

***pyrpipe* report**

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

Details

command

```
prefetch -0 /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 -0 /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 -0 /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 validating 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 validating 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/uniprotodb -m monocot_model/monocot.model -v -r
```

stdout

Predicted as neg: 1484: 0.2802114803625378
Predicted as pos: 3812: 0.7197885196374623

91m

```

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      |      | | \ \  | |__ | |
      _|      | _| \ \  \__ /

```

90m

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
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plncpro predict	0	20-01-22 23:27:31	0:15:10	 [91m _____ _ \ _ \ _ \ _ \) _ \)) _ \ _ \ _ \ _ \ _ \ (\ \ _ \ \ \ _ \ Valid commands are: predict build predtoseq
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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/uniprotodb -m monocot_model/monocot.model -v -r
```

stdout

Predicted as neg: 1504: 0.28355957767722473
Predicted as pos: 3800: 0.7164404223227753

[91m _____ |
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Valid
commands are: predict build
predtoseq

'_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'