

# Fábio Madeira

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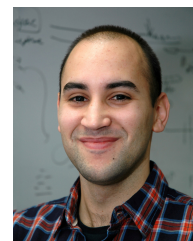
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🌐 <http://biomadeira.github.io>

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## EXPERIENCE

Since 2016

### **Postdoctoral Research Assistant in Bioinformatics**

Geoff Barton's Group, Division of Computational Biology, University of Dundee, UK. Currently Working on the Dundee Resources, "Tier-1" by the ELIXIR-UK Network (Protein Structure and Function), and developing new approaches to analyse structural and genomic data.

2012-2016

### **Wellcome Trust PhD in Computational Biology**

Geoff Barton's Group, Division of Computational Biology, University of Dundee, UK. My work focused on the analysis of genetic variation in protein structure interaction surfaces. The project was heavy on software development, data analysis and visualisation, development/benchmarking of machine learning classifiers, and web development.

2010-2012

### **Research Studentship in Bioinformatics and Artificial Intelligence**

Ludwig Krippahl's Group, Department of Computer Science, Universidade Nova de Lisboa, Portugal. The project involved software development and benchmarking of coevolution methods as constraints for protein docking, and development of new approaches to generate multiple sequence alignments.

## EDUCATION

2012-2016

### **PhD in Computational Biology**, *University of Dundee*

Supervisor: Prof Geoff J. Barton; Internal Examiner: Prof Helen Walden (University of Dundee); external Examiner: Prof David T. Jones (University College London). PhD Thesis: "Analysis of variation in protein domain families and interfaces". Viva voce passed with minor corrections.

2008-2010

### **MSc in Molecular Genetics**, *Universidade Nova de Lisboa*

Supervisors: Prof. Maria João Romão's and Prof. Ana Paula Leandro. Master Thesis: "Estudos estruturais e funcionais da fenilalanina hidroxilase humana" (Written in Portuguese). Santander-NOVA Merit Scholarship Award.

2004-2008

### **BSc in Biochemistry**, *Universidade Nova de Lisboa*

ECTN Chemistry Eurobachelor Degree. Ranked 2<sup>nd</sup> in class.

## PUBLICATIONS

Fábio Madeira, Thiago Britto-Borges, Stuart MacGowan and Geoffrey J. Barton (2017) **ProteoFAV: fast structural data integration with Pandas**. *About to be submitted to Bioinformatics*.

Peter V. Troshin, Alexander Sherstnev, James B. Procter, Daniel L. Barton, Fábio Madeira and Geoffrey J. Barton (2017) **JABAWS 2.2 Distributed Web Services for Bioinformatics: Protein Disorder, Conservation and RNA Secondary Structure**. *About to be submitted to Bioinformatics*.

Peter Troshin, Agnieszka Golicz, David Martin, Fábio Madeira, James B. Procter and Geoffrey J. Barton (2017) **AACon: A Fast Amino Acid Conservation Calculation Service**. *About to be submitted to Bioinformatics*.

Stuart A MacGowan, Fábio Madeira, Thiago Britto Borges, Melanie S Schmittner, Christian Cole, Geoffrey J. Barton (2017) **Human Missense Variation is Constrained by Domain Structure and Highlights Functional and Pathogenic Residues**. bioRxiv doi:10.1101/127050. *Submitted to Nature Genetics*.

Fábio Madeira, Michele Tinti, Gavuthami Murugesan, Emily Berrett, Margaret Stafford, Rachel Toth, Christian Cole, Carol MacKintosh and Geoffrey J. Barton (2015) **14-3-3-Pred: Improved methods to predict 14-3-3-binding phosphopeptides**. *Bioinformatics (Oxford)* 2015 Mar 3; doi:10.1093/bioinformatics/btv133

Michele Tinti, Fábio Madeira, Gavuthami Murugesan, Gerta Hoxhaj, Rachel Toth and Carol MacKintosh (2014) **ANIA - ANnotation and Integrated Analysis of the 14-3-3-interactome**. *Database (Oxford)* 2014 Feb 5; doi:10.1093/database/bat085

Ludwig Krippahl and Fábio Madeira (2014) **Improving Protein Docking with Constraining Programming and Coevolution Data**. bioRxiv doi:10.1101/002329

Ludwig Krippahl, Fábio Madeira and Pedro Barahona (2013) **Constraining Protein Docking with Coevolution Data for Medical Research**. *Proceedings of the 14th Conference on Artificial Intelligence in Medicine* pp 110-114. doi:10.1007/978-3-642-38326-7

Fábio Madeira and Ludwig Krippahl (2012) **PYCOEVOL - A Python Workflow to Study Protein-protein Coevolution**. *Proceedings of the International Conference on Bioinformatics Models, Methods and Algorithms* pp 143-149. doi:10.5220/0003737901430149

Marco Correia, Fábio Madeira, Pedro Barahona and Ludwig Krippahl (2011) **Improving Multiple Sequence Alignments with Constraint Programming and Local Search**. *Proceedings of the Workshop on Constraint Based Methods for Bioinformatics* pp 37-44. [www.dmi.unipg.it/WCB11/wcb11proc.pdf](http://www.dmi.unipg.it/WCB11/wcb11proc.pdf)

## POSTERS

Fábio Madeira and Geoffrey J. Barton (2015) **Analysis of protein domain interactions and genetic variation**. SLS PhD Poster Session at University of Dundee, Oct. 9. doi:10.6084/m9.figshare.1584880. Selected as Poster Prize Winner.

Fábio Madeira and Geoffrey J. Barton (2015) **Protein interactions and genetic variation**. ISMB/ECCB 2015 (23rd Annual International Conference on Intelligent Systems for Molecular Biology - 14th European Conference on Computational Biology) Dublin, Jul. 10-14. doi:10.6084/m9.figshare.1485641. Selected for Oral Poster Presentation and Travel Fellowship.

Fábio Madeira, Michele Tinti, Gerta Hoxhaj, Geoffrey J. Barton and Carol MacKintosh (2015) **Predicting and mapping the human 14-3-3 interactome to test a new signalling paradigm**. Wellcome Trust Retreat in Fribush, University of Dundee, May 23. doi:10.6084/m9.figshare.923439

Michele Tinti, Fábio Madeira, Catherine Johnson, Margaret Malcolm and Carol MacKintosh (2012) **Evolution of 14-3-3-binding sites and 2R-Ohnologue families**. PTMs in Cell Signaling, Copenhagen Denmark, Dec. 2-5. doi:10.6084/m9.figshare.923438

Paulo Roque Lino, Fábio Madeira, Isabel Tavares de Almeida and Paula Leandro (2010) **Alternative Answers to Everlasting Problems: Protein Engineering Towards New Approaches for Phenylketonuria Treatment**. SPDM Annual Symposium Albufeira, Portugal, Nov. 4-5.

Catarina Coelho, Fábio Madeira, Paulo Roque Lino, Isabel Tavares de Almeida, Paula Leandro and Maria João Romão (2010) **Crystallization of a Stable Form of Human Phenylalanine Hydroxylase: Towards the 3D Structure Determination**. UK-Portuguese Teams Meeting Protein-protein interaction and Protein folding. FCT-UNL, Mar. 29-31. doi:10.6084/m9.figshare.923437

## INITIATIVES

- 2015 **TEDx University of Dundee**  
Organization and development/design of the event's website and ticket sale.  
🌐 <http://tedxuod.github.io>
- 2014 **PiCLS Annual Symposium**  
Organization and development/design of the event's website.  
🌐 <http://picls-symposium.org/2014>
- 2013 **Biotechnology YES**  
Participated with a team project "IntelliGene: Empower your future" in the Biotechnology Young Entrepreneurs Scheme Competition.

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## SOFTWARE DEVELOPMENT

- 2017 **JABAWS**  
JABAWS 2.2: Distributed Web Services for Bioinformatics.  
🔗 <http://www.compbio.dundee.ac.uk/jabaws>
- 2017 **AACon**  
AACon 1.1: A Fast Amino Acid Conservation Calculation Service.  
🔗 <http://www.compbio.dundee.ac.uk/aacon>
- 2017 **BioDownloader**  
A Command Line Tool for downloading protein structures, protein sequences and multiple sequence alignments. 🐙 [biomadeira/BioDownloader](#)
- 2015 **pyPDBeREST**  
A python wrapper for the PDBe REST API powered by *Requests*.  
🐙 [biomadeira/pyPDBeREST](#)
- Since 2013 **ProIntVar**  
Python package for analysis of protein structures and genetic variants, developed in the Barton Group. Extensive use of the *Pandas* data structures and analysis tools. Source code available for review upon request.
- 2013-2015 **14-3-3-Pred**  
A webserver to predict 14-3-3-binding sites in proteins. Built with *Flask*, and related technologies.  
🔗 <http://www.compbio.dundee.ac.uk/1433pred>
- 2011-2012 **Pycoevol**  
A Python workflow to study protein-protein coevolution and interaction.  
🐙 [biomadeira/pycoevol](#)
- 2012 **BibYAML**  
A webserver for converting BibTeX bibliographies to YAML, deployed with *Google App Engine*. 🐙 [biomadeira/gae\\_bib2yaml](#)
- 2012 **Pubmed2Rss**  
Pubmed *Rss* ID Generator, deployed with *Google App Engine*.  
🐙 [biomadeira/gae\\_pubmed2rss](#)
- 2015 **Jasper**  
Full-featured clone of Ghost's default theme 'Casper' for GitHub pages powered by *Jekyll*. 🐙 [biomadeira/jasper](#)
- 2015 **Sustain**  
A personal blog theme developed with *Bootstrap* for GitHub pages powered by *Jekyll*. 🐙 [biomadeira/sustain](#)
- 2015 **Vitae**  
A personal resume theme developed with *Skeleton* for GitHub pages powered by *Jekyll*. 🐙 [biomadeira/vitae](#)

## TECHNICAL SKILLS

### Software Development

Adopter of Test-driven development practices. OOP Python 2 and 3 (Numpy, SciPy, IPython, Click, Unittests, Nose, Mock, etc.), Version control (Git/Github) and Continuous Integration (Travis-CI, Coveralls, Landscape.io, Virtualenv, Tox, etc.).

### Web Development

Python (Flask, webapp2, requests, jinja2, GAE, etc.), Java Servlet (Apache Tomcat), HTML/CSS frameworks (Bootstrap and Skeleton), JavaScript (jQuery) and static-site generators (Jekyll, liquid).

### Data Analysis and Visualisation

Python (pandas and matplotlib), Jupyter Notebooks, R/RStudio (ggplot2, ROCR, etc.), Plotly, Microsoft Excel, etc.

### Machine Learning

Feature selection and training/testing of Support-Vector Machines, Neural Networks, Random Forests, Naive Bayes, and other classification models, with Python (scikit-learn, PyML and TensorFlow) and R (RSNNS).

### Databases

Relational (MySQL and SQLite3) with Python SQLAlchemy and non-relational (MongoDB) with PyMongo. Data mangling with JSON and tabular data formats.

### Documentation

L<sup>A</sup>T<sub>E</sub>X, (R)Markdown, reStructuredText, Sphinx, ReadTheDocs, R Bookdown, etc.

### Others

Scripting/coding (Bash, Java, C and Perl), Build and distribution (Docker, Makefile, Common Workflow Language, Apache Ant, Maven, etc.), Linux/macOS Systems (Sun Grid Engine, TurnKey linux, CentOS, etc.).

### Bioinformatics

UCSF Chimera, PyMOL, Jalview, Biopython, HHMER, etc.

## SOFT-SKILLS

### Technical Writing

Wrote two dissertations, a few journal/conference papers and research reports.  
ORCID: 0000-0001-9892-9368

### Communication

Presented my research (oral/poster presentation) in several conferences and public meetings. Some of my talks are available online in *figshare*. Additionally, I have been an helper in Coding Courses, such as Software Carpentry, at the University of Dundee.

### Interpersonal

Problem solver, collaborative, supportive and respectful.

## WORKSHOPS ATTENDED

- Apr. 2017 **3<sup>rd</sup> BiVi Annual Meeting**  
Biological Visualisation Community Meeting, Edinburgh Napier University.
- Mar. 2016 **Error Statistics Analysis**  
Lecture Series on Error Analysis, Statistical Tests and P-values, by Marek Gierliński, University of Dundee.
- Nov. 2014 **PDBe API Workshop**  
PDBe Workshop for Programmers on Programmatic Access to Molecular Structure Information, EMBL-EBI Hinxton.
- Sept. 2014 **Data Visualisation and Infographics Design**  
Workshop on data visualisation by Andy Kirk, the curator of “Visualizing Data” ([www.visualisingdata.com](http://www.visualisingdata.com)). University of Dundee.
- May 2011 **Bioinformatics using Python for Biologists**  
Gulbenkian Training Programme in Bioinformatics with Allegra Via and Fabrizio Ferrè (Sapienza Università di Roma). Instituto Gulbenkian de Ciência.
- Feb. 2010 **Advanced Course in Protein Crystallography**  
Macromolecular Crystallography Laboratory, REQUIMTE-UNL.

## LANGUAGES

Portuguese (native) and English (proficient)

## HOBBIES AND INTERESTS

Music, Piano, Reading, Movies, Gaming, Running, Cycling, Swimming...

## REFERENCES

### Professor Geoff J. Barton

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School of Life Sciences  
University of Dundee  
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### Professor Carol MacKintosh

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