



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 Supérieure

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/Working Experience

Nykode Therapeutics AS

Oslo, Norway

BIOINFORMATICIAN

2022 - Present

University of Oslo

Oslo, Norway

POST-DOCTORAL RESEARCHER

2017 - 2022

- 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 TECNOLOGIA) SCHOLARSHIP FOR MASTER STUDIES

2013 - 2014

Teaching Experience

Aix-Marseille Universite

Marseille, France

ANALYSIS OF CIS-REGULATORY SEQUENCES

2017 - Present

- Teaching assistant. Master level

- Teaching assistant. Bachelor level

- 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. Santana-Garcia W*, **Castro-Mondragon JA***, Padilla-Galvez M, Nguyen NTT, Elizondo-Salas A, Ksouri N, Gerbes F, Thieffry D, Vincens P, Contreras-Moreira B#, van Helden J#, Thomas-Chollier M#, Medina-Rivera A#. *RSAT 2022: regulatory sequence analysis tools**. Nucleic Acids Research (2022)
2. **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)
3. 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)
4. 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)
5. 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)
6. 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)
7. 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)
8. 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)
9. 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)
10. 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)

11. Khan A*, Fornes O*, Stigliani A*, Gheorghe M, **Castro-Mondragon JA**, van der Lee R, Bessy A, Chèneby J, Kulka-rni 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)
12. Dao LM*, Galindo-Albarran AO*, **Castro-Mondragon JA**^, Andireu-Soler C^, Medina-Rivera A^, Souadi C, Char-bonnier 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)
13. **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)
14. **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)
15. Contreras-Moreira B#, **Castro-Mondragon JA**, Rioualen C, Cantalapiedra CP, van Helden J. *RSAT::Plants: Mo-tif Discovery Within Clusters of Upstream Sequences in Plant Genomes*. Plant Synthetic Promoters - Springer Protocol (2016)
16. Gama-Castro S*, Salgado H*, Santos-Zavaleta A, Ledezma-Tejeida D, Muñoz-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-Koutouchewa A, Del Moral-Chávez V, Rinaldi F, Collado-Vides J. *RegulonDB version 9.0: high-level integration of gene regula-tion, coexpression, motif clustering and beyond*. Nucleic Acids Research (2015)
17. 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)
18. 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 deregu-lation 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

COMBINING TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATION TO PREDICT MUTATIONS ALTERING THE GENE REGULATORY PROGRAM IN CANCER CELLS

Basel, Switzerland

2019 - 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.111300.2016).
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 GGLOT, 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@france-bioinformatique.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/>)