Alejandro Reyes

Curriculum Vitae (August 27, 2020)

✉ alejandro.reyes.ds@gmail.com
🖥 http://alejandroreyes.org
Birth date: February 12, 1989
ORCID: 0000-0001-8717-66
Google Scholar: 8QLuIWgAAAAJ
Publons: 389744
Twitter: @areyesq

Summary

I develop computational strategies that enable the translation of large amounts of data into biological knowledge. To ensure reproducibility of results and effective dissemination of code, I implement documented workflows, software packages and graphic interfaces.

Education

09/2011 - 10/2015 **Ph.D. in Bioinformatics**, European Molecular Biology Laboratory (EMBL) and Ruprecht Karl University of Heidelberg, Germany.
Summa cum laude.

08/2007 - 06/2011 **B.Sc. in Genomic Sciences**, National Autonomous University of Mexico (UNAM), Cuernavaca, Mexico.
With honours.

Work Experience

04/2020 - present **Principal Scientist I**, Novartis Institutes for BioMedical Research, Basel, Switzerland.

11/2016 - 03/2020 **Postdoctoral Research Fellow**, Dana-Farber Cancer Institute and Harvard T.H. Chan School of Public Health, Boston, USA.

- Advisor: Prof. Rafael Irizarry.

- Project 1 (ongoing): I am investigating how the epigenome and 3D structure of the genome is altered in colorectal cancer through the analysis and integration of multi-omic datasets.

- Designed an assay to identify the presence of circulating tumor DNA in the bloodstream based on the sensitive detection of allelic frecuency imbalances caused by large genomic copy number alterations; Co-authored three manuscripts, including one as corresponding author; Co-authored an R/Bioconductor package.

10/2015 - 09/2016 **Bridging Postdoctoral Fellow**, EMBL, 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.

09/2011 - 10/2015 **PhD Student**, EMBL, 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; Collaborated with experimentalists, participated in the design of research questions and experiments, and led the computational analysis of interdisciplinary projects; Published 9 scientific articles, of which 6 as first author; Authored 3 R/Bioconductor packages; Trained PhD students and postdocs during yearly courses and workshops.

08/2010 - 06/2011 **Research Trainee**, EMBL, Heidelberg, Germany.

- Advisor: Dr. Wolfgang Huber.

- Developed statistical methods to identify changes in transcript isoform regulation between different biological conditions.

06/2010 - 08/2010	**Research 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.
11/2009 – 06/2010	**Undergraduate Research Assistant**, UNAM, 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.

Submitted for peer review:

- Y Qi, **A Reyes**, ..., B Zhang. Data-driven polymer model for mechanistic exploration of diploid genome organization. *biorXiv*, 2020. doi: 10.1101/2020.02.27.968735

Selected publications:

- SE Johnstone*, **A Reyes***, ..., M Aryee† and BE Bernstein†. Large-scale topological changes restrain malignant progression in colorectal cancer. *Cell*, 2020. doi: 10.1016/j.cell.2020.07.030

- J Chávez*, C Barberena-Jonas*, JE Sotelo-Fonseca*, ..., L Collado-Torres† and **A Reyes**†. Programmatic access to bacterial regulatory networks with regutools. *Bioinformatics*, 2020. doi: 10.1093/bioinformatics/btaa575

- 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): becoming and remaining a member of the SNI requires demonstration of significant contributions in research and teaching.

Presentations and Posters

Invited talks

- Models, Inference and Algorithms Seminar. Broad Institute. Cambridge, USA, 2019.
- Alnylam Genomics Club. Alnylam Pharmaceuticals Inc. Cambridge, USA, 2018.
- LIIGH Seminar. International Laboratory for Human Research. Juriquilla, Mexico, 2018.
- Blue Seminar. EMBL, 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 workshop. 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. University of 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 Institute, Paris, France, 2013.
- BioC Conference. Fred Hutchison Cancer Research Center, Seattle, USA, 2013.

Abstracts selected for a talk

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

Poster presentations

- Single-cell Genomics Conference. Hubrecht Institute, Utrecht, Netherlands, 2015.
- Cancer Genomics Conference. EMBL, Heidelberg, Germany, 2012.

Teaching

Organizer

- "Building tidy tools" workshop. UNAM, Cuernavaca, Mexico, 2019.
- Latin American BioC Developers Workshop. UNAM, 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. UNAM, Juriquilla, Mexico, 2017.
- Replicathon2017: Consistency of Large Pharmacogenomic Studies. University of Puerto Rico Río Piedras, Puerto Rico, 2017.
- Statistics and Computing in Genome Data Science. University of Padua, Bressanone, Italy, 2015.
- Data Analysis for Genome Biology. University of Padua, Bressanone, Italy, 2014.
- Computational Statistics for Genome Biology. University of Padua, Bressanone, Italy, 2013.
- BioC Conference. Fred Hutchison Cancer Research Center, 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. University of Padua, Bressanone, Italy, 2012.
- Computational Statistics for Genome Biology.University of Padua, Bressanone, Italy, 2011.
- Introduction to R/Bioinformatics. UNAM, Cuernavaca, Mexico, 2010.

▬▬▬ Skills

Programming languages	R/Bioconductor, python, perl, C, LaTeX, mySQL
Languages	Spanish (native), English (advanced), Italian (advanced), German (basic)
Other	Piano