

Jaime A Castro-Mondragon

POST-DOCTORAL RESEARCHER

Computational biology and gene regulation group, University of Oslo

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Education

Aix-Marseille Universite

PHD IN BIOINFORMATICS

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

Marseille, France

2014–2017

Institute de biology de l'Ecole Normale Superieure

MASTER IN SYSTEMS BIOLOGY

- Thesis supervised by PhD Jacques van Helden.

Paris, France

2013–2014

Universidad Nacional Autonoma de Mexico

BACHELOR IN GENOMIC SCIENCES

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

Cuernavaca, Mexico

2009–2013

Research Experience

University of Oslo

POST-DOCTORAL RESEARCHER

- My main project focuses on study the likely association between mutations at cis-regulatory regions and dysregulation the miRNA networks

Oslo, Norway

2017–Present

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

ANALYSIS OF CIS-REGULATORY SEQUENCES

- Teaching assistant. Master level

Marseille, France

2017

Bachelor in genomic sciences program

PROGRAMMING WITH R

- Teaching assistant. Bachelor level

Cuernavaca, Mexico

2013

Bachelor in genomic sciences program

APPLICATIONS OF THE GENOMICS, SEMINARS.

- Teaching assistant. Bachelor level

Cuernavaca, Mexico

2013

Publications

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

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* = equal contributions (first-author)

^ = equal contributions (second-author)

= co-corresponding authors

1. 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)

2. 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)
3. 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)
4. **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)
5. **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)
6. 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)
7. 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)
8. 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)
9. 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)

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
- Perl
- Python
- HTML5
- Shell
- Make
- Snakemake
- ggplot
- D3