Jaime A Castro-Mondragon

BIOINFORMATICIAN (SCIENTIST LEVEL II)

Oslo, Norway

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I am a computational biologist with +10 years of experience in research, sequence analysis, methods development, and data visualisation. I have worked in both the academic and private sector. My main research expertise is related to sequence analysis and -omics integration. My experience in the private sector is related to the development and establishment of reproducible bioinformatic workflows as part of a vaccine design program.

Research/Working Experience

Nykode Therapeutics AS   *Oslo, Norway*

BIOINFORMATICIAN (SCIENTIST II)   *2022 - Present*

- Design and analysis of RNA-seq experiments. Development, establishment, and maintenance of bioinformatic workflows (prediction of MHC-binding peptides, protease cleavage sites, RNA secondary structure). Train ML models to highlight protein features explaining experimental observations.

University of Oslo   *Oslo, Norway*

POST-DOCTORAL RESEARCHER   *2017 - 2022*

- Multi-omics integration (WES, WGS, RNA-seq, sRNA-seq, CNAs) to associate mutations at cis-regulatory regions with dysregulation of miRNA networks. I co-lead two releases of the JASPAR database working on the clustering of motifs, data curation, and establishing a motif discovery pipeline. Supervisor: Anthony Mathelier.

Education

Aix-Marseille Universite   *Marseille, France*

PHD IN BIOINFORMATICS   *2014 - 2017*

- Development of methods to work with large collection of transcription factor binding motifs: clustering of motifs and enrichment of binding sites. Supervisor: PhD Jacques van Helden. 6 publication derived from this thesis. Graduated with honors.

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

MASTER IN SYSTEMS BIOLOGY   *2013 - 2014*

- Development of a method to cluster transcription factor binding motifs. Supervisor: PhD Jacques van Helden. Graduated with honors.

Universidad Nacional Autonoma de Mexico   *Cuernavaca, Mexico*

BACHELOR IN GENOMIC SCIENCES   *2009 - 2013*

- Detection of transcription factor binding motifs for uncharacterized transcritpion factors using sequence homology. Supervisors: PhD Julio Collado-Vides and PhD Alejandra Medina-Rivera. Graduated with honors.

Computational skills

R

PROFICIENT. USE OF GGPLOT, TIDYVERSE, RMARKDOWN, RCPP, S4 OBJECTS, PLOTLY.

Perl

PROFICIENT.

Git

PROFICIENT.

CI/CD (github actions)

BEGINNER

Snakemake

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

Python

Intermediate. Use of pandas, polars, seaborn, plotly, numpy, scikit-learn, object-oriented classes.

Docker

Intermediate

GNU make

Intermediate

Bash

Intermediate

D3

Intermediate. Development of interactive hierarchical trees.

aws S3

Beginner

nextflow

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

HTML / CSS

Intermediate. Development of interactive websites.

Other

Experience with biological databases like TCGA, ICGC, roadmap epigenomics, ENCODE, Human Protein Atlas

Languages

Spanish	English	French	Norwegian
Native	Fluent	Fluent	Intermediate (A2)

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, Hernandez-Alvarez AJ, **Castro-Mondragon JA**, and Encarnacion-Guervara S. *RhizoBindingSites v2.0 Is a Bioinformatic Database of DNA Motifs Potentially Involved in Transcriptional Regulation Deduced From Their Genomic Sites*. Bioinformatics and Biology Insights. (2024)

2. Rauluseviciute I, Launay T, Barzaghi G, Nikumbh S, Lenhard B, Krebs AR, **Castro-Mondragon JA**, and Mathelier A. *Identification of transcription factor co-binding patterns with non-negative matrix factorization.* Nucleic Acids Research (2024)

3. Rauluseviciute I*, Riudavets-Puig R*, Blanc-Mathieu R^, **Castro-Mondragon JA**^, Ferenc K^, Kumar V^, Berhanu Lemma R^, Lucas J^, Cheneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B#, Sandelin A#, Wasserman WW#, Parcy F#, and Mathelier A#. *JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles.* Nucleic Acids Research (2024)

4. **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 gene regulatory programs in cancers*. Nucleic Acids Research (2022)

5. Saha S*, Spinelli L*, **Castro-Mondragon JA**, Kervadec A, Lynott M, 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.* eLife (2022)

6. 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)

7. **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)

8. 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)

9. 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)

10. 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)

11. 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)

12. 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)

13. 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)

14. 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)

15. 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)

16. 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)

17. 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)

18. **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)

19. **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)

20. 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)

21. 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)

22. 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)

23. 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

No preprints at this moment.

Reviewed manuscripts

Web of Science (prev. 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.

Personalia

Date of birth

13/02/90

Citizenship

Mexican

References

Professor Jacques van Helden

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