Awk one-liners for blast results manipulation Cheat Sheet

by melissamlwong via cheatography.com/22270/cs/5331/

Introduction

This cheatsheet contains 10 useful AWK one-liners for tab delimited blast results. It is created as part of a series to help graduate students and biologists in learning some simple programming scripts. Each oneliner is usually accompanied by additional comments which start with a hash ("#"). Runnabble codes is available on http://code.runnable.com/VfItWNXUYTcrUkwn/10-awk-one-liners-for-blast-results-manipulation-for-shell-bash-and-bioinformatics

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Tab delimited blast results is a text-based files to show pairwise alignment between two sequences. It is generated using the option "-outfmt 6" or "-m 8". Each column is separated by a tab and represents queryId($1), subjectId($2), percIdentity($3), alnLength($4), mismatchCount($5), gapOpenCount($6), queryStart($7), queryEnd($8), subjectStart($9), subjectEnd($10), eValue($11) and bitScore($12) respectively

1. To filter alignment

```
awk '$1~/Medtr1g006460.1/' temp.blast #matching query name
awk '$2~/Medtr0/' temp.blast #matching reference name
awk '$12>=1000' temp.blast #score
awk '$3>=80' temp.blast #identity percentage
awk '$11<1e-30' temp.blast #e-value
```

2. To filter all against all blast results

```
#method 1 - remove blast results of the same sequence and apply filtering
blastn -task megablast -db database1 -query temp.fa -evalue 1E-10 -outfmt 6 | awk '$1!=$2 && $3>=40 && $4>=300'
#method 2 - remove blast results of the same sequence and apply filtering
blastn -task megablast -db database1 -query temp.fa -evalue 1E-10 -outfmt 6 | awk '{split($1,a,".");
split($1,b,"."); if (a[1]!=b[1] && $3>=40 && $4>=300) print }'
#method 3 - remove redundant alignments. Any alignment in all-against-all blast can appear twice as seq1\tseq2
and seq2\tseq1. Both alignments can sometimes vary in length by 1-2 bp, however, they always share the same score.
awk '{c=$1"\t"$2"\t"$12 ; b= $2"\t"$1"\t"$12; if ($1!=$2 && a[c]==0 && a[b]==0) a[$1"\t"$2"\t"$12]=$0}END{for (i
in a) print a[i]}' temp.txt > temp.blast #not so working well
```

3. To filter alignments based on sequence length

```
#method 1 - calculate sequence length, calculate percentage of alignment length against sequence length, filter
blast file
awk 'BEGIN{RS=">";FS="\n"}NR>1{seq="";for (i=2;i<=NF;i++) seq=seq""$i; print $1"\t"length(seq)}' temp.fa > len1
awk 'NR==FNR{a[NR]=$1"\t"$2"\t"$4;d[NR]=$0;sum+=1}NR>FNR{b[$1]=$2}END{for (i=1;i<=sum;i++) {split(a[i],c,"\t"); if
(c[3]/b[c[1]]>=0.8 && c[3]/b[c[2]]>=0.8) print d[i]}}' temp.blast len1 len1
#method 2 - if length information is included in fasta header
awk '{split($1,a,"_"); split($1,b,"_"); c=a[2];d=b[2]; if ($4/c>=0.8 && $4/d>=0.8) print $0}' temp.blast #if
length in header and separated by "_"
```

4. To count the number of queries

```
awk '! a[$1]++' temp.blast | wc -l
awk '{a[$1]++}END{for (i in a) sum+=1; print sum}' temp.blast #equivalent script but faster
```

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Published 5th October, 2015.
Last updated 21st April, 2016.

5. To count the number of alignments per query

```
awk '{a[$1]++}END{for (i in a) print i"\t"a[i]}' temp.blast
```

6. To find best hit for a query

```
#method 1 - Use the first alignment per sequence assuming the best hit is always listed first
awk '! a[$1]++' temp.blast
#method 2 - Use total score assuming each query can have multiple alignments to a reference sequence. In my opinion, this is the best way except in cases where multiple alignments to the same region of a pair of query and reference are reported.
awk '{b[$1]="0"; e[$1]="";if (a[$1,$2]=="0") a[$1,$2]=$12; else {score=a[$1,$2]+$12; a[$1,$2]=score}}END{for (i in b) for (j in a) {split(j,c,SUBSEP); if (c[1]==i && a[j]>b[i]) {b[i]=a[j];e[i]=c[2]}}; for (i in b) print i"\t"e[i]"\t"b[i]}' temp.blast
```

7. To find reciprocal best hit for a query

```
#An extension of the finding best hit script by making sure that a query is a reference's best hit and vice versa
awk '{a[$1]="0";b[$1]="";c[$2]="0";d[$2]="";if (e[$1,$2]==0) e[$1,$2]=$12; else {score=e[$1,$2]+$12; e[$1,$2]=score}}END{for (i in a) for (j in e) {split(j,f,SUBSEP); if (f[1]==i && e[j]>a[i]) {a[i]=e[j];b[i]=f[2]}}; for (i in c) for (j in e) {split(j,f,SUBSEP); if (f[2]==i && e[j]>c[i]) {c[i]=e[j];d[i]=f[1]}}; for (i in b) if (b[i] in d && d[b[i]]==i) print i"\t"b[i]"\t"a[i]"\t"c[b[i]]}' temp.blast
#need to debug
```

8. To extract one seqeunce

```
awk 'NR==FNR{if ($1~/Medtr1g006460.1/) a[$1]++}NR>FNR{if ($1 in a && $1!="") printf ">%s\n",$0}' RS="\n" FS="\t" temp.blast RS=">" FS="\n" temp.fa
```

9. To reduce blast file size

```
#replace unnecessary columns by replacing them with empty string. For example, we are only interested in the query name, reference name and score.
awk '{print $1"\t"$2"\t\t\t\t\t\t\t\t\t\t"$12}' temp.blast
```

10. To list all hits for each reference sequence

```
awk '{a[$1]++;b[$1,$2]++}END{for (i in a) {printf "%s", i; for (j in b) {split(j,c,SUBSEP); if (c[1]==i) printf " %s", c[2]};printf "\n"}}' temp.blast
```