

# TGAC - AllBio 2014

[bmpvieira.com/allbio14](http://bmpvieira.com/allbio14)

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Before:



Computational  
Biology & Population  
Genomics Group



geeklist  BBSRC



# Some problems I faced during my research:

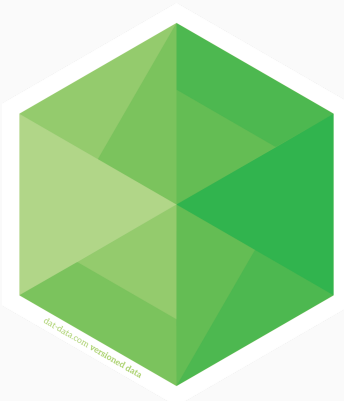
- Difficulty getting relevant descriptions and datasets from NCBI API using bio\* libs
  - For web projects, needed to implement the same functionality on browser and server
  - Difficulty writing scalable, reproducible and complex bioinformatic pipelines
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# 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](http://dat-data.com) |  [@maxogden](https://twitter.com/maxogden) |  [@mafintosh](https://twitter.com/mafintosh)

# bionode.io (online shell)

## Examples

### BASH

```
bionode-ncbi urls assembly Solenopsis invicta | grep genomic.fna
```

```
http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA\_000188075.1\_Si\_gnG/  
GCA\_000188075.1\_Si\_gnG\_genomic.fna.gz
```

```
bionode-ncbi download sra arthropoda | bionode-sra
```

```
bionode-ncbi download gff bacteria
```

### JavaScript

```
var ncbi = require('bionode-ncbi')  
ncbi.urls('assembly', 'Solenopsis invicta'), gotData)  
function gotData(urls) {  
  var genome = urls[0].genomic.fna  
  download(genome)  
})
```