



Jaime A Castro-Mondragon

BIOINFORMATICIAN

Oslo, Norway

[✉ jamondra@uio.no](mailto:jamondra@uio.no) | [。www.jaimicore.github.io](https://jaimicore.github.io) | [github.jaimicore](https://github.com/jaimicore) | [linkedin.jaime-castro-mondragon](https://www.linkedin.com/in/jaime-castro-mondragon/)

I am a computational biologist with 11 years of experience in research, sequence analysis, methods development and data visualisation. I have worked in both the academic and private sector. My main expertise is the development of algorithms to analyze multivariate data and apply them in a wider range of biomedical fields such as vaccine design or gene expression.

Working Experience

Akershus Universitetssykehus (Ahus)

Oslo, Norway

BIOINFORMATICIAN

2025 - Present

- Development and maintenance of bioinformatic workflows to analyze cancer samples (prediction of single nucleotide variants, structural variants, copy number alterations and gene fusions).
- Development of methods to provide evidence of clinically relevant variants.

Nykode Therapeutics AS

Oslo, Norway

BIOINFORMATICIAN (SCIENTIST II)

2022 - 2025

- Design and analysis of RNA-seq experiments to detect statistically significant changes in gene expression in human and mouse cells transfected with a vaccine candidate.
- Development, establishment, and maintenance of bioinformatic analysis pipelines (prediction of MHC-binding peptides, protease cleavage sites, RNA secondary structure).
- Train ML models to highlight protein features explaining experimental observations.
- Computational design of vaccine candidates (protein sequences) in 5 projects.
- Design of a NoSQL (JSON) protein sequence database.

University of Oslo

Oslo, Norway

POST-DOCTORAL RESEARCHER

2017 - 2022

- Co-lead the [JASPAR database](#) team (20 people) in the 2020 and 2022 releases (data QC, manual curation of results, development of [motif analysis pipeline](#) (R/python/Snakemake) and [added motif clusters to the website](#)).
- Development of a multi-omics (WES, WGS, RNA-seq, sRNA-seq, CNAs) [integration method](#) (written in R/Snakemake) to calculate the likely association of single-nucleotide variants with changes in gene expression in gene regulatory networks.
- +30 verified peer-reviews for scientific journals.
- Mentoring of 2 PhD and 3 master students.
- Supervisor: [Anthony Matelier](#).

Toolkit

What	Level	Category
Python	Proficient	Programming language
R	Proficient	
Perl	Proficient	
Bash	Intermediate	
HTML / CSS	Intermediate	
D3	Intermediate	
JavaScript	Beginner	
SQL	Beginner	Databases
Snakemake	Proficient	Pipeline Development
GNU make	Intermediate	
nextflow	Beginner	
Docker	Intermediate	Containerization
Apptainer	Intermediate	
Git	Proficient	Version Control
aws S3	Beginner	Cloud
CI/CD	Intermediate	Automation

Technical Skills: clustering, dimensionality reduction, exploratory data analysis (EDA), data wrangling, multivariate analysis, statistical tests, Markov chains, ML (Random Forest, Linear Regression, Logistic Regression, model evaluation), Deep Learning (neural networks), Data Curation, pattern discovery, pattern matching, unit tests.

Tools: jupyter notebooks, Rstudio, emacs, VS code, google docs, Linux (Ubuntu).

Education

Aix-Marseille Universite

PhD IN BIOINFORMATICS

Marseille, France

2014 - 2017

- Development of a computational methods to cluster transcription factor motifs. Development of a computational methods to detect enrichment of sequences. Design and implementation of software to create negative controls in DNA sequences. Supervisor: PhD Jacques van Helden. 6 publication derived from this thesis.

Institute de biology de l'Ecole Normale Supérieure

MASTER IN SYSTEMS BIOLOGY

Paris, France

2013 - 2014

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

Universidad Nacional Autonoma de Mexico

BACHELOR IN GENOMIC SCIENCES

Cuernavaca, Mexico

2009 - 2013

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

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. Ksouri N, Abdalrahem M, Montardit-Tarda F, **Castro-Mondragon JA**, van Helden J, Gorgorcena, Contreras-Moreira B#. *Web-Based Discovery of Regulatory Motifs in Non-model Plants Plant Transcription Factors*. Methods in Molecular Biology (2026)
2. Baydar DO, Rauluseviciute I, Aronsen DR^, Blanc-Mathieu R^, Bonthuis I^, de Beukelaer H^, Ferenc K^, Jegou A^, Kumar V^, Lemma RB^, Lucas J^, Pochon M^, Yun CM^, Ramalingam V^, Deshpande SS^, Patel A, Marinov GK, Wang AT, Aguirre A, **Castro-Mondragon JA**, Baranasic D, Chèneby J, Gundersen S, Johansen M, Khan A, Kuijjer ML, Hovig E, Lenhard B#, Sandelin A#, Vandepoele K, Wasserman WW#, Parcy F#, Kundaje A#, Mathelier A#. *Web-Based Discovery of Regulatory Motifs in Non-model Plants Plant Transcription Factors*. Methods in Molecular Biology (2026)
3. Taboada-Castro H, Hernandez-Alvarez AJ, **Castro-Mondragon JA**, and Encarnacion-Guerrero 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)
4. 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)
5. 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)
6. **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)

7. 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)
8. 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)
9. **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)
10. 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)
11. 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)
12. Ragle Aure M, Fleischer T, Bjørklund S, Ankil 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)
13. 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)
14. Taboada-Castro H, **Castro-Mondragon JA**, Aguilar-Vera A, Hernandez-Alvarez AJ, van Helden J, and Encarnacion-Guerrero S. *RhizoBindingSites, a Database of DNA-Binding Motifs in Nitrogen-Fixing Bacteria Inferred Using a Footprint Discovery Approach*. Frontiers in Microbiology (2020)
15. 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)
16. 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)
17. 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)
18. Khan A*, Fornes O*, Stigliani A*, Gheorghe M, **Castro-Mondragon JA**, van der Lee R, Bessy A, Cheneby 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)
19. Dao LM*, Galindo-Albaran AO*, **Castro-Mondragon JA**^A, Andireu-Soler C^A, Medina-Rivera A^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)
20. **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)
21. **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)
22. 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)
23. 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)
24. 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)
25. 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](#)

+30 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

Languages

SPANISH (NATIVE SPEAKER), ENGLISH (FLUENT), FRENCH (FLUENT), NORWEGIAN (INTERMEDIATE, A2 LEVEL)

References

Professor Jacques van Helden

PHD SUPERVISOR, COLLABORATOR

- Jacques.van-Helden@france-bioinformatique.fr (<https://orcid.org/0000-0002-8799-8584>)

Aix-Marseille Universite, Marseille,
France

PhD Alejandra Medina-Rivera

BACHELOR THESIS SUPERVISOR, COLLABORATOR

- amedina@liigh.unam.mx (<https://liigh.unam.mx/amedina/>)

Laboratorio International de
Investigacion sobre el Genoma
Humano, Queretaro, Mexico

PhD Anthony Mathelier

POSTDOC SUPERVISOR, COLLABORATOR

- anthony.mathelier@ncmm.uio.no (<https://mathelierlab.com/>)

Norway Centre of Molecular
Medicine, Oslo, Norway

PhD Andreas Midbøe Hoff

HEAD OF IN SILICO AND ARTIFICIAL INTELLIGENCE DEPARTMENT

- amhoff@nykode.com (linkedin.com/in/andreas-midbøe-hoff-853366b0)

Nykode Therapeutics AS, Oslo,
Norway