Rodrigo Dorantes-Gilardi

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COLMEX
Mexico City, September 2020

Born: April 24 1990
Nationality: Mexican/Spanish

Web: `https://rodogi.github.io`
GitHub: `https://github.com/rodogi`

Work

March 2020	Postdoctoral Fellow at Colegio de México
2019–2020	Postdoctoral Fellow at Instituto Nacional de Medicina Genómica
2018–2019	Data Scientist at Telcel

Education

April 24 2018	PhD Defense "Bio-mathematical aspects of the plasticity of protein folding" Thesis committee: Frédéric Cazals (INRIA), Lashuel Hilal (École Polytechnique Fédérale de Lausanne), Kavé Salamatian (Université de Savoie Mont-Blanc),
2014–2018	PhD Applied Mathematics Under supervision of Claire Lesieur and Laurent Vuillon, *IXXI Complex Systems Institute, ENS-Lyon, France.* *LAMA Mathematics Laboratory, Le Bourget-du-Lac, France.* "Bio-mathematical aspects of the plasticity of protein folding"
2014	Master thesis supervised by Gelasio Salazar, *Universidad Autónoma de San Luis Potosí, Mexico* "An algorithm in python on the minium crossing number of complete graphs".
2012–2014	Master degree in applied mathematics, *Universidad Autónoma de San Luis Potosí, Mexico.*
2008–2012	Bachelor degree in Economics, *Université de Toulouse Capitole, France.*
2005–2008	High School diploma, option: General Sciences, *Instituto Tecnológico de Estudios Superiores de Monterrey, Mexico.*

Publications

Peer reviewed

2020 (To Appear)
R. Dorantes-Gilardi, D. García-Cortés, Hiram Hernández-Ramos and J. Espinal-Enrquez
Eight years of homicide evolution in Monterrey, Mexico: a network approach.
In press

2020 (August)
R. Dorantes-Gilardi, D. García-Cortés, E. Hernandez-Lemus, and J. Espinal-Enrquez
Multilayer approach reveals organizational principles disrupted in breast cancer co-expression networks.
Applied Network Science

2018 (October)
R. Dorantes-Gilardi, L Bourgeat, L Vuillon, and C Lesieur
In proteins, the structural responses of a position to mutation rely on the Goldilocks principle: not too many links, not too few.
Phys. Chem. Chem. Phys., **20**, 25399 (2018)

2016 (December)
M. Achoch, **R. Dorantes-Gilardi**, C. Wymant, G. Feverati, K. Salamatian, L. Vuillon, and C. Lesieur
Protein structural robustness to mutations: an in silico investigation.
Phys. Chem. Chem. Phys., **18**, 13770 (2016)

Conference articles

2017 (December)
R. Dorantes-Gilardi, L. Vuillon, and C.Lesieur
Perturbation of amino acid networks: A statistical study of the defects introduced in proteins by mutations.
The 6th International Conference on Complex Networks and Their Applications

Teaching

2020 (Fall)
Mathematics
El Colegio de México.
Undergraduate

Talks

2020 (December)
Computational biology week at the INMEGEN
Gene co-expression networks.
Insituto Nacional de Médicina genómica.

2016 (May)
Workshop on Mechanisms underlying local to global signals in networks
Amino-acid network as a model of the protein's structure, an in silico investigation.
IXXI, École Normale Supérieure de Lyon, France.

2016 (March)
Workshop on Advanced mathematics for network analysis
Amino-acid networks used to capture protein structural changes caused by mutations.
Luchon, France.

2015 (June)
Workshop on protein fibers: from pathology to nanomaterial
Protein Graphs.
École Normale Supérieure de Lyon, France.

2015 (April)
IXXI Seminar
Tentative to relate functional and structural changes in protein, caused by mutations (perturbations) using amino-acid networks.
École Normale Supérieure de Lyon, France.

2014 (December)
Theoretical Approaches for the Genome and the proteome
What impact to expect on a whole protein from geometrical changes produced by local amino acid side chain perturbation (in silico amino acid mutation): resilience and innovation.
Bourget-du-Lac, France.

Posters

2017 (December)
The 6th International Conference on Complex Networks and Their Applications
Perturbation of amino acid networks: A statistical study of the defects introduced in proteins by mutations.
Lyon, France.

2015 (May)
Inter'Actions 2015
Statistics On Protein Graphs.
Grenoble, France.

Schools

2016 (April)	*Spring school of theoretical informatics.* CIRM, Marseille, France.
2016 (March)	*School for young researchers in mathematical informatics.* IMJ-PRG, Paris, France.
2015 (January)	*School Algorithms and Heuristics for Large-scale Data Sets.* École Normale Supérieure de Lyon, Lyon, France.
2014 (November)	*Lyon systems biology.* École Normale Supérieure de Lyon, Lyon, France.

Organization

2014 (December)	Theoretical Approaches for the Genome and the proteome Bourget-du-Lac, France.

Skills

Programming

Python	Advanced
R	Intermediate
Linux/GNU	Advanced (Bash)
Tex	Advanced
Lisp	Intermediate (Emacs)
SQL	Intermediate (Oracle and Netezza)
Git	Intermediate
HTML, CSS	Intermediate

Open Source Software

I have contributed to the following projects:

- networkx (`https://networkx.github.io/`)
- biopython (`http://biopython.org/`)

Bioinformatics

Pymol	Intermediate
YASARA	Intermediate
FoldX	Intermediate
Bio	Protein Data Bank: query (requests module in python), cleanse, analyze (numpy and pandas)
Bio-Structure	Database analysis (Biopython PDB module)
Bio-Space	Computational Algorithms using Delaunay triangulations and Convex hulls (Scipy spatial module)

Languages

Spanish	Reading, Writing, Speaking: Native language.
English	Reading, Writing, Speaking: Fluent.
French	Reading, Writing, Speaking: Fluent.

Recommendation Contacts

- Jesús Espinal-Enriquez Instituto Nacional de Medicina Genómica
  ✉ jespinal@inmegen.gob.mx
- Enrique Hernndez-Lemus Instituto Nacional de Medicina Genómica
  ✉ ehernandez@inmegen.gob.mx
- Claire Lesieur Laboratoire Ampère, Université Claude Bernard Lyon 1/ IXXI, ENS-Lyon
  ✉ claire.lesieur@ens-lyon.fr
- Gelasio Salazar Instituto de Física, Universidad Autónoma de San Luis Potosí
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