BIONODE.IO

Tutorial

LIVE CODING!

Module to get data from European Variation Archive EMBL-EBI

fish /home/bmpvieira/bionode-eva — docker ◂ -bash — 73×23

```
~/bionode-eva ▶ node index.js | json | head -n 21
{
  "apiVersion": "v1",
  "warning": "",
  "error": "",
  "queryOptions": {},
  "response": [
    {
      "time": 0,
      "dbTime": 9,
      "numResults": 15,
      "numTotalResults": 15,
      "resultType": "com.mongodb.BasicDBObject",
      "result": [
        {
          "studyId": "PRJEB8661",
          "studyName": "The Exome Aggregation Consortium (ExAC) v0.3"
        },
        {
          "studyId": "PRJEB6042",
          "studyName": "GEUVADIS: Genetic European Variation in Disease"
        },
~/bionode-eva ▶
```

PROCESS DATA IN CHUNKS

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request()
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Binary data
Buffer class
chunks of 16kb
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process
.stdout
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```

Live Coding Solution step 1 - get JSON

```
var url = require('url')
var request = require('request')

var urlObject = {
  protocol: 'http',
  host: 'www.ebi.ac.uk',
  pathname: '/eva/webservices/rest/v1/meta/studies/list',
  search: '?species=hsapiens_grch37'
}

var urlString = url.format(urlObject)

request(urlString).pipe(process.stdout)
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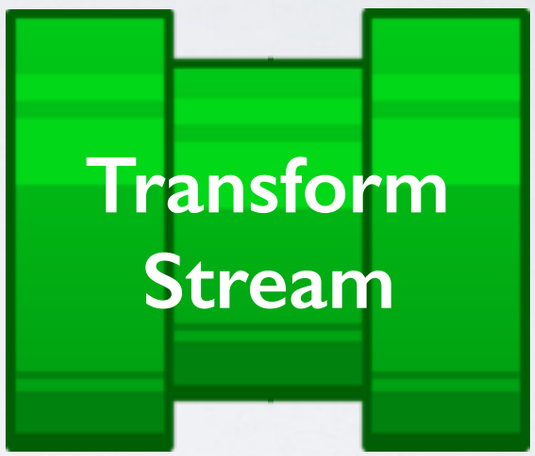


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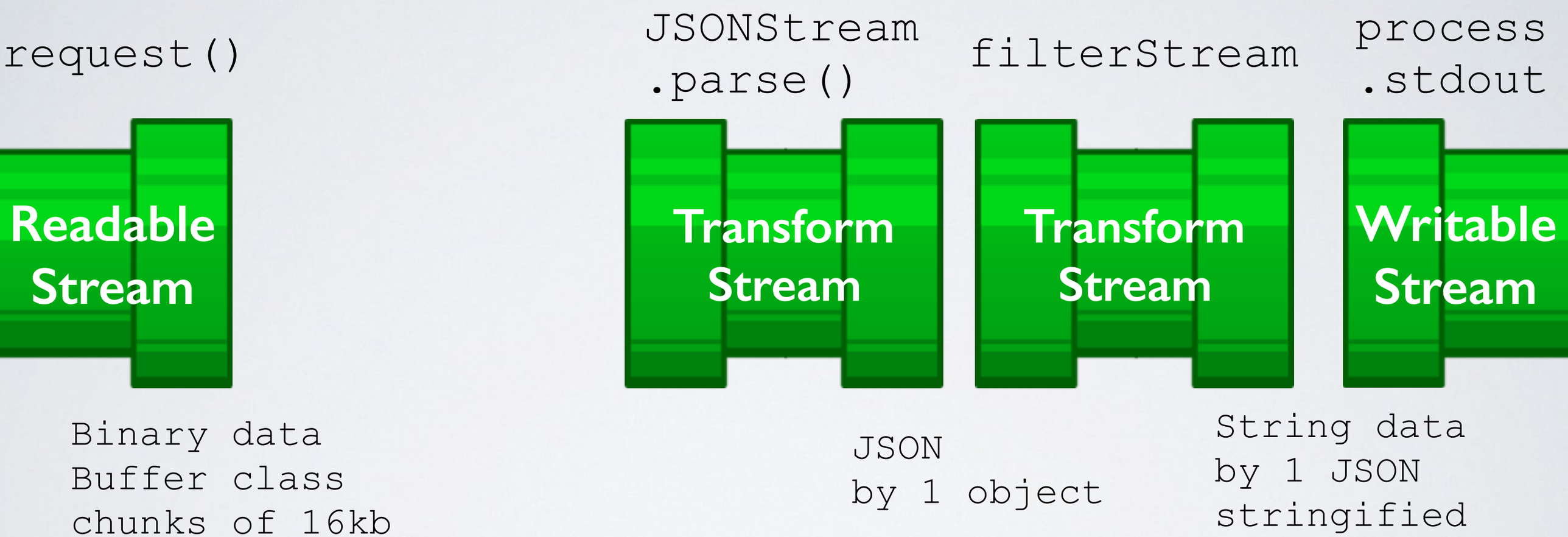
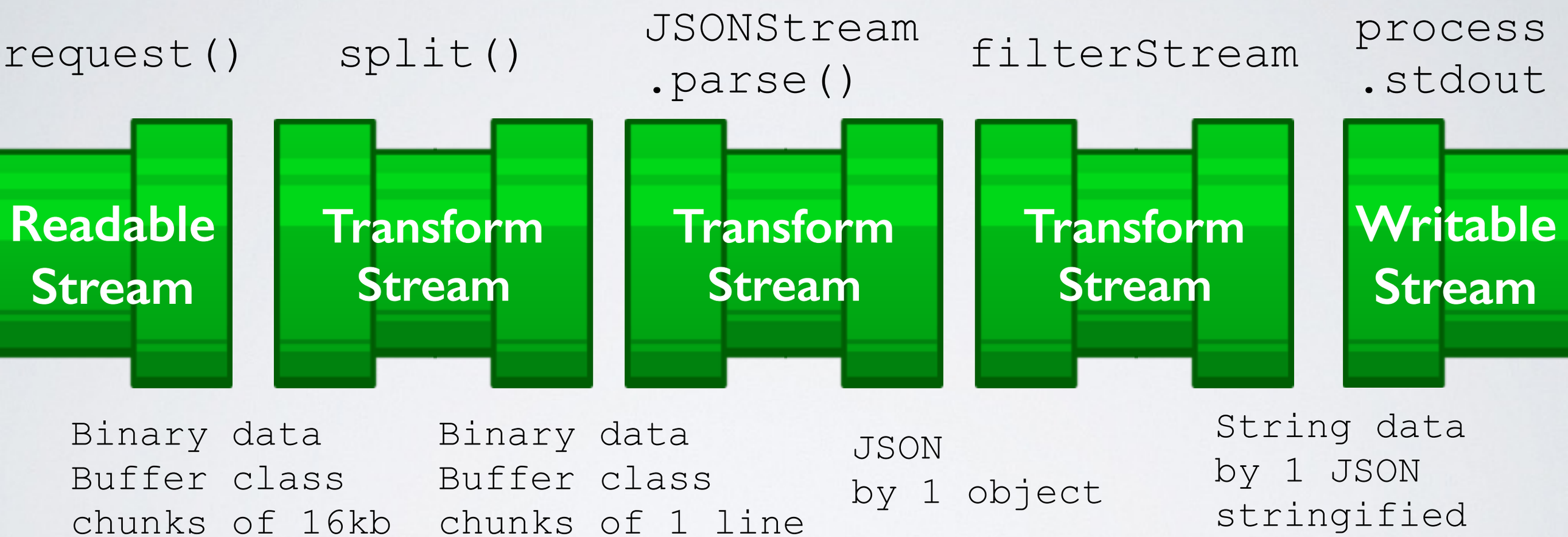


PROCESS DATA IN CHUNKS



Live Coding Solution step 2 - parse JSON

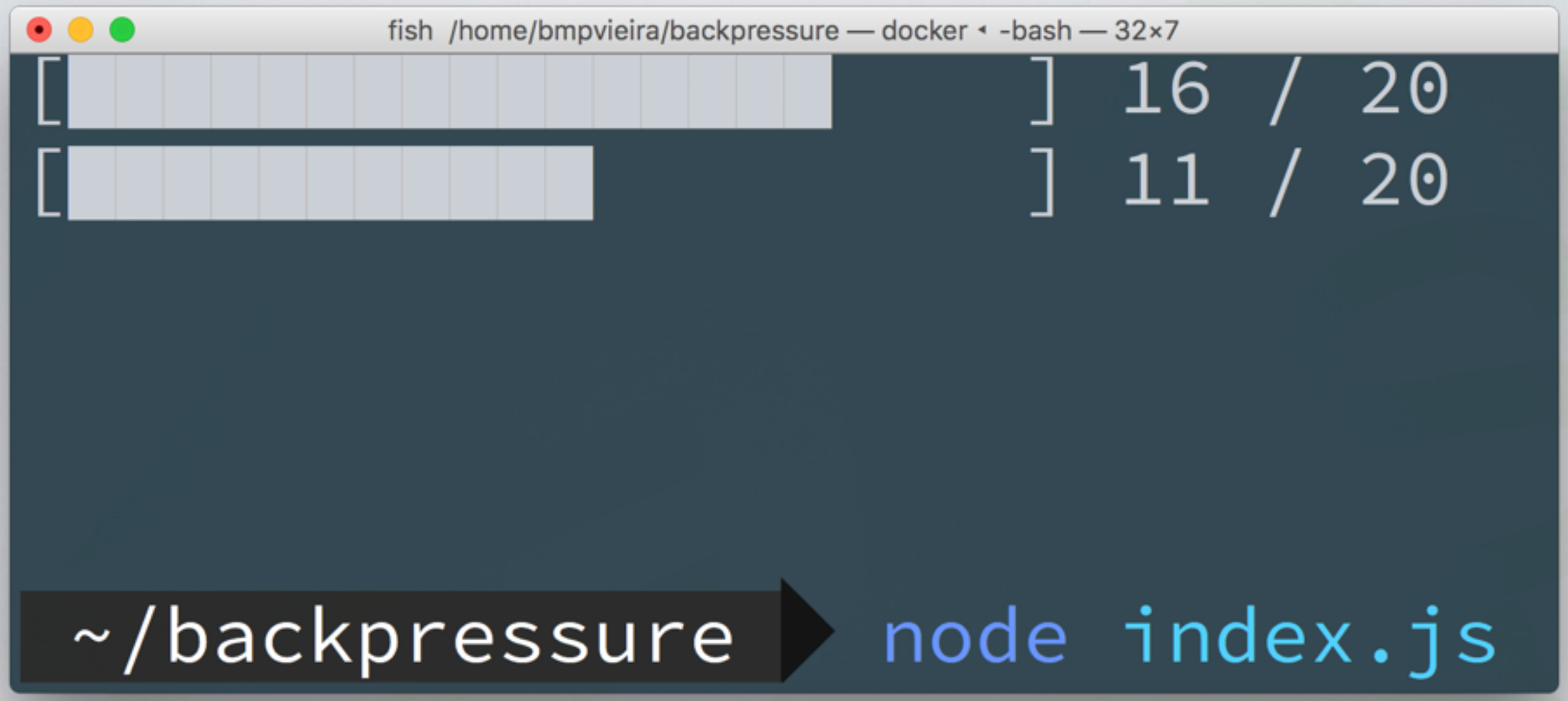
```
var url = require('url')
var split = require('split2')
var JSONstream = require('JSONstream')
var request = require('request')

var urlObject = {
  protocol: 'http',
  host: 'www.ebi.ac.uk',
  pathname: '/eva/webservices/rest/v1/meta/studies/list',
  search: '?species=hsapiens_grch37'
}

var filterStream = through.obj(filter)

function filter(object, encoding, callback) {
  this.push(JSON.stringify(object))
  callback()
}

var urlString = url.format(urlObject)

request(urlString)
.pipe(split())
.pipe(JSONStream.parse())
.pipe(filterStream)
.pipe(process.stdout)
```

Live Coding Solution step 3 - filter JSON

```
var os = require('os')
var url = require('url')
var miss = require('mississippi')
var split = require('split2')
var JSONstream = require('JSONstream')
var request = require('request')

var urlObject = {
  protocol: 'http',
  host: 'www.ebi.ac.uk',
  pathname: '/eva/webservices/rest/v1/meta/studies/list',
  search: '?species=hsapiens_grch37'
}

var urlString = url.format(urlObject)

var filterStream = through.obj(filter)

function filter(object, encoding, callback) {
  var self = this
  var results = object.response[0].result
  results.forEach(filterAndPush())
  function filterAndPush(result) {
    if (result.studyName.match('1000 Genomes')) {
      self.push(JSON.stringify(result) + os.EOL)
    }
  }
  callback()
}

request(urlString)
.pipe(split())
.pipe(JSONStream.parse())
.pipe(filterStream)
.pipe(process.stdout)
```

LIVE EXAMPLE

Show backpressure in action



```
var _ = require('lodash')
var through = require('through2')
var exec = require('child_process').exec;
var streamify = require('stream-array')
var multimeter = require('multimeter');
var multi = multimeter(process);

process.stdout.write('\033c'); // Clear the console

var jobs = 20

var progress = {
  fastStream: 1,
  slowStream: 1
}

var fastStreamProgressBar = multi(0, 1, {
    width : jobs,
    solid : { text : '▇'},
    empty : { text : ' ' },
})

var slowStreamProgressBar = multi(0, 2, {
    width : jobs,
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```
sourceStream = streamify(_.range(jobs))

var fastStream = through.obj({highWaterMark: 16}, function (obj, enc, next) {
  var self = this
  exec('sleep 1', function (err, stdout, stderr) {
    fastStreamProgressBar.ratio(progress.fastStream++, jobs)
    self.push(obj)
    next()
  })
})

var slowStream = through.obj({highWaterMark: 16}, function (obj, enc, next) {
  var self = this
  exec('sleep 2', function (err, stdout, stderr) {
    slowStreamProgressBar.ratio(progress.slowStream++, jobs)
    self.push(obj)
    next()
  })
})

sourceStream.pipe(fastStream).pipe(slowStream)

slowStream.resume()
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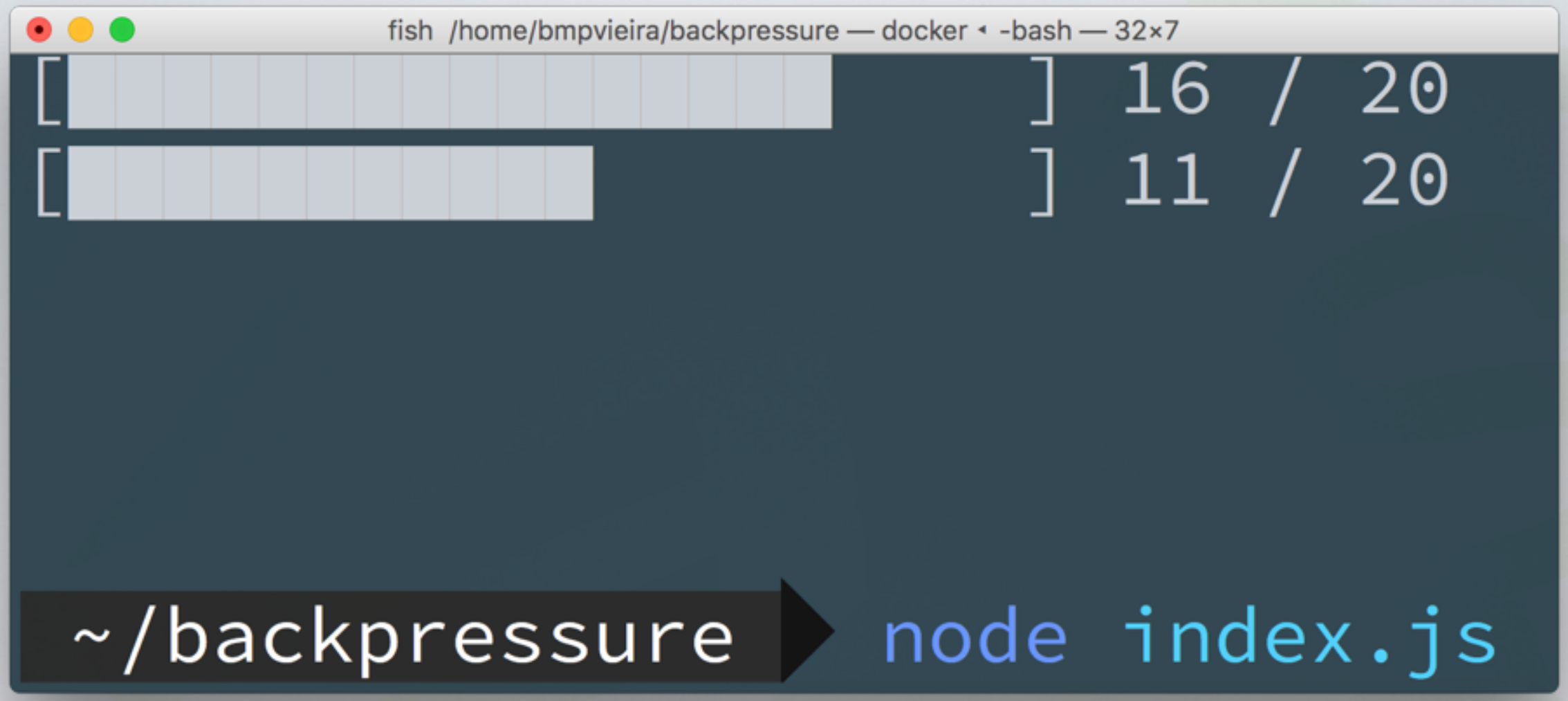

ACKNOWLEDGMENTS

Organisers

DNA digest

Community

bionode.io

Sponsor

repositive.io

Research group

WurmLab .github.io

Queen Mary University of London

Venue

CAMPUS LONDON

Friends

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