

# BRUNO VIEIRA

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## Personal Summary

Bioinformatician turned full stack developer.

My background has given me a diverse set of skills, from biological sciences to programming, including areas such as infrastructure and security.

I started coding in Java and R during my [MSc in Human Biology](#) in 2008. In 2010 I [became a bioinformatician](#) and [taught Python courses](#) at the University of Lisbon. Then I learned NodeJS in 2013 and my first project was to build the web platform and backend for organising a 1500 participants conference ([ESEB 2013](#)). After that, I was offered to start a [PhD in Bioinformatics in London](#) (2014). During my PhD, I founded the Open Source community project [Bionode.io](#) (modular and reusable bioinformatics in NodeJS) and won a [Mozilla Science fellowship](#) (one of four, out of 483 submissions) to [champion Open Science and Open Source around the world](#) (2016). After my PhD, I worked for some startups; became Co-CTO of [Resurgo Genetics](#) (therapeutics target discovery, 2019); and finally ended up at [Lifebit.ai](#) (large scale genomic data analysis platform, 2021).

## Experience Summary

### 2021-Present - Lifebit.ai | Senior Backend Developer

A precision medicine software company that builds enterprise data platforms for use by organisations with sensitive genomic and biomedical datasets, [empowering therapeutic leaders to access and analyse siloed biomedical data](#). I worked on:

- Integration with GitHub, GitLab, and authentication.
- No-code product for creating [Nextflow](#) bioinformatics pipelines.
- Interactive data analysis integration with Jupyter, RStudio, Dask, PySpark, etc. (one of our core products and greatly responsible for users' satisfaction).
- Client specific deployments on AWS, Azure, GCP, and Kubernetes.

- Docker containers, Packer, Terraform.
- Security issues resolution and prevention.

Skills: TypeScript, Node.js, React, AWS, K8S, Docker, Podman, Nix, Microservices, Nginx, MongoDB, Redis, GCP, Azure, Terraform, Packer, Hadoop, OpenAPI, Shell Scripting, Bioinformatics

## 2019-2021 - Resurgo Genetics | Co-Chief Technology Officer

An Entrepreneur First 8 cohort launched in 2017. It raised ~2M and was valued at ~10M. I joined in 2019 as Co-CTO in a small team of 4. I was focused more on the infrastructure, big genomic data analysis, and visualizations. We worked with data from our lab which was applying CRISPR and sequencing to multiple kinds of cancer cells. During the pandemic, we pivoted to analysing publicly available COVID19 data. We had a hacker/company house in Oxford, and I mostly worked on:

- Setting up the in-house servers with [NixOS](#)
- Setting up the bioinformatics and machine learning tooling
- Analysing sequencing data from the lab
- Preparing materials, [videos](#), and documents for funding

Skills: Nix, NixOS, NodeJS, Python, Dask, PyTorch, Datashader, HoloViews, Machine Learning, R, Bioinformatics, Linux System Administration, Video Editing, Funding Applications Writing, Biology

## 2018 (1 month) - Stencila.io via Code for Science and Society | Developer

Data-driven interactive documents. I worked on a [docker tool for researchers](#).

Skills: Nix, Docker, Open Source Development

## 2018 (6 months part-time) - Repositive.io | Bioinformatician

[Largest directory of preclinical cancer models](#). I worked on reproducible data analysis pipelines with Nix and Docker.

Skills: Nix, Docker, AWS, GCP, Kubernetes, Ember.js

## 2016 (10 months part-time) - Mozilla | Science Lab Fellow

I was 1 out of 4 fellows awarded this fellowship (483 applicants) to champion open science and open source [around the world](#). My [goal was to focus on Bionode](#) and reproducible science. Among other things, I wrote [blog posts](#), gave [talks](#), and organized [hackathons](#).

Skills: Open Source Development, Community Management, Workshop Development, Public Speaking, Node.js, JavaScript, Bioinformatics, Funding Applications Writing

### **2014-2018 (4 years) - Bionode.io Open-Source project during PhD | Founder**

Project to build scalable and streamable bioinformatics analysis by leveraging the NodeJS ecosystem. I mentored 3 Google Summer of Code students, organized several workshops and hackathons, and contributed to node modules. I also prototyped data analysis workflow engines.

Skills: Bioinformatics, Node.js, Data Streams, Community Management, Open Source Development, Workshops Development, Public Speaking, REST APIs, NCBI API

### **2014 - Dat project | Consultant**

Distributed data protocol. I advised for potential genetic data use cases and applications.

Skills: JavaScript, Data Streams, Open Source Development, Bioinformatics, Consulting, Node.js

### **2013 - Geekli.st | Intern developer**

First achievement based social platform and the largest online community for software developers. I was mostly responsible for the LinkedIn API integration.

Skills: Node.js, MongoDB, JavaScript

### **2012-2013 - ESEB 2013 at University of Lisbon | Full Stack Developer**

XIV Congress of the European Society for Evolutionary Biology (1500 participants). This was my first NodeJS project and my rite of passage to full stack development. I was the main developer and built the frontend, backend, registration process, talks/posters submissions and display, talks schedule, events notifications, rooms presentations synchronization, etc. I was offered a PhD in London in part thanks to this project.

Skills: Node.js, Express.js, MongoDB, Redis, CoffeeScript, Jade, Twitter Bootstrap, jQuery, Heroku

### **2009-2013 (4 years) - CoBiG<sup>2</sup> at Uni. of Lisbon | Bioinformatician**

Computational Biology & Population Genomics Group. I co-authored 4 papers; oversaw the groups high performance computing; taught Python courses for biologist (with novel in-browser interactive code examples and editor).

Skills: Bioinformatics, Python, R, High Performance Computing (HPC), Scientific Research, Scientific Writing, Courses Creation, Teaching, Unix Shell Scripting, Biology, Phylogeography, Phylogenetics, Genetics, Public Speaking, Linux Systems Administration, Arch Linux (btw), Ubuntu, LaTeX, Node.js, AngularJS, Joomla

## Education

### 2014-2018 | PhD in Bioinformatics @ Queen Mary, University of London

Thesis about genetic diversity of insects, looking at effective population size ( $N_e$ ). I co-authored 3 papers. At some point I had 40 TB of data on the cluster (biggest user). I worked on building scalable bioinformatics pipelines and founded the Bionode.io open-source project. I have submitted my thesis but not defended it yet.

Skills: Bioinformatics, Population Genomics, Python, R, Node.js, JavaScript, Scientific Research, Scientific Writing, Genomics, Biology, LaTeX, Teaching Assistant

### 2004-2009 | MSc in Human Biology & Environment @ Faculty of Sciences, U. of Lisbon

Thesis about antibiotics resistance. I did wet lab work and wrote an [ImageJ](#) Java plugin to [automatically count bacterial colonies](#).

Skills: R, Java, Scientific Research, Scientific Writing, Bacterial Cell Culture, PCR, Genetics

### 2010 | Extra classes from the MSc in Bioinformatics & Computational Biology @ Faculty of Sciences, U. of Lisbon

- **Fundamentals of Programming** from the MSc in Bioinformatics and Computational Biology Grade: 16/20
- **Introduction to Databases** from the MSc in Bioinformatics and Computational Biology Grade: 17/20

## Papers Published

- Vos RA, Katayama T, Mishima H, *et al.* (2020) [BioHackathon 2015: Semantics of data for life sciences and reproducible research](#) *F1000Research*
- Pina-Martins F, **Vieira BM**, Seabra SG, Batista D, Paulo OS (2016) [4Pipe4-A 454 data analysis pipeline for SNP detection in datasets with no reference sequence or strain information](#) *BMC Bioinformatics*
- Yachdav G, Goldberg T, Wilzback S, Dao D, Shih I, Choudhary S, Crouch S, Franz M, **Vieira B**, *et al.* (2015) [Anatomy of BioJS, an open source community for the life sciences](#) *eLife*
- Aleksic J, Alexa A, Attwood T, Hong NC, Dahlö M, Förstner K, Smith-Unna R, Schneider V, **Vieira B**, *et al.* (2014) [\\*\\* The Open Science Peer Review Oath\\*\\*](#) *F1000Research*
- **Vieira B\***, Sebastiana M\*, Lino-Neto T, Monteiro F, Figueiredo A, Sousa L, Pais MS, Tavares R, Paulo OS (2014): [Oak Root Response to Ectomycorrhizal](#)

## **Symbiosis Establishment: RNA-Seq Derived Transcript Identification and Expression Profiling.** *PLOS One*, **9**:5

- Talhinhas P, Azinheira HG, **Vieira B**, Loureiro A, Tavares S, Batista D, Morin E, Petitot AS, Paulo OS, Poulain J, Silva C, Duplessis S, Silva MC, Fernandez D (2014): **Overview of the functional virulent genome of the coffee leaf rust pathogen *Hemileia vastatrix* with an emphasis on early stages of infection.** *Frontiers in Plant Science*, **5**:88
- Bradnam KR, Fass JN, Alexandrov A, *et al* (2013): **Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species.** *GigaScience*, **2**:10

## **Talks Presented**

- **Vieira B** (2020): **My Journey Into Bioinformatics.** Presented at the Master's degree in Bioinformatics, Faculty of Sciences of the University of Lisbon, Portugal
- **Vieira B** (2019): **Automatically create containers using Dockta and Nixta.** Presented at the [The London Bioinformatics Frontiers Conference 2019](#), [Francis Crick Institute](#), London, UK
- **Vieira B** (2019): **My Journey Into Bioinformatics.** Presented at the Master's degree in Bioinformatics, Faculty of Sciences of the University of Lisbon, Portugal
- **Vieira B** (2019): **My Journey Into Bioinformatics.** Presented at the Undergrad in Bioinformatics, Escola Superior de Tecnologia do Barreiro, Portugal
- **Vieira B** (2018): **My Journey Into Bioinformatics.** Presented at the Master's degree in Bioinformatics, Faculty of Sciences of the University of Lisbon, Portugal
- **Vieira B** (2017): **Open Science.** Presented at the [2nd Biomed PhD Day](#), Barcelona, Spain
- **Vieira B** (2017): **A truly reproducible paper?** Presented at the [Springer Nature: Better Science through Better Data 2017](#), Wellcome Collection, London, UK
- **Vieira B**, Wurm Y (2016): **Bionode - Modular and universal bioinformatics.** Presented at the [Bioinformatics London meetup](#), Imperial College, London, England.
- **Vieira B**, Nichols R, Wurm Y (2015): **The effect of social evolution on the effective population size:** Presented at the 49th Population Genetics Group (PopGroup) meeting, Edinburgh, Scotland
- **Vieira B**, Wurm Y (2015): **An introduction to bionode - bioinformatics pipelines in Javascript.** Presented at the BioCoders meetup, Cambridge, England.
- **Vieira B**, Wurm Y (2015): **Bionode - Modular and universal bioinformatics.** Presented at the DBCLS BioHackathon 2015, Nagasaki University, Japan.

- **Vieira B**, Wurm Y (2015): **Bionode - Modular and universal bioinformatics**. Presented at the Bioinformatics Open Source Conference (BOSC). University of Dublin, Ireland.
- **Vieira B**, Wurm Y (2014): **Bionode**. Presented at the Collaborations Workshop, Software Sustainability Institute, Oxford, England.
- **Vieira B**, Nichols R, Wurm Y (2015): **Effective population size in insects**. Presented at the 48th Population Genetics Group (PopGroup) meeting, University of Sheffield, England
- **Vieira B**, Wurm Y (2014 Dec): **Effective population size and sociality**. Presented at the **X Encontro Nacional de Biologia Evolutiva**, National Museum of Natural History and Science, Lisbon, Portugal
- **Vieira B**, Wurm Y (2014 Dec): **Building collaborative workflows for scientific data**. Presented at the **Open Research Cambridge meetup**, England.
- **Vieira B**, Ogden M, Wurm Y (2014): **Bionode and Dat**. Presented at the Wellcome Trust Sanger Institute, Cambridge, England.
- **Vieira B** (2014 Mar 25): **Pairwise Sequentially Markovian Coalescent Model**. Presented at the Evolution Lab Jolly, SBCS, Queen Mary, University of London, London, England.
- **Vieira B** (2014): **Docker for reproducible science**. Presented at the Collaborations Workshop 2014, Software Sustainability Institute, University of Oxford, Oxford, England.
- **Vieira B** (2014): **Crowdsourcing Genome Annotation**. Presented at the Citizen Cyberscience Summit 2014, University College London (UCL), London, England.
- **Vieira BM**, Pina-Martins F, Seabra SG, Paulo OS (2010): **Analysis of software for the NGS technology: The Survival Guide**. Presented at the 24th European Conference on Operational Research. Faculty of Sciences of the University of Lisbon (FCUL), Lisbon, Portugal.

### Talks co-authored

- Pina-Martins F, **Vieira BM**, Seabra SG, Batista D, Paulo OS (2013): **Making the best of your 454 dataset using the 4Pipe4 analysis pipeline – from an unknown genome to a detailed SNPs analysis: A case study with a Quercus suber dataset**. Presented at the XIV Congress of the European Society for Evolutionary Biology (ESEB 2013). Faculty of Sciences of the University of Lisbon (FCUL), Lisbon, Portugal.

### Posters co-authored

- 2013 - Pina-Martins F, **Vieira BM**, Seabra SG, Batista D, Paulo OS (2013): **The 4Pipe4 analysis pipeline – how to exploit the hidden SNPs in your 454 dataset: a testcase with a quercus suber dataset**. Exhibited at the “XIII Congresso Luso-Espanhol de Fisiologia Vegetal”. Faculty of Sciences of the University of Lisbon, Lisbon, Portugal.

- 2013 - Talhinhos P, Azinheira HG, **Vieira BM**, Loureiro A, Tavares S, Batista D, Morin E, Petitot AS, Paulo OS, Poulain J, Silva C, Duplessis S, Silva MC, Fernandez D (2013): [Overview of the functional virulent genome of the coffee leaf rust pathogen, \*Hemileia vastatrix\*](#). Exhibited at the “XIII Congresso Luso-Espanhol de Fisiologia Vegetal”. Faculty of Sciences of the University of Lisbon, Lisbon, Portugal.
- 2010 - Talhinhos P, Azinheira HG, Vieira A, Loureiro A, **Vieira BM**, Pina-Martins F, Batista D, Tisserant E, Morin E, Petitot AS, Paulo OS, Duplessis S, Silva MC, Fernandez D (2010): [Transcriptomic analysis of \*Hemileia vastatrix\* in pre and post-penetration stages](#). Exhibited at the 9th Conference of the European Foundation for Plant Pathology (EFPP)/6th Congress of the Portuguese Society for Phytopathology (SPF). University of Évora (UE), Évora, Portugal.
- 2010 - Talhinhos P, Azinheira HG, Loureiro A, Batista D, **Vieira BM**, Pina-Martins F, Tisserant E, Petitot AS, Paulo OS, Duplessis S, Silva MC, Fernandez D (2010): [Overview of the functional virulent genome of the coffee leaf rust pathogen \*Hemileia vastatrix\*](#). Exhibited at the 23rd International Conference on Coffee Science from the Association for Science and Information on Coffee (ASIC). Indonesian Coffee and Cocoa Research Institute (ICCRI), Bali, Indonesia.

## Projects involved

- 2013-Present - [Bionode.io](#) - Modular and universal bioinformatics
- 2016 - [Google Summer of Code](#) mentoring of [Julian Mazzitelli](#) to build a “Bionode workflow engine for streamed data analysis”
- 2013-2014 - [Afra](#) - crowdsourcing gene feature annotation funded by BBSRC
- FCT Project: [SOBREIRO/0036/2009 Cork oak ESTs Consortium - Polymorphism detection and validation](#) Participation: 25% Institution: Fundação da Faculdade de Ciências (FFC/FC/UL) Budget: € 49 480,00

## Teaching experience

- 2013-Present - **Demonstrator** for master of bioinformatics and R practicals at Queen Mary University of London
- 2010 (Nov 25) - Class lecture about **Next-generation sequencing** for the MSc in Bioinformatics and Computational Biology

## Workshops organised

- 2015 - [Bionode](#) - Modular and universal bioinformatics at [Mozfest](#), London, England
- 2014 - [Dat Workshop: Dive into dat for dataset push, pull and clone](#) at [Mozfest](#), London, England



## Workshops attended

- 2015 - **Collaborations Workshop 2015**. Software Sustainability Institute, University of Oxford, Oxford, England
- 2014 (Mar 26-28) - **Collaborations Workshop 2014**. Software Sustainability Institute, University of Oxford, Oxford, England
- 2012 - **Node.js Workshop** by Mikeal Rogers and Daniel Shaw at Lisbon Javascript
- 2012 - “Cooking with Backbone and Socket.io 101” by Igor Soarez and João Duarte at Lisbon Javascript

## Courses organised

- 2012 - “**Python 101: by biologists for biologists**” at Faculty of Science of the University of Lisbon (FCUL) Some material that I gave:
  - presentation slides made in markdown and rendered with Node.js, Deck.js, CodeMirror and Skulpt
  - exercises made with iPython

## Courses attended

- 2010 - **Practical Course on Phylogenetics**, Centre for Environmental Biology (CBA), Lisbon, Portugal
- 2010 - **Practical Course on Phylogeography**, Centre for Environmental Biology (CBA), Lisbon, Portugal

## Online courses attended

- 2013 - **MongoDB University: M101P MongoDB for Developers** Score: 100% (top 6% of the 5,486 enrolled students. Course completion rate is 19%)
- 2013 - **MongoDB University: M102 MongoDB for DBAs** Score: 100% (top 8% of the 6,379 enrolled students. Course completion rate is 21%)
- 2013 - **MongoDB University: M101JS: MongoDB for Node.js Developers** Score: 100% (top 8% of the 7,599 enrolled students. Course completion rate is 20%)

## Conferences attended

- 2015 (Dec 15-18) - **The 49th UK Population Genetics Group**, Edinburgh, Scotland
- 2015 - **Mozilla Festival**. Ravensbourne, London, England
- 2015 (Aug 10-14) - **European Society for Evolutionary Biology (ESEB)**. The Department of Ecology and Evolution of the University of Lausanne, Switzerland
- 2015 (Jul 13-14) - **23rd annual international conference on Intelligent Systems for Molecular Biology (ISMB) and the 14th European Conference on Computational Biology (ECCB)**. International Society for Computational Biology (ISCB), University of Dublin, Ireland
- 2015 (Jul 10-11)- **Bioinformatics Open Source Conference (BOSC)**. University of Dublin, Ireland



- 2014 - **Mozilla Festival**. Ravensbourne, London, England
- 2014 (May 20) - **Neural circuits underpinning insect cognition**. Fogg Lecture Theatre, Fogg Building, Queen Mary University of London, London, England
- 2014 (May 2) - **Genomics of gene expression and ageing. EuroBATS Consortium at the Royal College of Physicians**
- 2014 (Feb 20-22) - **3rd Citizen Cyberscience Summit**. Royal Geographical Society and University College London, London, England
- 2014 - **London JS Conf**. Prince Charles Cinema, London, England
- 2013 (Nov 27) - **Beatles and Bioinformatics**. Center for Genomic Research at the University of Liverpool
- 2013 - **Mozilla Festival**. Ravensbourne, London, England
- 2013 - **LXJS Lisbon Javascript**. São Jorge Cinema, Lisbon, Portugal
- 2013 - **XIV Congress of the European Society for Evolutionary Biology**. Faculty of Sciences of the University of Lisbon (FCUL), Lisbon, Portugal
- 2012 - **LXJS Lisbon Javascript**. Ribeira Market, Lisbon, Portugal
- 2010 - **VI Encontro Nacional de Biologia Evolutiva**. Faculty of Sciences of the University of Lisbon (FCUL), Lisbon, Portugal
- 2010 - **Science 2010 - Meeting Science in Portugal**. Lisbon Congress Center, Portugal
- 2009 - **V Encontro Nacional de Biologia Evolutiva**. Instituto Superior de Psicologia Aplicada (ISPA), Lisbon, Portugal
- 2008 - **IV Encontro Nacional de Biologia Evolutiva**. Instituto de Biologia Molecular e Celular (IBMC), Porto, Portugal
- 2008 - **III Congresso da Ordem dos Biólogos: "Bioeconomia"**. Aula Magna, Lisbon, Portugal

## Hackathons organised

- 2016 (Jul 9) - **Bionode and DNAdigest Hackday - Crawling genomic datasets with node.js**, sponsored by [repositive.io](http://repositive.io). Google Campus London, England

## Hackathons attended

- 2015 (Sep 13-19) - **BioHackathon 2015**, Nagasaki University, Japan
- 2015 (Jul 8) - **OpenBio Codefest 2015**. The Open Bioinformatics Foundation (O|B|F), University of Dublin, Ireland
- 2014 (Apr 5) - **Prototyping a Data Discovery tool**. DNAdigest Hack Day, London, England

## Open Source Contributions

### Node.js Modules

- 2014-Present - **bionode** A Node.js JavaScript library for client and server side bioinformatics.

- 2013 - [xml2json-stream](#) Converts XML to JSON, using Streams and sax. This can be used with above-memory-limits XML files, as long as they're mostly composed of a repetitive tag.

## Software

- 2013-2014 - [Afra](#) - A web application for crowdsourcing genome annotation.
- 2013 - [CoBiG<sup>2</sup>](#) - An Angular.js web app that uses many APIs (LinkedIn, Mendeley, Facebook and GitHub) and will become CoBiG<sup>2</sup>'s new website.
- 2009 - [Colony Counter](#) - An ImageJ plugin for automatically enumerating *Escherichia coli* colonies. Published in *Comprehending the Cost of Antibiotics Resistance in Bacteria*. Masters thesis in Human Biology and Environment. Faculty of Sciences of the University of Lisbon

## Arch Linux AUR Packages Maintainer

- [casperjs-git](#), a browser navigation scripting & testing utility written in Javascript on top of PhantomJS
- [phantomjs-git](#), headless WebKit with JavaScript API
- [genepop](#), a population genetics software.
- [ima2](#), a program for fitting the isolation with migration model for multiple populations.
- [populations](#), population genetic software (individuals or populations distances, phylogenetic trees)
- [structure](#), program for using multi-locus genotype data to investigate population structure.

## Documentation

- 2012 - [Python101 Course Slides and Material](#)

## Design skills

### Posters designed

- 2012 - Poster for the course "[Python 101: by biologists for biologists](#)"
- 2010 - Poster for the "[Pós Graduação em Biodiversidade Adaptação e Alterações Globais](#)"

### Logos designed

- 2014 - Logo for the [bionode](#) Node.js module made with [Adobe Illustrator](#).
- 2010 - Logo for the [Computational Biology & Population Genomics Group \(CoBiG<sup>2</sup>\)](#) made with [Blender](#) and [Gimp](#).

## Musical skills

- Piano (4th degree) at the [Lisbon National Conservatory of Music](#)

## Sports skills

- Kung Fu (Choy Lee Fut) from 2007 to 2008 (6 months) and Karate during childhood