

Flux Capacitor error: java.lang.OutOfMemoryError: Java heap space with FLUX_MEM=16G

I have been using Flux Capacitor to quantify transcript abundance for samples in my RNA-seq study. However, for 2 of 126 samples, Flux Capacitor crashes with an out of memory error. I have increased the java heap space to 16G using the environmental variable FLUX_MEM=16G, but the error still occurs. The BAM file is about 2.4GB with about 42 million paired end reads. Do you have any idea what the problem could be? Strangely, I am telling Flux Capacitor to use only 2 threads, but it uses 22 threads on my server. So I wonder if it could be related to this?

```
/net/wonderland/home/cgillies/programs/flux-capacitor-1.6.1/bin/flux-capacitor -i /net/assembly/cgillies/data/NEPTUNE/RNA-Seq/11_24_2015//25870//final.bam -a /net/assembly/cgillies/data/NEPTUNE/RNA-Seq/11_24_2015/FLUX//gtf.filtered.sorted.gtf -m PAIRED -o /net/assembly/cgillies/data/NEPTUNE/RNA-Seq/11_24_2015/FLUX//25870.gtf --count-elements SPLICE_JUNCTIONS,INTRONS --threads 2 --force --tmp-dir /net/assembly/cgillies/data/NEPTUNE/RNA-Seq/11_24_2015/FLUX//25870_tmp/
```

[INFO] Flux-Capacitor v1.6.1 (Flux Library: 1.29)

[PRE-CHECK] I am checking availability of the required lpsolve JNI libs.

[PRE-CHECK] * successfully loaded lpsolve JNI (version 5.5,release 0,build 14)

Scanning annotation file Checking GTF ***** OK (00:00:09)

scanning OK (00:00:48)

[WARN] Skipped 268333 lines.

[INFO] 53182 loci, 215170 transcripts, 1306656 exons.

OK (00:00:48)

Scanning mapping file [SAM] Setting validation stringency to SILENT

[INFO] The Flux Capacitor is not using the SAM flags for counting the number of reads in the mapping file.

[WARN] This process can be long for big files!

OK (00:14:23)

[INFO] 85007194 mapped reads, 85007194 mappings: R-factor 1.0

[INFO] 76440206 entire, 8566988 split mappings (10.077957%)

OK (00:14:23)

[INFO] Annotation and mapping input checked

[HEHO] We are set, so let's go!

[ANNOTATION_FILE] /net/assembly/cgillies/data/NEPTUNE/RNA-Seq/11_24_2015/FLUX/gtf.filtered.sorted.gtf

[MAPPING_FILE] /net/assembly/cgillies/data/NEPTUNE/RNA-Seq/11_24_2015/25870/final.bam

[INFO] minimum intron length 24

[SORT_IN_RAM] true

[TMP_DIR] /net/assembly/cgillies/data/NEPTUNE/RNA-Seq/11_24_2015/FLUX/25870_tmp

[STDOUT_FILE] /net/assembly/cgillies/data/NEPTUNE/RNA-Seq/11_24_2015/FLUX/25870.gtf

[INFO] mate pairing information considered

[PROFILE] Loading profile

[PROFILE] Scanning the input and getting the attributes.

profiling Exception in thread "Thread-5" java.lang.OutOfMemoryError: Java heap space

at net.sf.samtools.DefaultSAMRecordFactory.createBAMRecord(DefaultSAMRecordFactory.java:30)

at net.sf.samtools.BAMRecordCodec.decode(BAMRecordCodec.java:201)
at net.sf.samtools.BAMFileReader\$BAMFileIterator.getNextRecord(BAMFileReader.java:557)
at net.sf.samtools.BAMFileReader\$BAMFileIndexIterator.getNextRecord(BAMFileReader.java:664)
at net.sf.samtools.BAMFileReader\$BAMFileIterator.advance(BAMFileReader.java:531)
at net.sf.samtools.BAMFileReader\$BAMFileIterator.next(BAMFileReader.java:521)
at net.sf.samtools.BAMFileReader\$BAMFileIterator.next(BAMFileReader.java:480)
at net.sf.samtools.BAMFileReader\$BAMQueryFilteringIterator.advance(BAMFileReader.java:749)
at net.sf.samtools.BAMFileReader\$BAMQueryFilteringIterator.next(BAMFileReader.java:719)
at net.sf.samtools.BAMFileReader\$BAMQueryFilteringIterator.next(BAMFileReader.java:672)
at net.sf.samtools.SAMFileReader\$AssertableIterator.next(SAMFileReader.java:664)
at net.sf.samtools.SAMFileReader\$AssertableIterator.next(SAMFileReader.java:642)
at barna.io.sam.SAMMappingSortedIterator\$1.run(SAMMappingSortedIterator.java:103)
at java.lang.Thread.run(Thread.java:744)