

Curriculum Vitae

Information:

Name: CASTRO MONDRAGÓN Jaime Abraham.
Born: 13th February, 1990.
Birth place: Chilpancingo de los Bravo, Guerrero, México.
Citizenship: Mexican
e-mail: jcastro@lcg.unam.mx

Education:

2009 - 2013 **Bachelor in Genomic Sciences**, UNAM. Cuernavaca, Morelos, México.
Graduated with honors.

2013 - 2014 **Master in Systems Biology**, ENS. Paris, France.

2014 - PhD student in Bioinformatics, TAGC. Marseille, France.

Workshops and Conferences:

2014 Models, epigenetics and evolution. EpiGeneSys. Paris, France.

Research experience:

2008
(Jul-Dec) Research internship at department of ocular microbiology and infectology of 'Instituto de Oftalmología Conde de Valenciana' Mexico City, Mexico.

2009
(Jan-Jun) Research internship at department of ocular microbiology and infectology of 'Instituto de Oftalmología Conde de Valenciana' Mexico City, Mexico.

2011
(Jan-Dec) Research internship at Computational Genomics Program Laboratory at Center of Genomic Sciences. Cuernavaca, Morelos, México.

2012

(Jan-Dec) Research internship at Computational Genomics Program Laboratory at Center of Genomic Sciences. Cuernavaca, Morelos, México.

2013

(Jan-Aug) Research internship at Computational Genomics Program Laboratory at Center of Genomic Sciences. Cuernavaca, Morelos, México.

(Jan-Mar) Research Internship at Environmental and Symbiotic Microbiology Research Program Laboratory at Center of Genomic Sciences. Cuernavaca, Morelos, México.

2014

(Jan-) Research internship at Technological Advances for Genomics and Clinics (TAGC) laboratory. Inserm Unité 1090. Marseille, France.

2015

PhD student in Bioinformatics. Technological Advances for Genomics and Clinics (TAGC) laboratory. Inserm Unité 1090. Marseille, France.

Congress:

2011:

5th IECA Conference 2011. *Gene Regulatory Networks in the Enterobacteriaceae*. Cancún, México.

2014:

13th ECCB (European Conference on Computational Biology), Strasbourg, France.

2015:

12th BC2 (Basel Computational Biology Conference), Basel, Switzerland.

Posters:

2011: "Novel computational predictions of regulons based on the observed autoregulation of the network" at 5th IECA Conference 2011. *Gene Regulatory Networks in the Enterobacteriaceae*.

2014: "Comparing, clustering and aligning Transcription Factor Binding Motifs with RSAT" at 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))

2015: "Comparing and clustering multiple collections of DNA motifs using RSAT" at 12th BC2. (doi: [10.7490/f1000research.1111391.1](https://doi.org/10.7490/f1000research.1111391.1))

Teaching experience:

2013

(Feb- May) Teaching assistant of subject 'Applications of genomics' at undergraduate program in genomic sciences. UNAM.

(Aug) Teaching assistant in subject 'Programming with R' at undergraduate program in genomic sciences. UNAM.

2015

Teaching assistant in subject 'Analysis of Cis-Regulatory Sequences'. Aix-Marseille Université.

Languages:

Mother Tongue: Spanish.

Other Languages: English, French.

Computer skills:

- Programing skills in R, Perl, Python, HTML5, JavaScript, Shell, Make, Snakemake.

Publications:

1. Contreras-Moreira B et al. (2016) **RSAT::Plants: Motif Discovery Within Clusters of Upstream Sequences in Plant Genomes**. Springer protocols - Plant Synthetic Promoters.
2. Castro-Mondragon JA et al. (2016) **RSAT:: Plants: Motif Discovery in ChIP-Seq Peaks of Plant Genomes**. Springer protocols - Plant Synthetic Promoters
3. Castro-Mondragon JA et al. (2016) **RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections**. In revision
4. Gama-Castro S et al. (2015) **RegulonDB version 9.0: high-level integration of gene regulation, coexpression, motif clustering and beyond**. Nucleic Acids Research.
5. Medina-Rivera A et al. (2015) **RSAT 2015: Regulatory Sequence Analysis Tools**. Nucleic Acids Research.
6. Rogel M et al. (2014) **Genomic basis of symbiovar mimosae in Rhizobium etli**. BMC Genomics.