pyrpipe report

file name:pyrpipe_logs/2020-01-22-18_14_47_pyrpipe.log

Summary

Time start: 2020-01-22 18:14:47 Time end: 2020-01-22 23:56:24
Total time: 5:41:37

Num commands: 15

Num failed commands: 1

Num passed commands: 14

Total programs: 7

Programs: trim_galore,prefetch,stringtie,fasterq-dump,gffread,plncpro predict,STAR

Details

command

```
prefetch -O /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746 SRR3098746
```

stdout

```
2020-01-22T23:14:50 prefetch.2.10.0: 1) Downloading 'SRR3098746'...
2020-01-22T23:14:50 prefetch.2.10.0:  Downloading via https...
2020-01-22T23:23:00 prefetch.2.10.0:  https download succeed
2020-01-22T23:23:00 prefetch.2.10.0: 1) 'SRR3098746' was downloaded successfully
2020-01-22T23:23:00 prefetch.2.10.0: 'SRR3098746' has 0 unresolved dependencies
```

stderr

Program	Return code	Start	Runtime	Version
prefetch	0	20-01-22 18:14:49	0:08:11	/pylon5/mc5pl7p/usingh/lib/sratoolkit.2.10.0-centos_linux64/bin/prefetch : 2.10.0

---

command

```
prefetch -O /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098745 SRR3098745
```

stdout

```
2020-01-22T23:23:01 prefetch.2.10.0: 1) Downloading 'SRR3098745'...
2020-01-22T23:23:01 prefetch.2.10.0:  Downloading via https...
2020-01-22T23:28:35 prefetch.2.10.0 int: timeout exhausted while reading file within network system module - Cannot KStreamRead: https://sra-downloadb.be-md.ncbi.nlm.nih.gov/sos2/sra-pub-run-7/SRR3098745/SRR3098745.1
2020-01-22T23:28:35 prefetch.2.10.0:  https download failed
2020-01-22T23:28:35 prefetch.2.10.0: 1) failed to download SRR3098745
```

stderr

Program	Return code	Start	Runtime	Version
prefetch	3	20-01-22 18:23:00	0:05:35	/pylon5/mc5pl7p/usingh/lib/sratoolkit.2.10.0-centos_linux64/bin/prefetch : 2.10.0

---

command

```
prefetch -O /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744 SRR3098744
```

stdout

```
2020-01-22T23:28:38 prefetch.2.10.0: 1) Downloading
```

```
'SRR3098744'...
2020-01-22T23:28:38 prefetch.2.10.0:  Downloading via
https...
2020-01-22T23:35:21 prefetch.2.10.0:  https download succeed
2020-01-22T23:35:21 prefetch.2.10.0: 1) 'SRR3098744' was
downloaded successfully
2020-01-22T23:35:21 prefetch.2.10.0: 'SRR3098744' has 0
unresolved dependencies
```

stderr

Program	Return code	Start	Runtime	Version
prefetch	0	20-01-22 18:28:35	0:06:46	/pylon5/mc5pl7p/usingh/lib/sratoolkit.2.10.0-centos_linux64/bin/prefetch : 2.10.0

---

command

```
fasterq-dump -e 20 -f -t /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize -O /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098746 -o SRR3098746.fastq /
pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/
SRR3098746/SRR3098746.sra
```

stdout

```
spots read      : 85,732,311
reads read      : 171,464,622
reads written   : 171,464,622
```

stderr

Program	Return code	Start	Runtime	Version
fasterq-dump	0	20-01-22 18:35:21	0:01:15	

---

command

```
trim_galore --cores 10 --paired -o /pylon5/mc5pl7p/usingh/
urmi/pyrpipeTest/testDir/maize/SRR3098746 /pylon5/mc5pl7p/
usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746/
SRR3098746_1.fastq /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098746/SRR3098746_2.fastq
```

stdout

```
Using an excessive number of cores has a diminishing return!
It is recommended not to exceed 8 cores per trimming process
(you asked for 10 cores). Please consider re-specifying
Path to Cutadapt set as: 'cutadapt' (default)
Cutadapt seems to be working fine (tested command 'cutadapt
--version')
Cutadapt version: 2.6
Cutadapt seems to be using Python 3! Proceeding with multi-
core enabled Cutadapt using 10 cores
Parallel gzip (pigz) detected. Proceeding with multicore
(de)compression using 10 cores

No quality encoding type selected. Assuming that the data
provided uses Sanger encoded Phred scores (default)

Output will be written into the directory: /pylon5/mc5pl7p/
usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746/


AUTO-DETECTING ADAPTER TYPE
============================
Attempting to auto-detect adapter type from the first 1
million sequences of the first file (>> /pylon5/mc5pl7p/
usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746/
SRR3098746_1.fastq <<)

Found perfect matches for the following adapter sequences:
Adapter type    Count   Sequence        Sequences
analysed        Percentage
Illumina        10739   AGATCGGAAGAGC   1000000 1.07
smallRNA        0       TGGAATTCTCGG    1000000 0.00
Nextera 0       CTGTCTCTTATA    1000000 0.00
Using Illumina adapter for trimming (count: 10739). Second
best hit was smallRNA (count: 0)

Writing report to '/pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098746/
SRR3098746_1.fastq_trimming_report.txt'

SUMMARISING RUN PARAMETERS
==========================
Input filename: /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098746/SRR3098746_1.fastq
Trimming mode: paired-end
Trim Galore version: 0.6.4_dev
Cutadapt version: 2.6
Python version: 3.6.3 :: Intel Corporation
Number of cores used for trimming: 10
Quality Phred score cutoff: 20
Quality encoding type selected: ASCII+33
```

```
Adapter sequence: 'AGATCGGAAGAGC' (Illumina TruSeq, Sanger
iPCR; auto-detected)
Maximum trimming error rate: 0.1 (default)
Minimum required adapter overlap (stringency): 1 bp
Minimum required sequence length for both reads before a
sequence pair gets removed: 20 bp

Cutadapt seems to be fairly up-to-date (version 2.6).
Setting -j 10
Writing final adapter and quality trimmed output to
SRR3098746_1_trimmed.fq


  >>> Now performing quality (cutoff '-q 20') and adapter
trimming in a single pass for the adapter sequence:
'AGATCGGAAGAGC' from file /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098746/SRR3098746_1.fastq <<<
10000000 sequences processed
20000000 sequences processed
30000000 sequences processed
40000000 sequences processed
50000000 sequences processed
60000000 sequences processed
70000000 sequences processed
80000000 sequences processed
This is cutadapt 2.6 with Python 3.6.3
Command line parameters: -j 10 -e 0.1 -q 20 -O 1 -a
AGATCGGAAGAGC /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098746/SRR3098746_1.fastq
Processing reads on 10 cores in single-end mode ...
Finished in 200.35 s (2 us/read; 25.67 M reads/minute).

=== Summary ===

Total reads processed:              85,732,311
Reads with adapters:                21,391,002 (25.0%)
Reads written (passing filters):    85,732,311 (100.0%)

Total basepairs processed: 10,802,271,186 bp
Quality-trimmed:              131,091,920 bp (1.2%)
Total written (filtered):  10,608,673,685 bp (98.2%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13;
Trimmed: 21391002 times.

No. of allowed errors:
0-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:
  A: 27.4%
```

```
  C: 32.4%
  G: 22.5%
  T: 17.6%
  none/other: 0.1%

Overview of removed sequences
length  count   expect  max.err error counts
1       13192893        21433077.8      0       13192893
2       5112936 5358269.4       0       5112936
3       1098625 1339567.4       0       1098625
4       389713  334891.8        0       389713
5       113158  83723.0 0       113158
6       98100   20930.7 0       98100
7       89746   5232.7  0       89746
8       78166   1308.2  0       78166
9       50635   327.0   0       49825 810
10      94576   81.8    1       92306 2270
11      31106   20.4    1       29945 1161
12      56660   5.1     1       55404 1256
13      70914   1.3     1       69391 1523
14      33934   1.3     1       33115 819
15      63389   1.3     1       62005 1384
16      23403   1.3     1       22731 672
17      45683   1.3     1       44411 1272
18      62366   1.3     1       61084 1282
19      22113   1.3     1       21452 661
20      52382   1.3     1       51374 1008
21      25385   1.3     1       24745 640
22      33807   1.3     1       33092 715
23      40007   1.3     1       39201 806
24      22327   1.3     1       21772 555
25      49372   1.3     1       48554 818
26      5074    1.3     1       4842 232
27      31287   1.3     1       30612 675
28      38546   1.3     1       37871 675
29      14784   1.3     1       14436 348
30      28962   1.3     1       28580 382
31      14838   1.3     1       14560 278
32      29229   1.3     1       28768 461
33      9613    1.3     1       9425 188
34      21462   1.3     1       21113 349
35      9728    1.3     1       9505 223
36      21908   1.3     1       21635 273
37      4881    1.3     1       4773 108
38      14504   1.3     1       14250 254
39      13204   1.3     1       12954 250
40      10913   1.3     1       10625 288
41      11776   1.3     1       11562 214
42      10515   1.3     1       10350 165
43      13334   1.3     1       13175 159
44      3805    1.3     1       3698 107
45      5264    1.3     1       5176 88
```

```
46      2136    1.3     1       2070 66
47      6800    1.3     1       6693 107
48      3946    1.3     1       3868 78
49      6945    1.3     1       6840 105
50      3233    1.3     1       3166 67
51      5023    1.3     1       4956 67
52      1915    1.3     1       1871 44
53      4105    1.3     1       4021 84
54      4279    1.3     1       4192 87
55      3798    1.3     1       3724 74
56      1079    1.3     1       1028 51
57      2741    1.3     1       2688 53
58      2841    1.3     1       2788 53
59      1079    1.3     1       1037 42
60      2676    1.3     1       2636 40
61      1571    1.3     1       1526 45
62      939     1.3     1       874 65
63      2064    1.3     1       2014 50
64      1698    1.3     1       1636 62
65      882     1.3     1       796 86
66      1218    1.3     1       1157 61
67      1146    1.3     1       1081 65
68      1164    1.3     1       1044 120
69      1217    1.3     1       1064 153
70      1183    1.3     1       996 187
71      1266    1.3     1       947 319
72      1345    1.3     1       956 389
73      1718    1.3     1       951 767
74      2634    1.3     1       956 1678
75      11847   1.3     1       1175 10672
76      11015   1.3     1       3209 7806
77      6050    1.3     1       1577 4473
78      3394    1.3     1       545 2849
79      1928    1.3     1       232 1696
80      1256    1.3     1       154 1102
81      718     1.3     1       120 598
82      528     1.3     1       107 421
83      374     1.3     1       75 299
84      308     1.3     1       76 232
85      303     1.3     1       76 227
86      267     1.3     1       67 200
87      260     1.3     1       72 188
88      191     1.3     1       41 150
89      194     1.3     1       54 140
90      191     1.3     1       50 141
91      167     1.3     1       56 111
92      123     1.3     1       32 91
93      136     1.3     1       47 89
94      126     1.3     1       35 91
95      144     1.3     1       42 102
96      146     1.3     1       36 110
97      117     1.3     1       25 92
```

```
98      122     1.3     1       24 98
99      137     1.3     1       41 96
100     119     1.3     1       32 87
101     106     1.3     1       20 86
102     114     1.3     1       24 90
103     102     1.3     1       23 79
104     101     1.3     1       22 79
105     83      1.3     1       15 68
106     86      1.3     1       18 68
107     87      1.3     1       18 69
108     89      1.3     1       11 78
109     64      1.3     1       19 45
110     83      1.3     1       10 73
111     71      1.3     1       6 65
112     88      1.3     1       18 70
113     98      1.3     1       17 81
114     97      1.3     1       21 76
115     83      1.3     1       19 64
116     74      1.3     1       15 59
117     78      1.3     1       10 68
118     84      1.3     1       8 76
119     102     1.3     1       6 96
120     122     1.3     1       9 113
121     151     1.3     1       12 139
122     182     1.3     1       7 175
123     267     1.3     1       7 260
124     414     1.3     1       7 407
125     856     1.3     1       5 851
126     9495    1.3     1       33 9462

RUN STATISTICS FOR INPUT FILE: /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098746/SRR3098746_1.fastq
=============================================
85732311 sequences processed in total
The length threshold of paired-end sequences gets evaluated
later on (in the validation step)

Writing report to '/pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098746/
SRR3098746_2.fastq_trimming_report.txt'

SUMMARISING RUN PARAMETERS
==========================
Input filename: /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098746/SRR3098746_2.fastq
Trimming mode: paired-end
Trim Galore version: 0.6.4_dev
Cutadapt version: 2.6
Python version: 3.6.3 :: Intel Corporation
Number of cores used for trimming: 10
Quality Phred score cutoff: 20
Quality encoding type selected: ASCII+33
```

```
Adapter sequence: 'AGATCGGAAGAGC' (Illumina TruSeq, Sanger
iPCR; auto-detected)
Maximum trimming error rate: 0.1 (default)
Minimum required adapter overlap (stringency): 1 bp
Minimum required sequence length for both reads before a
sequence pair gets removed: 20 bp

Cutadapt seems to be fairly up-to-date (version 2.6).
Setting -j -j 10
Writing final adapter and quality trimmed output to
SRR3098746_2_trimmed.fq


  >>> Now performing quality (cutoff '-q 20') and adapter
trimming in a single pass for the adapter sequence:
'AGATCGGAAGAGC' from file /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098746/SRR3098746_2.fastq <<<
10000000 sequences processed
20000000 sequences processed
30000000 sequences processed
40000000 sequences processed
50000000 sequences processed
60000000 sequences processed
70000000 sequences processed
80000000 sequences processed
This is cutadapt 2.6 with Python 3.6.3
Command line parameters: -j 10 -e 0.1 -q 20 -O 1 -a
AGATCGGAAGAGC /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098746/SRR3098746_2.fastq
Processing reads on 10 cores in single-end mode ...
Finished in 197.75 s (2 us/read; 26.01 M reads/minute).

=== Summary ===

Total reads processed:              85,732,311
Reads with adapters:                21,262,166 (24.8%)
Reads written (passing filters):    85,732,311 (100.0%)

Total basepairs processed: 10,802,271,186 bp
Quality-trimmed:              206,049,532 bp (1.9%)
Total written (filtered):  10,533,933,416 bp (97.5%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13;
Trimmed: 21262166 times.

No. of allowed errors:
0-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:
  A: 30.3%
```

```
  C: 24.9%
  G: 30.0%
  T: 14.8%
  none/other: 0.0%

Overview of removed sequences
length  count   expect  max.err error counts
1       11558505        21433077.8      0       11558505
2       7023316 5358269.4       0       7023316
3       820195  1339567.4       0       820195
4       240848  334891.8        0       240848
5       138298  83723.0 0       138298
6       104106  20930.7 0       104106
7       134985  5232.7  0       134985
8       66205   1308.2  0       66205
9       16805   327.0   0       15264 1541
10      112019  81.8    1       107082 4937
11      11324   20.4    1       7965 3359
12      91518   5.1     1       88212 3306
13      16178   1.3     1       14909 1269
14      100010  1.3     1       96361 3649
15      29918   1.3     1       28799 1119
16      17937   1.3     1       16981 956
17      87866   1.3     1       85018 2848
18      6390    1.3     1       5864 526
19      68018   1.3     1       66435 1583
20      32789   1.3     1       32002 787
21      2049    1.3     1       1743 306
22      37629   1.3     1       36382 1247
23      36520   1.3     1       35215 1305
24      71308   1.3     1       69427 1881
25      17821   1.3     1       17213 608
26      24906   1.3     1       24289 617
27      3932    1.3     1       3631 301
28      42457   1.3     1       41727 730
29      2339    1.3     1       2109 230
30      42208   1.3     1       41388 820
31      3777    1.3     1       3556 221
32      27739   1.3     1       27216 523
33      19306   1.3     1       18835 471
34      4352    1.3     1       4112 240
35      24939   1.3     1       24423 516
36      6747    1.3     1       6463 284
37      13986   1.3     1       13647 339
38      17084   1.3     1       16744 340
39      8819    1.3     1       8590 229
40      6307    1.3     1       6029 278
41      11286   1.3     1       11000 286
42      15099   1.3     1       14830 269
43      890     1.3     1       768 122
44      8117    1.3     1       7916 201
45      11792   1.3     1       11518 274
```

```
46      4590    1.3     1       4472 118
47      2649    1.3     1       2524 125
48      4913    1.3     1       4808 105
49      6011    1.3     1       5857 154
50      2633    1.3     1       2536 97
51      8081    1.3     1       7923 158
52      3254    1.3     1       3153 101
53      2108    1.3     1       2005 103
54      1492    1.3     1       1412 80
55      3210    1.3     1       3062 148
56      1954    1.3     1       1854 100
57      2671    1.3     1       2550 121
58      1937    1.3     1       1834 103
59      2113    1.3     1       1993 120
60      2050    1.3     1       1931 119
61      2028    1.3     1       1850 178
62      2082    1.3     1       1825 257
63      2057    1.3     1       1773 284
64      1954    1.3     1       1590 364
65      2117    1.3     1       1485 632
66      2859    1.3     1       1500 1359
67      18586   1.3     1       1927 16659
68      15630   1.3     1       8000 7630
69      5371    1.3     1       1597 3774
70      2308    1.3     1       424 1884
71      1421    1.3     1       181 1240
72      769     1.3     1       133 636
73      585     1.3     1       100 485
74      427     1.3     1       85 342
75      319     1.3     1       75 244
76      331     1.3     1       91 240
77      253     1.3     1       70 183
78      214     1.3     1       65 149
79      240     1.3     1       81 159
80      211     1.3     1       67 144
81      240     1.3     1       66 174
82      219     1.3     1       79 140
83      207     1.3     1       49 158
84      186     1.3     1       70 116
85      175     1.3     1       61 114
86      140     1.3     1       53 87
87      145     1.3     1       51 94
88      159     1.3     1       46 113
89      116     1.3     1       30 86
90      120     1.3     1       43 77
91      137     1.3     1       43 94
92      106     1.3     1       25 81
93      141     1.3     1       37 104
94      115     1.3     1       30 85
95      128     1.3     1       38 90
96      109     1.3     1       42 67
97      111     1.3     1       20 91
```

```
98      77      1.3     1       15 62
99      99      1.3     1       30 69
100     99      1.3     1       18 81
101     87      1.3     1       17 70
102     73      1.3     1       16 57
103     74      1.3     1       16 58
104     110     1.3     1       13 97
105     92      1.3     1       9 83
106     92      1.3     1       7 85
107     93      1.3     1       6 87
108     87      1.3     1       5 82
109     80      1.3     1       2 78
110     65      1.3     1       6 59
111     75      1.3     1       2 73
112     91      1.3     1       4 87
113     76      1.3     1       1 75
114     79      1.3     1       2 77
115     91      1.3     1       3 88
116     93      1.3     1       2 91
117     96      1.3     1       1 95
118     95      1.3     1       0 95
119     144     1.3     1       3 141
120     131     1.3     1       3 128
121     143     1.3     1       1 142
122     218     1.3     1       1 217
123     318     1.3     1       2 316
124     407     1.3     1       1 406
125     790     1.3     1       2 788
126     7570    1.3     1       21 7549

RUN STATISTICS FOR INPUT FILE: /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098746/SRR3098746_2.fastq
=============================================
85732311 sequences processed in total
The length threshold of paired-end sequences gets evaluated
later on (in the validation step)

Validate paired-end files SRR3098746_1_trimmed.fq and
SRR3098746_2_trimmed.fq
file_1: SRR3098746_1_trimmed.fq, file_2:
SRR3098746_2_trimmed.fq


>>>>> Now validing the length of the 2 paired-end infiles:
SRR3098746_1_trimmed.fq and SRR3098746_2_trimmed.fq <<<<<
Writing validated paired-end Read 1 reads to
SRR3098746_1_val_1.fq
Writing validated paired-end Read 2 reads to
SRR3098746_2_val_2.fq

Total number of sequences analysed: 85732311
```

```
Number of sequence pairs removed because at least one read
was shorter than the length cutoff (20 bp): 464084 (0.54%)

Deleting both intermediate output files
SRR3098746_1_trimmed.fq and SRR3098746_2_trimmed.fq

================================================================
=====================================
```

stderr

Program	Return code	Start	Runtime	Version
trim_galore	0	20-01-22 18:36:39	0:13:02	Quality-/Adapter-/RRBS-/ Speciality-Trimming [powered by Cutadapt] version 0.6.4_dev Last update: 24 09 2019

---

command

```
fasterq-dump -e 20 -f -t /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize -O /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098744 -o SRR3098744.fastq /
pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/
SRR3098744/SRR3098744.sra
```

stdout

```
spots read      : 92,170,823
reads read      : 184,341,646
reads written   : 184,341,646
```

stderr

Program	Return code	Start	Runtime	Version
fasterq-dump	0	20-01-22 18:49:41	0:01:29	

---

command

```
trim_galore --cores 10 --paired -o /pylon5/mc5pl7p/usingh/
urmi/pyrpipeTest/testDir/maize/SRR3098744 /pylon5/mc5pl7p/
usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/
```

```
SRR3098744_1.fastq /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098744/SRR3098744_2.fastq
```

stdout

```
Using an excessive number of cores has a diminishing return!
It is recommended not to exceed 8 cores per trimming process
(you asked for 10 cores). Please consider re-specifying
Path to Cutadapt set as: 'cutadapt' (default)
Cutadapt seems to be working fine (tested command 'cutadapt
--version')
Cutadapt version: 2.6
Cutadapt seems to be using Python 3! Proceeding with multi-
core enabled Cutadapt using 10 cores
Parallel gzip (pigz) detected. Proceeding with multicore
(de)compression using 10 cores

No quality encoding type selected. Assuming that the data
provided uses Sanger encoded Phred scores (default)

Output will be written into the directory: /pylon5/mc5pl7p/
usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/


AUTO-DETECTING ADAPTER TYPE
============================
Attempting to auto-detect adapter type from the first 1
million sequences of the first file (>> /pylon5/mc5pl7p/
usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/
SRR3098744_1.fastq <<)

Found perfect matches for the following adapter sequences:
Adapter type    Count   Sequence        Sequences
analysed        Percentage
Illumina        9450    AGATCGGAAGAGC   1000000 0.95
smallRNA        1       TGGAATTCTCGG    1000000 0.00
Nextera 0       CTGTCTCTTATA    1000000 0.00
Using Illumina adapter for trimming (count: 9450). Second
best hit was smallRNA (count: 1)

Writing report to '/pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098744/
SRR3098744_1.fastq_trimming_report.txt'

SUMMARISING RUN PARAMETERS
==========================
Input filename: /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098744/SRR3098744_1.fastq
Trimming mode: paired-end
Trim Galore version: 0.6.4_dev
Cutadapt version: 2.6
Python version: 3.6.3 :: Intel Corporation
```

```
Number of cores used for trimming: 10
Quality Phred score cutoff: 20
Quality encoding type selected: ASCII+33
Adapter sequence: 'AGATCGGAAGAGC' (Illumina TruSeq, Sanger
iPCR; auto-detected)
Maximum trimming error rate: 0.1 (default)
Minimum required adapter overlap (stringency): 1 bp
Minimum required sequence length for both reads before a
sequence pair gets removed: 20 bp

Cutadapt seems to be fairly up-to-date (version 2.6).
Setting -j 10
Writing final adapter and quality trimmed output to
SRR3098744_1_trimmed.fq


  >>> Now performing quality (cutoff '-q 20') and adapter
trimming in a single pass for the adapter sequence:
'AGATCGGAAGAGC' from file /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098744/SRR3098744_1.fastq <<<
10000000 sequences processed
20000000 sequences processed
30000000 sequences processed
40000000 sequences processed
50000000 sequences processed
60000000 sequences processed
70000000 sequences processed
80000000 sequences processed
90000000 sequences processed
This is cutadapt 2.6 with Python 3.6.3
Command line parameters: -j 10 -e 0.1 -q 20 -O 1 -a
AGATCGGAAGAGC /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098744/SRR3098744_1.fastq
Processing reads on 10 cores in single-end mode ...
Finished in 214.22 s (2 us/read; 25.82 M reads/minute).

=== Summary ===

Total reads processed:              92,170,823
Reads with adapters:                23,552,072 (25.6%)
Reads written (passing filters):    92,170,823 (100.0%)

Total basepairs processed: 11,613,523,698 bp
Quality-trimmed:              106,029,323 bp (0.9%)
Total written (filtered):  11,443,573,255 bp (98.5%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13;
Trimmed: 23552072 times.

No. of allowed errors:
```

```
0-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:
  A: 27.3%
  C: 31.6%
  G: 22.5%
  T: 18.6%
  none/other: 0.0%

Overview of removed sequences
length  count   expect  max.err error counts
1       14510201        23042705.8      0       14510201
2       5810228 5760676.4       0       5810228
3       1241422 1440169.1       0       1241422
4       432848  360042.3        0       432848
5       134720  90010.6 0       134720
6       93190   22502.6 0       93190
7       89969   5625.7  0       89969
8       65179   1406.4  0       65179
9       62171   351.6   0       61148 1023
10      86505   87.9    1       84050 2455
11      36022   22.0    1       34725 1297
12      62459   5.5     1       60854 1605
13      63202   1.4     1       61554 1648
14      40957   1.4     1       39786 1171
15      55176   1.4     1       53743 1433
16      32828   1.4     1       31838 990
17      42093   1.4     1       40901 1192
18      50655   1.4     1       49417 1238
19      31203   1.4     1       30339 864
20      40974   1.4     1       39990 984
21      33552   1.4     1       32773 779
22      36470   1.4     1       35585 885
23      30988   1.4     1       30308 680
24      27642   1.4     1       26962 680
25      37290   1.4     1       36635 655
26      14824   1.4     1       14488 336
27      26269   1.4     1       25730 539
28      28532   1.4     1       28008 524
29      19037   1.4     1       18652 385
30      22067   1.4     1       21708 359
31      18520   1.4     1       18153 367
32      23824   1.4     1       23417 407
33      10400   1.4     1       10167 233
34      15432   1.4     1       15111 321
35      20250   1.4     1       19967 283
36      6074    1.4     1       5903 171
37      16645   1.4     1       16412 233
38      6575    1.4     1       6426 149
39      11146   1.4     1       10954 192
40      11345   1.4     1       11103 242
41      8966    1.4     1       8790 176
```

```
42      7025    1.4     1       6910 115
43      11531   1.4     1       11374 157
44      3758    1.4     1       3642 116
45      5037    1.4     1       4938 99
46      3420    1.4     1       3313 107
47      5164    1.4     1       5048 116
48      4451    1.4     1       4323 128
49      5231    1.4     1       5086 145
50      3799    1.4     1       3681 118
51      4087    1.4     1       3975 112
52      3088    1.4     1       3010 78
53      3464    1.4     1       3368 96
54      3185    1.4     1       3069 116
55      3689    1.4     1       3579 110
56      1309    1.4     1       1240 69
57      2588    1.4     1       2505 83
58      2160    1.4     1       2094 66
59      1631    1.4     1       1579 52
60      2373    1.4     1       2322 51
61      1459    1.4     1       1400 59
62      1354    1.4     1       1296 58
63      1915    1.4     1       1856 59
64      1438    1.4     1       1389 49
65      1087    1.4     1       1025 62
66      1293    1.4     1       1230 63
67      1077    1.4     1       1017 60
68      1056    1.4     1       995 61
69      1143    1.4     1       1051 92
70      1093    1.4     1       961 132
71      1013    1.4     1       872 141
72      1119    1.4     1       865 254
73      1256    1.4     1       863 393
74      1852    1.4     1       951 901
75      9184    1.4     1       1105 8079
76      8395    1.4     1       3093 5302
77      5164    1.4     1       1773 3391
78      3653    1.4     1       767 2886
79      2559    1.4     1       476 2083
80      1380    1.4     1       297 1083
81      869     1.4     1       236 633
82      627     1.4     1       179 448
83      368     1.4     1       127 241
84      349     1.4     1       128 221
85      301     1.4     1       112 189
86      308     1.4     1       109 199
87      236     1.4     1       77 159
88      224     1.4     1       76 148
89      180     1.4     1       65 115
90      202     1.4     1       67 135
91      175     1.4     1       47 128
92      204     1.4     1       68 136
93      152     1.4     1       55 97
```

```
94      158     1.4     1       60 98
95      183     1.4     1       51 132
96      159     1.4     1       36 123
97      145     1.4     1       41 104
98      148     1.4     1       35 113
99      111     1.4     1       35 76
100     122     1.4     1       28 94
101     138     1.4     1       35 103
102     162     1.4     1       37 125
103     124     1.4     1       21 103
104     130     1.4     1       32 98
105     85      1.4     1       18 67
106     130     1.4     1       36 94
107     143     1.4     1       23 120
108     106     1.4     1       21 85
109     91      1.4     1       20 71
110     128     1.4     1       24 104
111     107     1.4     1       22 85
112     93      1.4     1       18 75
113     114     1.4     1       23 91
114     105     1.4     1       18 87
115     127     1.4     1       21 106
116     127     1.4     1       21 106
117     113     1.4     1       16 97
118     127     1.4     1       14 113
119     137     1.4     1       7 130
120     139     1.4     1       7 132
121     186     1.4     1       17 169
122     220     1.4     1       14 206
123     378     1.4     1       22 356
124     494     1.4     1       16 478
125     1054    1.4     1       42 1012
126     8763    1.4     1       167 8596

RUN STATISTICS FOR INPUT FILE: /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098744/SRR3098744_1.fastq
=============================================
92170823 sequences processed in total
The length threshold of paired-end sequences gets evaluated
later on (in the validation step)

Writing report to '/pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098744/
SRR3098744_2.fastq_trimming_report.txt'

SUMMARISING RUN PARAMETERS
==========================
Input filename: /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098744/SRR3098744_2.fastq
Trimming mode: paired-end
Trim Galore version: 0.6.4_dev
Cutadapt version: 2.6
```

```
Python version: 3.6.3 :: Intel Corporation
Number of cores used for trimming: 10
Quality Phred score cutoff: 20
Quality encoding type selected: ASCII+33
Adapter sequence: 'AGATCGGAAGAGC' (Illumina TruSeq, Sanger
iPCR; auto-detected)
Maximum trimming error rate: 0.1 (default)
Minimum required adapter overlap (stringency): 1 bp
Minimum required sequence length for both reads before a
sequence pair gets removed: 20 bp

Cutadapt seems to be fairly up-to-date (version 2.6).
Setting -j -j 10
Writing final adapter and quality trimmed output to
SRR3098744_2_trimmed.fq


  >>> Now performing quality (cutoff '-q 20') and adapter
trimming in a single pass for the adapter sequence:
'AGATCGGAAGAGC' from file /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098744/SRR3098744_2.fastq <<<
10000000 sequences processed
20000000 sequences processed
30000000 sequences processed
40000000 sequences processed
50000000 sequences processed
60000000 sequences processed
70000000 sequences processed
80000000 sequences processed
90000000 sequences processed
This is cutadapt 2.6 with Python 3.6.3
Command line parameters: -j 10 -e 0.1 -q 20 -O 1 -a
AGATCGGAAGAGC /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098744/SRR3098744_2.fastq
Processing reads on 10 cores in single-end mode ...
Finished in 214.07 s (2 us/read; 25.83 M reads/minute).

=== Summary ===

Total reads processed:              92,170,823
Reads with adapters:                22,417,052 (24.3%)
Reads written (passing filters):    92,170,823 (100.0%)

Total basepairs processed: 11,613,523,698 bp
Quality-trimmed:             186,415,642 bp (1.6%)
Total written (filtered):  11,364,862,692 bp (97.9%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13;
Trimmed: 22417052 times.
```

```
No. of allowed errors:
0-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:
  A: 31.4%
  C: 24.6%
  G: 28.3%
  T: 15.7%
  none/other: 0.0%

Overview of removed sequences
length  count   expect  max.err error counts
1       12169032        23042705.8      0       12169032
2       7535213 5760676.4       0       7535213
3       831524  1440169.1       0       831524
4       291075  360042.3        0       291075
5       171719  90010.6 0       171719
6       105099  22502.6 0       105099
7       137323  5625.7  0       137323
8       55681   1406.4  0       55681
9       25340   351.6   0       23611 1729
10      113308  87.9    1       108103 5205
11      9891    22.0    1       6216 3675
12      82903   5.5     1       79400 3503
13      25085   1.4     1       23479 1606
14      91895   1.4     1       88301 3594
15      22230   1.4     1       21080 1150
16      29592   1.4     1       28217 1375
17      81606   1.4     1       78817 2789
18      6254    1.4     1       5606 648
19      65446   1.4     1       63462 1984
20      34914   1.4     1       33813 1101
21      2909    1.4     1       2540 369
22      34917   1.4     1       33619 1298
23      32896   1.4     1       31581 1315
24      63855   1.4     1       61709 2146
25      14579   1.4     1       13937 642
26      22214   1.4     1       21481 733
27      7301    1.4     1       6821 480
28      40437   1.4     1       39289 1148
29      2108    1.4     1       1807 301
30      36408   1.4     1       35355 1053
31      3940    1.4     1       3641 299
32      23660   1.4     1       22955 705
33      18082   1.4     1       17518 564
34      5631    1.4     1       5319 312
35      21464   1.4     1       20815 649
36      6259    1.4     1       5910 349
37      11647   1.4     1       11221 426
38      14175   1.4     1       13738 437
39      7493    1.4     1       7201 292
40      8248    1.4     1       7853 395
```

```
41      9166    1.4     1       8853 313
42      12958   1.4     1       12603 355
43      1301    1.4     1       1164 137
44      6602    1.4     1       6381 221
45      10196   1.4     1       9883 313
46      3629    1.4     1       3457 172
47      2815    1.4     1       2639 176
48      5270    1.4     1       5094 176
49      4281    1.4     1       4123 158
50      3466    1.4     1       3303 163
51      7116    1.4     1       6898 218
52      3000    1.4     1       2855 145
53      1973    1.4     1       1853 120
54      1678    1.4     1       1565 113
55      3011    1.4     1       2849 162
56      2072    1.4     1       1941 131
57      2244    1.4     1       2111 133
58      2080    1.4     1       1957 123
59      1886    1.4     1       1772 114
60      1984    1.4     1       1857 127
61      1916    1.4     1       1726 190
62      1911    1.4     1       1715 196
63      1852    1.4     1       1613 239
64      1765    1.4     1       1486 279
65      1963    1.4     1       1486 477
66      2473    1.4     1       1479 994
67      14715   1.4     1       1735 12980
68      14201   1.4     1       7932 6269
69      4906    1.4     1       1771 3135
70      2119    1.4     1       516 1603
71      1234    1.4     1       201 1033
72      737     1.4     1       182 555
73      599     1.4     1       125 474
74      423     1.4     1       117 306
75      326     1.4     1       97 229
76      333     1.4     1       114 219
77      254     1.4     1       83 171
78      238     1.4     1       88 150
79      249     1.4     1       86 163
80      213     1.4     1       71 142
81      235     1.4     1       75 160
82      215     1.4     1       91 124
83      221     1.4     1       67 154
84      191     1.4     1       78 113
85      202     1.4     1       67 135
86      176     1.4     1       70 106
87      156     1.4     1       58 98
88      184     1.4     1       51 133
89      157     1.4     1       51 106
90      166     1.4     1       36 130
91      138     1.4     1       36 102
92      130     1.4     1       42 88
```

```
93      158     1.4     1       41 117
94      160     1.4     1       53 107
95      131     1.4     1       44 87
96      120     1.4     1       20 100
97      154     1.4     1       29 125
98      91      1.4     1       27 64
99      109     1.4     1       22 87
100     113     1.4     1       25 88
101     97      1.4     1       17 80
102     100     1.4     1       20 80
103     107     1.4     1       13 94
104     125     1.4     1       22 103
105     101     1.4     1       8 93
106     91      1.4     1       10 81
107     110     1.4     1       10 100
108     132     1.4     1       11 121
109     120     1.4     1       10 110
110     88      1.4     1       4 84
111     91      1.4     1       6 85
112     99      1.4     1       4 95
113     91      1.4     1       9 82
114     76      1.4     1       3 73
115     116     1.4     1       5 111
116     110     1.4     1       5 105
117     124     1.4     1       3 121
118     123     1.4     1       4 119
119     160     1.4     1       5 155
120     166     1.4     1       4 162
121     182     1.4     1       1 181
122     256     1.4     1       9 247
123     347     1.4     1       9 338
124     416     1.4     1       5 411
125     915     1.4     1       3 912
126     6994    1.4     1       29 6965

RUN STATISTICS FOR INPUT FILE: /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098744/SRR3098744_2.fastq
=============================================
92170823 sequences processed in total
The length threshold of paired-end sequences gets evaluated
later on (in the validation step)

Validate paired-end files SRR3098744_1_trimmed.fq and
SRR3098744_2_trimmed.fq
file_1: SRR3098744_1_trimmed.fq, file_2:
SRR3098744_2_trimmed.fq


>>>>> Now valiging the length of the 2 paired-end infiles:
SRR3098744_1_trimmed.fq and SRR3098744_2_trimmed.fq <<<<<
Writing validated paired-end Read 1 reads to
SRR3098744_1_val_1.fq
```

```
Writing validated paired-end Read 2 reads to
SRR3098744_2_val_2.fq

Total number of sequences analysed: 92170823

Number of sequence pairs removed because at least one read
was shorter than the length cutoff (20 bp): 469354 (0.51%)

Deleting both intermediate output files
SRR3098744_1_trimmed.fq and SRR3098744_2_trimmed.fq

================================================================
=====================================
```

stderr

Program	Return code	Start	Runtime	Version
trim_galore	0	20-01-22 18:51:10	0:13:56	Quality-/Adapter-/RRBS-/ Speciality-Trimming [powered by Cutadapt] version 0.6.4_dev Last update: 24 09 2019

---

command

```
STAR --outFilterType BySJout --runThreadN 8 --outSAMtype BAM
SortedByCoordinate --genomeDir /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/maize_data/starindex --
readFilesIn /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/
maize/SRR3098746/SRR3098746_1_trimgalore.fastq /pylon5/
mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746/
SRR3098746_2_trimgalore.fastq --outFileNamePrefix /pylon5/
mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746/
```

stdout

```
Jan 22 19:05:07 ..... started STAR run
Jan 22 19:05:07 ..... loading genome
Jan 22 19:05:40 ..... started mapping
Jan 22 20:47:54 ..... finished mapping
Jan 22 20:47:57 ..... started sorting BAM
Jan 22 20:52:21 ..... finished successfully
```

stderr

Program	Return code	Start	Runtime	Version
STAR	0	20-01-22 19:05:07	1:47:28	2.7.3a

---

command

```
stringtie -G maize_data/Zea_mays.B73_RefGen_v4.46.gtf -p 25 -
o /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/
SRR3098746/Aligned.sortedByCoord.out_stringtie.gtf /pylon5/
mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746/
Aligned.sortedByCoord.out.bam
```

stdout

stderr

Program	Return code	Start	Runtime	Version
stringtie	0	20-01-22 20:52:36	0:20:09	2.0.3

---

command

```
STAR --outFilterType BySJout --runThreadN 8 --outSAMtype BAM
SortedByCoordinate --genomeDir /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/maize_data/starindex --
readFilesIn /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/
maize/SRR3098744/SRR3098744_1_trimgalore.fastq /pylon5/
mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/
SRR3098744_2_trimgalore.fastq --outFileNamePrefix /pylon5/
mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/
```

stdout

```
Jan 22 21:12:45 ..... started STAR run
Jan 22 21:12:45 ..... loading genome
Jan 22 21:13:25 ..... started mapping
Jan 22 23:01:59 ..... finished mapping
Jan 22 23:02:01 ..... started sorting BAM
Jan 22 23:06:09 ..... finished successfully
```

stderr

Program	Return code	Start	Runtime	Version
STAR	0	20-01-22 21:12:45	1:53:37	2.7.3a

---

command

```
stringtie -G maize_data/Zea_mays.B73_RefGen_v4.46.gtf -p 25 -
o /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/
SRR3098744/Aligned.sortedByCoord.out_stringtie.gtf /pylon5/
mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/
Aligned.sortedByCoord.out.bam
```

stdout

stderr

Program	Return code	Start	Runtime	Version
stringtie	0	20-01-22 23:06:22	0:19:58	2.0.3

---

command

```
gffread -w /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/
maize/SRR3098746/transcripts.fa -g maize_data/
Zea_mays.B73_RefGen_v4.dna.toplevel.1_10.fa /pylon5/mc5pl7p/
usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746/
Aligned.sortedByCoord.out_stringtie.gtf
```

stdout

stderr

Program	Return code	Start	Runtime	Version
gffread	0	20-01-22 23:27:18	0:00:09	0.11.5

---

command

```
plncpro predict -i /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098746/transcripts_filter.fa -o /pylon5/
mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746/
plncpro_out -p plncpro_predictions -t 25 -d uniprot/
uniprotdb -m monocot_model/monocot.model -v -r
```

stdout

```
                Predicted as neg: 1484: 0.2802114803625378
                Predicted as pos: 3812: 0.7197885196374623
[91m
                                    _____  _
_____    _____     ____            |  __ \| |
|  __ \  |  __ \   / __ \           | |__) | |  _ __     ___  |
|__) | | |__) | | |  | |           |  ___/| | |  _ \   / __|
|  ___/  |  _  /  | |  | |          | |    | | | | | | | (__  |
|      | | \ \  | |__| |           |_|    |_| |_| |_|  \___| |
_|      |_|  \_\  \____/
[0m
Reading Input File...
Extracting Features...
Extracting Framefinder Features...
Running BLASTX...This might take some time depending on your
input.
blastx -query /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098746/transcripts_filter.fa -db uniprot/
uniprotdb -outfmt '6 qseqid sseqid pident evalue qcovs
qcovhsp score bitscore qframe sframe' -out /pylon5/mc5pl7p/
usingh/urmi/pyrpipeTest/testDir/maize/SRR3098746/
transcripts_filter.fa_blastres -qcov_hsp_perc 30 -
num_threads 25
Parsing Blast Results...
Merging all Features...
Predicting...
python /pylon5/mc5pl7p/usingh/lib/myAnacondaInstallation/
envs/pyrpipeTest/lib/python3.7/site-packages/plncpro/bin/rf/
predict.py /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/
maize/SRR3098746/transcripts_filter.fa_all_features
monocot_model/monocot.model /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/plncpro_predictions false
Removing temp files...
All outputs saved to: /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098746/plncpro_out
END
```

stderr

Program	Return code	Start	Runtime	Version

<table>
<tr><td>plncpro predict</td><td>0</td><td>20-01-22 23:27:31</td><td>0:15:10</td><td>␛[91m _____ _ _____ _____ ____ | __ \| | | __ \ | __ \ / __ \ | |__) | | _ __ ___ | |__) | | |__) | | | | | | ___/| | | _ \ / __| | ___/ | _ / | | | | | | | | | | | | (__ | | | | \ \ | |__| | |_| |_| |_| |_| ___| |_| |_| _\ ____/ ␛[0m Valid commands are: predict build predtoseq</td></tr>
</table>

---

command

```
gffread -w /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/transcripts.fa -g maize_data/Zea_mays.B73_RefGen_v4.dna.toplevel.1_10.fa /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/Aligned.sortedByCoord.out_stringtie.gtf
```

stdout

stderr

Program	Return code	Start	Runtime	Version
gffread	0	20-01-22 23:42:41	0:00:07	0.11.5

---

command

```
plncpro predict -i /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/transcripts_filter.fa -o /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/plncpro_out -p plncpro_predictions -t 25 -d uniprot/uniprotdb -m monocot_model/monocot.model -v -r
```

stdout

```
                Predicted as neg: 1504: 0.28355957767722473
                Predicted as pos: 3800: 0.7164404223227753
␛[91m
                                  _____  _
_____    _____    ____
                                 |  __ \| |
|  __ \  |  __ \   / __ \
                                 | |__) | |  _ __     ___  |
|__) | | |__) | | |  | |
                                 |  ___/| | |  _ \   / __|
```

```
|  ___/  |  _  /  | |  | |                                                 | |    | | | | | | | (__  |
|      | | \ \  | |__| |                                                 |_|    |_| |_| |_|  \___| |
_|      |_|  \_\  \____/
[0m
Reading Input File...
Extracting Features...
Extracting Framefinder Features...
Running BLASTX...This might take some time depending on your
input.
blastx -query /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/
testDir/maize/SRR3098744/transcripts_filter.fa -db uniprot/
uniprotdb -outfmt '6 qseqid sseqid pident evalue qcovs
qcovhsp score bitscore qframe sframe' -out /pylon5/mc5pl7p/
usingh/urmi/pyrpipeTest/testDir/maize/SRR3098744/
transcripts_filter.fa_blastres -qcov_hsp_perc 30 -
num_threads 25
Parsing Blast Results...
Merging all Features...
Predicting...
python /pylon5/mc5pl7p/usingh/lib/myAnacondaInstallation/
envs/pyrpipeTest/lib/python3.7/site-packages/plncpro/bin/rf/
predict.py /pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/
maize/SRR3098744/transcripts_filter.fa_all_features
monocot_model/monocot.model /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/plncpro_predictions false
Removing temp files...
All outputs saved to: /pylon5/mc5pl7p/usingh/urmi/
pyrpipeTest/testDir/maize/SRR3098744/plncpro_out
END
```

stderr

Program	Return code	Start	Runtime	Version
plncpro predict	0	20-01-22 23:42:49	0:13:35	[91m _____ _ _____ _____ ____ | | __ \ | __ \ / __ \ | |__) | | _ __ ___ | |__) | | |__) | | | | | ___/| | | _ \ / __| | ___/ | _ / | | | | | | | | | | | (__ | | | \ \ | |__| | |_| |_| |_| |_| ___| |_| |_| _\ \ ____/ [0m Valid commands are: predict build predtoseq

---

Environment Information

Programs		
name	**version**	**path**
trim_galore	Quality-/Adapter-/RRBS-/ Speciality-Trimming [powered by Cutadapt] version 0.6.4_dev Last update: 24 09 2019	/pylon5/mc5pl7p/usingh/lib/ TrimGalore-0.6.5/trim_galore
prefetch	/pylon5/mc5pl7p/usingh/ lib/sratoolkit.2.10.0- centos_linux64/bin/ prefetch : 2.10.0	/pylon5/mc5pl7p/usingh/lib/ sratoolkit.2.10.0- centos_linux64/bin/prefetch
stringtie	2.0.3	/pylon5/mc5pl7p/usingh/lib/ stringtie/ stringtie-2.0.3.Linux_x86_64/ stringtie
fasterq-dump		/pylon5/mc5pl7p/usingh/lib/ sratoolkit.2.10.0- centos_linux64/bin/fasterq-dump
gffread	0.11.5	/pylon5/mc5pl7p/usingh/lib/ gffread/gffread
plncpro predict	[91m _____ _ _____ _____ ____ | __ \\| | | __ \ | __ \ / __ \ | |__) | | _ __ ___ | |__) | | |__) | | | | | ___/| | | _ \ / __| | ___/ | _ / | | | | | | | | | | | (__ | | | \ \ | |__| | |_| |_| |_| |_| ___| |_| |_| _\ _____/ [0m Valid commands are: predict build predtoseq	/pylon5/mc5pl7p/usingh/lib/ myAnacondaInstallation/envs/ pyrpipeTest/bin/plncpro
STAR	2.7.3a	/pylon5/mc5pl7p/usingh/lib/ STAR-2.7.3a/bin/Linux_x86_64/ STAR

System Information	
Time at collection	20-01-22 18:14:47
Python	Python 3.7.5 (default, Oct 25 2019, 15:51:11) [GCC 7.3.0]
Operating system	Linux-3.10.0-957.27.2.el7.x86_64-x86_64-with-centos-7.6.1810-Core
CPU	28 logical CPU cores

sys.modules
'sys'
'builtins'
'_frozen_importlib'

'_imp'
'_thread'
'_warnings'
'_weakref'
'zipimport'
'_frozen_importlib_external'
'_io'
'marshal'
'posix'
'encodings'
'codecs'
'_codecs'
'encodings.aliases'
'encodings.utf_8'
'_signal'
'__main__'
'encodings.latin_1'
'io'
'abc'
'_abc'
'_bootlocale'
'_locale'
'site'
'os'
'stat'
'_stat'
'posixpath'
'genericpath'
'os.path'
'_collections_abc'
'_sitebuiltins'
'pyrpipe'
'pyrpipe.sra'
'pyrpipe.pyrpipe_utils'
'datetime'
'time'
'math'
'_datetime'
'pyrpipe.pyrpipe_engine'
'subprocess'
'signal'
'functools'
'_functools'
'collections'

'operator'
'_operator'
'keyword'
'heapq'
'_heapq'
'itertools'
'reprlib'
'_collections'
'enum'
'types'
'warnings'
'errno'
'_posixsubprocess'
'select'
'selectors'
'collections.abc'
'threading'
'traceback'
'linecache'
'tokenize'
're'
'sre_compile'
'_sre'
'sre_parse'
'sre_constants'
'copyreg'
'token'
'_weakrefset'
'logging'
'weakref'
'string'
'_string'
'atexit'
'platform'
'multiprocessing'
'multiprocessing.context'
'multiprocessing.process'
'multiprocessing.reduction'
'pickle'
'struct'
'_struct'
'_compat_pickle'
'_pickle'
'socket'

'_socket'
'array'
'__mp_main__'
'json'
'json.decoder'
'json.scanner'
'_json'
'json.encoder'

sys.path
'/pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/testDir/maize'
'/pylon5/mc5pl7p/usingh/lib/myAnacondaInstallation/envs/pyrpipeTest/lib/python37.zip'
'/pylon5/mc5pl7p/usingh/lib/myAnacondaInstallation/envs/pyrpipeTest/lib/python3.7'
'/pylon5/mc5pl7p/usingh/lib/myAnacondaInstallation/envs/pyrpipeTest/lib/python3.7/lib-dynload'
'/pylon5/mc5pl7p/usingh/lib/myAnacondaInstallation/envs/pyrpipeTest/lib/python3.7/site-packages'
'/pylon5/mc5pl7p/usingh/urmi/pyrpipeTest/pyrpipe'