

Nextflow workflow report

[confident_volta]

Workflow execution completed unsuccessfully!

The exit status of the task that caused the workflow execution to fail was: 1 .

The full error message was:

✕ Nextflow Report

Process `NeoFuse`:

Process `NeoFuse (sample1)` terminated with an error exit status (1)

Command executed:

```
NeoFuse_single -1 sample1_tumor_RNA_trimmed_R1.fastq.gz -2 sample1_tumor_RNA_trimmed_R2.fastq.gz \
  -d sample1 \
  -o . \
  -m 8 \
  -M 11 \
  -n 40 \
  -t 500 \
  -T 2 \
  -c L \
  -s star \
  -g GRCh38.d1.vd1.fa \
  -a gencode.v33.primary_assembly.annotation.gtf \
  -N false \
  -C sample1_hlas.txt \
  -v sample1_somaticSV.vcf.gz \
  -k true

mv sample1/NeoFuse/MHC_I/sample1_MHCI_filtered.tsv
sample1/NeoFuse/MHC_I/sample1_NeoFuse_MHC_Class_I_filtered.tsv
mv sample1/NeoFuse/MHC_I/sample1_MHCI_unfiltered.tsv
sample1/NeoFuse/MHC_I/sample1_NeoFuse_MHC_Class_I_unfiltered.tsv
mv sample1/NeoFuse/MHC_I/sample1_unsupported.txt
sample1/NeoFuse/MHC_I/sample1_NeoFuse_MHC_Class_I_unsupported.txt
mv sample1/NeoFuse/MHC_II/sample1_MHCII_filtered.tsv
sample1/NeoFuse/MHC_II/sample1_NeoFuse_MHC_Class_II_filtered.tsv
mv sample1/NeoFuse/MHC_II/sample1_MHCII_unfiltered.tsv
sample1/NeoFuse/MHC_II/sample1_NeoFuse_MHC_Class_II_unfiltered.tsv
mv sample1/NeoFuse/MHC_II/sample1_unsupported.txt
sample1/NeoFuse/MHC_II/sample1_NeoFuse_MHC_Class_II_unsupported.txt
mv sample1/NeoFuse/MHC_II/sample1_mixMHC2pred_conf.txt
sample1/NeoFuse/MHC_II/sample1_NeoFuse_MHC_Class_II_mixMHC2pred_conf.txt
```

Command exit status:

1

Command output:

```
[----- [NeoFuse] -----]

[NeoFuse] Paired End (PE) Reads detected: commencing processing
[NeoFuse] Processing files sample1_tumor_RNA_trimmed_R1.fastq.gz - sample1_tumor_RNA_trimmed_R2.fastq.gz
[NeoFuse] STAR Run started at: 02:58:17
[NeoFuse] Arriba Run started at: 02:58:17
[NeoFuse] Parsing custom HLA list: 04:08:07
[NeoFuse] featureCounts Run started at: 04:08:07
[NeoFuse] Converting Raw Counts to TPM and FPKM: 07:12:23
[NeoFuse] Searching for MHC I peptides of length 8 9 10 11 : 07:12:26
[NeoFuse] Searching for MHC II peptides of length 15 16 17 18 19 20 21 22 23 24 25 : 07:12:26
[NeoFuse] MHCFlurry Run started at: 07:12:26
An error occurred while creating the MHCFlurry temp files, check ./sample1/LOGS/sample1_MHCI_final.log for more
details
```

Command wrapper:

```
[----- [NeoFuse] -----]

[NeoFuse] Paired End (PE) Reads detected: commencing processing
[NeoFuse] Processing files sample1_tumor_RNA_trimmed_R1.fastq.gz - sample1_tumor_RNA_trimmed_R2.fastq.gz
[NeoFuse] STAR Run started at: 02:58:17
[NeoFuse] Arriba Run started at: 02:58:17
[NeoFuse] Parsing custom HLA list: 04:08:07
[NeoFuse] featureCounts Run started at: 04:08:07
[NeoFuse] Converting Raw Counts to TPM and FPKM: 07:12:23
[NeoFuse] Searching for MHC I peptides of length 8 9 10 11 : 07:12:26
[NeoFuse] Searching for MHC II peptides of length 15 16 17 18 19 20 21 22 23 24 25 : 07:12:26
[NeoFuse] MHCFlurry Run started at: 07:12:26
An error occurred while creating the MHCFlurry temp files, check ./sample1/LOGS/sample1_MHCI_final.log for more
details
```

Nextflow Report

/data/SBCS-BessantLab/Antara/nextNEOpi/work/a9/f5d9ded3bc5bc9dfbb2f33b7f58074

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``

Run times

23-May-2022 18:01:45 - 25-May-2022 07:23:02 (duration: **1d 13h 21m 17s**)

538 succeeded

Nextflow command

```
nextflow run nextNEOpi.nf --batchFile batchFile.csv -config conf/params.config --outputDir /data/SBCS-BessantLab/Antara/nextNEOpi/myResults --trim_adapters true --trim_adapters_RNaseq true --use_NetChop false --tmpDir /data/SBCS-BessantLab/Antara/nextNEOpi/tmpDir -profile singularity,cluster --accept_license
```

CPU-Hours

2'425.8 (46.9% failed)

Launch directory

/data/SBCS-BessantLab/Antara/nextNEOpi

Work directory

/data/SBCS-BessantLab/Antara/nextNEOpi/work

Project directory

/data/SBCS-BessantLab/Antara/nextNEOpi

Script name

nextNEOpi.nf

Script ID

78ab17de50910f7101f161256f7a29e0

Workflow session

114a38e1-6b16-43d6-ad2a-80c443a09ad2

Workflow profile

singularity,cluster

Nextflow version

version 22.04.3, build 5703 (18-05-2022 19:22 UTC)

Resource Usage

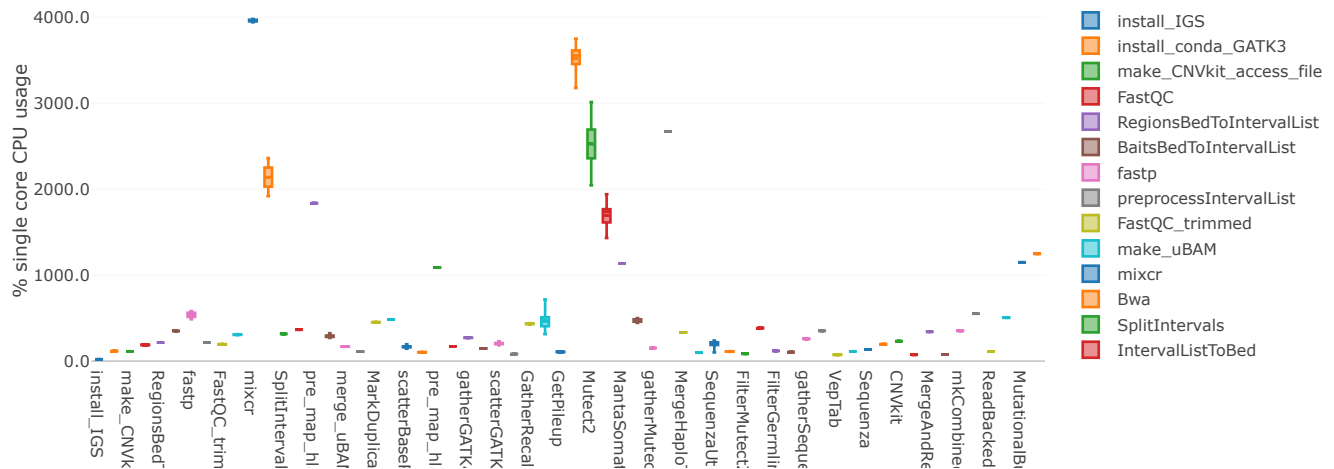
These plots give an overview of the distribution of resource usage for each process.

CPU

Raw Usage

% Allocated

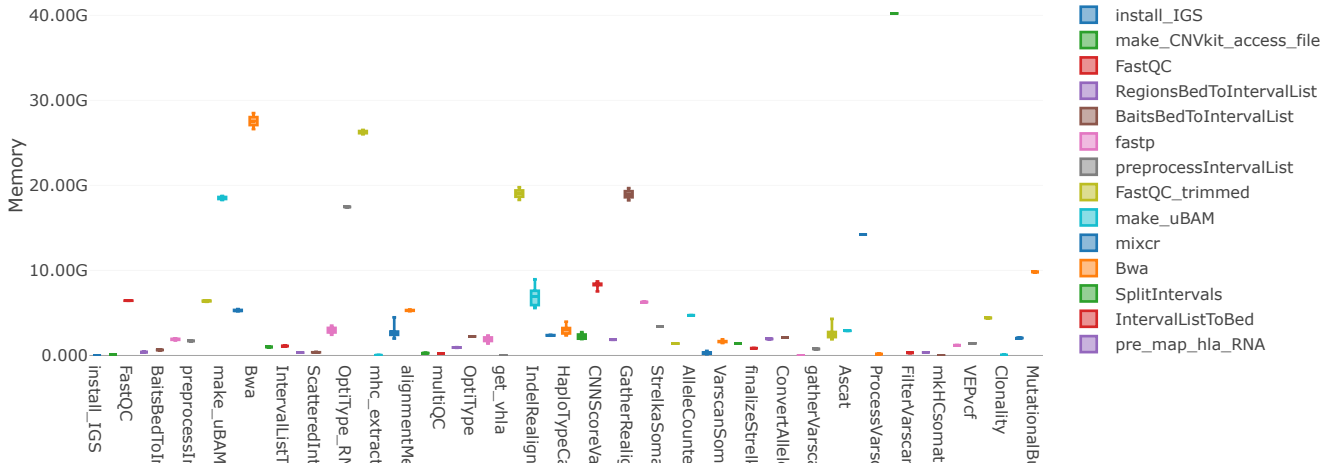
CPU Usage



Nextflow Report

Physical (RAM) virtual (RAM + DISK swap) % RAM Allocated

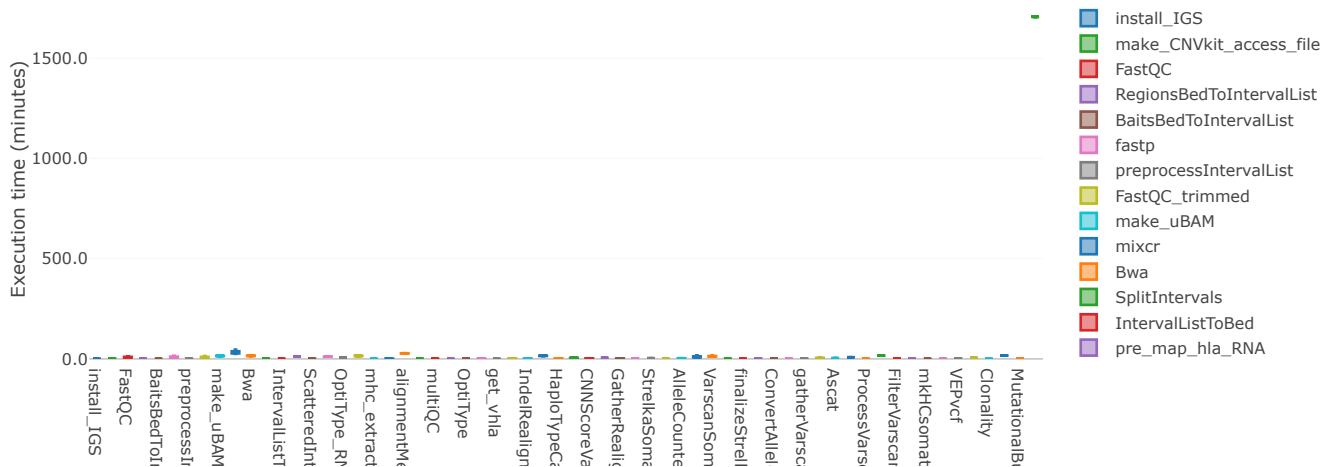
Physical Memory Usage



Job Duration

Raw Usage % Allocated

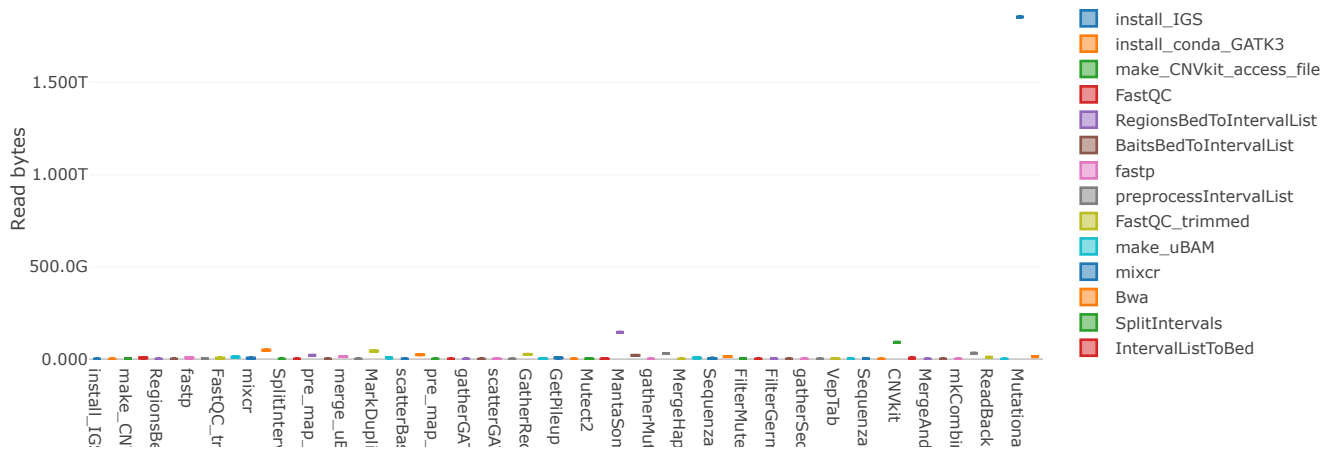
Task execution real-time



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:

Show entries

Filter: Search:

task_id	process	tag	status	hash	allocated cpus	%cpu	allocated memory	%mem
1	RegionsBedToIntervalList	RegionsBedToIntervalList	COMPLETED	1d/ed0e83	40	214.9	-	0.1
2	BaitsBedToIntervalList	BaitsBedToIntervalList	COMPLETED	85/473f68	40	350.0	-	0.1
3	FastQC	sample1 : tumor_DNA	COMPLETED	98/14d09e	40	186.3	-	1.0
4	FastQC	sample1 : normal_DNA	COMPLETED	4d/6d1742	40	184.4	-	1.0
5	FastQC	sample1 : tumor_RNA	COMPLETED	65/053dea	40	195.5	-	1.0
6	fastp	sample1 : tumor_DNA	COMPLETED	0b/2404da	40	581.4	-	0.3
7	fastp	sample1 : normal_DNA	COMPLETED	f4/20cf10	40	486.0	-	0.3
8	fastp	sample1 : tumor_RNA	COMPLETED	ae/d320d1	40	542.7	-	0.3
9	install_conda_GATK3	install GATK3	COMPLETED	9c/c80d4a	40	116.5	-	0.0

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 Nextflow Report

11	install_IGS	install IGS	COMPLETED	e5/ddbffe	40	21.1	-	0.0
12	preprocessIntervallList	preprocessIntervallList	COMPLETED	8d/1fc191	40	216.1	-	0.3
13	FastQC_trimmed	sample1 : tumor_DNA	COMPLETED	12/0721e0	40	193.6	-	1.0
14	make_uBAM	sample1 : tumor_DNA	COMPLETED	44/78aacf	40	302.4	-	3.0
15	Bwa	sample1 : tumor_DNA	COMPLETED	6b/e08271	40	1918.4	-	4.2
16	mixcr	sample1 : tumor_DNA	COMPLETED	aa/f20005	40	3980.0	-	0.9
17	FastQC_trimmed	sample1 : normal_DNA	COMPLETED	1a/ceb1a1	40	190.6	-	1.0
18	Bwa	sample1 : normal_DNA	COMPLETED	24/527038	40	2362.3	-	4.4
19	make_uBAM	sample1 : normal_DNA	COMPLETED	50/fb036e	40	313.0	-	2.9
20	mixcr	sample1 : normal_DNA	COMPLETED	7e/c9ffe1	40	3941.7	-	0.8
21	IntervalListToBed	BedFromIntervallList	COMPLETED	44/47541d	40	364.6	-	0.2
22	SplitIntervals	SplitIntervals	COMPLETED	a2/8d87dd	40	315.8	-	0.2



 Nextflow Report

24	pre_map_hla_RNA	sample1	COMPLETED	c8/7738fb	40	1837.7	-	0.0
25	mixcr	sample1 : tumor_RNA	COMPLETED	48/eade48	40	3962.4	-	0.8

Showing 1 to 25 of 539 entries

Previous 1 2 3 4 5 ... 22 Next