



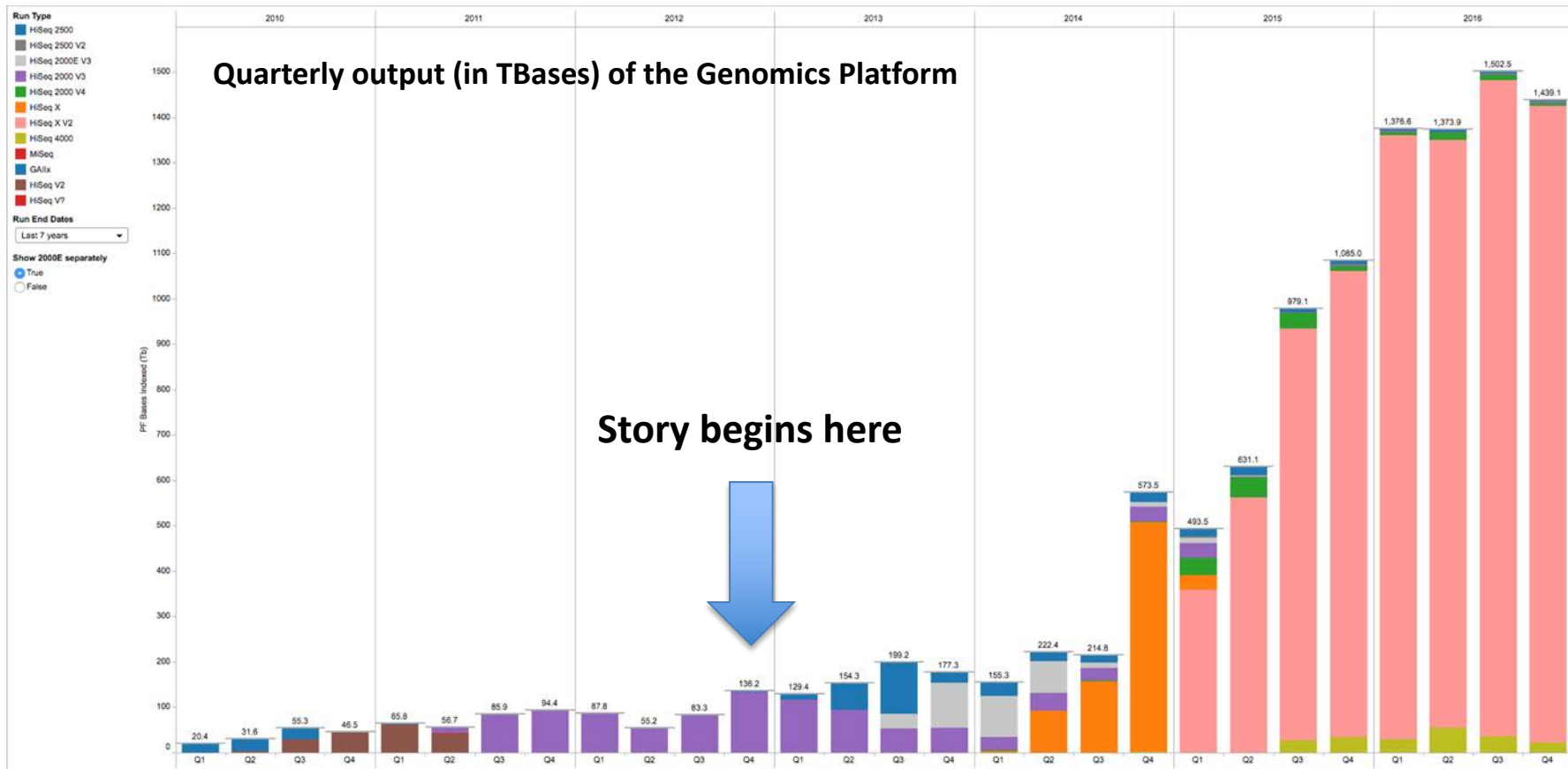
Getting started with WDL & Cromwell

Bioinformatics workflows at any scale

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Data Sciences Platform
Broad Institute

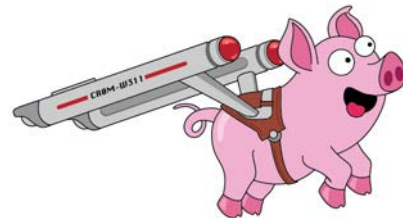


The backdrop: data generation set to explode

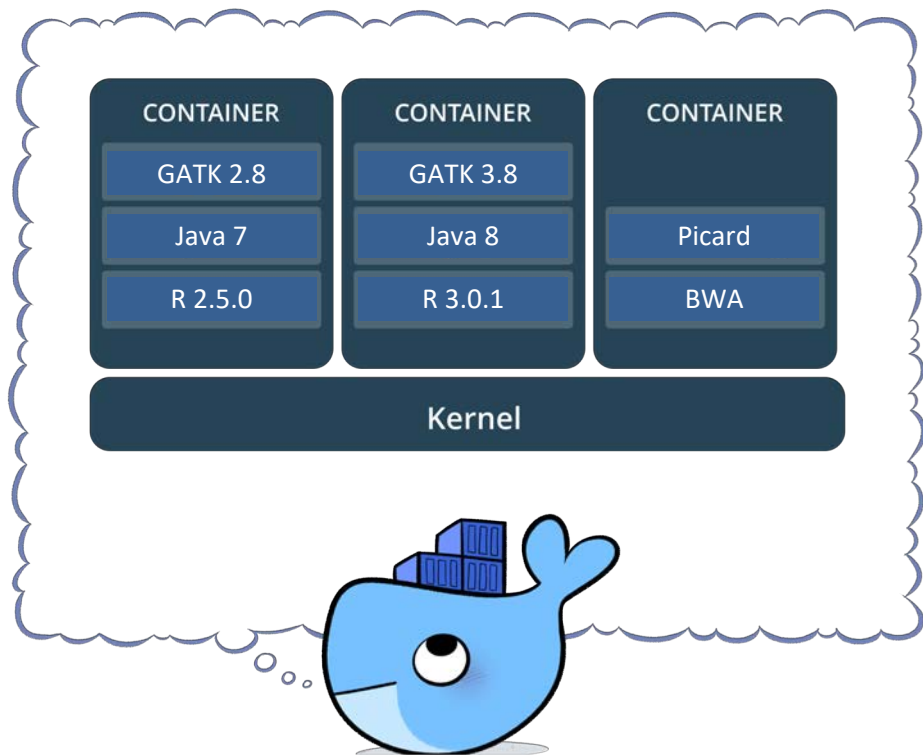


Meet Cromwell & WDL

- Execution engine that can
 - Run on any platform (HPC *and* on Cloud)
 - Seamlessly scale based on workflow needs
 - Provide maximal flexibility for all use cases
 - <https://github.com/broadinstitute/cromwell>
- Workflow language that humans can read/write
 - Methods developers and biomedical scientists at large
 - <https://github.com/openwdl/wdl/>



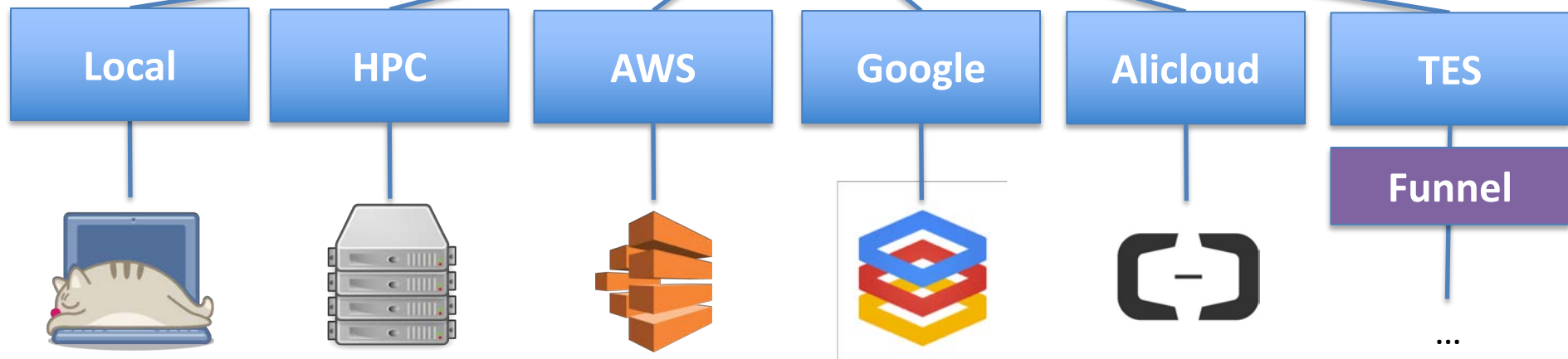
Use containers for portability & reproducibility



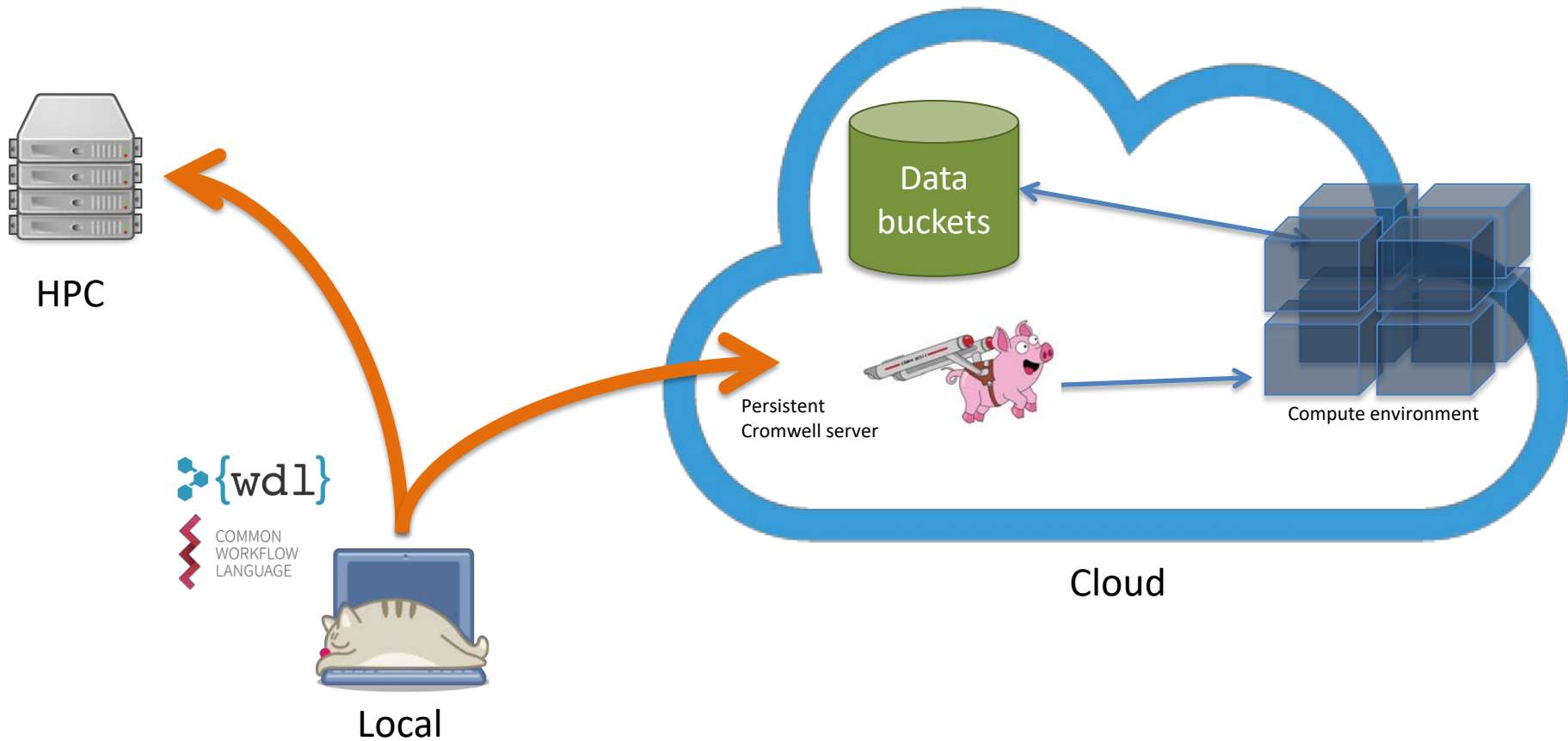
A container encapsulates all the software dependencies associated with running a program

Takes the guesswork out of running workflows on different platforms!

Use a workflow execution engine that runs anywhere



Run using HPC and Cloud resources!





Two main ways to run Cromwell

Command Line

- Simple, self-contained command
- Appropriate for independent analysts
- Call Caching

```
java -jar cromwell.jar \  
  run hello.wdl \  
  hello_inputs.json
```

Server

- API endpoints
- More scalable, appropriate for production environments
- Call caching

Cromwell Server REST API ³⁰

[/swagger/cromwell.yaml](#)

Describes the REST API provided by a Cromwell server

[BSD](#)

Workflows ▾

- POST** `/api/workflows/{version}` Submit a workflow for execution
- POST** `/api/workflows/{version}/batch` Submit a batch of workflows for execution

HPC Backend Configuration

Managing data

- Root directory
- Data handling strategies
- Support for object stores

```
backend.providers.MyHPCBackend {  
  config.root = "/path/to/execution_directory"  
  filesystems {  
    local {  
      localization: [  
        "hard-link", "soft-link", "copy"  
      ]  
    },  
    gcs { ... },  
    s3 { ... }  
  }  
}
```

<https://cromwell.readthedocs.io/en/stable/tutorials/HPCIntro/>

HPC Backend Configuration



Managing resources

- CPU
- Memory
- Custom attributes

```
backend.providers.SGE.config {  
  runtime-attributes = ""  
  Int cpu = 1  
  Float? memory_gb  
  String? sge_queue  
  String? sge_project  
  ""  
}
```

<https://cromwell.readthedocs.io/en/stable/tutorials/HPCIntro/>

HPC Backend Configuration

Run command

- Built-in variables
- Full flexibility

```
backend.providers.SGE.config {  
  check-alive = "qstat -j ${job_id}"  
}
```

```
backend.providers.SGE.config {  
  kill = "qdel ${job_id}"  
}
```

```
backend.providers.SGE.config {  
  submit = ""  
  qsub \  
  -terse \  
  -V \  
  -b y \  
  -N ${job_name} \  
  -wd ${cwd} \  
  -o ${out}.qsub \  
  -e ${err}.qsub \  
  -pe smp ${cpu} \  
  ${"-l mem_free=" + memory_gb + "g"} \  
  ${"-q " + sge_queue} \  
  ${"-P " + sge_project} \  
  /usr/bin/env bash ${script}  
  ""  
}
```

<https://cromwell.readthedocs.io/en/stable/tutorials/HPCIntro/>

Plenty of workflow solutions to go around



So of course we decided to create a new one.

Workflow description Language (WDL)



```
workflow myWorkflowName {
```

```
File my_ref  
File my_input  
String name
```

```
call task_A {
```

```
input: ref= my_ref, in= my_input, id= name
```

```
}
```

```
call task_B {
```

```
input: ref= my_ref, in= task_A.out
```

```
}
```

```
}
```

```
task task_A { ... }
```

```
task task_B { ... }
```

```
task task_A {
```

```
File ref  
File in  
String id
```

```
command {
```

```
do_stuff -R ${ref} -I ${in} -O ${id}.ext
```

```
}
```

```
runtime {
```

```
docker: "my_project/do_stuff:1.2.0"
```

```
}
```

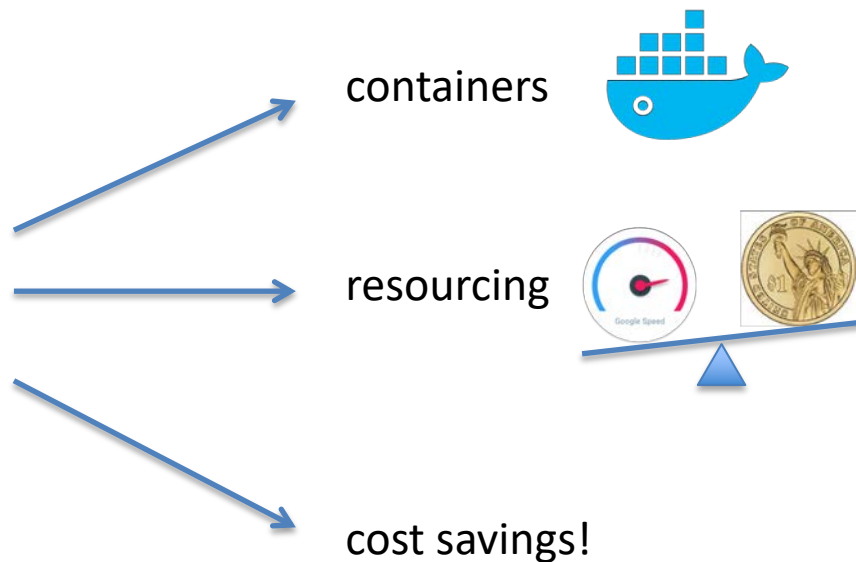
```
output {
```

```
File out= "${id}.ext"
```

```
}
```

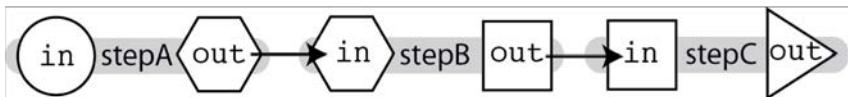
```
}
```

```
task echoHelloWorld {  
  command {  
    echo 'Hello, World!'  
  }  
  runtime {  
    docker: "phusion/baseimage"  
    disks: "local-disk 10 HDD"  
    memory: "1 GB"  
    preemptible: 3  
  }  
}  
  
workflow printHelloAndGoodbye {  
  call echoHelloWorld  
}
```



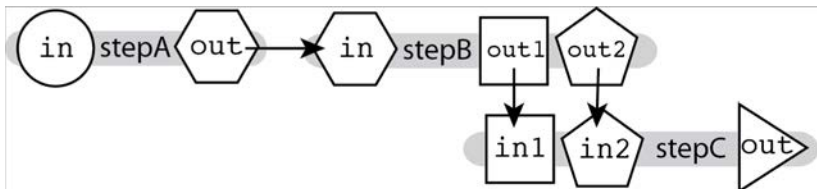
Basic WDL plumbing options

LINEAR CHAINING



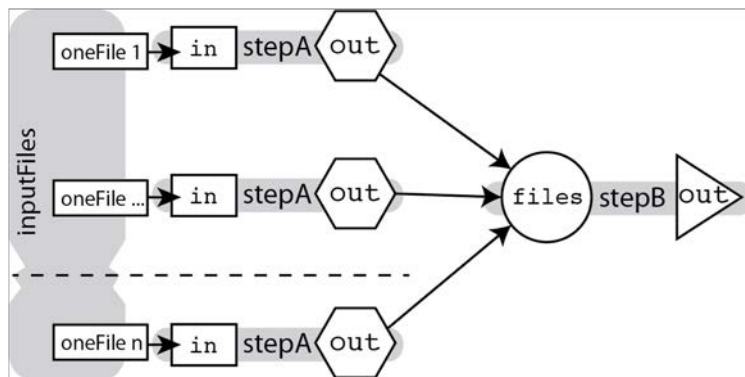
```
call stepA
call stepB { input: in=stepA.out }
call stepC { input: in=stepB.out }
```

MULTI-IN/OUT



```
call stepC { input :
    in1=stepB.out1,
    in2=stepB.out2 }
```

SCATTER-GATHER



```
Array[File] inputFiles

scatter(oneFile in inputFiles) {
    call stepA { input: in=oneFile }
}

call stepB { input: files=stepA.out }
```

But what about CWL?



Randall Munroe, XKCD
<https://www.xkcd.com/1739/>



Multiple workflow languages coming to Cromwell, starting with CWL

Posted by jgentry on 2 Jan 2018

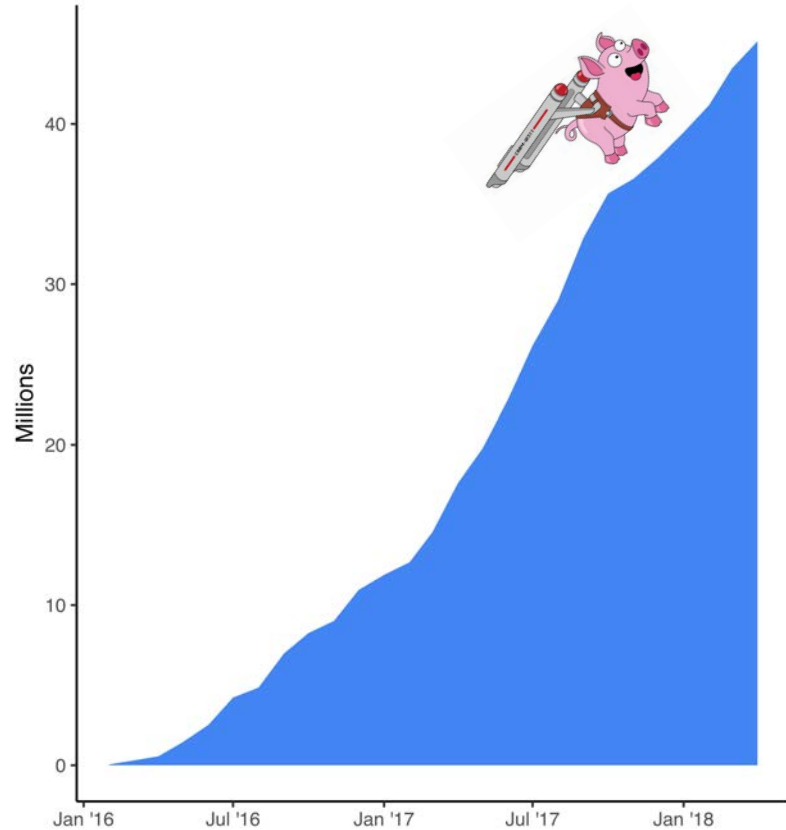
Thanks to our **Workflow Object Model (WOM)**, Cromwell now supports multiple versions of WDL as well as CWL 1.0!

Cromwell has been busy

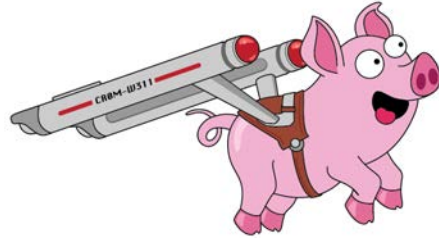
Cromwell in production at Broad:

Processed **47.5 million jobs**
over the last two years

And this is just the tip of the iceberg!



Want to discuss further?



My Email:

rmunshi@broadinstitute.org

More Information:

Docs: <http://cromwell.readthedocs.io/en/develop/>

Github: <https://www.github.com/broadinstitute/cromwell>

WDL: <http://www.openwdl.org>

Example Pipelines: <https://github.com/gatk-workflows>