

polcuscó

bioinformatician && machine learning geek

contact



polcusco@gmail



linkedin/pol-cusco



researchgate/PoL_Cusco2



github.com/nanakiksc



+34 684 200 939

languages

catalan & spanish
english
portuguese

programming



Python

C & C#

HTML & CSS

Shell scripting

L^AT_EX

interests

genomics, machine learning, big data, data visualization

education

- | | | |
|------------|---|---|
| since 2013 | PhD in Biomedicine
<i>Machine learning approach to the study of chromatin</i>
Thesis. | Universitat Pompeu Fabra |
| 2010–2011 | MSc in Pharmaceutical Industry & Biotechnology | Universitat Pompeu Fabra |
| 2005–2010 | BSc in Biology
Specialization in Human Biology | Universitat Pompeu Fabra |
| 2012–2013 | Research Scholar
I was enrolled at the Department of Mechanical Engineering, where I conducted research on autonomous underwater vehicles and underwater wireless communications. | Massachusetts Institute of Technology, Cambridge (MA) |

experience

- | | | |
|-----------|--|-------------------------------------|
| 2019 | Gastrointestinal and Endocrine Tumor Group
<i>Bioinformatician</i>
I developed and maintained NGS analysis pipelines, working mostly with whole-exome sequencing data from both tumors and cfDNA. I also wrote scripts for custom analyses and performed data visualization tasks. | Vall d'Hebron Institute of Oncology |
| 2017–2019 | Bioinformatics Unit
<i>Bioinformatician</i>
I also worked with different research groups in the institute and gave them bioinformatics support. I helped them decide which data analyses they needed in their projects and then I conducted them. It was also my responsibility to communicate the results of such analyses to help guide their research. | Vall d'Hebron Institute of Oncology |
| 2013–2017 | Genome Architecture Lab
<i>PhD student</i>
I worked from raw genomics data, especially ChIP-seq. I used both supervised and unsupervised machine learning methods and developed of our own (see publications). I have a solid grasp of best practices in machine learning and how to avoid common pitfalls (see publications).
Lab website. | Centre for Genomic Regulation |

2011–2012	Neuropharmacology Lab Technician	Department of Experimental and Health Sciences, UPF
2011	Central Nervous System Unit Researcher during my MSc internship	Pharmaceutical R&D Centre, Ferrer Internacional
2010	Keypoint CRO Clinical Research Associate during my BSc internship	Grupo Keypoint
2008	Neuropharmacology Lab Student during a summer internship	Department of Experimental and Health Sciences, UPF

publications

- Cuscó P, Filion GJ. Zerone: a ChIP-seq discretizer for multiple replicates with built-in quality control. *Bioinformatics*. 2016;32(19):2896-902.
- Corrales M, Cuscó P, Usmanova DR, Chen HC, Bogatyreva NS, Filion GJ, Ivankov DN. Machine Learning: How Much Does It Tell about Protein Folding Rates? *PLoS One*. 2015;10(11):e0143166.
- Zorita E, Cuscó P, Filion GJ. Starcode: sequence clustering based on all-pairs search. *Bioinformatics*. 2015;31(12):1913-9.

courses

2017	From Science to Market A course on entrepreneurship focused on technology-based companies.	Universitat de Barcelona / Universitat Politècnica de Catalunya
2014	Algorithms: Design and Analysis, Part 1 An in-depth review of classical algorithms and data structures.	Stanford University
2013	Machine Learning A reference on the fundamentals and good practices of machine learning.	Stanford University
2012	Web Fundamentals, JavaScript, jQuery, PHP, Python Several courses on different programming languages.	Codecademy
2012	Introduction to Computing Principles An introduction to the key ideas of computing.	Stanford University