Rodrigo Dorantes-Gilardi

\bowtie rdorantes@colmex.mx

COLMEX Born: April 24 1990

Mexico City, September 2020 Nationality: Mexican/Spanish

Web: https://rodogi.github.io

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

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 R. Dorantes-Gilardi, D. García-Cortés, Hiram Hernández-Ramos and J. Espinal-Enrquez

(To Appear) | Eight years of homicide evolution in Monterrey, Mexico: a network approach. In press

2020 R. Dorantes-Gilardi, D. García-Cortés, E. Hernandez-Lemus, and J. Espinal-Enrquez

(August) Multilayer approach reveals organizational principles disrupted in breast cancer co-expression networks.

Applied Network Science

2018 R. Dorantes-Gilardi, L Bourgeat, L Vuillon, and C Lesieur

(October) 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 M. Achoch, **R. Dorantes-Gilardi**, C. Wymant, G. Feverati, K. Salamatian, L. Vuillon, and C. Lesieur

(December) Protein structural robustness to mutations: an in silico investigation. Phys. Chem. Phys., 18, 13770 (2016)

Conference articles

2017 | R. Dorantes-Gilardi, L. Vuillon, and C.Lesieur

(December) | 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 | Mathematics

(Fall) | El Colegio de México.

Undergraduate

Awards

2020 | Sistema Nacional de Investigadores

(SNI) | Candidate

Area 1 (Interdisciplinary and applied math)

Reviewing

2019 | PLOS One

Talks

2020 Computational biology week at the INMEGEN (December) Gene co-expression networks. Insituto Nacional de Médicina genómica. 2016 Workshop on Mechanisms underlying local to global signals in networks (May) Amino-acid network as a model of the protein's structure, an in silico investigation. IXXI, École Normale Supérieure de Lyon, France. 2016 Workshop on Advanced mathematics for network analysis (March) Amino-acid networks used to capture protein structural changes caused by mutations.Luchon, France. 2015 Workshop on protein fibers: from pathology to nanomaterial (June) Protein Graphs. École Normale Supérieure de Lyon, France. 2015 IXXI Seminar (April) Tentative to relate functional and structural changes in protein, caused by mutations (perturbations) using amino-acid networks. École Normale Supérieure de Lyon, France. 2014 Theoretical Approaches for the Genome and the proteome (December) What impact to expect on a whole protein from geometrical changes produced by

Posters

and innovation.

Bourget-du-Lac, France.

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

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

local amino acid side chain perturbation (in silico amino acid mutation): resilience

Schools

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

Organization

2014 Theoretical Approaches for the Genome and the proteome (December) 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
$\operatorname{Fold}X$	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
- 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

 ⊠ gelasio.salazar@gmail.com