



Jaime A Castro-Mondragon

POST-DOCTORAL RESEARCHER

Computational biology and gene regulation group, University of Oslo

✉ j.a.c.mondragon@ncmm.uio.no | 🏠 jaimicore.github.io | 📺 [jaimicore](#) | 🐦 [jaimicore](#)

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

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

- 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. 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)
2. 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)
3. 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)
4. Khan A*, Fornes O*, Stigliani A*, Gheorghe M, **Castro-Mondragon JA**, van der Lee R, Bessy A, Chèneby J, Kulcarini 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)
5. 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)
6. **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)
7. **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)
8. 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)
9. 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-Koutouchéva 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)
10. 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)
11. 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. **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)
2. Ragle Aure M, Fleischer T, Bjørklund S, Ankill J, **Castro-Mondragon JA**, OSBREAC (Oslo Breast Cancer Research Consortium), Børresen-Dale AL, Sahlberg KK, Mathelier A, Tekpli X#, Kristensen VN#. *Crosstalk between microRNA expression and DNA methylation drive the hormone-dependent phenotype of breast cancer*. *bioRxiv* (2020)

3. Ksouri N, **Castro-Mondragon JA**, Montardit-Tarda F, van Helden J, Contreras-Moreira B#, and Gogorcena Y#. *Motif analysis in co-expression networks reveals regulatory elements in plants: The peach as a model*. bioRxiv (2020)
4. 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*. bioRxiv (2018)

Reviewed manuscripts

Publons profile: 1499198

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

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

1st Student Symposium on Computational Genomics

Mainz, Germany

RSAT MATRIX-CLUSTERING: DYNAMIC EXPLORATION AND REDUNDANCY REDUCTION OF TRANSCRIPTION FACTOR BINDING MOTIF COLLECTIONS.

2016

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.

Perl

PROFICIENT

Git

PROFICIENT

Snakemake

PROFICIENT. DEVELOPMENT OF PIPELINES FOR ANALYSIS OG HIGH-THROUGHPUT DATA

Python

INTERMEDIATE

Make

INTERMEDIATE

Bash

INTERMEDIATE

D3

INTERMEDIATE

Other

EXPERIENCE WITH BIOLOGICAL DATABASES LIKE TCGA, ROADMAP EPIGENOMICS, ENCODE.