

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) and other institutions, 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 a board member of the [Community of Bioinformatics Software Developers](#). In order to provide a supportive and stimulating research environment at LIBD, my group provides [Data Science guidance sessions](#) open to any LIBD staff member and organizes 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. I became a principal investigator in September 2020.

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](#). In the past, I also served on the [Bioconductor Community Advisory Board](#) and the advisory board for [rOpenSci's Statistical Software Peer Review](#).

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



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CONTACT

- ✉ lcolladotor@gmail.com
- 🐦 [lcolladotor](#)
- 👤 [lcolladotor](#)
- 🔗 [lcolladotor.github.io](#)
- 🌐 [Team website](#)
- linkedin [Icollado](#)
- ORCID [ORCID](#)
- Google Scholar [Google Scholar](#)
- Speaker Deck [Speaker Deck](#)
- Slideshare [slideshare](#)
- Publons [publons](#)
- NIH Reporter [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 2023-06-20.

- Languages

EDUCATION

2016
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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
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2005

B.S., Genomic Sciences

National Autonomous University of Mexico (UNAM)

 Cuernavaca, Morelos, Mexico

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

2005
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2002

H.S.

ITESM Campus Cuernavaca

 Cuernavaca, Morelos, Mexico

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- 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

2023
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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
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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
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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
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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
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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
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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
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2006

Undergrad research assistant at Roberto Kolter's lab

Harvard University

📍 Boston, MA, US

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- 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
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2010

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.

2010
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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.

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](#).

2022
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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](#).

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

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

2018

Bioinformatics Peer Prize III

announcement

- [Competition website](#), and our [winning entry](#).

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2023

PUBLICATIONS

escheR: Unified multi-dimensional visualizations with Gestalt principles

R/Bioconductor package

- Boyi Guo, Louise A. Huuki-Myers, Melissa Grant-Peters, **Leonardo Collado-Torres**, Stephanie C. Hicks. escheR: Unified multi-dimensional visualizations with Gestalt principles. *bioRxiv* (2023) doi: [10.1101/2023.03.18.533302](https://doi.org/10.1101/2023.03.18.533302).

* indicates equal contribution, † indicates corresponding author

2023

Activity-regulated gene expression across cell types of the mouse hippocampus

iSEE app, code

- Erik D. Nelson, Kristen R. Maynard, Kyndall R. Nicholas, Matthew N. Tran, Heena R. Divecha, **Leonardo Collado-Torres**, Stephanie C. Hicks †, Keri Martinowich †. Activity-regulated gene expression across cell types of the mouse hippocampus. *Hippocampus* (2023) doi: [10.1002/hipo.23548](https://doi.org/10.1002/hipo.23548)
bioRxiv (2022) doi: [10.1101/2022.11.23.517593](https://doi.org/10.1101/2022.11.23.517593)
- Supporting role
- [pre-print Twitter summary](#)

2023

Influence of Alzheimer's disease related neuropathology on local microenvironment gene expression in the human inferior temporal cortex

[project website](#), code

- Sang Ho Kwon, Sowmya Parthiban, Madhavi Tippani, Heena R. Divecha, Nicholas J. Eagles, Jashandeep S. Lobana, Stephen R. Williams, Michelle Mak, Rahul A. Bharadwaj, Joel E. Kleinman, Thomas M. Hyde, Stephanie C. Page, Stephanie C. Hicks †, Keri Martinowich †, Kristen R. Maynard †, **Leonardo Collado-Torres** †. Influence of Alzheimer's disease related neuropathology on local microenvironment gene expression in the human inferior temporal cortex. *bioRxiv* (2023) doi: [10.1101/2023.04.20.537710](https://doi.org/10.1101/2023.04.20.537710).
- Co-corresponding author
- [pre-print Twitter summary](#)

|

2022

2023

Integrated single cell and unsupervised spatial transcriptomic analysis defines molecular anatomy of the human dorsolateral prefrontal cortex
[project website](#), [code](#), [snRNA-seq code](#)

- Louise A. Huuki-Myers, Abby Spangler, Nicholas J. Eagles, Kelsey D. Montgomery, Sang Ho Kwon, Boyi Guo, Melissa Grant-Peters, Heena R. Divecha, Madhavi Tippani, Chaichontat Sriworarat, Annie B. Nguyen, Prashanthi Ravichandran, Matthew N. Tran, Arta Seyedian, PsychENCODE consortium, Thomas M. Hyde, Joel E. Kleinman, Alexis Battle, Stephanie C. Page, Mina Ryten, Stephanie C. Hicks, Keri Martinowich, **Leonardo Collado-Torres** †, Kristen R. Maynard †. Integrated single cell and unsupervised spatial transcriptomic analysis defines molecular anatomy of the human dorsolateral prefrontal cortex. *bioRxiv* (2023) doi: [10.1101/2023.02.15.528722](https://doi.org/10.1101/2023.02.15.528722)
- Co-corresponding author
- [pre-print Twitter summary](#)

2023

Splicing accuracy varies across human introns, tissues and age
[code](#)

- S García-Ruiz, D Zhang, E K Gustavsson, G Rocamora-Perez, M Grant-Peters, A Fairbrother-Browne, R H Reynolds, J W Brenton, A L Gil-Martínez, Z Chen, D C Rio, J A Botia, S Guelfi, **Leonardo Collado-Torres**, M Ryten. Splicing accuracy varies across human introns, tissues and age. *bioRxiv* (2023) doi: [10.1101/2023.03.29.534370](https://doi.org/10.1101/2023.03.29.534370)
- Second to last author
- [pre-print Twitter summary](#)

2023

Genetic and environmental contributions to ancestry differences in gene expression in the human brain
[code](#)

- Kynon J.M. Benjamin, Qiang Chen, Nicholas J. Eagles, Louise A. Huuki-Myers, **Leonardo Collado-Torres**, Joshua M. Stoltz, Joo Heon Shin, Apuā C.M. Paquola, Thomas M. Hyde, Joel E. Kleinman, Andrew E. Jaffe, Shizhong Han †, Daniel R. Weinberger †. Genetic and environmental contributions to ancestry differences in gene expression in the human brain. *bioRxiv* (2023) doi: [10.1101/2023.03.28.534458](https://doi.org/10.1101/2023.03.28.534458)
- Supporting role

2023

Performant web-based interactive visualization tool for spatially-resolved transcriptomics experiments
[Samui Browser](#), [code](#)

- Chaichontat Sriworarat, Annie Nguyen, Nicholas J. Eagles, **Leonardo Collado-Torres**, Keri Martinowich, Kristen R. Maynard †, Stephanie C. Hicks †. Performant web-based interactive visualization tool for spatially-resolved transcriptomics experiments. *bioRxiv* (2023) doi: [10.1101/2023.01.28.525943](https://doi.org/10.1101/2023.01.28.525943)
- Supporting role
- [pre-print Twitter summary](#)

2023
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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

IntroVerse: a comprehensive database of introns across human tissues

[IntroVerse](#), [code](#)

- Sonia Garcia Ruiz, Emil K Gustavsson, David Zhang, Regina H Reynolds, Zhongbo Chen, Aine Fairbrother-Browne, Ana Luisa Gil-Martínez, Juan A Botia, **Leonardo Collado-Torres**, Mina Ryten. IntroVerse: a comprehensive database of introns across human tissues. *Nucleic Acids Research* (2022) doi: [10.1093/nar/gkac1056](https://doi.org/10.1093/nar/gkac1056)
- Second to last author
- [Twitter summary](#)

2022
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2020

Analysis of the caudate nucleus transcriptome in individuals with schizophrenia highlights effects of antipsychotics and new risk genes

- Kynon JM Benjamin, Qiang Chen, Andrew E Jaffe, Joshua M. Stoltz, **Leonardo Collado-Torres**, Louise A. Huuki-Myers, Emily E Burke, Ria Arora, Arthur S Feltrin, André Rocha Barbosa, Eugenia Radulescu, Giulio Pergola, 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 †. Analysis of the caudate nucleus transcriptome in individuals with schizophrenia highlights effects of antipsychotics and new risk genes. *Nature Neuroscience* (2022) doi: [10.1038/s41593-022-01182-7](https://doi.org/10.1038/s41593-022-01182-7) *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](#)

2022

Transcriptional and genetic sex differences for schizophrenia across the dorsolateral prefrontal cortex, hippocampus, and caudate nucleus

[code](#)

- Kynon JM Benjamin †, **Ria Arora**, Joshua M. Stoltz, Laura D'Ignazio, **Leonardo Collado-Torres**, Thomas M Hyde, Joel E Kleinman, Daniel R Weinberger †, Apuã CM Paquola †, Jennifer A Erwin †. Transcriptional and genetic sex differences for schizophrenia across the dorsolateral prefrontal cortex, hippocampus, and caudate nucleus. *medRxiv* (2022) doi: [10.1101/2022.09.30.22280452](https://doi.org/10.1101/2022.09.30.22280452)
- Supporting role

2022

Comment on: What genes are differentially expressed in individuals with schizophrenia? A systematic review

- Gabriel E. Hoffman †, Andrew E. Jaffe †, Michael J. Gandal †, **Leonardo Collado-Torres**, Solveig K. Sieberts, Bernie Devlin, Daniel H. Geschwind, Daniel R. Weinberger, Panos Roussos. Comment on: What genes are differentially expressed in individuals with schizophrenia? A systematic review. *Molecular Psychiatry* (2022) doi: [10.1038/s41380-022-01781-7](https://doi.org/10.1038/s41380-022-01781-7)
- Supporting role

2022

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2021

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. *BMC Genomics* (2022) doi: [10.1186/s12864-022-08601-w](https://doi.org/10.1186/s12864-022-08601-w) *bioRxiv* (2021) doi: [10.1101/2021.04.29.440149](https://doi.org/10.1101/2021.04.29.440149).
- Corresponding author
- [pre-print Twitter summary](#)

2022

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2021

VistoSeg: processing utilities for high-resolution Visium/Visium-IF images for spatial transcriptomics data

Documentation, code

- Madhavi Tippani, Heena R. Divecha, Joseph L. Catallini II, Sang Ho Kwon, Lukas M. Weber, Abby Spangler, Andrew E. Jaffe, Stephanie C. Hicks, Keri Martinowich, **Leonardo Collado-Torres**, Stephanie C. Page †, Kristen R. Maynard †. VistoSeg: processing utilities for high-resolution Visium/Visium-IF images for spatial transcriptomics data. *bioRxiv* (2022) doi: [10.1101/2021.08.04.452489](https://doi.org/10.1101/2021.08.04.452489)
- Supporting role
- [pre-print Twitter summary](#)

2022

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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) *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
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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
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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](#)

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

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](#)

|

2019

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 Vandrovčova, 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 Hoeppner, 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.122231](https://doi.org/10.12688/f1000research.122231). 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).

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- 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

all_purpose: R, Ranked 311/37,473 (top 0.83%) in the US and 1,132/356,811 (top 0.32%) worldwide by [Star Dev](#) as of May 9th, 2023. Does not take into account contributions at GitHub organizations.
statistics: Stata
scripting: bash
markup: LaTeX, markdown
OS: Linux
cluster queue: Son of Grid Engine

2014
|
2021

Bioconductor: author role

[recount3](#): Explore and download data from the recount3 project – 9324 downloads. [biocthis](#): Automate package and project setup for Bioconductor packages – 6176 downloads. [megadepth](#): BigWig and BAM related utilities – 4251 downloads. [spatialLIBD](#): LIBD Visium spatial transcriptomics human pilot data inspector – 6589 downloads. [GenomicState](#): data for derfinder analyses – 3627 downloads. [recount](#): Explore and download data from the recount2 project – 45965 downloads. [derfinder](#): Annotation-agnostic differential expression analysis of RNA-seq data at base-pair resolution via the DER Finder approach – 58293 downloads. [derfinderPlot](#): plotting functions for derfinder results – 18805 downloads. [regionReport](#): Generate HTML or PDF reports for a set of genomic regions or DESeq2/edgeR results – 21847 downloads. [derfinderHelper](#): helper functions for derfinder package – 50144 downloads. [derfinderData](#): data for derfinder examples – 5325 downloads.

2023
|
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

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LEADERSHIP AND SERVICE

2023

|
2011

Open-source software

Develop and maintain open-source biostatistical software

2023

|
2013

Peer Review

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

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

2023

|
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 Mexico.

2023

|
2018

LIBD rstats club

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

Baltimore, MD, USA

2021

Conference Abstracts Review

useR!2021.

2016

JHBSPH Student rep

Student representative for the Centennial celebration of the Department of Biostatistics.

Baltimore, MD, USA

2016

|
2012

JHBSPH Biostatistics Cultural Mixers

Organized *Cultural Mixer* events for the Department of Biostatistics with [Amanda Mejia](#) for raising cultural awareness.

Baltimore, MD, USA

2014

Professional memberships

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

JHBSPH Genomics for students

Organized the *Genomics for Students* group ([website](#)).

Baltimore, MD, USA

2011	IBT-UNAM Genomics Journal Club	
	Organized a Genomics Journal Club at IBT-UNAM.	
2009		📍 Cuernavaca, Morelos, Mexico
2009	LCG-UNAM Student rep	
	Elected class representative for the LCG Academic Committee. Class representative for Administration Unit for Technology Information committee.	
2008		📍 Cuernavaca, Morelos, Mexico
2008	NNB-UNAM forum launch	
	Helped start the National Node of Bioinformatics (Mexico) online forum .	
		📍 Cuernavaca, Morelos, Mexico
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MENTORING EXPERIENCE

2023	Daianna González Padilla	
	LCG-UNAM student: 3rd year lab rotation	📍 Remotely
2022		
2021	Brenda Pardo	
	LCG-UNAM student: 3rd year lab rotation	📍 Remotely
2020		
2020	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
2019		
2018	Amy Peterson	
	MPH practicum and MPH capstone advisor.	📍 Baltimore, MD, USA
2017		
2018	Ashkaun Razmara	
	MPH practicum and MPH capstone advisor.	📍 Baltimore, MD, USA
2017		
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

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TEACHING EXPERIENCE

2023

Statistical Analysis of Genome Scale Data

Cold Spring Harbor Laboratory

📍 Cold Spring Harbor, NY, USA

- Instructor for this [CSHL course](#).

2023

Introduction to RNA-seq data analysis with Bioconductor

LCG-UNAM

📍 Cuernavaca, Morelos, Mexico

- Instructor for [rnaseq_LCG-UNAM_2023](#).

2022

CDSB

CDSB at LCG-UNAM

📍 Virtual event

- Instructor for the [CDSB 2022 workshop: advanced metagenomics analysis. Building workflows with R/Bioconductor..](#)

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 believe in giving back to your own community by passing on the knowledge you acquired at a course or conference. Historically, that's what launched my career in R and I still learn a lot from teaching.

2021	Getting started with scRNA-seq analyses with Bioconductor Human Cell Atlas (HCA) Latin America workshop <ul style="list-style-type: none">• Instructor for a 2 hour workshop.	 Virtual event
2021	Introduction to RNA-seq data analysis with Bioconductor LCG-UNAM <ul style="list-style-type: none">• Instructor for rnaseq_LCG-UNAM_2021.	 Virtual event
2020	R/Bioconductor Data Science bootcamps LIBD <ul style="list-style-type: none">• Taught 8 bootcamp sessions (materials).	 Virtual event
2020	CDSB CDSB at LCG-UNAM <ul style="list-style-type: none">• Organizer and instructor for the CDSB 2020 workshop.	 Virtual event
2020	Analyzing scRNA-seq data with Bioconductor LCG-EJ-UNAM <ul style="list-style-type: none">• Instructor for OSCA_LIIGH_UNAM_2020.	 Virtual event
2019	CDSB CDSB at LCG-UNAM <ul style="list-style-type: none">• Organizer and instructor for the CDSB 2019 workshop.	 Cuernavaca, Morelos, Mexico
2016	Kandahar University Training Johns Hopkins University <ul style="list-style-type: none">• Instructor for a Biostatistics and Stata workshop for Kandahar University Faculty, organized by Johns Hopkins University (website).	 Dubai, UAE
2016	Genomeeting INMGEN <ul style="list-style-type: none">• Instructor for Genomeeting 2016.	 Mexico City, CDMX, Mexico
2016 2014	Statistical Methods in Public Health Johns Hopkins Bloomberg School of Public Health <ul style="list-style-type: none">• Lead teaching assistant for Statistical Methods in Public Health I and II.	 Baltimore, MD, USA
2016 2014	MPH capstone project Johns Hopkins Bloomberg School of Public Health <ul style="list-style-type: none">• Teaching assistant for the MPH capstone projects. 30 min one-on-one consulting sessions (biostatistics, Stata coding).• Develop and maintain the MPHcapstoneTA shiny application.	 Baltimore, MD, USA

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

2009	Enrique Morett Lab 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 (website)	
2009	Seminar III: R/Bioconductor LCG-UNAM	📍 Cuernavaca, Morelos, Mexico
	• Organizer and instructor for an in-depth Bioconductor course (website)	

2009	Principles of Statistics LCG-UNAM	📍 Cuernavaca, Morelos, Mexico
	• Basic R (website).	

2008	Bioinformatics and Statistics I LCG-UNAM	📍 Cuernavaca, Morelos, Mexico
	• R and Bioconductor overview (website).	Table of Contents



COURSES, MEETINGS, TALKS, AND POSTERS

2023	2023 NIA/LNG Neurodegenerative Diseases Seminar Series	📍 Virtual seminar
	• Presented a talk on "Harnessing the power of spatially-resolved transcriptomics one step at a time" (slides)	Most recent slides are available via speakerdeck or slideshare .
2023	UCL Queen Square Institute of Neurology	📍 University College London, UK
	• Presented a talk on "Harnessing the power of spatially-resolved transcriptomics one step at a time" (slides)	
2023	The Francis Crick Institute	📍 The Francis Crick Institute, UK
	• Presented a talk on "Lessons from working on the edge of human brain transcriptomics with spatially-resolved transcriptomics and deconvolution" (slides)	
2023	UCL Great Ormond Street Institute of Child Health	📍 University College London, UK
	• Presented a talk on "Navigating human brain gene expression measurements at different resolutions to study psychiatric disorders" (slides)	

2023	Genomics of Brain Disorders GBD2023	📍 Wellcome Genome Campus, UK
	• Presented a talk on “Applying Visium Spatial Proteogenomics (Visium-SPG) to study Alzheimer’s Disease” (slides)	
2023	Chan-Zuckerberg Initiative Latin America Meeting Accelerating Open Science in Latin America	📍 Buenos Aires, Argentina
2022	Biological Data Science BDS2022	📍 Cold Spring Harbor, NY, USA
2022	Human Cell Atlas Latin America	📍 Virtual event
	• Presented a talk on “Spatially-resolved Transcriptomics Analysis with R/Bioconductor and Beyond” (slides)	
2022	R/Medicine	📍 Virtual event
	• Presented a talk on “Spatially-resolved Transcriptomics Analysis with R/Bioconductor and Beyond” (slides)	
2022	BioC Seattle Children's Hospital	📍 Seattle, WA, USA
2022	Montgomery College RNA-seq Workshop	📍 Hybrid event
	• Presented a talk on “Applications, limitations, and future directions of spatial transcriptomics technology in the human brain” (slides)	
2022	IBANGS The International Behavioural and Neural Genetics Society	📍 Hybrid event
	• Presented a talk with Kristen R Maynard on “Applications, limitations, and future directions of spatial transcriptomics technology in the human brain” (slides)	
2022	Biology of Genomes (BoG) Biology of Genomes (BoG)	📍 Cold Spring Harbor, NY, USA
	• Presented a poster on “Spatial Transcriptomics Analysis of Aβ-tau Synergy in the Inferior Temporal Cortex of the Human Brain in Alzheimer’s Disease”.	
2022	Psychgenomics Ichan School of Medicine	📍 Virtual event
	• Presented an invited seminar on “Deconvolution of RNA-seq data in the postmortem human brain: the present and preparing the future” (slides)	

2021	Spatial Biology US	 Virtual event
	• Presented a talk on "Extending Spatial Analysis with R/Bioconductor and beyond" (slides)	
2021	NIH	 Virtual event
	NIH Data Science Bootcamp	
	• Presented and participated in the "finding data" panel (slides)	
2021	HBHL	 Virtual event
	HBHL 2021 keynote	
	• Presented a keynote (slides)	
2021	Biology of Genomes (BoG)	 Virtual event
	Biology of Genomes (BoG)	
2021	BioTuring webinar	 Virtual event
	• Presented the spatialLIBD project together with Kristen Maynard during a webinar with ~200 registered individuals that you can watch here . (slides)	
2021	Genomics of Brain Disorders	 Virtual event
	Wellcome Genome Campus	
2021	CDC/ATSDR R User Group	 Virtual event
	• Presented a talk on spatialLIBD and recount3 (slides).	
2021	ConectaR	 Virtual event
	• Presented a virtual poster on how to use "biocthis for making R/Bioconductor packages" (slides).	
2021	RStudio Global	 Virtual event
2021	Ryten lab	 Virtual event
	• Guest presentation for Mina Ryten's lab on "Making R/Bioconductor packages with biocthis; recount3 use case" (slides)	
2020	ASHG	 Virtual event

2020	CDSB LCG-UNAM	 Virtual event
	• Launch of the CDSB 2020 workshop (slides) and keynote on the spatialLIBD project (slides).	
2020	JSM	 Virtual event
	• Gave a talk on “Promoting the next wave of R/Bioconductor developers in Latin America starting in Mexico” (slides).	
2020	BioC Dana-Farber Cancer Research Institute	 Virtual event
	• Presented a poster on the spatialLIBD project, taught a workshop on recount2 and related projects, organized and presented at the Birds of a Feather: CDSB event, and was involved in the Community Advisory Board presentation.	
2020	useR! Saint Louis University	 Virtual event
	• Presented on the “ Latin American Communities and Organizations ” panel and wrote a blog post for the R Consortium .	
2020	The Scientist webinar	 Virtual event
	• Presented the spatialLIBD project together with Kristen Maynard during a webinar with ~600 registered individuals that you can watch here . (slides)	
2020	rstudio::conf	 San Francisco, CA, USA
	• Attended the JavaScript for Shiny users workshop taught by Garrick Aden-Buie.	
2019	ASHG	 Houston, TX, USA
	• Platform talk: Regional heterogeneity in gene expression, regulation, and coherence in the frontal cortex and hippocampus across development and schizophrenia (slides).	
2019	Visitors Research Seminar LIIGH-UNAM	 Juriquilla, Qro, Mexico
	• Analyzing BrainSeq Phase II and generating the recount-brain resource (slides).	
2019	CDSB LCG-UNAM	 Cuernavaca, Morelos, Mexico
	• Launch of the CDSB 2019 workshop (slides).	

2019	BioC Rockefeller University	 New York, NY, USA
	<ul style="list-style-type: none">• Using the recount2 resource and related tools workshop (slides).Lightning talk on the Community of Bioinformatics Software Developers (slides).• Also remotely for CONABIO's bioinformatics course on 2019-10-07 organized by Alicia Mastretta-Yanes.	
2019	Biology of Genomes (BoG) Cold Spring Harbor Laboratory	 Cold Spring Harbor, NY, USA
	<ul style="list-style-type: none">• recount-brain: a curated repository of human brain RNA-seq datasets metadata (poster).	
2019	Staff Seminar Series LIBD	 Baltimore, MD, USA
	<ul style="list-style-type: none">• Analyzing BrainSeq Phase II and generating the recount-brain resource (slides).	
2019	rstudio::conf	 Austin, TX, USA
	<ul style="list-style-type: none">• Attended the Building Tidy Tools workshop by Charlotte and Hadley Wickham.	
2019	Pacific Symposium on Biocomputing (PSB)	 Hawaii, HI, USA
	<ul style="list-style-type: none">• Reproducible RNA-seq analysis with recount2 (slides). Regional heterogeneity in gene expression, regulation and coherence in hippocampus and dorsolateral prefrontal cortex across development and in schizophrenia (poster).	
2018	Joint Genomic Meeting Johns Hopkins University	 Baltimore, MD, USA
	<ul style="list-style-type: none">• recount-brain: a curated repository of human brain RNA-seq datasets metadata (slides).	
2018	Biological Data Science Cold Spring Harbor Laboratory	 Cold Spring Harbor, NY, USA
	<ul style="list-style-type: none">• Regional heterogeneity in gene expression, regulation and coherence in hippocampus and dorsolateral prefrontal cortex across development and in schizophrenia (poster).	
2018	ASHG	 San Diego, CA, USA
	<ul style="list-style-type: none">• Regional heterogeneity in gene expression, regulation and coherence in hippocampus and dorsolateral prefrontal cortex across development and in schizophrenia (poster).	

2018	CDSB Keynote <ul style="list-style-type: none">From learning to using to teaching to developing R (remote presentation) (slides).	Remotely
2018	SAGES <ul style="list-style-type: none">BrainSeq Phase II: schizophrenia-associated expression differences between the hippocampus and the dorsolateral prefrontal cortex (poster).	Philadelphia, PA, USA
2018	LCG-UNAM Remote Talks LCG-UNAM <ul style="list-style-type: none">Reproducible RNA-seq analysis with recount2 and recount-brain (slides).	Remotely
2018	SOBP <ul style="list-style-type: none">Unique Molecular Correlates of Schizophrenia and Its Genetic Risk in the Hippocampus Compared to Frontal Cortex (slides).	New York, NY, USA
2018	Biology of Genomes (BoG) Cold Spring Harbor Laboratory <ul style="list-style-type: none">BrainSeq Phase II: Schizophrenia-associated expression differences between the hippocampus and the dorsolateral prefrontal cortex (slides).	Cold Spring Harbor, NY, USA
2018	rOpenSci Unconf <ul style="list-style-type: none">Worked on pkgsinspector.	Seattle, WA, USA
2018	Journal Club by Dennis Lal <ul style="list-style-type: none">recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor (slides).	Remotely
2017	IDIES Johns Hopkins University <ul style="list-style-type: none">Getting started with recount2 and accessing it via R (poster).	Baltimore, MD, USA
2017	JSM <ul style="list-style-type: none">Guiding principles for interactive graphics based on LIBD data science projects (slides).	Baltimore, MD, USA
2017	Summer Institute Johns Hopkins University <ul style="list-style-type: none">Reproducible Research and Bioinformatics (slides).	Baltimore, MD, USA

2017	BioC Dana-Farber Cancer Institute • Reproducible RNA-seq analysis with recount2 workshop (slides) .	 Boston, MA, USA
2017	ICSA • Reproducible RNA-seq analysis with recount2 (slides) .	 Chicago, IL, USA
2017	SOBP • RNA-seq samples beyond the known transcriptome with derfinder and recount (slides) .	 San Diego, CA, USA
2016	Kandahar University Training Johns Hopkins University • Introduction at Kandahar University MPH training event (slides) .	 Dubai, UAE
2016	Genomeeting INMEGEN • recount: facilitando el análisis de miles de muestras de RNA-seq (slides) .	 Mexico City, CDMX, Mexico
2016	SACNAS • Using Data Science to Study Human Brain Genomic Measurements (slides) .	 Long Beach, CA, USA
2016	ENAR • Annotation-agnostic differential expression analysis (slides) .	 Austin, TX, USA
2015	Joint Genomic Meeting Johns Hopkins University • dbFinder (slides) .	 Baltimore, MD, USA
2015	IDIES Johns Hopkins University • Annotation-agnostic RNA-seq differential expression analysis software (poster) .	 Baltimore, MD, USA
2015	Genomics and Bioinformatics Symposium Johns Hopkins University • Annotation-agnostic differential expression analysis (slides) .	 Baltimore, MD, USA

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

2014	LCG-UNAM 10 year anniversary Johns Hopkins University	 Cuernavaca, Morelos, Mexico
	• Fast differential expression analysis annotation-agnostic across groups with biological replicates (slides).	
2013	Genomics and Bioinformatics Symposium Johns Hopkins University	 Baltimore, MD, USA
	• Fast annotation-agnostic differential expression analysis (poster).	
2013	Genomics for Students Johns Hopkins University	 Baltimore, MD, USA
	• Introduction to ggbio (slides).	
2013	Joint Genomic Meeting Johns Hopkins University	 Baltimore, MD, USA
	• Fast differential expression analysis annotation-agnostic across groups with biological replicates (slides).	
2013	Biostatistics Journal Club Johns Hopkins University	 Baltimore, MD, USA
	• Fast differential expression analysis annotation-agnostic across groups with biological replicates (slides).	
2013	useR!	 Albacete, Spain
	• Differential expression analysis of RNA-seq data at base-pair resolution in multiple biological replicates (slides).	
2013	Biostatistics Department Retreat Johns Hopkins University	 Philadelphia, PA, USA
	• Differential expression RNA-seq analysis with a large data set from brain samples (poster).	
2013	Biostatistics Computing Club Johns Hopkins University	 Baltimore, MD, USA
	• Introduction to knitr (slides).	
2013	Genomics for Students Johns Hopkins University	 Baltimore, MD, USA
	• Introduction to High-Throughput Sequencing and RNA-seq (slides).	
2012	Genomics for Students Johns Hopkins University	 Baltimore, MD, USA
	• DEXSeq paper discussion (slides).	

2012	LCG-UNAM Remote Talks LCG-UNAM	Remotely
	• Introduction to R and Biostatistics (slides).	
2012	Biostatistics Computing Club Johns Hopkins University	Baltimore, MD, USA
	• Introducing Git while making your academic webpage (slides).	
2011	LCG-UNAM Remote Talks LCG-UNAM	Remotely
	• Introducing Biostatistics to first year LCG students (slides).	
2011	BioC Fred Hutchinson Cancer Research Center	Seattle, WA, USA
2010	Bioconductor Developer Meeting EMBL	Heidelberg, Germany
	• BacterialTranscription: a R package to identify Transcription Start Sites and Transcription Units (slides).	
2010	From Functional Genomics to System Biology EMBL	Heidelberg, Germany
	• Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes (poster).	
2010	National Bioinformatics Week Organized by NNB-UNAM at CCG-UNAM	Cuernavaca, Morelos, Mexico
	• Introduction to using Bioconductor for High Throughput Sequencing Analysis instructor (slides).	
2010	BioC Fred Hutchinson Cancer Research Center	Seattle, WA, USA
	• Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes (poster).	
2009	LCG-UNAM Third Generation Symposium CCG-UNAM	Cuernavaca, Morelos, Mexico
	• Bacteriophages: analyzing their diversity (slides).	
2009	BioC Fred Hutchinson Cancer Research Center	Seattle, WA, USA
2009	Course on Oral Communication CCG-UNAM	Cuernavaca, Morelos, Mexico
	• Taught by the master Rafael Popoca.	

2008	BioC Fred Hutchinson Cancer Research Center	📍 Seattle, WA, USA
2008	A Short R/Bioconductor Course LCG-UNAM • Taught by James Bullard from UC Berkeley, Ph.D. student in Sandrine Dudoit's lab at the time.	📍 Cuernavaca, Morelos, Mexico
2007	Boston Bacterial Meeting	📍 Boston, MA, USA
2007	Department of Microbiology and Molecular Genetics Retreat Harvard University	📍 Boston, MA, USA
2006	Winter School in Genomics CCG-UNAM	📍 Cuernavaca, Morelos, Mexico
2005	HUGO	📍 Kyoto, Japan

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LANGUAGES

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

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