

***pyrpipe* report**

file name:pyrpipe_logs/2020-01-29-12_00_45_pyrpipe.log

Summary

Time start: 2020-01-29 12:00:45 Time end: 2020-01-29 12:21:38
Total time: 0:20:53

Num commands: 22

Num failed commands: 0

Num passed commands: 22

Total programs: 7

rq-
dump

Details

command

```
prefetch -0 athal_out/SRR976159 SRR976159
```

stdout

```
2020-01-29T18:02:08 prefetch.2.10.0: 1) Downloading  
'SRR976159'...  
2020-01-29T18:02:08 prefetch.2.10.0: Downloading via  
https...  
2020-01-29T18:02:16 prefetch.2.10.0: https download succeed  
2020-01-29T18:02:16 prefetch.2.10.0: 1) 'SRR976159' was  
downloaded successfully
```

stderr

Program	Return code	Start	Runtime	Version
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prefetch	0	20-01-29 12:02:04	0:00:12	/home/usingh/lib_urmi/ softwares/sratoolkit.2.10.0- centos_linux64/bin/prefetch : 2.10.0
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command

prefetch -0 athal_out/SRR978411 SRR978411

stdout

```
2020-01-29T18:02:18 prefetch.2.10.0: 1) Downloading
'SRR978411'...
2020-01-29T18:02:18 prefetch.2.10.0: Downloading via
https...
2020-01-29T18:02:26 prefetch.2.10.0: https download succeed
2020-01-29T18:02:26 prefetch.2.10.0: 1) 'SRR978411' was
downloaded successfully
```

stderr

Program	Return code	Start	Runtime	Version
prefetch	0	20-01-29 12:02:17	0:00:09	/home/usingh/lib_urmi/ softwares/sratoolkit.2.10.0- centos_linux64/bin/prefetch : 2.10.0

command

prefetch -0 athal_out/SRR971778 SRR971778

stdout

```
2020-01-29T18:02:27 prefetch.2.10.0: 1) Downloading
'SRR971778'...
2020-01-29T18:02:27 prefetch.2.10.0: Downloading via
https...
2020-01-29T18:02:37 prefetch.2.10.0: https download succeed
2020-01-29T18:02:37 prefetch.2.10.0: 1) 'SRR971778' was
downloaded successfully
```

stderr

Program	Return code	Start	Runtime	Version
prefetch	0	20-01-29 12:02:26	0:00:11	/home/usingh/lib_urmi/softwares/sratoolkit.2.10.0-centos_linux64/bin/prefetch : 2.10.0

command

```
fasterq-dump -e 8 -f -t athal_out -O athal_out/SRR976159 -o SRR976159.fastq athal_out/SRR976159/SRR976159.sra
```

stdout

```
spots read      : 4,728,806
reads read      : 9,457,612
reads written    : 9,457,612
```

stderr

Program	Return code	Start	Runtime	Version
fasterq-dump	0	20-01-29 12:03:54	0:00:14	

command

```
fasterq-dump -e 8 -f -t athal_out -O athal_out/SRR978411 -o SRR978411.fastq athal_out/SRR978411/SRR978411.sra
```

stdout

```
spots read      : 4,200,625
reads read      : 8,401,250
reads written    : 8,401,250
```

stderr

Program	Return code	Start	Runtime	Version
fasterq-dump	0	20-01-29 12:04:09	0:00:26	

command

```
fasterq-dump -e 8 -f -t athal_out -O athal_out/SRR971778 -o SRR971778.fastq athal_out/SRR971778/SRR971778.sra
```

stdout

```
spots read      : 5,432,321
reads read      : 10,864,642
reads written   : 10,864,642
```

stderr

Program	Return code	Start	Runtime	Version
fasterq-dump	0	20-01-29 12:04:35	0:00:30	

command

```
bbduk.sh ktrim=r k=23 mink=11 qtrim='rl' trimq=10
ref=adapters2.fa in=athal_out/SRR976159/SRR976159_1.fastq
in2=athal_out/SRR976159/SRR976159_2.fastq out=athal_out/
SRR976159/SRR976159_1_bbduk.fastq out2=athal_out/SRR976159/
SRR976159_2_bbduk.fastq -Xmx2g
```

stdout

```
java -ea -Xmx2g -Xms2g -cp /home/usingh/lib_urmi/software/
bbmap/current/ jgi.BBDuk ktrim=r k=23 mink=11 qtrim='rl'
trimq=10 ref=adapters2.fa in=athal_out/SRR976159/
SRR976159_1.fastq in2=athal_out/SRR976159/SRR976159_2.fastq
out=athal_out/SRR976159/SRR976159_1_bbduk.fastq
out2=athal_out/SRR976159/SRR976159_2_bbduk.fastq -Xmx2g
Executing jgi.BBDuk [ktrim=r, k=23, mink=11, qtrim=rl,
trimq=10, ref=adapters2.fa, in=athal_out/SRR976159/
SRR976159_1.fastq, in2=athal_out/SRR976159/
SRR976159_2.fastq, out=athal_out/SRR976159/
SRR976159_1_bbduk.fastq, out2=athal_out/SRR976159/
SRR976159_2_bbduk.fastq, -Xmx2g]
Version 38.73
```

```
maskMiddle was disabled because useShortKmers=true
0.017 seconds.
```

```
Initial:
```

```
Memory: max=2058m, total=2058m, free=2015m, used=43m
```

```
Added 3297 kmers; time:          0.024 seconds.
```

```
Memory: max=2058m, total=2058m, free=1961m, used=97m
```

```
Input is being processed as paired
```

```
Started output streams: 0.012 seconds.
```

```

Processing time:          9.963 seconds.

Input:                   9457612 reads
680948064 bases.
QTrimmed:                319597 reads (3.38%)
1867256 bases (0.27%)
KTrimmed:                10427 reads (0.11%)
483899 bases (0.07%)
Total Removed:           1408 reads (0.01%)
2351155 bases (0.35%)
Result:                  9456204 reads (99.99%)
678596909 bases (99.65%)

Time:                    10.002 seconds.
Reads Processed:         9457k    945.61k reads/sec
Bases Processed:         680m     68.08m bases/sec

```

stderr

Program	Return code	Start	Runtime	Version
bbduk.sh	0	20-01-29 12:10:30	0:00:11	java -ea -Xmx4580m -Xms4580m -cp /home/usingh/lib_urmi/ softwares/bbmap/current/ jgi.BBDuk --version BBMap version 38.73 For help, please run the shellscript with no parameters, or look in /docs/.

command

```

bbduk.sh ktrim=r k=23 mink=11 qtrim='rl' trimq=10
ref=adapters2.fa in=athal_out/SRR978411/SRR978411_1.fastq
in2=athal_out/SRR978411/SRR978411_2.fastq out=athal_out/
SRR978411/SRR978411_1_bbduk.fastq out2=athal_out/SRR978411/
SRR978411_2_bbduk.fastq -Xmx2g

```

stdout

```

java -ea -Xmx2g -Xms2g -cp /home/usingh/lib_urmi/softwares/
bbmap/current/ jgi.BBDuk ktrim=r k=23 mink=11 qtrim='rl'
trimq=10 ref=adapters2.fa in=athal_out/SRR978411/
SRR978411_1.fastq in2=athal_out/SRR978411/SRR978411_2.fastq
out=athal_out/SRR978411/SRR978411_1_bbduk.fastq
out2=athal_out/SRR978411/SRR978411_2_bbduk.fastq -Xmx2g
Executing jgi.BBDuk [ktrim=r, k=23, mink=11, qtrim=rl,
trimq=10, ref=adapters2.fa, in=athal_out/SRR978411/
SRR978411_1.fastq, in2=athal_out/SRR978411/

```

```

SRR978411_2.fastq, out=athal_out/SRR978411/
SRR978411_1_bbduk.fastq, out2=athal_out/SRR978411/
SRR978411_2_bbduk.fastq, -Xmx2g]
Version 38.73

maskMiddle was disabled because useShortKmers=true
0.017 seconds.
Initial:
Memory: max=2058m, total=2058m, free=2015m, used=43m

Added 3297 kmers; time:          0.021 seconds.
Memory: max=2058m, total=2058m, free=1961m, used=97m

Input is being processed as paired
Started output streams: 0.004 seconds.
Processing time:                31.490 seconds.

Input:                          8401250 reads
604890000 bases.
QTrimmed:                      247216 reads (2.94%)
1358333 bases (0.22%)
KTrimmed:                      8251 reads (0.10%)
373837 bases (0.06%)
Total Removed:                 1128 reads (0.01%)
1732170 bases (0.29%)
Result:                        8400122 reads (99.99%)
603157830 bases (99.71%)

Time:                          31.516 seconds.
Reads Processed:               8401k    266.57k reads/sec
Bases Processed:               604m     19.19m bases/sec

```

stderr

Program	Return code	Start	Runtime	Version
bbduk.sh	0	20-01-29 12:10:42	0:00:32	java -ea -Xmx4580m -Xms4580m -cp /home/usingh/lib_urmi/ softwares/bbmap/current/ jgi.BBDuk --version BBMap version 38.73 For help, please run the shellscript with no parameters, or look in /docs/.

command

```

bbduk.sh ktrim=r k=23 mink=11 qtrim='rl' trimq=10
ref=adapters2.fa in=athal_out/SRR971778/SRR971778_1.fastq

```

```
in2=athal_out/SRR971778/SRR971778_2.fastq out=athal_out/  
SRR971778/SRR971778_1_bbduk.fastq out2=athal_out/SRR971778/  
SRR971778_2_bbduk.fastq -Xmx2g
```

stdout

```
java -ea -Xmx2g -Xms2g -cp /home/usingh/lib_urmi/software/   
bbmap/current/ jgi.BBDuk ktrim=r k=23 mink=11 qtrim='rl'   
trimq=10 ref=adapters2.fa in=athal_out/SRR971778/   
SRR971778_1.fastq in2=athal_out/SRR971778/SRR971778_2.fastq   
out=athal_out/SRR971778/SRR971778_1_bbduk.fastq   
out2=athal_out/SRR971778/SRR971778_2_bbduk.fastq -Xmx2g   
Executing jgi.BBDuk [ktrim=r, k=23, mink=11, qtrim=rl,   
trimq=10, ref=adapters2.fa, in=athal_out/SRR971778/   
SRR971778_1.fastq, in2=athal_out/SRR971778/   
SRR971778_2.fastq, out=athal_out/SRR971778/   
SRR971778_1_bbduk.fastq, out2=athal_out/SRR971778/   
SRR971778_2_bbduk.fastq, -Xmx2g]   
Version 38.73
```

```
maskMiddle was disabled because useShortKmers=true   
0.012 seconds.
```

```
Initial:
```

```
Memory: max=2058m, total=2058m, free=2015m, used=43m
```

```
Added 3297 kmers; time: 0.212 seconds.
```

```
Memory: max=2058m, total=2058m, free=1961m, used=97m
```

```
Input is being processed as paired
```

```
Started output streams: 0.008 seconds.
```

```
Processing time: 54.414 seconds.
```

```
Input: 10864642 reads
```

```
782254224 bases.
```

```
QTrimmed: 196217 reads (1.81%)
```

```
1170368 bases (0.15%)
```

```
KTrimmed: 13593 reads (0.13%)
```

```
576005 bases (0.07%)
```

```
Total Removed: 1042 reads (0.01%)
```

```
1746373 bases (0.22%)
```

```
Result: 10863600 reads (99.99%)
```

```
780507851 bases (99.78%)
```

```
Time: 54.636 seconds.
```

```
Reads Processed: 10864k 198.86k reads/sec
```

```
Bases Processed: 782m 14.32m bases/sec
```

stderr

Program	Return code	Start	Runtime	Version
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bbduk.sh	0	20-01-29 12:11:14	0:00:55	java -ea -Xmx4580m -Xms4580m -cp /home/usingh/lib_urmi/ softwares/bbmap/current/ jgi.BBDuk --version BBDuk version 38.73 For help, please run the shellscript with no parameters, or look in /docs/.
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command

```
hisat2-build -p 8 -a -q athal_out/  
Arabidopsis_thaliana.TAIR10.dna.toplevel.fa athal_out/  
athalIndex/athalInd
```

stdout

stderr

Program	Return code	Start	Runtime	Version
hisat2- build	0	20-01-29 12:12:33	0:00:37	hisat2-build version 2.1.0 64-bit Built on login-node03 Wed Jun 7 15:52:43 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 -msse2 -funroll-loops - g3 -DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}

command

```
hisat2 --dta-cufflinks -p 10 -x athal_out/athalIndex/  
athalInd -1 athal_out/SRR976159/SRR976159_1_bbduk.fastq -2  
athal_out/SRR976159/SRR976159_2_bbduk.fastq -S athal_out/  
SRR976159/SRR976159_hisat2.sam
```

stdout

```
4728102 reads; of these:  
  4728102 (100.00%) were paired; of these:  
    206364 (4.36%) aligned concordantly 0 times  
    4408659 (93.24%) aligned concordantly exactly 1 time  
    113079 (2.39%) aligned concordantly >1 times  
  ----
```



```

    206364 pairs aligned concordantly 0 times; of these:
      41813 (20.26%) aligned discordantly 1 time
    ----
    164551 pairs aligned 0 times concordantly or
discordantly; of these:
      329102 mates make up the pairs; of these:
        180243 (54.77%) aligned 0 times
        143912 (43.73%) aligned exactly 1 time
        4947 (1.50%) aligned >1 times
98.09% overall alignment rate

```

stderr

Program	Return code	Start	Runtime	Version
hisat2	0	20-01-29 12:13:33	0:01:05	/home/usingh/lib_urmi/software/ hisat2-2.1.0/hisat2-align-s version 2.1.0 64-bit Built on login-node03 Wed Jun 7 15:53:42 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 -msse2 -funroll-loops -g3 -DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}

command

```

hisat2 --dta-cufflinks -p 10 -x athal_out/athalIndex/
athalInd -1 athal_out/SRR978411/SRR978411_1_bbduk.fastq -2
athal_out/SRR978411/SRR978411_2_bbduk.fastq -S athal_out/
SRR978411/SRR978411_hisat2.sam

```

stdout

```

4200061 reads; of these:
  4200061 (100.00%) were paired; of these:
    197399 (4.70%) aligned concordantly 0 times
    3894707 (92.73%) aligned concordantly exactly 1 time
    107955 (2.57%) aligned concordantly >1 times
  ----
    197399 pairs aligned concordantly 0 times; of these:
      41081 (20.81%) aligned discordantly 1 time
  ----
    156318 pairs aligned 0 times concordantly or
discordantly; of these:
      312636 mates make up the pairs; of these:
        173950 (55.64%) aligned 0 times

```

133563 (42.72%) aligned exactly 1 time
5123 (1.64%) aligned >1 times
97.93% overall alignment rate

stderr

Program	Return code	Start	Runtime	Version
hisat2	0	20-01-29 12:14:38	0:01:07	/home/usingh/lib_urmi/software/hisat2-2.1.0/hisat2-align-s version 2.1.0 64-bit Built on login-node03 Wed Jun 7 15:53:42 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 -msse2 -funroll-loops -g3 -DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}

command

```
hisat2 --dta-cufflinks -p 10 -x athal_out/athalIndex/  
athalInd -1 athal_out/SRR971778/SRR971778_1_bbduk.fastq -2  
athal_out/SRR971778/SRR971778_2_bbduk.fastq -S athal_out/  
SRR971778/SRR971778_hisat2.sam
```

stdout

```
5431800 reads; of these:  
  5431800 (100.00%) were paired; of these:  
    643040 (11.84%) aligned concordantly 0 times  
    4607044 (84.82%) aligned concordantly exactly 1 time  
    181716 (3.35%) aligned concordantly >1 times  
    ----  
    643040 pairs aligned concordantly 0 times; of these:  
      17694 (2.75%) aligned discordantly 1 time  
    ----  
    625346 pairs aligned 0 times concordantly or  
discordantly; of these:  
      1250692 mates make up the pairs; of these:  
        1132019 (90.51%) aligned 0 times  
        112860 (9.02%) aligned exactly 1 time  
        5813 (0.46%) aligned >1 times  
89.58% overall alignment rate
```

stderr

Program	Return code	Start	Runtime	Version
hisat2	0	20-01-29 12:15:45	0:01:17	/home/usingh/lib_urmi/software/ hisat2-2.1.0/hisat2-align-s version 2.1.0 64-bit Built on login-node03 Wed Jun 7 15:53:42 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 -msse2 -funroll-loops -g3 -DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}

command

```
samtools view -@ 8 -o athal_out/SRR976159/
SRR976159_hisat2.bam -b athal_out/SRR976159/
SRR976159_hisat2.sam
```

stdout

stderr

Program	Return code	Start	Runtime	Version
samtools	0	20-01-29 12:17:11	0:00:33	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

command

```
samtools sort -@ 8 -o athal_out/SRR976159/
SRR976159_hisat2_sorted.bam athal_out/SRR976159/
SRR976159_hisat2.bam
```

stdout

```
[bam_sort_core] merging from 0 files and 8 in-memory
blocks...
```

stderr

Program	Return code	Start	Runtime	Version
samtools	0	20-01-29 12:17:44	0:00:20	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

command

```
samtools view -@ 8 -o athal_out/SRR978411/
SRR978411_hisat2.bam -b athal_out/SRR978411/
SRR978411_hisat2.sam
```

stdout

stderr

Program	Return code	Start	Runtime	Version
samtools	0	20-01-29 12:18:04	0:00:24	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

command

```
samtools sort -@ 8 -o athal_out/SRR978411/
SRR978411_hisat2_sorted.bam athal_out/SRR978411/
SRR978411_hisat2.bam
```

stdout

```
[bam_sort_core] merging from 0 files and 8 in-memory
blocks...
```

stderr

Program	Return code	Start	Runtime	Version
samtools	0	20-01-29 12:18:28	0:00:18	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

command

```
samtools view -@ 8 -o athal_out/SRR971778/  
SRR971778_hisat2.bam -b athal_out/SRR971778/  
SRR971778_hisat2.sam
```

stdout

stderr

Program	Return code	Start	Runtime	Version
samtools	0	20-01-29 12:18:47	0:00:30	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

command

```
samtools sort -@ 8 -o athal_out/SRR971778/  
SRR971778_hisat2_sorted.bam athal_out/SRR971778/  
SRR971778_hisat2.bam
```

stdout

```
[bam_sort_core] merging from 0 files and 8 in-memory  
blocks...
```

stderr

Program	Return code	Start	Runtime	Version
samtools	0	20-01-29 12:19:17	0:00:24	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

command

```
stringtie -G athal_out/Arabidopsis_thaliana.TAIR10.45.gtf -o  
athal_out/SRR976159/SRR976159_hisat2_sorted_stringtie.gtf  
athal_out/SRR976159/SRR976159_hisat2_sorted.bam
```

stdout

stderr

Program	Return code	Start	Runtime	Version
stringtie	0	20-01-29 12:19:40	0:00:40	2.0.4

command

```
stringtie -G athal_out/Arabidopsis_thaliana.TAIR10.45.gtf -o  
athal_out/SRR978411/SRR978411_hisat2_sorted_stringtie.gtf  
athal_out/SRR978411/SRR978411_hisat2_sorted.bam
```

stdout

stderr

Program	Return code	Start	Runtime	Version
stringtie	0	20-01-29 12:20:20	0:00:36	2.0.4

command

```
stringtie -G athal_out/Arabidopsis_thaliana.TAIR10.45.gtf -o  
athal_out/SRR971778/SRR971778_hisat2_sorted_stringtie.gtf  
athal_out/SRR971778/SRR971778_hisat2_sorted.bam
```

stdout

stderr

Program	Return code	Start	Runtime	Version
stringtie	0	20-01-29 12:20:56	0:00:42	2.0.4

Environment Information

Programs		
name	version	path

stringtie	2.0.4	/home/usingh/lib_urmi/ softwares/ stringtie-2.0.4.Linux_x86_64/ stringtie
bbduk.sh	java -ea -Xmx4580m - Xms4580m -cp /home/usingh/ lib_urmi/softwares/bbmap/ current/ jgi.BBDuk --version BBMap version 38.73 For help, please run the shellscript with no parameters, or look in / docs/.	/home/usingh/lib_urmi/ softwares/bbmap/bbduk.sh
hisat2- build	hisat2-build version 2.1.0 64- bit Built on login-node03 Wed Jun 7 15:52:43 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 - msse2 -funroll-loops -g3 - DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}	/home/usingh/lib_urmi/ softwares/hisat2-2.1.0/hisat2- build
samtools	samtools 1.9 Using htlib 1.9 Copyright (C) 2018 Genome Research Ltd.	/home/usingh/lib_urmi/ softwares/samtools-1.9/ samtools-1.9/bin/samtools
prefetch	/home/usingh/lib_urmi/ softwares/sratoolkit.2.10.0- centos_linux64/bin/prefetch : 2.10.0	/home/usingh/lib_urmi/ softwares/sratoolkit.2.10.0- centos_linux64/bin/prefetch
hisat2	/home/usingh/lib_urmi/ softwares/hisat2-2.1.0/hisat2- align-s version 2.1.0 64-bit Built on login-node03 Wed Jun 7 15:53:42 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 - msse2 -funroll-loops -g3 - DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}	/home/usingh/lib_urmi/ softwares/hisat2-2.1.0/hisat2
fasterq- dump		/home/usingh/lib_urmi/ softwares/sratoolkit.2.10.0- centos_linux64/bin/fasterq- dump

System Information	
Time at collection	20-01-29 12:00:45
Python	Python 3.7.5 (default, Oct 25 2019, 15:51:11) [GCC 7.3.0]

Operating system	Linux-3.16.0-4-amd64-x86_64-with-debian-8.9
CPU	8 logical CPU cores

sys.modules
'sys'
'builtins'
'_frozen_importlib'
'_imp'
'_thread'
'_warnings'
'_weakref'
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