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

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 validing 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

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

---

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
stringtie	2.0.3	/pylon5/mc5pl7p/usingh/lib/ stringtie/ stringtie-2.0.3.Linux_x86_64/ stringtie
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
fasterq-dump		/pylon5/mc5pl7p/usingh/lib/ sratoolkit.2.10.0-centos_linux64/bin/fasterq-dump
STAR	2.7.3a	/pylon5/mc5pl7p/usingh/lib/ STAR-2.7.3a/bin/Linux_x86_64/ STAR
plncpro predict	▒[91m ____ _ ____ ____ ___ | _ \\\| | _ \ | _ \/ _ \ | |_) | | _ | _ | |_) | | _) | | | | | | ___/| | | _ \/ _| | ___/ | _ / | | | | | | | | | | | | (__ | | | | \\ | |_| | |_| |_| |_| |_| ___| |_| |_| _\\ ___/ ▒[0m Valid commands are: predict build predtoseq	/pylon5/mc5pl7p/usingh/lib/ myAnacondaInstallation/envs/ pyrpipeTest/bin/plncpro
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
gffread	0.11.5	/pylon5/mc5pl7p/usingh/lib/ gffread/gffread

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'