***BLAST***

#!/bin/bash

##THIS SCRIPT BLASTS ALL THE GREEN PROTEIN QUERIES FROM GALLUS GALLUS TO THE PARUS MAJOR GENOME

#To export the blast software and to define the paths of the inputs and outputs:
export PATH=/cursos/BI/bin/ncbiblast/x64/bin:$PATH #Blast
PATH\_db=/cursos/20428/BI/genomes/2016/Parus\_major/genome.fa #Parus majus genome database
PATH\_outputg=/home/u104639/Bioinformatica/Parus/Green #Output's directory
PATH\_proteinsg=/home/u104639/Bioinformatica/Gallus/Green #Directory of Gallus gallus Selenoproteins from SelenoDB

#To change directory to the protein's path and to define the proteins variable
cd $PATH\_proteinsg
proteinsg="eEFsec.fa MsrA.fa SBP2\_1.fa SECp43.fa SELENOH.fa SELENOO\_2.fa GPx7.fa MSRB3.fa SBP2\_2.fa SecS\_1.fa SELENOK\_2.fa SELENOO\_4.fa GPx8.fa PSTK.fa SBP2\_3.fa SecS\_2.fa SELENOK\_3.fa SEPHS.fa "

#Make the output directory
mkdir $PATH\_outputg

#To enter a loop for each protein
for protein in $proteinsg
do
 #To run the blastall software for each protein (-i) to the genome database(-d)
 tblastn -query $PATH\_proteinsg/$protein -db $PATH\_db -out $PATH\_outputg/$protein.blast
done

echo "Blast finished!"
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#!/bin/bash

##THIS SCRIPT BLASTS ALL THE RED PROTEIN QUERIES FROM GALLUS GALLUS TO THE PARUS MAJOR GENOME

#To export the blast software and to define the paths of the inputs and outputs:
export PATH=/cursos/BI/bin/ncbiblast/x64/bin:$PATH #Blast
PATH\_db=/cursos/20428/BI/genomes/2016/Parus\_major/genome.fa #Parus majus genome database
PATH\_output=/home/u104639/Bioinformatica/Parus/Red #Output's directory
PATH\_proteins=/home/u104639/Bioinformatica/Gallus/Red #Directory of Gallus gallus Selenoproteins from SelenoDB

#To change directory to the protein's path and to define the proteins variable
cd $PATH\_proteins
proteins="DIO1.fa GPx3.fa SELENOI.fa SELENOO1.fa SELENOP2.fa SELENOU1.fa TXNRD3.fa DIO2.fa MSRB1.fa SELENOK.fa SELENOO3.fa SELENOS.fa TXNRD1.fa DIO3.fa Sel15.fa SELENON.fa SELENOP1.fa SELENOT.fa TXNRD2.fa "

#Make the output directory
mkdir $PATH\_output

#To enter a loop for each protein
for protein in $proteins
do
 #To run the blastall software for each protein (-i) to the genome database(-d)
 tblastn -query $PATH\_proteins/$protein -db $PATH\_db -out $PATH\_output$protein.blast
done

echo "Blast finished!"