

# Sergio Castillo Lara

Data Scientist



## PERSONAL INFORMATION

Address	Barcelona, Spain	Email	✉ <a href="mailto:s.cast.lara@gmail.com">s.cast.lara@gmail.com</a>
Telephone	☎ +34 657926201	LinkedIn	<a href="https://www.linkedin.com/sergiocastillolara">linkedin.com/sergiocastillolara</a>
Date of birth	October 27th, 1992	Github	<a href="https://github.com/scastlara">github.com/scastlara</a>

## EXPERIENCE

### 2017 - Present

#### Ph.D. Fellow

*Computational Genomics Lab, University of Barcelona*

Supervised by: Josep F. Abril ([jabril@ub.edu](mailto:jabril@ub.edu))

- Trained and applied machine-learning models to predict gene regulatory networks and protein-protein interactions.
- Developed Django and Flask web applications to integrate and visualize predictions and other heterogeneous biological data from multiple data sources.
- Set up and managed multiple databases using Neo4j and MySQL.
- Analyzed large sequence datasets using various pipelines involving different statistical approaches (descriptive statistics, clustering, visualization, statistical inference, and so on),
- Assistant teacher of the courses: “Introduction to Algorithmics”: Msc. Bioinformatics for Health Sciences at UPF; “Bioinformatics”: BSc. Biochemistry at UB; “Computational Genomics”: BSc. Bioinformatics at UPF/UPC/UB.

### 2014 - 2017

#### Research Intern

*Computational Genomics Lab, University of Barcelona*

- Prediction of an interactions network of planarian genes and proteins using sequence homology information and machine learning.
- Implementation of a pipeline to retrieve protein-protein interactions from scientific literature using natural language processing.

## EDUCATION

### 2015 - 2017

#### M.Sc. Bioinformatics for health sciences

*Universitat Pompeu Fabra, Barcelona, Spain*

### 2010 - 2015

B.Sc. Biology

*Universitat de Barcelona, Barcelona, Spain*

## PROFESSIONAL SKILLS

<b>Programming</b>	Python, Perl, R, JavaScript, Bash
<b>Databases</b>	Neo4j, Cypher Query Language, SQL
<b>Data Science</b>	Machine-learning, ggplot2, scikit-learn, numpy, R caret
<b>Web</b>	HTML5, CSS, Django, Flask, jQuery, Bootstrap, Cytoscape.js, plotly.js
<b>Other</b>	Statistics, RNA-seq, Linux, git, LaTeX

## LANGUAGES

<b>English</b>	Full professional proficiency
Spanish & Catalan	Native language

## PUBLICATIONS



R. Arenas-Galnares<sup>†</sup>, **S. Castillo-Lara<sup>†</sup>**, V. Toulis, D. Boloc, R. González-Duarte, G. Marfany, J.F. Abril (2019) <sup>†</sup> *Contributed equally*  
[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*, AOP.



**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



R. Arenas-Galnares<sup>†</sup>, **S. Castillo-Lara<sup>†</sup>**, V. Toulis, D. Boloc, R. González-Duarte, G. Marfany, J.F. Abril (2019) <sup>†</sup> *Contributed equally*  
[RPGeNet v2.0: expanding the universe of retinal disease gene interactions network.](#)  
*Database*, Volume 2019, baz120.