Alejandro Reyes

Curriculum Vitae (June 8, 2022)

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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 - 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 **Senior Expert I Data Science**, Novartis Institutes for BioMedical Research, Basel, Switzerland

- Lead data science efforts of drug-development projects to understand mechanisms of action and to identify novel targets (transcriptomics, genetics, epigenetics, compound profiling, etc).
- Develop and implement software for the analysis of high-dimensional multi-omic datasets.
- Mentor interns, masters students and postdocs; coordinate stakeholders across NIBR divisions to advance computational pipelines and drug-development projects.

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.
- Investigated 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.

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:

- C Gubser-Keller, ..., **A Reyes**, ..., R Sivasankaran. An orally available, brain penetrant, small molecule lowers huntingtin levels by enhancing pseudoexon inclusion. *Nature Communications*, 2022. doi: 10.1038/s41467-022-28653-6
- N Di Nanni, **A Reyes**, ..., A de Weck. TRAWLING: a Transcriptome Reference Aware of spLIciNG events. *bioRXiv*, 2021. doi: 10.1101/2021.12.03.471115
- Y Qi, **A Reyes**, ..., B Zhang. Data-driven polymer model for mechanistic exploration of diploid genome organization. *Biophysical Journal*, 2020. doi: 10.1016/j.bpj.2020.09.009
- 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 (B1)
Other	Piano