



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 Supérieure

Paris, France

MASTER IN SYSTEMS BIOLOGY

2013–2014

- Thesis supervised by PhD Jacques van Helden.

Universidad Nacional Autónoma de México

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)

PEER-REVIEWED

1. Fornes O*, **Castro-Mondragon JA***, Khan A*, van der Lee Robin, Zhang X, Richmond PA, Modi BP, Corread 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)
2. 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)
3. 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)
4. 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)
5. **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)
6. **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)
7. 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)
8. 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 regula-tion, coexpression, motif clustering and beyond*. Nucleic Acids Research (2015)
9. 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)
10. 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 OF HIGH-THROUGHPUT DATA

Python

INTERMEDIATE

Make

INTERMEDIATE

Bash

INTERMEDIATE

D3

INTERMEDIATE

Other

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