

Leonardo Collado-Torres

Education

- 2011-present **PhD in Biostatistics**, *Johns Hopkins Bloomberg School of Public Health*, Baltimore, US.
- 2005-2009 **Bachelor in Genomic Sciences (LCG)**, *National Autonomous University of Mexico (UNAM)*, Cuernavaca, MX, *Grade 9.71/10*.
- 2002-2005 **High school**, *ITESM Campus Cuernavaca*, Cuernavaca, MX, *Grade 97.8/100*.

PhD thesis

- title *Developing single-base RNA-seq methods and software to understand neuropsychiatric disorders and more.*
- advisors **Jeffrey T. Leek** and **Andrew E. Jaffe**.
- description The goal is 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 will allow researchers to correct for technological variation and study the biological variation driving their phenotype of interest. Then apply these methods to further our understanding of neuropsychiatric disorders using the Lieber Institute for Brain Development human brains collection (> 1000 samples).

Honors and awards

- 2011 Awarded CONACyT Mexico scholarship for PhD studies outside Mexico.
- 2009 *Summa Cum Laude* for bachelor in Genomic Sciences studies at LCG-UNAM.
- 2005 Best high school average (~ 200 students): awarded ITESM system 90% scholarship for college studies, declined to join LCG-UNAM.

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📄 <http://lcolladotor.github.io/about.html>

Experience

Vocational

2009–2011 **Scientific executive**, *Winter Genomics*, Cuernavaca, MX.

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.

- First scientific staff member at Winter Genomics;
- Projects completed:
 - de novo genome assembly simulations,
 - assembly and annotation of the *phiVC8* bacteriophage genome,
 - 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.

Research

2009–2011 **Bioinformatician**, *Enrique Morett lab*, IBT-UNAM, Cuernavaca, MX.

Identified transcriptions start sites and transcription units in *Escherichia coli* and *Geobacter sulfurreducens* with RNA-seq data.

Developed the *BacterialTranscription* R package.

2007–2009 **Undergraduate research assistant**, *Guillermo Dávila lab*, CCG-UNAM, Cuernavaca, MX.

Determined bacteriophage ecological groups by developing a method based on codon distribution of all phage sequenced genomes.

Joint work with Sur Herrera Paredes.

2007 **Undergraduate research assistant**, *Roberto Kolter lab*, Harvard, Boston, 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*.

Publications

Peer-reviewed

1. **Collado-Torres L**, Jaffe AE and Leek JT. regionReport: Interactive reports for region-based analyses. *F1000Research* 2015, 4:105. doi: 10.12688/f1000research.6379.1.
2. 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.* 2014. doi: 10.1038/nn.3898.
3. 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.
4. 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,

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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.

Pre-prints

1. Nellore A, **Collado-Torres L**, Jaffe AE, Morton J, Pritt J, Alquicira-Hernández J, Leek JT, Langmead B. Rail-RNA: Scalable analysis of RNA-seq splicing and coverage. *bioRxiv* 019067 (2015). doi:10.1101/019067.
2. **Collado-Torres L**, Jaffe AE, Leek JT. regionReport: Interactive reports for region-based analyses. *bioRxiv* 016659 (2015). doi:10.1101/016659.
3. **Collado-Torres L**, Frazee AC, Love MI, Irizarry RA, Jaffe AE, Leek JT. derfinder: Software for annotation-agnostic RNA-seq differential expression analysis. *bioRxiv* 015370 (2015). doi:10.1101/015370.

Books

1. 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.

Public profiles

Google Scholar <https://scholar.google.com/citations?user=h57-MykAAAAJ>

ORCID <http://orcid.org/0000-0003-2140-308X>

LinkedIn <https://www.linkedin.com/in/lcollado>

Epernicus <http://www.epernicus.com/lc40>

GitHub <https://github.com/lcolladotor>

Referee for

Since 2015 Bioinformatics

Since 2013 Biostatistics

Presentations

Talks at conferences

- 2015 **Collado-Torres L**, Frazee AC, Love MI, Irizarry RA, Jaffe AE, Leek JT. Annotation-agnostic differential expression analysis, *Genomics and Bioinformatics Symposium*, Center for Computational Genomics, Hopkins, Baltimore – US.
- 2015 Jaffe AE, Shin J, **Collado-Torres L**, Leek JT, et al. Dissecting human brain development at high resolution using RNA-seq, *ENAR*, Miami – US.
- 2014 Jaffe AE, Shin J, **Collado-Torres L**, Leek JT, et al. Developmental regulation of human cortex transcription at base-pair resolution, *is3b: 1st International Summer Symposium on Systems Biology*, INMEGEN, Mexico City – MX.

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- 2014 **Collado-Torres L**, Frazee AC, Love MI, Irizarry RA, Jaffe AE, Leek JT. Fast differential expression analysis annotation-agnostic across groups with biological replicates, LCG 10 year anniversary, LCG-UNAM, Cuernavaca – MX.
- 2013 **Collado-Torres L**, Frazee AC, Irizarry RA, Jaffe AE, Leek JT. Differential expression analysis of RNA-seq data at base-pair resolution in multiple biological replicates, *useR2013*, Albacete – Spain.
- 2010 **Collado-Torres L**, Reyes-Quiroz A, Cuéllar-Partida G, Moreno-Mayar V, Vargas-Chávez C, Collado-Vides J. BacterialTranscription: a R package to identify Transcription Start Sites and Transcription Units, *Bioconductor Developer Meeting*, EMBL, Heidelberg – Germany.

Posters

- 2015 **Collado-Torres L**, Frazee AC, Love MI, Irizarry RA, Jaffe AE, Leek JT. Annotation-agnostic RNA-seq differential expression analysis software, *ASHG2015* and *IDIES2015*, Baltimore – US.
- 2014 **Collado-Torres L**, Frazee AC, Love MI, Irizarry RA, Jaffe AE, Leek JT. Fast annotation-agnostic differential expression analysis, *ENAR* and *Delta Omega Poster Competition (JHSPH)*, Baltimore – US.
- 2013 **Collado-Torres L**, Jaffe AE, Leek JT. Fast annotation-agnostic differential expression analysis, *Genomics and Bioinformatics Symposium*, Center for Computational Genomics, Hopkins, Baltimore – US.
- 2010 **Collado-Torres L**, Reyes-Quiroz A, Cuéllar-Partida A, Moreno-Mayar V, Taboada B, Vega-Alvarado L, Jiménez-Jacinto V, Mendoza-Vargas A, Grande R, Olvera L, Olvera M, Vargas-Chávez C, Juárez K, Collado-Vides J, Morett E. Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes, *From Functional Genomics to Systems Biology*, EMBL, Heidelberg – Germany.
- 2010 **Collado-Torres L**, Reyes-Quiroz A, Cuéllar-Partida A, Moreno-Mayar V, Taboada B, Vega-Alvarado L, Jiménez-Jacinto V, Mendoza-Vargas A, Grande R, Olvera L, Olvera M, Vargas-Chávez C, Juárez K, Collado-Vides J, Morett E. Global Analysis of Transcription Start Sites and Transcription Units in Bacterial Genomes, *BioC2010*, FHCRC, Seattle – US.

Other talks

- 2015 dbFinder, *Joint Genomic Meeting*, JHSPH, Baltimore – US.
- 2015 Easy parallel computing with BiocParallel and HTML reports with knitrBootstrap, *Biostatistics Computing Club*, JHSPH, Baltimore – US.
- 2015 Does mapping simulated RNA-seq reads provide information?, *Joint Genomic Meeting*, JHSPH, Baltimore – US.
- 2014 Git for research, *Biostatistics Computing Club*, JHSPH, Baltimore – US.
- 2013 Introduction to ggbio, *Genomics for Students*, JHSPH, Baltimore – US.
- 2013 Introduction to knitr, *Biostatistics Computing Club*, JHSPH, Baltimore – US.

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- 2013 Introduction to High-Throughput Sequencing and RNA-seq, *Genomics for Students*, JHSPH, Baltimore – US.
- 2012 DEXSeq paper discussion, *Genomics for Students*, JHSPH, Baltimore – US.
- 2012 Introduction to R and Biostatistics, LCG-UNAM via Skype.
- 2012 Introducing Git while making your academic webpage, *Biostatistics Computing Club*, JHSPH, Baltimore – US.
- 2011 Introducing Biostatistics to first year LCG students, LCG-UNAM via Skype.
- 2010 Introduction to using Bioconductor for High Throughput Sequencing Analysis, *National Bioinformatics Week*, CCG-UNAM, Cuernavaca – MX.
- 2009 Bacteriophages: analyzing their diversity, *LCG third generation symposium*, CCG-UNAM, Cuernavaca – MX.

Courses and Meetings Attendance

- 2015 *ENAR*, Miami – US.
- 2014 *is3b*, INMEGEN, Mexico City – MX.
- 2014 *BioC2014*, Harvard, Boston – US.
- 2014 *IDIES2014*, Johns Hopkins University, Baltimore – US.
- 2014 *ENAR*, Baltimore – US.
- 2014 *Delta Omega Poster Competition*, Johns Hopkins University, Baltimore – US.
- 2014 LCG 10 year anniversary, LCG-UNAM, Cuernavaca – MX.
- 2013 *Genomics and Bioinformatics Symposium*, Johns Hopkins University, Baltimore – US.
- 2013 *useR2013*, Albacete – Spain.
- 2011 *BioC2011*, FHCRC, Seattle – US.
- 2010 *From Functional Genomics to Systems Biology*, EMBL, Heidelberg – Germany.
- 2010 *BioC2010*, FHCRC, Seattle – US.
- 2009 *BioC2009*, FHCRC, Seattle – US.
- 2009 Course on Oral Communication taught by the master Rafael Popoca, CCG-UNAM, Cuernavaca – MX.
- 2008 *BioC2008*, FHCRC, Seattle – US.
- 2008 *A Short R/Bioconductor Course* by James Bullard from UC Berkeley, LCG-UNAM, Cuernavaca – MX.
- 2007 *Boston Bacterial Meeting*, Boston – US.
- 2007 *Retreat of the Department of Microbiology and Molecular Genetics - Harvard*, Boston – US.
- 2006 *Winter School in Genomics*, CCG-UNAM, Cuernavaca – MX.
- 2005 *HUGO 2005*, Kyoto – Japan.

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Software

Bioconductor – main author

- 2014 derfinder: Annotation-agnostic differential expression analysis of RNA-seq data at base-pair resolution via the DER Finder approach – 3024 downloads in last 12 months.
- 2014 derfinderPlot: plotting functions for derfinder results – 2366 downloads in past 12 months.
- 2014 regionReport: generate HTML reports for exploring a set of regions – 2246 downloads in last 12 months.
- 2014 derfinderHelper: helper functions for derfinder package – 2671 downloads in last 12 months.
- 2014 derfinderData: data for derfinder examples – 658 downloads in past 12 months.

Bioconductor – contributor role

- 2015 bumphunter
- 2014 ballgown

Other R packages

- 2014 dots: simplify function calls <https://github.com/lcolladotor/dots>.
- 2013 fitbitR: visualize your FitBit data <https://github.com/lcolladotor/fitbitR>.
- 2011 BacterialTranscription: identify TSSs and TUs from RNA-seq data.

shiny applications

- 2014–2016 MPH capstone TA office hours sign up <https://github.com/lcolladotor/MPHcapstoneTA>
- 2014 Simple mortgage calculator <https://github.com/lcolladotor/mortgage>

Computer skills

- all-purpose **R** *Ranked 152/5661 in the US and 418/53325 worldwide by <http://github-awards.com/users/lcolladotor> as of January 28, 2016. Does not take into account contributions at <https://github.com/leekgroup>.*
- statistics **Stata**
- scripting **bash, Perl**
- markup **LaTeX, markdown**
- OS **Linux**
- cluster queue **Sun Grid Engine**

Teaching Experience

Instructor

- o PDCB-UNAM, Cuernavaca, MX

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- 2011 Invited instructor for the course *Introduction to R and Biostatistics* <http://lcolladotor.github.io/courses/PDCB-Biostats.html> ~ 10 enrollment.
- 2010 *Analysis of High-Throughput Sequencing data with Bioconductor* for Biomedical Sciences PhD Program students <http://lcolladotor.github.io/courses/PDCB-HTS.html> ~ 10 enrollment.
- CCG-UNAM, Cuernavaca, MX
 - 2010 *Introduction to Using Bioconductor for High-Throughput Sequencing Analysis* practice lab at the *National Bioinformatics Week* ~ 40 enrollment.
- IBT-UNAM, Cuernavaca, MX
 - 2010 *Introduction to R and plotting with R* course for Morett's lab ~ 10 enrollment.
 - 2010 Organized and gave a lecture for the course on *Statistical Methods and Analysis of Genomic Data* <http://lcolladotor.github.io/courses/MEyAddDG.html> ~ 20 enrollment.
 - 2009 Organized the course *Introduction to Bioinformatics* for Morett's lab and served as instructor for the *Introduction to R and plotting with R* module <http://lcolladotor.github.io/courses/mIntroR.html> ~ 10 enrollment.
- LCG-UNAM, Cuernavaca, MX
 - 2009 *Seminar III: R/Bioconductor*. In-depth Bioconductor course <http://www.lcg.unam.mx/~lcollado/B/> ~ 30 enrollment.

Guest lecturer

- JHSPH, Baltimore, US
 - 2015 *Introduction to R for Public Health Researchers: Reproducible research module* ~ 20 enrollment.
- LCG-UNAM, Cuernavaca, MX
 - 2012 *Introduction to R and Biostatistics* lecture for *Seminar 1: Introduction to Bioinformatics* course ~ 30 enrollment.
 - 2011 *Introduction to R and Biostatistics* lecture for *Seminar 1: Introduction to Bioinformatics* course ~ 30 enrollment.

Lead teaching assistant

- JHSPH, Baltimore, US
 - 2015–2016 *Statistical Methods in Public Health II* ~ 550 enrollment.
 - 2014–2015 *Statistical Methods in Public Health I and II* ~ 550 enrollment.

Teaching assistant

- JHSPH, Baltimore, US
 - 2014–2016 *MPH capstone project*: 30 min one-on-one consulting sessions (biostatistics, Stata coding) ~ 500 enrollment. Develop and maintain <https://lcolladotor.shinyapps.io/MPHcapstoneTA/>.
 - 2015–2016 *Statistical Methods in Public Health I* ~ 550 enrollment.

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- 2015 *Introduction to R for Public Health Researchers* ~ 20 enrollment.
- 2013–2014 *Statistical Methods in Public Health I and II* ~ 550 enrollment.
- 2012–2013 *Statistical Methods in Public Health I, II, III, and IV* ~ 550 enrollment.
- LCG-UNAM, Cuernavaca, MX
 - 2009 *Principles of Statistics*. Basic R <http://www.lcg.unam.mx/~lcollado/E/> ~ 30 enrollment.
 - 2008 *Bioinformatics and Statistics I*. R and Bioconductor overview <http://www.lcg.unam.mx/~lcollado/R/> ~ 40 enrollment.

Mentoring

- 2015 Mentored Alquicira-Hernández J, LCG-UNAM student visiting Jeff Leek's group.
- 2009–2011 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.
- 2009 Trained 3 LCG-UNAM students to take over the R/Bioconductor course: Reyes-Quiroz A, Moreno-Mayar V, and Reyes-López J.

Other

- 2016 Student representative for the Centennial celebration of the Department of Biostatistics.
- 2012–2014 Organized the *Genomics for Students* group <http://lcolladotor.github.io/courses/GenomicsForStudents.html>
- 2012–2014 Organized *Cultural Mixer* events for the Department of Biostatistics with Amanda Mejia for raising cultural awareness.
- 2009–2011 Organized a Genomics Journal Club at IBT-UNAM.
- 2008–2009 Elected class representative for the LCG Academic Committee.
- 2008–2009 Class representative for Administration Unit for Technology Information committee.
- 2008 Helped start the National Node of Bioinformatics online forum <http://foros.nnb.unam.mx/>.

Languages

Native Spanish
 Bilingual English
 Basic French

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