

# LEONARDO COLLADO-TORRES

At the Lieber Institute for Brain Development, I am part of the Data Science team whose goals include better understanding and characterizing genomics signatures in the human brain. We use high-throughput technologies such as DNA methylation and RNA sequencing. I help mentor other team members, provide support for LIBD projects and I am advancing my academic career as part of [Andrew Jaffe's lab](#).

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 the [Department of Biostatistics](#) at [Johns Hopkins Bloomberg School of Public Health](#) thanks to a [CONACyT scholarship](#) awarded in 2011. I worked with [Jeff Leek](#) and Andrew Jaffe in developing [derfinder](#), [regionReport](#), [recount](#) as well as other applied 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 [CDSBMexico](#) community of R and Bioconductor developers in Latin America.

## EDUCATION

2016  
|  
2011

- **PhD., Biostatistics**

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

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

2009  
|  
2005

- **B.S., Genomic Sciences**

National Autonomous University of Mexico (UNAM)  
📍 Cuernavaca, Morelos, Mexico

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



[Download a PDF of this CV](#)

## CONTACT

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- 🐦 [fellgernon](#)
- 👤 [lcolladotor](#)
- 🔗 [lcolladotor.github.io](#)
- 💻 [lcollado](#)
- 🏛 [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 2020-03-06.

2005  
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2002

- **H.S.**  
ITESM Campus Cuernavaca 📍 Cuernavaca, Morelos, Mexico
  - 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

2016  
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2011

- **Jeff Leek lab**  
Johns Hopkins Bloomberg School of Public Health 📍 Baltimore, MD, USA
  - Research Assistant

2011  
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2009

- **Enrique Morett Lab**  
IBT-UNAM 📍 Cuernavaca, Morelos, Mexico
  - Bioinformatician
  - Identified transcriptions start sites and transcription units in *Escherichia coli* and *Geobacter sulfurreducens* with RNA-seq data. Developed the `BacterialTranscription` R package.

2009  
|  
2007

- **Guillermo Dávila Lab**  
CCG-UNAM 📍 Cuernavaca, Morelos, Mexico
  - Undergrad research assistant
  - Determined bacteriophage ecological groups by developing a method based on codon distribution of all phage sequenced genomes. Joint work with [Sur Herrera-Paredes](#).

2007

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

<b>● Andrew Jaffe Lab</b>	 Baltimore, MD, USA
Lieber Institute for Brain Development	
<ul style="list-style-type: none"> <li>• Staff Scientist II</li> <li>• At LIBD, Dr. Collado-Torres is part of the Data Science team which goals include better understanding and characterizing genomics signatures in the human brain, including DNA methylation and gene expression. Leonardo helps mentor other team members, provides support for LIBD projects and is advancing his academic career as part of Andrew Jaffe's lab. He is also a co-founder of the <a href="#">LIBD rstats club</a> and <a href="#">CDSB</a>.</li> </ul>	

## INDUSTRY EXPERIENCE

2011  
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2009

<b>● Data Science Division Leader</b>	 Cuernavaca, Morelos, Mexico
Winter Genomics	
<ul style="list-style-type: none"> <li>• Responsible for recruiting and hiring new personnel, overseeing and supervising bioinformaticians, training new employees, writing research reports and presenting them to colleagues, and organizing all scientific projects.</li> <li>• First scientific staff member at Winter Genomics; Projects completed: - de novo genome assembly simulations,</li> <li>• assembly and annotation of the phiVC8 bacteriophage genome,</li> <li>• integrated analysis of more than 20 RNA-seq samples for determination of transcription initiation in Escherichia coli reported in Gama-Castro et al., <a href="#">PMID 21051347</a>,</li> <li>• de novo assembly of four Escherichia coli strains and lead to Aguilar et al., <a href="#">PMID 22884033</a>; Designed training material for new employees.</li> </ul>	

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.

## HONORS AND AWARDS

2019  
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2010

<b>● Travel awards</b>	
BioC2019, BioC2017, BioC2014, useR2013, BioC2011, From Functional Genomics to Systems Biology 2010 and BioDevelEurope 2010	
<ul style="list-style-type: none"> <li>• Taught a <a href="#">workshop on recount</a> at BioC2017. Taught a <a href="#">workshop on recount</a> at BioC2017, Gave a talk on BacterialTranscription at BioDevelEurope2010.</li> <li>• BioC2019 <a href="#">scholarship application</a></li> </ul>	
<b>● rstudio::conf 2019 diversity award recipient</b>	
<ul style="list-style-type: none"> <li>• <a href="#">announcement</a></li> <li>• <a href="#">Scholarship application</a>.</li> </ul>	
<b>● Early Career Clinical Research Symbiont Award</b>	
<ul style="list-style-type: none"> <li>• <a href="http://researchsymbionts.org">http://researchsymbionts.org</a></li> <li>• For our work on <a href="#">recount2</a>.</li> </ul>	

- 2018
  - **National Researcher level 1 announcement** 📍 CONACyT, Mexico
  - **rOpenSci Unconf 2018** [unconf18 participants](#) and [application](#)
    - Worked on [pkginspector](#).
  - **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 Tippangi, 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
  - **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

\* indicates equal contribution, † indicates corresponding author

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, Regína 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, Adaiakalan 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

- **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 Shibani, 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 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

- **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  
|  
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  
|  
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  
|  
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  
|  
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.63792](https://doi.org/10.12688/f1000research.63792) 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

2014

|

2020

## SOFTWARE

- Bioconductor: author role

**spatialLIBD:** LIBD Visium spatial transcriptomics human pilot data inspector – (Not Available on 2020-03-06) downloads. **GenomicState:** data for derfinder analyses – (Not Available on 2020-03-06) downloads. **recount:** Explore and download data from the recount project – 20813 downloads. **derfinder:** Annotation-agnostic differential expression analysis of RNA-seq data at base-pair resolution via the DER Finder approach – 29714 downloads. **derfinderPlot:** plotting functions for derfinder results – 12422 downloads. **regionReport:** Generate HTML or PDF reports for a set of genomic regions or DESeq2/edgeR results – 14383 downloads. **derfinderHelper:** helper functions for derfinder package – 24388 downloads. **derfinderData:** data for derfinder examples – 2863 downloads.

2020

- Mentor role

**regutools**

📍 Remotely

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

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.

**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

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. My most direct way of helping 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 learn a lot from teaching.

- 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           <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> </li> </ul>	📍 Cuernavaca, Morelos, Mexico
2009	<ul style="list-style-type: none"> <li>● <b>Seminar III: R/Bioconductor</b> LCG-UNAM           <ul style="list-style-type: none"> <li>• Organizer and instructor for an in-depth Bioconductor course (<a href="#">website</a>)</li> </ul> </li> </ul>	📍 Cuernavaca, Morelos, Mexico
2009	<ul style="list-style-type: none"> <li>● <b>Principles of Statistics</b> LCG-UNAM           <ul style="list-style-type: none"> <li>• Basic R (<a href="#">website</a>).</li> </ul> </li> </ul>	📍 Cuernavaca, Morelos, Mexico
2008	<ul style="list-style-type: none"> <li>● <b>Bioinformatics and Statistics I</b> LCG-UNAM           <ul style="list-style-type: none"> <li>• R and Bioconductor overview (<a href="#">website</a>).</li> </ul> </li> </ul>	📍 Cuernavaca, Morelos, Mexico

## 💻 COURSES, MEETINGS, TALKS, AND POSTERS

2020	<ul style="list-style-type: none"> <li>● <b>rstudio::conf</b> <ul style="list-style-type: none"> <li>• Attended the <i>JavaScript for Shiny users</i> workshop taught by Garrick Aden-Buie.</li> </ul> </li> </ul>	📍 San Francisco, CA, USA
2019	<ul style="list-style-type: none"> <li>● <b>ASHG</b> <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> </li> </ul>	📍 Houston, TX, USA
2019	<ul style="list-style-type: none"> <li>● <b>Visitors Research Seminar</b> LIIGH-UNAM           <ul style="list-style-type: none"> <li>• Analyzing BrainSeq Phase II and generating the recount-brain resource (<a href="#">slides</a>).</li> </ul> </li> </ul>	📍 Juriquilla, Qro, Mexico
2019	<ul style="list-style-type: none"> <li>● <b>CDSB launch keynote</b> LCG-UNAM           <ul style="list-style-type: none"> <li>• Launch of the CDSB 2019 workshop (<a href="#">slides</a>).</li> </ul> </li> </ul>	📍 Cuernavaca, Morelos, Mexico

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

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

- 2018
- **CDSB**  
Keynote  
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  
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  
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  
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  
Reproducible Research and Bioinformatics ([slides](#)).

2017	<ul style="list-style-type: none"><li>● <b>BioC</b> Dana-Farber Cancer Institute<ul style="list-style-type: none"><li>• Reproducible RNA-seq analysis with recount2 <a href="#">workshop (slides)</a>.</li></ul></li></ul>	 Boston, MA, USA
2017	<ul style="list-style-type: none"><li>● <b>ICSA</b><ul style="list-style-type: none"><li>• Reproducible RNA-seq analysis with recount2 <a href="#">(slides)</a>.</li></ul></li></ul>	 Chicago, IL, USA
2017	<ul style="list-style-type: none"><li>● <b>SOBP</b><ul style="list-style-type: none"><li>• RNA-seq samples beyond the known transcriptome with derfinder and recount <a href="#">(slides)</a>.</li></ul></li></ul>	 San Diego, CA, USA
2016	<ul style="list-style-type: none"><li>● <b>Kandahar University Training</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Introduction at Kandahar University MPH training event <a href="#">(slides)</a>.</li></ul></li></ul>	 Dubai, UAE
2016	<ul style="list-style-type: none"><li>● <b>Genomeeting</b> INMEGEN<ul style="list-style-type: none"><li>• recount: facilitando el análisis de miles de muestras de RNA-seq <a href="#">(slides)</a>.</li></ul></li></ul>	 Mexico City, CDMX, Mexico
2016	<ul style="list-style-type: none"><li>● <b>SACNAS</b><ul style="list-style-type: none"><li>• Using Data Science to Study Human Brain Genomic Measurements <a href="#">(slides)</a>.</li></ul></li></ul>	 Long Beach, CA, USA
2016	<ul style="list-style-type: none"><li>● <b>ENAR</b><ul style="list-style-type: none"><li>• Annotation-agnostic differential expression analysis <a href="#">(slides)</a>.</li></ul></li></ul>	 Austin, TX, USA
2015	<ul style="list-style-type: none"><li>● <b>Joint Genomic Meeting</b> Johns Hopkins University<ul style="list-style-type: none"><li>• dbFinder <a href="#">(slides)</a>.</li></ul></li></ul>	 Baltimore, MD, USA
2015	<ul style="list-style-type: none"><li>● <b>IDIES</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Annotation-agnostic RNA-seq differential expression analysis software <a href="#">(poster)</a>.</li></ul></li></ul>	 Baltimore, MD, USA
2015	<ul style="list-style-type: none"><li>● <b>Genomics and Bioinformatics Symposium</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Annotation-agnostic differential expression analysis <a href="#">(slides)</a>.</li></ul></li></ul>	 Baltimore, MD, USA
2015	<ul style="list-style-type: none"><li>● <b>ASHG</b><ul style="list-style-type: none"><li>• Annotation-agnostic RNA-seq differential expression analysis software <a href="#">(poster)</a>.</li></ul></li></ul>	 Baltimore, MD, USA

2015	<ul style="list-style-type: none"><li>● <b>Biostatistics Computing Club</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Easy parallel computing with BiocParallel and HTML reports with knitr-Bootstrap (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2015	<ul style="list-style-type: none"><li>● <b>ENAR</b><ul style="list-style-type: none"><li>• Dissecting human brain development at high resolution using RNA-seq (<a href="#">slides</a>).</li></ul></li></ul>	 Miami, FL, USA
2015	<ul style="list-style-type: none"><li>● <b>Joint Genomic Meeting</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Does mapping simulated RNA-seq reads provide information? (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2014	<ul style="list-style-type: none"><li>● <b>Jeff Leek lab</b> Johns Hopkins University<ul style="list-style-type: none"><li>• derfinder tutorial (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2014	<ul style="list-style-type: none"><li>● <b>is3b: International Summer Symposium on Systems Biology</b> INMEGEN<ul style="list-style-type: none"><li>• Developmental regulation of human cortex transcription at base-pair resolution (<a href="#">slides</a>).</li></ul></li></ul>	 Mexico City, CDMX, Mexico
2014	<ul style="list-style-type: none"><li>● <b>BioC</b> Dana-Farber Cancer Institute</li></ul>	 Boston, MA, USA
2014	<ul style="list-style-type: none"><li>● <b>Biostatistics Computing Club</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Git for research (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2014	<ul style="list-style-type: none"><li>● <b>IDIES</b> Johns Hopkins University</li></ul>	 Baltimore, MD, USA
2014	<ul style="list-style-type: none"><li>● <b>ENAR</b><ul style="list-style-type: none"><li>• Fast annotation-agnostic differential expression analysis (<a href="#">poster</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2014	<ul style="list-style-type: none"><li>● <b>Delta Omega Poster Competition</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Fast annotation-agnostic differential expression analysis (<a href="#">poster</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2014	<ul style="list-style-type: none"><li>● <b>LCG-UNAM 10 year anniversary</b><ul style="list-style-type: none"><li>• Fast differential expression analysis annotation-agnostic across groups with biological replicates (<a href="#">slides</a>).</li></ul></li></ul>	 Cuernavaca, Morelos, Mexico

2013	<ul style="list-style-type: none"><li>● <b>Genomics and Bioinformatics Symposium</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Fast annotation-agnostic differential expression analysis (<a href="#">poster</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2013	<ul style="list-style-type: none"><li>● <b>Genomics for Students</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Introduction to ggbio (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2013	<ul style="list-style-type: none"><li>● <b>Joint Genomic Meeting</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Fast differential expression analysis annotation-agnostic across groups with biological replicates (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2013	<ul style="list-style-type: none"><li>● <b>Biostatistics Journal Club</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Fast differential expression analysis annotation-agnostic across groups with biological replicates (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2013	<ul style="list-style-type: none"><li>● <b>useR!</b>  Albacete, Spain<ul style="list-style-type: none"><li>• Differential expression analysis of RNA-seq data at base-pair resolution in multiple biological replicates (<a href="#">slides</a>).</li></ul></li></ul>	
2013	<ul style="list-style-type: none"><li>● <b>Biostatistics Department Retreat</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Differential expression RNA-seq analysis with a large data set from brain samples (<a href="#">poster</a>).</li></ul></li></ul>	 Philadelphia, PA, USA
2013	<ul style="list-style-type: none"><li>● <b>Biostatistics Computing Club</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Introduction to knitr (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2013	<ul style="list-style-type: none"><li>● <b>Genomics for Students</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Introduction to High-Throughput Sequencing and RNA-seq (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2012	<ul style="list-style-type: none"><li>● <b>Genomics for Students</b> Johns Hopkins University<ul style="list-style-type: none"><li>• DEXSeq paper discussion (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA
2012	<ul style="list-style-type: none"><li>● <b>LCG-UNAM Remote Talks</b> LCG-UNAM<ul style="list-style-type: none"><li>• Introduction to R and Biostatistics (<a href="#">slides</a>).</li></ul></li></ul>	 Remotely
2012	<ul style="list-style-type: none"><li>● <b>Biostatistics Computing Club</b> Johns Hopkins University<ul style="list-style-type: none"><li>• Introducing Git while making your academic webpage (<a href="#">slides</a>).</li></ul></li></ul>	 Baltimore, MD, USA

2011	<ul style="list-style-type: none"><li>● <b>LCG-UNAM Remote Talks</b> LCG-UNAM • Introducing Biostatistics to first year LCG students (<a href="#">slides</a>).</li></ul>	Remotely
2011	<ul style="list-style-type: none"><li>● <b>BioC</b> Fred Hutchinson Cancer Research Center</li></ul>	Seattle, WA, USA
2010	<ul style="list-style-type: none"><li>● <b>Bioconductor Developer Meeting</b> EMBL • BacterialTranscription: a R package to identify Transcription Start Sites and Transcription Units (<a href="#">slides</a>).</li></ul>	Heidelberg, Germany
2010	<ul style="list-style-type: none"><li>● <b>From Functional Genomics to System Biology</b> EMBL • Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes (<a href="#">poster</a>).</li></ul>	Heidelberg, Germany
2010	<ul style="list-style-type: none"><li>● <b>National Bioinformatics Week</b> Organized by NNB-UNAM at CCG-UNAM • Introduction to using Bioconductor for High Throughput Sequencing Analysis instructor (<a href="#">slides</a>).</li></ul>	Cuernavaca, Morelos, Mexico
2010	<ul style="list-style-type: none"><li>● <b>BioC</b> Fred Hutchinson Cancer Research Center • Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes (<a href="#">poster</a>).</li></ul>	Seattle, WA, USA
2009	<ul style="list-style-type: none"><li>● <b>LCG-UNAM Third Generation Symposium</b> CCG-UNAM • Bacteriophages: analyzing their diversity (<a href="#">slides</a>).</li></ul>	Cuernavaca, Morelos, Mexico
2009	<ul style="list-style-type: none"><li>● <b>BioC</b> Fred Hutchinson Cancer Research Center</li></ul>	Seattle, WA, USA
2009	<ul style="list-style-type: none"><li>● <b>Course on Oral Communication</b> CCG-UNAM • Taught by the master Rafael Popoca.</li></ul>	Cuernavaca, Morelos, Mexico
2008	<ul style="list-style-type: none"><li>● <b>BioC</b> Fred Hutchinson Cancer Research Center</li></ul>	Seattle, WA, USA
2008	<ul style="list-style-type: none"><li>● <b>A Short R/Bioconductor Course</b> LCG-UNAM • Taught by James Bullard from UC Berkeley, Ph.D. student in Sandrine Dudoit's lab at the time.</li></ul>	Cuernavaca, Morelos, Mexico
2007	<ul style="list-style-type: none"><li>● <b>Boston Bacterial Meeting</b></li></ul>	Boston, MA, USA

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

 LANGUAGES

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