

Nextflow workflow report

[intergalactic_knuth]

Workflow execution completed unsuccessfully!

The exit status of the task that caused the workflow execution to fail was: 2 .

The full error message was:



```
Caused by:
  Process `LONGREADS_ONLY:wtdbg2 (sample_5)` terminated
  with an error exit status (2)

Command executed:

# run wtdbg2
wtdbg2.pl \
  -t 6 \
  -x sq \
  -g 800m \
  -o sample_5 \
  \
  HMW_DNA_m84126_231020_112323_s3.hifi_reads.fastq.gz

# rename results
cp sample_5.cns.fa wtdbg2_assembly.fasta

Command exit status:
2

Command output:
(empty)

Command error:
36900000
37200000
37500000
37800000
38100000
38400000
38700000
39000000
39300000
39600000
39900000
40200000
40500000
40800000
41100000
41400000
41700000
42000000
42300000
42600000
42900000
43200000
43500000
43800000
44100000
44400000
44700000
45000000
45300000
45600000
45900000
46200000
46500000
46800000
47100000
47400000
47700000
48000000
48300000
48600000
48900000
49200000
49500000
49800000
50100000
50400000
50700000
51000000
51300000The following command returns non-zero code:
/home/guyh/.nextflow/assets/fmalmeida/mpgap/bin/wtdbg2
-x sq -g 800m -t 6 -fo sample_5 -i
HMW_DNA_m84126_231020_112323_s3.hifi_reads.fastq.gz

Work dir:

/mnt/data/guyh/Trifolium/Revio/work/3e/e8ad46fad2a48746213d

Tip: you can try to figure out what's wrong by changing to
the process work dir and showing the script file named
`.command.sh`
```

6 failed

Nextflow command

```
nextflow -bg run fmalmeida/mpgap --output _ASSEMBLY --max_cpus 20 -
-skeep_wtdbg2 --genome_size 800m --input MPGAP_samplesheet1.yml -
profile docker
```

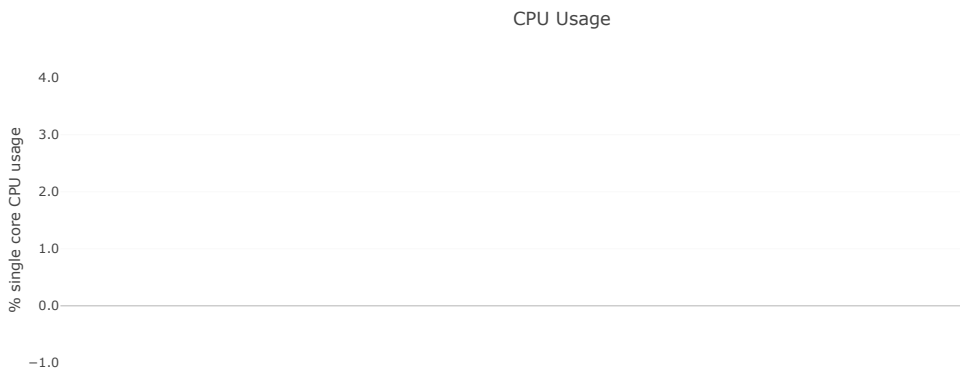
CPU-Hours	34.7 (100% failed)
Launch directory	/mnt/data/guyh/Trifolium/Revio
Work directory	/mnt/data/guyh/Trifolium/Revio/work
Project directory	/home/guyh/.nextflow/assets/fmalmeida/mpgap
Script name	main.nf
Script ID	e554427da6b0720fd518c3cf195d7533
Workflow session	f50fa786-80f9-4116-ba65-28d3d8a7c025
Workflow repository	https://github.com/fmalmeida/mpgap , revision <code>master</code> (commit hash <code>df86d76b7b3cdd2ade860d767ed8d309c69edd</code>)
Workflow profile	docker
Workflow container	fmalmeida/mpgap:v3.1
Container engine	docker
Nextflow version	version 23.04.3, build 5875 (11-08-2023 18:37 UTC)

Resource Usage

These plots give an overview of the distribution of resource usage for each process.

CPU

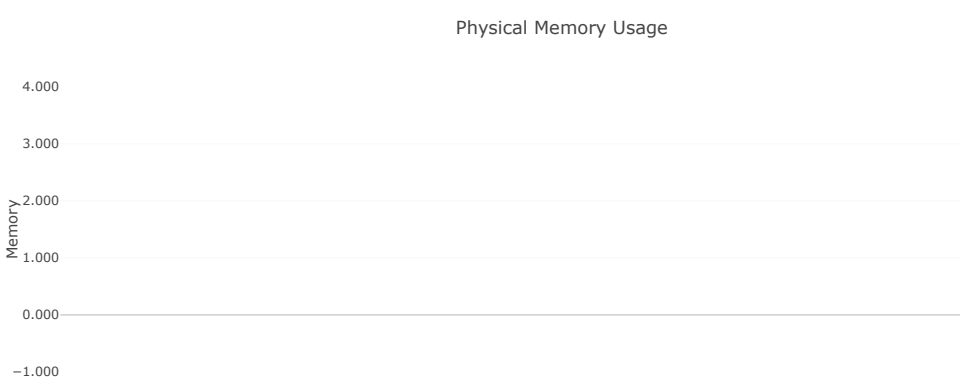
Raw Usage **% Allocated**



Memory

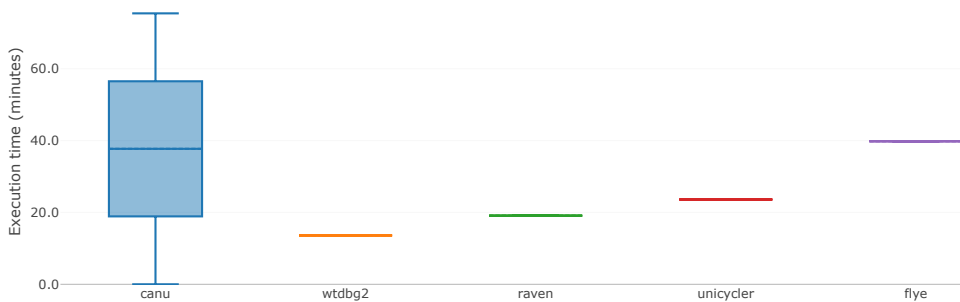
Physical (RAM) **Virtual (RAM + Disk swap)**

% RAM Allocated



Raw Usage % Allocated

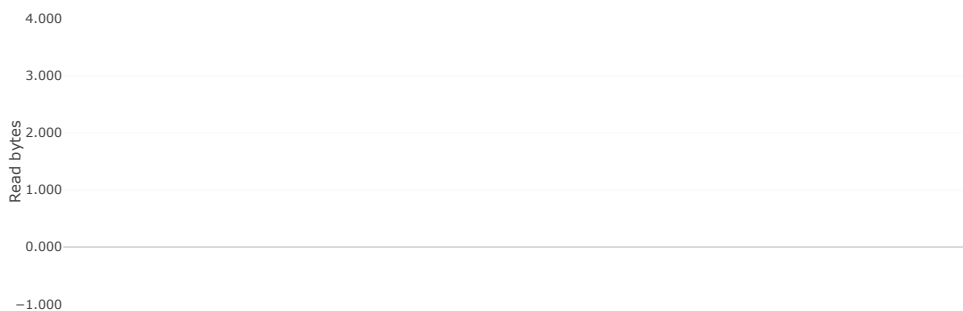
Task execution real-time



I/O

Read Write

Number of bytes read



Tasks

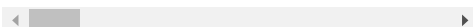
This table shows information about each task in the workflow. Use the search box on the right to filter rows for specific values. Clicking headers will sort the table by that value and scrolling side to side will reveal more columns.

Values shown as: Human readable

Show 25 entries

Filter: Metrics Metadata All Search:

task_id	process	tag	status	h
2	LONGREADS_ONLY:raven	sample_5	FAILED	
3	LONGREADS_ONLY:wtdbg2	sample_5	FAILED	
4	LONGREADS_ONLY:flye	sample_5	FAILED	
5	LONGREADS_ONLY:canu	sample_5	FAILED	
6	LONGREADS_ONLY:unicycler	sample_5	FAILED	
7	LONGREADS_ONLY:canu	sample_5	FAILED	





PREVIOUS | 1 | NEXT

Generated by [Nextflow](#), version 23.04.3