

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

Search or jump to...

Pull requests

Issues

Marketplace

Explore

DeborahBambil / PmiRSelect

Public

Pin

Unwatch 1

Fork 0

Star 0

<> Code

Issues

Pull requests

Actions

Projects

Wiki

Security

Insights

Settings

main 1 branch 0 tags

Go to file

Add file

Code

DeborahBambil

Add files via upload

edd8aff in 3 hours 60 commits

| | | |
|------------------------------|----------------------|--------------|
| CMBUILD_CMCALIBRAT.rar | Add files via upload | now |
| CMBUILD_CMCALIBRAT_Part1.rar | Add files via upload | now |
| PlantMiRNAsFamilies.fa | Add files via upload | now |
| PlantMiRNAsFamiliesBLAST.nhr | Add files via upload | now |
| PlantMiRNAsFamiliesBLAST.nin | Add files via upload | now |
| PlantMiRNAsFamiliesBLAST.nsq | Add files via upload | now |
| README.md | Update README.md | 22 hours ago |
| 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 |

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



Make Download

 Search or jump to...

Pull requestsIssuesMarketplaceExplore

DeborahBambil / PmiRSelectPublic

PinUnwatch1Fork0Star0

<> CodeIssuesPull requestsActionsProjectsWikiSecurityInsightsSettings

main1 branch0 tags

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 |

Go to fileAdd fileCode

Clone

HTTPSSSHGitHub 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/PmiRSelect

Use a password-protected SSH key.

Download ZIP

About

No description, website, or topics provided.

Readme

0 stars

1 watching

0 forks

Releases

No releases published

[Create a new release](#)

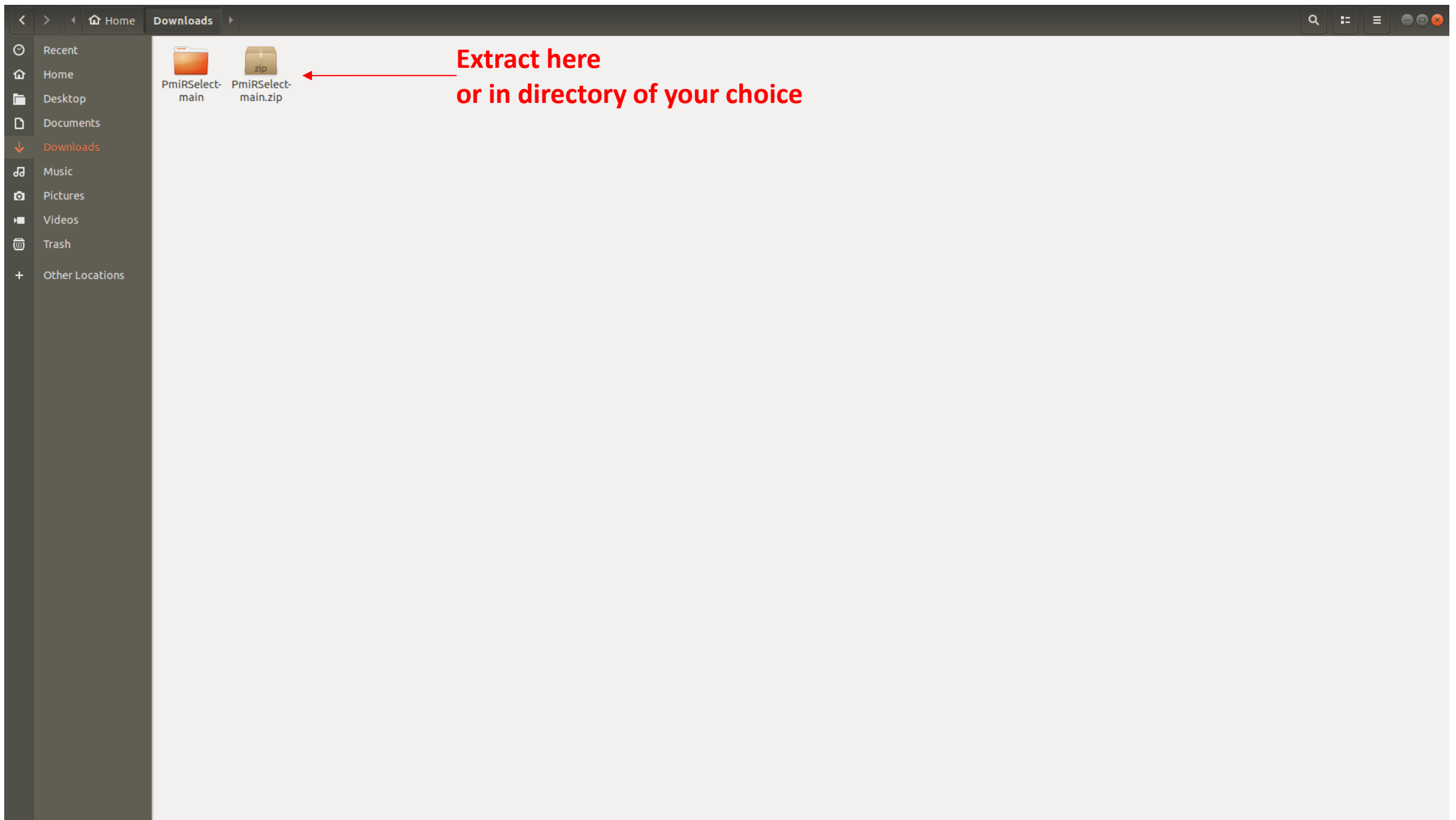
Packages

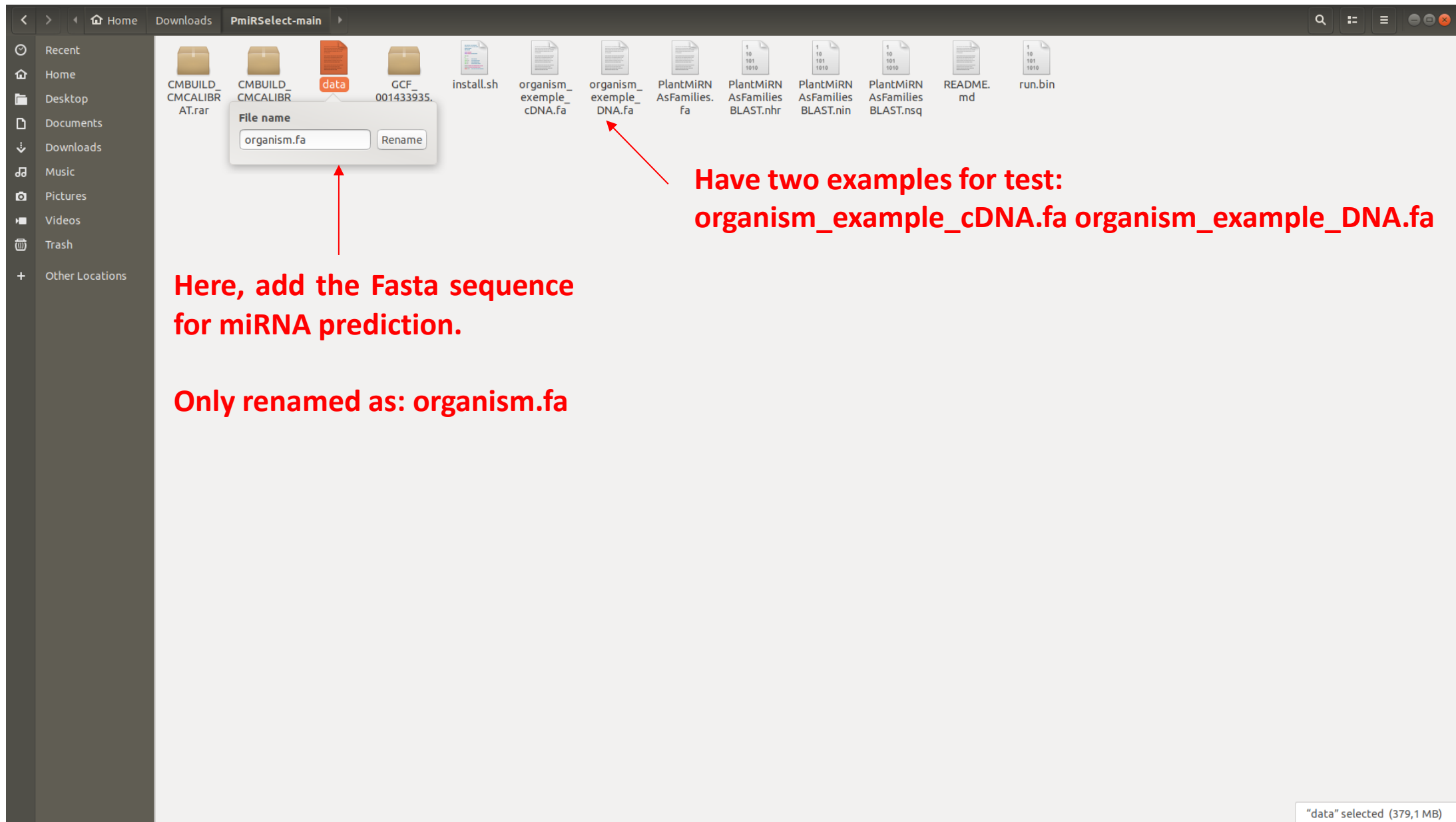
No packages published

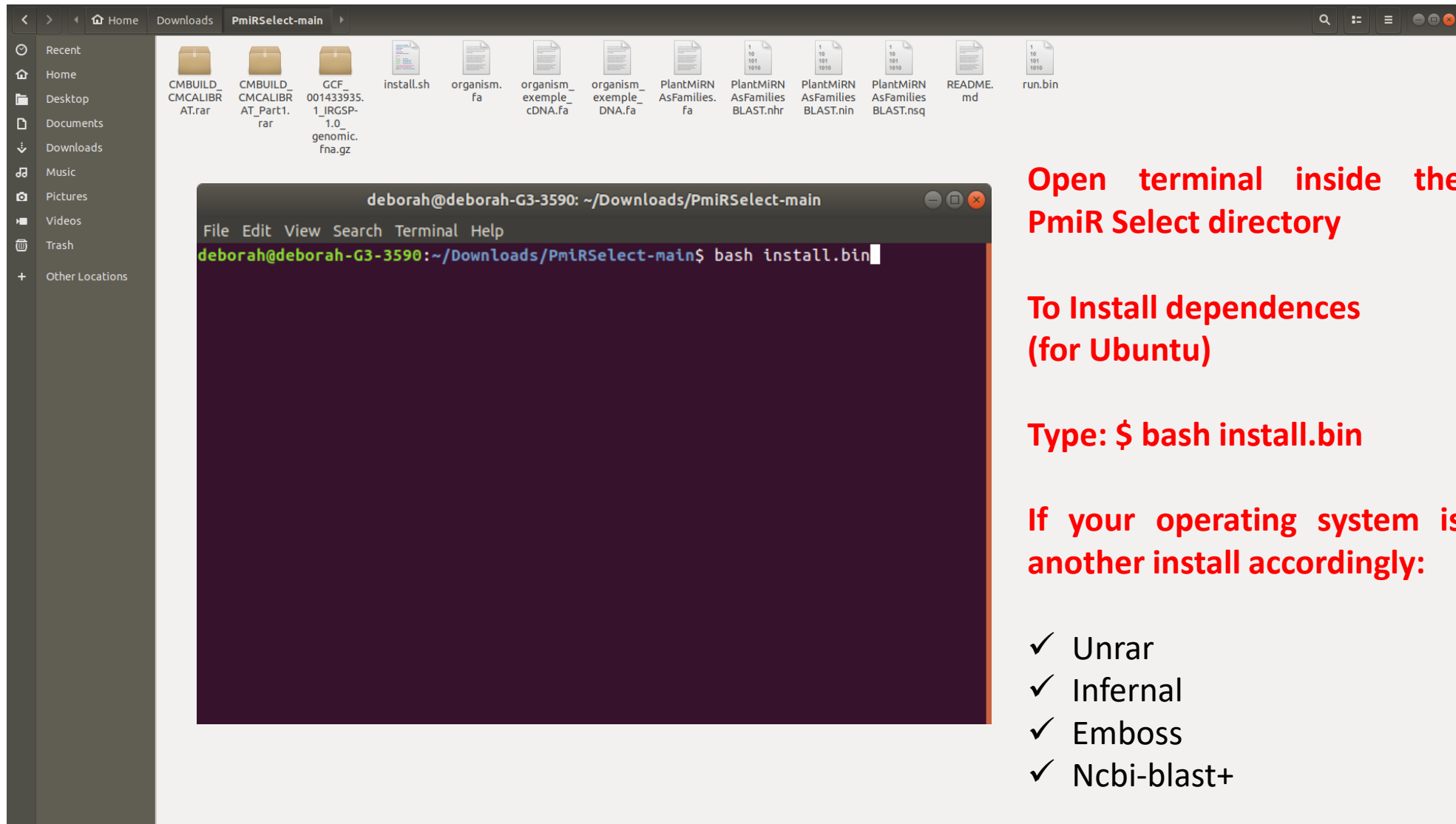
[Publish your first package](#)

README.md

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







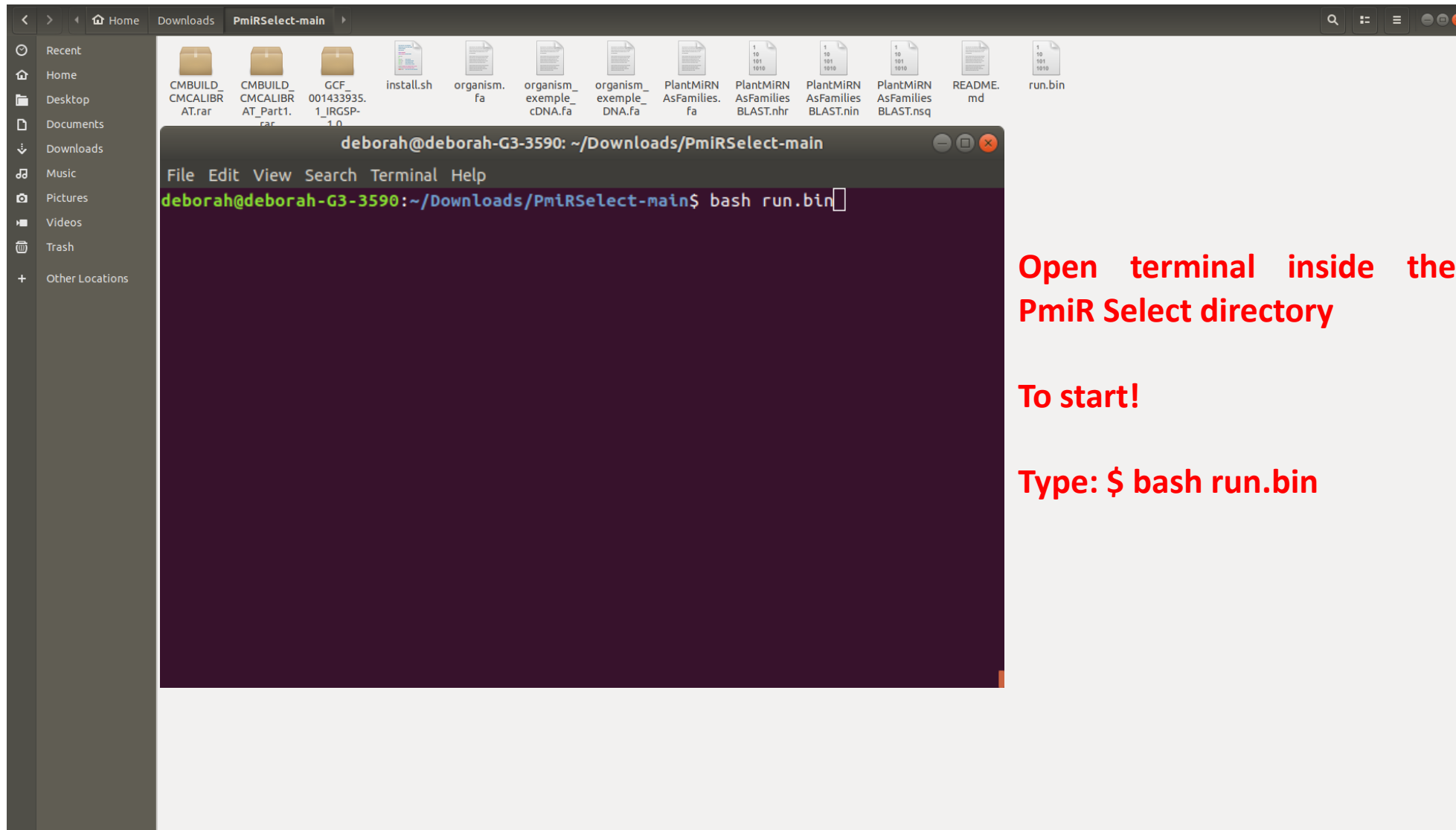
Open terminal inside the PmiR Select directory

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!

```
deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main
File Edit View Search Terminal Help
# sequence reporting threshold:      E-value <= 0.05
# number of worker threads:         8
# - - - - -

Error: no E-value parameters were read for CM: MIR12176

# 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_Part1/MIR12177.cm
# target sequence database:         organism.fa
# MSA of significant hits saved to file: CMSEARCH/MIR12177
# sequence reporting threshold:     E-value <= 0.05
# number of worker threads:         8
# - - - - -

Error: no E-value parameters were read for CM: MIR12177

Extract regions from a sequence alignment
Regions to extract (eg: 4-57,78-94) [1-262]: 
```

Here, press Enter!


```
deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main
File Edit View Search Terminal Help
Error: Unable to read sequence 'CMSEARCH/MIR5214'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5215'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5216'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5217'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5218'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5219'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5221'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5222'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
```

```
deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main
File Edit View Search Terminal Help
Error: Unable to read sequence 'Curated/MIR1080'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1081'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1082'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1083'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1084'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1085'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1086'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1087'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
```

```
deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main
File Edit View Search Terminal Help
ed/MIR1439'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1440'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1441'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1442'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1444'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1445'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1446'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1447'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1448'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1449'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1450'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1507'
```

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!

```
deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main
File Edit View Search Terminal Help
CMSEARCH/MIR8672
CMSEARCH/MIR4375
CMSEARCH/MIR2665
CMSEARCH/MIR5554
CuratedIdentical/MIR437
CuratedIdentical/MIR167
CuratedIdentical/MIR858
CuratedIdentical/MIR529
CuratedIdentical/MIR1435
CuratedIdentical/MIR390
CuratedIdentical/MIR5049
CuratedIdentical/MIR530
CuratedIdentical/MIR1030
CuratedIdentical/MIR168
CuratedIdentical/MIR166
CuratedIdentical/MIR159
deborah@deborah-G3-3590:~/Downloads/PmiRSelect-main$
deborah@deborah-G3-3590:~/Downloads/PmiRSelect-main$
deborah@deborah-G3-3590:~/Downloads/PmiRSelect-main$
deborah@deborah-G3-3590:~/Downloads/PmiRSelect-main$
deborah@deborah-G3-3590:~/Downloads/PmiRSelect-main$
deborah@deborah-G3-3590:~/Downloads/PmiRSelect-main$
deborah@deborah-G3-3590:~/Downloads/PmiRSelect-main$
deborah@deborah-G3-3590:~/Downloads/PmiRSelect-main$
```

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

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

Size

Modified

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

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

CuratedIdentical = Separate the repeated sequences

CuratedNonIdentical = Separate the repeated sequences