Jaime A Castro-Mondragon

Post-doctoral researcher

Computational biology and gene regulation group, University of Oslo

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Personalia

Date of birth

13/02/90

Citizenship

Mexican

Children

1

Paternity leave

Spring 2021

Education

Aix-Marseille Universite — *Marseille, France*

PhD in bioinformatics — *2014 - 2017*

- Graduated with honors. Thesis supervised by PhD Jacques van Helden. 6 publication derived from the thesis work.

Institute de biology de l'Ecole Normale Superieure — *Paris, France*

Master in systems biology — *2013 - 2014*

- Thesis supervised by PhD Jacques van Helden.

Universidad Nacional Autonoma de Mexico — *Cuernavaca, Mexico*

Bachelor in genomic sciences — *2009 - 2013*

- Graduated with honors. Thesis supervised by PhD Julio Collado-Vides and PhD Alejandra Medina-Rivera

Research Experience

University of Oslo — *Oslo, Norway*

Post-doctoral researcher — *2017 - Present*

- My main project focuses on study the likely association between mutations at cis-regulatory regions and dysregulation the miRNA networks. Besides this project, I am leading the latest release of the JASPAR database. Supervisor: Anthony Matelier.

Awards and Honors

Travel fellowship to present a talk at ISMB/ECCB 2019 — *2019*

PhD scholarship from Ecole Doctorale Sciences de la Vie et de la Sancte — *2014 - 2017*

CONACYT (Consejo NAcional de ciencia y Teconologia) scholarship for Master studies — *2013 - 2014*

Teaching Experience

Aix-Marseille Universite — *Marseille, France*

Analysis of Cis-Regulatory Sequences — *2017 - Present*

- Teaching assistant. Master level

Bachelor in genomic sciences program — *Cuernavaca, Mexico*

Programming with R — *2013*

- Teaching assistant. Bachelor level

Bachelor in genomic sciences program *Cuernavaca, Mexico*

Applications of the genomics, seminars. *2013*

- Teaching assistant. Bachelor level

Publications

See the complete list of publications (including preprints) and citations in my google scholar profile: *pcevKk0AAAA*

ORCID profile: 0000-0003-4069-357X

* = equal contributions (first-author)

^ = equal contributions (second-author)

= co-corresponding authors

Peer-reviewed

1. **Castro-Mondragon JA***, Riudavets-Puig R*, Rauluseviciute I*, Berhanu Lemma R, Turchi L, Blanc-Mathieu R, Lucas J, Boddie P, Khan A, Manosalva Perez N, Fornes O, Leung TY, Aguirre A, Hammal F, Schmelter D, Baranasic D, Ballester B, Sandelin A#, Lenhard B#, Vandepoele K, Wasserman WW#, Parcy F#, and Mathelier A#. *JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles*. Nucleic Acids Research (2021)
2. Santiago-Algarra D, Souaid C, Singh H, Dao TML, Hussain S, Medina-Rivera A, Ramirez-Navarro L, **Castro-Mondragon JA**, Sadouni N, Charbonnier G, Spicuglia S. *Epromoters function as a hub to recruit key transcription factors required for the inflammatory response*. Nature Communications (2021)
3. Riudavets-Puig R, Boddie P, Khan A, **Castro-Mondragon JA**, and Mathelier A. *UniBind: maps of high-confidence direct TF-DNA interactions across nine species*. BMC Genomics (2021)
4. Ragle Aure M, Fleischer T, Bjørklund S, Ankill J, **Castro-Mondragon JA**, OSBREAC (Oslo Breast Cancer Research Consortium), Børresen-Dale AL, Tost J, Sahlberg KK, Mathelier A, Tekpli X#, Kristensen VN#. *Crosstalk between microRNA expression and DNA methylation drives the hormone-dependent phenotype of breast cancer*. Genome Medicine (2021)
5. Ksouri N, **Castro-Mondragon JA**, Montardit-Tarda F, van Helden J, Contreras-Moreira B#, and Gogorcena Y#. *Tuning promoter boundaries improves regulatory motif discovery in non-model plants: the peach example*. Plant Physiology (2021)
6. Taboada-Castro H, **Castro-Mondragon JA**, Aguilar-Vera A, Hernandez-Alvarez AJ, van Helden J, and Encarnacion-Guervara S. *RhizoBindingSites, a Database of DNA-Binding Motifs in Nitrogen-Fixing Bacteria Inferred Using a Footprint Discovery Approach*. Frontiers in Microbiology (2020)
7. Fornes O*, **Castro-Mondragon JA***, Khan A*, van der Lee Robin, Zhang X, Richmond PA, Modi BP, Correard S, Gheorghe M, Baranasic D, Santana-Garcia Walter, Tan G, Cheneby J, Ballester B, Parcy F, Sandelin A#, Lenhard B#, Wasserman WW#, and Mathelier A#. *JASPAR 2020: update of the open-access database of transcription factor binding profiles*. Nucleic Acids Research (2019)
8. Nguyen NTT*, Contreras-Moreira B*, **Castro-Mondragon JA**, Santana-Garcia W, Ossio R, Robles-Espinoza CD, Bahin M, Collombet S, Vincens P, Thieffry D, van Helden J#, Medina-Rivera A#, Thomas-Chollier M#. *RSAT 2018: regulatory sequence analysis tools 20th anniversary*. Nucleic Acids Research (2018)
9. Taboada H*, Meneses N*, Dunn MF*, Vargas-Lagunas C, Buchs N, **Castro-Mondragon JA**, Heller M, and Encarnacion S. *Proteins in the periplasmic space and outer membrane vesicles of Rhizobium etli CE3 grown in minimal medium are largely distinct and change with growth phase*. Microbiology (2018)
10. Khan A*, Fornes O*, Stigliani A*, Gheorghe M, **Castro-Mondragon JA**, van der Lee R, Bessy A, Chèneby J, Kulkarni S, Tan G, Baranasic D, Arenillas D, Sandelin A#, Vandepoele K, Lenhard B#, Ballester B, Wasserman W#, Parcy F, Mathelier A#. *JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework*. Nucleic Acids Research (2017)
11. Dao LM*, Galindo-Albarran AO*, **Castro-Mondragon JA**^, Andireu-Soler C^, Medina-Rivera A^, Souadi C, Charbonnier G, Griffon A, Vanhille L, Stephen S, Alomairi J, Soler C, Stephen T, Martin D, Torres M, Fernandez N,

Soler E, van Helden J, Puthier D, Spicuglia S. *Genome-wide characterization of mammalian promoters with distal enhancer functions*. Nature Genetics (2017)

12. **Castro-Mondragon JA**, Jaeger S, Thieffry D, Thomas-Chollier M#, and van Helden J#. *RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections*. Nucleic Acids Research (2017)
13. **Castro-Mondragon JA***, Rioualen C*, Contreras-Moreira B, van Helden J. *RSAT::Plants: Motif Discovery in ChIP-Seq Peaks of Plant Genomes*. Plant Synthetic Promoters - Springer Protocol (2016)
14. Contreras-Moreira B#, **Castro-Mondragon JA**, Rioualen C, Cantalapiedra CP, van Helden J. *RSAT::Plants: Motif Discovery Within Clusters of Upstream Sequences in Plant Genomes*. Plant Synthetic Promoters - Springer Protocol (2016)
15. Gama-Castro S*, Salgado H*, Santos-Zavaleta A, Ledezma-Tejeida D, Muñiz-Rascado L, García-Sotelo JS, Alquicira-Hernández K, Martínez-Flores I, Pannier L, **Castro-Mondragon JA**, Medina-Rivera A, Solano-Lira H, Bonavides-Martínez C, Pérez-Rueda E, Alquicira-Hernández S, Porrón-Sotelo L, López-Fuentes A, Hernández-Koutoucheva A, Del Moral-Chávez V, Rinaldi F, Collado-Vides J. *RegulonDB version 9.0: high-level integration of gene regulation, coexpression, motif clustering and beyond*. Nucleic Acids Research (2015)
16. Medina-Rivera A*, Defrance M*, Sand O*, Herrmann C, **Castro-Mondragon JA**, Delerce J, Jaeger S, Blanchet C, Vincens P, Caron C, Staines DM, Contreras-Moreira B, Artufel M, Charbonnier–Khamvongsa L, Hernandez C, Thieffry D, Thomas-Chollier M#, van Helden J#. * RSAT 2015 : Regulatory Sequence Analysis Tools*. Nucleic Acids Research (2015)
17. Rogel MA, Bustos P, Santamaría RI, González V, Romero D, Miguel AC, Lozano L, **Castro-Mondragon JA**, Martínez-Romero J, Ormeño-Orrillo E, Martínez-Romero E. *Genomic basis of symbiovar mimosae in Rhizobium etli*. BMC Genomics (2014)

Preprints

1. Saha S*, Spinelli L*, **Castro-Mondragon JA**, Kervadec A, Kremmer L, Roder L, Sallouha J, Torres M, Brun C, Vogler G, Bodmer R, Colas AR#, Ocorr K#, and Perrin L#. *Genetic architecture of natural variations of cardiac performance in flies*. bioRxiv (2021)
2. **Castro-Mondragon JA**, Ragle Aure M, Lingjærde OC, Langerød A, Martens JWM, Børresen-Dale AL, Kristensen VN, and Mathelier A. *Cis-regulatory mutations associate with transcriptional and post-transcriptional deregulation of the gene regulatory program in cancers*. bioRxiv (2020)

Reviewed manuscripts

Publons profile: 1499198

Reviewed manuscripts in the following journals: Bioinformatics, Genetics, Molecular Plant, Nucleic Acids Research, Genome biology, Genome Biology and Evolution, Frontiers in Genetics, eLife.

Presentations

Talks

ISMB/ECCB 2019 — *Basel, Switzerland*

Combining transcriptional and post-transcriptional regulation to predict mutations altering the gene regulatory program in cancer cells — *2019 - Present*

1st Student Symposium on Computational Genomics — *Mainz,Germany*

RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections. — *2016 - Present*

Posters

1. *Combining transcriptional and post-transcriptional regulation to predict mutations altering the gene regulatory program in cancer cells*. ISM/ECCB, 2019. (doi: `https://f1000research.com/posters/8-1286`)
2. *Characterization of mutations that dysregulate driver microRNAs in cancer*. 4th anual NORBIS conference, 2018.

3. *Clustering and redundancy reduction of transcription factor binding motifs*. 1st Student Symposium on Computational Genomics, 2016.
4. *Clustering and redundancy reduction of transcription factor binding motifs*. 15th ECCB (doi: 10.7490/f1000research.1113 2016.
5. *Comparing and clustering multiple collections of DNA motifs using RSAT* 12th BC2 (doi: 10.7490/f1000research.1111391.1 2015.
6. *Comparing, clustering and aligning Transcription Factor Binding Motifs with RSAT*. 13th ECCB. (**Castro J**, Thomas-Chollier M, Thieffry D and van Helden J Comparing, clustering and aligning transcription factor binding motifs with RSAT. F1000Posters 2014,5:1845 (poster)), 2014.
7. *Novel computational predictions of regulons based on the observed autoregulation of the network*. 5th IECA Conference 2011. Gene Regulatory Networks in the Enterobacteriaceae, 2011.

Languages

Spanish
- Native speaker

English
- Fluent

French
- Fluent

Computational skills

R

Proficient. Use of ggplot, tidyverse, Rmarkdown, Rcpp.

Perl

Proficient

Git

Proficient

Snakemake

Proficient. Development of pipelines for analysis of high-throughput data

Python

Intermediate

Make

Intermediate

Bash

Intermediate

D3

Intermediate

Other

Experience with biological databases like TCGA, ICGC, roadmap epigenomics, ENCODE.

References

Professor Jacques van Helden

Aix-Marseille Universite, Marseille, France

PhD Supervisor
- Jacques.van-Helden@univ-amu.fr (https://orcid.org/0000-0002-8799-8584)

PhD Alejandra Medina-Rivera

Laboratorio Internacional de Investigacion sobre el Genoma Humano, Queretaro, Mexico

Bachelor Thesis Supervisor

- amedina@liigh.unam.mx (https://liigh.unam.mx/amedina/)

PhD Anthony Mathelier

Norway Centre of Molecular Medicine, Oslo, Norway

Postdoc Supervisor

- anthony.mathelier@ncmm.uio.no (https://mathelierlab.com/)