

# Alejandro Reyes

Curriculum Vitae (April 8, 2020)

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## 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 - **Ph.D. in Bioinformatics**, European Molecular Biology Laboratory (EMBL) and Ruprecht Karl University of Heidelberg, Germany.  
10/2015 *Summa cum laude.*
- 08/2007 - **B.Sc. in Genomic Sciences**, National Autonomous University of Mexico (UNAM), Cuernavaca, Mexico.  
06/2011 With honours.

## Work Experience

- 04/2020 - **Principal Scientist I**, Novartis Institutes for BioMedical Research, Basel, Switzerland.  
present
- 11/2016 - **Postdoctoral Research Fellow**, Dana-Farber Cancer Institute and Harvard T.H. Chan School of Public Health, Boston, USA.  
03/2020
- 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 frequency 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 - **Bridging Postdoctoral Fellow**, EMBL, Heidelberg, Germany.  
09/2016
- 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 - **PhD Student**, EMBL, Heidelberg, Germany.  
10/2015
- 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 - **Research Trainee**, EMBL, Heidelberg, Germany.  
06/2011
- Advisor: Dr. Wolfgang Huber.
  - Developed statistical methods to identify changes in transcript isoform regulation between different biological conditions.

06/2010 - **Research Trainee**, Weizmann Institute of Science, Rehovot, Israel.

08/2010 • Advisor: Prof. Doron Lancet.

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

11/2009 – **Undergraduate Research Assistant**, UNAM, Cuernavaca, Mexico.

06/2010 • 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:

- SE Johnstone\*, **A Reyes**\*, ..., M Aryee† and BE Bernstein†. A survey of genome topology in colorectal tumors reveals large-scale compartmental changes that restrain malignant progression. (Under 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:

- 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 Krijgsvel† 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/nm.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.

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## Skills

Programming languages R/Bioconductor, python, perl, C,  $\LaTeX$ , mySQL

Languages Spanish (native), English (advanced), Italian (advanced), German (basic)

Other Piano