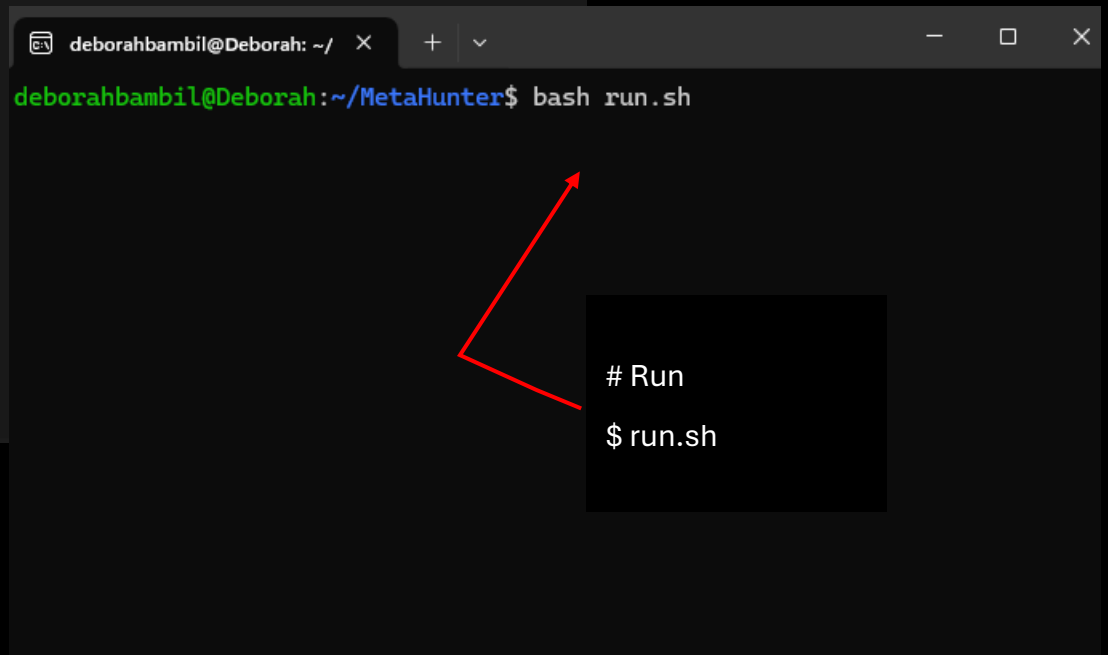
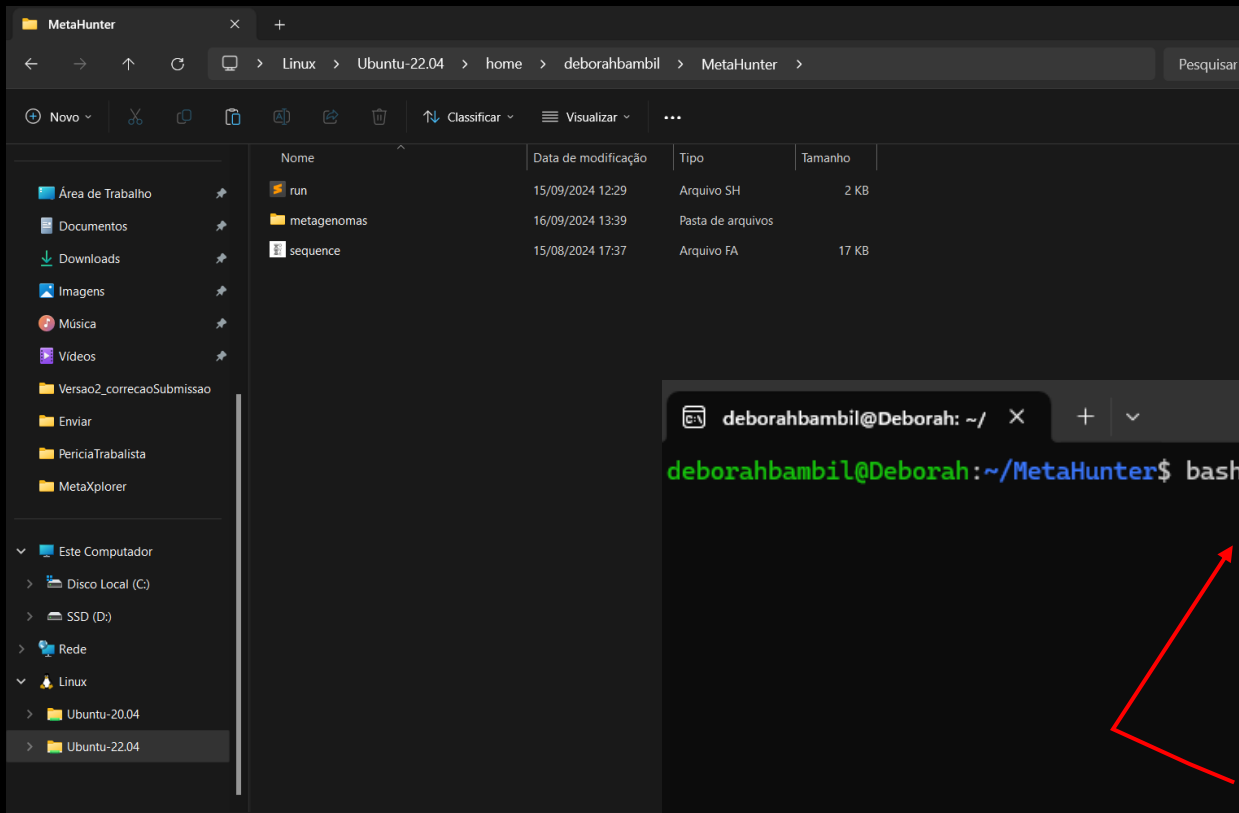
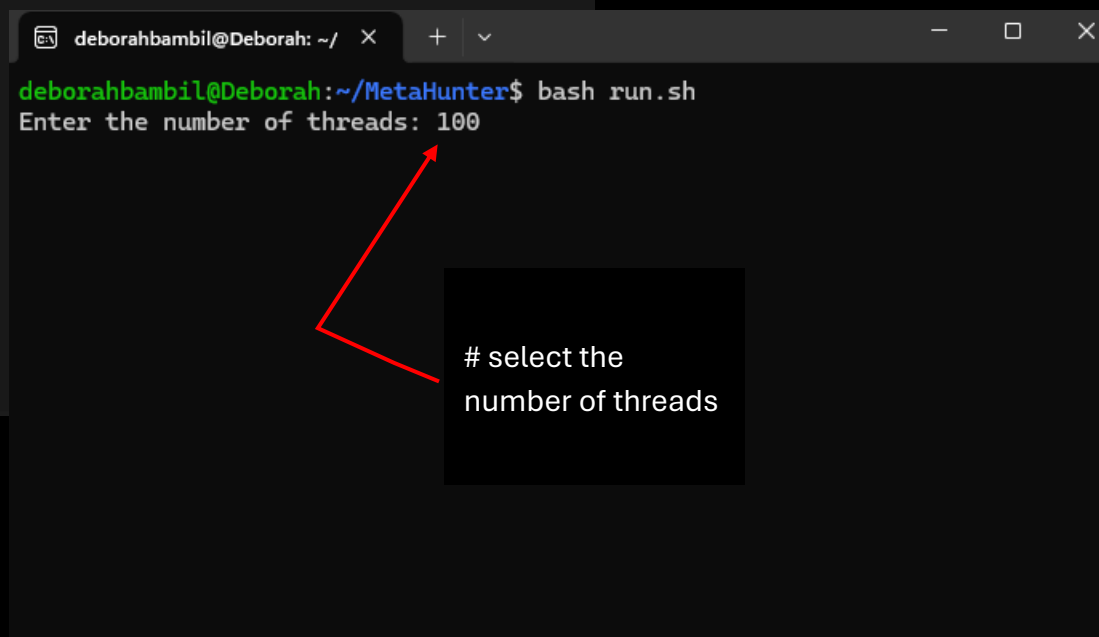
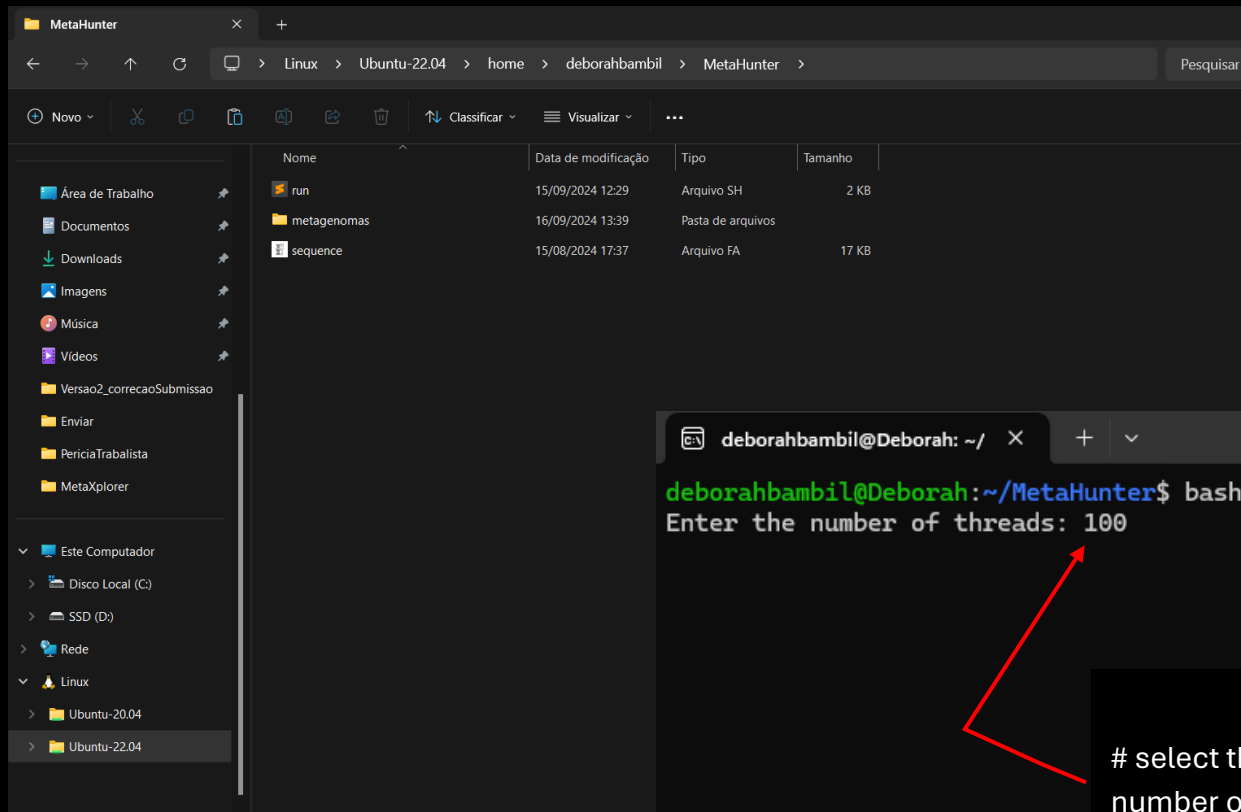


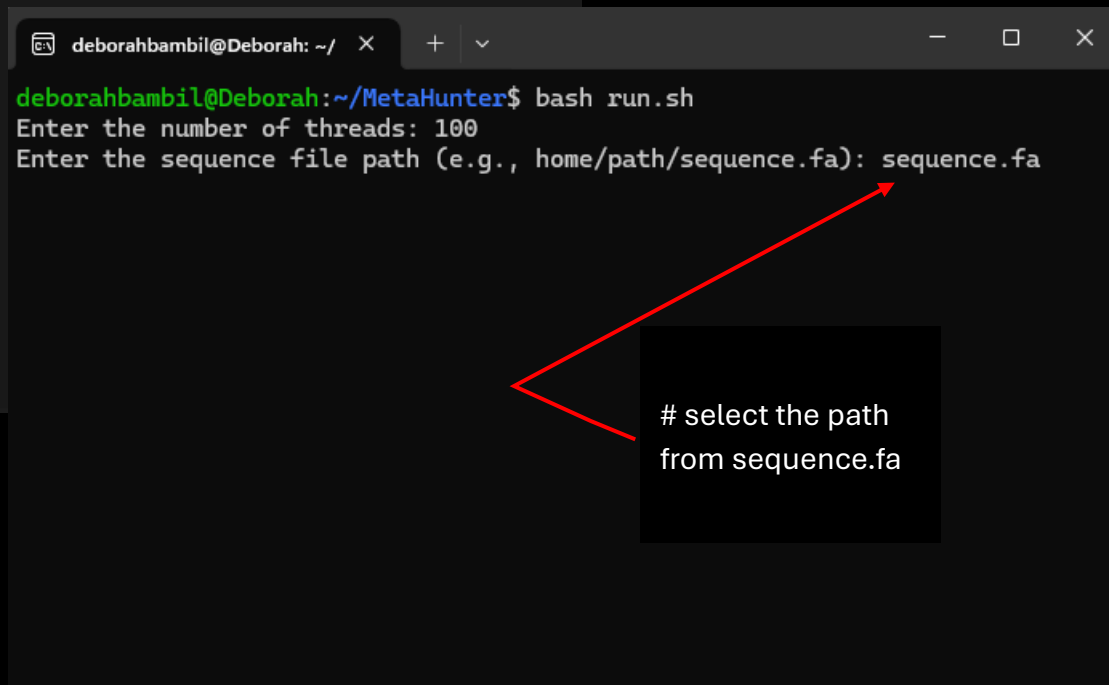
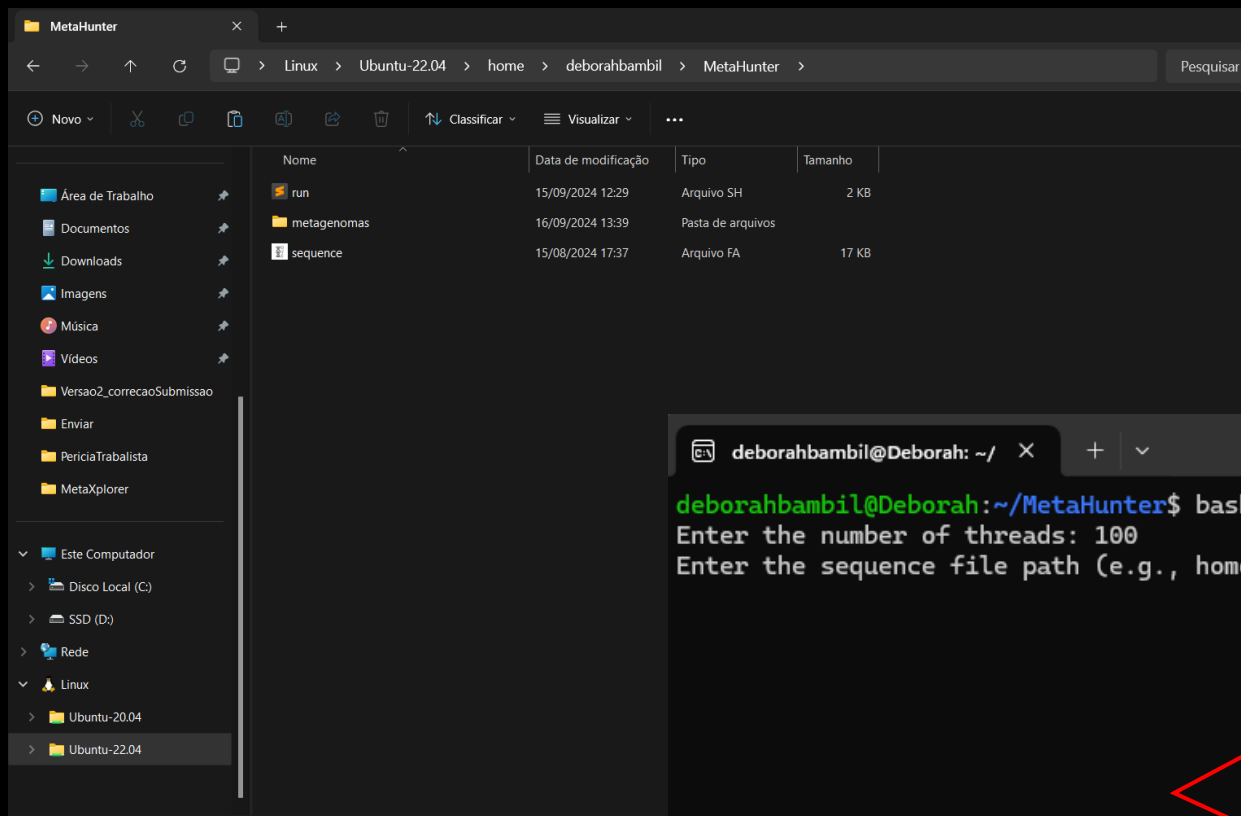
# MetaHunter

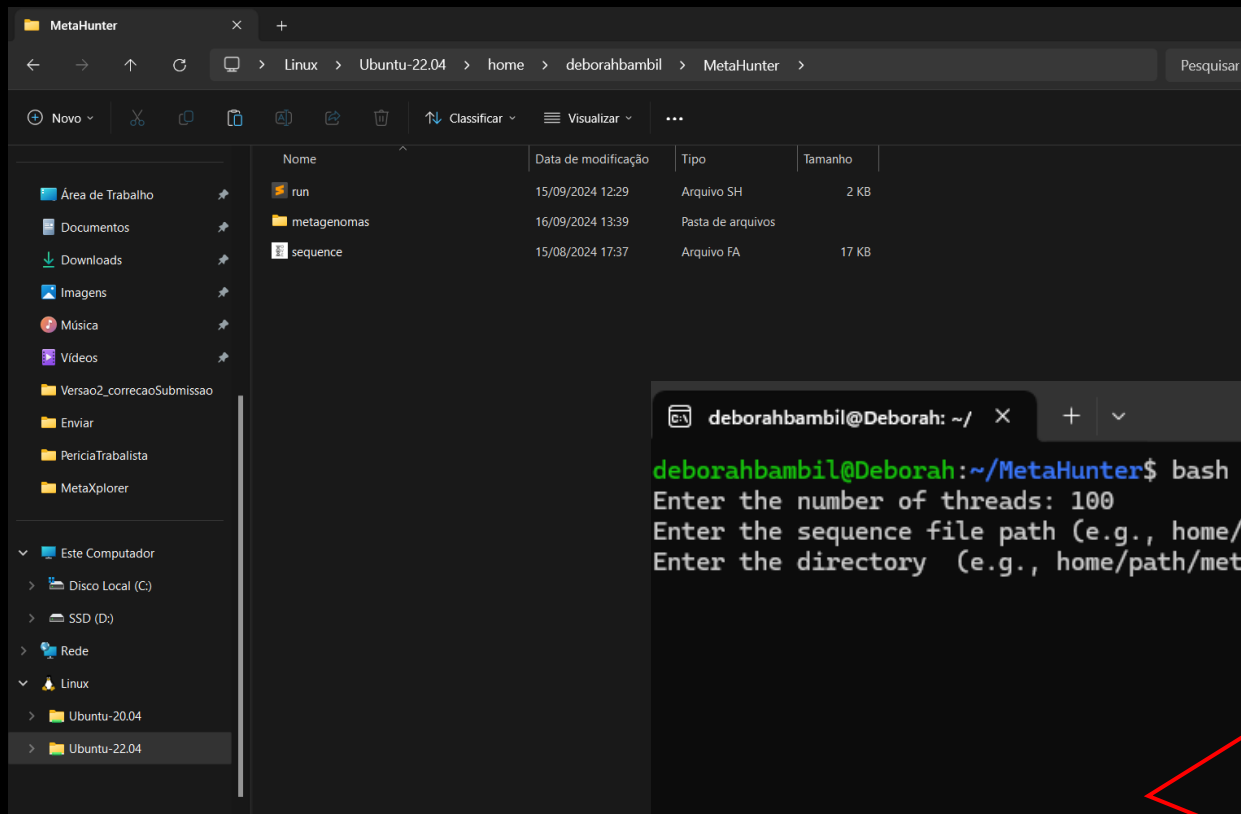


User Guide



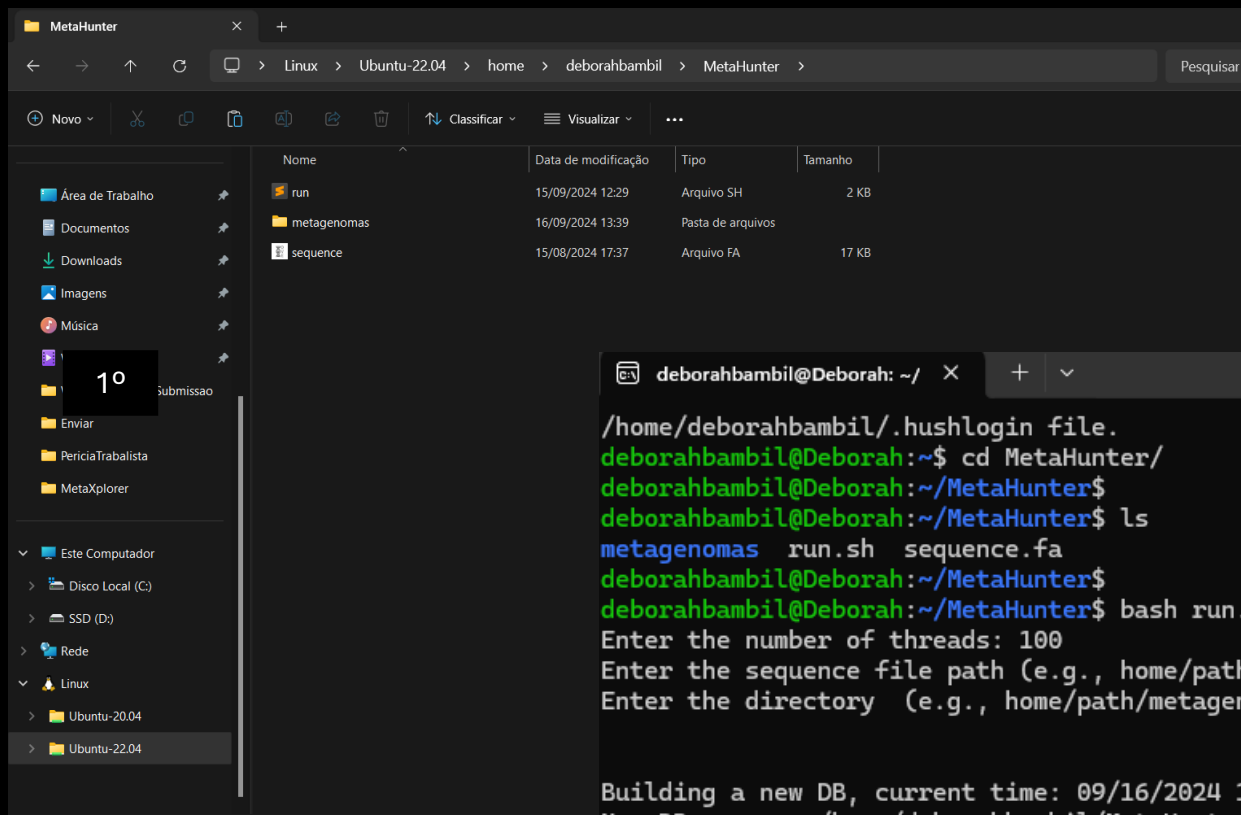




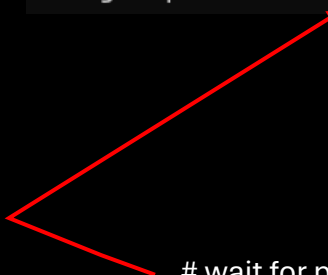


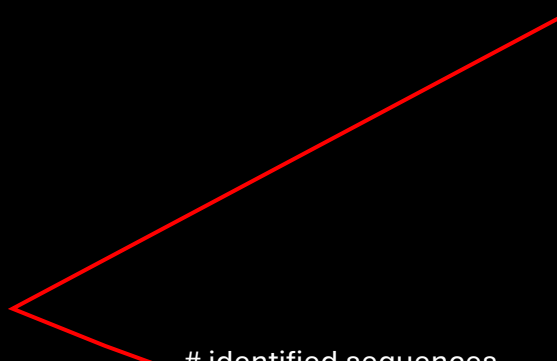
```
deborahbambil@Deborah: ~/MetaHunter$ bash run.sh
Enter the number of threads: 100
Enter the sequence file path (e.g., home/path/sequence.fa): sequence.fa
Enter the directory (e.g., home/path/metagenomes): metagenomes
```

# select the path from metagenomes



```
deborahbambil@Deborah: ~/  + -  
  
/home/deborahbambil/.hushlogin file.  
deborahbambil@Deborah:~$ cd MetaHunter/  
deborahbambil@Deborah:~/MetaHunter$  
deborahbambil@Deborah:~/MetaHunter$ ls  
metagenomas run.sh sequence.fa  
deborahbambil@Deborah:~/MetaHunter$  
deborahbambil@Deborah:~/MetaHunter$ bash run.sh  
Enter the number of threads: 100  
Enter the sequence file path (e.g., home/path/sequence.fa): sequence.fa  
Enter the directory (e.g., home/path/metagenomes): metagenomes  
  
Building a new DB, current time: 09/16/2024 13:50:38  
New DB name: /home/deborahbambil/MetaHunter/sequence  
New DB title: sequence.fa  
Sequence type: Protein  
Keep MBits: T  
Maximum file size: 1000000000B  
Adding sequences from FASTA; added 38 sequences in 0.00576687 seconds.
```

 # wait for processing



metagenomes	16/09/2024 13:39	Pasta de arquivos	
Output	16/09/2024 13:50	Pasta de arquivos	
Seq	16/09/2024 13:50	Pasta de arquivos	
run	15/09/2024 12:29	Arquivo SH	2 KB
sequence	15/08/2024 17:37	Arquivo FA	17 KB
sequence.pdb	16/09/2024 13:50	Arquivo PDB	20 KB
sequence.phr	16/09/2024 13:50	Arquivo PHR	5 KB
sequence.pin	16/09/2024 13:50	Arquivo PIN	1 KB
sequence	16/09/2024 13:50	Modelo do Micros...	1 KB
sequence.psq	16/09/2024 13:50	Arquivo PSQ	15 KB
sequence.ptf	16/09/2024 13:50	Arquivo PTF	16 KB
sequence.pto	16/09/2024 13:50	Arquivo PTO	1 KB

- ✓ The identified sequences will be in the "Output" directory, remembering that the metagenomes and sequece.fa files may be in other directories, just enter the correct path.