

Sergio Castillo Lara

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Back end developer with proven experience in both academia and industry, proficient in several technologies such as Python, Django, Perl, R, and others.

EXPERIENCE

SOFTWARE DEVELOPER 04/2020 – Present
Elements Interactive

- Developed RESTful APIs using Python/Django.
- Made use of Docker, Kubernetes, and CI/CD for scaling and delivering applications.

PREDOCTORAL RESEARCHER 04/2017 – 04/2020
Computational Genomics Lab, University of Barcelona

- Created web applications to integrate and visualize biological data using Django, Flask, Plotly, MySQL, and Neo4j.
- Developed bioinformatics software, machine learning pipelines, and other research tools.
- Analyzed large sequence datasets: RNA-seq, single-cell RNA-seq, ChIP-seq, ATAC-seq.

RESEARCH INTERN 07/2014 – 04/2017
Computational Genomics Lab, University of Barcelona

- Analyzed protein-protein graph/network related to retinitis pigmentosa disease.
- Implemented a text mining pipeline to extract interactions from articles.

EDUCATION

Ph.D. in Genetics

Universitat de Barcelona, Barcelona, Spain

2017 – Present

Thesis project: *"Development of computational methods for the integration of multiple omics data sources over gene-protein networks"*

M.Sc. Bioinformatics for health sciences

Universitat Pompeu Fabra, Barcelona, Spain

2015 – 2017

B.Sc. Biology

Universitat de Barcelona, Barcelona, Spain

2010 - 2015

PROFESSIONAL SKILLS

Programming	Python, Perl, R, Bash
Databases	Neo4j, Cypher Query Language, SQL
Data Science	Machine learning, Statistics, ggplot2, scikit-learn
Frameworks	Django, Flask
Other	Docker, git, RNA-seq, Linux

LANGUAGES

English	Full professional proficiency
Spanish & Catalan	Native language

PUBLICATIONS

- R. Arenas-Galnares[†], S. Castillo-Lara[†], V. Toulis, D. Boloc, R. González-Duarte, G. Marfany, J.F. Abril (2019)
[†] Contributed equally as first authors
[RPGeNet v2.0: expanding the universe of retinal disease gene interactions network.](#)
Database, Volume 2019, baz120.
- S. Castillo-Lara, E. Pascual-Carreras, J.F. Abril (2019)
[PlanExp: intuitive integration of complex RNA-seq datasets with planarian omics resources.](#) Bioinformatics, 36(6): pp. 1889–1895,
- S. Castillo-Lara, J.F. Abril (2018)
[PPaxe: easy extraction of protein occurrence and interactions from the scientific literature.](#)
Bioinformatics, 35(14): pp. 2523–2524.
- S. Castillo-Lara, J.F. Abril (2017)
[PlanNET: Homology-based predicted interactome for multiple planarian transcriptomes.](#)
Bioinformatics, 34(6): pp. 1016–1023.
- D. Boloc, S. Castillo-Lara, G. Marfany, R. González-Duarte, J.F. Abril (2015)
[Distilling a visual network of retinitis pigmentosa gene-protein interactions to uncover new disease candidates.](#)
PLOS ONE, 10(8): e0135307

TEACHING EXPERIENCE

- 2018 - 2019 Teaching Assistant – Computational Genomics
B.Sc. Bioinformatics, UPF/UPC/UB
- 2017 - 2019 Teaching Assistant – Introduction to Algorithmics
M.Sc. Bioinformatics for Health Sciences, Universitat Pompeu fabra
- 2017 - 2019 Teaching Assistant – Bioinformatics
B.Sc. Biochemistry / Biotechnology, Universitat de Barcelona