BRUNO VIEIRA

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 Full CV: github.com/bmpvieira/bmpvieira/blob/main/cv.md

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've 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.

Main tech used: TypeScript, React, AWS, K8S, Docker, Podman, Nix, Microservices, Nginx, MongoDB, Redis, GCP, Azure, Terraform, Packer, Hadoop, OpenAPI

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

Main tech used: Nix, NodeJS, Python, Dask, PyTorch, Bioinformatics

2018 (1 month) - Stencila.io via Code for Science and Society | Developer
Data-driven interactive documents. I worked on a docker tool for researchers.
Tech: Nix and Docker

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.
Tech: 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.

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.
Tech: NodeJS Streams, Bioinformatics, NCBI API

2014 - Dat project | Consultant
Distributed data protocol. I advised for potential genetic data use cases and applications.
Tech: NodeJS Streams

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.
Tech: NodeJS, MongoDB

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.
Tech used: NodeJS, Express.js, MongoDB, Coffee Script, Jade, Twitter Bootstrap, jQuery.

2009-2013 (4 years) - CoBiG² 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).
Tech: Bioinformatics, Python, R, Arch Linux (btw), AngularJS

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've submitted my thesis but not defended it yet.

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.