

TGAC - AllBio 2014

Who

bmpvieira.com/allbio2014

Bruno Vieira |  [@bmpvieira](https://twitter.com/bmpvieira)

Phd Student @  Queen Mary
University of London

Bioinformatics and
Population Genomics



Supervisor:

Yannick Wurm |  [@yannick__](https://twitter.com/yannick__)

Before

2004-2009

Master in Human Biology and Environment
Licentiate in Cell Biology and Biotechnology



2009-2013

Bioinformatician and SysAdmin



**Computational
Biology & Population
Genomics Group**

2012-2013

Full Stack Web Developer - Built everything with
Node.js, Express.js, Bootstrap, MongoDB and Redis



2013

Full Stack Web Developer - Worked on integration
with LinkedIn API



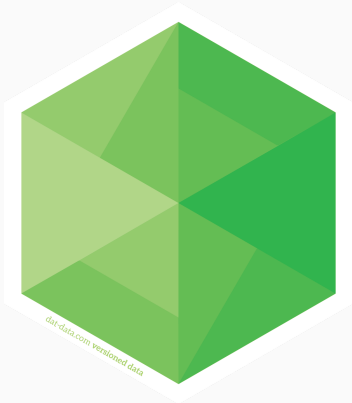
What

Bionode.io – *Modular and universal bioinformatics*

Pipeable UNIX command line tools and
JavaScript / Node.js APIs for bioinformatic
analysis workflows on the server and browser.



Collaborates with **BioJS** – *Represent biological data on the web*



Dat – *Build data pipelines*

Provides a streaming interface between every file
format and data storage backend. *"git for data"*

Why Bionode / Why Node.js?

- Reusable, small and tested modules
- Same language everywhere (JavaScript)
- JavaScript is **fast enough**
- Package Manager that works (**NPM**)
- Huge number modules (**93327, 199/day**)
- Use other JS projects (**Dat, BioJS, NoFlo**)
- **Streams** applies well to Bioinformatics
- Easy to write CLI wrappers for Streams
- Possible to write Desktop GUI apps in JS