09/07/2024

Sunday, September 01, 2024   4:03 PM

- Error occurred when running stringtie merge on data.

SRR7757114 Time Metrics

HK1_SRR7757114 upload: 42 minutes 14 seconds
HK1 Uncompressed: 10 minutes
FastQC: 9 minutes 11 seconds
Trim Galore: 24 minutes 56 seconds
FastQC on Trim Galore:

SRR7757113 Time Metrics:

C666_1:SRR7757113: 38 minutes 33 seconds
C666_1: 10 minutes
FastQC: 11 minutes 42 seconds
Trim Galore: 24 minutes 56 seconds

SRR7757114 Size Metrics

HK1 Size: 6.33 GB
HK1 Uncompressed: 5.9 GB
FastQC: 610 KB
Trim Galore: 27.6 GB
FastQC on Trim Galore:

SRR7757113 Size Metrics:

C666_1:SRR7757113: 5.77GB
C666_1 uncompressed: 25.4 GB
FastQC: 580 KB
Trim Galore: 25.4 GB

User data and job quotas

Jobs that have low memory and CPU requirements are subject to the following limits:

Maximum total accounts per user	1 registered/unregistered
Maximum total user data on server	250GB for registered users, 5GB for unregistered users
Maximum concurrent jobs	6 for registered users, 1 for unregistered users

Tools utilizing multiple CPUs and over 8 Gb of RAM are subject to stricted limits:

Resource	Per-resource job concurrency quotas
Increased memory tools	1 registered/unregistered
Galaxy cluster	2 registered, unregistered not allowed
Jetstream	4 registered, unregistered not allowed
TACC Stampede	4 registered, unregistered not allowed

All test/development resources are limited to 1 registered, unregistered not allowed.

Choosing computational resources

Tools that can run on more than one computational resource are, by default, automatically directed to the most suitable and readily available resource automatically by Galaxy. However, these tools also have the option for you to manually select the resource. Although not designed for typical usage, manual selection can be a good idea if you know (or strongly suspect) that a tool will exceed the allocation (time limit or memory) on a given resource. On the form for these tools, a **Job Resource Parameters** parameter is available that, if selected, will display a **Compute Resources** selection parameter. The possible options (not all are available for every tool) for this parameter are:

Resource	Characteristics

Galaxy cluster	36 hour walltime, 6 cores, 30 GB memory, short/moderate wait
Jetstream	36 hour walltime, 10 cores, 30 GB memory, short/moderate wait
TACC Stampede2 normal (KNL) partition	48 hour walltime, 64 low-frequency cores, 96 GB memory, moderate/long wait
TACC Stampede2 SKX partition	48 hour walltime, 48 cores, 192 GB memory, long/very long wait
PSC Bridges	variable walltime, variable cores, variable memory, moderate/long wait

SRR7767114 Time Metrics

SRR7767113 Processing Time: 37 minutes 52 seconds
SRR7767113 Uncompressing time: 6 minutes 2 seconds
FastQC on uncompressed file: 10 minutes 1 second
Trim Galore time: 19 minutes 49 seconds
FastQC on trim galore: 6 minutes
Genome Upload Speed for all 3 files:
HISAT2 Tool: 13 minutes 23 seconds
StringTie Tool:
StringTie Merge:

SRR7767114 Size Metrics

SRR7767113 Size upload: 6.33 GB
SRR7767113 Uncompressed Size: 30.07 GB
FastQC on uncompressed file: < 1 MB
Trim Galore size: 28.6 GB
FastQC on trim galore: All files around 620 KB
Genome Upload Size for all 3 files:
HISAT2 Tool: 6.3 GB
StringTie Tool:
StringTie Merge:

SRR7767113 Time Metrics

SRR7767113 Processing Time: 1 min 4 seconds
SRR7767113 Uncompressing time: 11 seconds
FastQC on uncompressed file: 53 seconds
Trim Galore time: 19 seconds
FastQC on trim galore: 25 seconds
Genome Upload Speed for all 3 files: 16 seconds
HISAT2 Tool: 21 seconds
StringTie Tool: Once started processing, took less than a second. However, post processing took one minute to start.
StringTie Merge:

SRR7767113 Size Metrics

SRR7767113 Size upload: 57.7 MB
SRR7767113 Uncompressed Size: 254.3 MB
FastQC on uncompressed file: 3 MB
Trim Galore size: 248 MB
FastQC on trim galore: 10 MB
Genome Upload Size for all 3 files: 472.5 KB when uploaded
HISAT2 Tool: 52.2 MB
StringTie Tool: Too small to notice.
StringTie Merge: