# Alejandro Reyes, PhD

## Curriculum Vitae (June 10, 2019)

✉ *alejandro.reyes.ds@gmail.com*
*Twitter: @areyesq*
*ORCID: 0000-0001-8717-66*
*Google Scholar: 8QLuIWgAAAAJ*
*Publons: 389744*

## Summary

My research is focused on developing analysis strategies that enable the translation of large amounts of data into biological knowledge. Broadly, I am interested in (1) understanding processes by which transcript isoforms contribute to cellular phenotypes and disease conditions and (2) integrating multi-omic data to unravel the molecular consequences of mutations in cancer. In order to ensure reproducibility of results and effective dissemination of code, I implement my analyses in documented workflows, software packages and graphic interphases.

## Education

09/11 - 10/15 **Ph.D. in Biology**, European Molecular Biology Laboratory / University of Heidelberg, Heidelberg, Germany.
*Summa cum laude.*

08/07 - 06/11 **B.Sc. in Genomic Sciences**, National Autonomous University of Mexico, Cuernavaca, Mexico.
With honours.

## Research Experience

11/16 - today **Postdoctoral Research Fellow**, Dana-Farber Cancer Institute and Harvard T.H. Chan School of Public Health, Boston, USA.

- Advisor: Prof. Rafael Irizarry.
- My current research is focused on the characterization of molecular phenotypes in cancer through the integration of multi-omic data. I am investigating how DNA methylation alters the three-dimensional structure of the genome and leads to activation of oncogenes.

10/15 - 09/16 **Bridging Postdoctoral Fellow**, European Molecular Biology Laboratory, Heidelberg, Germany.

- Advisor: Dr. Wolfgang Huber.
- Analyzed data from the Genotype-Tissue Expression project to study transcript isoform dynamics across human tissues; Published a first author article.

09/11 - 10/15 **PhD Student**, European Molecular Biology Laboratory, Heidelberg, Germany.

- Advisor: Dr. Wolfgang Huber.
- Developed statistical software to analyze RNA-seq data; Used public datasets to investigate transcript isoform dynamics across tissues and species; Engaged in collaborations with experimentalist, participated in the design of research questions and experiments, and led the computational analysis; Published 9 scientific articles, 6 as first author; Authored 3 R/Bioconductor packages; Trained PhD students and postdocs during yearly courses and workshops.

08/10 - 06/11 **Trainee**, European Molecular Biology Laboratory, Heidelberg, Germany.

- Advisor: Dr. Wolfgang Huber.
- Developed statistical methods to identify differences in transcript isoform regulation between different conditions.

06/10 - 08/10 **Trainee**, Weizmann Institute of Science, Rehovot, Israel.

- Advisor: Prof. Doron Lancet.
- Developed a computational pipeline to identify human genetic variants affecting olfactory receptors; Co-authored a peer-reviewed article.

11/09 – 06/10 **Undergraduate Research Assistant**, National Autonomous University of Mexico, Cuernavaca, Mexico.

- Advisors: Prof. Julio Collado-Vides and Prof. Enrique Morett.
- Evaluated methods to map transcription start sites in *E. coli* using high-throughput sequencing data.

## Scientific publications

* Contributed equally. † Shared last authorship.

**Selected publications:**

- P Kimes* and **A Reyes***. Reproducible and replicable comparisons using SummarizedBenchmark. *Bioinformatics*, 2018. doi: 10.1093/bioinformatics/bty627
- **A Reyes**† and W Huber†. Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. *Nucleic Acids Research*, 2017. doi: 10.1093/nar/gkx1165
- P Brennecke*, **A Reyes***, S Pinto*, K Rattay*, ..., W Huber†, B Kyewski† and LM Steinmetz†. Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. *Nature Immunology*, 2015. doi: 10.1038/ni.3246
- D Klimmeck*, N Cabezas-Wallscheid*, **A Reyes***, ..., W Huber† and A Trumpp†. Transcriptome-wide profiling and posttranscriptional analysis of hematopoietic stem/progenitor cell differentiation toward myeloid commitment. *Stem Cell Reports*, 2014. doi: 10.1016/j.stemcr.2014.08.012
- N Cabezas-Wallscheid*, D Klimmeck*, J Hansson*, DB Lipka*, **A Reyes***, ..., W Huber†, MD Milsom†, C Plass†, J Krijgsveld† and A Trumpp†. Identification of regulatory networks in HSCs and their immediate progeny via integrated proteome, transcriptome, and DNA methylome analysis. *Cell Stem Cell*, 2014. doi: 10.1016/j.stem.2014.07.005
- **A Reyes***, S Anders*, ..., W Huber. Drift and conservation of differential exon usage across tissues in primate species. *PNAS*, 2013. doi: 10.1073/pnas.1307202110
- S Anders*, **A Reyes*** and W Huber. Detecting differential usage of exons from RNA-seq data. *Genome Research*, 2012. doi: 10.1101/gr.133744.111

**Other publications:**

- K Korthauer*, P Kimes*, ... , **A Reyes**, ..., SC Hicks. A practical guide to methods controlling false discoveries in computational biology. *Genome Biology*, 2019. doi: 10.1186/s13059-019-1716-1
- M Ruiz-Velasco, ..., **A Reyes**, ..., JB Zaugg. CTCF-mediated chromatin loops between promoter and gene body regulate alternative splicing across individuals. *Cell Systems*, 2017. doi: 10.1016/j.cels.2017.10.018
- MM Parker, ..., **A Reyes**, ..., PJ Casaldi. RNA sequencing identifies novel non-coding RNA and exon-specific effects associated with cigarette smoking. *BMC Medical Genomics*, 2017. doi: 10.1186/s12920-017-0295-9
- R Scognamiglio, ..., **A Reyes**, ..., A Trumpp. Myc depletion induces a pluripotent dormant state mimicking diapause. *Cell*, 2016. doi: 10.1016/j.cell.2015.12.033
- W Huber, ..., **A Reyes**, ..., M Morgan. Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods*, 2015. doi: 10.1038/ni.3246
- **A Reyes**, ..., W Huber. Mutated SF3B1 is associated with transcript isoform changes of the genes UQCC and RPL31 both in CLLs and uveal melanomas. *bioRxiv*, 2013. doi: 10.1101/000992
- K Zarnack*, J König*, ..., **A Reyes**, ..., NM Luscombe† and J Ule†. Direct competition between hnRNP C and U2AF65 protects the transcriptome from the uncontrolled exonization of Alu elements. *Cell*, 2013. doi: 10.1016/j.cell.2012.12.023
- T Olender, ..., **A Reyes**, ..., D Lancet. Personal receptor repertoires: olfaction as a model. *BMC Genomics*, 2012. doi: 10.1186/1471-2164-13-414

## Software development

- DEXSeq: Inference of differential exon usage from RNA-seq data. *R/Bioconductor*.
- pasilla: Package with count data of a pasilla knock-down RNA-seq experiment. *R/Bioconductor*.
- Single.mTEC.Transcriptomes: Transcriptome data and analysis of mouse mTECs. *R/Bioconductor*.
- SummarizedBenchmark: Inference of differential exon usage from RNA-seq data. *R/Bioconductor*.

## Honors

- Mexican National System of Researchers (SNI I).

## Presentations and Posters

**Invited talks**

- MIA Seminar. Broad Institute. Cambridge, USA, 2019.
- Alnylam Genomics Club. Cambridge, USA, 2018.
- LIIGH Seminar. Juriquilla, Mexico, 2018.
- Blue Seminar. European Molecular Biology Laboratory, Heidelberg, Germany, 2017.
- Evolution of Biological Traits. Center for Advanced Studies (LMU), Munich, Germany, 2017.
- Seminarios de Investigación. Universidad del Valle de Atemajac, Queretaro, Mexico, 2017.
- Genomeeting. National Institute of Genomic Medicine, Mexico city, Mexico, 2016.
- 15th Annual BCI-McGill Workshop. Bellairs Research Institute, Holetown, Barbados, 2016.
- C1omics Workshop. Manchester Cancer Research Centre, Manchester, UK, 2015.
- Interpretation of Next Generation Sequencing Data Workshop. Heidelberg University, Heidelberg, Germany, 2015.
- RADIANT General Meeting. Telethon Institute of Genetics and Medicine, Pozzuoli, Italy, 2015.
- "Manejo Inteligente de Datos e Información". Mexican Institute of Transportation, Queretaro, Mexico, 2014.
- European Conference on Computational Biology *RADIANT* Workshop. Strasbourg, France, 2014.
- Statistical Analysis of RNA-seq Data. Pasteur Institut, Paris, France, 2013.
- BioC Conference. Fred Hutchison Cancer Research Center, Seattle, USA, 2013.

**Selected talks**

- The Biology of Genomes. Cold Spring Harbor Laboratory, Cold Spring Harbor, USA, 2014.

**Poster presentations**

- Single-cell Genomics Conference. Hubrecht Institute, Utrecht, Netherlands, 2015.
- BioC Conference. Fred Hutchison Cancer Research Center, Seattle, USA, 2012.
- Cancer Genomics Conference. European Molecular Biology Laboratory, Heidelberg, Germany, 2012.

## Teaching

**Organizer**

- Latin American BioC Developers Workshop. Cuernavaca, Mexico, 2018.

**Mentor and lecturer**

- Detecting differentially expressed genes with RNA-seq Data, Dana-Farber Cancer Institute. Boston, USA, 2019.
- Productivity tools in Unix, Dana-Farber Cancer Institute. Boston, USA, 2019.
- Workshop on Transcriptomics, Harvard University. Cambridge, USA, 2017.
- UNAM's II Summer School in Bioinformatics. Juriquilla, Mexico, 2017.
- Replicathon2017: Consistency of Large Pharmacogenomic Studies. Bayamón, Puerto Rico, 2017.
- Genomeeting Workshop: Analysis of RNA-seq data. Mexico city, Mexico, 2016.
- Statistics and Computing in Genome Data Science. Bressanone, Italy, 2015.
- Data Analysis for Genome Biology. Bressanone, Italy, 2014.
- Computational Statistics for Genome Biology. Bressanone, Italy, 2013.
- BioC Conference. Seattle, USA, 2012.

**Teaching assistant**

- Introduction to Data Science: BST260. Harvard T.H. Chan School of Public Health, Boston, USA, 2017.
- Advanced topics in Evolutionary Genomics. Černý Krumov, Czech Republic, 2013.
- Computational Statistics for Genome Biology. Bressanone, Italy, 2012.
- Computational Statistics for Genome Biology. Bressanone, Italy, 2011.
- Introduction to R/Bioinformatics. National Autonomous University of Mexico. Cuernavaca, Mexico, 2010.