yes, we have a deluge of data

and sometimes, it does seem very big...

and yes, there are ways to crunch it fast…

flowr

Streamlining Workflows

speed up analysis using a computing cluster

why bother?

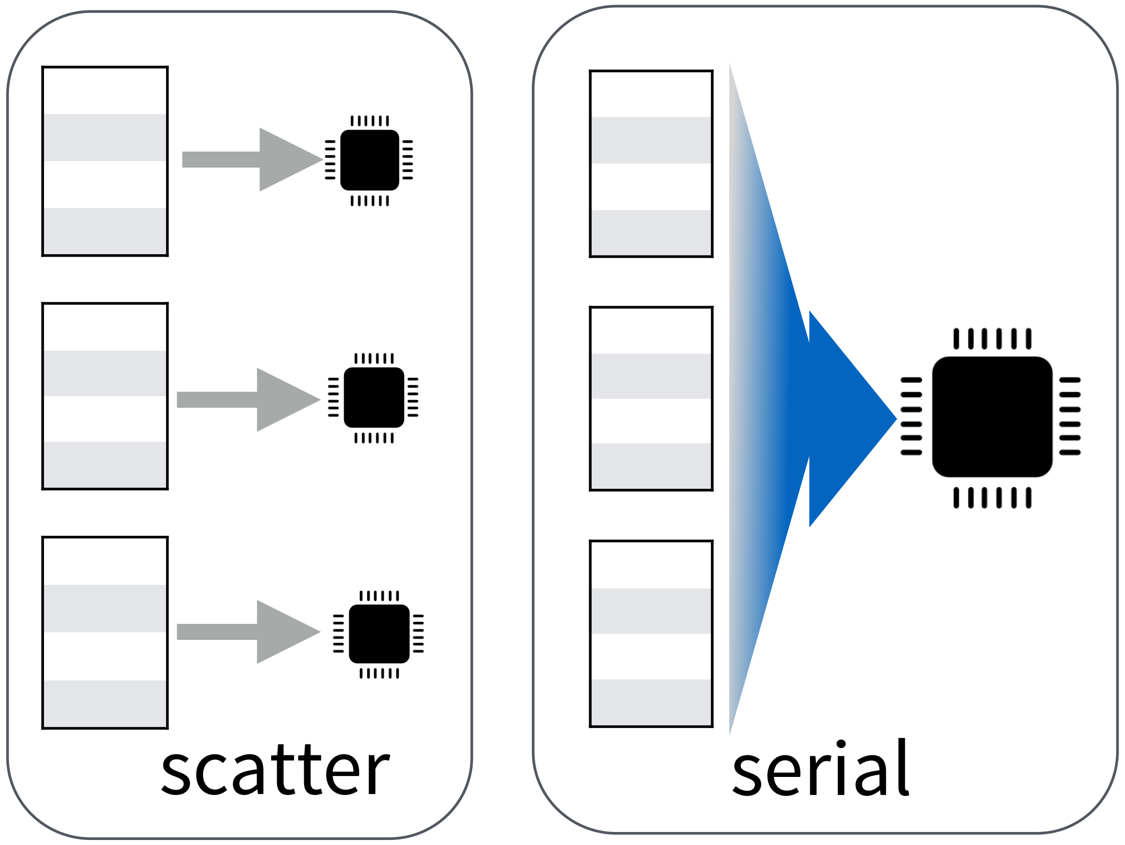
- ➡when one needs to wrangle a lot of data
- ➡and there are multiple steps involved
- ➡esp. when some of the steps can be further broken down and processed in parallel
- ➡use a computing cluster, submit a web of jobs

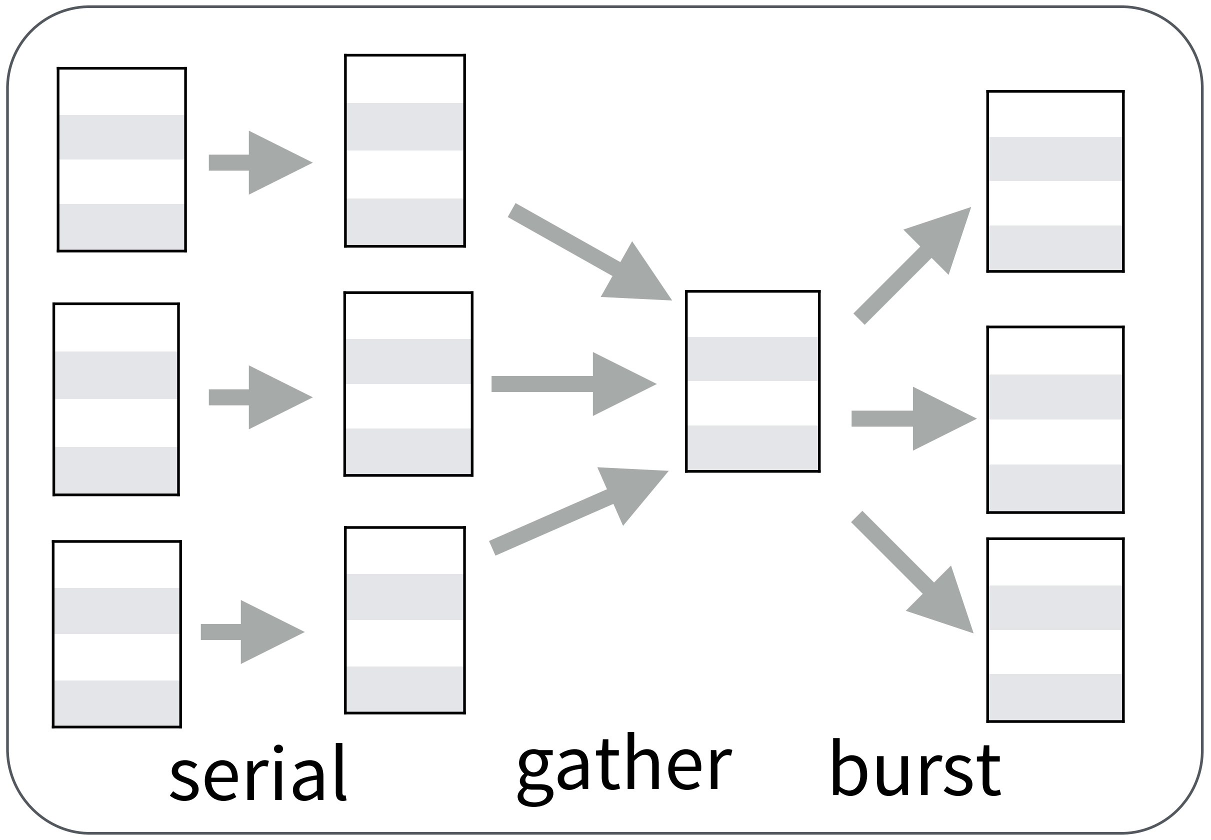
- ✓ Effectively process a **multi-step pipeline**, spawning it across the computing cluster
- ✓ **Reproducible** and **transparent**, with cleanly structured execution logs
- ✓ **Track** and **re-run** flows
- ✓ **Lean** and **Portable**, with easy installation
- ✓ Run the same pipeline in the cloud (using star cluster) OR a local machine
- ✓ Supports **multiple cluster computing platforms** (torque, lsf, sge, slurm …)

five simple terms, defining all relationships

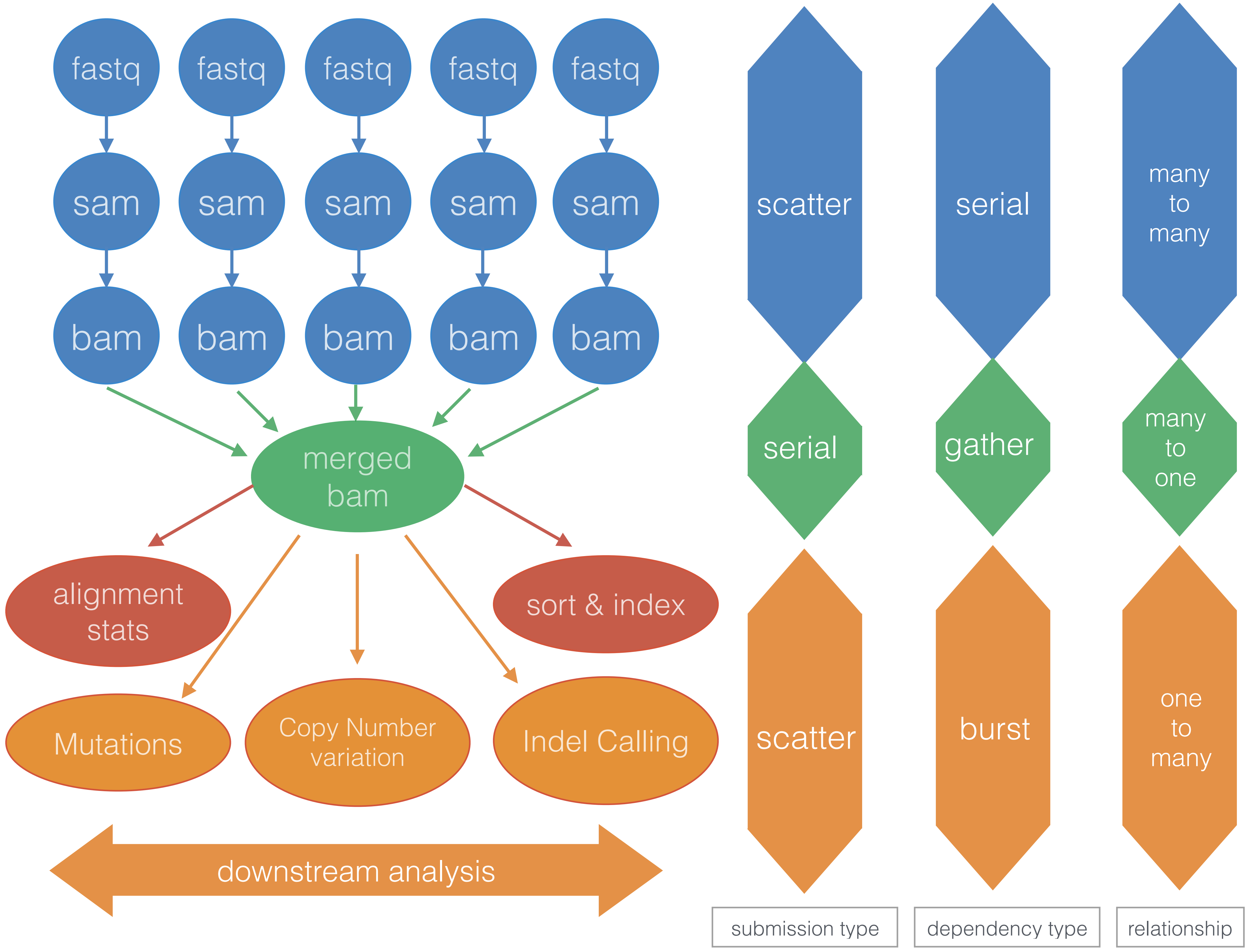
submission types

dependency types





Using a genomics example flow, with flowr concepts



All attributes of this flow can be defined using these concepts

a simple pipeline, where

- ★ we would sleep for a few seconds
- ★ create a few small files
- ★ merge those files
- ★ get the size of the resulting merged file

simple pipeline in bash

say Hello to the world

wait for a few seconds…

create two small files

merge the two files

check the size of the resulting file

```
echo 'Hello World !'

sleep 5
sleep 5

cat $RANDOM > tmp1
cat $RANDOM > tmp2

cat tmp1 tmp2 > tmp

du -sh tmp
```

- ★ we would sleep for a few seconds
- ★ create a few small files
- ★ merge those files
- ★ get the size of the resulting merged file

wrap bash commands into R

say Hello to the world

wait for a few seconds…

create two small files

merge the two files

check the size of the resulting file

```
hello='echo Hello World !'

sleep=c('sleep 5', 'sleep 5')

tmp=c('cat $RANDOM > tmp1',
       'cat $RANDOM > tmp2')

merge='cat tmp1 tmp2 > tmp'

size='du -sh tmp'
```

- ★ we would sleep for a few seconds
- ★ create a few small files
- ★ merge those files
- ★ get the size of the resulting merged file

create a table of all commands

```
hello='echo Hello World !'

sleep=c('sleep 5', 'sleep 5')

tmp=c('cat $RANDOM > tmp1',
         'cat $RANDOM > tmp2')

merge='cat tmp1 tmp2 > tmp'

size='du -sh tmp'
```

```
library(flowr)
lst = list(hello=hello,
           sleep=sleep,
           tmp=tmp,
           merge=merge,
           size=size)

flowmat = to_flowmat(lst, "samp1")
```

create a **named** list

create a table

```
|samplename |jobname |cmd                 |
|:----------|:-------|:-------------------|
|samp1      |hello   |echo Hello World !  |
|samp1      |sleep   |sleep 5             |
|samp1      |sleep   |sleep 5             |
|samp1      |tmp     |cat $RANDOM > tmp1  |
|samp1      |tmp     |cat $RANDOM > tmp2  |
|samp1      |merge   |cat tmp1 tmp2 > tmp |
|samp1      |size    |du -sh tmp          |
```

a simple tab-delim table

connect the dots…

flow definition decides the sequence of steps

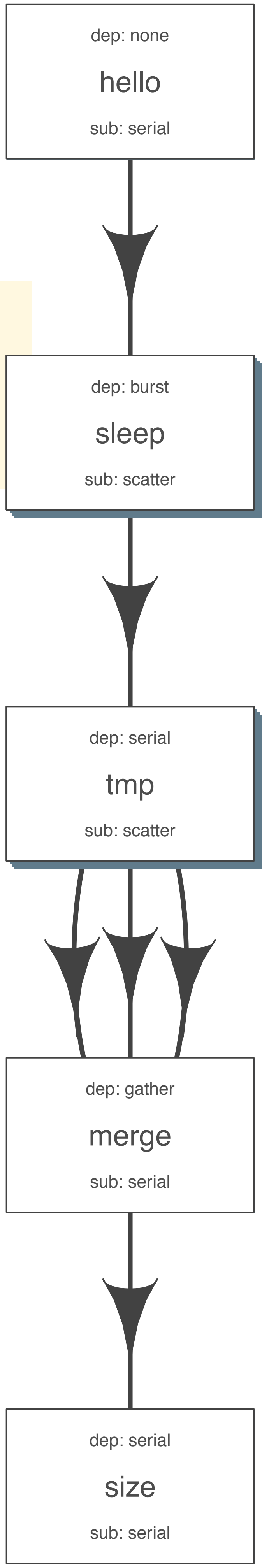
create a flow definition

```
flowdef = to_flowdef(flowmat,
         sub_type = c("serial", "scatter", "scatter", "serial", "serial"),
         dep_type = c("none", "burst", "serial", "gather", "serial"),
         platform = "local")
```

```
|jobname |sub_type |prev_jobs |dep_type | cpu|
|:-------|:--------|:---------|:--------|---:|
|hello   |serial   |none      |none     |   1|
|sleep   |scatter  |hello     |burst    |   1|
|tmp     |scatter  |sleep     |serial   |   1|
|merge   |serial   |tmp       |gather   |   1|
|size    |serial   |merge     |serial   |   1|
```

a simple tab-delim table

```
plot_flow(flowdef)
```



stitch a flow…

use a flow mat and flow def,
to create a flow object

flow mat

```
|samplename |jobname |cmd                  |
|:----------|:-------|:--------------------|
|samp1      |hello   |echo Hello World !   |
|samp1      |sleep   |sleep 5              |
|samp1      |sleep   |sleep 5              |
|samp1      |tmp     |cat $RANDOM > tmp1   |
|samp1      |tmp     |cat $RANDOM > tmp2   |
|samp1      |merge   |cat tmp1 tmp2 > tmp  |
|samp1      |size    |du -sh tmp           |
```

+

flow def

```
|jobname  |sub_type  |prev_jobs  |dep_type  | cpu|
|:--------|:---------|:----------|:---------|---:|
|hello    |serial    |none       |none      |   1|
|sleep    |scatter   |hello      |burst     |   1|
|tmp      |scatter   |sleep      |serial    |   1|
|merge    |serial    |tmp        |gather    |   1|
|size     |serial    |merge      |serial    |   1|
```

stitch & submit to the cluster (cloud or server)

```
fobj = to_flow(flowmat, flowdef, execute = TRUE)
```

```
Flow is being processed. Track it from R/Terminal using:
flowr status x=~/flowr/runs/flowname-samp1-20151005-16-01-38-M8WniKJo
OR from R using:
status(x='~/flowr/runs/flowname-samp1-20151005-16-01-38-M8WniKJo')
```

```
Working on: hello
  |=====                                   |  25%
Working on: sleep
  |=================                       |  50%
Working on: merge
  |========================================| 100%
Working on: size
```

submit a flow, then...

`status()`

monitor the status of a single flow
OR multiple flows

`kill()`

kill all the associated jobs, of one or many flows

`rerun()`

One can rerun the flow from a intermediate step github.com/sahilseth/flowr

complete documentation: docs.flowr.space

email: sahil.seth@me.com

Extra details

Flow mat

samplename	jobname	cmd
sample1	A	sleep 2 && sleep 5;echo hello
sample1	A	sleep 13 && sleep 7;echo hello
sample1	B	head -c 100000 /dev/urandom > tmp1
sample1	B	head -c 100000 /dev/urandom > tmp1
sample1	C	cat tmp1 tmp2 tmp3 > merged
sample1	D	du -sh merged
sample1	D	ls merged

- use any language to create a flow mat (a tsv file)
- cmd column defines commands to run

Flow Definition

	Define Relationships			Resource Requirements				
jobname	**submission type**	**previous job(s)**	**dependency type**	**queue**	**memory**	**time**	**cpu**	**platform**
A	scatter	none	none	medium	163185	23:00	1	lsf
B	scatter	A	serial	medium	163185	23:00	1	lsf
C	serial	B	gather	medium	163185	23:00	1	lsf
D	scatter	C	burst	medium	163185	23:00	1	lsf

- creativily define relationships using submission and dependency types
- each row describes resources for **one** step, providing full flexibility