

TGAC - AllBio 2014

Who

bmpvieira.com/allbio2014

Bruno Vieira |  @bmpvieira

Phd Student @  Queen Mary
University of London

Bioinformatics and
Population Genomics



Supervisor:

Yannick Wurm |  @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



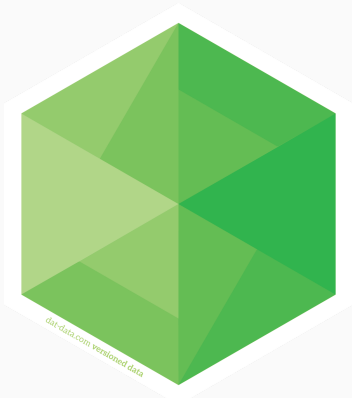
What

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"*

dat-data.com |  [@maxogden](https://twitter.com/maxogden) |  [@mafintosh](https://twitter.com/mafintosh)

Why Bionode / 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