

Script 1. Blast parser

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#!/usr/bin/python
from Bio.Blast import NCBIXML
import sys
import re

output = open("f113vsnr2xmlb.tab", 'w')
output.write('Query\tHit\tTaxon\tCoverage\tIdentities\tPerIdentities\tPositives\tPercentPositives\tE-Value\tBit Score\n')
result_handle = open("f113vsnr2.xml")
blast_records = NCBIXML.parse(result_handle)
for blast_record in blast_records:
    for alignment in blast_record.alignments:
        queryprot = blast_record.query
        sqquery = re.match('(.+)( \[])', queryprot)
        query = sqquery.group(1)
        hitprot = alignment.hit_def
        searchobj = re.match('gi\|.+?\|.+?\|(.+\[).(\.+)(\])', hitprot)
        protein=searchobj.group(1)
        specie = searchobj.group(3)
        for hsp in alignment.hsps:
            identities = hsp.identities
            percidentities=round(float(identities)/float(hsp.align_length)*100,1)
            coverage = round(float(alignment.length) / float(hsp.align_length) * 100, 1)
            positives = hsp.positives
            percpositives=round(float(positives)/float(hsp.align_length)*100, 1)
            evalor= hsp.expect
            score= hsp.score
            output.write(str(query) + '\t' + str(protein) + '\t' + str(specie) + '\t' +
str(coverage) + '%\t' + str(identities) + '\t' +
str(percidentities) + '\t' + str(positives) + '\t' + str(percpositives) + '\t' +
str(evalor) + '\t' + str(score) '\n')
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Script 2. Concatenation of sequences

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#!/usr/bin/Python
import sys
import os
import re

r16S = open('r16S', 'r')
gyrB = open('gyrB', 'r')
rpoB = open('rpoB', 'r')
rpoD = open('rpoD', 'r')
out = open('output', 'w')

with open('del_16S', 'w') as del_16S:
    for line in r16S:
        line = line.rstrip('\n')
        if '>' in line:
            line = '\n'+line+'|'
            del_16S.write(line)
        else:
            del_16S.write(line)
    del_16S.closed

with open('del_gyrB', 'w') as del_gyrB:
    for line in gyrB:
        line = line.rstrip('\n')
        if '>' in line:
            line = '\n'+line+'|'
            del_gyrB.write(line)
        else:
            del_gyrB.write(line)
    del_gyrB.closed

with open('del_rpoB', 'w') as del_rpoB:
    for line in rpoB:
        line = line.rstrip('\n')
        if '>' in line:
            line = '\n'+line+'|'
            del_rpoB.write(line)
        else:
            del_rpoB.write(line)
    del_rpoB.closed

with open('del_rpoD', 'w') as del_rpoD:
    for line in rpoD:
        line = line.rstrip('\n')
        if '>' in line:
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        line = '\n'+line+'|'
        del_rpoD.write(line)
    else:
        del_rpoD.write(line)
del_rpoD.closed

del_16S_r = open('del_16S', 'r')
del_gyrB_r = open('del_gyrB', 'r')
del_rpoB_r = open('del_rpoB', 'r')
del_rpoD_r = open('del_rpoD', 'r')

for a, b, c, d in zip(sorted(del_16S_r), sorted(del_gyrB_r), sorted(del_rpoB_r),
sorted(del_rpoD_r)):
    if re.match('^$', a):
        pass
    else:
        match_16S = re.match('(>.*))\|(.*)', a)
        match_gyrB = re.match('(>.*))\|(.*)', b)
        match_rpoB = re.match('(>.*))\|(.*)', c)
        match_rpoD = re.match('(>.*))\|(.*)', d)

        out.write(match_16S.group(1)+'\n'+match_16S.group(3)+match_gyrB.group(3)
+match_rpoB.group(3)+match_rpoD.group(3)+'\n')

```