





José Guilherme de Almeida

PhD, computational biologist (they/them)

✉ jose.almeida@research.fchampalimaud.org  0000-0002-1887-0157
 josegcpa.ml  github.com/josegcpa  bitbucket.org/josegcpa

Education

Oct 2017 – 2022	European Bioinformatics Institute and University of Cambridge <i>PhD in Computational Biology</i>
Sep 2015 – Sep 2017	Universidade de Coimbra <i>MSc in Cell and Molecular Biology</i> with honours
Sep 2012 – Jul 2015	Universidade de Coimbra <i>BSc in Biochemistry</i>

Relevant Research Experience

2022-current	Computational Clinical Imaging Group @ Champalimaud Foundation Under Nikolaos Papanikolaou <i>Post-doctoral fellow</i> <ul style="list-style-type: none">▪ Development of robust machine- and deep-learning methods for prostate cancer detection and segmentation in multi-parametric magnetic resonance imaging▪ Creation of reproducible pipelines for image registration and radiomic feature extraction
2017 - 2022	Cancer data science group @ EMBL-EBI Supervised by Moritz Gerstung and George S. Vassiliou <i>PhD fellow</i> <ul style="list-style-type: none">▪ Development of machine- and deep-learning methods to detect and characterize vast collections of cells in digitalised whole blood slides in a haematological cancer context. Predictive modelling of disease genotype using machine-learning methods to uncover cytomorphological profiles▪ Statistical and Bayesian modelling of longitudinal targeted sequencing experiments to uncover the genetic and non-genetic factors driving clonal expansion. Phylogenetic and phylodynamic modelling of the lifelong trajectories of clones using single-cell colonies in healthy individuals
2016 - 2017	Data-driven molecular design group @ CNC-UC Supervised by Irina S. Moreira <i>MSc student</i> <ul style="list-style-type: none">▪ Development of machine-learning protocols to determine hot-spots (important residues) in the binding interfaces of proteins▪ Structural and statistical analysis of large collections of protein-protein complexes and structural characterization of complexes with no known structure

Professional certificates

2023	Docker & Kubernetes: The Practical Guide <i>Academind (online)</i>
2021	Probability theory: foundations for data science <i>Colorado Boulder University (online)</i>
2021	Econometrics: methods and applications <i>Erasmus University Rotterdam (online)</i>

Technical skills

Programming	Python (advanced user), R (advanced user), C (beginner)
Machine-learning	Machine-learning — scikit-learn (Python), caret (R) Deep-learning — pytorch, lightning, MONAI, tensorflow, and related packages (Python)
Computer-vision	scikit-image, OpenCV (Python)
Statistical analysis	Frequentist methods Bayesian methods (particularly MCMC)
Data visualization	ggplot2 (R)
Workflows	Containerisation (Docker) Workflow management (snakemake)

Teaching Experience

2019	EMBL Heidelberg <i>2019 EMBL Lautenschlager Summer School</i> Teaching young graduate students about practical bioimage analysis
2016	Universidade de Coimbra <i>Workshops on Introductory Programming</i> Teaching young students about programming in Python and R

Fellowships, awards and honors

2017	Universidade de Coimbra <i>Merit fellowship for exceptional curricular performance during my MSc</i>
2017 - 2022	European Molecular Biology Laboratory and support from the National Health Research Institute <i>PhD fellowship</i>

Peer-reviewed research grants

2018-2021	Fundação para Ciências e Tecnologia Deep learning in cancer drug discovery: a pipeline for the generation of new therapies <i>Role: team member</i>
2018-2021	Fundação para Ciências e Tecnologia Membrane proteins development of new computational approaches and its application to GPCRs <i>Role: team member</i>

Other activities

2016 - 2017	Junior Enterprise for Science and Technology (JEST) <i>Co-founder</i> JEST is a junior initiative I founded with a few colleagues that is dedicated to data science training among young students and services to external businesses
2018	20th EMBL PhD Symposium <i>Organization, speaker contact</i> Contacted different high-profile researchers to invite them to present at the 20th EMBL PhD Symposium
2019	EBI-Sanger-Cambridge PhD Symposium (eSCAMPS) 2019 <i>Website design</i> Developed and designed the website for the 2019 eSCAMPS

Languages

Portuguese	Native
English	Proficient
Spanish	Beginner

Scientific publications

- | | |
|------|---|
| 2022 | 1. De Almeida, J. G. , Gudgin, E., Besser, M., Dunn, W. G., <i>et al.</i> Computational analysis of peripheral blood smears detects disease-associated cytomorphologies. <i>medRxiv</i> (2022). |
| | 2. Fabre, M. A., de Almeida, J. G. , Fiorillo, E., Mitchell, E., <i>et al.</i> The longitudinal dynamics and natural history of clonal haematopoiesis. <i>Nature (shared first-authorship with M Fabre)</i> , 1–8 (2022). |
| 2021 | 3. Preto, A. J., Matos-Filipe, P., de Almeida, J. G. , Mourão, J. & Moreira, I. S. in <i>Artificial Neural Networks</i> 267–288 (Springer, 2021). |
| 2020 | 4. Preto, A. J., Barreto, C. A., Baptista, S. J., Almeida, J. G. d., <i>et al.</i> Understanding the binding specificity of G-Protein coupled receptors toward G-proteins and arrestins: Application to the dopamine receptor family. <i>Journal of Chemical Information and Modeling</i> 60 , 3969–3984 (2020). |
| 2019 | 5. R Magalhães, P., Machuqueiro, M., G Almeida, J., Melo, A., <i>et al.</i> Dynamical rearrangement of human epidermal growth factor receptor 2 upon antibody binding: effects on the dimerization. <i>Biomolecules</i> 9 , 706 (2019). |
| 2018 | 6. Lemos, A., Melo, R., Preto, A. J., Almeida, J. G. , <i>et al.</i> In silico studies targeting G-protein coupled receptors for drug research against Parkinson's disease. <i>Current neuropharmacology</i> 16 , 786–848 (2018). |
| | 7. Melo, R., Lemos, A., Preto, A. J., Almeida, J. G. , <i>et al.</i> Computational approaches in antibody-drug conjugate optimization for targeted cancer therapy. <i>Current topics in medicinal chemistry</i> 18 , 1091–1109 (2018). |
| | 8. Melo, R., Lemos, A., Preto, A. J., Bueschbell, B., <i>et al.</i> An Overview of Antiretroviral Agents for Treating HIV Infection in Paediatric Population. <i>Current medicinal chemistry</i> (2018). |
| | 9. Preto, A. J., Almeida, J. G. , Schaarschmidt, J., Xue, L. C., <i>et al.</i> Computational Tools for the Structural Characterization of Proteins and Their Complexes from Sequence-Evolutionary Data. <i>Encyclopedia of Analytical Chemistry: Applications, Theory and Instrumentation</i> , 1–19 (2018). |
| 2017 | 10. Almeida, J. G. , Preto, A. J., Koukos, P. I., Bonvin, A. M. & Moreira, I. S. Membrane proteins structures: A review on computational modeling tools. <i>Biochimica et Biophysica Acta (BBA)-Biomembranes</i> 1859 , 2021–2039 (2017). |
| | 11. Bastos, F. C., Corceiro, V. N., Lopes, S. A., de Almeida, J. G. , <i>et al.</i> Effect of tolbutamide on tetraethylammonium-induced postsynaptic zinc signals at hippocampal mossy fiber-CA3 synapses. <i>Canadian Journal of Physiology and Pharmacology</i> 95 , 1058–1063 (2017). |
| | 12. Moreira, I. S., Koukos, P. I., Melo, R., Almeida, J. G. , <i>et al.</i> SpotOn: high accuracy identification of protein-protein interface hot-spots. <i>Scientific reports</i> 7 , 1–11 (2017). |
| | 13. Sensoy, O., Almeida, J. G. , Shabbir, J., Moreira, I. S. & Morra, G. in <i>Methods in Cell Biology</i> 205–245 (Academic Press, 2017). |

Conference presentations

- | | | |
|------|--|--|
| 2021 | | The Natural History of Clonal Haematopoiesis, <i>CRUK Cambridge Centre Early Detection Programme 6th Annual Symposium</i> , Cambridge |
| 2020 | | Leveraging Automated Blood Cell Morphology for Myelodysplastic Syndrome Diagnosis and Prognosis Prediction, <i>Quantitative BioImaging Conference</i> , Oxford |
| 2017 | | Using big-data to understand the protein interface landscape, <i>Encontro de Jovens Investigadores de Biologia Computacional Estrutural</i> , Coimbra |
| 2016 | | A Machine Learning Based Protein-Protein Hot-Spot Prediction Method — SpotOn, <i>Encontro de Jovens Investigadores de Biologia Computacional Estrutural</i> , Lisbon |