

Rodrigo Dorantes-Gilardi

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INMEGEN
Mexico City

Born: April 24 1990
Nationality: Mexican/Spanish

Web: <https://rodogi.github.io>
GitHub: <https://github.com/rodogi>

Work

March 2019	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, <i>IXXI Complex Systems Institute, ENS-Lyon, France.</i> <i>LAMA Mathematics Laboratory, Le Bourget-du-Lac, France.</i> “Bio-mathematical aspects of the plasticity of protein folding”
2014	Master thesis supervised by Gelasio Salazar, <i>Universidad Autónoma de San Luis Potosí, Mexico</i> “An algorithm in python on the minium crossing number of complete graphs”.
2012–2014	Master degree in applied mathematics, <i>Universidad Autónoma de San Luis Potosí, Mexico.</i>
2008–2012	Bachelor degree in Economics, <i>Université de Toulouse Capitole, France.</i>
2005–2008	High School diploma, option: General Sciences, <i>Instituto Tecnológico de Estudios Superiores de Monterrey, Mexico.</i>

Publications

Articles

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| 2018
(October) | R. Dorantes-Gilardi , L Bourgeat, L Vuillon, and C Lesieur
<i>In proteins, the structural responses of a position to mutation rely on the Goldilocks principle: not too many links, not too few.</i>
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
<i>Protein structural robustness to mutations: an in silico investigation.</i>
Phys. Chem. Chem. Phys., 18 , 13770 (2016) |

Chapters

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| 2018
(July) | C. Lesieur, R. Dorantes-Gilardi , and L. Vuillon
<i>Chapter: Induced Graphs: surfing on protein structures.</i>
Book: Allostery and protein dynamics: from physical chemistry to drug discovery
To appear in Springer <i>Methods in Molecular Biology</i> |
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Proceedings

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

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| 2016
(May) | Workshop on Mechanisms underlying local to global signals in networks
<i>Amino-acid network as a model of the protein's structure, an in silico investigation.</i>
IXXI, École Normale Supérieure de Lyon, France. |
| 2016
(March) | Workshop on Advanced mathematics for network analysis
<i>Amino-acid networks used to capture protein structural changes caused by mutations.</i>
Luchon, France. |
| 2015
(June) | Workshop on protein fibers: from pathology to nanomaterial
<i>Protein Graphs.</i>
École Normale Supérieure de Lyon, France. |
| 2015
(April) | IXXI Seminar
<i>Tentative to relate functional and structural changes in protein, caused by mutations (perturbations) using amino-acid networks.</i>
École Normale Supérieure de Lyon, France. |
| 2014
(December) | Theoretical Approaches for the Genome and the proteome
<i>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.</i>
Bourget-du-Lac, France. |

Posters

2017 (December)	The 6th International Conference on Complex Networks and Their Applications <i>Perturbation of amino acid networks: A statistical study of the defects introduced in proteins by mutations.</i> Lyon, France.
2015 (May)	Inter'Actions 2015 <i>Statistics On Protein Graphs.</i> Grenoble, France.

Conferences and Schools

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

Organization

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

Programing

Python	Advanced (pandas, numpy, sklearn, pyspark, matplotlib, networkx, biopython)
R	Intermediate (data.table)
Tex	Advanced
Elisp	Intermediate (Emacs)
C	basic
SQL	Intermediate (Oracle and Netezza)
Git	Intermediate
Linux/GNU	Advanced (Bash)
HTML, CSS	Intermediate

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)

Open Source Software

I have contributed to the following projects:

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

Languages

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

Recommendation Contacts

- Claire Lesieur Laboratoire Ampère, Université Claude Bernard Lyon 1/ IXXI, ENS-Lyon
✉ claire.lesieur@ens-lyon.fr
- Laurent Vuillon Laboratoire de Mathématiques, Université de Savoie Mont-Blanc
✉ laurent.vuillon@gmail.com
- Gelasio Salazar Instituto de Física, Universidad Autónoma de San Luis Potosí
✉ gelasio.salazar@gmail.com