

# 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! ^\_~



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## CONTACT

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- [Icolladotor](https://orcid.org/0000-0002-4358-352X)
- [Icolladotor.github.io](https://github.com/icolladotor)
- [Icollado](https://www.linkedin.com/in/icollado)
- [orcid](https://orcid.org/0000-0002-4358-352X)
- [scholar](https://scholar.google.com/citations?user=HkzLcQAAAAJ&hl=en)
- [speaker-deck](https://speakerdeck.com/icolladotor)
- [slideshare](https://www.slideshare.net/icolladotor)
- [publons](https://publons.com/authors/1139213)

## 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).

## LANGUAGE SKILLS



Made with the R package [pagedown](#).

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

Last updated on 2020-03-16.

<p>2009   2005</p>	<ul style="list-style-type: none"> <li>● <b>B.S., Genomic Sciences</b>            National Autonomous University of Mexico (UNAM)   Cuernavaca, Morelos, Mexico             <ul style="list-style-type: none"> <li>• Grade 9.71/10</li> <li>• Third generation at <a href="#">LCG-UNAM</a></li> </ul> </li> </ul>
<p>2005   2002</p>	<ul style="list-style-type: none"> <li>● <b>H.S.</b>            ITESM Campus Cuernavaca  Cuernavaca, Morelos, Mexico             <ul style="list-style-type: none"> <li>• Grade 97.8/100</li> <li>• Best high school average ( 200 students): awarded ITESM system 90% scholarship for college studies, declined to join LCG-UNAM.</li> </ul> </li> </ul>



## RESEARCH EXPERIENCE

<p>2020   2019</p>	<ul style="list-style-type: none"> <li>● <b>Research Scientist</b>            Lieber Institute for Brain Development  Baltimore, MD, USA             <ul style="list-style-type: none"> <li>• Affiliated to Andrew Jaffe's Data Science Team I.</li> <li>• Currently building a team and developing research ideas for grant submission.</li> <li>• Applying for a formal JHU joint appointment.</li> <li>• 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.</li> <li>• 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.</li> <li>• LIBD rstats club and CDSB Mexico lead.</li> </ul> </li> <li>● <b>Staff Scientist II at Andrew Jaffe's lab</b>            Lieber Institute for Brain Development  Baltimore, MD, USA             <ul style="list-style-type: none"> <li>• Innovation and research head at Andrew Jaffe's Data Science Team I.</li> <li>• Last author for the recount-brain project.</li> <li>• Senior role in a collaborative project with Mina Ryten.</li> <li>• Co-first author in the spatialLIBD project along with Kristen R Maynard. Also established a collaboration with Stephanie Hicks and Lukas M Weber.</li> <li>• Presented research findings at conferences such as ASHG.</li> <li>• Created or contributed to the sgejobs, libdRSE, brainflowprobes, GemonicState and spatialLIBD R packages.</li> <li>• Led the LIBD rstats club and CDSB Mexico.</li> </ul> </li> </ul>
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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.
- 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

- 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

## 💼 INDUSTRY EXPERIENCE

### ● Data Science Division Leader

Winter Genomics

📍 Cuernavaca, Morelos, Mexico

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

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.

2019  
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2010

## ❖ HONORS AND AWARDS

### ● 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](#)

2019

### ● rstudio::conf 2019 diversity award recipient

[announcement](#)

- [Scholarship application](#).

2019

### ● Early Career Clinical Research Symbiont Award

<http://researchsymbionts.org>

- For our work on [recount2](#).

2018

### ● National Researcher level 1

[announcement](#)

📍 CONACyT, Mexico

2018

### ● rOpenSci Unconf 2018

[unconf18 participants](#) and [application](#)

- Worked on [pkginspector](#).

2018

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

## PUBLICATIONS

2020

- **Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex**  
[shiny app](#), [R/Bioconductor package](#), [analysis code](#)
  - Kristen E 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](#)

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, Adaikala-van 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](#)

\* indicates equal contribution, † indicates corresponding author

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 Shabbani, Gregory R Hamersky, Marcelo Diaz Bustamante, BaDoi N Phan, William S Ulrich, Cristian Valencia, Amrittha 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

- 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. *bioRxiv* 823781 (2019). doi: [10.1101/823781](https://doi.org/10.1101/823781)
- 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 numbertwo](#)

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

- Incomplete annotation of OMIM genes is likely to be limiting the diagnostic yield of genetic testing, particularly for 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. *bioRxiv* 499103 (2018). doi: [10.1101/499103](https://doi.org/10.1101/499103)
- Supervisor role, data generation, overall project advice
- [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/btw575](https://doi.org/10.1093/bioinformatics/btw575) *bioRxiv* 019067 (2015). doi: [10.1101/019067](https://doi.org/10.1101/019067)
- Supporting role: analysis
- [Twitter summary](#)

2016

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



## SOFTWARE

2014  
I  
2020

- Bioconductor: author role

**spatialLIBD**: LIBD Visium spatial transcriptomics human pilot data inspector – (Not Available on 2020-03-16) downloads. **GenomicState**: data for derfinder analyses – (Not Available on 2020-03-16) downloads. **recount**: Explore and download data from the recount project – 21027 downloads. **derfinder**: Annotation-agnostic differential expression analysis of RNA-seq data at base-pair resolution via the DER Finder approach – 29921 downloads. **derfinderPlot**: plotting functions for derfinder results – 12475 downloads. **regionReport**: Generate HTML or PDF reports for a set of genomic regions or DESeq2/edgeR results – 14455 downloads. **derfinderHelper**: helper functions for derfinder package – 24567 downloads. **derfinderData**: data for derfinder examples – 2882 downloads.

2020

- Mentor role

**regutools**

📍 Remotely

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

**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
- **Bioconductor: contributor role**  
[brainflowprobes](#), [bumphunter](#), [ballgown](#)
  - **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.
- 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  
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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
- **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, 2018-2019), American Statistical Association (2015-2017, 2020), ENAR student member (2014-2016), American Public Health Association (2014).
- 2014 | **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.  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.  Cuernavaca, Morelos, Mexico
- 2008 | **NNB-UNAM forum launch**  
 Helped start the National Node of Bioinformatics (Mexico) [online forum](#).  Cuernavaca, Morelos, Mexico

## MENTORING EXPERIENCE

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

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.

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](#).

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.



## TEACHING EXPERIENCE

- 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
- **Statistical Methods and Analysis of Genomic Data**  
IBT-UNAM  
📍 Cuernavaca, Morelos, Mexico
    - Organizer and instructor ([website](#)).

2009	<ul style="list-style-type: none"> <li> <b>Enrique Morett Lab</b>            IBT-UNAM         </li> </ul>	 Cuernavaca, Morelos, Mexico
	<ul style="list-style-type: none"> <li>• Organizer and instructor for the course <i>Introduction to Bioinformatics</i> for Morett's lab where I taught the <i>Introduction to R and plotting with R</i> module (<a href="#">website</a>)</li> </ul>	
2009	<ul style="list-style-type: none"> <li> <b>Seminar III: R/Bioconductor</b>            LCG-UNAM         </li> </ul>	 Cuernavaca, Morelos, Mexico
	<ul style="list-style-type: none"> <li>• Organizer and instructor for an in-depth Bioconductor course (<a href="#">website</a>)</li> </ul>	
2009	<ul style="list-style-type: none"> <li> <b>Principles of Statistics</b>            LCG-UNAM         </li> </ul>	 Cuernavaca, Morelos, Mexico
	<ul style="list-style-type: none"> <li>• Basic R (<a href="#">website</a>).</li> </ul>	
2008	<ul style="list-style-type: none"> <li> <b>Bioinformatics and Statistics I</b>            LCG-UNAM         </li> </ul>	 Cuernavaca, Morelos, Mexico
	<ul style="list-style-type: none"> <li>• R and Bioconductor overview (<a href="#">website</a>).</li> </ul>	

## COURSES, MEETINGS, TALKS, AND POSTERS

2020	<ul style="list-style-type: none"> <li> <b>rstudio::conf</b> </li> </ul>	 San Francisco, CA, USA
	<ul style="list-style-type: none"> <li>• Attended the <a href="#">JavaScript for Shiny users</a> workshop taught by Garrick Aden-Buie.</li> </ul>	
2019	<ul style="list-style-type: none"> <li> <b>ASHG</b> </li> </ul>	 Houston, TX, USA
	<ul style="list-style-type: none"> <li>• Platform talk: Regional heterogeneity in gene expression, regulation, and coherence in the frontal cortex and hippocampus across development and schizophrenia (<a href="#">slides</a>).</li> </ul>	Most recent slides are available via <a href="#">speakerdeck</a> or <a href="#">slideshare</a> .
2019	<ul style="list-style-type: none"> <li> <b>Visitors Research Seminar</b>            LIIGH-UNAM         </li> </ul>	 Juriquilla, Qro, Mexico
	<ul style="list-style-type: none"> <li>• Analyzing BrainSeq Phase II and generating the recount-brain resource (<a href="#">slides</a>).</li> </ul>	
2019	<ul style="list-style-type: none"> <li> <b>CDSB launch keynote</b>            LCG-UNAM         </li> </ul>	 Cuernavaca, Morelos, Mexico
	<ul style="list-style-type: none"> <li>• Launch of the CDSB 2019 workshop (<a href="#">slides</a>).</li> </ul>	

- 2019 ● **BioC**  
Rockefeller University  New York, NY, USA
- 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
- recount-brain: a curated repository of human brain RNA-seq datasets metadata ([poster](#)).
- 2019 ● **Staff Seminar Series**  
LIBD  Baltimore, MD, USA
- Analyzing BrainSeq Phase II and generating the recount-brain resource ([slides](#)).
- 2019 ● **rstudio::conf**  
 Austin, TX, USA
- Attended the [Building Tidy Tools](#) workshop by Charlotte and Hadley Wickham.
- 2019 ● **Pacific Symposium on Biocomputing (PSB)**  
 Hawaii, HI, USA
- 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
- 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
- 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
- Regional heterogeneity in gene expression, regulation and coherence in hippocampus and dorsolateral prefrontal cortex across development and in schizophrenia ([poster](#)).

- 2018 ● **CDSB**  
Keynote  Remotely  
• From learning to using to teaching to developing R (remote presentation) ([slides](#)).
- 2018 ● **SAGES**  Philadelphia, PA, USA  
• BrainSeq Phase II: schizophrenia-associated expression differences between the hippocampus and the dorsolateral prefrontal cortex ([poster](#)).
- 2018 ● **LCG-UNAM Remote Talks**  
LCG-UNAM  Remotely  
• Reproducible RNA-seq analysis with recount2 and recount-brain ([slides](#)).
- 2018 ● **SOBP**  New York, NY, USA  
• Unique Molecular Correlates of Schizophrenia and Its Genetic Risk in the Hippocampus Compared to Frontal Cortex ([slides](#)).
- 2018 ● **Biology of Genomes (BoG)**  
Cold Spring Harbor Laboratory  Cold Spring Harbor, NY, USA  
• BrainSeq Phase II: Schizophrenia-associated expression differences between the hippocampus and the dorsolateral prefrontal cortex ([slides](#)).
- 2018 ● **rOpenSci Unconf**  Seattle, WA, USA  
• Worked on [pkginspector](#).
- 2018 ● **Journal Club by Dennis Lal**  Remotely  
• recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor ([slides](#)).
- 2017 ● **IDIES**  
Johns Hopkins University  Baltimore, MD, USA  
• Getting started with recount2 and accessing it via R ([poster](#)).
- 2017 ● **JSM**  Baltimore, MD, USA  
• Guiding principles for interactive graphics based on LIBD data science projects ([slides](#)).
- 2017 ● **Summer Institute**  
Johns Hopkins University  Baltimore, MD, USA  
• Reproducible Research and Bioinformatics ([slides](#)).

- 2017 ● **BioC**  
Dana-Farber Cancer Institute  Boston, MA, USA  
• Reproducible RNA-seq analysis with recount2 [workshop \(slides\)](#).
- 2017 ● **ICSA**  
 Chicago, IL, USA  
• Reproducible RNA-seq analysis with recount2 [\(slides\)](#).
- 2017 ● **SOBP**  
 San Diego, CA, USA  
• RNA-seq samples beyond the known transcriptome with derfinder and recount [\(slides\)](#).
- 2016 ● **Kandahar University Training**  
Johns Hopkins University  Dubai, UAE  
• Introduction at Kandahar University MPH training event [\(slides\)](#).
- 2016 ● **Genomeeting**  
INMEGEN  Mexico City, CDMX, Mexico  
• recount: facilitando el análisis de miles de muestras de RNA-seq [\(slides\)](#).
- 2016 ● **SACNAS**  
 Long Beach, CA, USA  
• Using Data Science to Study Human Brain Genomic Measurements [\(slides\)](#).
- 2016 ● **ENAR**  
 Austin, TX, USA  
• Annotation-agnostic differential expression analysis [\(slides\)](#).
- 2015 ● **Joint Genomic Meeting**  
Johns Hopkins University  Baltimore, MD, USA  
• dbFinder [\(slides\)](#).
- 2015 ● **IDIES**  
Johns Hopkins University  Baltimore, MD, USA  
• Annotation-agnostic RNA-seq differential expression analysis software [\(poster\)](#).
- 2015 ● **Genomics and Bioinformatics Symposium**  
Johns Hopkins University  Baltimore, MD, USA  
• Annotation-agnostic differential expression analysis [\(slides\)](#).
- 2015 ● **ASHG**  
 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 knitr-Bootstrap ([slides](#)).
- 2015 ● **ENAR**  
 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**  
 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**  
 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  Cuernavaca, Morelos, Mexico  
• Taught by James Bullard from UC Berkeley, Ph.D. student in Sandrine Dudoit's lab at the time.
- 2007 ● **Boston Bacterial Meeting**  
 Boston, MA, USA

- |      |  |   |
|------|--|---|
| 2007 | <b>Department of Microbiology and Molecular Genetics Retreat</b><br>Harvard University |  Boston, MA, USA             |
| 2006 | <b>Winter School in Genomics</b><br>CCG-UNAM   |  Cuernavaca, Morelos, Mexico |
| 2005 | <b>HUGO</b>  |  Kyoto, Japan                |

## LANGUAGES

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