



SLURM pipeline

Processing 115 billion NGS reads

Terry Jones
Dept. of Zoology
University of Cambridge
tcj25@cam.ac.uk



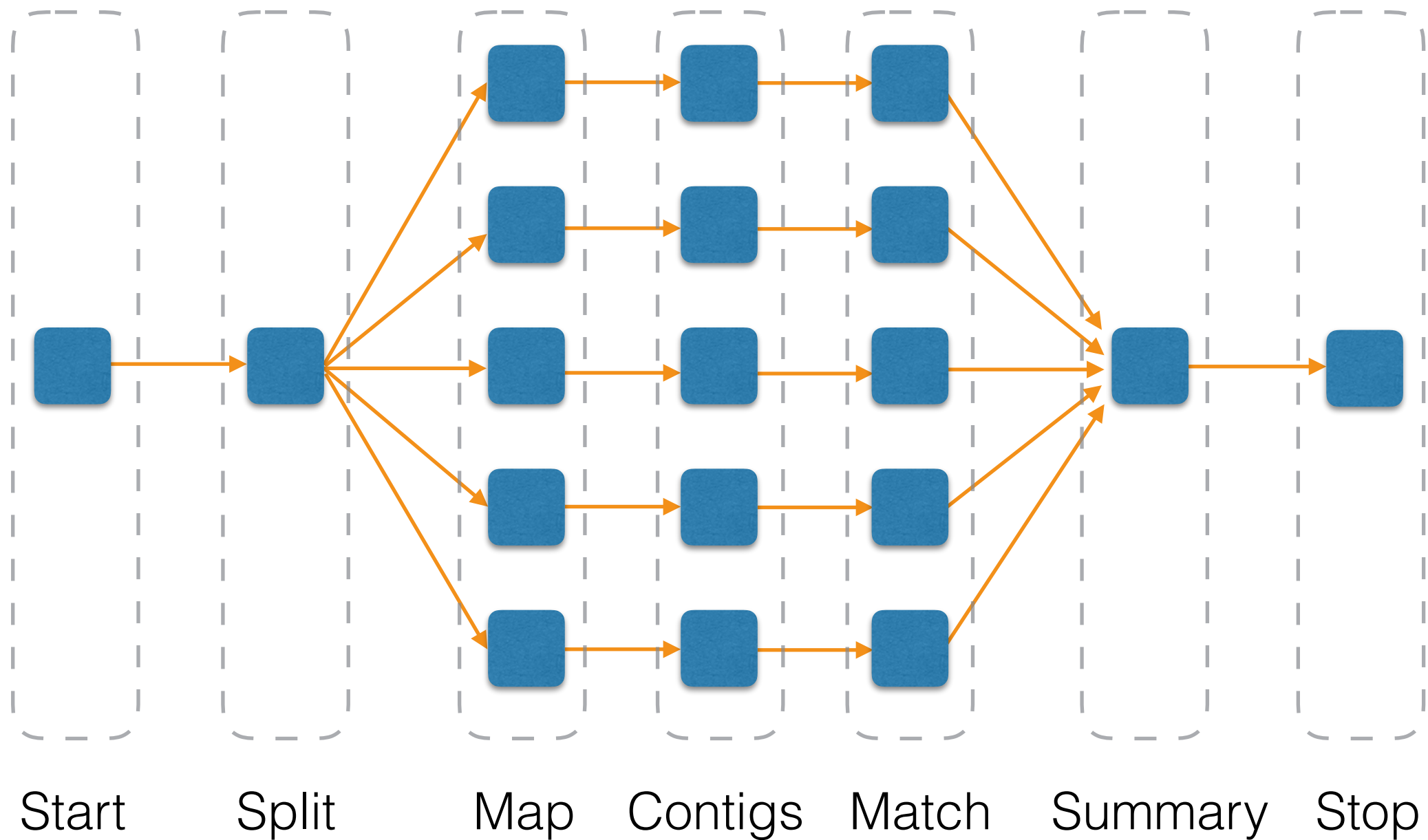
Ceci n'est pas une pipe.

Magritte
Lunpi

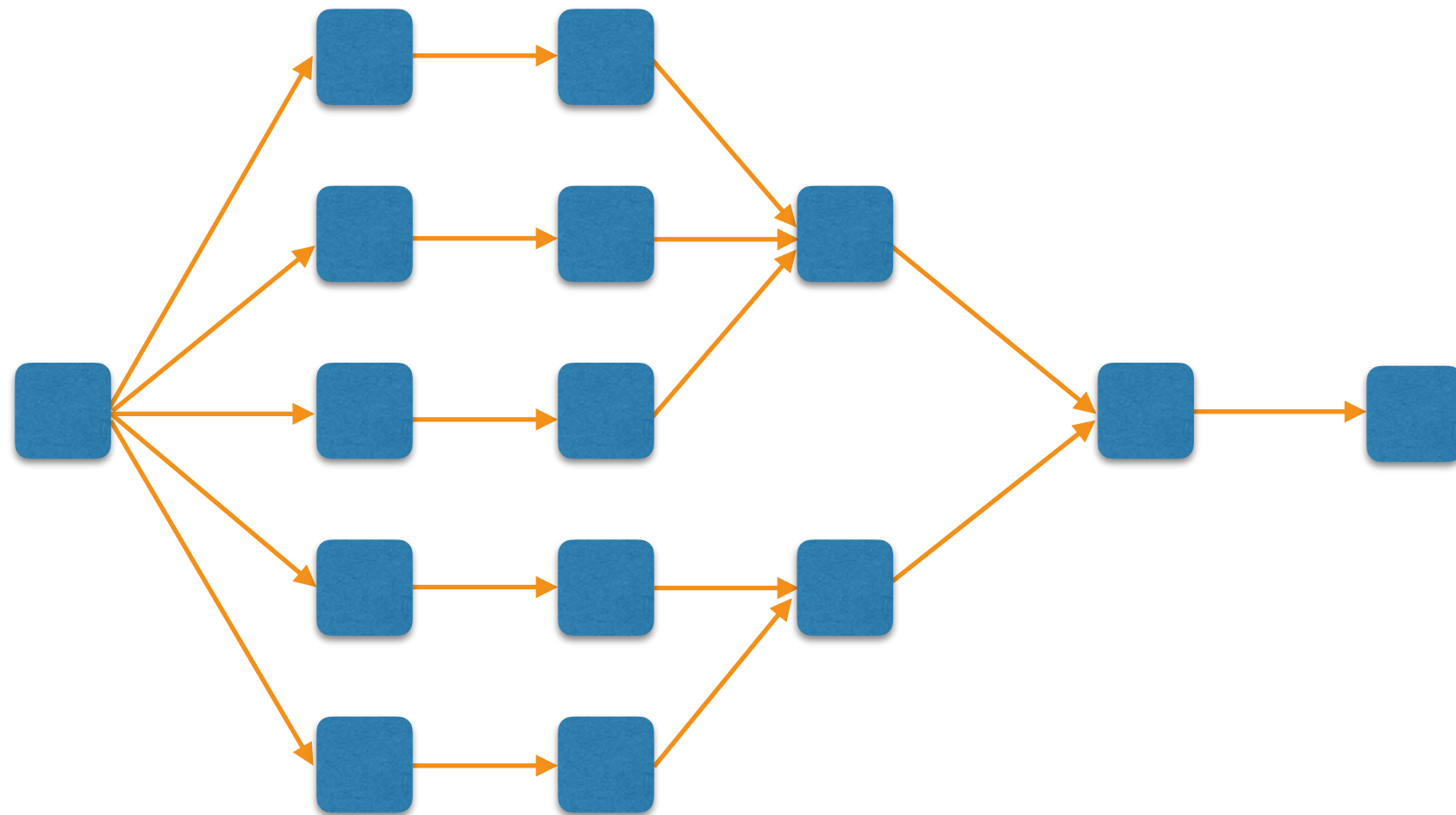


- Simple Linux Utility for Resource Management
- Resource allocation, job launch, manage queues
- Used on ~60% of the TOP500 supercomputers
- Open source (<https://slurm.schedmd.com/>)

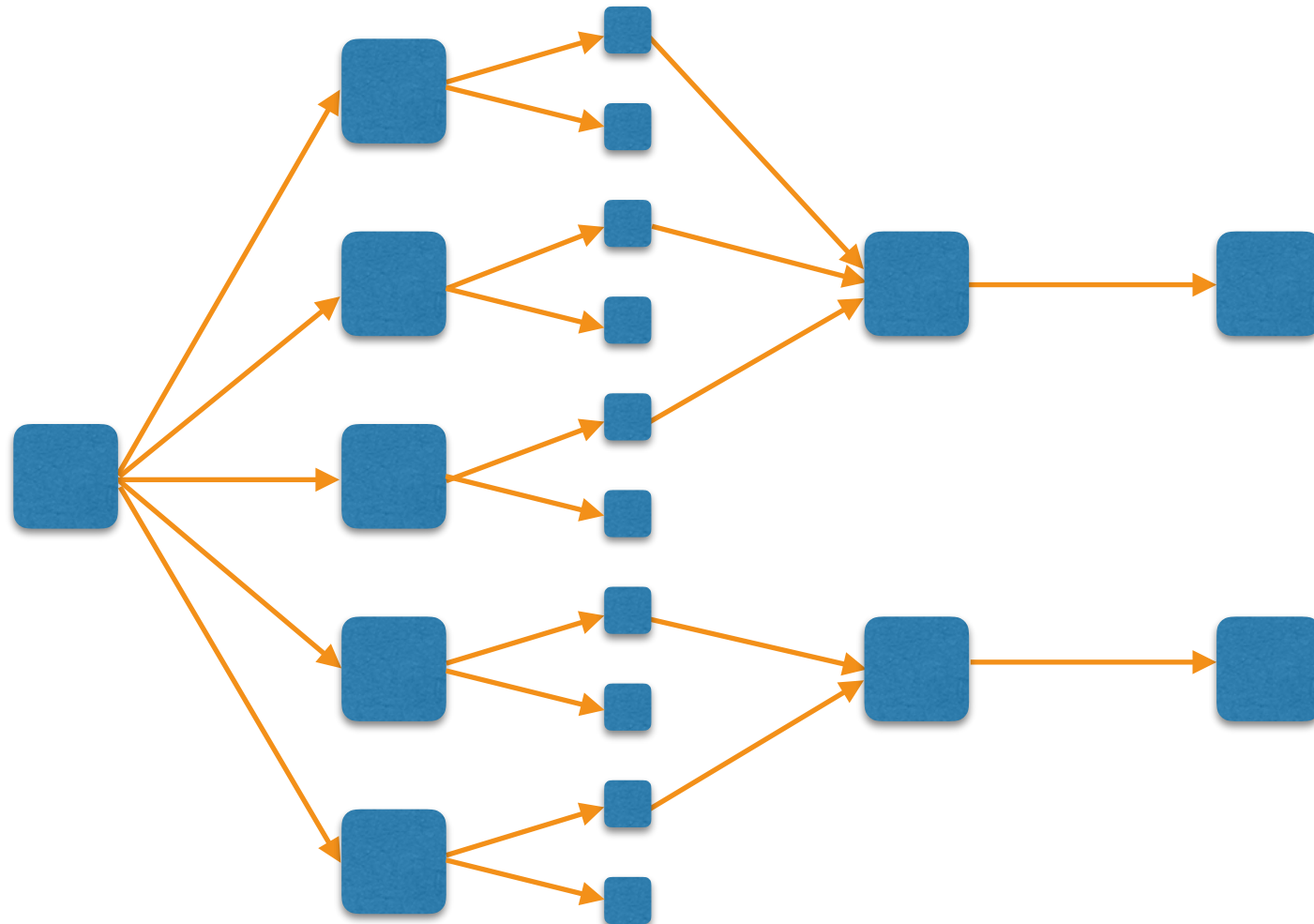
Typical NGS data flow



Alternate data flow



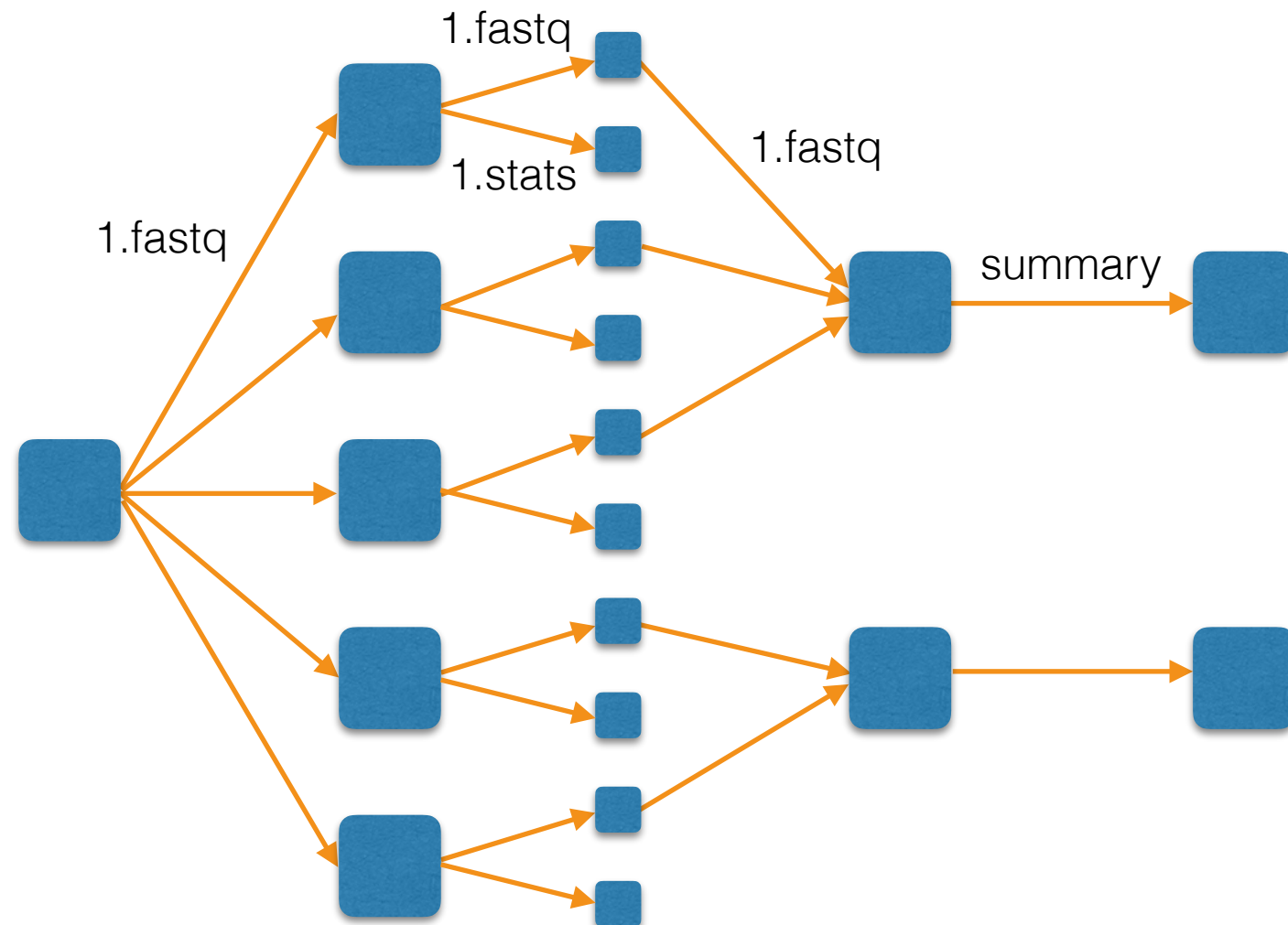
Yet another data flow



Aims

- Allow for these kinds of workflows
- Make specification as simple as possible
- Make no assumptions about underlying operations
- A formal framework for our pipelines

Steps and tasks



Steps are
conceptual,
tasks are
concrete

Steps: { { { { {

Tasks: → named tasks are emitted by steps

Pipeline specification (JSON)

```
{
  "steps": [
    {
      "name": "start-log",
      "script": "start-log.sh"
    },
    {
      "name": "split",
      "script": "split-fasta.sh"
    },
    {
      "dependencies": ["split"],
      "name": "blast",
      "script": "blast.sh"
    },
    {
      "collect": true,
      "dependencies": ["blast"],
      "name": "summarize",
      "script": "summarize.sh"
    },
    {
      "dependencies": ["summarize"],
      "name": "end",
      "script": "summarize.sh"
    }
  ]
}
```

The specification gives an ordered list of steps & their dependencies

A “collect” step runs after all the *tasks* emitted by its dependent steps are finished

Extras

- Start / stop at arbitrary pipeline steps
- Allow simulation and step skipping
- Add tools to inspect, cancel, start after jobs

Open source

- Written in Python
- <https://github.com/acorg/slurm-pipeline>
- Documentation, tests, examples
- We built multiple pipelines, to process 115 billion NGS reads in various ways