressed region analysis for RNA-seq with *derfinder*.

- **Collado-Torres L**, Nellore A, Frazee AC, Wilks C, Love MI, Langmead B, Irizarry RA, Leek JT, Jaffe AE. Flexible expressed region analysis for RNA-seq with *derfinder*. *Nucl. Acids Res.* 2016. doi: [10.1093/nar/gkw852](https://doi.org/10.1093/nar/gkw852) *bioRxiv* (2016). doi: [10.1101/015370](https://doi.org/10.1101/015370)
- First author
- [pre-print Twitter summary](#)

2016

|

2015

## Rail-RNA: Scalable analysis of RNA-seq splicing and coverage.

- Nellore A, **Collado-Torres L**, Jaffe AE, Alquicira-Hernández J, Wilks C, Pritt J, Morton J, Leek JT, Langmead B. Rail-RNA: Scalable analysis of RNA-seq splicing and coverage. *Bioinformatics* 2016. doi: [10.1093/bioinformatics/btw575](https://doi.org/10.1093/bioinformatics/btw575) *bioRxiv* (2015). doi: [10.1101/019067](https://doi.org/10.1101/019067)
- Supporting role: analysis
- [Twitter summary](#)

2016  
|  
2015

## regionReport: Interactive reports for region-level and feature-level genomic analyses

- Collado-Torres L, Jaffe AE and Leek JT. regionReport: Interactive reports for region-level and feature-level genomic analyses [version2; referees: 2 approved, 1 approved with reservations]. *F1000Research* 2016, 4:105. doi: [10.12688/f1000research.6379.2](https://doi.org/10.12688/f1000research.6379.2) *bioRxiv* (2015). doi: [10.1101/016659](https://doi.org/10.1101/016659)
- First author
- [Twitter summary](#)

2015

## Developmental regulation of human cortex transcription and its clinical relevance at single base resolution.

- Jaffe AE, Shin J, Collado-Torres L, Leek JT, et al. Developmental regulation of human cortex transcription and its clinical relevance at single base resolution. *Nat. Neurosci.* 2015. doi: [10.1038/nn.3898](https://doi.org/10.1038/nn.3898)
- Supporting role: analysis
- [Twitter summary](#)

2014

## Book chapter: Measurement, Summary, and Methodological Variation in RNA-sequencing

- Frazee AC, Collado-Torres L, Jaffe AE, Langmead B, Leek JT. Measurement, Summary, and Methodological Variation in RNA-sequencing in Statistical Analysis of Next Generation Sequencing Data, *Springer*, 2014, 115-128.

2011

## Interspecies interactions that result in *Bacillus subtilis* forming biofilms are mediated mainly by members of its own genus.

- Shank EA, Klepac-Ceraj V, Collado-Torres L, Powers GE, Losick R, Kolter R. Interspecies interactions that result in *Bacillus subtilis* forming biofilms are mediated mainly by members of its own genus. *Proc. Natl. Acad. Sci. U.S.A.* 2011 Nov;108(48):E1236–1243. doi: [10.1073/pnas.1103630108](https://doi.org/10.1073/pnas.1103630108)
- Supporting role: performed initial experiments
- *Twitter summary from 2011? No such thing back then*

2011

## RegulonDB version 7.0: transcriptional regulation of *Escherichia coli* K-12 integrated within genetic sensory response units (Gensor Units).

[Table of Contents](#)

- Gama-Castro S, Salgado H, Peralta-Gil M, Santos-Zavaleta A, Muñiz-Rascado L, Solano-Lira H, Jimenez-Jacinto V, Weiss V, García-Sotelo JS, López-Fuentes A, Porrón-Sotelo L, Alquicira-Hernández S, Medina-Rivera A, Martínez-Flores I, Alquicira-Hernández K, Martínez-Adame R, Bonavides-Martínez C, Miranda-Ríos J, Huerta AM, Mendoza-Vargas A, Collado-Torres L, Taboada B, Vega-Alvarado L, Olvera M, Olvera L, Grande R, Morett E, Collado-Vides J. RegulonDB version 7.0: transcriptional regulation of *Escherichia coli* K-12 integrated within genetic sensory response units (Gensor Units). *Nucleic Acids Res.* 2011 Jan;39(Database issue):D98–105. doi: [10.1093/nar/gkq1110](https://doi.org/10.1093/nar/gkq1110)

## SOFTWARE

2014  
|  
2021

### Bioconductor: author role

[recount3](#): Explore and download data from the recount3 project – 3385 downloads. [biocthis](#): Automate package and project setup for Bioconductor packages – 3096 downloads. [megadepth](#): BigWig and BAM related utilities – 2373 downloads. [spatialLIBD](#): LIBD Visium spatial transcriptomics human pilot data inspector – 3353 downloads. [GenomicState](#): data for derfinder analyses – 2520 downloads. [recount](#): Explore and download data from the recount2 project – 38725 downloads. [derfinder](#): Annotation-agnostic differential expression analysis of RNA-seq data at base-pair resolution via the DER Finder approach – 49133 downloads. [derfinderPlot](#): plotting functions for derfinder results – 16938 downloads. [regionReport](#): Generate HTML or PDF reports for a set of genomic regions or DESeq2/edgeR results – 19964 downloads. [derfinderHelper](#): helper functions for derfinder package – 41678 downloads. [derfinderData](#): data for derfinder examples – 4492 downloads.

[all\\_purpose](#): R, Ranked 295/34,440 (top 0.9%) in the US and 1,110/320,722 (top 0.35%) worldwide by [Star Dev](#) as of May 1st, 2021. Does not take into account contributions at GitHub organizations.

[statistics](#): Stata

[scripting](#): bash

[markup](#): LaTeX, markdown

[OS](#): Linux

[cluster queue](#): Son of Grid Engine

2022  
|  
2020

### Bioconductor: mentor role

[qsvar](#) for correcting confounding by degradation in postmortem human brain, [TREG](#) for identifying genes that consistently predict RNA abundance across cell types, [regutools](#): mentored 3 CDSB alumni remotely

2021  
|  
2014

### Bioconductor: contributor role

[dasper](#), [brainflowprobes](#), [bumphunter](#), [ballgown](#).

2021  
|  
2014

### shiny web applications

[recount3-study-explorer](#), [spatialLIBD](#), [recount-brain](#): explore recount-brain interactively. [wgbsExprs](#): LIBD WGBS Expression explorer for the methylation and expression associations described by Price et al, 2019. [shinycsv](#): explore a table interactively. [recount](#): analysis-ready RNA-seq gene and exon counts datasets. MPH capstone TA [office hours sign up](#). [Simple mortgage calculator](#).

- Deployed links: [recount3-study-explorer](#), [spatialLIBD](#), [recount-brain](#), [wgbsExprs](#), [recount](#), [shinycsv](#).

2019  
|  
2011

### Misc R packages

[sgejobs](#): Helper functions for SGE jobs at JHPCE. [easyweb](#): A fast and easy way to build your own website. [libdRSE](#): Custom RSE objects from genomic coordinates on LIBD data. [blogdown](#): contributed the *Insert Image* and *New Post* addins. [recount.bwtool](#): Compute coverage matrices from recount quickly using bwtool. [jaffelab](#): commonly used functions by the Jaffe lab. [shinycsv](#): explore a table interactively. [enrichedRanges](#): identify enrichment between two sets of genomic ranges. [dots](#): simplify function calls. [fitbitR](#): visualize your FitBit data. [BacterialTranscription](#): identify TSSs and TUs from RNA-seq data.

2016

### JHU thesis template

[GitHub](#) and [Overleaf](#)

[Table of Contents](#)



## LEADERSHIP AND SERVICE

2022  
|  
2011

### Open-source software

Develop and maintain open-source biostatistical software

2022  
|  
2013

### Peer Review

Bioinformatics, Biological Psychiatry, Biostatistics, F1000Research, Nucleic Acids Research, Scientific Reports, Statistical Applications in Genetics and Molecular Biology.

- Full details available [through Publons](#).

2022  
|  
2018

### Community of Bioinformatics Software Developers (CDSB in Spanish)

Co-founder and Board Member of [CDSB](#) which is a community of R and Bioconductor developers in Latin America.

2022  
|  
2018

### LIBD rstats club

Co-founder and Maintainer of the [LIBD rstats club](#).

Baltimore, MD, USA

2021	<b>Conference Abstracts Review</b> useR!2021.	
2016	<b>JHBSPH Student rep</b> Student representative for the Centennial celebration of the Department of Biostatistics.	📍 Baltimore, MD, USA
2016   2012	<b>JHBSPH Biostatistics Cultural Mixers</b> Organized <i>Cultural Mixer</i> events for the Department of Biostatistics with <a href="#">Amanda Mejia</a> for raising cultural awareness.	📍 Baltimore, MD, USA
2014	<b>Professional memberships</b> International Society for Computational Biology (2019), American Society of Human Genetics (2015, 2018-2021), American Statistical Association (2015-2017, 2020), ENAR student member (2014-2016), American Public Health Association (2014).	
2014   2012	<b>JHBSPH Genomics for students</b> Organized the <i>Genomics for Students</i> group ( <a href="#">website</a> ).	📍 Baltimore, MD, USA
2011   2009	<b>IBT-UNAM Genomics Journal Club</b> Organized a Genomics Journal Club at IBT-UNAM.	📍 Cuernavaca, Morelos, Mexico
2009   2008	<b>LCG-UNAM Student rep</b> Elected class representative for the LCG Academic Committee. Class representative for Administration Unit for Technology Information committee.	📍 Cuernavaca, Morelos, Mexico
2008	<b>NNB-UNAM forum launch</b> Helped start the National Node of Bioinformatics (Mexico) <a href="#">online forum</a> .	<a href="#">Table of Contents</a> 📍 Cuernavaca, Morelos, Mexico



## MENTORING EXPERIENCE

2021   2020	<b>Brenda Pardo</b> LCG-UNAM student: 3rd year lab rotation	📍 Remotely
-------------------	--	------------

2020  
|  
2019

### CDSB regutools project

Along with Alejandro Reyes, co-mentored Joselyn Chávez, Carmina Barberena-Jonas and Jesus Emiliano Sotelo-Fonseca for the CDSB [regutools](#) R/Bioconductor package project.

📍 Remotely

2018  
|  
2017

### Amy Peterson

MPH practicum and MPH capstone advisor.

📍 Baltimore, MD, USA

2018  
|  
2017

### Ashkaun Razmara

MPH practicum and MPH capstone advisor.

📍 Baltimore, MD, USA

2015

### José Alquicira-Hernández

LCG-UNAM student visiting Jeff Leek's group.

📍 Baltimore, MD, USA

2011  
|  
2009

### Winter Genomics mentees

Advised and trained 13 LCG-UNAM students and alumni while working at *Winter Genomics*: Riveros-McKay F, Vargas-Chávez C, Dulanto-Acevedo V, Romero-Martínez S, Samaniego-Castruita J, Zepeda-Mendoza L, Vargas-Velázquez A, Noé-González M, Soto Jiménez LM, López Moyado I, Medina-Abarca H., Izquierdo-Rangel E, and Berrocal-Quezada NA.

📍 Cuernavaca, Morelos, Mexico

2009

### LCG-UNAM mentees

Trained 3 LCG-UNAM students to take over the R/Bioconductor course: Reyes-Quiroz A, Moreno-Mayar V, and Reyes-López J.

📍 Cuernavaca, Morelos, Mexico

[Table of Contents](#)



## TEACHING EXPERIENCE

2022

### Introduction to RNA-seq data analysis with Bioconductor

LCG-UNAM

📍 Virtual event

- Instructor for [rnaseq\\_LCG-UNAM\\_2022](#).

2021

### CDSB

CDSB at LCG-UNAM

📍 Virtual event

- Organizer and instructor for the [CDSB 2021 workshop: analysis of scRNA-seq data with Bioconductor](#).

2021

### Interactive exploration of RNA-seq data with iSEE

CDSB, RMB and NNB-CCG (UNAM)

📍 Virtual event

- Instructor for a workshop that is part of the [mini courses series organized by CDSB, RMB and NNB-CCG \(UNAM\)](#).

I am a strong believer that access to education is important, but also having [mentors and sponsors](#) and as such as I aim to be a good mentor and help others by promoting them among my peers and helping them become more visible in the research community, particularly through Twitter. Locally, I help through [Data Science guidance sessions](#) at LIBD as well as through the [LIBD rstats club](#). My most direct way of helping Mexicans and Latino Americans is through the [Community of Bioinformatics Software Developers](#) that aims to help R/Bioconductor users become R/Bioconductor developers. I also strongly

2021	<b>Getting started with scRNA-seq analyses with Bioconductor</b> Human Cell Atlas (HCA) Latin America workshop	 Virtual event
	• Instructor for a 2 hour workshop.	
2021	<b>Introduction to RNA-seq data analysis with Bioconductor</b> LCG-UNAM	 Virtual event
	• Instructor for rnaseq_LCG-UNAM_2021.	
2020	<b>R/Bioconductor Data Science bootcamps</b> LIBD	 Virtual event
	• Taught 8 bootcamp sessions ( <a href="#">materials</a> ).	
2020	<b>CDSB</b> CDSB at LCG-UNAM	 Virtual event
	• Organizer and instructor for the <a href="#">CDSB 2020 workshop</a> .	
2020	<b>Analyzing scRNA-seq data with Bioconductor</b> LCG-EJ-UNAM	 Virtual event
	• Instructor for <a href="#">OSCA_LIIGH_UNAM_2020</a> .	
2019	<b>CDSB</b> CDSB at LCG-UNAM	 Cuernavaca, Morelos, Mexico
	• Organizer and instructor for the <a href="#">CDSB 2019 workshop</a> .	
2016	<b>Kandahar University Training</b> Johns Hopkins University	 Dubai, UAE
	• Instructor for a Biostatistics and Stata workshop for Kandahar University Faculty, organized by Johns Hopkins University ( <a href="#">website</a> ).	
2016	<b>Genomeeting</b> INMGEN	 Mexico City, CDMX, Mexico
	• Instructor for <a href="#">Genomeeting 2016</a> .	
2016   2014	<b>Statistical Methods in Public Health</b> Johns Hopkins Bloomberg School of Public Health	 Baltimore, MD, USA
	• Lead teaching assistant for Statistical Methods in Public Health I and II.	
2016   2014	<b>MPH capstone project</b> Johns Hopkins Bloomberg School of Public Health	 Baltimore, MD, USA
	• Teaching assistant for the MPH capstone projects. 30 min one-on-one consulting sessions (biostatistics, Stata coding). • Develop and maintain the <a href="#">MPHcapstoneTA shiny application</a> .	

2016   2012	<b>Statistical Methods in Public Health</b> Johns Hopkins Bloomberg School of Public Health  Baltimore, MD, USA <ul style="list-style-type: none"><li>Teaching assistant for Statistical Methods in Public Health I, II, III and IV.</li></ul>
2015	<b>Summer Institute</b> Johns Hopkins Bloomberg School of Public Health  Baltimore, MD, USA <ul style="list-style-type: none"><li>Guest lecturer: Introduction to R for Public Health Researchers, Reproducible research module.</li></ul>
2015	<b>Introduction to R for Public Health Researchers</b> Johns Hopkins Bloomberg School of Public Health  Baltimore, MD, USA <ul style="list-style-type: none"><li>Teaching assistant</li></ul>
2012   2011	<b>Introduction to R and Biostatistics</b> LCG-UNAM  Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"><li>Guest lecturer: Seminar 1, Introduction to Bioinformatics course</li></ul>
2011	<b>PDCB-UNAM</b> CCG-UNAM  Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"><li>Instructor for the course <i>Introduction to R and Biostatistics</i> for Biomedical Sciences Ph.D. students (<a href="#">website</a>).</li></ul>
2010	<b>PDCB-UNAM</b> CCG-UNAM  Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"><li>Instructor for <i>Analysis of High-Throughput Sequencing data with Bioconductor</i> for Biomedical Sciences Ph.D. students (<a href="#">website</a>).</li></ul>
2010	<b>National Bioinformatics Week</b> Organized by NNB-UNAM at CCG-UNAM  Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"><li>Instructor of the <i>Introduction to Using Bioconductor for High-Throughput Sequencing Analysis</i> practice lab at the <i>National Bioinformatics Week</i>.</li></ul>
2010	<b>Enrique Morett Lab</b> IBT-UNAM  Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"><li>Instructor for the <i>Introduction to R and plotting with R</i> course for Morett's lab.</li></ul>
2010	<b>Statistical Methods and Analysis of Genomic Data</b> IBT-UNAM  Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"><li>Organizer and instructor (<a href="#">website</a>).</li></ul>

2009	<b>Enrique Morett Lab</b> IBT-UNAM	📍 Cuernavaca, Morelos, Mexico
	• Organizer and instructor for the course <i>Introduction to Bioinformatics</i> for Morett's lab where I taught the <i>Introduction to R and plotting with R</i> module ( <a href="#">website</a> )	
2009	<b>Seminar III: R/Bioconductor</b> LCG-UNAM	📍 Cuernavaca, Morelos, Mexico
	• Organizer and instructor for an in-depth Bioconductor course ( <a href="#">website</a> )	
2009	<b>Principles of Statistics</b> LCG-UNAM	📍 Cuernavaca, Morelos, Mexico
	• Basic R ( <a href="#">website</a> ).	
2008	<b>Bioinformatics and Statistics I</b> LCG-UNAM	📍 Cuernavaca, Morelos, Mexico
	• R and Bioconductor overview ( <a href="#">website</a> ).	<a href="#">Table of Contents</a>



## COURSES, MEETINGS, TALKS, AND POSTERS

2021	<b>Biology of Genomes (BoG)</b> Cold Spring Harbor Laboratory	📍 Virtual event
2021	<b>BioTuring webinar</b>	📍 Virtual event
	• Presented the spatialLIBD project together with Kristen Maynard during a webinar with ~200 registered individuals that you can watch <a href="#">here</a> . ( <a href="#">slides</a> )	Most recent slides are available via <a href="#">speakerdeck</a> or <a href="#">slideshare</a> .
2021	<b>Genomics of Brain Disorders</b> Wellcome Genome Campus	📍 Virtual event
2021	<b>CDC/ATSDR R User Group</b>	📍 Virtual event
	• Presented a talk on spatialLIBD and recount3 ( <a href="#">slides</a> ).	
2021	<b>ConectaR</b>	📍 Virtual event
	• Presented a virtual poster on how to use "biocthis for making R/Bioconductor packages" ( <a href="#">slides</a> ).	
2021	<b>RStudio Global</b>	📍 Virtual event

2021	<b>Ryten lab</b>	Virtual event
	• Guest presentation for Mina Ryten's lab on "Making R/Bioconductor packages with biocthis; recount3 use case" ( <a href="#">slides</a> )	
2020	<b>ASHG</b>	Virtual event
2020	<b>CDSB</b> LCG-UNAM	Virtual event
	• Launch of the CDSB 2020 workshop ( <a href="#">slides</a> ) and keynote on the spatialLIBD project ( <a href="#">slides</a> ).	
2020	<b>JSM</b>	Virtual event
	• Gave a talk on "Promoting the next wave of R/Bioconductor developers in Latin America starting in Mexico" ( <a href="#">slides</a> ).	
2020	<b>BioC</b> Dana-Farber Cancer Research Institute	Virtual event
	• Presented a <a href="#">poster</a> on the spatialLIBD project, taught a <a href="#">workshop</a> on recount2 and related projects, organized and presented at the <a href="#">Birds of a Feather: CDSB</a> event, and was involved in the Community Advisory Board presentation.	
2020	<b>useR!</b> Saint Louis University	Virtual event
	• Presented on the " <a href="#">Latin American Communities and Organizations</a> " panel and wrote a blog post for the <a href="#">R Consortium</a> .	
2020	<b>The Scientist webinar</b>	Virtual event
	• Presented the spatialLIBD project together with Kristen Maynard during a webinar with ~600 registered individuals that you can watch <a href="#">here</a> . ( <a href="#">slides</a> )	
2020	<b>rstudio::conf</b>	San Francisco, CA, USA
	• Attended the <a href="#">JavaScript for Shiny users</a> workshop taught by Garrick Aden-Buie.	
2019	<b>ASHG</b>	Houston, TX, USA
	• Platform talk: Regional heterogeneity in gene expression, regulation, and coherence in the frontal cortex and hippocampus across development and schizophrenia ( <a href="#">slides</a> ).	

2019	<b>Visitors Research Seminar</b> IIGH-UNAM	Juriquilla, Qro, Mexico
	• Analyzing BrainSeq Phase II and generating the recount-brain resource ( <a href="#">slides</a> ).	
2019	<b>CDSB</b> LCG-UNAM	Cuernavaca, Morelos, Mexico
	• Launch of the CDSB 2019 workshop ( <a href="#">slides</a> ).	
2019	<b>BioC</b> Rockefeller University	New York, NY, USA
	• Using the recount2 resource and related tools <a href="#">workshop (slides)</a> . Lightning talk on the Community of Bioinformatics Software Developers ( <a href="#">slides</a> ). • Also remotely for CONABIO's bioinformatics course on 2019-10-07 organized by Alicia Mastretta-Yanes.	
2019	<b>Biology of Genomes (BoG)</b> Cold Spring Harbor Laboratory	Cold Spring Harbor, NY, USA
	• recount-brain: a curated repository of human brain RNA-seq datasets metadata ( <a href="#">poster</a> ).	
2019	<b>Staff Seminar Series</b> LIBD	Baltimore, MD, USA
	• Analyzing BrainSeq Phase II and generating the recount-brain resource ( <a href="#">slides</a> ).	
2019	<b>rstudio::conf</b>	Austin, TX, USA
	• Attended the <a href="#">Building Tidy Tools</a> workshop by Charlotte and Hadley Wickham.	
2019	<b>Pacific Symposium on Biocomputing (PSB)</b>	Hawaii, HI, USA
	• Reproducible RNA-seq analysis with recount2 ( <a href="#">slides</a> ). Regional heterogeneity in gene expression, regulation and coherence in hippocampus and dorsolateral prefrontal cortex across development and in schizophrenia ( <a href="#">poster</a> ).	
2018	<b>Joint Genomic Meeting</b> Johns Hopkins University	Baltimore, MD, USA
	• recount-brain: a curated repository of human brain RNA-seq datasets metadata ( <a href="#">slides</a> ).	

2018	<b>Biological Data Science</b> Cold Spring Harbor Laboratory	📍 Cold Spring Harbor, NY, USA
	• Regional heterogeneity in gene expression, regulation and coherence in hippocampus and dorsolateral prefrontal cortex across development and in schizophrenia ( <a href="#">poster</a> ).	
2018	<b>ASHG</b>	📍 San Diego, CA, USA
	• Regional heterogeneity in gene expression, regulation and coherence in hippocampus and dorsolateral prefrontal cortex across development and in schizophrenia ( <a href="#">poster</a> ).	
2018	<b>CDSB</b> Keynote	📍 Remotely
	• From learning to using to teaching to developing R (remote presentation) ( <a href="#">slides</a> ).	
2018	<b>SAGES</b>	📍 Philadelphia, PA, USA
	• BrainSeq Phase II: schizophrenia-associated expression differences between the hippocampus and the dorsolateral prefrontal cortex ( <a href="#">poster</a> ).	
2018	<b>LCG-UNAM Remote Talks</b> LCG-UNAM	📍 Remotely
	• Reproducible RNA-seq analysis with recount2 and recount-brain ( <a href="#">slides</a> ).	
2018	<b>SOBP</b>	📍 New York, NY, USA
	• Unique Molecular Correlates of Schizophrenia and Its Genetic Risk in the Hippocampus Compared to Frontal Cortex ( <a href="#">slides</a> ).	
2018	<b>Biology of Genomes (BoG)</b> Cold Spring Harbor Laboratory	📍 Cold Spring Harbor, NY, USA
	• BrainSeq Phase II: Schizophrenia-associated expression differences between the hippocampus and the dorsolateral prefrontal cortex ( <a href="#">slides</a> ).	
2018	<b>rOpenSci Unconf</b>	📍 Seattle, WA, USA
	• Worked on <a href="#">pkginspector</a> .	
2018	<b>Journal Club by Dennis Lal</b>	📍 Remotely
	• recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor ( <a href="#">slides</a> ).	

2017	<b>IDIES</b> Johns Hopkins University	 Baltimore, MD, USA
	• Getting started with recount2 and accessing it via R ( <a href="#">poster</a> ).	
2017	<b>JSM</b>	 Baltimore, MD, USA
	• Guiding principles for interactive graphics based on LIBD data science projects ( <a href="#">slides</a> ).	
2017	<b>Summer Institute</b> Johns Hopkins University	 Baltimore, MD, USA
	• Reproducible Research and Bioinformatics ( <a href="#">slides</a> ).	
2017	<b>BioC</b> Dana-Farber Cancer Institute	 Boston, MA, USA
	• Reproducible RNA-seq analysis with recount2 <a href="#">workshop</a> ( <a href="#">slides</a> ).	
2017	<b>ICSA</b>	 Chicago, IL, USA
	• Reproducible RNA-seq analysis with recount2 ( <a href="#">slides</a> ).	
2017	<b>SOBP</b>	 San Diego, CA, USA
	• RNA-seq samples beyond the known transcriptome with derfinder and recount ( <a href="#">slides</a> ).	
2016	<b>Kandahar University Training</b> Johns Hopkins University	 Dubai, UAE
	• Introduction at Kandahar University MPH training event ( <a href="#">slides</a> ).	
2016	<b>Genomeeting</b> INMEGEN	 Mexico City, CDMX, Mexico
	• recount: facilitando el análisis de miles de muestras de RNA-seq ( <a href="#">slides</a> ).	
2016	<b>SACNAS</b>	 Long Beach, CA, USA
	• Using Data Science to Study Human Brain Genomic Measurements ( <a href="#">slides</a> ).	
2016	<b>ENAR</b>	 Austin, TX, USA
	• Annotation-agnostic differential expression analysis ( <a href="#">slides</a> ).	
2015	<b>Joint Genomic Meeting</b> Johns Hopkins University	 Baltimore, MD, USA
	• dbFinder ( <a href="#">slides</a> ).	

2015	<b>IDIES</b> Johns Hopkins University	 Baltimore, MD, USA
	• Annotation-agnostic RNA-seq differential expression analysis software ( <a href="#">poster</a> ).	
2015	<b>Genomics and Bioinformatics Symposium</b> Johns Hopkins University	 Baltimore, MD, USA
	• Annotation-agnostic differential expression analysis ( <a href="#">slides</a> ).	
2015	<b>ASHG</b> Johns Hopkins University	 Baltimore, MD, USA
	• Annotation-agnostic RNA-seq differential expression analysis software ( <a href="#">poster</a> ).	
2015	<b>Biostatistics Computing Club</b> Johns Hopkins University	 Baltimore, MD, USA
	• Easy parallel computing with BiocParallel and HTML reports with knitrBootstrap ( <a href="#">slides</a> ).	
2015	<b>ENAR</b> Johns Hopkins University	 Miami, FL, USA
	• Dissecting human brain development at high resolution using RNA-seq ( <a href="#">slides</a> ).	
2015	<b>Joint Genomic Meeting</b> Johns Hopkins University	 Baltimore, MD, USA
	• Does mapping simulated RNA-seq reads provide information? ( <a href="#">slides</a> ).	
2014	<b>Jeff Leek lab</b> Johns Hopkins University	 Baltimore, MD, USA
	• derfinder tutorial ( <a href="#">slides</a> ).	
2014	<b>is3b: International Summer Symposium on Systems Biology</b> INMEGEN	 Mexico City, CDMX, Mexico
	• Developmental regulation of human cortex transcription at base-pair resolution ( <a href="#">slides</a> ).	
2014	<b>BioC</b> Dana-Farber Cancer Institute	 Boston, MA, USA
2014	<b>Biostatistics Computing Club</b> Johns Hopkins University	 Baltimore, MD, USA
	• Git for research ( <a href="#">slides</a> ).	
2014	<b>IDIES</b> Johns Hopkins University	 Baltimore, MD, USA

2014	<b>ENAR</b>	 Baltimore, MD, USA
	• Fast annotation-agnostic differential expression analysis ( <a href="#">poster</a> ).	
2014	<b>Delta Omega Poster Competition</b>	 Baltimore, MD, USA
	Johns Hopkins University	
	• Fast annotation-agnostic differential expression analysis ( <a href="#">poster</a> ).	
2014	<b>LCG-UNAM 10 year anniversary</b>	 Cuernavaca, Morelos, Mexico
	• Fast differential expression analysis annotation-agnostic across groups with biological replicates ( <a href="#">slides</a> ).	
2013	<b>Genomics and Bioinformatics Symposium</b>	 Baltimore, MD, USA
	Johns Hopkins University	
	• Fast annotation-agnostic differential expression analysis ( <a href="#">poster</a> ).	
2013	<b>Genomics for Students</b>	 Baltimore, MD, USA
	Johns Hopkins University	
	• Introduction to ggbio ( <a href="#">slides</a> ).	
2013	<b>Joint Genomic Meeting</b>	 Baltimore, MD, USA
	Johns Hopkins University	
	• Fast differential expression analysis annotation-agnostic across groups with biological replicates ( <a href="#">slides</a> ).	
2013	<b>Biostatistics Journal Club</b>	 Baltimore, MD, USA
	Johns Hopkins University	
	• Fast differential expression analysis annotation-agnostic across groups with biological replicates ( <a href="#">slides</a> ).	
2013	<b>useR!</b>	 Albacete, Spain
	• Differential expression analysis of RNA-seq data at base-pair resolution in multiple biological replicates ( <a href="#">slides</a> ).	
2013	<b>Biostatistics Department Retreat</b>	 Philadelphia, PA, USA
	Johns Hopkins University	
	• Differential expression RNA-seq analysis with a large data set from brain samples ( <a href="#">poster</a> ).	
2013	<b>Biostatistics Computing Club</b>	 Baltimore, MD, USA
	Johns Hopkins University	
	• Introduction to knitr ( <a href="#">slides</a> ).	

2013	<b>Genomics for Students</b> Johns Hopkins University	 Baltimore, MD, USA
	• Introduction to High-Throughput Sequencing and RNA-seq ( <a href="#">slides</a> ).	
2012	<b>Genomics for Students</b> Johns Hopkins University	 Baltimore, MD, USA
	• DEXSeq paper discussion ( <a href="#">slides</a> ).	
2012	<b>LCG-UNAM Remote Talks</b> LCG-UNAM	 Remotely
	• Introduction to R and Biostatistics ( <a href="#">slides</a> ).	
2012	<b>Biostatistics Computing Club</b> Johns Hopkins University	 Baltimore, MD, USA
	• Introducing Git while making your academic webpage ( <a href="#">slides</a> ).	
2011	<b>LCG-UNAM Remote Talks</b> LCG-UNAM	 Remotely
	• Introducing Biostatistics to first year LCG students ( <a href="#">slides</a> ).	
2011	<b>BioC</b> Fred Hutchinson Cancer Research Center	 Seattle, WA, USA
2010	<b>Bioconductor Developer Meeting</b> EMBL	 Heidelberg, Germany
	• BacterialTranscription: a R package to identify Transcription Start Sites and Transcription Units ( <a href="#">slides</a> ).	
2010	<b>From Functional Genomics to System Biology</b> EMBL	 Heidelberg, Germany
	• Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes ( <a href="#">poster</a> ).	
2010	<b>National Bioinformatics Week</b> Organized by NNB-UNAM at CCG-UNAM	 Cuernavaca, Morelos, Mexico
	• Introduction to using Bioconductor for High Throughput Sequencing Analysis instructor ( <a href="#">slides</a> ).	
2010	<b>BioC</b> Fred Hutchinson Cancer Research Center	 Seattle, WA, USA
	• Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes ( <a href="#">poster</a> ).	

2009	<b>LCG-UNAM Third Generation Symposium</b> CCG-UNAM • Bacteriophages: analyzing their diversity ( <a href="#">slides</a> ).	📍 Cuernavaca, Morelos, Mexico
2009	<b>BioC</b> Fred Hutchinson Cancer Research Center	📍 Seattle, WA, USA
2009	<b>Course on Oral Communication</b> CCG-UNAM • Taught by the master Rafael Popoca.	📍 Cuernavaca, Morelos, Mexico
2008	<b>BioC</b> Fred Hutchinson Cancer Research Center	📍 Seattle, WA, USA
2008	<b>A Short R/Bioconductor Course</b> LCG-UNAM • Taught by James Bullard from UC Berkeley, Ph.D. student in Sandrine Dudoit's lab at the time.	📍 Cuernavaca, Morelos, Mexico
2007	<b>Boston Bacterial Meeting</b>	📍 Boston, MA, USA
2007	<b>Department of Microbiology and Molecular Genetics Retreat</b> Harvard University	📍 Boston, MA, USA
2006	<b>Winter School in Genomics</b> CCG-UNAM	📍 Cuernavaca, Morelos, Mexico
2005	<b>HUGO</b>	📍 Kyoto, Japan
		<a href="#">Table of Contents</a>



- Native: Spanish (Mexico)
- Bilingual: English
- Basic: French

[Table of Contents](#)