

A

```

ct seq library.txt
ct seq bin_1.txt
ct seq bin_2.txt
:
:
ct seq bin_9.txt

```

B

files.txt

bin	file
0	library.txt
1	bin_1.txt
2	bin_2.txt
3	bin_3.txt
4	bin_4.txt
5	bin_5.txt
6	bin_6.txt
7	bin_7.txt
8	bin_8.txt
9	bin_9.txt

C

```

bin file file list
files.txt

```

gatherseqs

```

ct_0 ct_1 ... ct_9 seq dataset
data.txt

```

profile_info

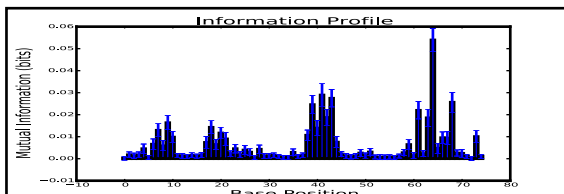
```

pos info info_err information profile
info.txt

```

draw

info.pdf



D



E

```

$ sortseq gatherseqs -i files.txt -o data.txt
$ sortseq profile_info -i data.txt -o info.txt
$ sortseq draw -i info.txt -o info.pdf

```

Figure 5