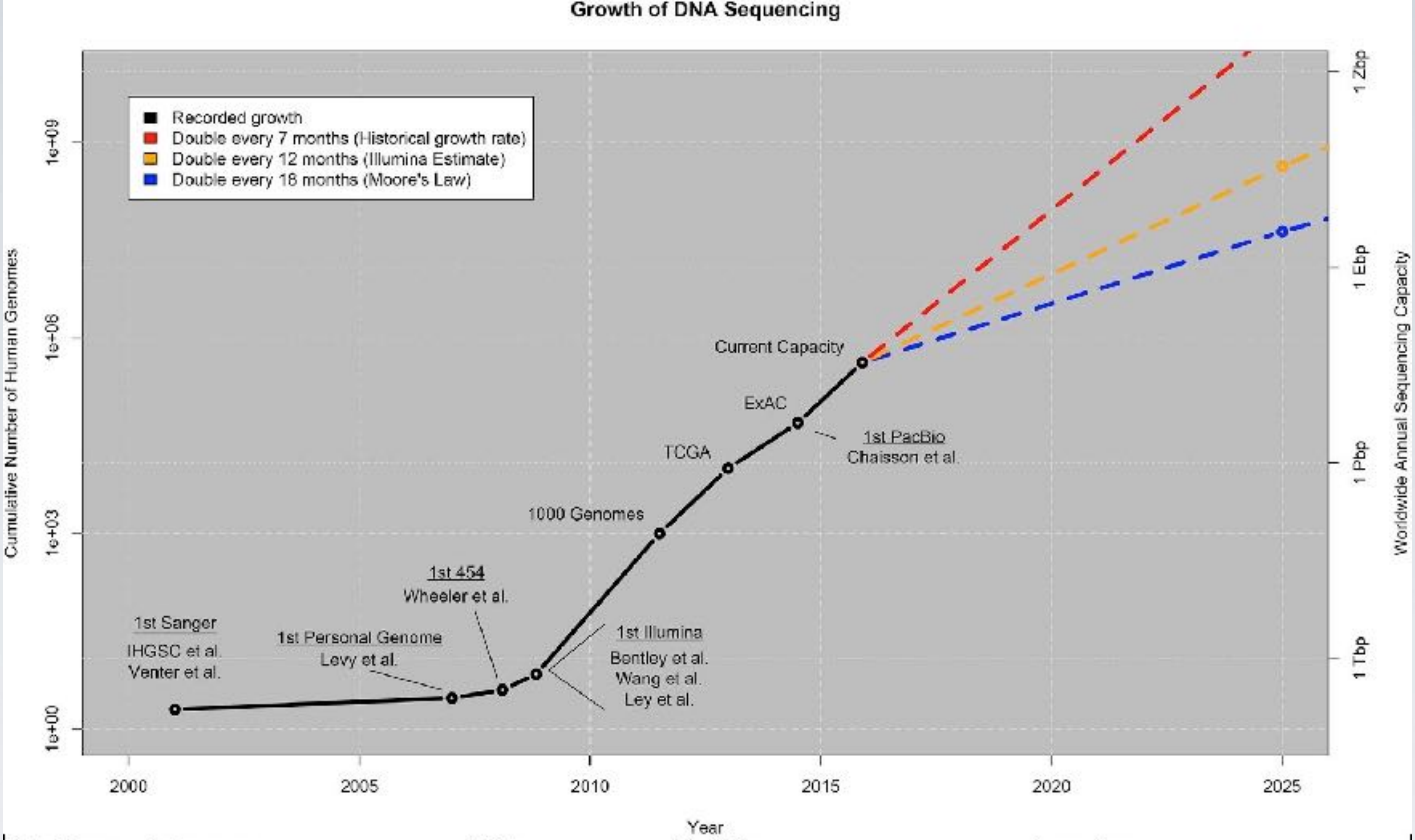
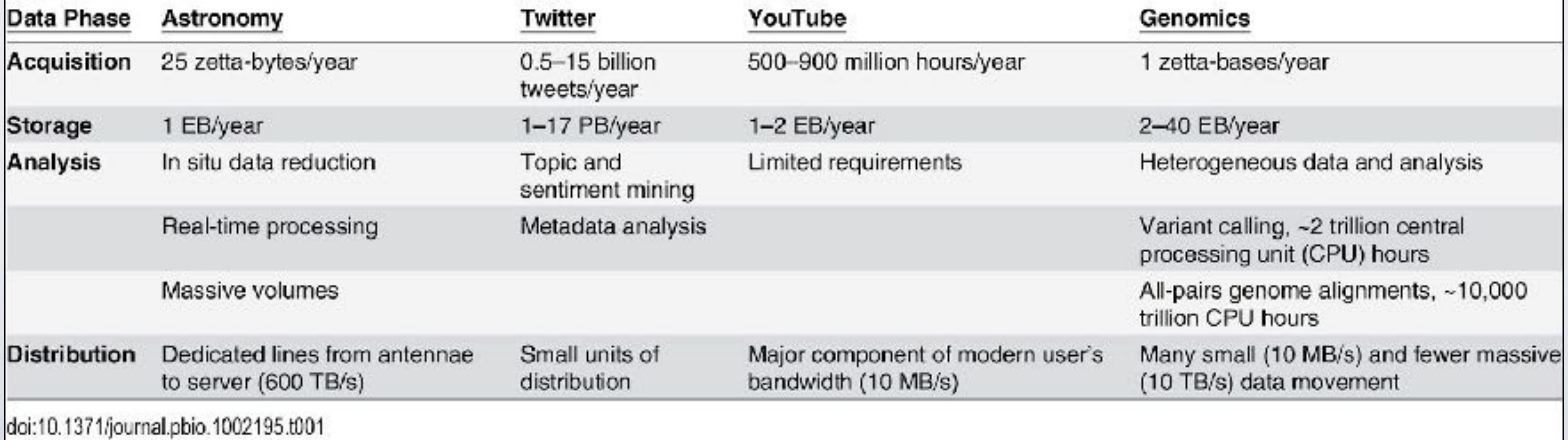
BIONODE.IO

#MozFest 2016

github.com/bionode

gitter.im/bionode/bionode





Data Phase	Astronomy	Twitter	YouTube	Genomics
Acquisition	25 zetta-bytes/year	0.5–15 billion tweets/year	500–900 million hours/year	1 zetta-bases/year
Storage	1 EB/year	1–17 PB/year	1–2 EB/year	2–40 EB/year
Analysis	In situ data reduction	Topic and sentiment mining	Limited requirements	Heterogeneous data and analysis
	Real-time processing	Metadata analysis		Variant calling, ~2 trillion central processing unit (CPU) hours
	Massive volumes			All-pairs genome alignments, ~10,000 trillion CPU hours
Distribution	Dedicated lines from antennae to server (600 TB/s)	Small units of distribution	Major component of modern user's bandwidth (10 MB/s)	Many small (10 MB/s) and fewer massive (10 TB/s) data movement

doi:10.1371/journal.pbio.1002195.t001

WHAT

Modular and universal bioinformatics

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- Each tool tries to do one thing well

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☝ Each tool tries to do one thing well

♻ Provides highly reusable code and tools

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Using Node.js

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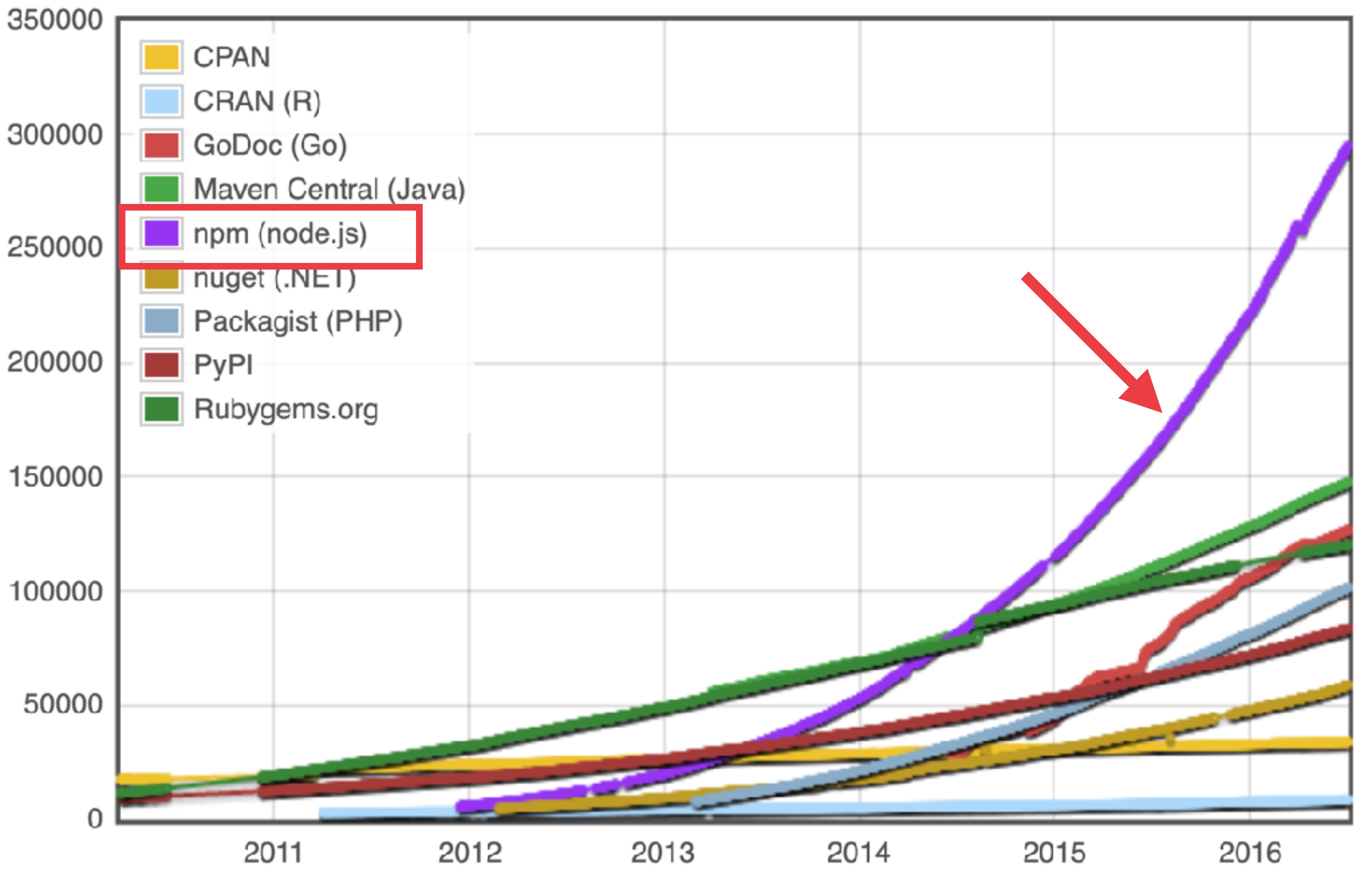
Using Node.js

- Highly modular
- Very open community on GitHub
- Scales by using Streams
- Runs everywhere

Modules count



HOW

Using Node.js

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- Scales by using Streams
- Runs everywhere

HOW

Using Node.js

- Highly modular
- Very open community on GitHub
- Provides native implementation of Streams
- Runs everywhere

HOW

Using Node.js

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

ORIGIN

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During my PhD at

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Compare genetic diversity of social vs solitary species

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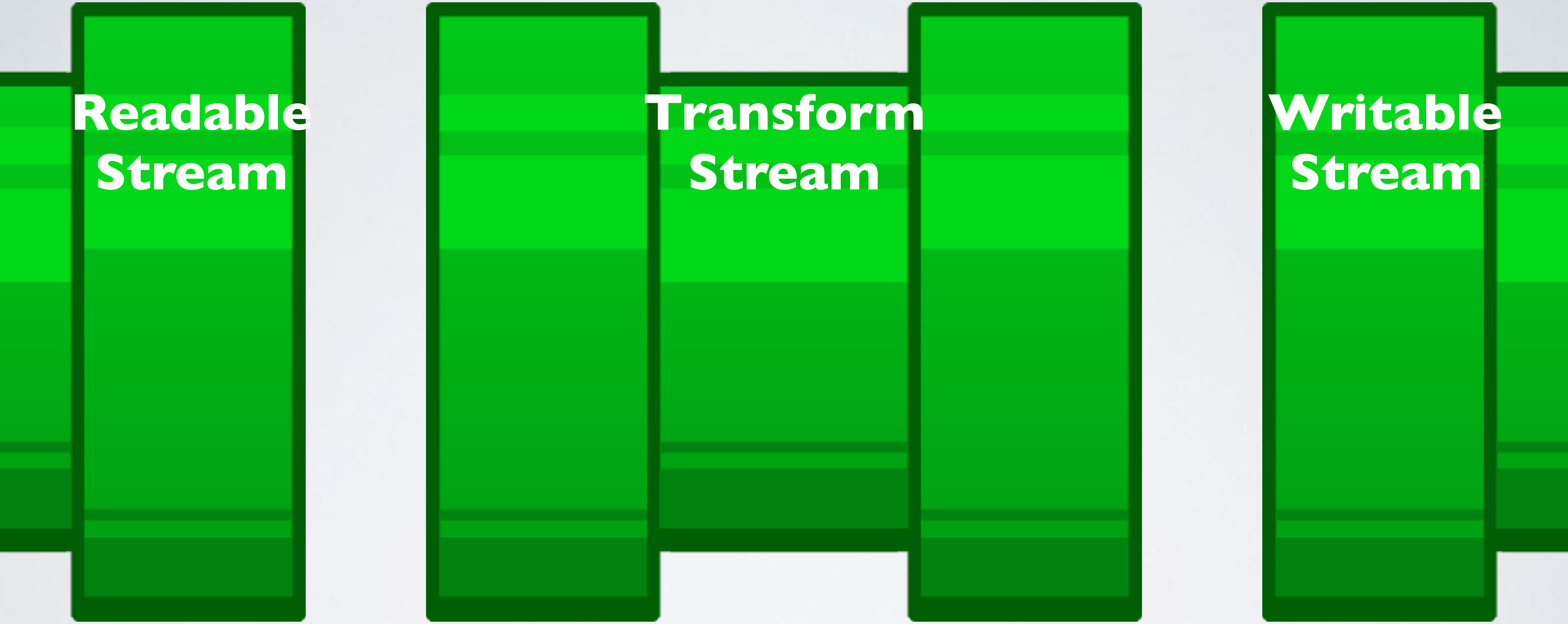
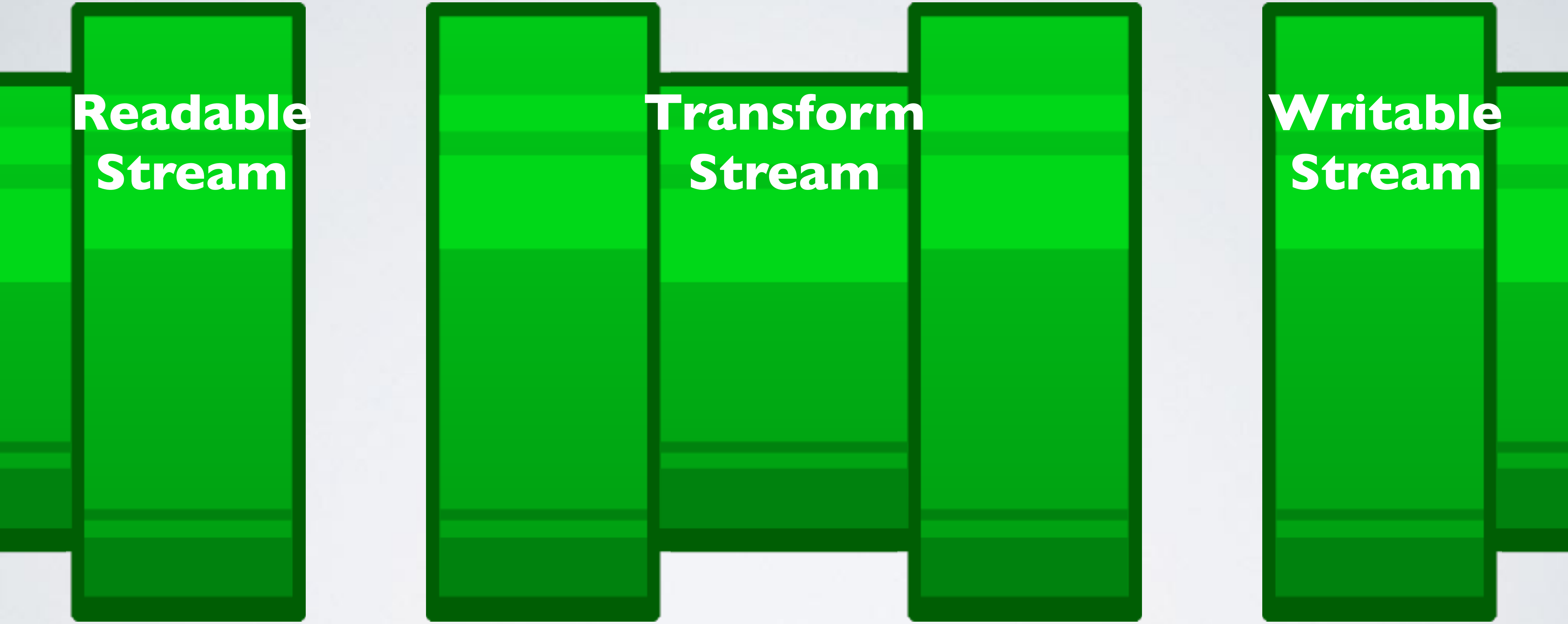
During my PhD at

Compare genetic diversity of social vs solitary species

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


Readable Stream
Transform Stream
Writable Stream



Readable Stream

Transform Stream

Writable Stream

PROCESS DATA IN CHUNKS

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fs.createReadStream(file)

request(url)

process.stdin()

PROCESS DATA IN CHUNKS

.pipe( )

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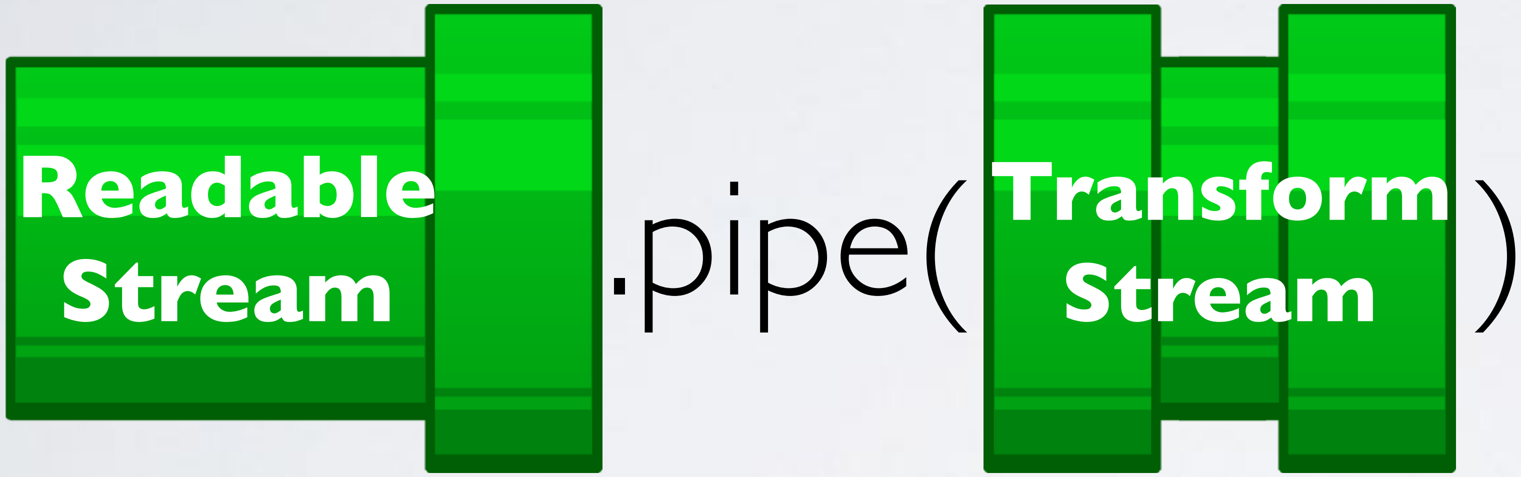
PROCESS DATA IN CHUNKS



fs.createReadStream(file)

request(url)

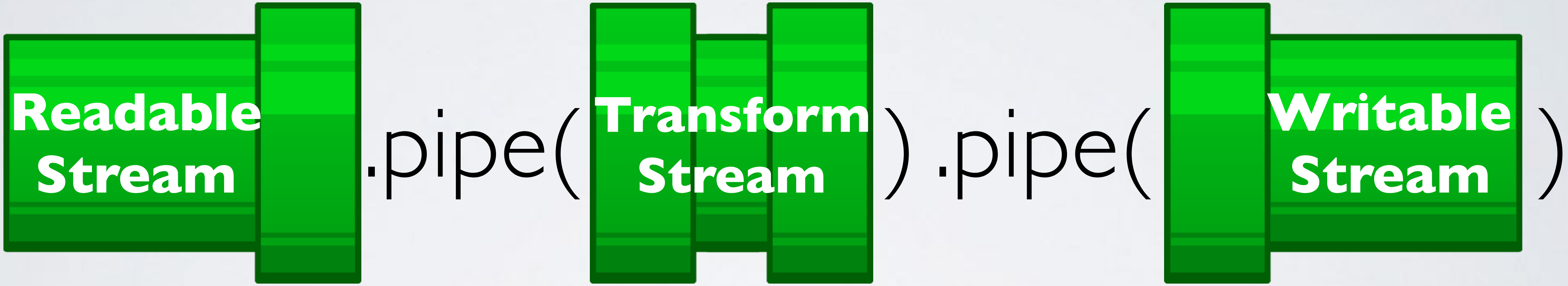
process.stdin()

JSONStream.parse()

filterFunction()

multithreadAnalysis()

PROCESS DATA IN CHUNKS



Readable Stream .pipe(Transform Stream) .pipe(Writable Stream)

fs.createReadStream(file)

request(url)

process.stdin()

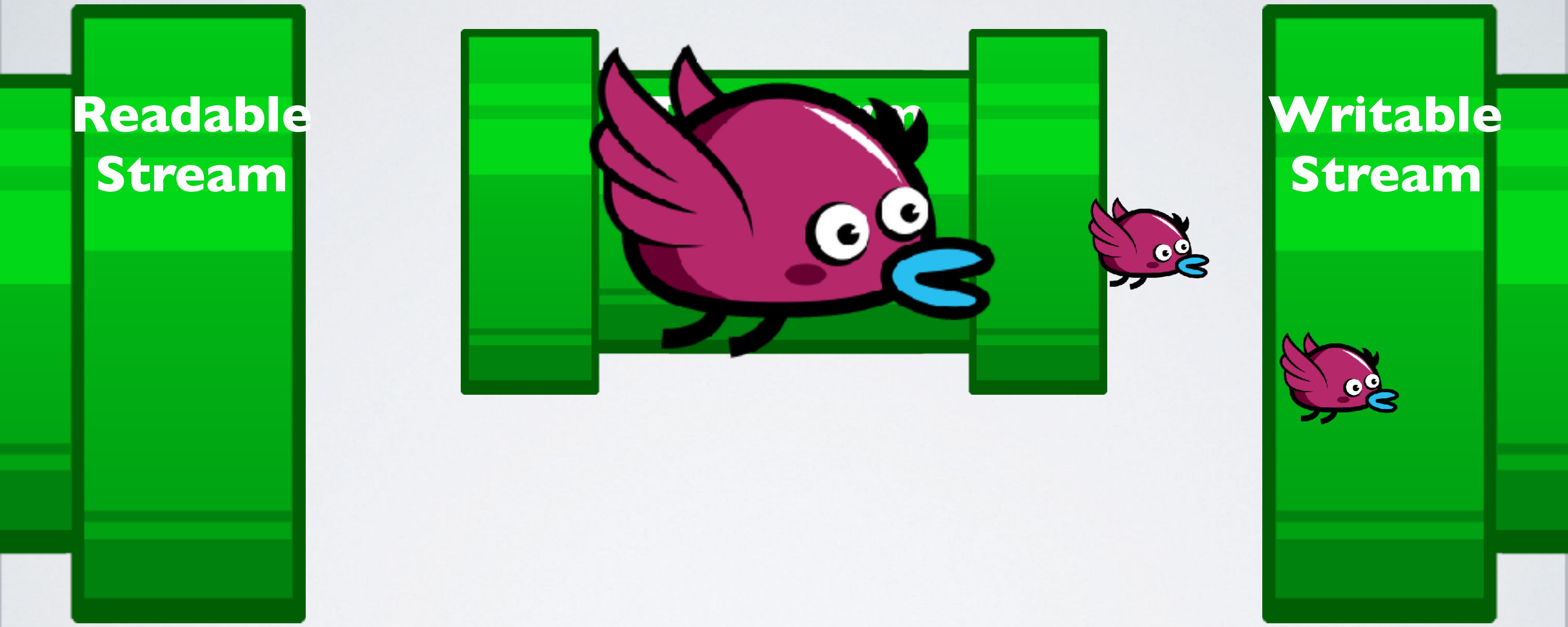
JSONStream.parse()

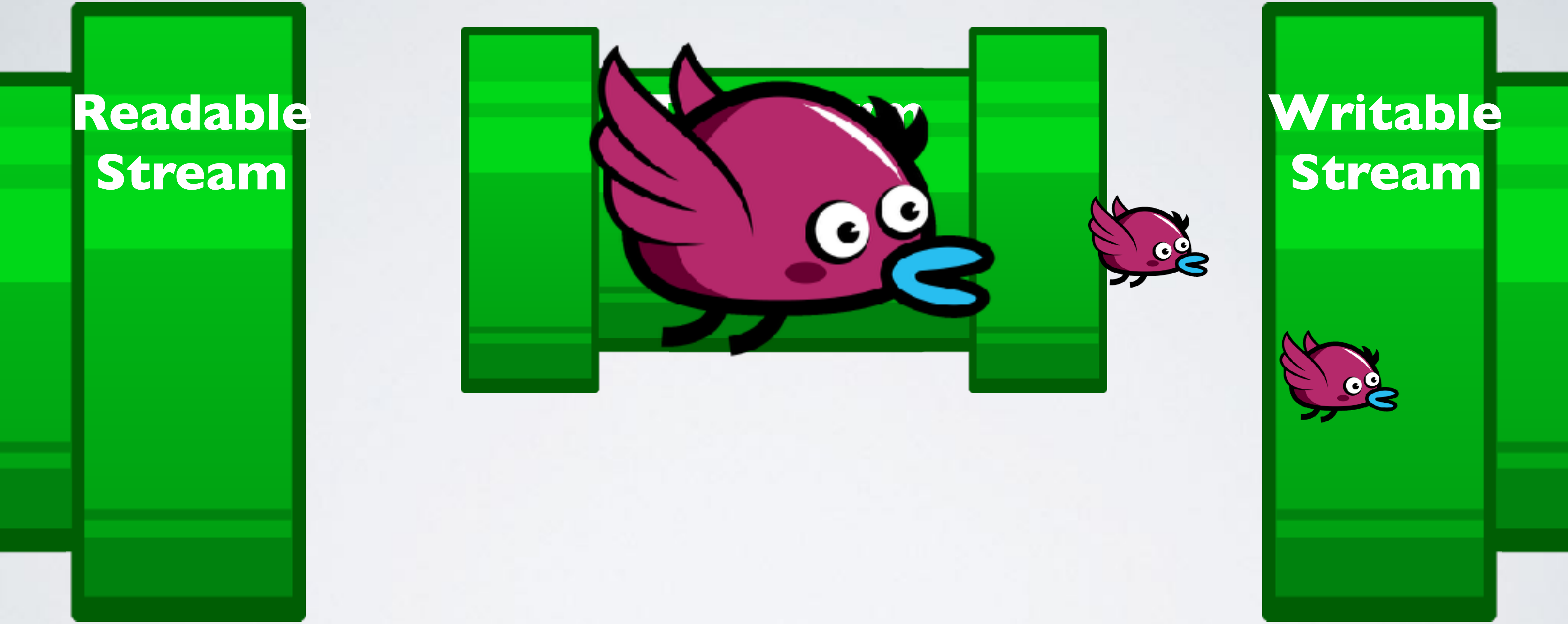
filterFunction()

multithreadAnalysis()

fs.createWriteStream(file)

process.stdout()


Readable Stream
Writable Stream



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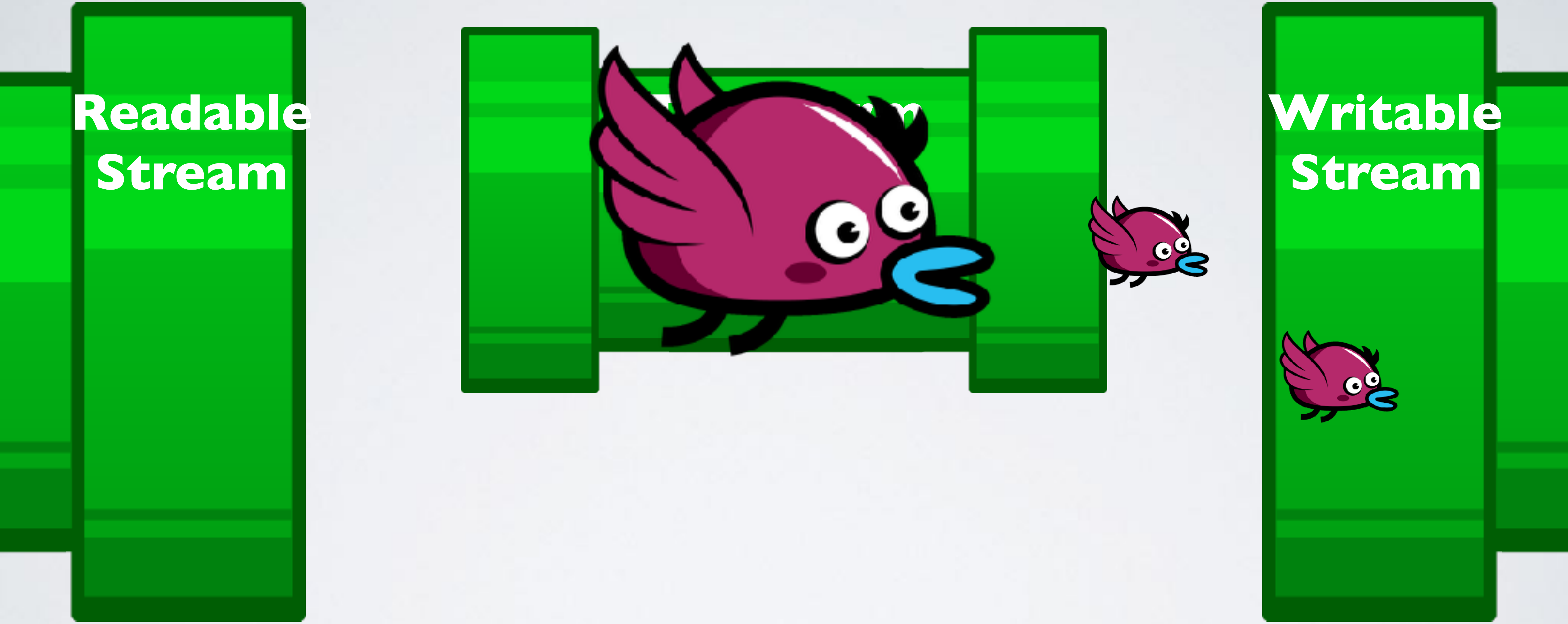
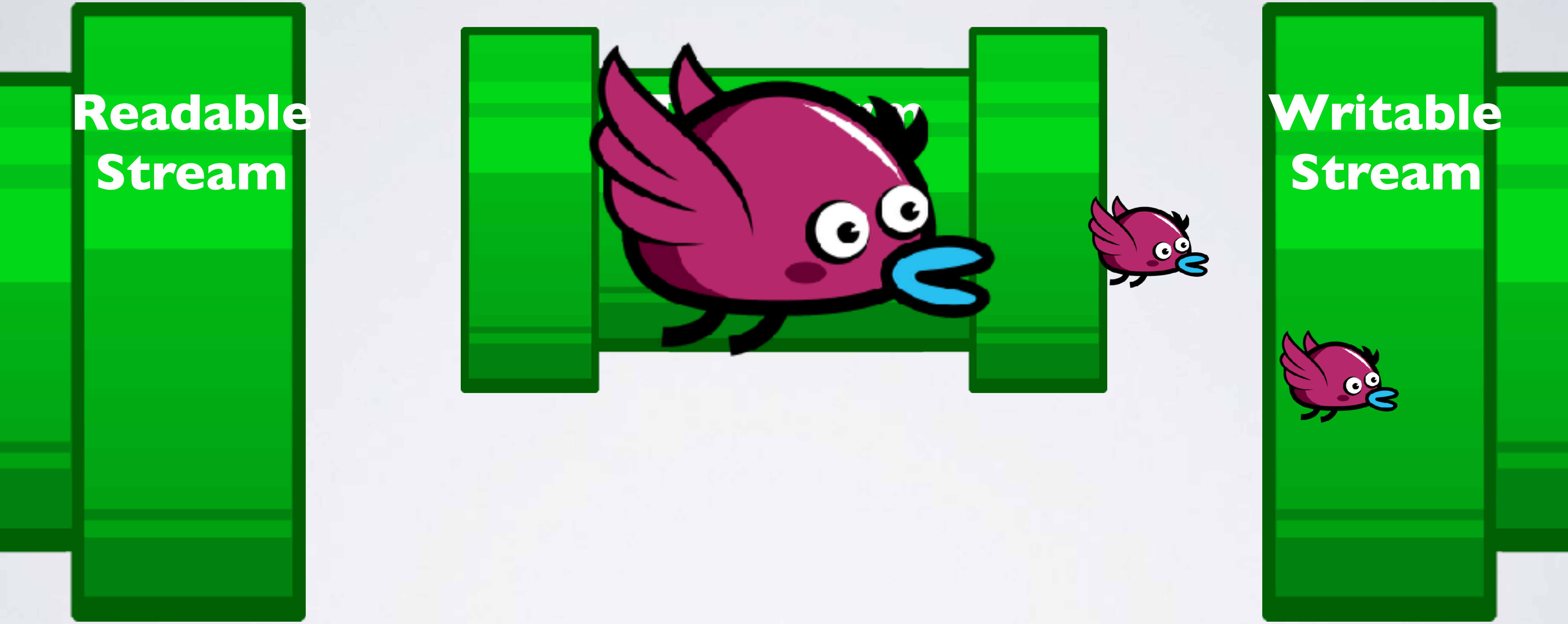
Writable Stream



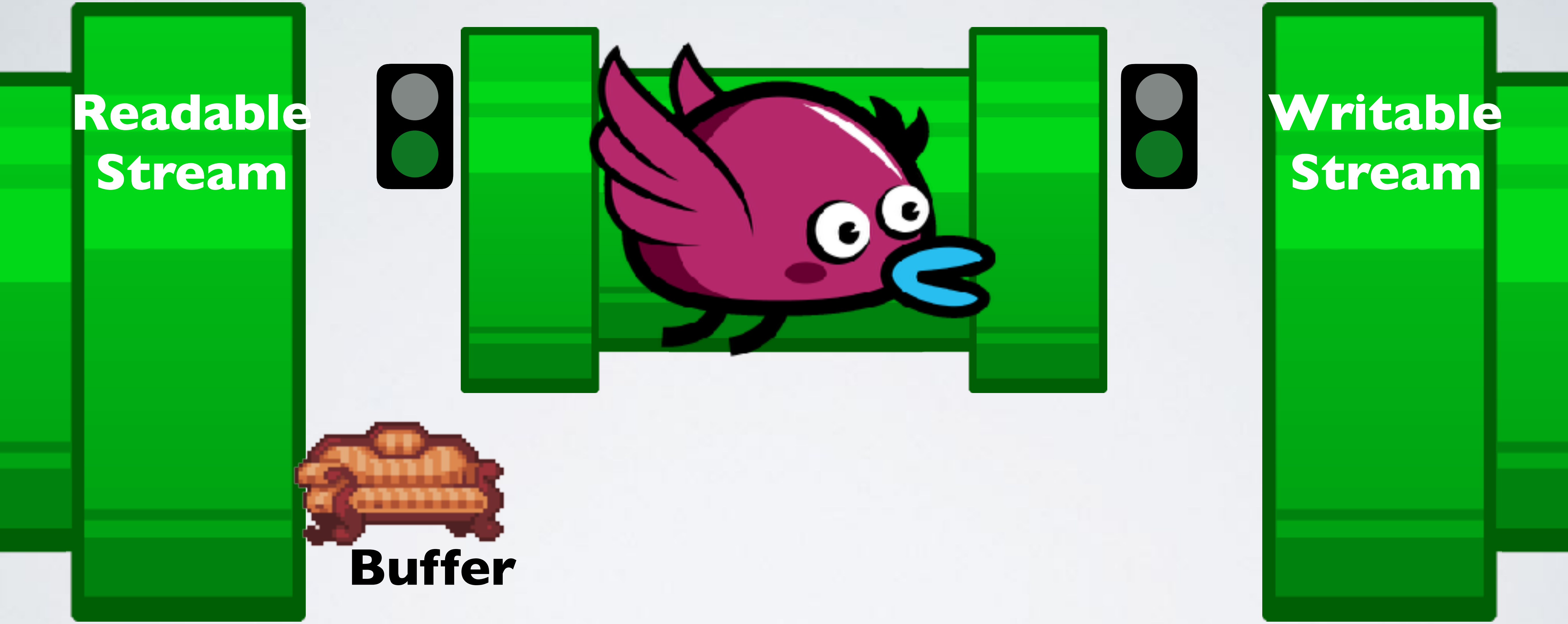
Readable Stream

Writable Stream



Readable Stream

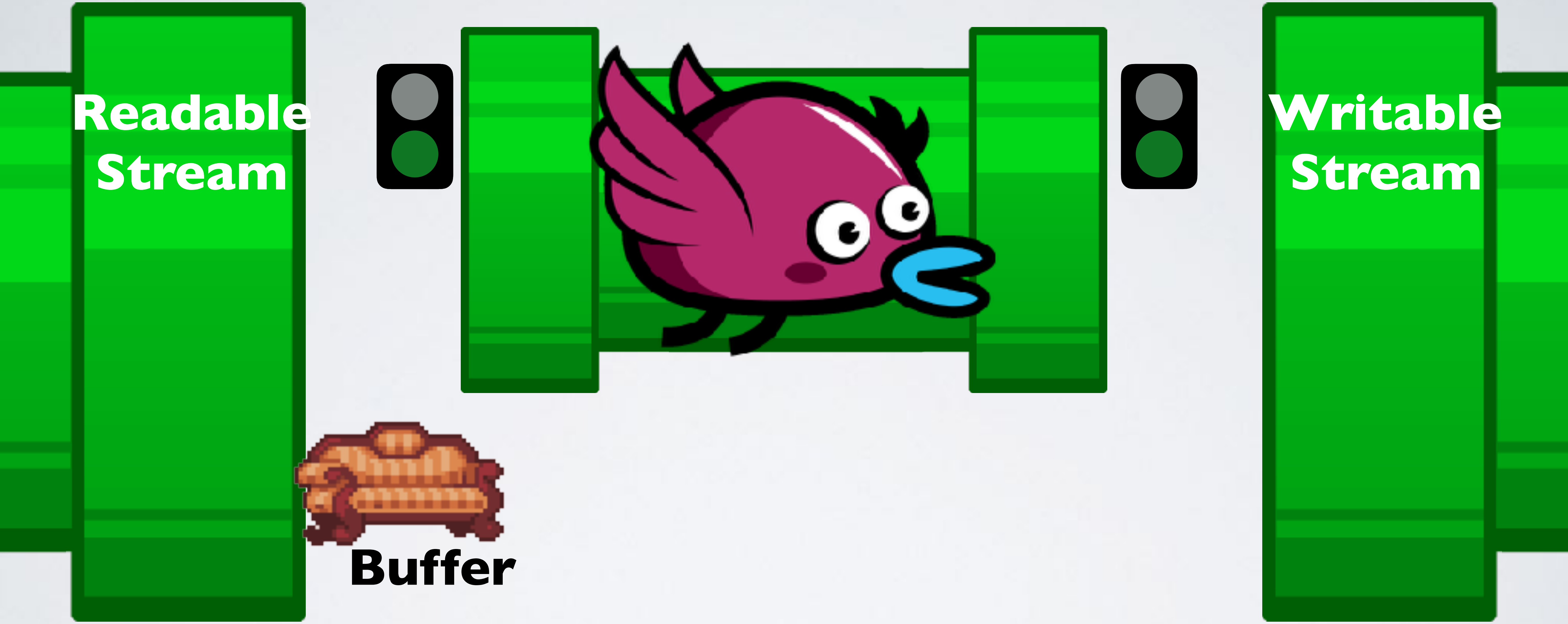
Writable Stream



Readable Stream

Writable Stream

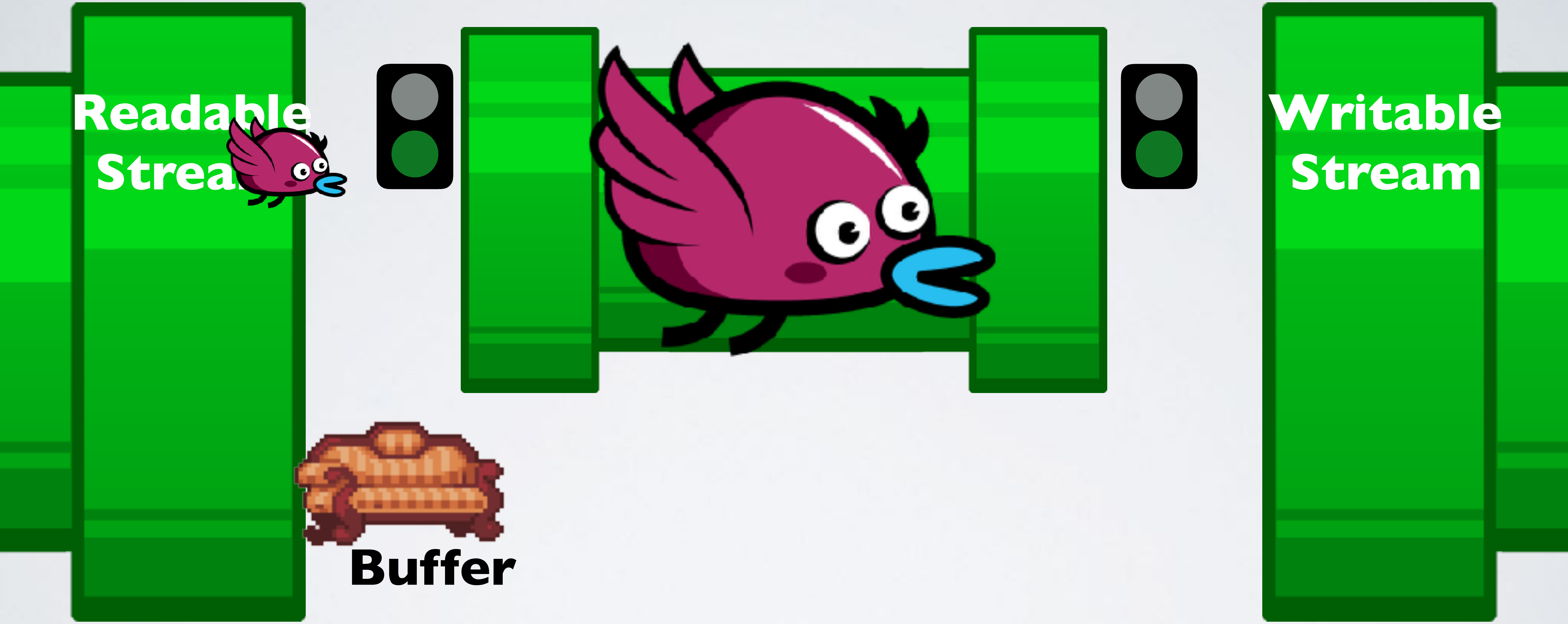
Buffer



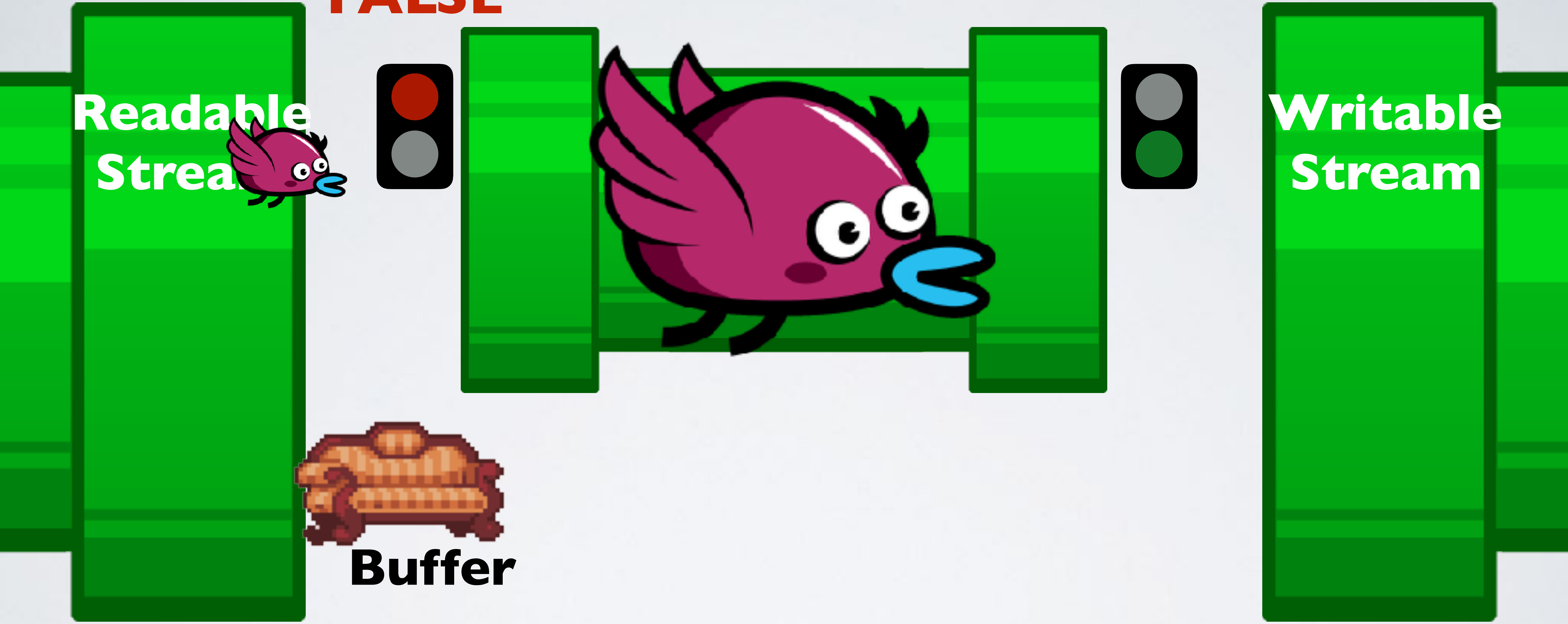
Readable Stream

Writable Stream

Buffer


Readable
Strea
Buffer
Writable
Stream

this.push(data)
FALSE



Readable Strea

Writable Stream

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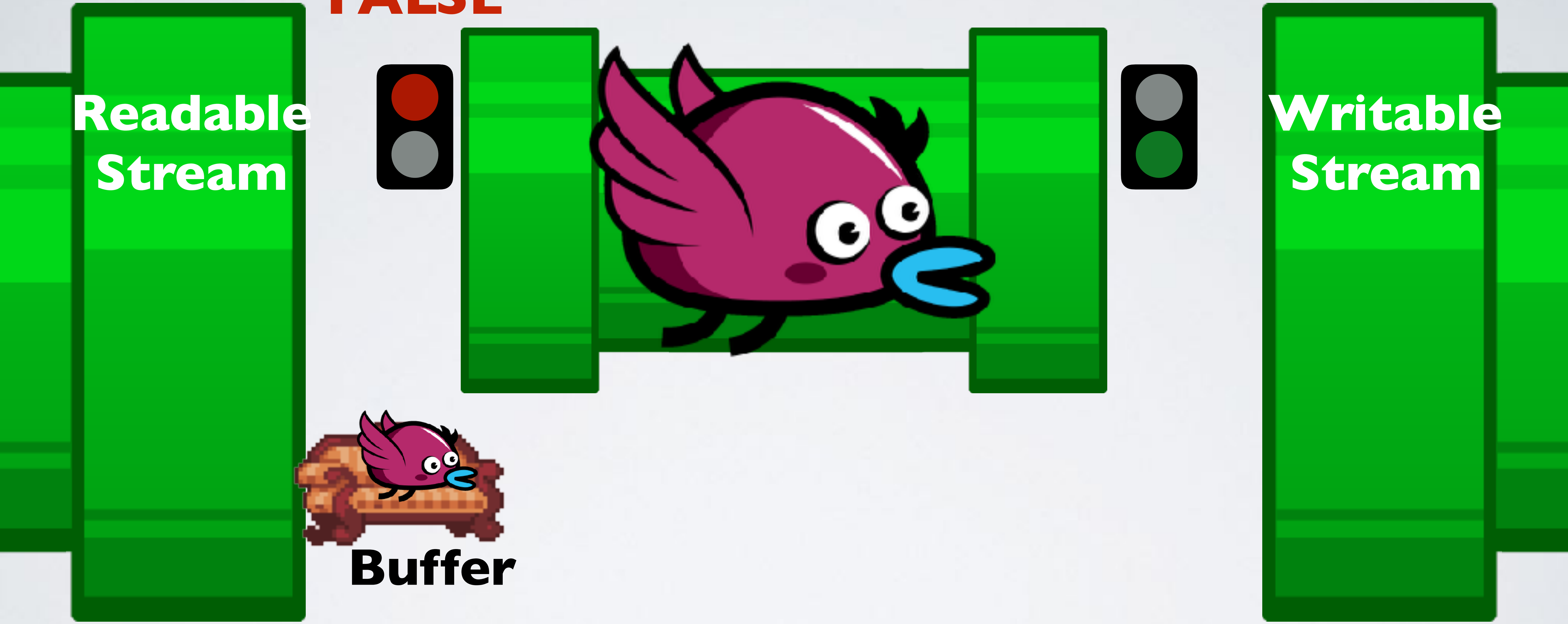

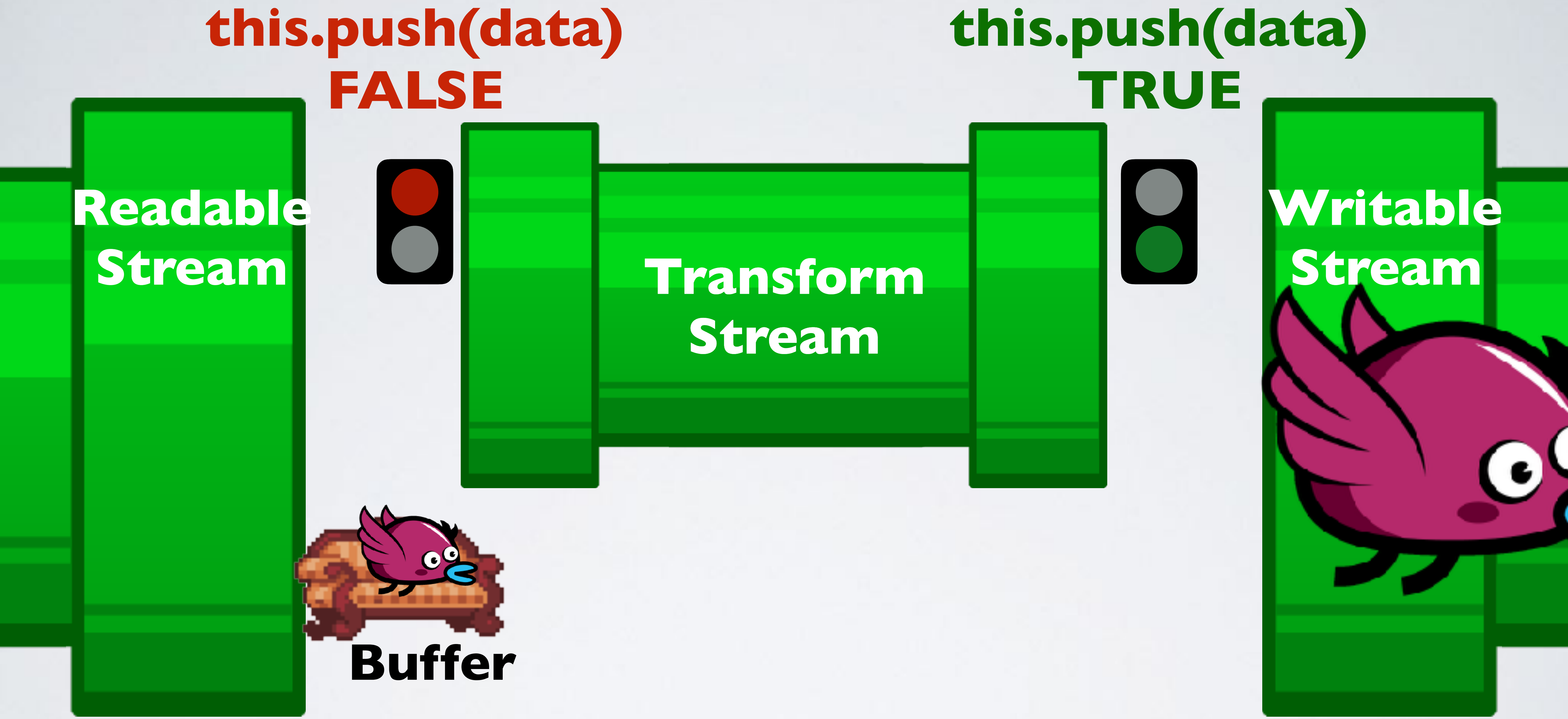

this.push(data)
FALSE

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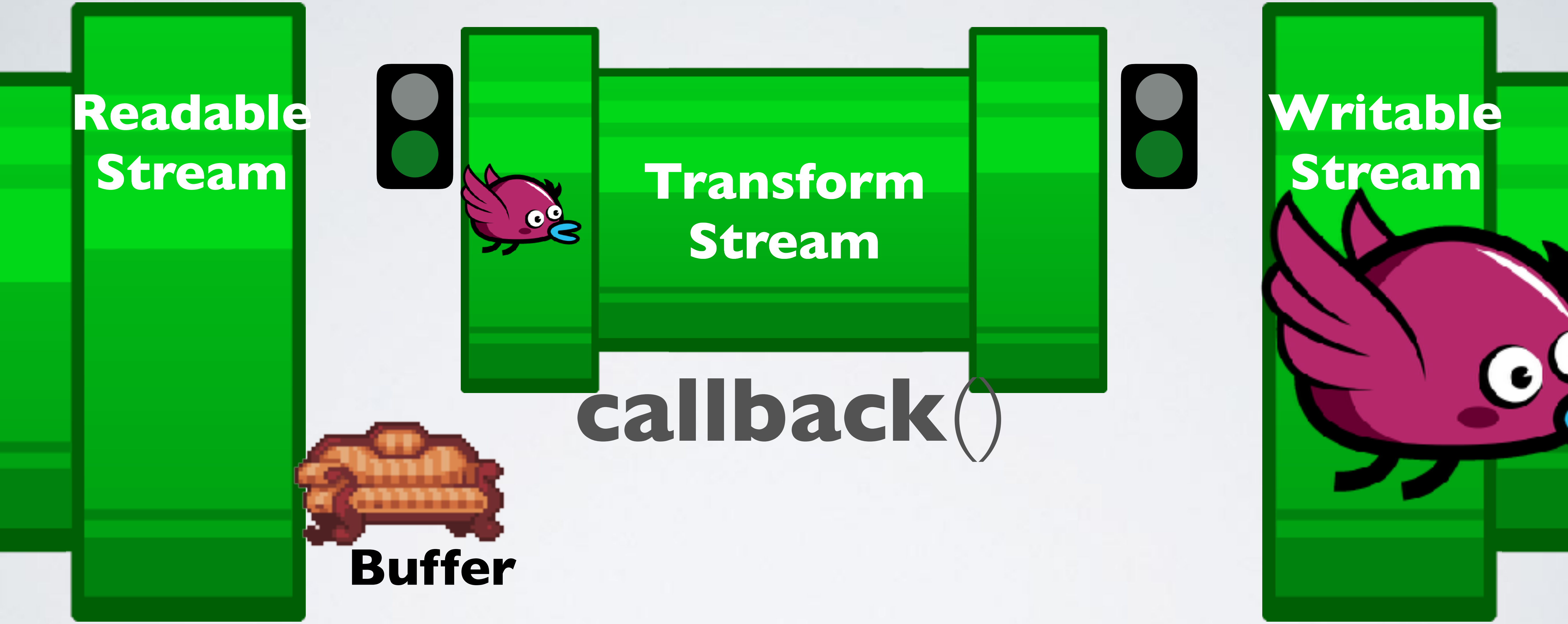
TRUE

Readable Stream

Transform Stream

Writable Stream

Buffer



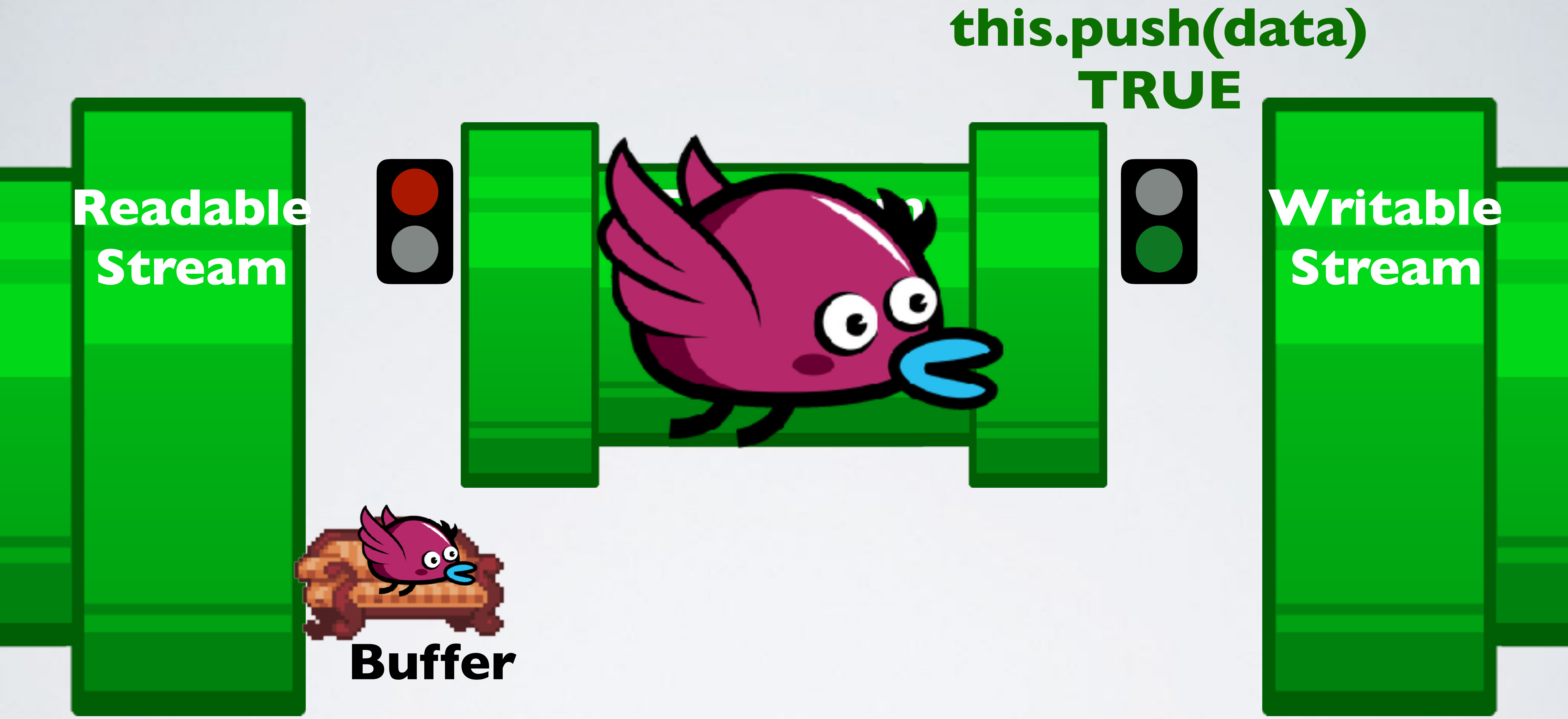
Readable Stream

Transform Stream

Writable Stream

callback()

Buffer



this.push(data)
TRUE
Readable Stream
Writable Stream
Buffer

this.push(data)
TRUE

Readable Stream

Writable Stream

Buffer

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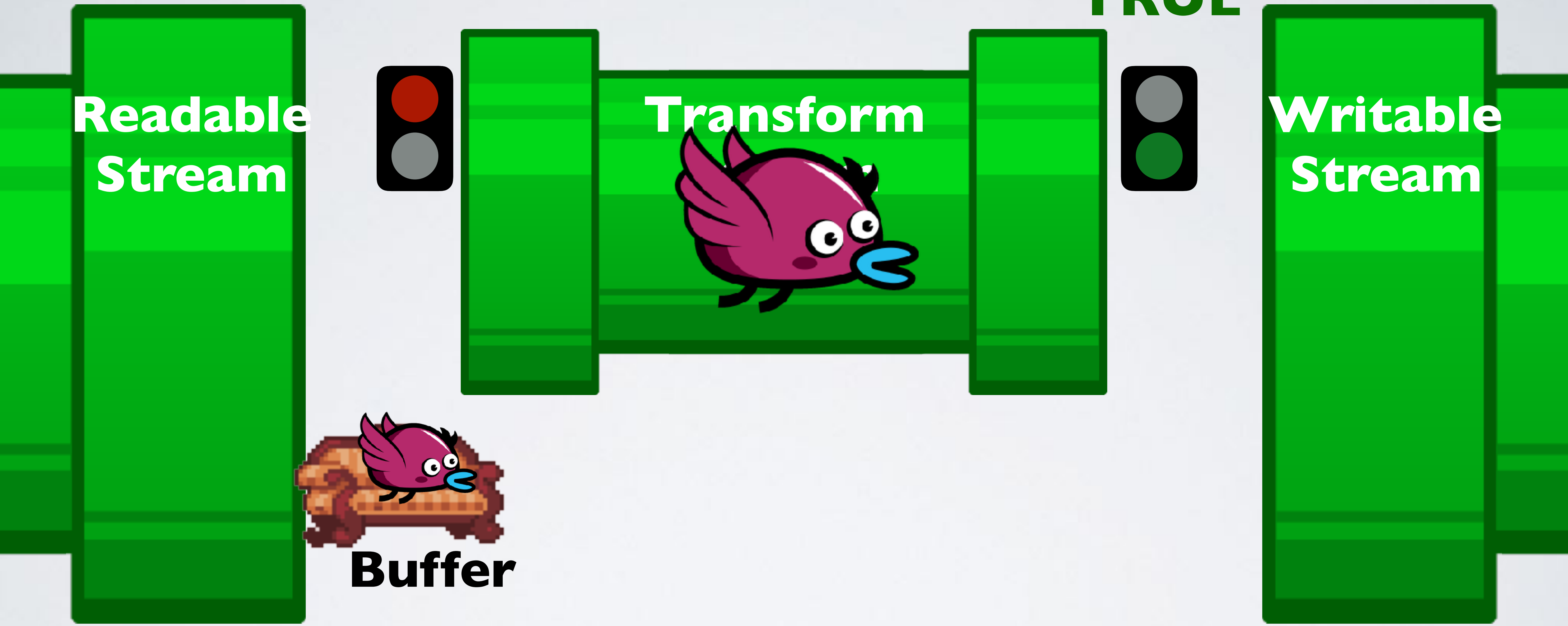
TRUE



Readable Stream

Transform

Writable Stream

Buffer

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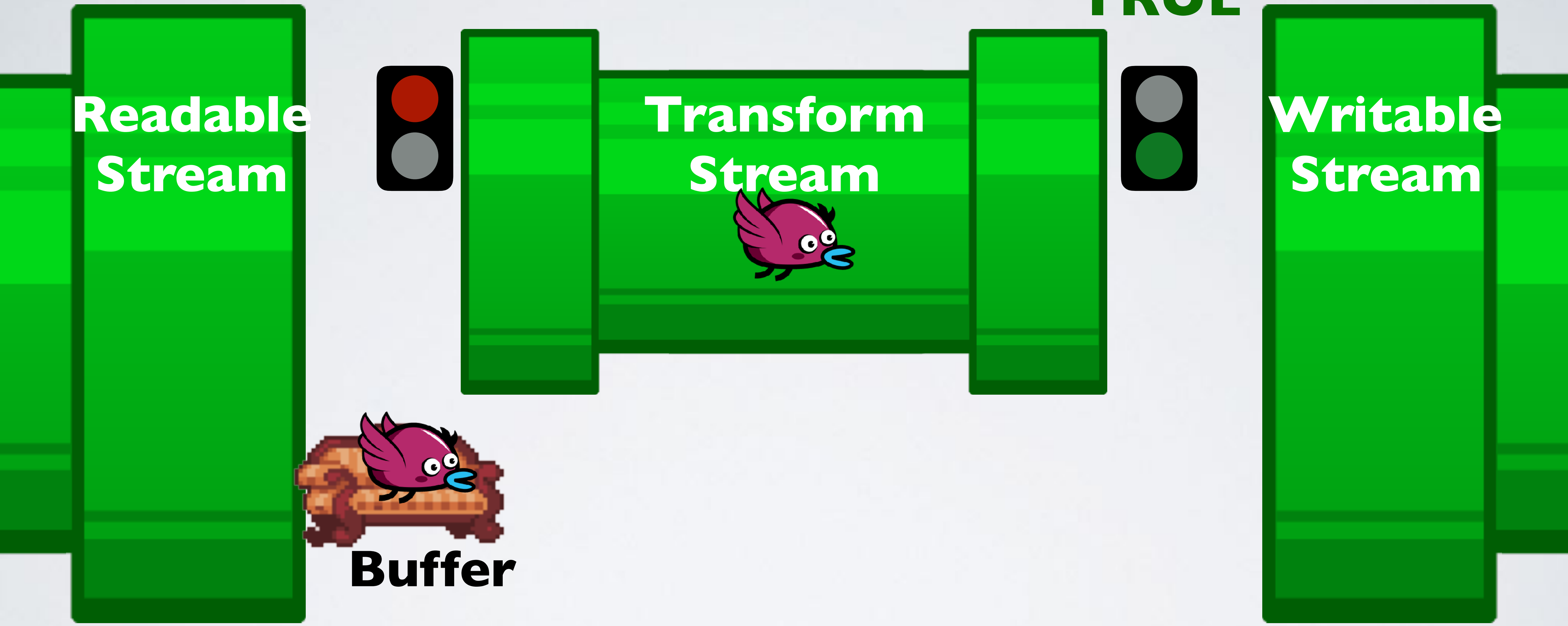

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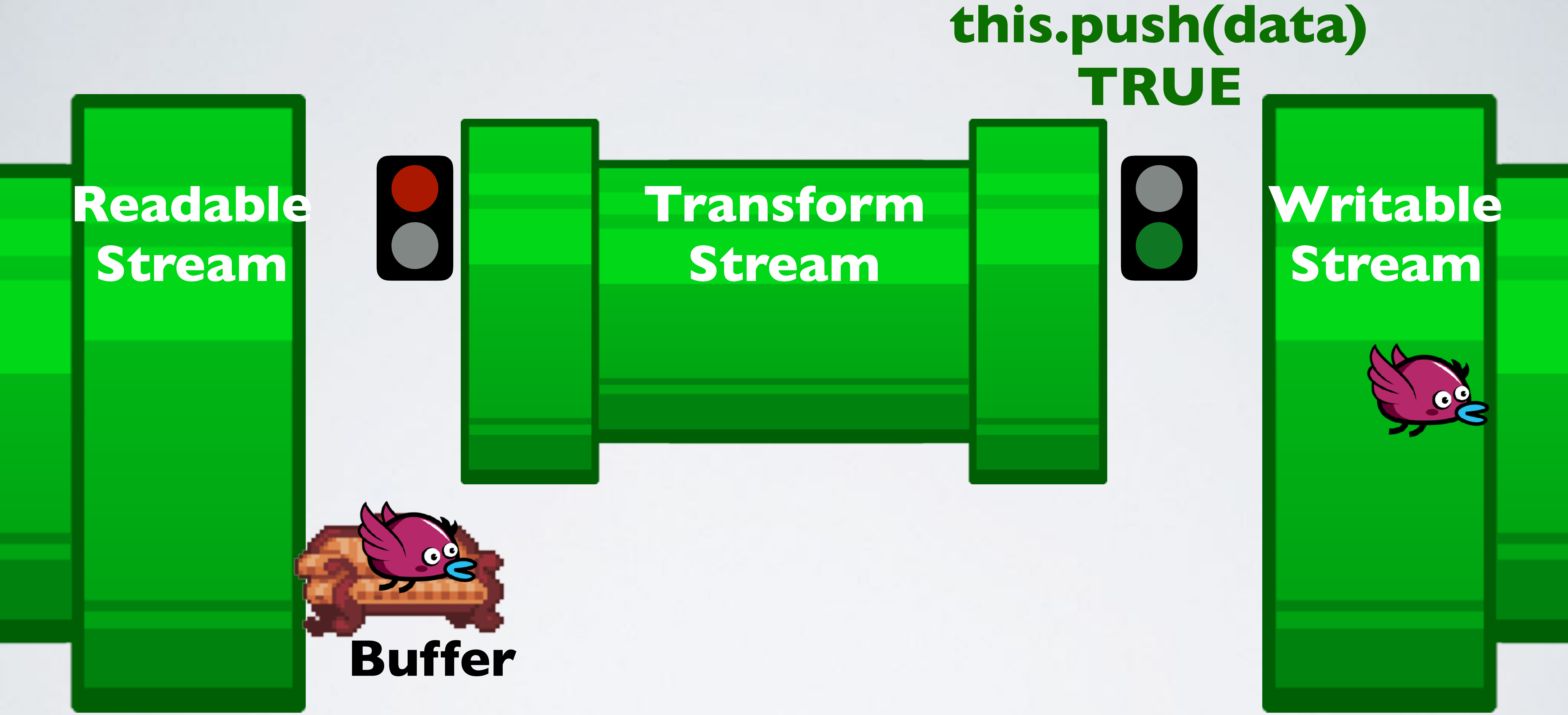

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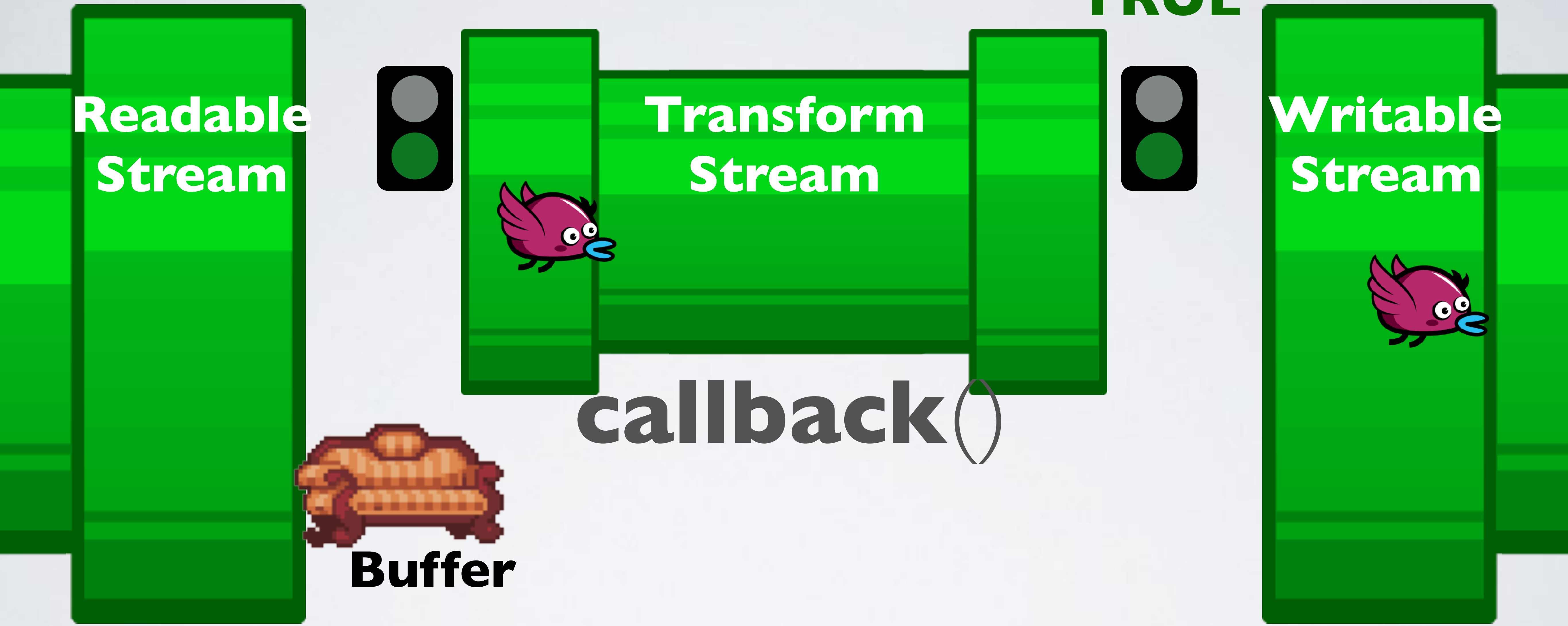

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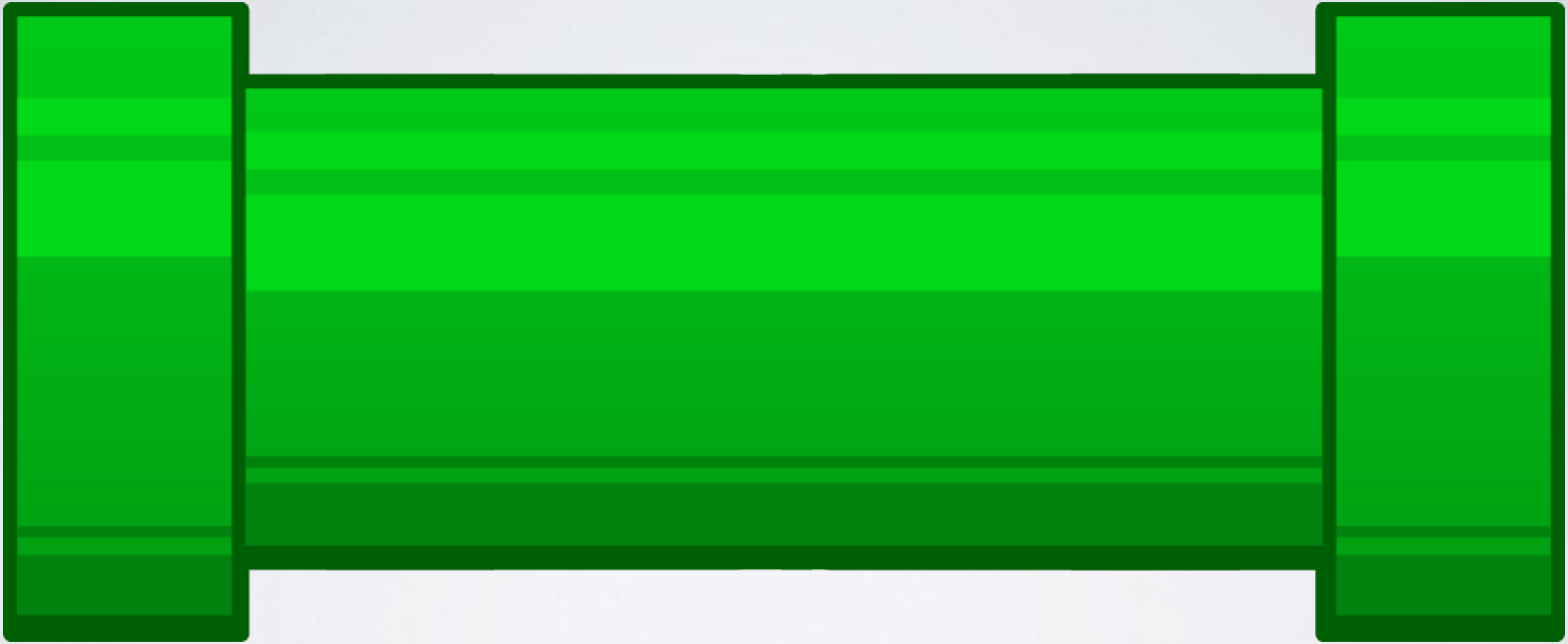
DUPLEX STREAM



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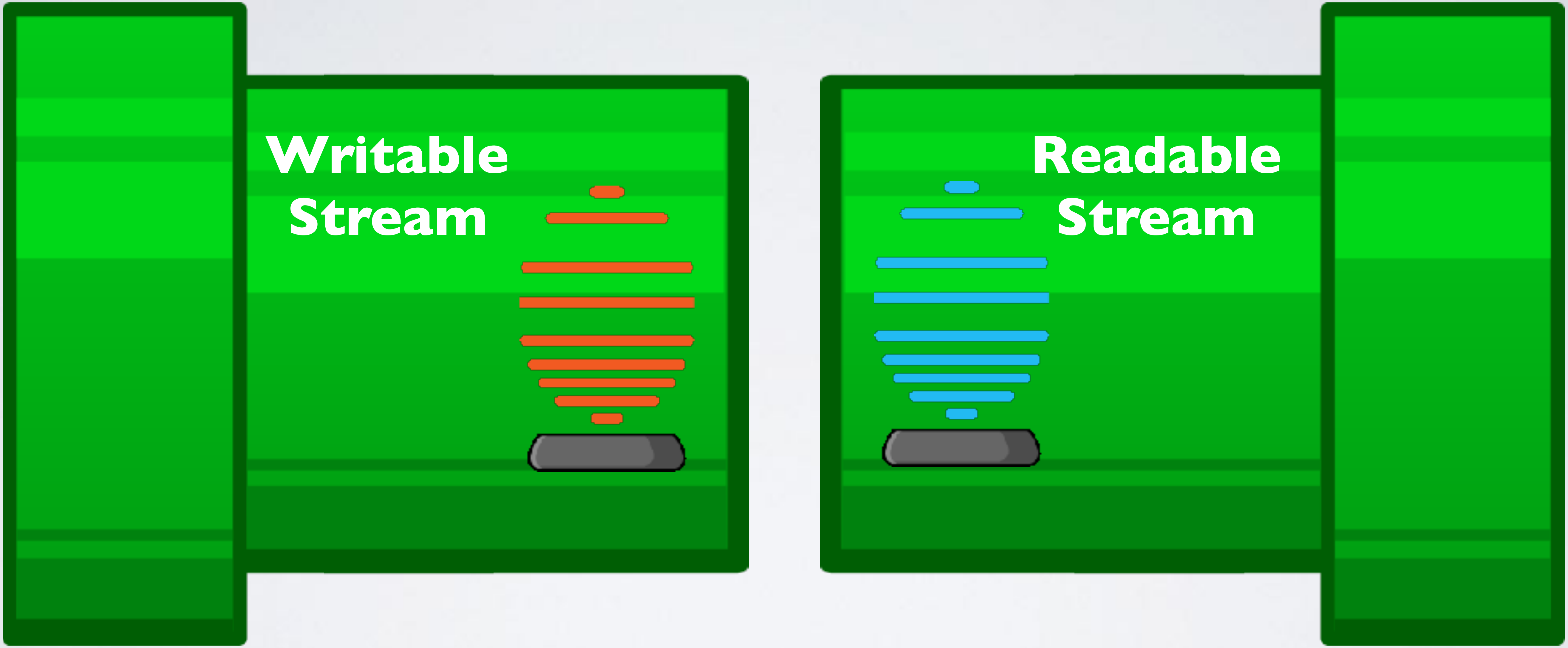

PASSTHROUGH STREAM

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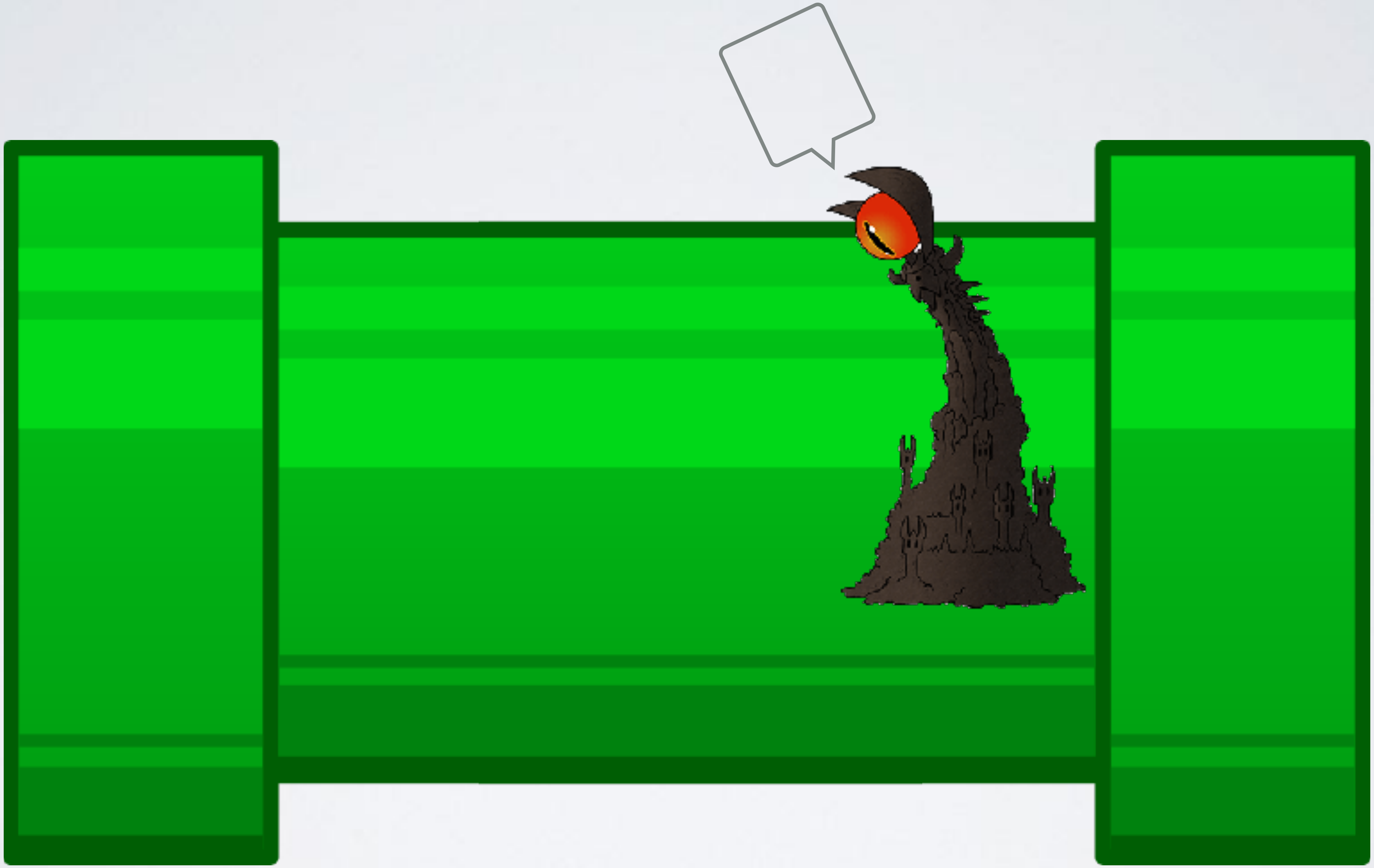

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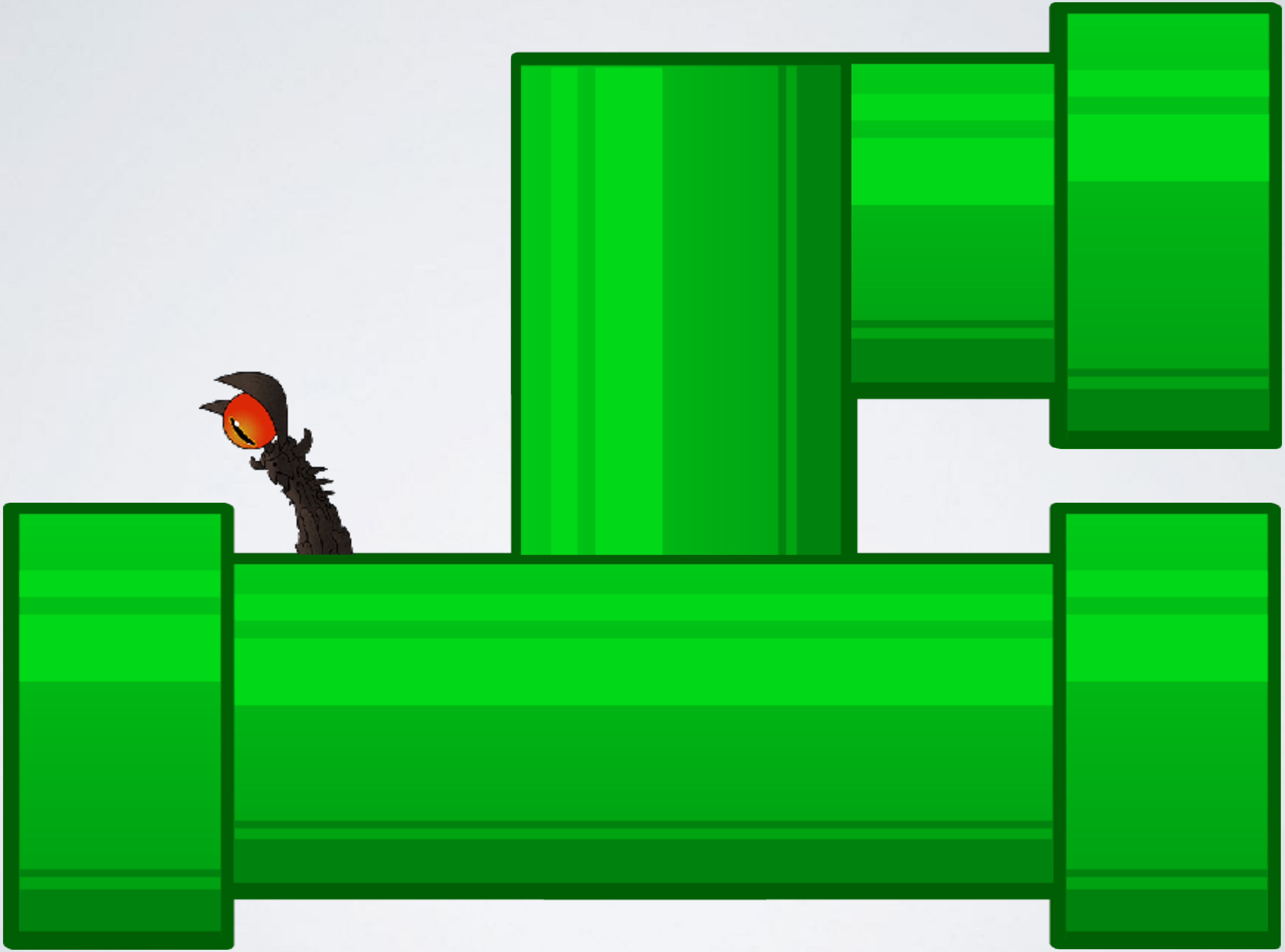

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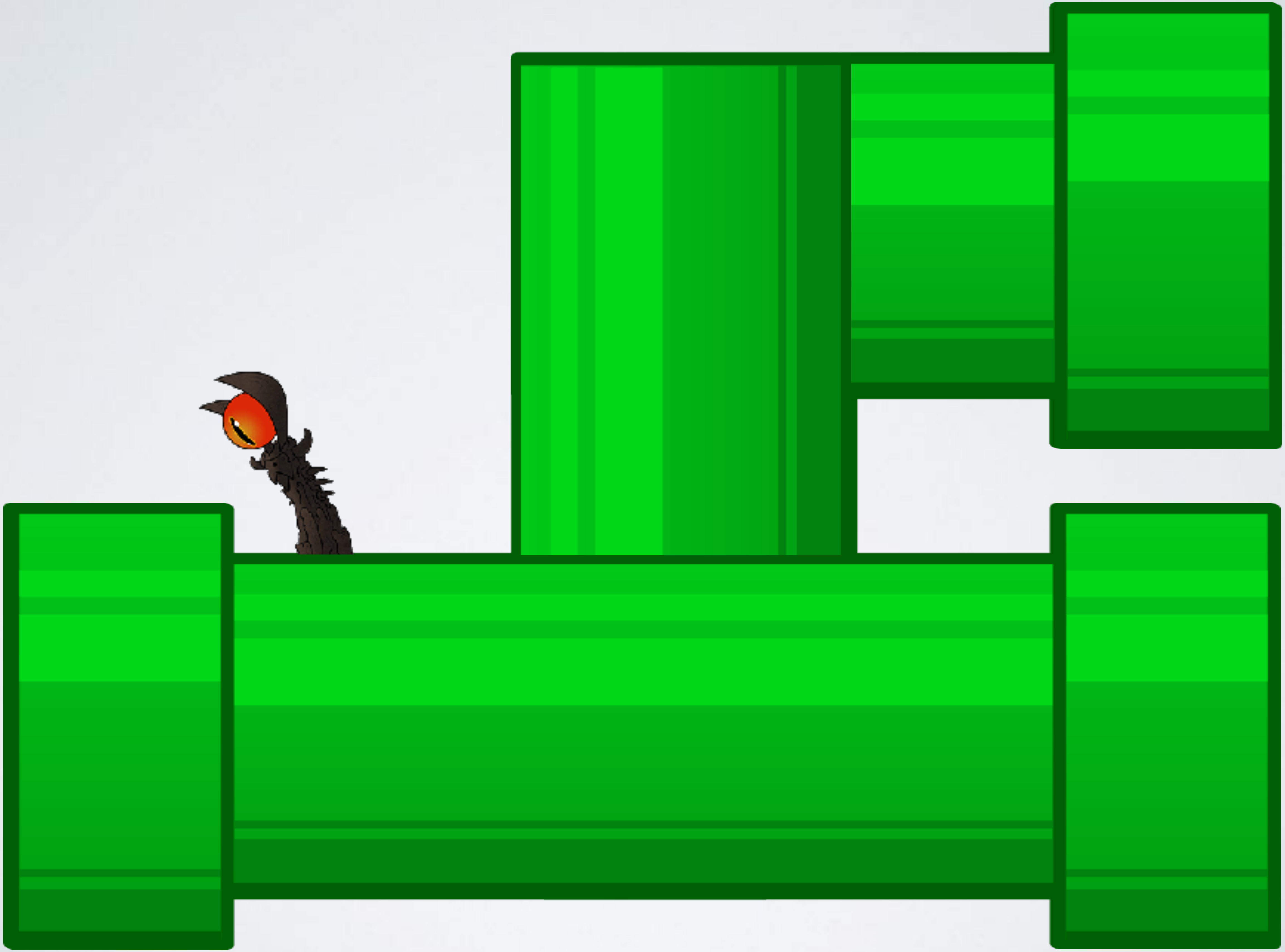

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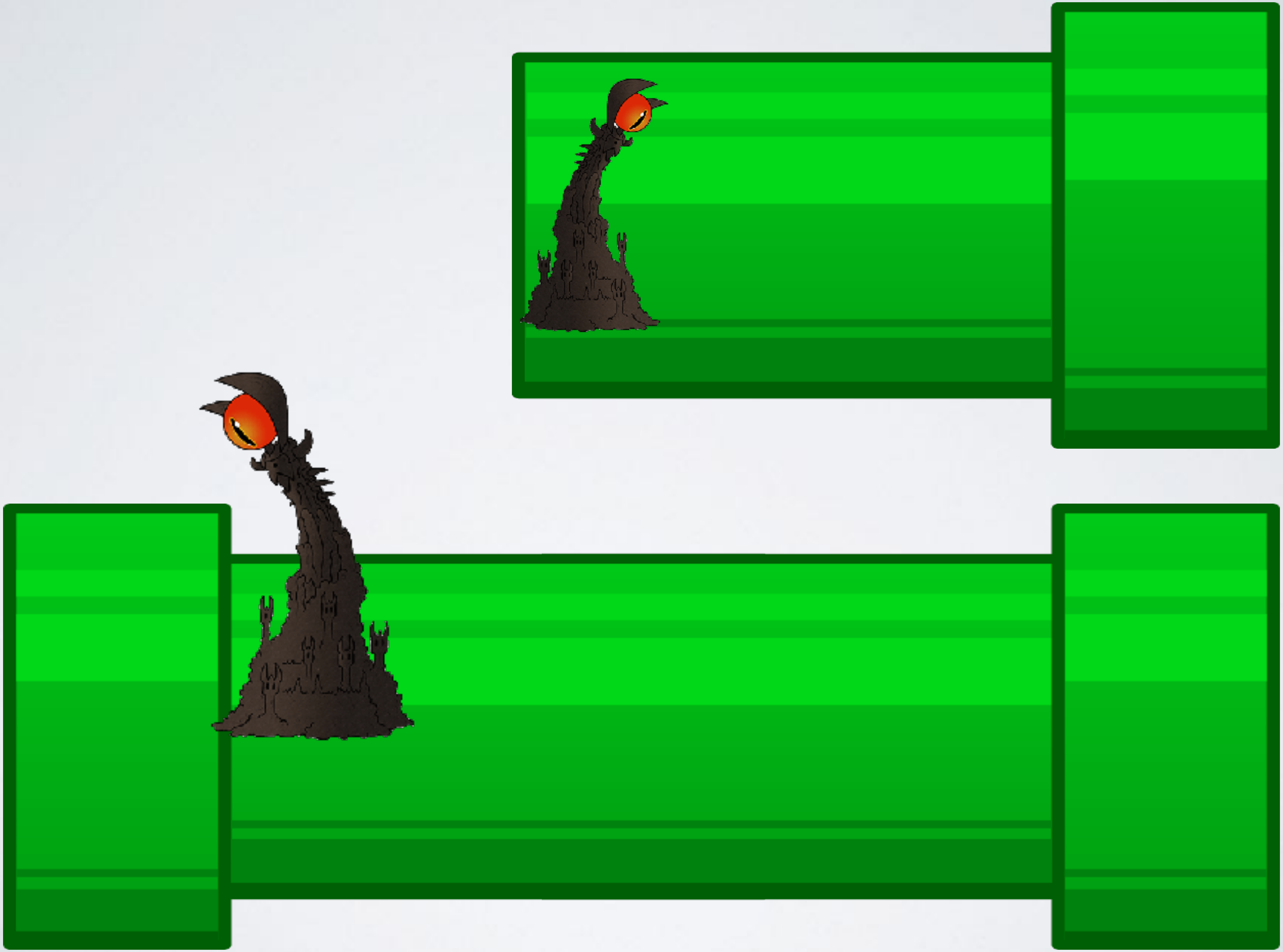

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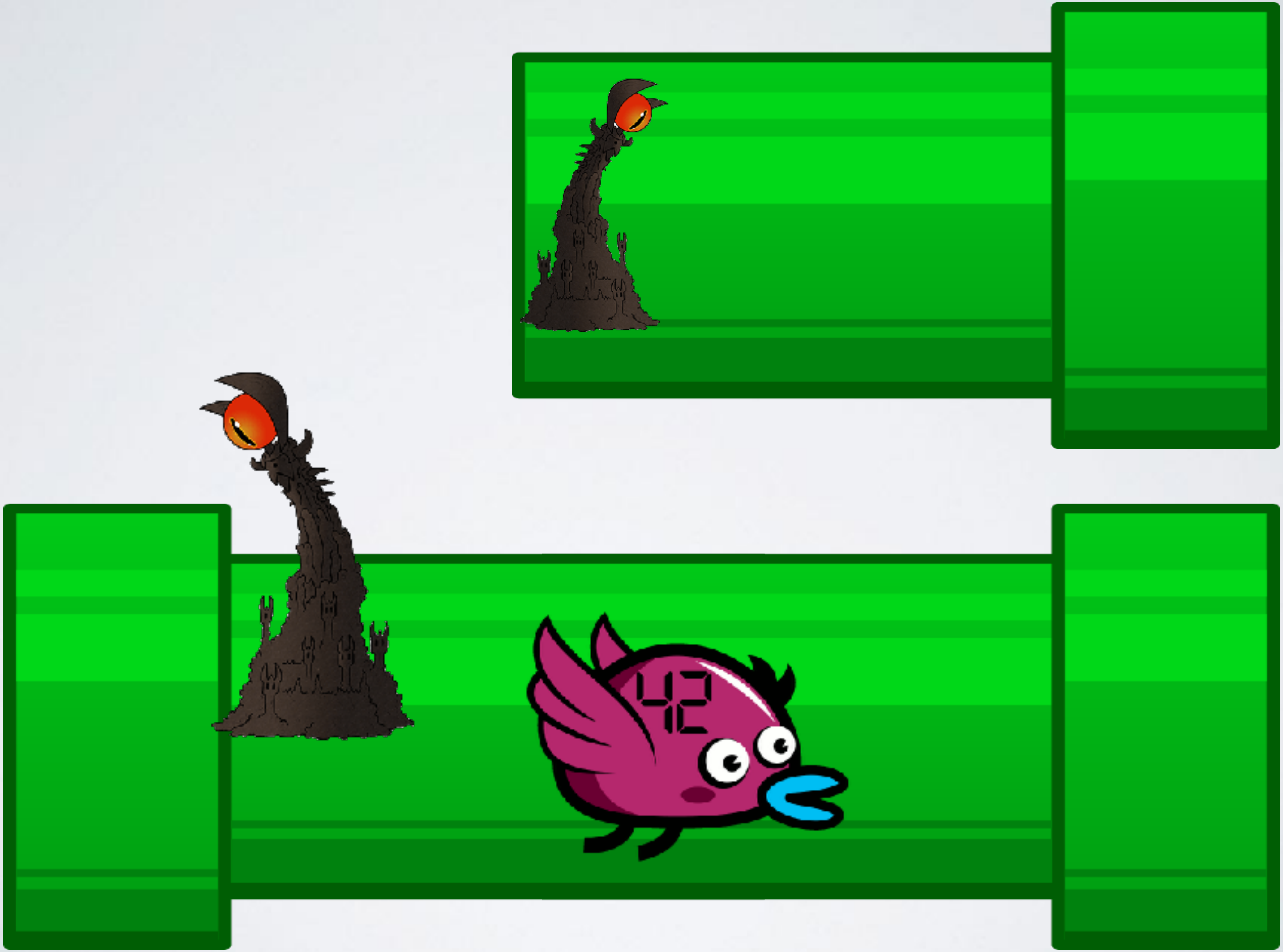

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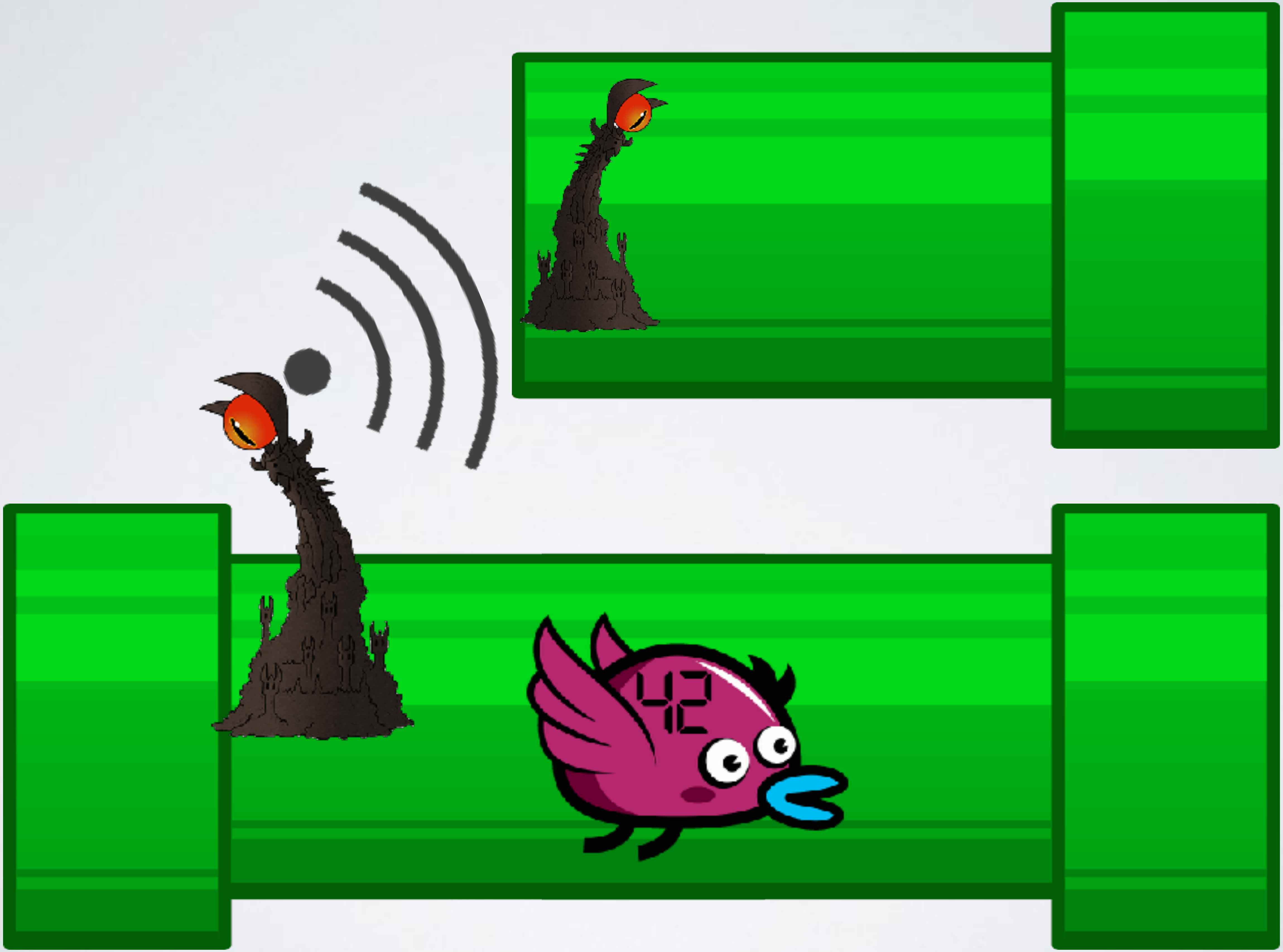

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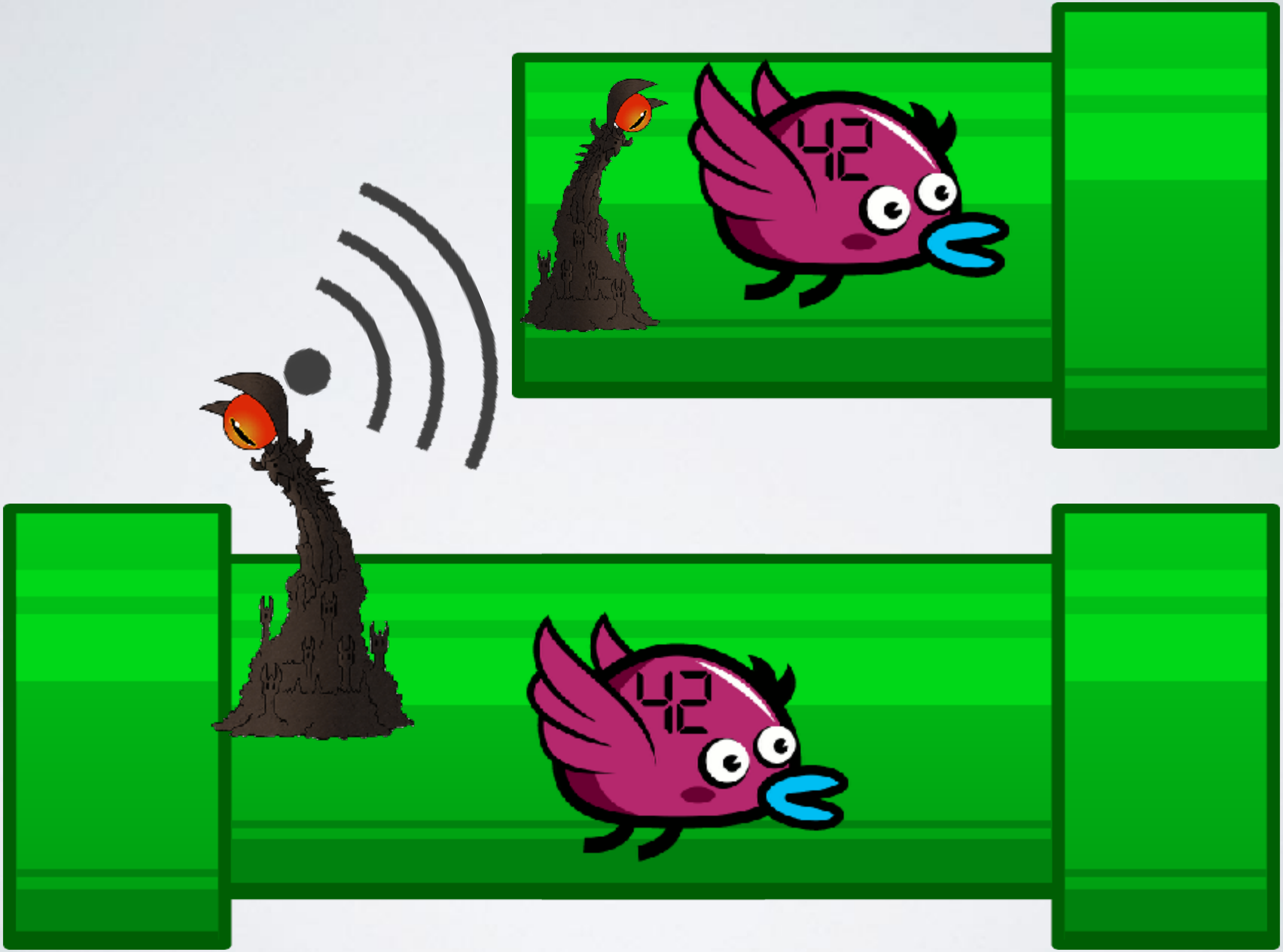
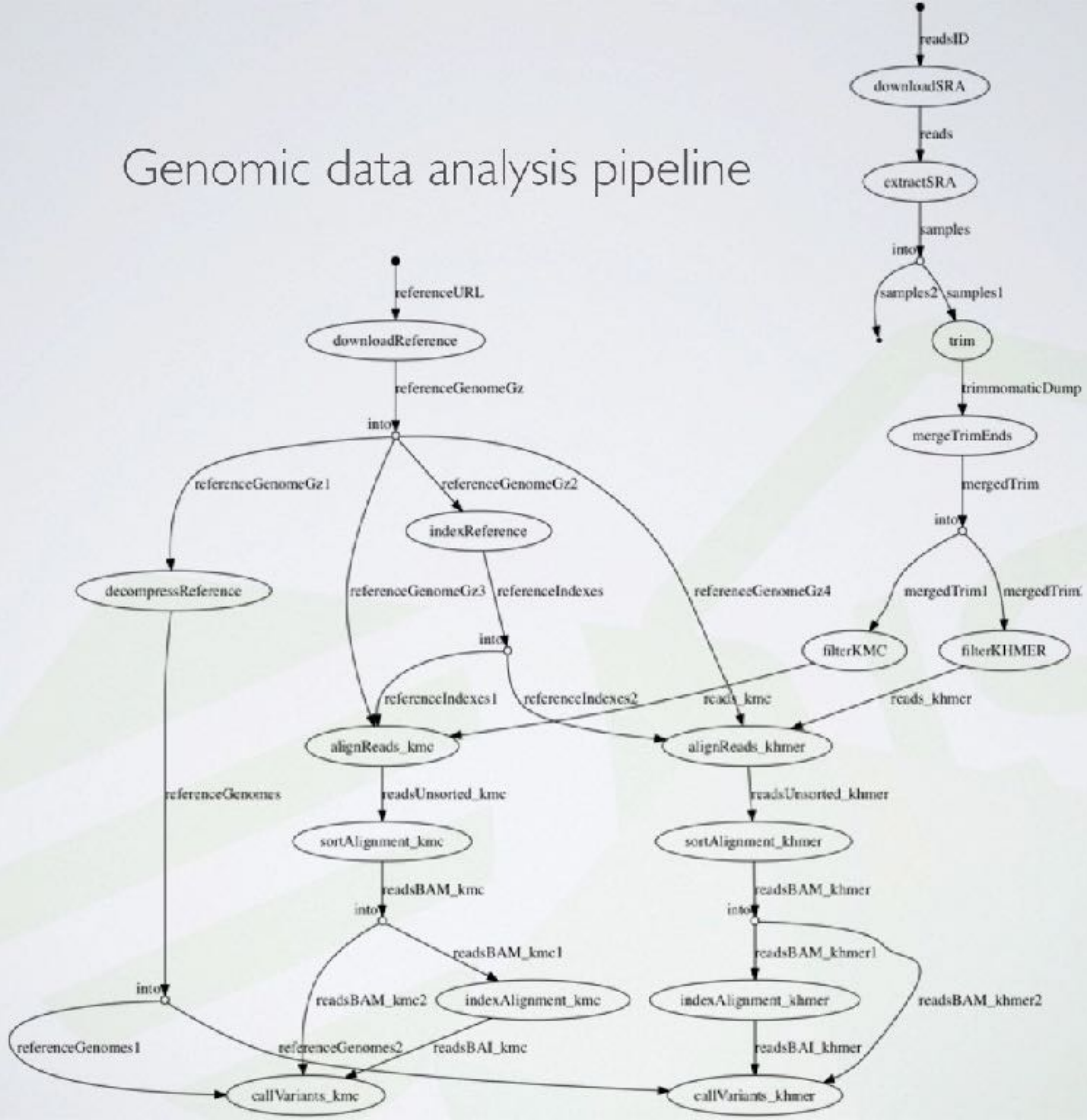


PASSTHROUGH STREAM

Genomic data analysis pipeline



bionode-watermill

A Streaming Workflow Engine for bioinformatics and other big data explorations

Google Summer of Code 2016

OBF

```
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

repositive.io

dat DATA

BioJS

mozilla Science Lab

- **More self-sustainable**

mozilla Science Lab

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  - Organise more hackathons to attract contributors, especially with more technical Node/JS background

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  - Use our existing connections to other projects like Dat (data versioning and distribution), BioJS (biological visualisation), CWL (common workflow language) to see if together we can build something amazing for Open Genomics

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  - Use the Mozilla fellowship to make new collaborations

SUNDAY 11:00

bionode.io

@bmpvieira

ACKNOWLEDGMENTS

Community

bionode.io

Research group

WurmLab
.github.io

Queen Mary
University of London

Funding

THE LEONA M. AND HARRY B.
HELMSLEY
CHARITABLE TRUST

mozilla
Science Lab

Friends

DNA
digest

repositive.io

dat
DATA

BioJS

COMMON
WORKFLOW
LANGUAGE

IMAGES SOURCES

http://opengameart.org/content/bevouliin-green-flappy-bird-sprite-sheets

http://neoriceisgood.deviantart.com/art/100-furniture-sprites-405058884

http://android272.deviantart.com/art/Teeworlds-Teleport-570298308

http://www.how-to-draw-cartoons-online.com/eye-of-sauron.html