

LEONARDO COLLADO-TORRES

At the Lieber Institute for Brain Development, I am part of the Data Science Team I led by [Andrew E Jaffe](#). My research aims to better understand the roots and signatures of disease (particularly psychiatric disorders) by zooming in across dimensions of gene activity: from studying gene expression at all feature levels (genes to exons to exon-exon junctions and un-annotated regions of expression), to using different gene expression measurement technologies (bulk RNA-seq, single cell/nuclei RNA-seq to spatial transcriptomics) that provide finer biological resolution and localization of gene expression. I'm interested in both hypothesis-driven projects as well as building general resources such as [recount2](#) that enable us to contextualize our findings across all of the public human gene expression landscape. I use the [R programming language](#) for nearly all my work and like to organize my code in R packages that I share mostly through the [Bioconductor project](#). From my position at LIBD, I'm able to interact with and collaborate with fantastic biologists, data scientists, researchers at Johns Hopkins University and beyond. Furthermore, I officially help mentor LIBD employees in data science and R tools.

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](#). I worked with [Jeff Leek](#) and Andrew Jaffe in developing [derfinder](#) and [recount](#). I then worked ~3.5 years as a Staff Scientist in Andrew Jaffe's lab on a variety of data analysis projects.

Every day I use [R](#) and [Bioconductor](#). Occasionally I blog 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.

If you want to join my team, please get in touch! ^_~

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).

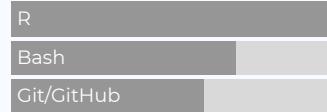


[Download a PDF of this CV](#)

CONTACT

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- 🏛 [orcid](#)
- 💻 [scholar](#)
- 💻 [speaker-deck](#)
- 💻 [slideshare](#)
- 💻 [publons](#)

LANGUAGE SKILLS



Made with the R package [page-down](#).

The source code is available at [github.com/lcolladotor/cv](#) and is powered by [nstrayer/cv](#).

Last updated on 2020-08-11.

<p>2009 2005</p>	<ul style="list-style-type: none"> ● B.S., Genomic Sciences National Autonomous University of Mexico (UNAM) 📍 Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"> • Grade 9.71/10 • Third generation at LCG-UNAM
<p>2005 2002</p>	<ul style="list-style-type: none"> ● H.S. ITESM Campus Cuernavaca 📍 Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"> • 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

<p>2020 2019</p>	<ul style="list-style-type: none"> ● Research Scientist Lieber Institute for Brain Development 📍 Baltimore, MD, USA <ul style="list-style-type: none"> • Affiliated to Andrew Jaffe's Data Science Team I. • Currently building a team and developing research ideas for grant submission. • Applying for a formal JHU joint appointment. • Official data science mentoring role at LIBD through: weekly LIBD rstats club sessions; individual 30 min guidance sessions (as in my JHBSPH MPH capstone TA years); and occasional internal LIBD courses. • Working on research projects with LIBD collaborators such as Andrew E Jaffe, Kristen R Maynard, and Keri Martinowich, JHU collaborators including Stephanie Hicks, Lukas M Weber, Ben Langmead, Christopher Wilks and Kasper Daniel Hansen, as well as external collaborators such as David Zhang, Mina Ryten, and Nicholas Clifton. • LIBD rstats club and CDSB Mexico lead. ● Staff Scientist II at Andrew Jaffe's lab Lieber Institute for Brain Development 📍 Baltimore, MD, USA <ul style="list-style-type: none"> • 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, GeonomicState and spatialLIBD R packages. • Led the LIBD rstats club and CDSB Mexico.
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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.
 - JHSPH 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.

- **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.

- **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.

- **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](#).

- **Undergrad research assistant at Roberto Kolter's lab**
Harvard University 📍 Boston, MA, US
 - 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*.

2016
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2011

2011
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2009

2009
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2007

2007
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2006

INDUSTRY EXPERIENCE

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.

- **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](#).

2010
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2009

HONORS AND AWARDS

2019
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2010

- **Travel awards**
[BioC2019](#), [BioC2017](#), [BioC2014](#), [useR2013](#), [BioC2011](#), From Functional Genomics to Systems Biology 2010 and [BiocDevelEurope 2010](#).
 - Taught a [workshop on recount](#) at BioC2017. Taught a [workshop on recount](#) at BioC2017, Gave a talk on [BacterialTranscription](#) at BiocDevelEurope2010.
 - BioC2019 [scholarship application](#)

- **rstudio::conf 2019 diversity award recipient**
[announcement](#)
 - [Scholarship application](#).

- **Early Career Clinical Research Symbiont Award**
<http://researchsymbionts.org>
 - For our work on [recount2](#).

- **National Researcher level 1**
[announcement](#) 📍 CONACYT, Mexico

- **rOpenSci Unconf 2018**
[unconf18 participants](#) and [application](#)
 - Worked on [pkginspector](#).

2018

- **Bioinformatics Peer Prize III announcement**
 - Competition website, and our [winning entry](#).

2020

■ PUBLICATIONS

- **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 †. *Oxford Bioinformatics* (2020). doi: [10.1093/bioinformatics/btaa575](https://doi.org/10.1093/bioinformatics/btaa575). *bioRxiv* 068551 (2020). doi: [10.1101/2020.04.29.068551](https://doi.org/10.1101/2020.04.29.068551)
 - Co-corresponding author
 - [Twitter summary](#)
- **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. *eLife* (2020) doi: [10.7554/eLife.56273](https://doi.org/10.7554/eLife.56273). *bioRxiv* 922013 (2020). doi: [10.1101/2020.01.28.922013](https://doi.org/10.1101/2020.01.28.922013)
 - Supporting role: analysis
 - [Twitter summary](#)
- **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 †. *Nature Neuroscience* (2020). doi: [10.1038/s41593-020-0604-z](https://doi.org/10.1038/s41593-020-0604-z)
 - Supporting role: analysis
 - [Twitter summary](#)
- **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 †. *bioRxiv* 969931 (2020). doi: [10.1101/2020.02.28.969931](https://doi.org/10.1101/2020.02.28.969931)
 - Co-first author
 - [Twitter summary](#)

* indicates equal contribution, † indicates corresponding author

2020
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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* 823781 (2019). doi: [10.1101/823781](https://doi.org/10.1101/823781)
- Supporting role: analysis
- [Twitter summary](#)

2020
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2019

● Recounting the FANTOM CAGE–Associated Transcriptome

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

- Eddie-Luidy 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* 659490 (2019). doi: [10.1101/659490](https://doi.org/10.1101/659490)
- Supporting role: data preparation and advice
- [Twitter summary](#)

2020
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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, Adaikalanathan 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* 591156 (2019). doi: [10.1101/591156](https://doi.org/10.1101/591156)
- Supporting role: data preparation and advice
- [Twitter summary](#)

2020
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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 Petersen, 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* 499103 (2018). doi: [10.1101/499103](https://doi.org/10.1101/499103)

- Supervisor role, data generation, overall project advice

- Twitter summary

2020
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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 Shibbani, 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* 380758 (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* 618025 (2019). doi: [10.1101/618025](https://doi.org/10.1101/618025)

- Corresponding author

- Twitter summary

2019
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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* 428391 (2018). doi: [10.1101/428391](https://doi.org/10.1101/428391)

• Co-first author

• [Twitter summary](#) and [summary number two](#)

2019
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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* 426213 (2018). doi: [10.1101/426213](https://doi.org/10.1101/426213)

• First-author

• [Twitter summary](#)

2019
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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* 445437 (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
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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* 430603 (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* 247346 (2018). doi: [10.1101/247346](https://doi.org/10.1101/247346)

• Supporting role

• [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* 384172 (2018). doi: [10.1101/384172](https://doi.org/10.1101/384172)

• Supporting role: data preparation and advice

• [Twitter summary](#)

2018
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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* 236968 (2017). doi: [10.1101/236968](https://doi.org/10.1101/236968)
- Supporting role: analysis
- [Twitter summary](#)

2018
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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* 124321 (2017). doi: [10.1101/145656](https://doi.org/10.1101/145656)
- Supporting role: analysis
- [Twitter summary](#)

2018
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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* 145656 (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* 068478 (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* 038224 (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* 015370 (2016). doi: [10.1101/015370](https://doi.org/10.1101/015370)
 - First author
 - [Twitter summary](#)

2016
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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/btv575](https://doi.org/10.1093/bioinformatics/btv575) *bioRxiv* 019067 (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 016659 (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).

· Gama-Castro S, Salgado H, Peralta-Gil M, Santos-Zavaleta A, Muñiz-Rascado L, Solano-Lira H, Jiménez-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

💻 SOFTWARE

2014
|
2020

- Bioconductor: author role

[spatialLIBD](#): LIBD Visium spatial transcriptomics human pilot data inspector – 256 downloads. [GenomicState](#): data for derfinder analyses – 483 downloads. [recount](#): Explore and download data from the recount project – 25592 downloads. [derfinder](#): Annotation-agnostic differential expression analysis of RNA-seq data at base-pair resolution via the DER Finder approach – 34586 downloads. [derfinderPlot](#): plotting functions for derfinder results – 13623 downloads. [regionReport](#): Generate HTML or PDF reports for a set of genomic regions or DESeq2/edgeR results – 15720 downloads. [derfinderHelper](#): helper functions for derfinder package – 28497 downloads. [derfinderData](#): data for derfinder examples – 3328 downloads.

📍 Remotely

[regutools](#)

· Mentored three CDSB alumni while they developed their first R/Bioconductor package.

2020

- Mentor role

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

2019
|
2014

- Bioconductor: contributor role

[biocthis](#), [automate](#), [easyweb](#)

[biocore](#): Automate package and project setup for Bioconductor 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. [jaf-felab](#): 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.

2019
|
2011

- Misc R packages

[all_purpose](#): R, Ranked 220/8606 (top 2.5%) in the US and 799/72425 (top 1%) worldwide by [GitHub Awards](#) as of March 1st, 2020. Does not take into account contributions at GitHub organizations.

[statistics](#): Stata

[scripting](#): bash

[markup](#): LaTeX, markdown

[OS](#): Linux

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

- 2019
|
2014
- **shiny web applications**
[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: [recount-brain](#), [wgbsExprs](#), [recount](#), [shinycsv](#).
- 2016
- **JHU thesis template**
[GitHub](#) and [Overleaf](#)
- LEADERSHIP AND SERVICE**
- 2020
|
2011
- **Open-source software**
Develop and maintain open-source biostatistical software
- 2020
|
2013
- **Peer Review**
Biostatistics, Bioinformatics, F1000Research, Nucleic Acids Research, Scientific Reports, Statistical Applications in Genetics and Molecular Biology.
 - Full details available [through Publons](#).
- 2020
|
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.
- 2020
|
2018
- **LIBD rstats club**
Co-founder and Maintainer of the [LIBD rstats club](#).
📍 Baltimore, MD, USA
- 2016
- **JHSPH Student rep**
Student representative for the Centennial celebration of the Department of Biostatistics.
📍 Baltimore, MD, USA
- 2016
|
2012
- **JHSPH 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, 2018-2019), American Statistical Association (2015-2017, 2020), ENAR student member (2014-2016), American Public Health Association (2014).
- 2014
|
2012
- **JHSPH Genomics for students**
Organized the *Genomics for Students* group ([website](#)).
📍 Baltimore, MD, USA
- 2011
|
2009
- **IBT-UNAM Genomics Journal Club**
Organized a Genomics Journal Club at IBT-UNAM.
📍 Cuernavaca, Morelos, Mexico

- 2009 |
2008
- **LCG-UNAM Student rep**
Elected class representative for the LCG Academic Committee. Class representative for Administration Unit for Technology Information committee.
📍 Cuernavaca, Morelos, Mexico
 - **NNB-UNAM forum launch**
Helped start the National Node of Bioinformatics (Mexico) [online forum](#).
📍 Cuernavaca, Morelos, Mexico

MENTORING EXPERIENCE

- 2020 |
2019
- 2018 |
2017
- 2018 |
2017
- 2015
- 2011 |
2009
- **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
 - **Amy Peterson**
MPH practicum and MPH capstone advisor.
📍 Baltimore, MD, USA
 - **Ashkaun Razmara**
MPH practicum and MPH capstone advisor.
📍 Baltimore, MD, USA
 - **José Alquicira-Hernández**
LCG-UNAM student visiting Jeff Leek's group.
📍 Baltimore, MD, USA
 - **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

2020

- **CDSB**

CDSB at LCG-UNAM
📍 Virtual event

- Organizer and instructor for the [CDSB 2020 workshop](#).

2020

- **Analyzing scRNA-seq data with Bioconductor**

LCG-EJ-UNAM
📍 Virtual event

- Instructor for [OSCA_LIIGH_UNAM_2020](#).

2019

- **CDSB**

CDSB at LCG-UNAM
📍 Cuernavaca, Morelos, Mexico

- Organizer and instructor for the [CDSB 2019 workshop](#).

2016

- **Kandahar University Training**

Johns Hopkins University
📍 Dubai, UAE

- Instructor for a Biostatistics and Stata workshop for Kandahar University Faculty, organized by Johns Hopkins University ([website](#)).

2016

- **Genomeeting**

INMEGEN
📍 Mexico City, CDMX, Mexico

- Instructor for [Genomeeting 2016](#).

2016

|

2014

- **Statistical Methods in Public Health**

Johns Hopkins Bloomberg School of Public Health
📍 Baltimore, MD, USA

- Lead teaching assistant for Statistical Methods in Public Health I and II.

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 one-on-one 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.

- 2016
|
2014
- **MPH capstone project**
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 [MPHcapstoneTA shiny application](#).
- 2016
|
2012
- **Statistical Methods in Public Health**
Johns Hopkins Bloomberg School of Public Health  Baltimore, MD, USA
 - 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
 - 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
 - Teaching assistant
- 2012
|
2011
- **Introduction to R and Biostatistics**
LCG-UNAM  Cuernavaca, Morelos, Mexico
 - Guest lecturer: Seminar 1, Introduction to Bioinformatics course
- 2011
- **PDCB-UNAM**
CCG-UNAM  Cuernavaca, Morelos, Mexico
 - Instructor for the course *Introduction to R and Biostatistics* for Biomedical Sciences Ph.D. students ([website](#)).
- 2010
- **PDCB-UNAM**
CCG-UNAM  Cuernavaca, Morelos, Mexico
 - Instructor for *Analysis of High-Throughput Sequencing data with Bioconductor* for Biomedical Sciences Ph.D. students ([website](#)).
- 2010
- **National Bioinformatics Week**
Organized by NNB-UNAM at CCG-UNAM  Cuernavaca, Morelos, Mexico
 - Instructor of the *Introduction to Using Bioconductor for High-Throughput Sequencing Analysis* practice lab at the *National Bioinformatics Week*.
- 2010
- **Enrique Morett Lab**
IBT-UNAM  Cuernavaca, Morelos, Mexico
 - Instructor for the *Introduction to R and plotting with R* course for Morett's lab.

2010	<ul style="list-style-type: none"> ● Statistical Methods and Analysis of Genomic Data IBT-UNAM <ul style="list-style-type: none"> • Organizer and instructor (website). 	📍 Cuernavaca, Morelos, Mexico
2009	<ul style="list-style-type: none"> ● Enrique Morett Lab IBT-UNAM <ul style="list-style-type: none"> • 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) 	📍 Cuernavaca, Morelos, Mexico
2009	<ul style="list-style-type: none"> ● Seminar III: R/Bioconductor LCG-UNAM <ul style="list-style-type: none"> • Organizer and instructor for an in-depth Bioconductor course (website) 	📍 Cuernavaca, Morelos, Mexico
2009	<ul style="list-style-type: none"> ● Principles of Statistics LCG-UNAM <ul style="list-style-type: none"> • Basic R (website). 	📍 Cuernavaca, Morelos, Mexico
2008	<ul style="list-style-type: none"> ● Bioinformatics and Statistics I LCG-UNAM <ul style="list-style-type: none"> • R and Bioconductor overview (website). 	📍 Cuernavaca, Morelos, Mexico

👤 COURSES, MEETINGS, TALKS, AND POSTERS

2020	<ul style="list-style-type: none"> ● CDSB LCG-UNAM <ul style="list-style-type: none"> • Launch of the CDSB 2019 workshop (slides) and keynote on the spatialLIBD project (slides). 	📍 Virtual event
2020	<ul style="list-style-type: none"> ● JSM <ul style="list-style-type: none"> • Gave a talk on "Promoting the next wave of R/Bioconductor developers in Latin America starting in Mexico" (slides). 	📍 Virtual event
2020	<ul style="list-style-type: none"> ● BioC Dana-Farber Cancer Research Institute <ul style="list-style-type: none"> • Presented a poster on the spatialLIBD project, taught a workshop on re-count2 and related projects, organized and presented at the Birds of a Feather: CDSB event, and was involved in the Community Advisory Board presentation. 	📍 Virtual event

Most recent slides are available via [speakerdeck](#) or [slideshare](#).

2020	<ul style="list-style-type: none">● useR! Saint Louis University 📍 Virtual event<ul style="list-style-type: none">• Presented on the “Latin American Communities and Organizations” panel and wrote a blog post for the R Consortium.
2020	<ul style="list-style-type: none">● The Scientist webinar 📍 Virtual event<ul style="list-style-type: none">• Presented the spatialLIBD project together with Kristen Maynard during a webinar with ~600 registered individuals that you can watch here.
2020	<ul style="list-style-type: none">● rstudio::conf 📍 San Francisco, CA, USA<ul style="list-style-type: none">• Attended the JavaScript for Shiny users workshop taught by Garrick Aden-Buie.
2019	<ul style="list-style-type: none">● ASHG 📍 Houston, TX, USA<ul style="list-style-type: none">• Platform talk: Regional heterogeneity in gene expression, regulation, and coherence in the frontal cortex and hippocampus across development and schizophrenia (slides).
2019	<ul style="list-style-type: none">● Visitors Research Seminar 📍 Juriquilla, Qro, Mexico<ul style="list-style-type: none">• Analyzing BrainSeq Phase II and generating the recount-brain resource (slides).
2019	<ul style="list-style-type: none">● CDSB 📍 Cuernavaca, Morelos, Mexico<ul style="list-style-type: none">• Launch of the CDSB 2019 workshop (slides).
2019	<ul style="list-style-type: none">● BioC 📍 New York, NY, USA<ul style="list-style-type: none">• Using the recount2 resource and related tools workshop (slides). Lighting 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	<ul style="list-style-type: none">● Biology of Genomes (BoG) 📍 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	<ul style="list-style-type: none">● Staff Seminar Series 📍 Baltimore, MD, USA<ul style="list-style-type: none">• Analyzing BrainSeq Phase II and generating the recount-brain resource (slides).

2019	<ul style="list-style-type: none">● rstudio::conf Austin, TX, USA<ul style="list-style-type: none">· Attended the Building Tidy Tools workshop by Charlotte and Hadley Wickham.
2019	<ul style="list-style-type: none">● 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	<ul style="list-style-type: none">● 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	<ul style="list-style-type: none">● 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	<ul style="list-style-type: none">● 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	<ul style="list-style-type: none">● CDSB Keynote Remotely<ul style="list-style-type: none">· From learning to using to teaching to developing R (remote presentation) (slides).
2018	<ul style="list-style-type: none">● SAGES Philadelphia, PA, USA<ul style="list-style-type: none">· BrainSeq Phase II: schizophrenia-associated expression differences between the hippocampus and the dorsolateral prefrontal cortex (poster).
2018	<ul style="list-style-type: none">● LCG-UNAM Remote Talks LCG-UNAM Remotely<ul style="list-style-type: none">· Reproducible RNA-seq analysis with recount2 and recount-brain (slides).
2018	<ul style="list-style-type: none">● SOBP New York, NY, USA<ul style="list-style-type: none">· Unique Molecular Correlates of Schizophrenia and Its Genetic Risk in the Hippocampus Compared to Frontal Cortex (slides).

2018	<ul style="list-style-type: none">● 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).
2018	<ul style="list-style-type: none">● rOpenSci Unconf  Seattle, WA, USA<ul style="list-style-type: none">• Worked on pkginspector.
2018	<ul style="list-style-type: none">● Journal Club by Dennis Lal  Remotely<ul style="list-style-type: none">• recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor (slides).
2017	<ul style="list-style-type: none">● IDIES Johns Hopkins University  Baltimore, MD, USA<ul style="list-style-type: none">• Getting started with recount2 and accessing it via R (poster).
2017	<ul style="list-style-type: none">● JSM  Baltimore, MD, USA<ul style="list-style-type: none">• Guiding principles for interactive graphics based on LIBD data science projects (slides).
2017	<ul style="list-style-type: none">● Summer Institute Johns Hopkins University  Baltimore, MD, USA<ul style="list-style-type: none">• Reproducible Research and Bioinformatics (slides).
2017	<ul style="list-style-type: none">● BioC Dana-Farber Cancer Institute  Boston, MA, USA<ul style="list-style-type: none">• Reproducible RNA-seq analysis with recount2 workshop (slides).
2017	<ul style="list-style-type: none">● ICSA  Chicago, IL, USA<ul style="list-style-type: none">• Reproducible RNA-seq analysis with recount2 (slides).
2017	<ul style="list-style-type: none">● SOBP  San Diego, CA, USA<ul style="list-style-type: none">• RNA-seq samples beyond the known transcriptome with derfinder and recount (slides).
2016	<ul style="list-style-type: none">● Kandahar University Training Johns Hopkins University  Dubai, UAE<ul style="list-style-type: none">• Introduction at Kandahar University MPH training event (slides).
2016	<ul style="list-style-type: none">● Genomeeting INMEGEN  Mexico City, CDMX, Mexico<ul style="list-style-type: none">• recount: facilitando el análisis de miles de muestras de RNA-seq (slides).

2016	<ul style="list-style-type: none">• SACNAS Long Beach, CA, USA<ul style="list-style-type: none">• Using Data Science to Study Human Brain Genomic Measurements (slides).
2016	<ul style="list-style-type: none">• ENAR Austin, TX, USA<ul style="list-style-type: none">• Annotation-agnostic differential expression analysis (slides).
2015	<ul style="list-style-type: none">• Joint Genomic Meeting Johns Hopkins University Baltimore, MD, USA<ul style="list-style-type: none">• dbFinder (slides).
2015	<ul style="list-style-type: none">• IDIES Johns Hopkins University Baltimore, MD, USA<ul style="list-style-type: none">• Annotation-agnostic RNA-seq differential expression analysis software (poster).
2015	<ul style="list-style-type: none">• Genomics and Bioinformatics Symposium Johns Hopkins University Baltimore, MD, USA<ul style="list-style-type: none">• Annotation-agnostic differential expression analysis (slides).
2015	<ul style="list-style-type: none">• ASHG Baltimore, MD, USA<ul style="list-style-type: none">• Annotation-agnostic RNA-seq differential expression analysis software (poster).
2015	<ul style="list-style-type: none">• Biostatistics Computing Club Johns Hopkins University Baltimore, MD, USA<ul style="list-style-type: none">• Easy parallel computing with BiocParallel and HTML reports with knitr-Bootstrap (slides).
2015	<ul style="list-style-type: none">• ENAR Miami, FL, USA<ul style="list-style-type: none">• Dissecting human brain development at high resolution using RNA-seq (slides).
2015	<ul style="list-style-type: none">• Joint Genomic Meeting Johns Hopkins University Baltimore, MD, USA<ul style="list-style-type: none">• Does mapping simulated RNA-seq reads provide information? (slides).
2014	<ul style="list-style-type: none">• Jeff Leek lab Johns Hopkins University Baltimore, MD, USA<ul style="list-style-type: none">• derfinder tutorial (slides).

- | | |
|------|---|
| 2014 | <ul style="list-style-type: none">● is3b: International Summer Symposium on Systems Biology
INMEGEN<ul style="list-style-type: none">• Developmental regulation of human cortex transcription at base-pair resolution (slides). |
| | <p style="text-align: right;">📍 Mexico City, CDMX, Mexico</p> |
| 2014 | <ul style="list-style-type: none">● BioC
Dana-Farber Cancer Institute<ul style="list-style-type: none">• Boston, MA, USA |
| | <p style="text-align: right;">📍 Boston, MA, USA</p> |
| 2014 | <ul style="list-style-type: none">● Biostatistics Computing Club
Johns Hopkins University<ul style="list-style-type: none">• Baltimore, MD, USA• Git for research (slides). |
| | <p style="text-align: right;">📍 Baltimore, MD, USA</p> |
| 2014 | <ul style="list-style-type: none">● IDIES
Johns Hopkins University<ul style="list-style-type: none">• Baltimore, MD, USA |
| | <p style="text-align: right;">📍 Baltimore, MD, USA</p> |
| 2014 | <ul style="list-style-type: none">● ENAR<ul style="list-style-type: none">• Baltimore, MD, USA• Fast annotation-agnostic differential expression analysis (poster). |
| | <p style="text-align: right;">📍 Baltimore, MD, USA</p> |
| 2014 | <ul style="list-style-type: none">● Delta Omega Poster Competition
Johns Hopkins University<ul style="list-style-type: none">• Baltimore, MD, USA• Fast annotation-agnostic differential expression analysis (poster). |
| | <p style="text-align: right;">📍 Baltimore, MD, USA</p> |
| 2014 | <ul style="list-style-type: none">● LCG-UNAM 10 year anniversary<ul style="list-style-type: none">• Cuernavaca, Morelos, Mexico• Fast differential expression analysis annotation-agnostic across groups with biological replicates (slides). |
| | <p style="text-align: right;">📍 Cuernavaca, Morelos, Mexico</p> |
| 2013 | <ul style="list-style-type: none">● Genomics and Bioinformatics Symposium
Johns Hopkins University<ul style="list-style-type: none">• Baltimore, MD, USA• Fast annotation-agnostic differential expression analysis (poster). |
| | <p style="text-align: right;">📍 Baltimore, MD, USA</p> |
| 2013 | <ul style="list-style-type: none">● Genomics for Students
Johns Hopkins University<ul style="list-style-type: none">• Baltimore, MD, USA• Introduction to ggbio (slides). |
| | <p style="text-align: right;">📍 Baltimore, MD, USA</p> |
| 2013 | <ul style="list-style-type: none">● Joint Genomic Meeting
Johns Hopkins University<ul style="list-style-type: none">• Baltimore, MD, USA• Fast differential expression analysis annotation-agnostic across groups with biological replicates (slides). |
| | <p style="text-align: right;">📍 Baltimore, MD, USA</p> |
| 2013 | <ul style="list-style-type: none">● Biostatistics Journal Club
Johns Hopkins University<ul style="list-style-type: none">• Baltimore, MD, USA• Fast differential expression analysis annotation-agnostic across groups with biological replicates (slides). |
| | <p style="text-align: right;">📍 Baltimore, MD, USA</p> |

2013	<ul style="list-style-type: none">● useR!<ul style="list-style-type: none">• Differential expression analysis of RNA-seq data at base-pair resolution in multiple biological replicates (slides).
2013	<ul style="list-style-type: none">● Biostatistics Department Retreat<ul style="list-style-type: none">• Johns Hopkins University• Philadelphia, PA, USA• Differential expression RNA-seq analysis with a large data set from brain samples (poster).
2013	<ul style="list-style-type: none">● Biostatistics Computing Club<ul style="list-style-type: none">• Johns Hopkins University• Baltimore, MD, USA• Introduction to knitr (slides).
2013	<ul style="list-style-type: none">● Genomics for Students<ul style="list-style-type: none">• Johns Hopkins University• Baltimore, MD, USA• Introduction to High-Throughput Sequencing and RNA-seq (slides).
2012	<ul style="list-style-type: none">● Genomics for Students<ul style="list-style-type: none">• Johns Hopkins University• Baltimore, MD, USA• DEXSeq paper discussion (slides).
2012	<ul style="list-style-type: none">● LCG-UNAM Remote Talks<ul style="list-style-type: none">• LCG-UNAM• Remotely• Introduction to R and Biostatistics (slides).
2012	<ul style="list-style-type: none">● Biostatistics Computing Club<ul style="list-style-type: none">• Johns Hopkins University• Baltimore, MD, USA• Introducing Git while making your academic webpage (slides).
2011	<ul style="list-style-type: none">● LCG-UNAM Remote Talks<ul style="list-style-type: none">• LCG-UNAM• Remotely• Introducing Biostatistics to first year LCG students (slides).
2011	<ul style="list-style-type: none">● BioC<ul style="list-style-type: none">• Fred Hutchinson Cancer Research Center• Seattle, WA, USA
2010	<ul style="list-style-type: none">● Bioconductor Developer Meeting<ul style="list-style-type: none">• EMBL• Heidelberg, Germany• BacterialTranscription: a R package to identify Transcription Start Sites and Transcription Units (slides).
2010	<ul style="list-style-type: none">● From Functional Genomics to System Biology<ul style="list-style-type: none">• EMBL• Heidelberg, Germany• Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes (poster).

2010	<ul style="list-style-type: none"> National Bioinformatics Week Organized by NNB-UNAM at CCG-UNAM 📍 Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"> · Introduction to using Bioconductor for High Throughput Sequencing Analysis instructor (slides).
2010	<ul style="list-style-type: none"> BioC Fred Hutchinson Cancer Research Center 📍 Seattle, WA, USA <ul style="list-style-type: none"> · Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes (poster).
2009	<ul style="list-style-type: none"> LCG-UNAM Third Generation Symposium CCG-UNAM 📍 Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"> · Bacteriophages: analyzing their diversity (slides).
2009	<ul style="list-style-type: none"> BioC Fred Hutchinson Cancer Research Center 📍 Seattle, WA, USA
2009	<ul style="list-style-type: none"> Course on Oral Communication CCG-UNAM 📍 Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"> · Taught by the master Rafael Popoca.
2008	<ul style="list-style-type: none"> BioC Fred Hutchinson Cancer Research Center 📍 Seattle, WA, USA
2008	<ul style="list-style-type: none"> A Short R/Bioconductor Course LCG-UNAM 📍 Cuernavaca, Morelos, Mexico <ul style="list-style-type: none"> · Taught by James Bullard from UC Berkeley, Ph.D. student in Sandrine Dudoit's lab at the time.
2007	<ul style="list-style-type: none"> Boston Bacterial Meeting 📍 Boston, MA, USA
2007	<ul style="list-style-type: none"> Department of Microbiology and Molecular Genetics Retreat Harvard University 📍 Boston, MA, USA
2006	<ul style="list-style-type: none"> Winter School in Genomics CCG-UNAM 📍 Cuernavaca, Morelos, Mexico
2005	<ul style="list-style-type: none"> HUGO 📍 Kyoto, Japan

LANGUAGES

- Native: Spanish
- Bilingual: English
- Basic: French