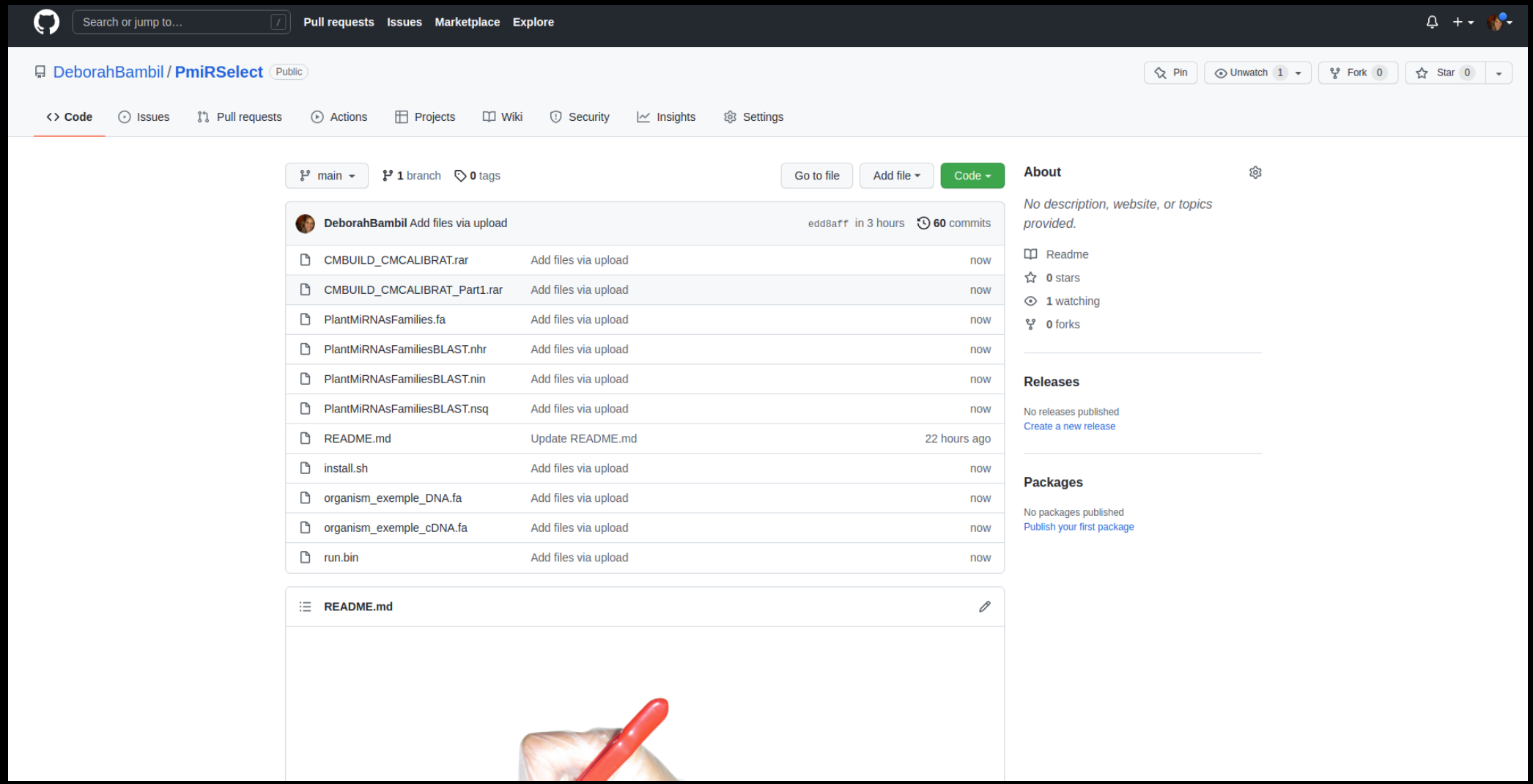
PmiR
Select

Access the GitHub for Download platform PmiRSelect:
https://github.com/DeborahBambil/PmiRSelect



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main 1 branch 0 tags

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DeborahBambil Add files via upload

CMBUILD_CMCALIBRAT.rar	Add files via upload	
CMBUILD_CMCALIBRAT_Part1.rar	Add files via upload	
PlantMiRNAsFamilies.fa	Add files via upload	
PlantMiRNAsFamiliesBLAST.nhr	Add files via upload	
PlantMiRNAsFamiliesBLAST.nin	Add files via upload	
PlantMiRNAsFamiliesBLAST.nsq	Add files via upload	
README.md	Update README.md	
install.sh	Add files via upload	now
organism_exemple_DNA.fa	Add files via upload	now
organism_exemple_cDNA.fa	Add files via upload	now
run.bin	Add files via upload	now

Clone

HTTPS SSH GitHub CLI

You don't have any public SSH keys in your GitHub account. You can add a new public key, or try cloning this repository via HTTPS.

git@github.com:DeborahBambil/PmiRSelec

Use a password-protected SSH key.

Download ZIP

README.md

About

No description, website, or topics provided.

Readme
0 stars
1 watching
0 forks

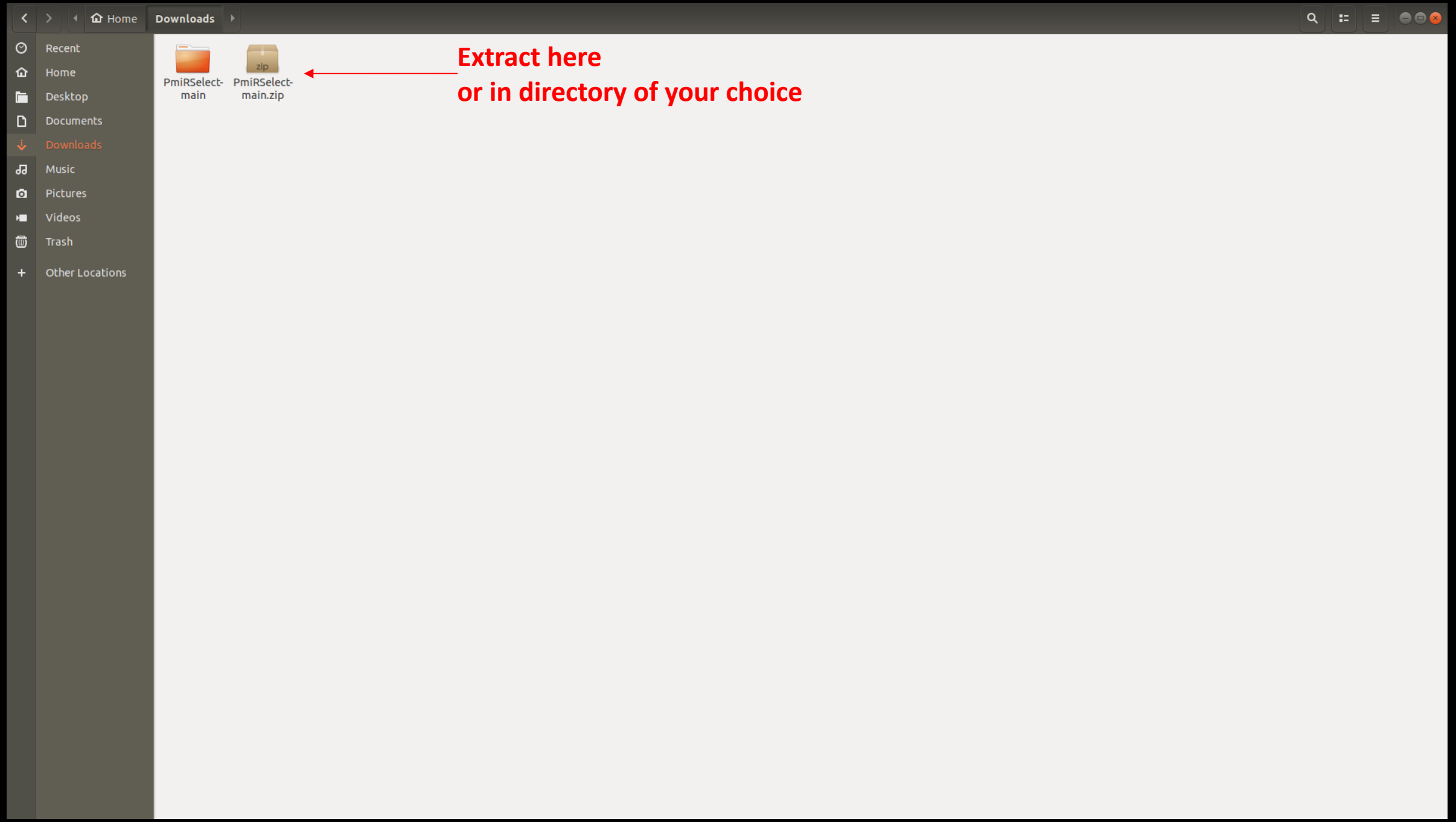
Releases

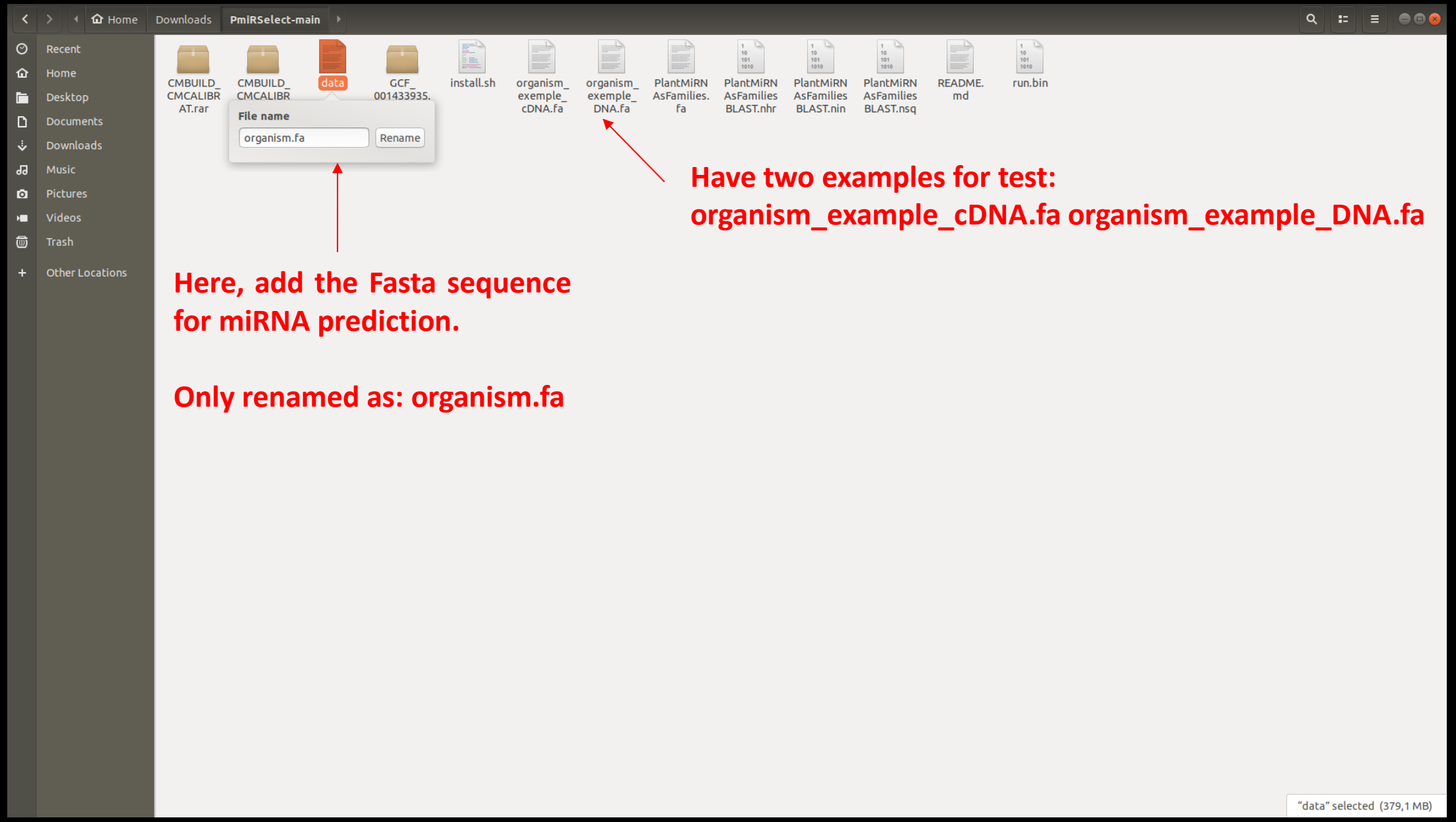
No releases published
Create a new release

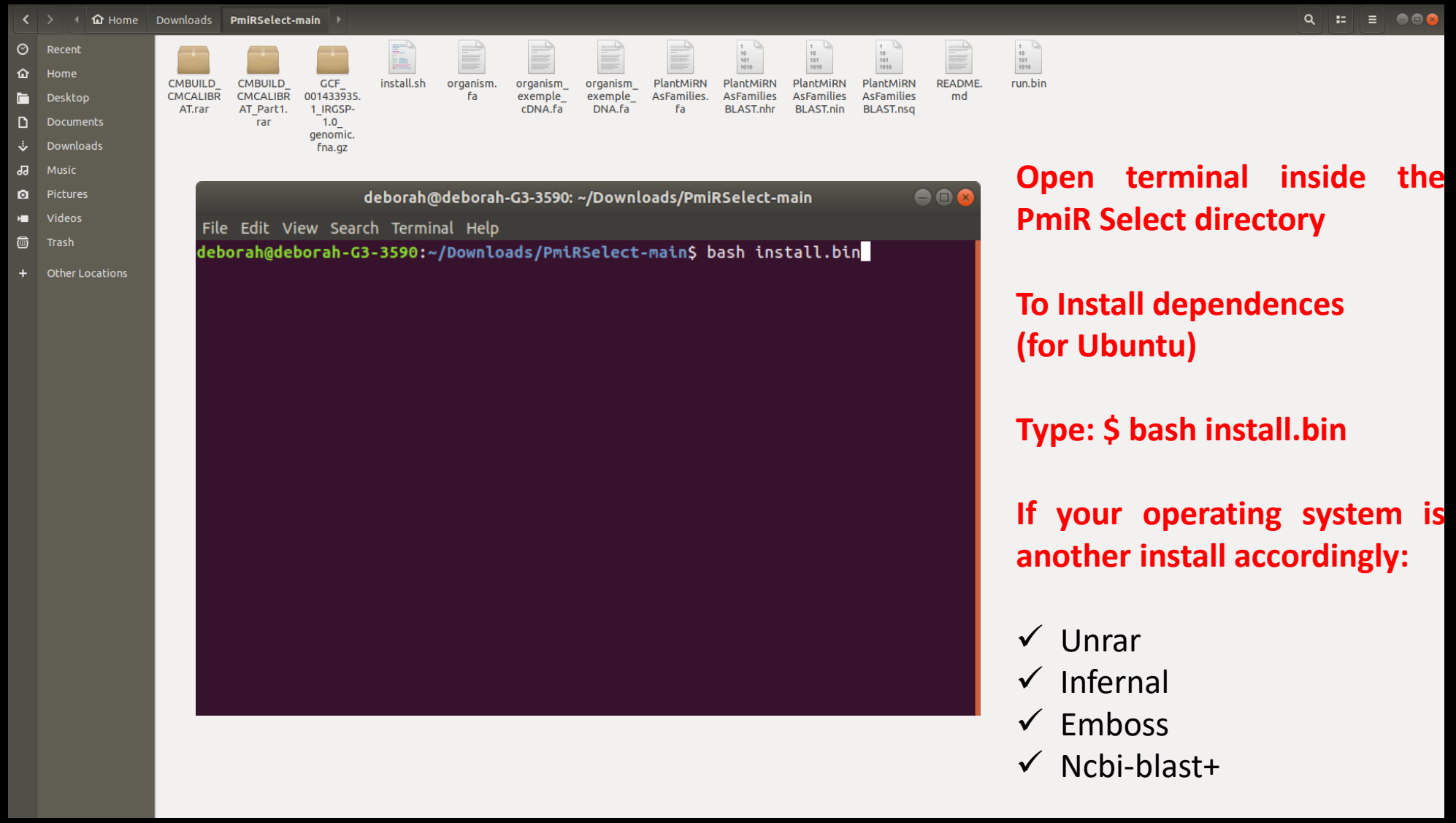
Packages

No packages published
Publish your first package

https://github.com/DeborahBambil/PmiRSelect/archive/refs/heads/main.zip


Home
Downloads
Recent
Home
Desktop
Documents
Downloads
Music
Pictures
Videos
Trash
Other Locations
PmiRSelect-main
PmiRSelect-main.zip
zip
Extract here
or in directory of your choice


Home
Downloads
PmiRSelect-main
Recent
Home
Desktop
Documents
Downloads
Music
Pictures
Videos
Trash
Other Locations
CMBUILD_CMCALIBRAT.rar
CMBUILD_CMCALIBR
data
GCF_001433935.
install.sh
organism_exemple_cDNA.fa
organism_exemple_DNA.fa
PlantMiRNAsFamilies.fa
PlantMiRNAsFamiliesBLAST.nhr
PlantMiRNAsFamiliesBLAST.nin
PlantMiRNAsFamiliesBLAST.nsq
README.md
run.bin
File name
organism.fa
Rename
Here, add the Fasta sequence for miRNA prediction.
Only renamed as: organism.fa
Have two examples for test: organism_example_cDNA.fa organism_example_DNA.fa
"data" selected (379,1 MB)



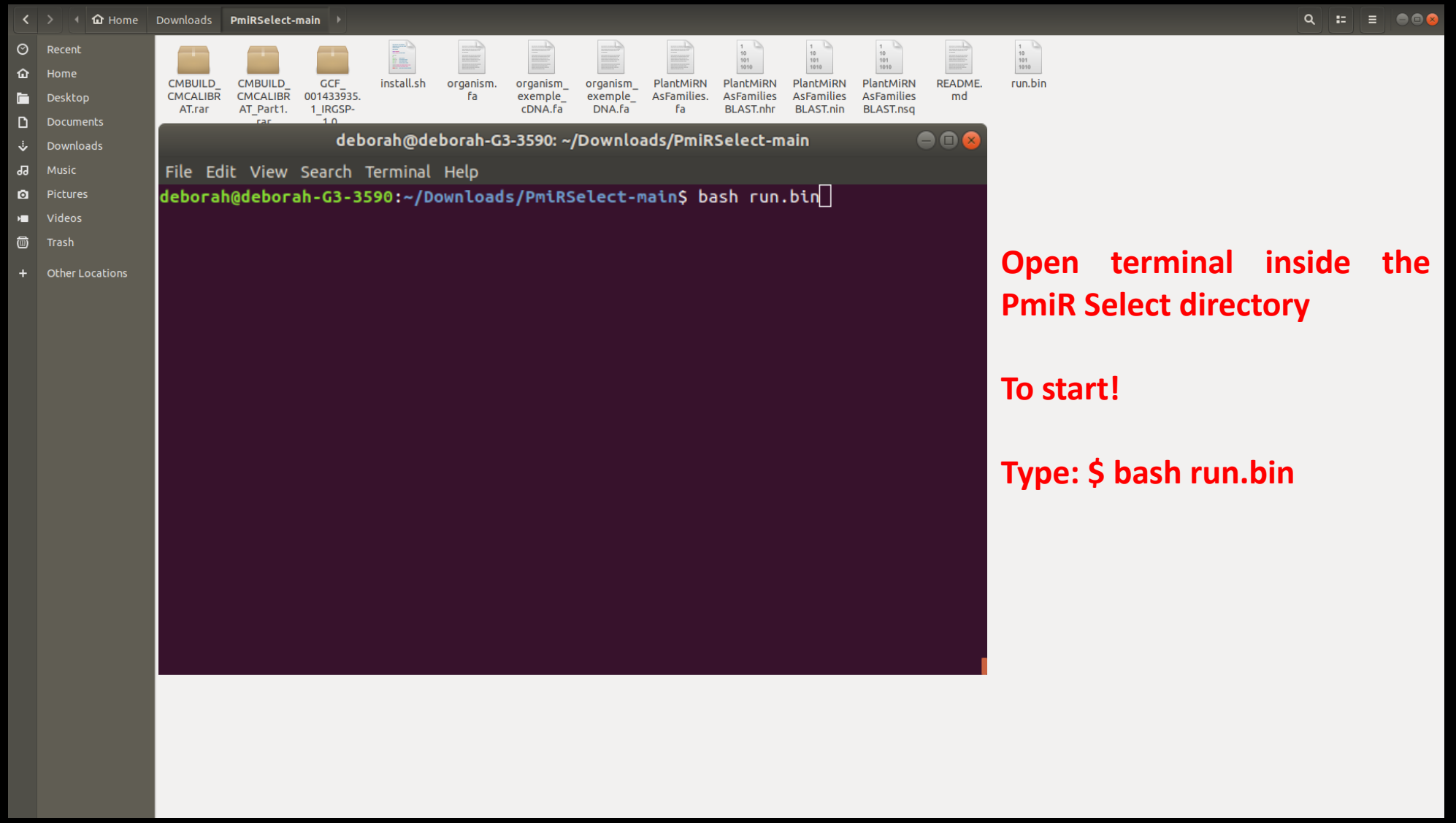
Open terminal inside the PmiR Select directory

To Install dependences (for Ubuntu)

Type: $ bash install.bin

If your operating system is another install accordingly:

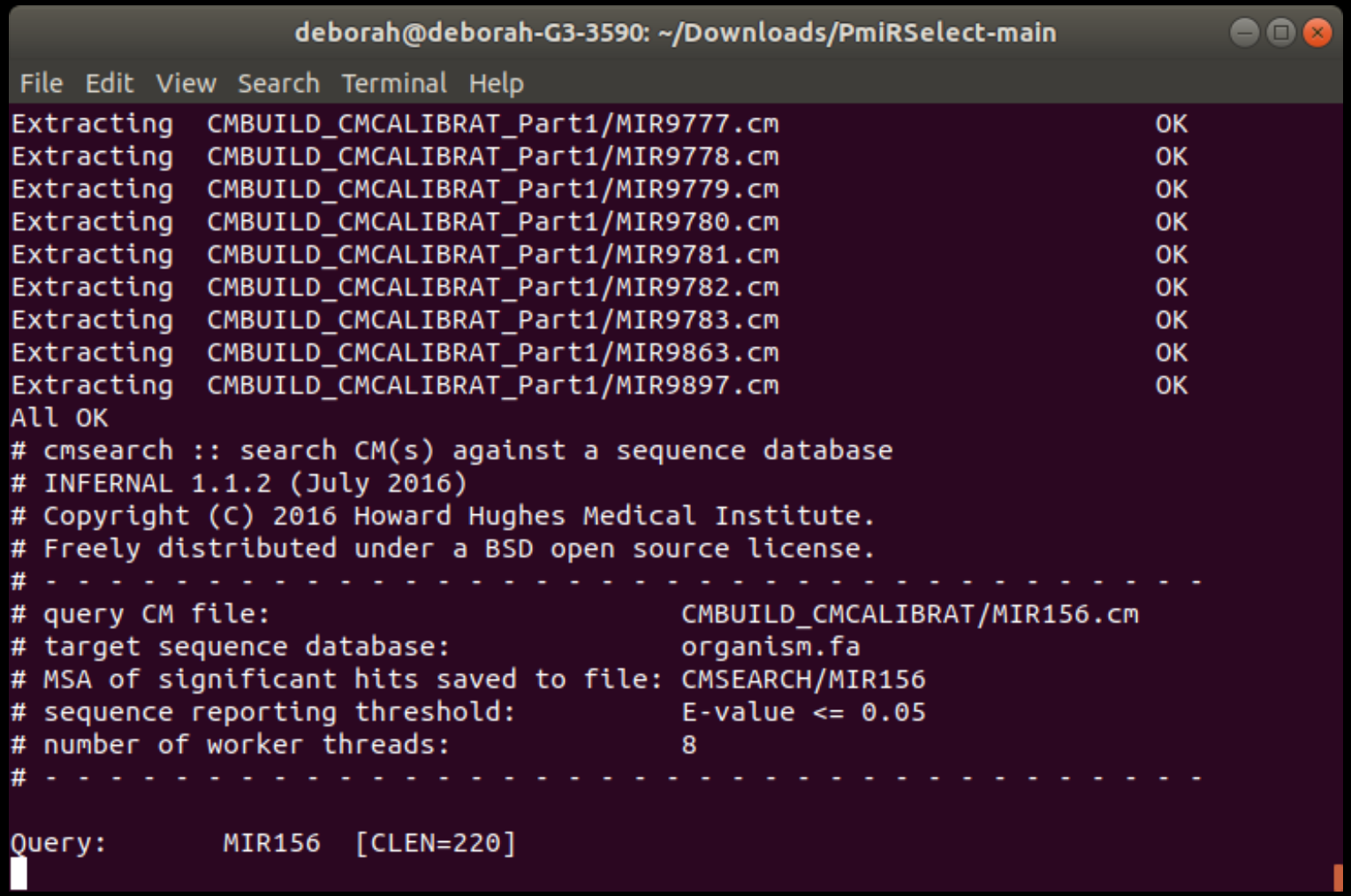
- ✓ Unrar
- ✓ Infernal
- ✓ Emboss
- ✓ Ncbi-blast+



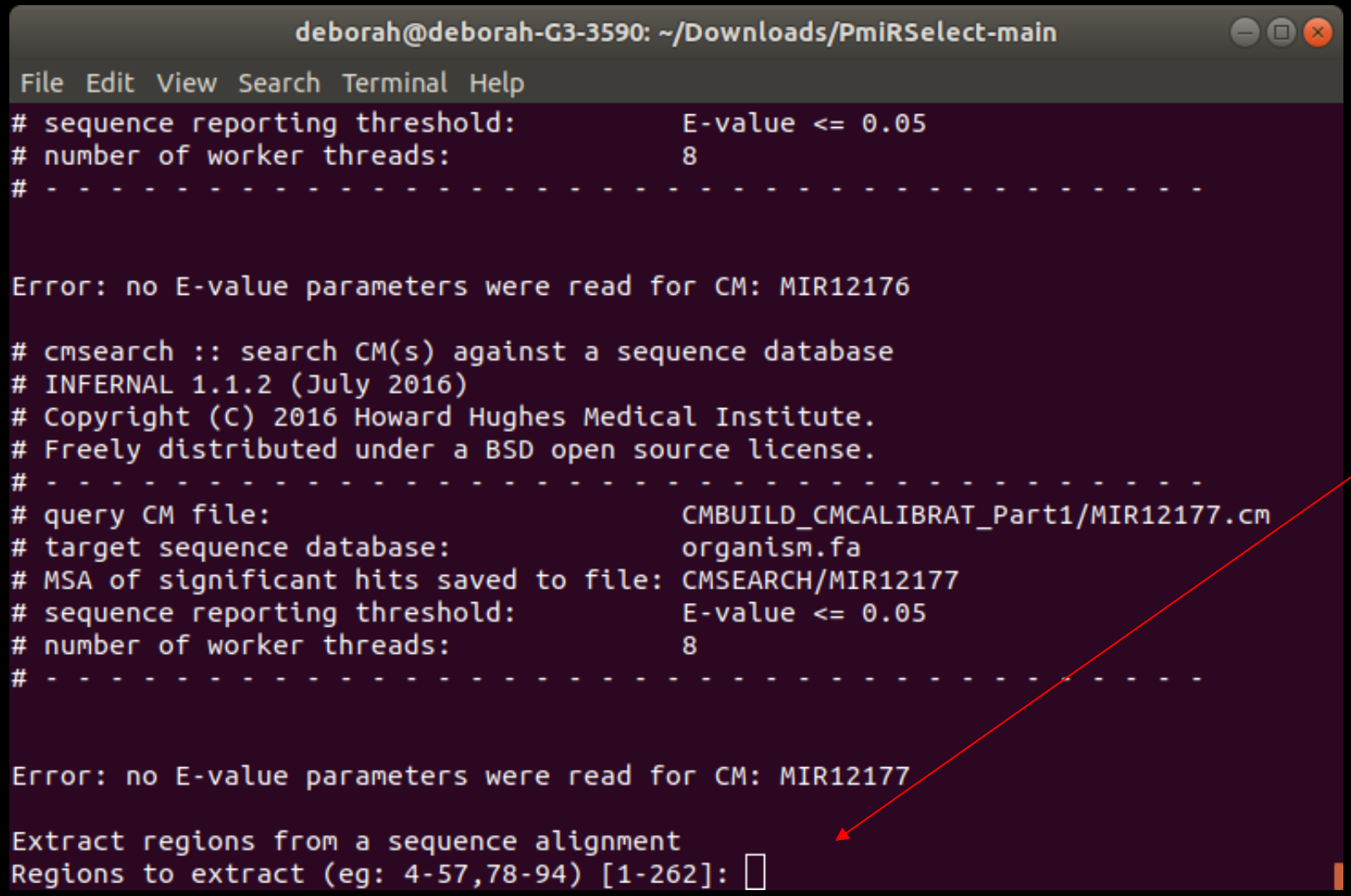
Open terminal inside the PmiR Select directory

To start!

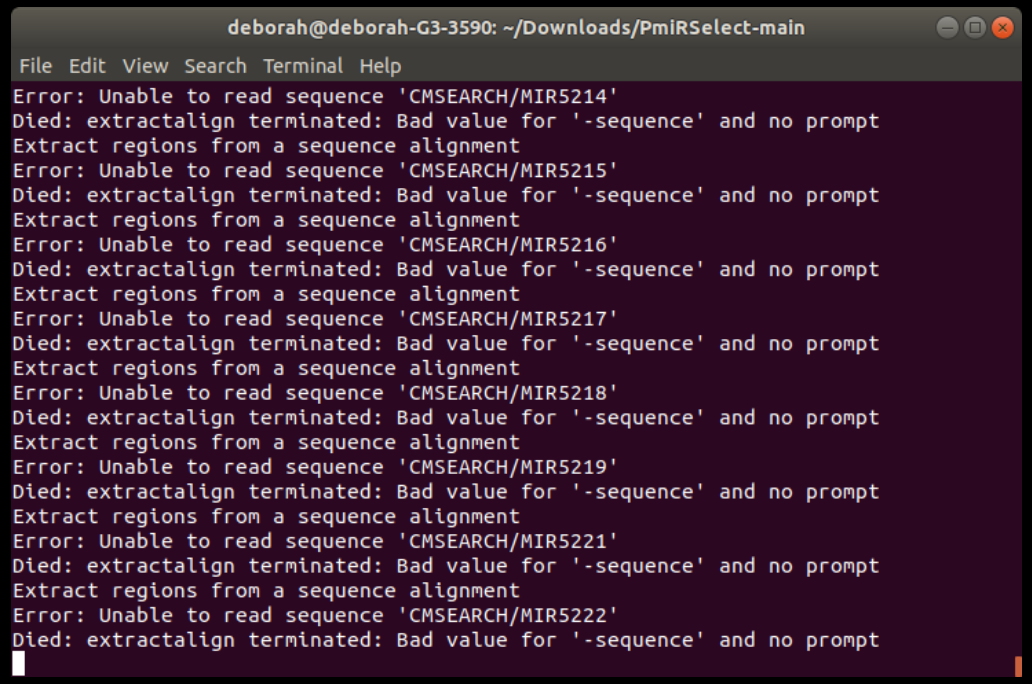
Type: $ bash run.bin

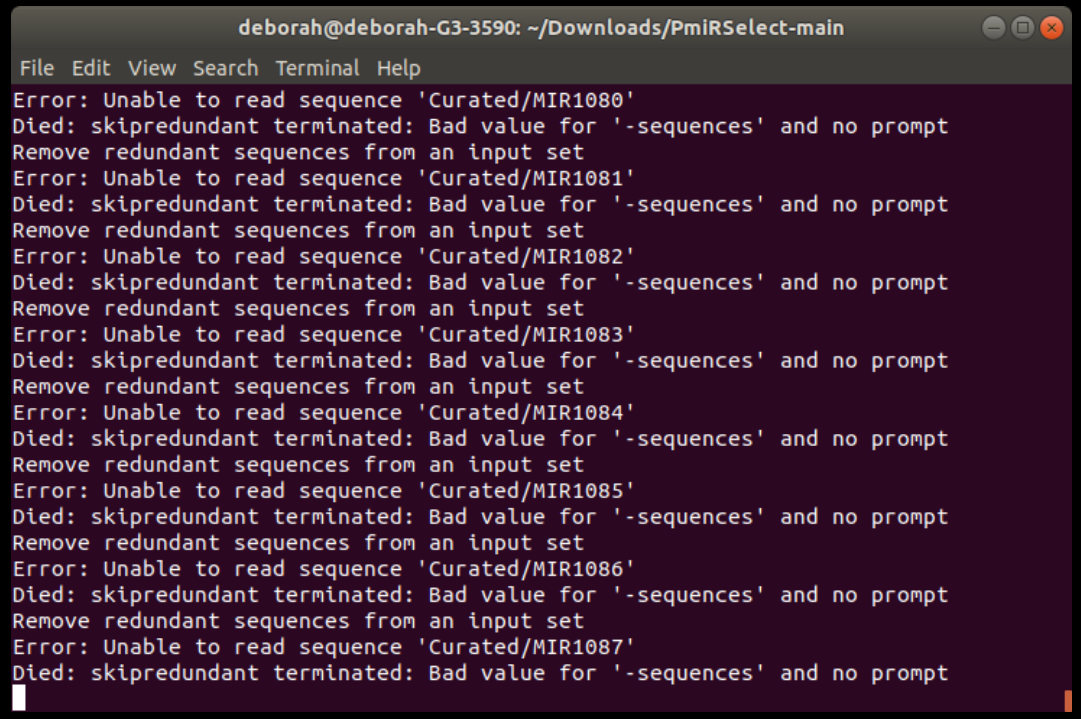

deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main
File Edit View Search Terminal Help
Extracting CMBUILD_CMCALIBRAT_Part1/MIR9777.cm OK
Extracting CMBUILD_CMCALIBRAT_Part1/MIR9778.cm OK
Extracting CMBUILD_CMCALIBRAT_Part1/MIR9779.cm OK
Extracting CMBUILD_CMCALIBRAT_Part1/MIR9780.cm OK
Extracting CMBUILD_CMCALIBRAT_Part1/MIR9781.cm OK
Extracting CMBUILD_CMCALIBRAT_Part1/MIR9782.cm OK
Extracting CMBUILD_CMCALIBRAT_Part1/MIR9783.cm OK
Extracting CMBUILD_CMCALIBRAT_Part1/MIR9863.cm OK
Extracting CMBUILD_CMCALIBRAT_Part1/MIR9897.cm OK
All OK
cmsearch :: search CM(s) against a sequence database
INFERNAL 1.1.2 (July 2016)
Copyright (C) 2016 Howard Hughes Medical Institute.
Freely distributed under a BSD open source license.
-
query CM file: CMBUILD_CMCALIBRAT/MIR156.cm
target sequence database: organism.fa
MSA of significant hits saved to file: CMSEARCH/MIR156
sequence reporting threshold: E-value <= 0.05
number of worker threads: 8
-
Query: MIR156 [CLEN=220]

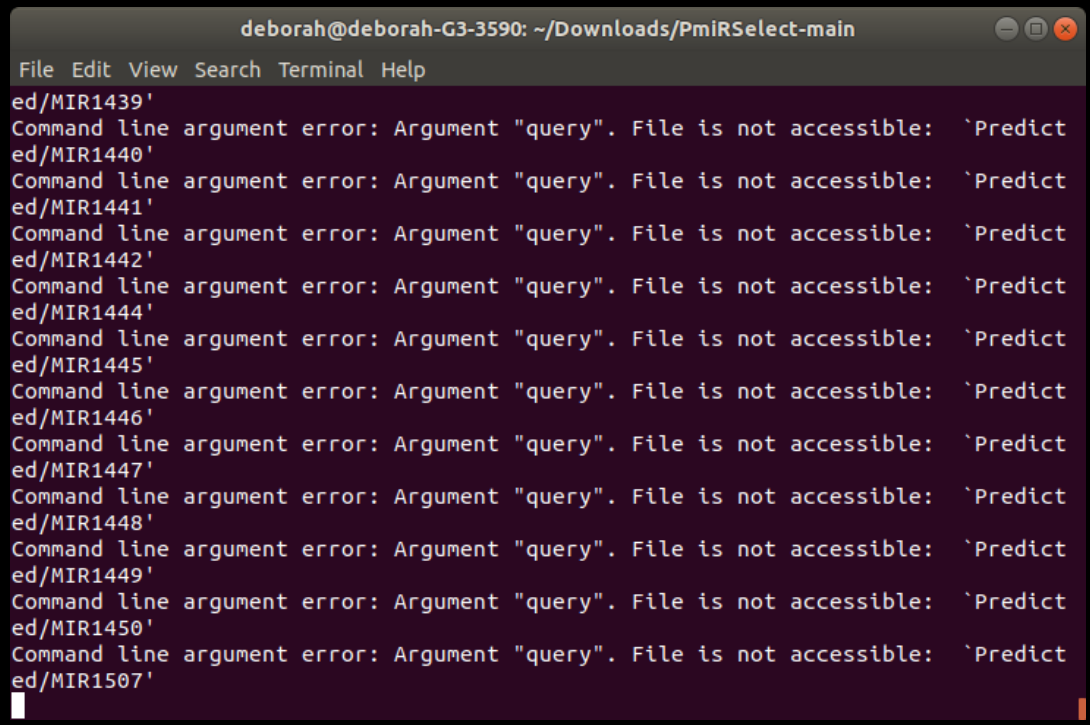
Start!



Here, press Enter!





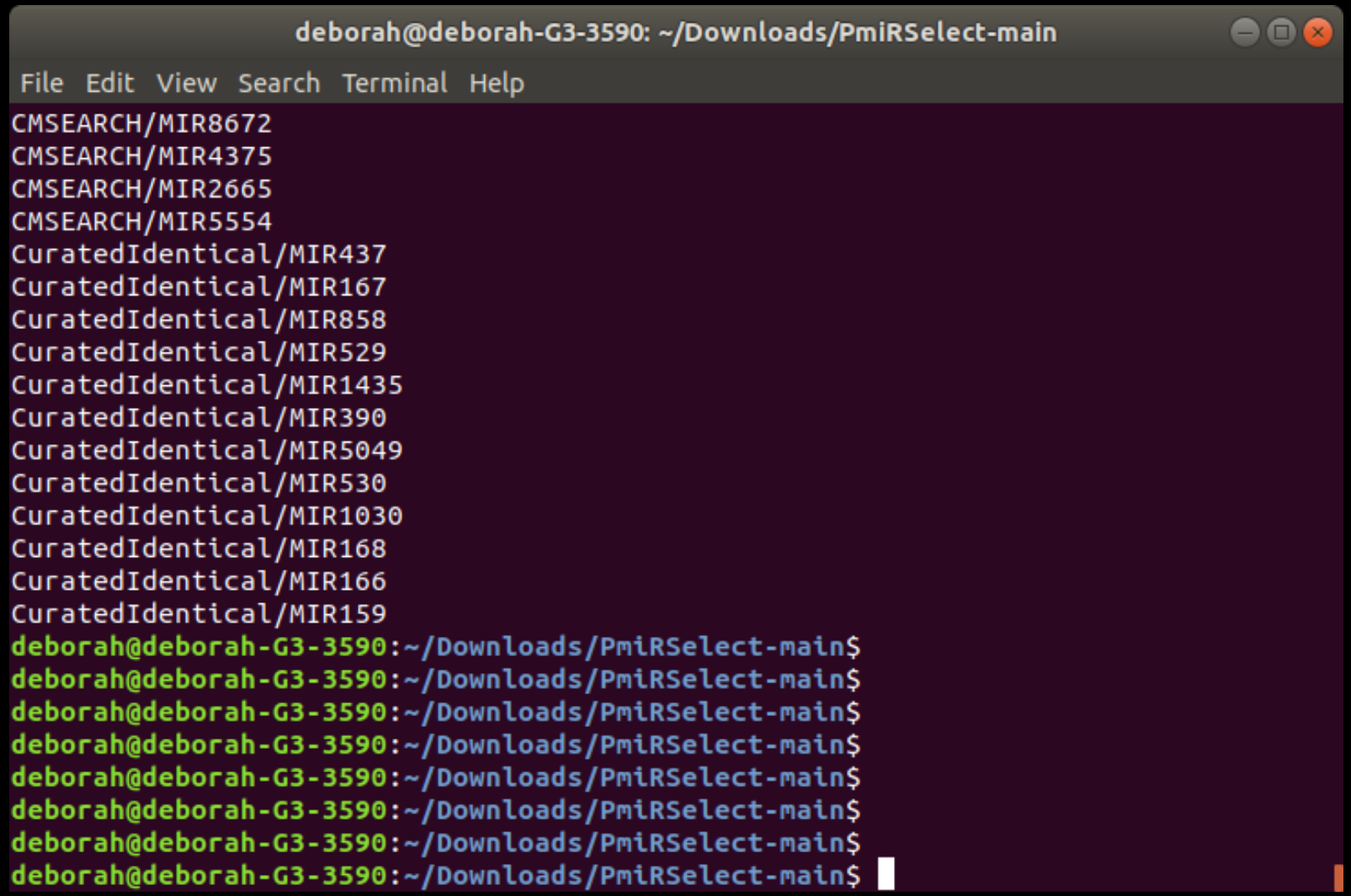


If these "errors" screens showed.

Do not worry!

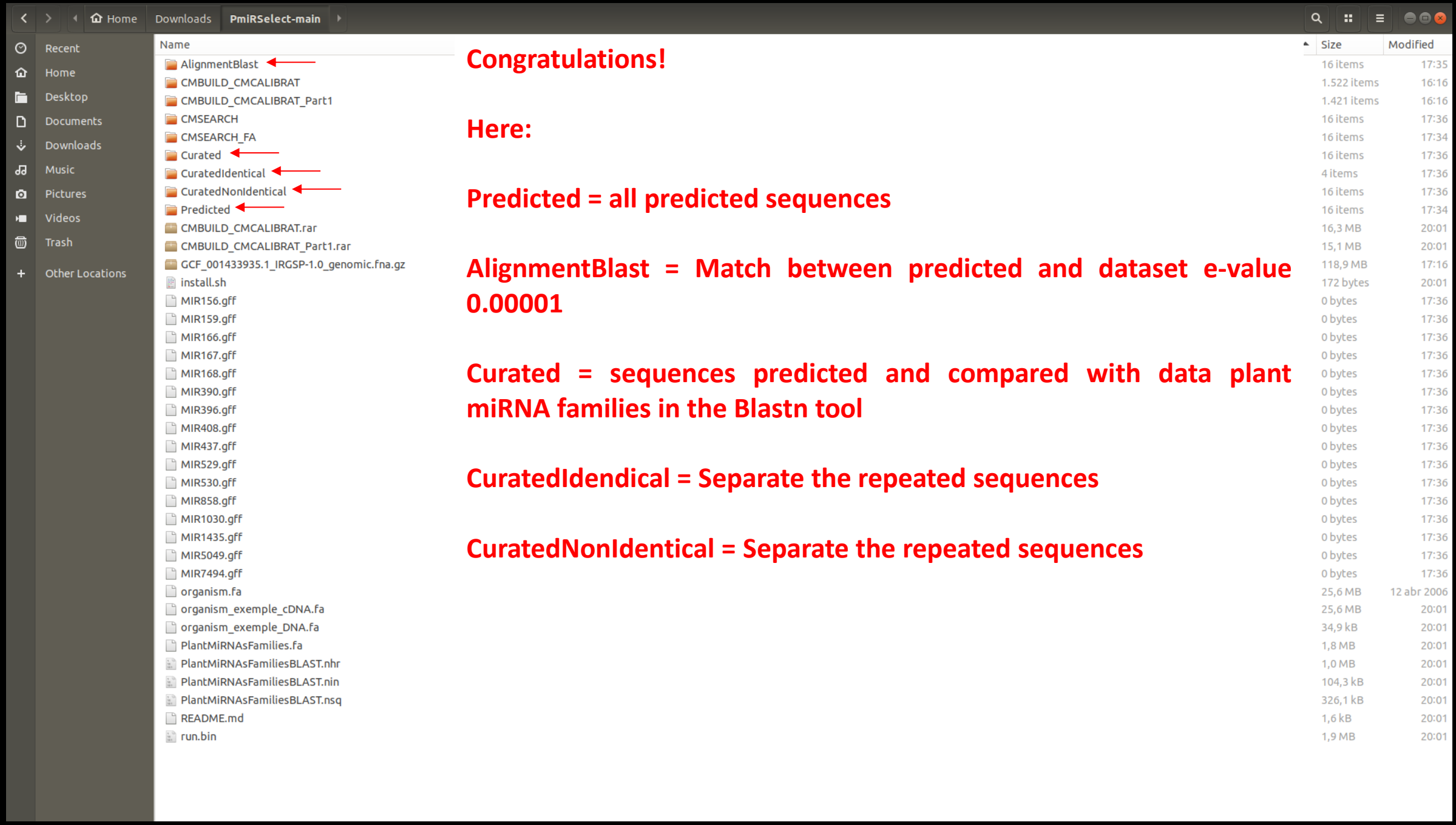
It's just the families that didn't find homologs.

Keep Calm, wait, the predicts are already being selected!



Finish!

Go to the directory to see the predicts and analyze the data!


Home
Downloads
PmiRSelect-main
Recent
Home
Desktop
Documents
Downloads
Music
Pictures
Videos
Trash
Other Locations
Name
Size
Modified
AlignmentBlast
CMBUILD_CMCALIBRAT
CMBUILD_CMCALIBRAT_Part1
CMSEARCH
CMSEARCH_FA
Curated
CuratedIdentical
CuratedNonIdentical
Predicted
CMBUILD_CMCALIBRAT.rar
CMBUILD_CMCALIBRAT_Part1.rar
GCF_001433935.1_IRGSP-1.0_genomic.fna.gz
install.sh
MIR156.gff
MIR159.gff
MIR166.gff
MIR167.gff
MIR168.gff
MIR390.gff
MIR396.gff
MIR408.gff
MIR437.gff
MIR529.gff
MIR530.gff
MIR858.gff
MIR1030.gff
MIR1435.gff
MIR5049.gff
MIR7494.gff
organism.fa
organism_exemple_cDNA.fa
organism_exemple_DNA.fa
PlantMiRNAsFamilies.fa
PlantMiRNAsFamiliesBLAST.nhr
PlantMiRNAsFamiliesBLAST.nin
PlantMiRNAsFamiliesBLAST.nsq
README.md
run.bin
16 items 17:35
1.522 items 16:16
1.421 items 16:16
16 items 17:36
16 items 17:34
16 items 17:36
4 items 17:36
16 items 17:36
16 items 17:34
16,3 MB 20:01
15,1 MB 20:01
118,9 MB 17:16
172 bytes 20:01
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
0 bytes 17:36
25,6 MB 12 abr 2006
25,6 MB 20:01
34,9 kB 20:01
1,8 MB 20:01
1,0 MB 20:01
104,3 kB 20:01
326,1 kB 20:01
1,6 kB 20:01
1,9 MB 20:01
Congratulations!
Here:
Predicted = all predicted sequences
AlignmentBlast = Match between predicted and dataset e-value 0.00001
Curated = sequences predicted and compared with data plant miRNA families in the Blastn tool
CuratedIdendical = Separate the repeated sequences
CuratedNonIdentical = Separate the repeated sequences