bmpvieira.com

#bionodehack

BIONODE.IO

Introduction

github.com/bionode-hack/discussions

gitter.im/bionode-hack/discussions

WHAT

Modular and universal bioinformatics

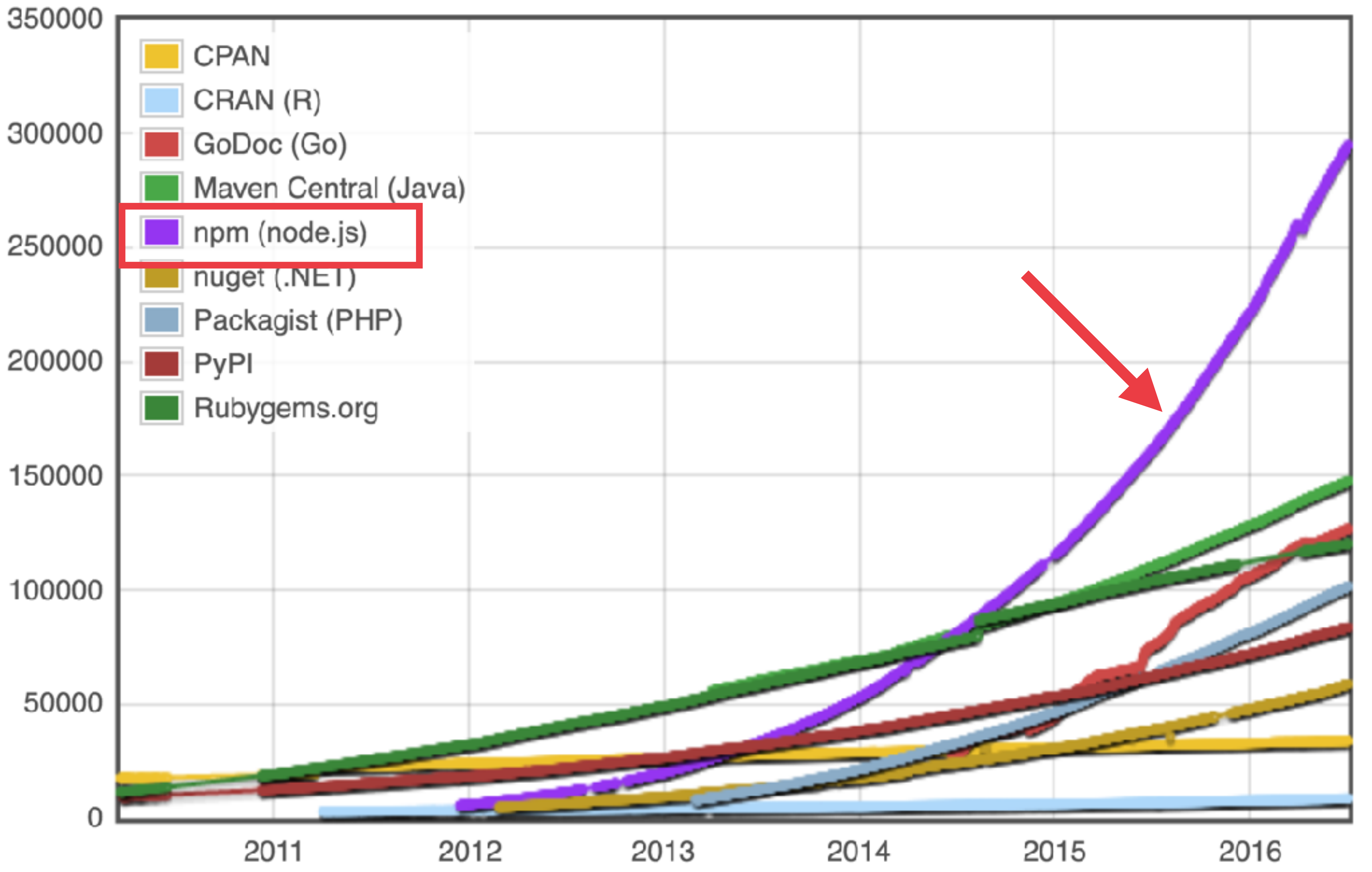
- Tries to do one thing well
- Provides highly reusable code and tools
- Scales by using Streams
- Runs everywhere

HOW

Using Node.js

- 👆 Highly modular
- ♻️ Very open community on GitHub

Modules count



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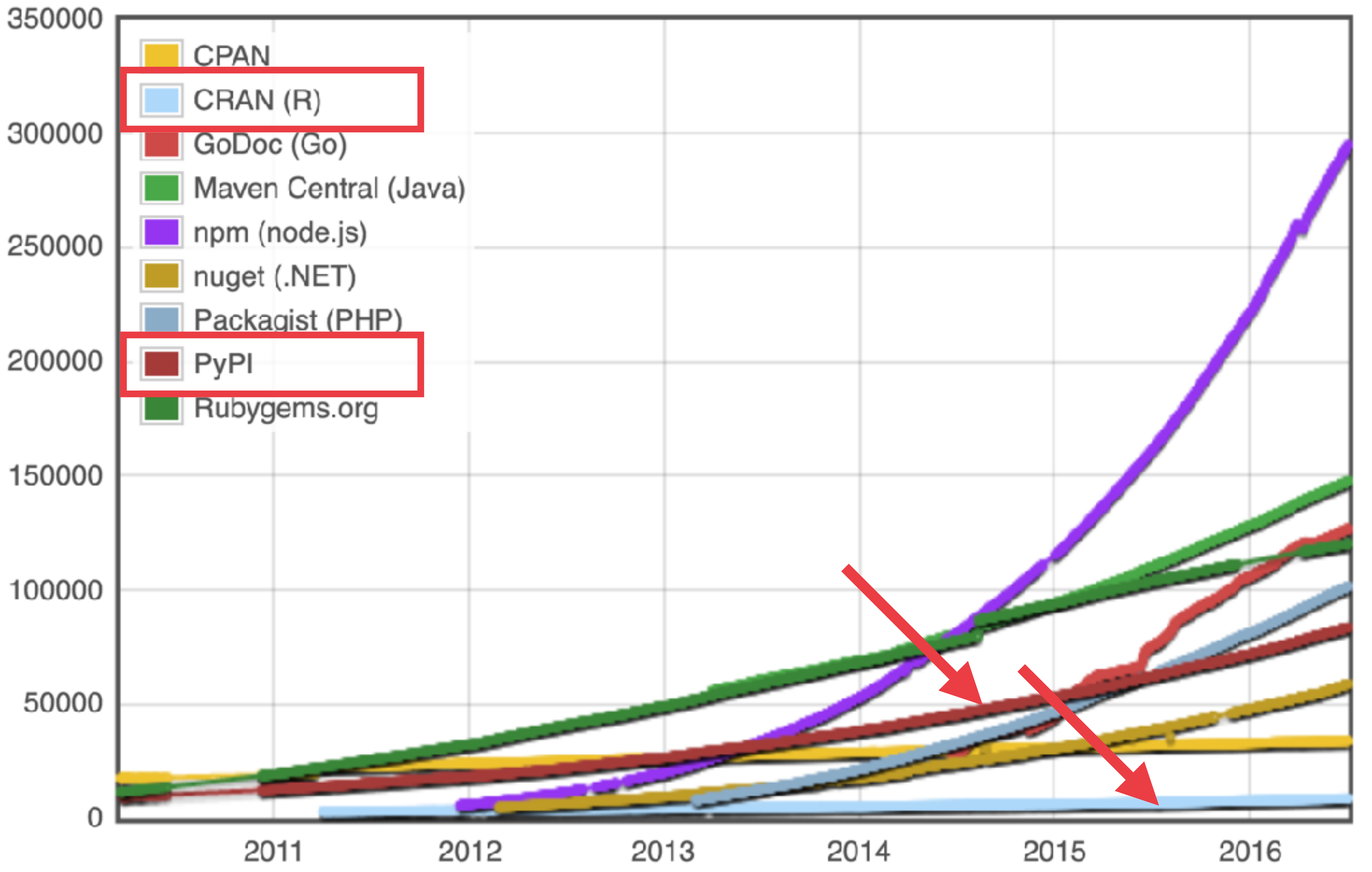
bit.ly/biohack16

Modules count



HOW

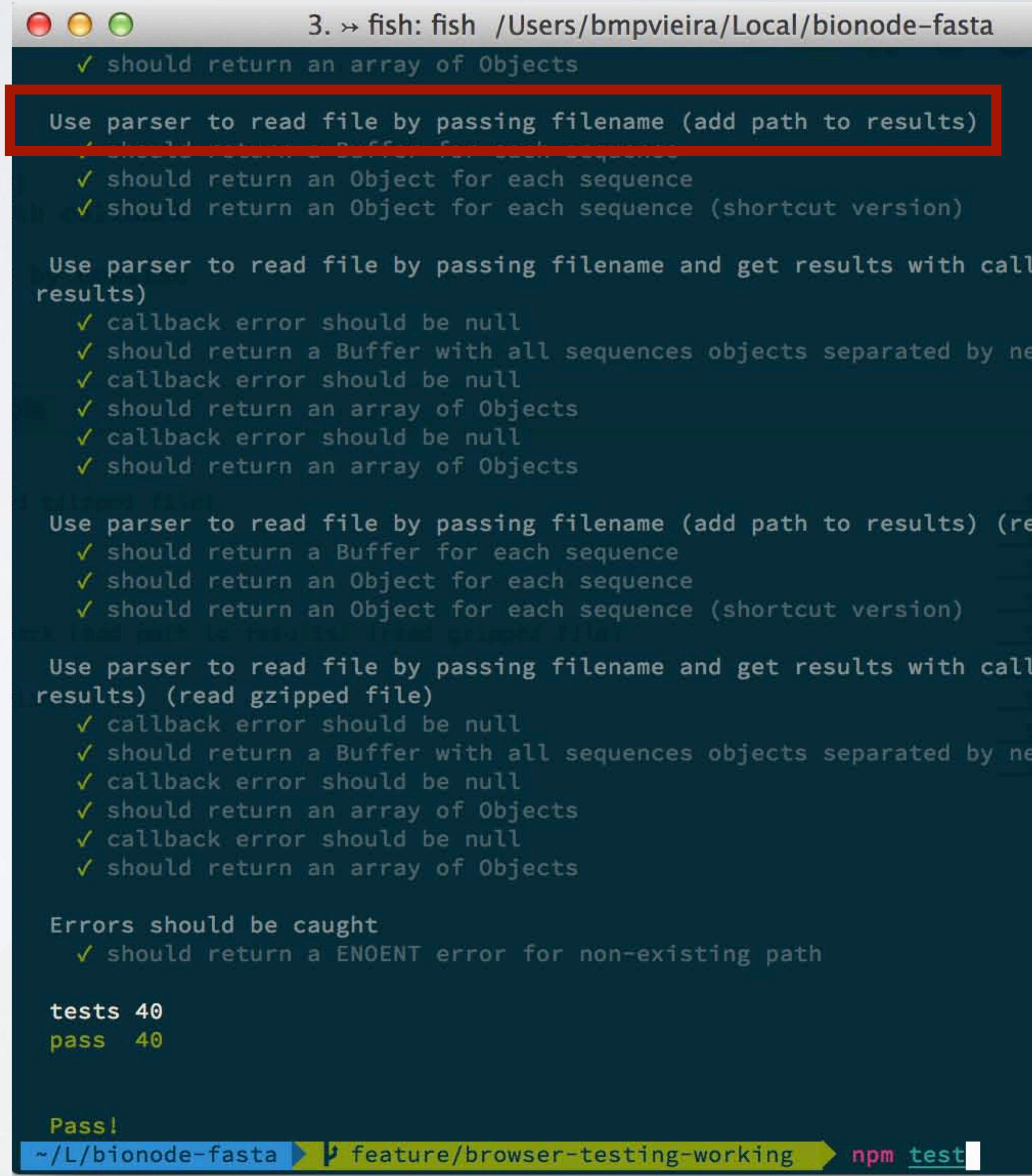
Using Node.js

- Highly modular
- Very open community on GitHub
- Provides native implementation of Streams
- Run same JavaScript code on browser or CLI

Run same JavaScript code on browser or CLI

FASTA file format
> X-gene
ATGCGTACTGCATCATG
ACGTACTGCATTCATGC
GTGCTAGGGGTTTACGT

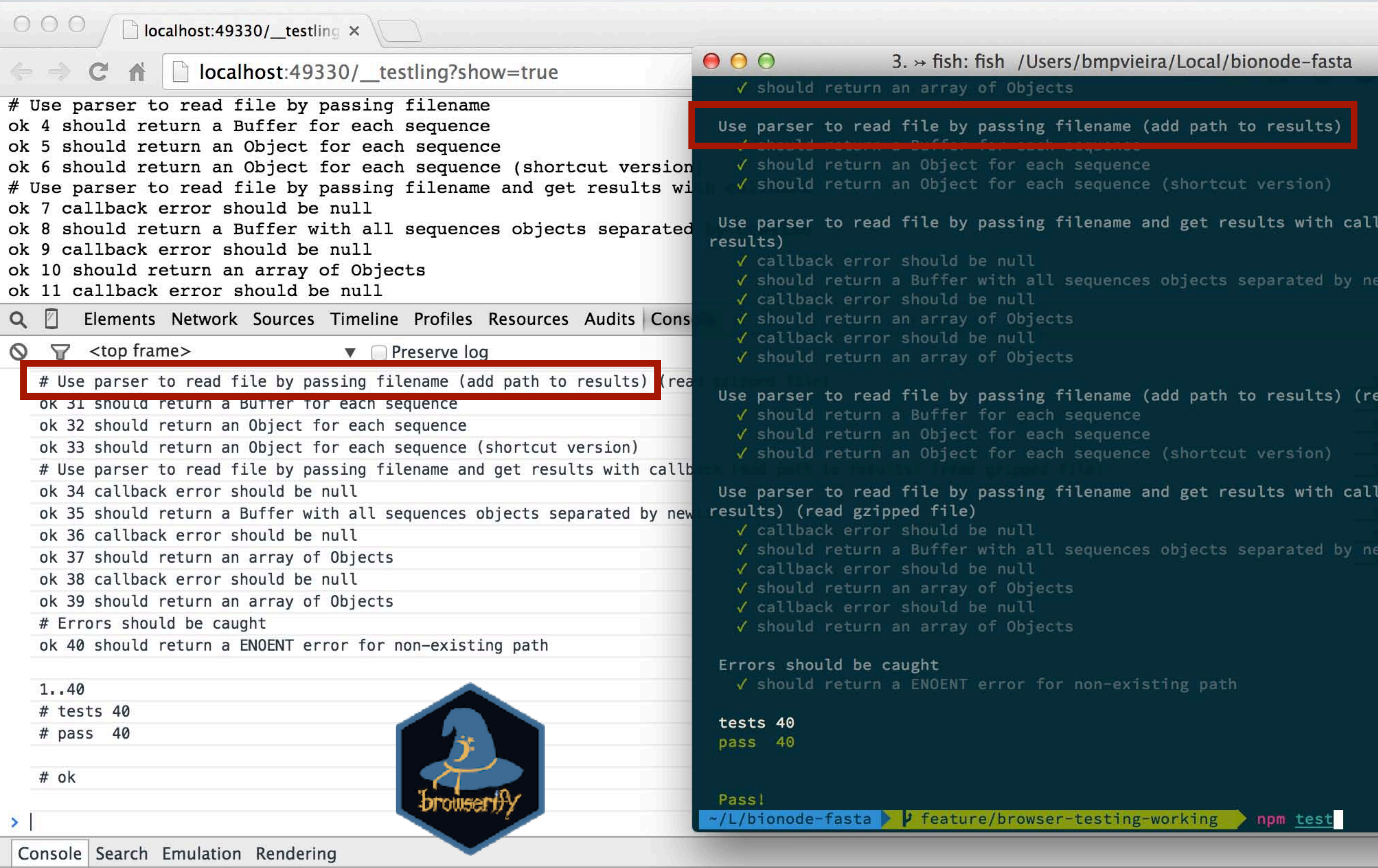
JSON (JavaScript Object Notation)
{
 "id": "X-gene",
 "seq": "ATGCGTACTGCATCAT
GACGTACTGCATTCATGCGTG
CTAGGGGTTTACGT"
}



3. ↣ fish: fish /Users/bmpvieira/Local/bionode-fasta

```
    ✓ should return an array of Objects

  Use parser to read file by passing filename (add path to results)
    ✓ should return a Buffer for each sequence
    ✓ should return an Object for each sequence
    ✓ should return an Object for each sequence (shortcut version)

  Use parser to read file by passing filename and get results with call
 results)
    ✓ callback error should be null
    ✓ should return a Buffer with all sequences objects separated by ne
    ✓ callback error should be null
    ✓ should return an array of Objects
    ✓ callback error should be null
    ✓ should return an array of Objects

  Use parser to read file by passing filename (add path to results) (re
    ✓ should return a Buffer for each sequence
    ✓ should return an Object for each sequence
    ✓ should return an Object for each sequence (shortcut version)

  Use parser to read file by passing filename and get results with call
 results) (read gzipped file)
    ✓ callback error should be null
    ✓ should return a Buffer with all sequences objects separated by ne
    ✓ callback error should be null
    ✓ should return an array of Objects
    ✓ callback error should be null
    ✓ should return an array of Objects

  Errors should be caught
    ✓ should return a ENOENT error for non-existing path

  tests 40
  pass  40


  Pass!
 ~/L/bionode-fasta  feature/browser-testing-working  npm test
```

Run same JavaScript code on browser or CLI


localhost:49330/__testling
localhost:49330/__testling?show=true
Elements Network Sources Timeline Profiles Resources Audits Cons
<top frame>
Preserve log
Console Search Emulation Rendering
browserify
3. ↣ fish: fish /Users/bmpvieira/Local/bionode-fasta

```
# Use parser to read file by passing filename
ok 4 should return a Buffer for each sequence
ok 5 should return an Object for each sequence
ok 6 should return an Object for each sequence (shortcut version
# Use parser to read file by passing filename and get results wi
ok 7 callback error should be null
ok 8 should return a Buffer with all sequences objects separated
ok 9 callback error should be null
ok 10 should return an array of Objects
ok 11 callback error should be null
```

```
# Use parser to read file by passing filename (add path to results) (rea
ok 31 should return a Buffer for each sequence
ok 32 should return an Object for each sequence
ok 33 should return an Object for each sequence (shortcut version)
# Use parser to read file by passing filename and get results with callb
ok 34 callback error should be null
ok 35 should return a Buffer with all sequences objects separated by new
ok 36 callback error should be null
ok 37 should return an array of Objects
ok 38 callback error should be null
ok 39 should return an array of Objects
# Errors should be caught
ok 40 should return a ENOENT error for non-existing path

1..40
# tests 40
# pass  40

# ok
```

```
  ✓ should return an array of Objects

Use parser to read file by passing filename (add path to results)
  ✓ should return a Buffer for each sequence
  ✓ should return an Object for each sequence
  ✓ should return an Object for each sequence (shortcut version)

Use parser to read file by passing filename and get results with call
results)
  ✓ callback error should be null
  ✓ should return a Buffer with all sequences objects separated by ne
  ✓ callback error should be null
  ✓ should return an array of Objects
  ✓ callback error should be null
  ✓ should return an array of Objects

Use parser to read file by passing filename (add path to results) (re
  ✓ should return a Buffer for each sequence
  ✓ should return an Object for each sequence
  ✓ should return an Object for each sequence (shortcut version)

Use parser to read file by passing filename and get results with call
results) (read gzipped file)
  ✓ callback error should be null
  ✓ should return a Buffer with all sequences objects separated by ne
  ✓ callback error should be null
  ✓ should return an array of Objects
  ✓ callback error should be null
  ✓ should return an array of Objects

Errors should be caught
  ✓ should return a ENOENT error for non-existing path

tests 40
pass  40


Pass!
~/L/bionode-fasta  feature/browser-testing-working  npm test
```

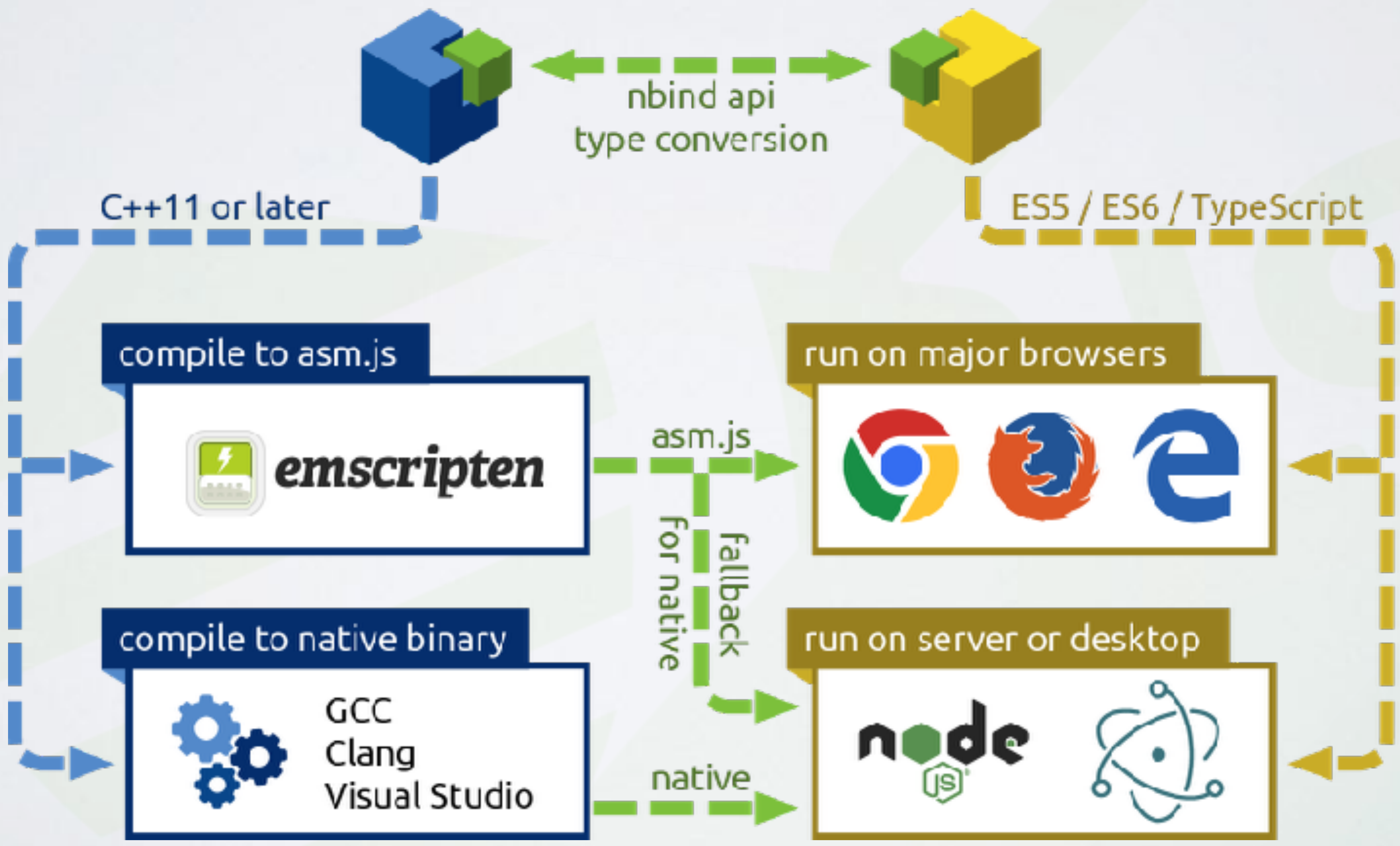
Run same JavaScript code on browser or CLI

JavaScript not suitable for heavy scientific computation?

C++ preferred?

Run C++ from JavaScript

#include nbind in C++ & call effortlessly from JavaScript without changes.



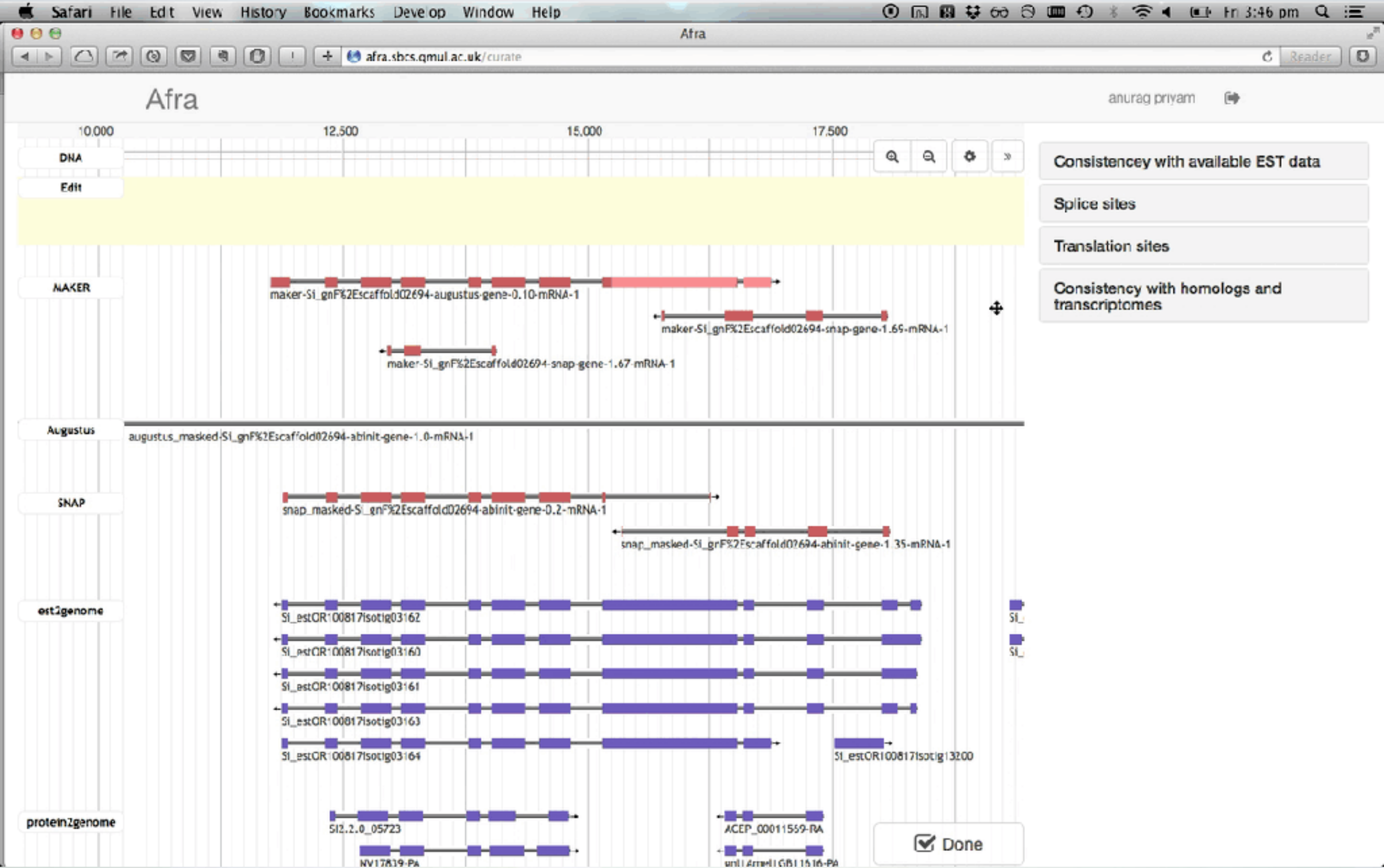
ORIGIN

During my PhD at

- Involved in biological web projects that need JS

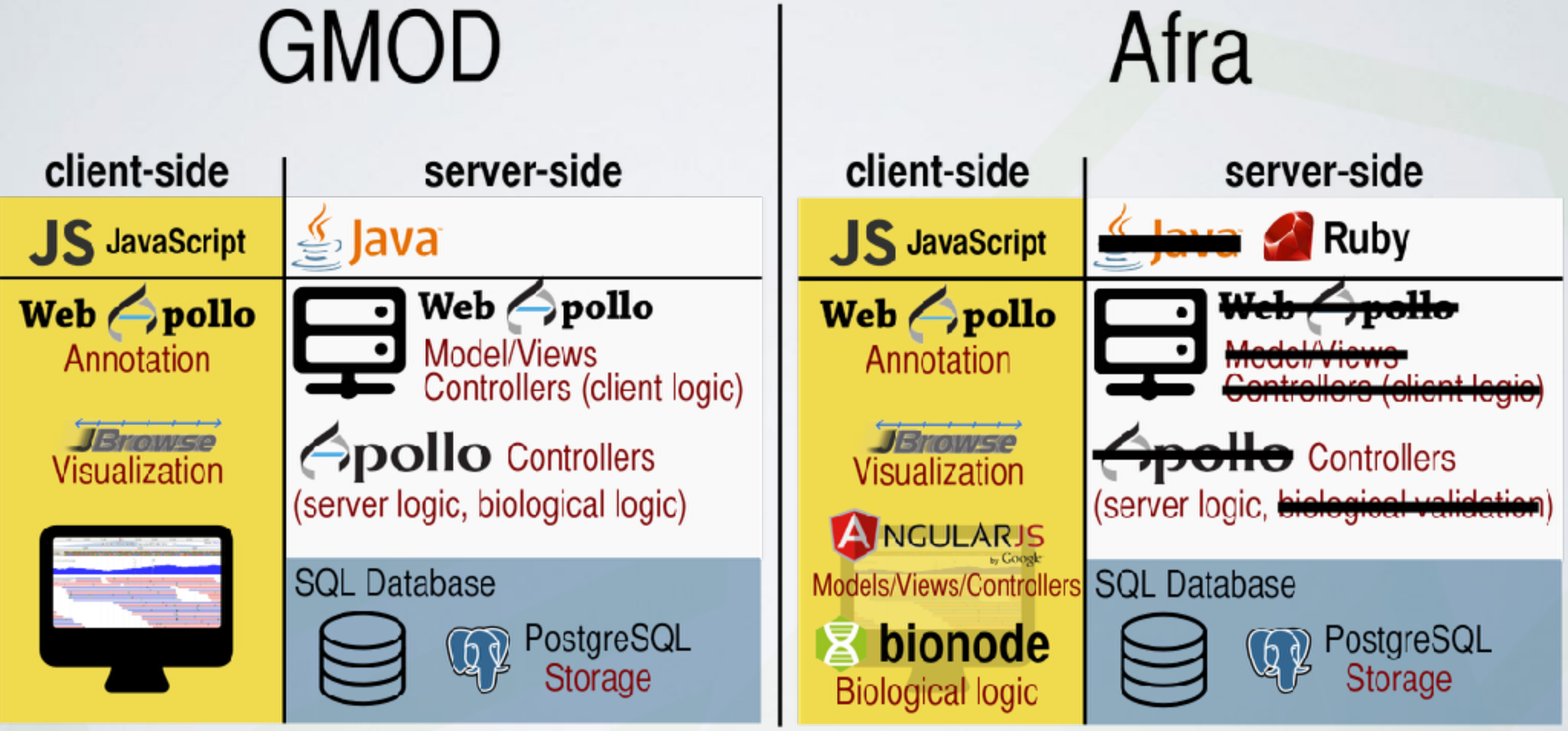
Involved in biological web projects that need JS

wurmlab.github.io

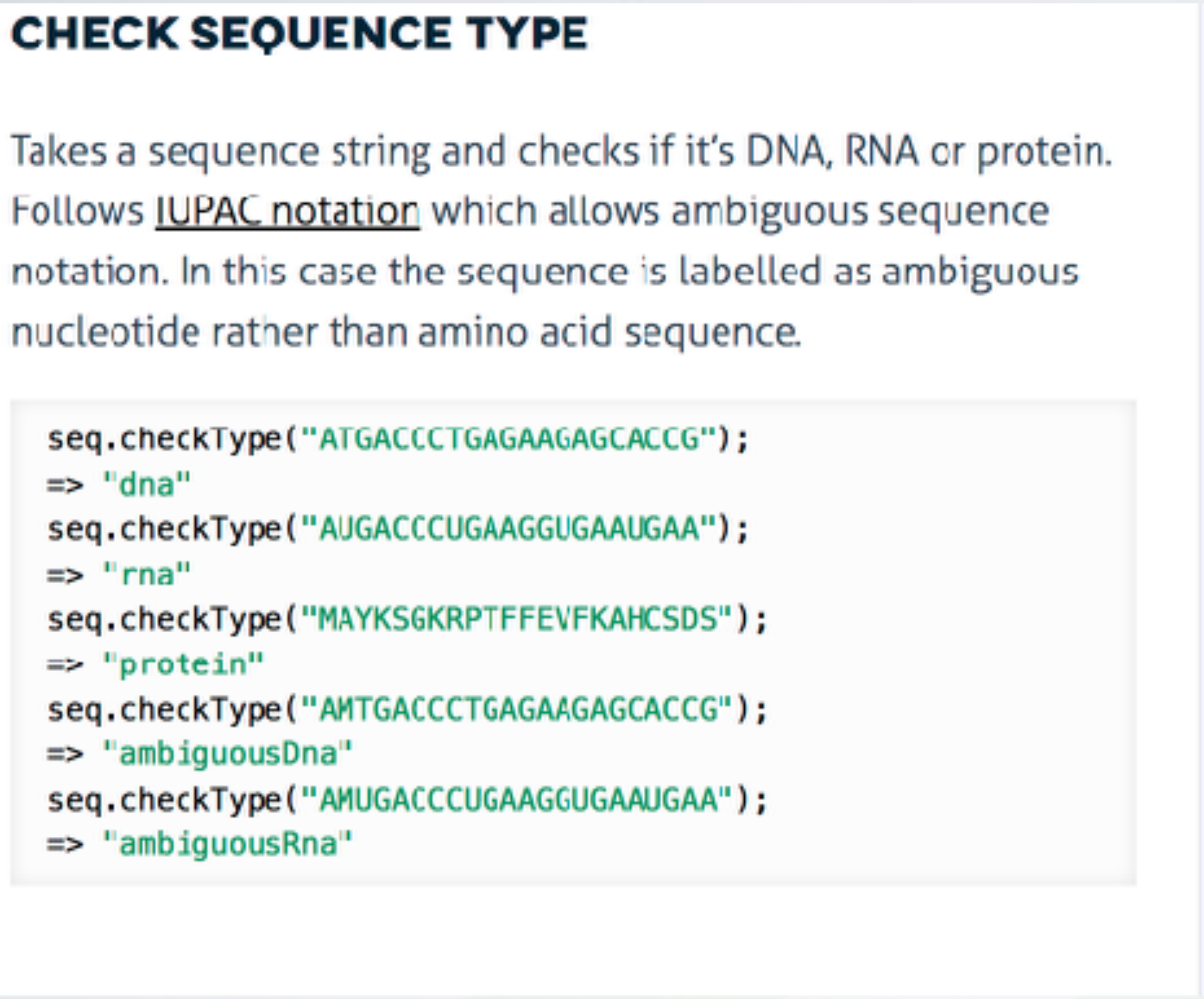

Safari File Edit View History Bookmarks Develop Window Help
Fri 3:46 pm
Afra
afra.sbcs.qmul.ac.uk/curate
Reader
Afra
anurag priyam
10,000
12,500
15,000
17,500
DNA
Edit
MAKER
maker-SI_gnF%2Escaffold02694-augustus-gene-0.10-mRNA-1
maker-SI_gnF%2Escaffold02694-snap-gene-1.65-mRNA-1
maker-SI_gnF%2Escaffold02694-snap-gene-1.67-mRNA-1
Augustus
augustus_masked-SI_gnF%2Escaffold02694-abinit-gene-1.0-mRNA-1
SNAP
snap_masked-SI_gnF%2Escaffold02694-abinit-gene-0.2-mRNA-1
snap_masked-SI_gnF%2Escaffold02694-abinit-gene-1.35-mRNA-1
est2genome
SI_estOR100817isotig03162
SI_estOR100817isotig03160
SI_estOR100817isotig03161
SI_estOR100817isotig03163
SI_estOR100817isotig03164
SI_estOR100817isotig13200
protein2genome
SI2.2.0_05723
NV17839-PA
ACEP_00011559-RA
Done
Consistencey with available EST data
Splice sites
Translation sites
Consistency with homologs and transcriptomes

Involved in biological web projects that need JS

wurmlab.github.io



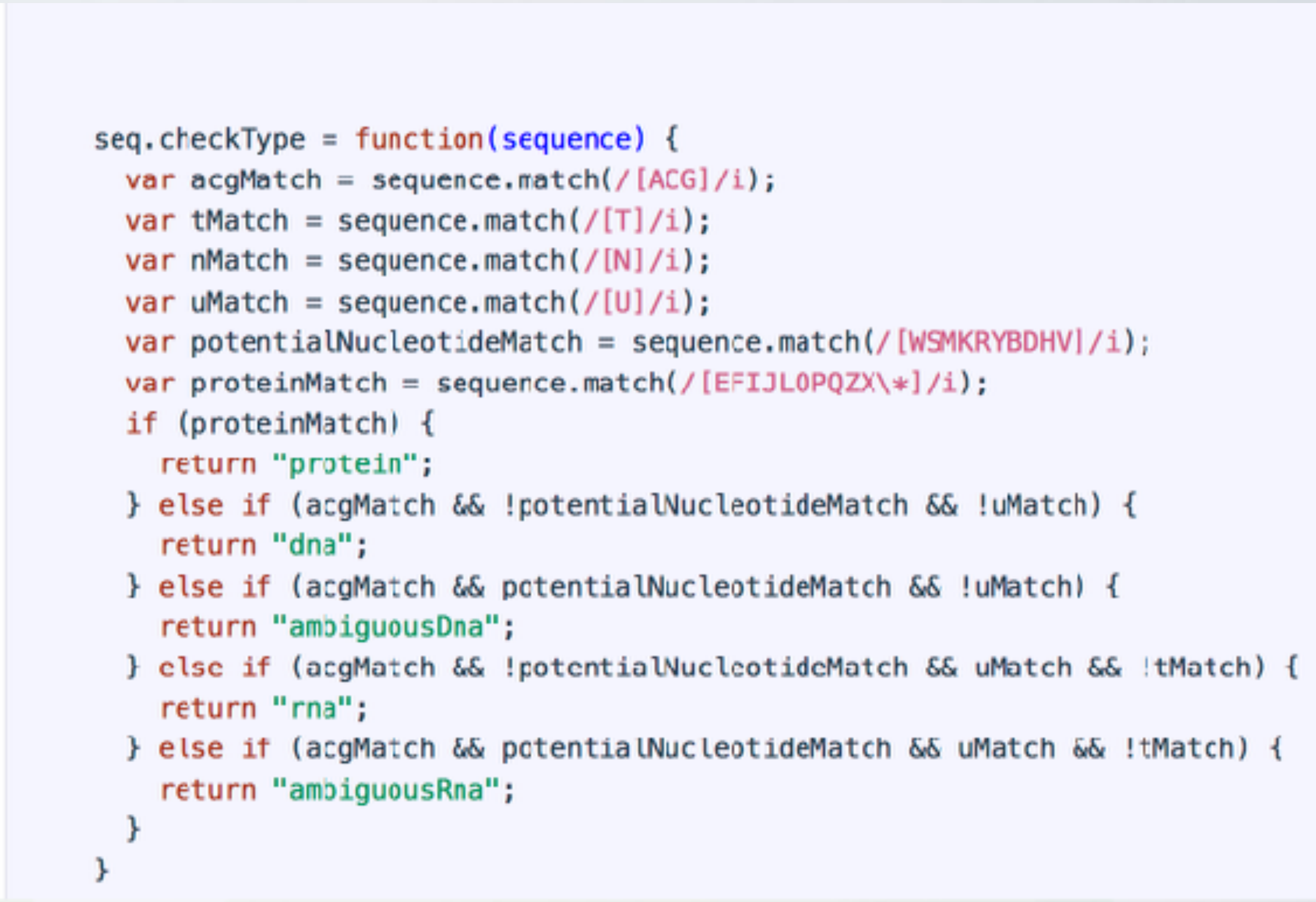
bionode-seq



CHECK SEQUENCE TYPE

Takes a sequence string and checks if it's DNA, RNA or protein. Follows IUPAC notation which allows ambiguous sequence notation. In this case the sequence is labelled as ambiguous nucleotide rather than amino acid sequence.

```
seq.checkType("ATGACCCTGAGAAGAGCACCG");
=> "dna"
seq.checkType("AUGACCCUGAAGGUGAAUGAA");
=> "rna"
seq.checkType("MAYKSGKRPTFFEVFKAHCSDS");
=> "protein"
seq.checkType("AMTGACCCTGAGAAGAGCACCG");
=> "ambiguousDna"
seq.checkType("AMUGACCCUGAAGGUGAAUGAA");
=> "ambiguousRna"
```



```
seq.checkType = function(sequence) {
  var acgMatch = sequence.match(/[ACG]/i);
  var tMatch = sequence.match(/[T]/i);
  var nMatch = sequence.match(/[N]/i);
  var uMatch = sequence.match(/[U]/i);
  var potentialNucleotideMatch = sequence.match(/[WSMKRYBDHV]/i);
  var proteinMatch = sequence.match(/[EFIJLOPQZX\*]/i);
  if (proteinMatch) {
    return "protein";
  } else if (acgMatch && !potentialNucleotideMatch && !uMatch) {
    return "dna";
  } else if (acgMatch && potentialNucleotideMatch && !uMatch) {
    return "ambiguousDna";
  } else if (acgMatch && !potentialNucleotideMatch && uMatch && !tMatch) {
    return "rna";
  } else if (acgMatch && potentialNucleotideMatch && uMatch && !tMatch) {
    return "ambiguousRna";
  }
}
```

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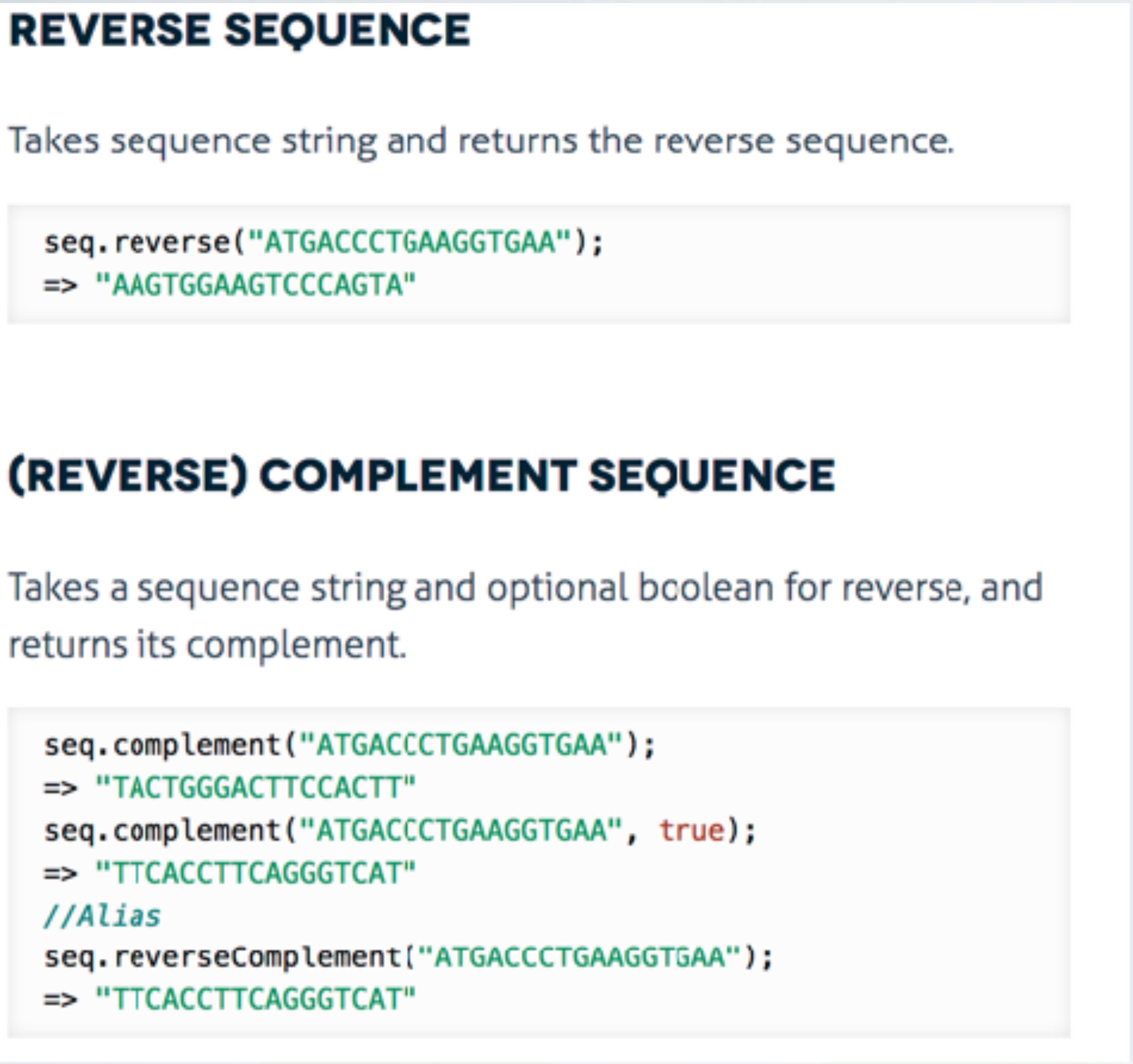
bionode-seq

#bionodehack



REVERSE SEQUENCE

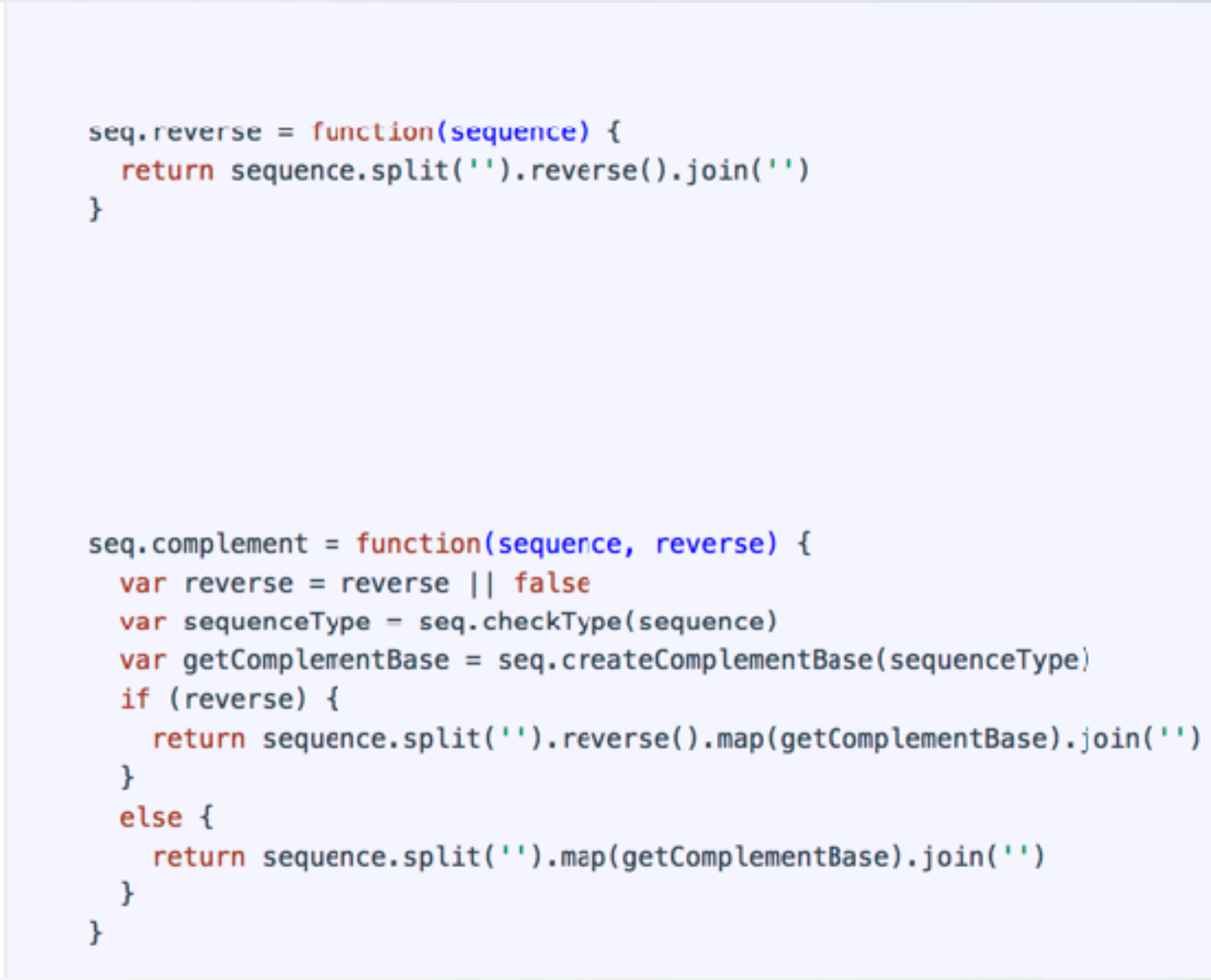
Takes sequence string and returns the reverse sequence.

```
seq.reverse("ATGACCCTGAAGGTGAA");
=> "AAGTGGAAGTCCCAGTA"
```

(REVERSE) COMPLEMENT SEQUENCE

Takes a sequence string and optional boolean for reverse, and returns its complement.

```
seq.complement("ATGACCCTGAAGGTGAA");
=> "TACTGGGACTTCCACTT"
seq.complement("ATGACCCTGAAGGTGAA", true);
=> "TTCACCTTCAGGGTCAT"
//Alias
seq.reverseComplement("ATGACCCTGAAGGTGAA");
=> "TTCACCTTCAGGGTCAT"
```



```
seq.reverse = function(sequence) {
  return sequence.split('').reverse().join('')
}
```

```
seq.complement = function(sequence, reverse) {
  var reverse = reverse || false
  var sequenceType = seq.checkType(sequence)
  var getComplementBase = seq.createComplementBase(sequenceType)
  if (reverse) {
    return sequence.split('').reverse().map(getComplementBase).join('')
  }
  else {
    return sequence.split('').map(getComplementBase).join('')
  }
}
```

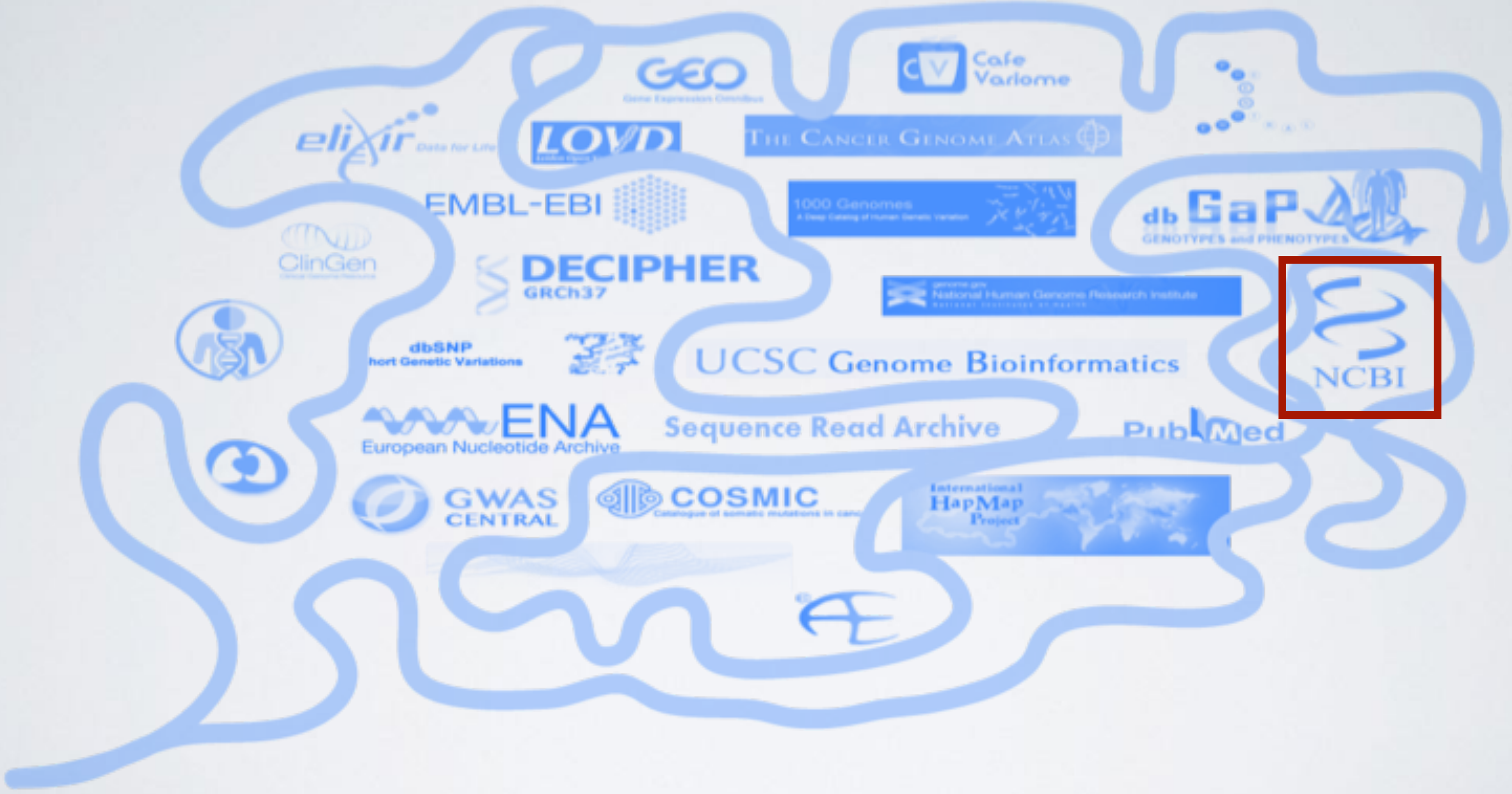
ORIGIN

During my PhD at

- Involved in biological web projects that need JS
- Had to find and get TB of data online

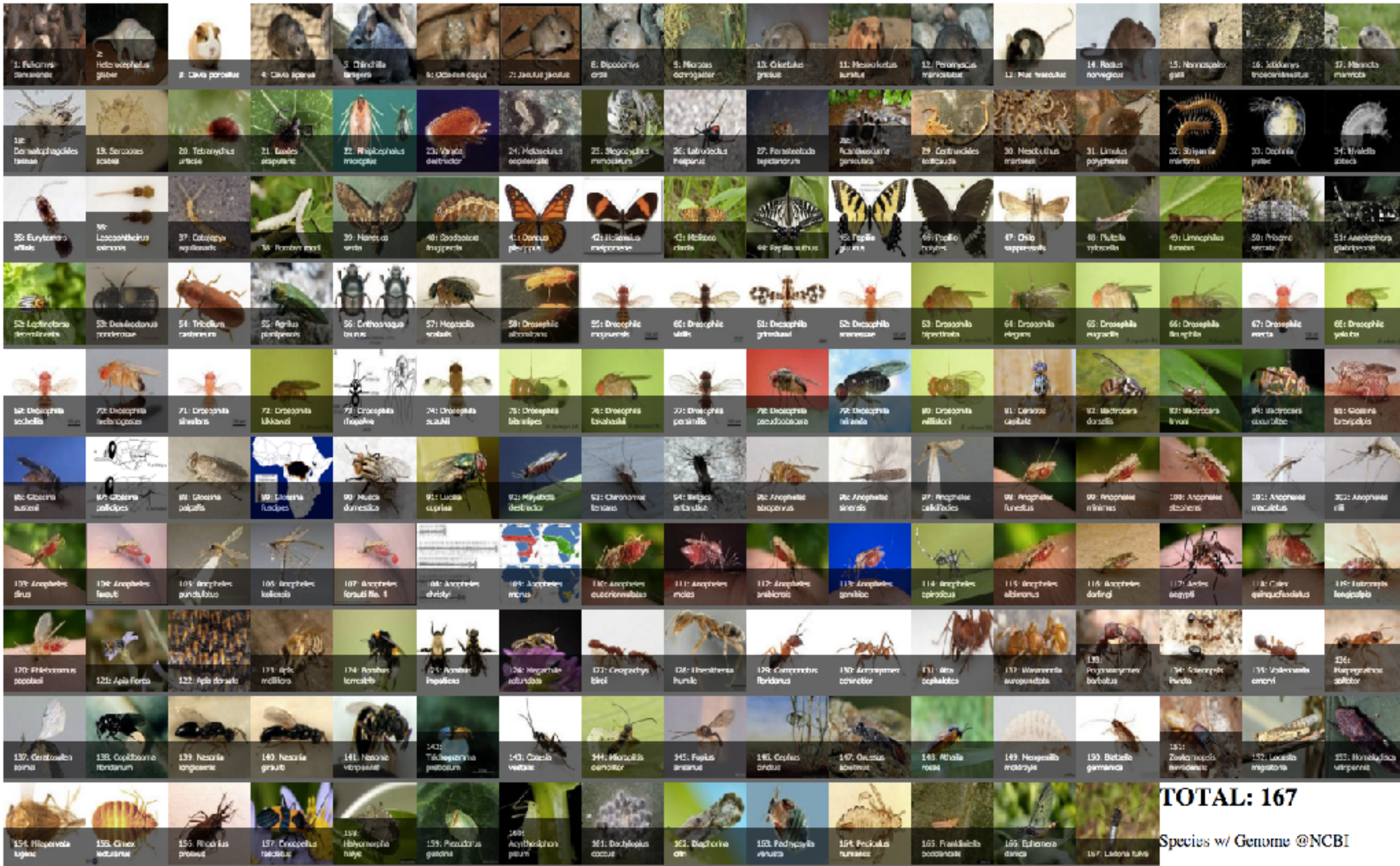
Compare genetic diversity of social vs solitary species

Maze of data sources



Had to find and get TB of data online

All Insects and Rodents



Had to find and get TB of data online
Social (red) - Solitary (blue)

TOTAL: 167

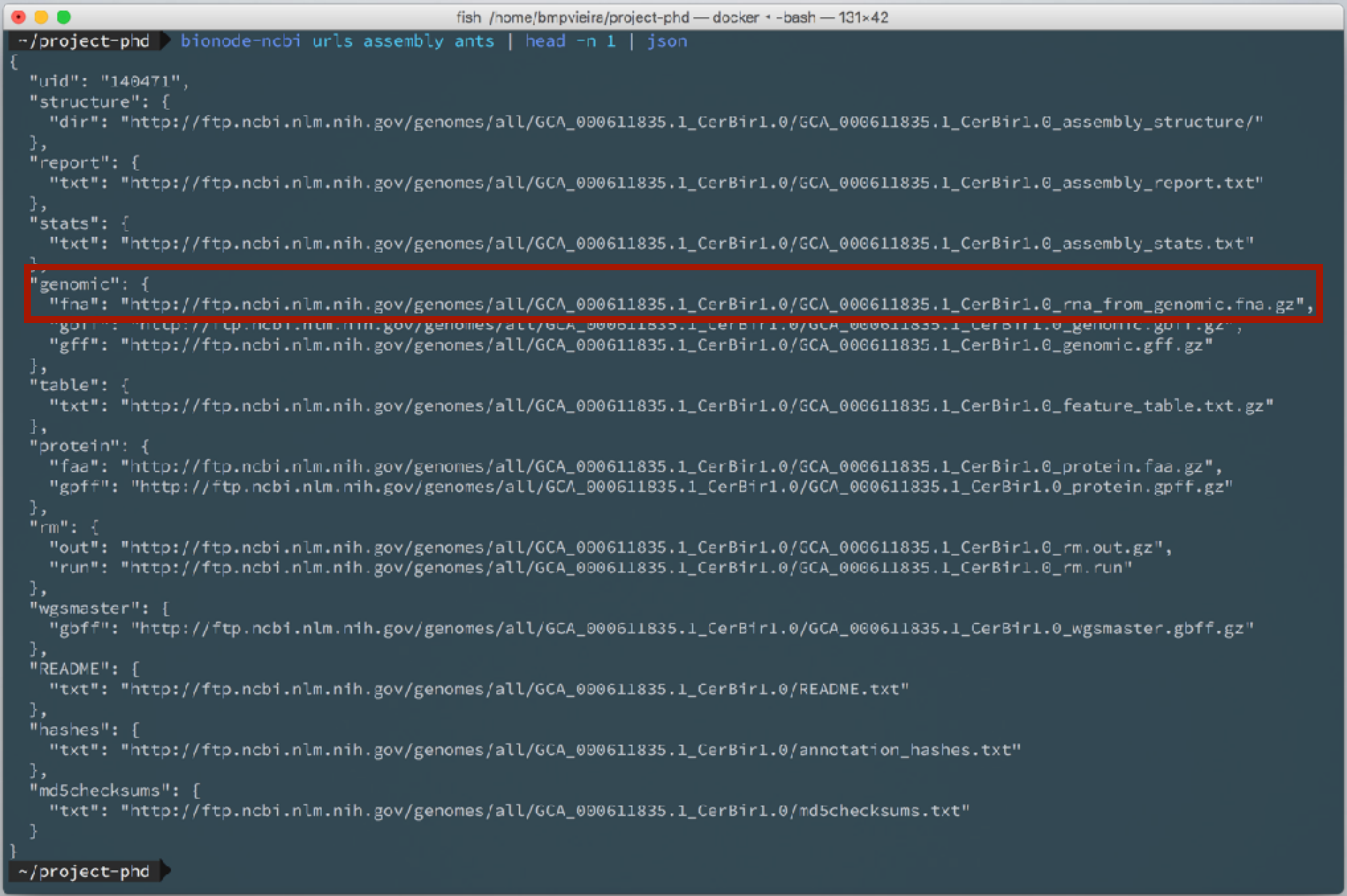
Blue solitary, Red social

bionode-ncbi

How to get the URLs for genomic dataset?

for example raw data of genome assembly:

ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000188075.1_Si_gnG



fish /home/bmpvieira/project-phd — docker ◂ -bash — 131×42

```
~/project-phd  bionode-ncbi urls assembly ants | head -n 1 | json
{
  "uid": "140471",
  "structure": {
    "dir": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_assembly_structure/"
  },
  "report": {
    "txt": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_assembly_report.txt"
  },
  "stats": {
    "txt": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_assembly_stats.txt"
  },
  "genomic": {
    "fna": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_rna_from_genomic.fna.gz",
    "gbff": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_genomic.gbff.gz",
    "gff": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_genomic.gff.gz"
  },
  "table": {
    "txt": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_feature_table.txt.gz"
  },
  "protein": {
    "faa": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_protein.faa.gz",
    "gpff": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_protein.gpff.gz"
  },
  "rm": {
    "out": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_rm.out.gz",
    "run": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_rm.run"
  },
  "wgsmaster": {
    "gbff": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/GCA_000611835.1_CerBir1.0_wgsmaster.gbff.gz"
  },
  "README": {
    "txt": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/README.txt"
  },
  "hashes": {
    "txt": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/annotation_hashes.txt"
  },
  "md5checksums": {
    "txt": "http://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000611835.1_CerBir1.0/md5checksums.txt"
  }
}
~/project-phd
```

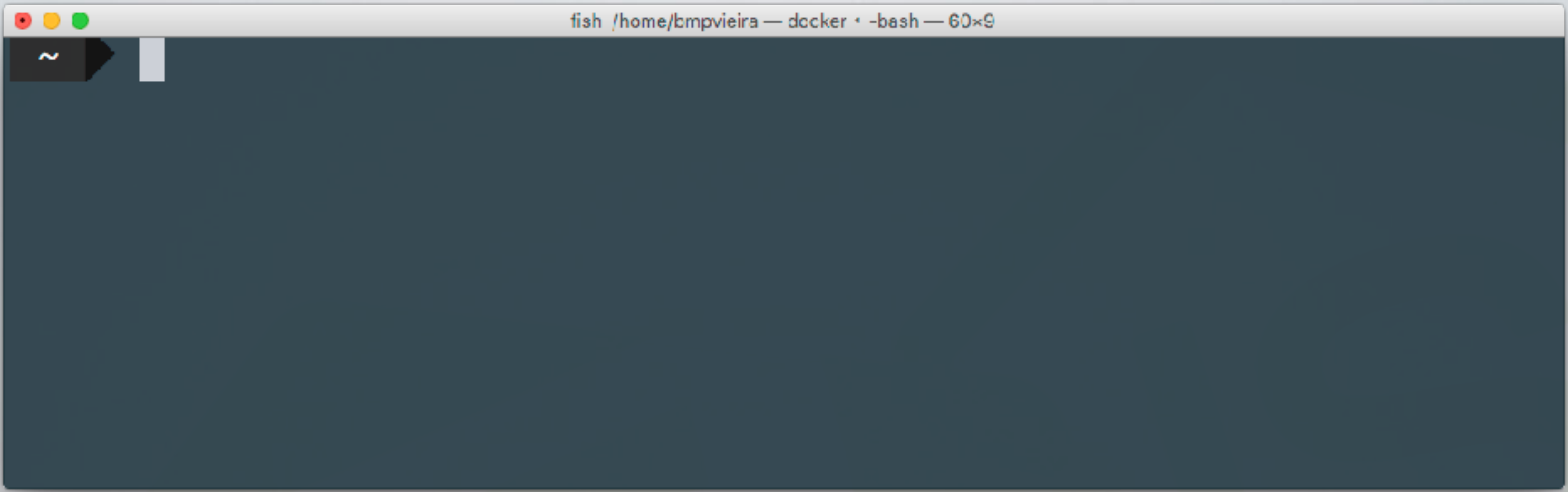
bionode-ncbi

```
var bio = require('bionode')

// Callback pattern
bio.ncbi.urls('assembly', 'ants', function(urls) {
  console.log(urls[0].genomic.fna)
})


// Event pattern
bio.ncbi.urls('assembly', ‘ants’)
.on('data', printGenomeURL)

function printGenomeURL(urls) {
  console.log(urls[0].genomic.fna)
})
```

bionode-ncbi

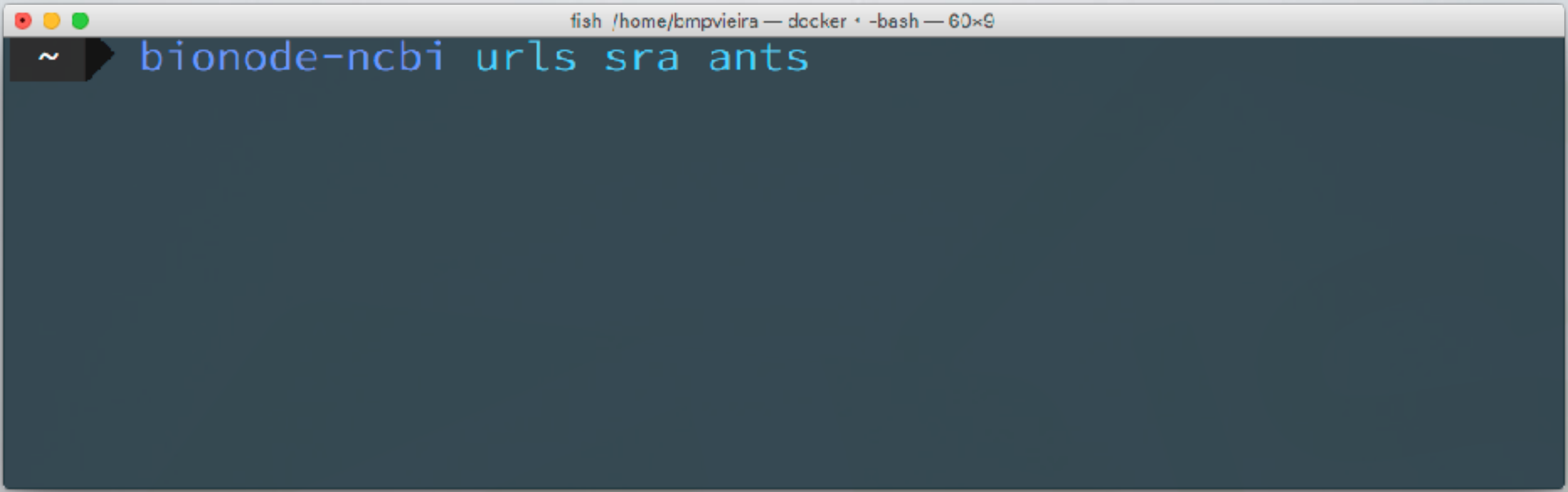
```
// Pipe pattern
var ncbi = require('bionode-ncbi')
var ndjson = require(‘ndjson')

ncbi.urls('genomes', 'ants')
.pipe(ndjson.stringify())
.pipe(process.stdout)
```

bionode-ncbi



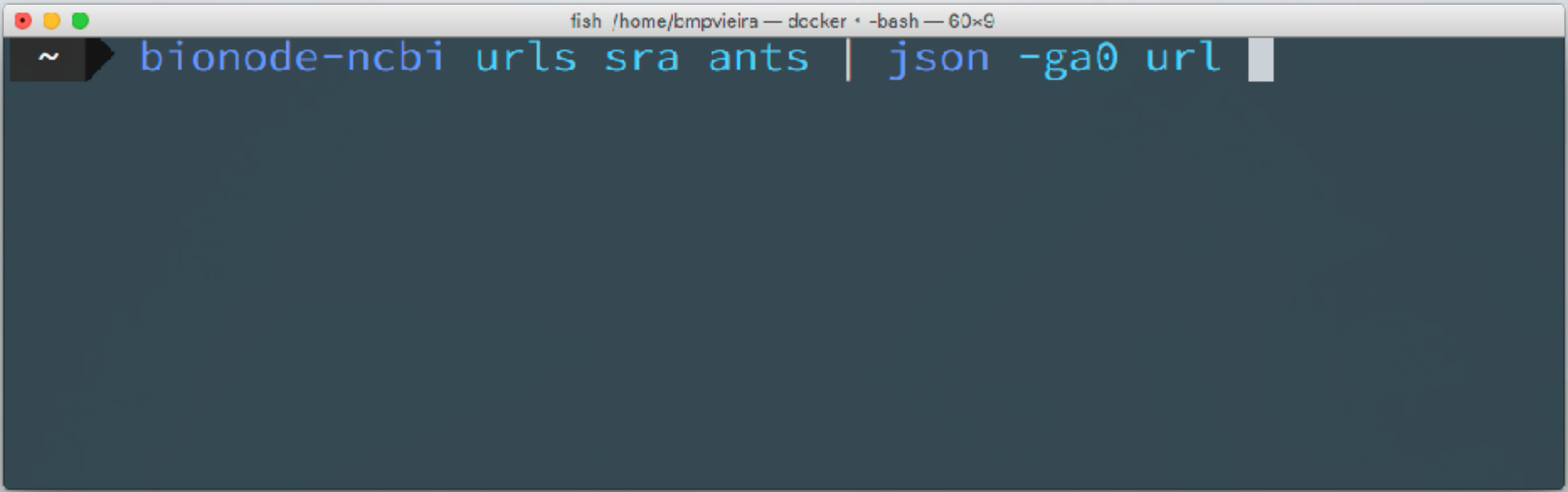
```
~
```

bionode-ncbi



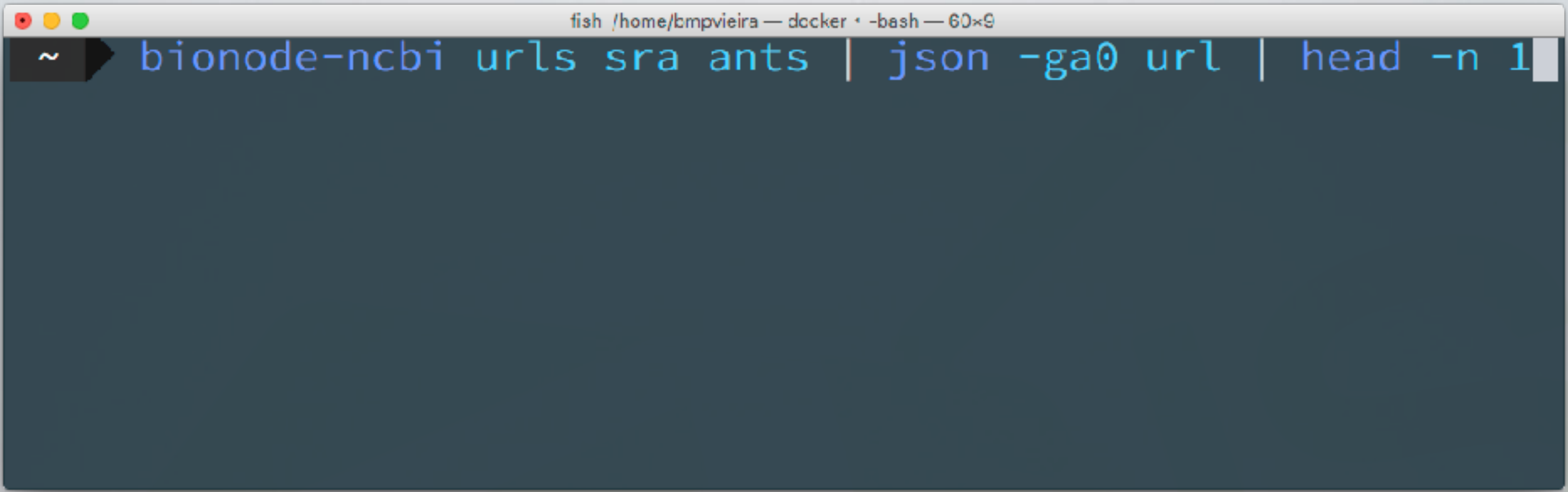
```
~ bionode-ncbi urls sra ants
```

bionode-ncbi



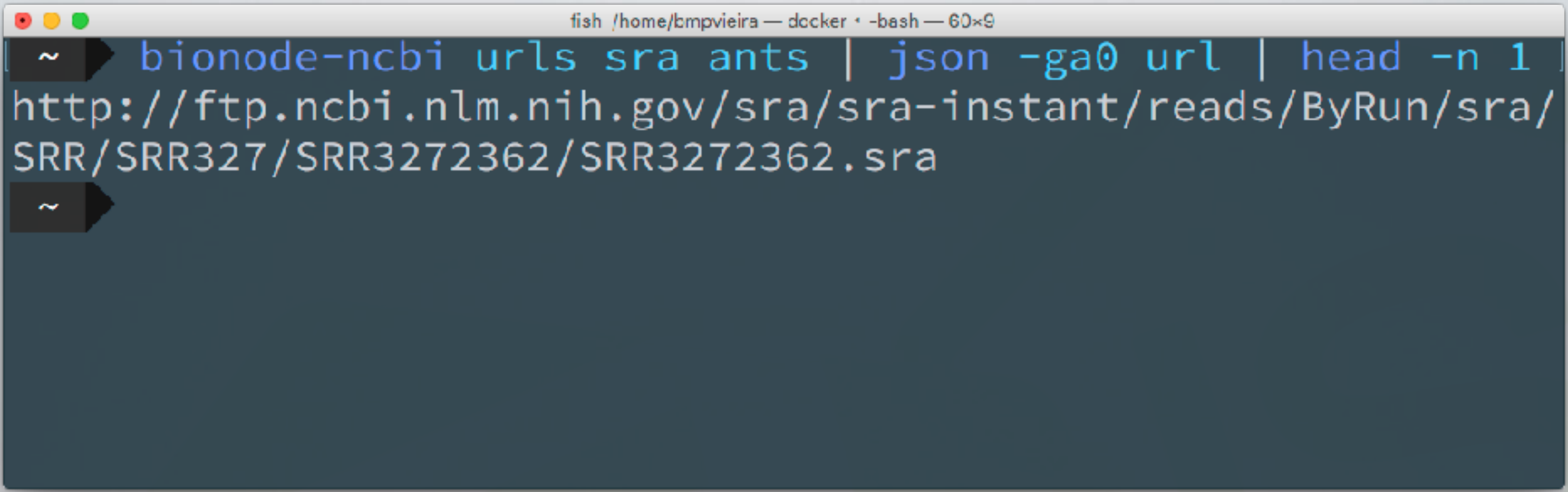
```
~ bionode-ncbi urls sra ants | json -ga0 url
```

bionode-ncbi



```
~ bionode-ncbi urls sra ants | json -ga0 url | head -n 1
```

bionode-ncbi



```
 ~  bionode-ncbi urls sra ants | json -ga0 url | head -n 1
http://ftp.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/
SRR/SRR327/SRR3272362/SRR3272362.sra
 ~ 
```

Had to find and get TB of data online
Social (red) - Solitary (blue)

TOTAL: 167

Blue solitary, Red social

Had to find and get TB of data online
Remove non-wild samples

TOTAL: 119

No Droso., Aedes, Anoph., Mus or R

Had to find and get TB of data online
Remove missing WGS

TOTAL: 88

Usable reads (genomic, wgs, etc)

Had to find and get TB of data online
Remove low coverage

Had to find and get TB of data online
Remove unusable for PSMC

TOTAL: 45

30x manually curated (no haploids, p
inbreds, etc)

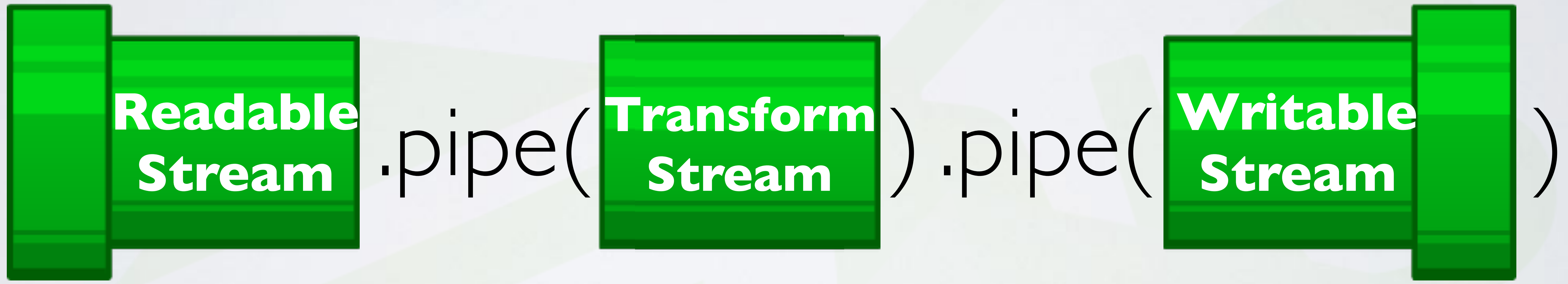
ORIGIN

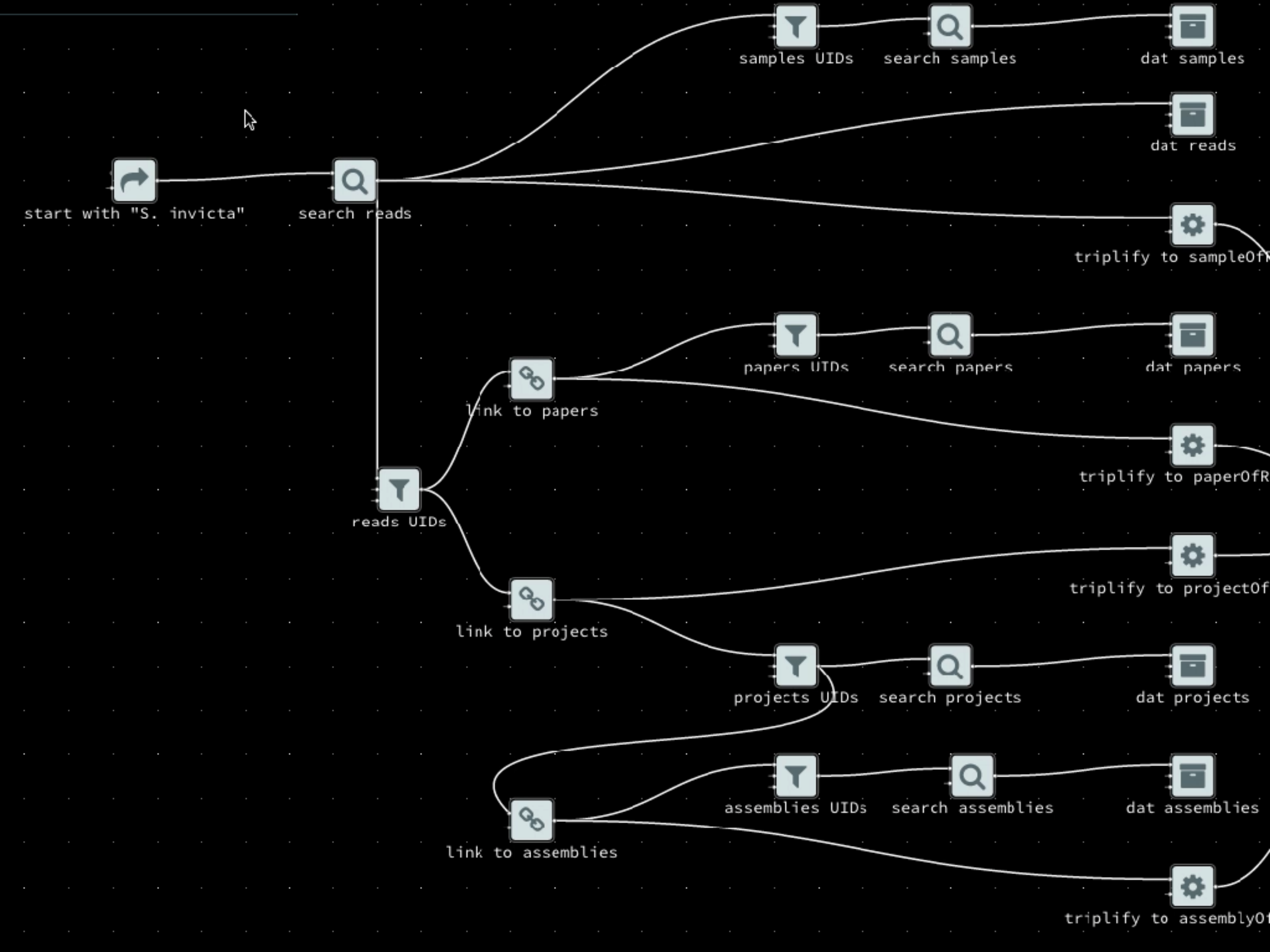
During my PhD at WurmLab.github.io

Queen Mary
University of London

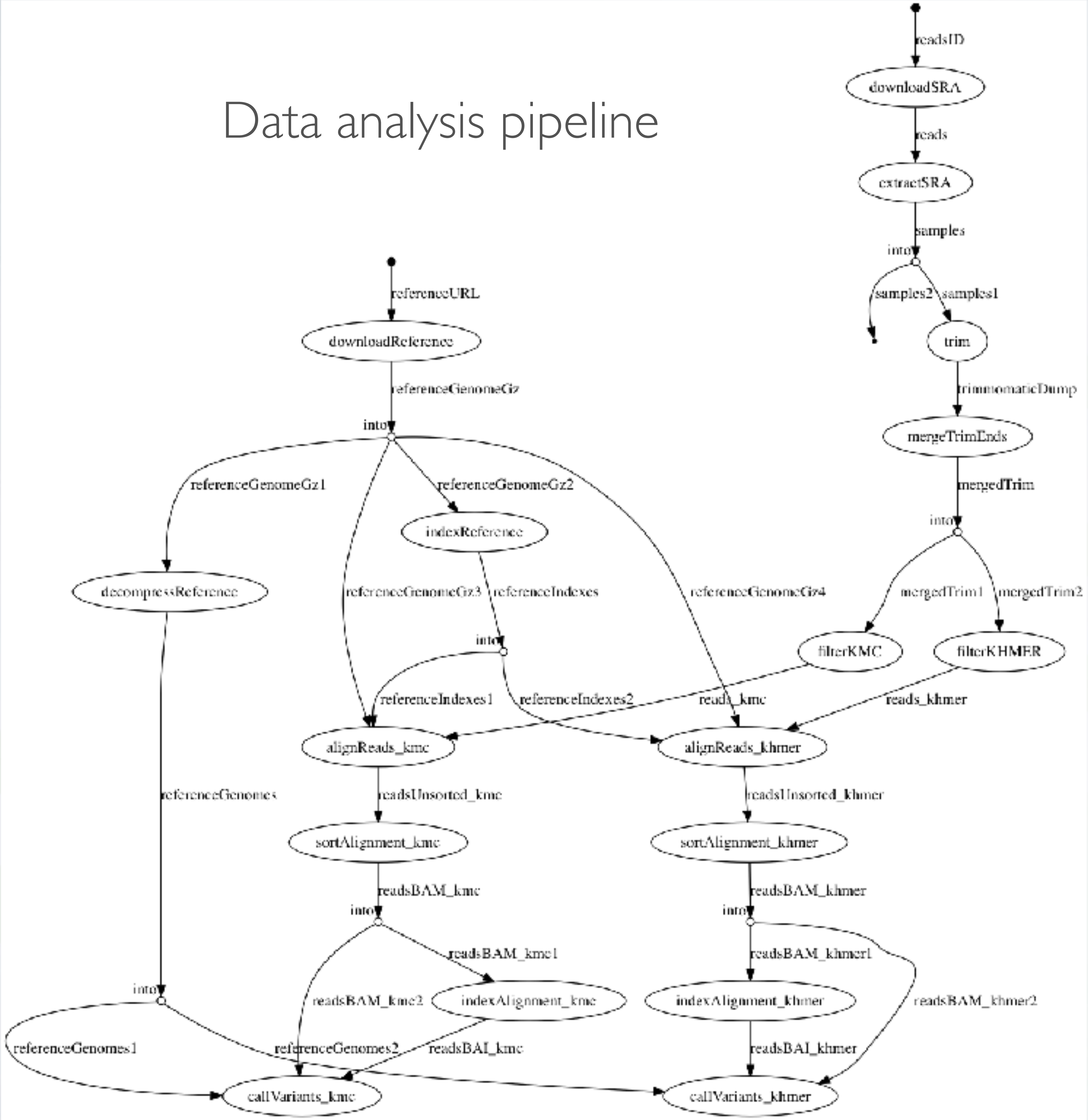
- Involved in biological web projects that need JS
- Had to find and get TB of data online
- Had to build complicated bioinformatic pipelines

DATA PROCESSING



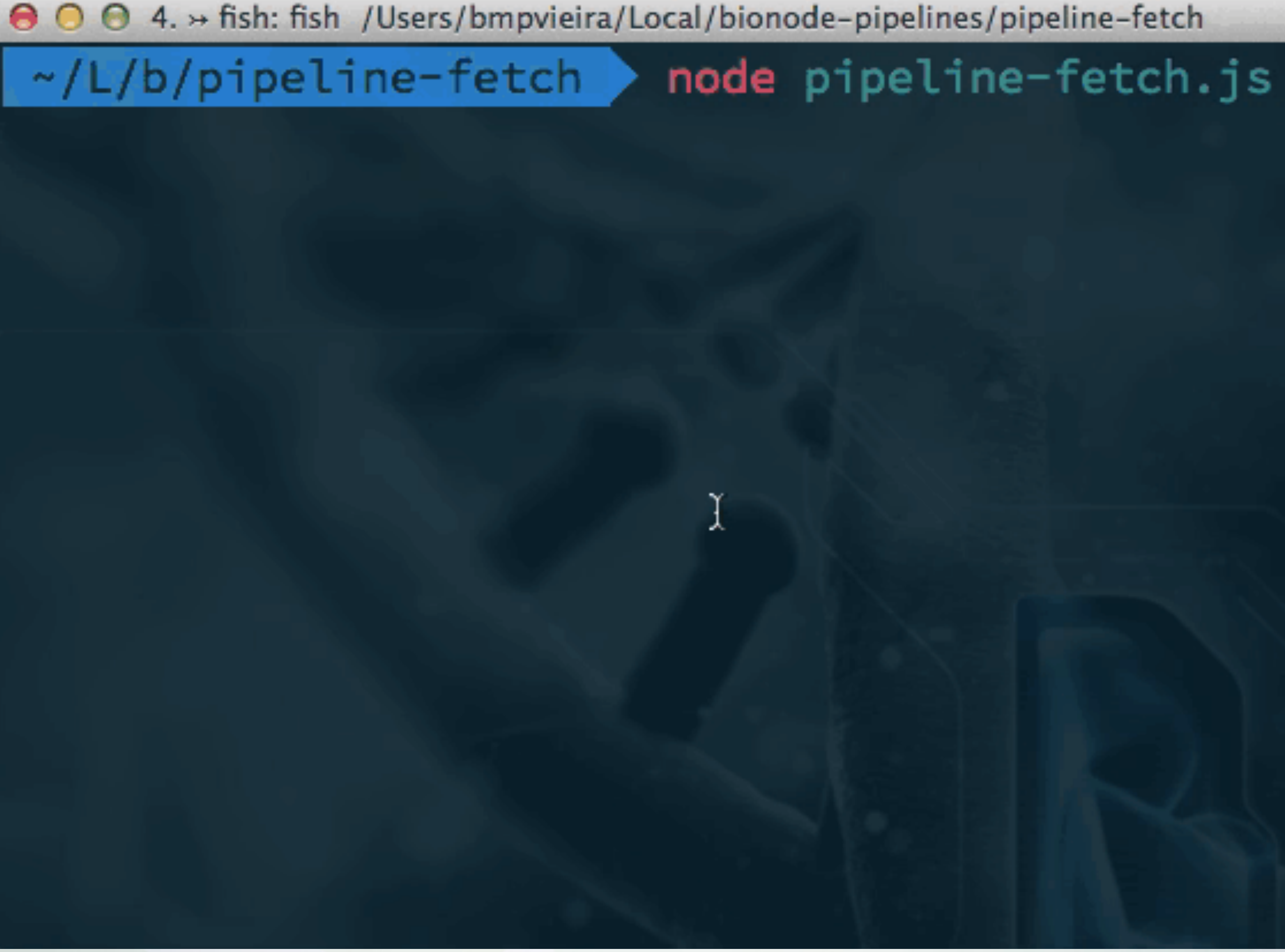

start with "S. invicta"
search reads
samples UIDs
search samples
dat samples
dat reads
triplify to sampleOf
reads UIDs
link to papers
papers UIDs
search papers
dat papers
triplify to paperOfR
triplify to projectOf
link to projects
projects UIDs
search projects
dat projects
assemblies UIDs
search assemblies
dat assemblies
link to assemblies
triplify to assemblyOf

Data analysis pipeline



Metadata pipeline

```
ncbi
.search('sra', 'Solenopsis invicta')
.pipe(fork1)
.pipe(dat.reads)

fork1
.pipe(tool.extractProperty('expxml.Biosample.id'))
.pipe(ncbi.search('biosample'))
.pipe(dat.samples)

fork1
.pipe(tool.extractProperty('uid'))
.pipe(ncbi.link('sra', 'pubmed'))
.pipe(ncbi.search('pubmed'))
.pipe(fork2)
.pipe(dat.papers)
```



```
4. ↣ fish: fish  /Users/bmpvieira/Local/bionode-pipelines/pipeline-fetch
~/L/b/pipeline-fetch  node pipeline-fetch.js
```

bionode-waterwheel

A Streaming Workflow Engine for bioinformatics and other big data explorations

Google Summer of Code 2016

```
const samples = task({
  input: {
    db: 'sra',
    accession: config.sraAccession
  },
  output: '**/*.sra'
}, ({ input }) => ncbi.download(input.db, input.accession) )

const fastqDump = task({
  input: new File('**/*.sra'),
  output: [1, 2].map(n => new File(`*_${n}.fastq.gz`))
}, ({ input }) => shell(`fastq-dump --split-files --skip-technical --gzip ${input}`) )
```

BIONODE COMMUNITY

WurmLab .github.io

Queen Mary University of London

DNA digest

dat DATA

BioJS

ACKNOWLEDGMENTS

mozilla Science Lab

Research group

WurmLab .github.io

Queen Mary University of London

Community

bionode.io

Friends

dat DATA