




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




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	README.md	Update README.md	22 days ago
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README.md



About



No description, website, or topics provided.

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Releases

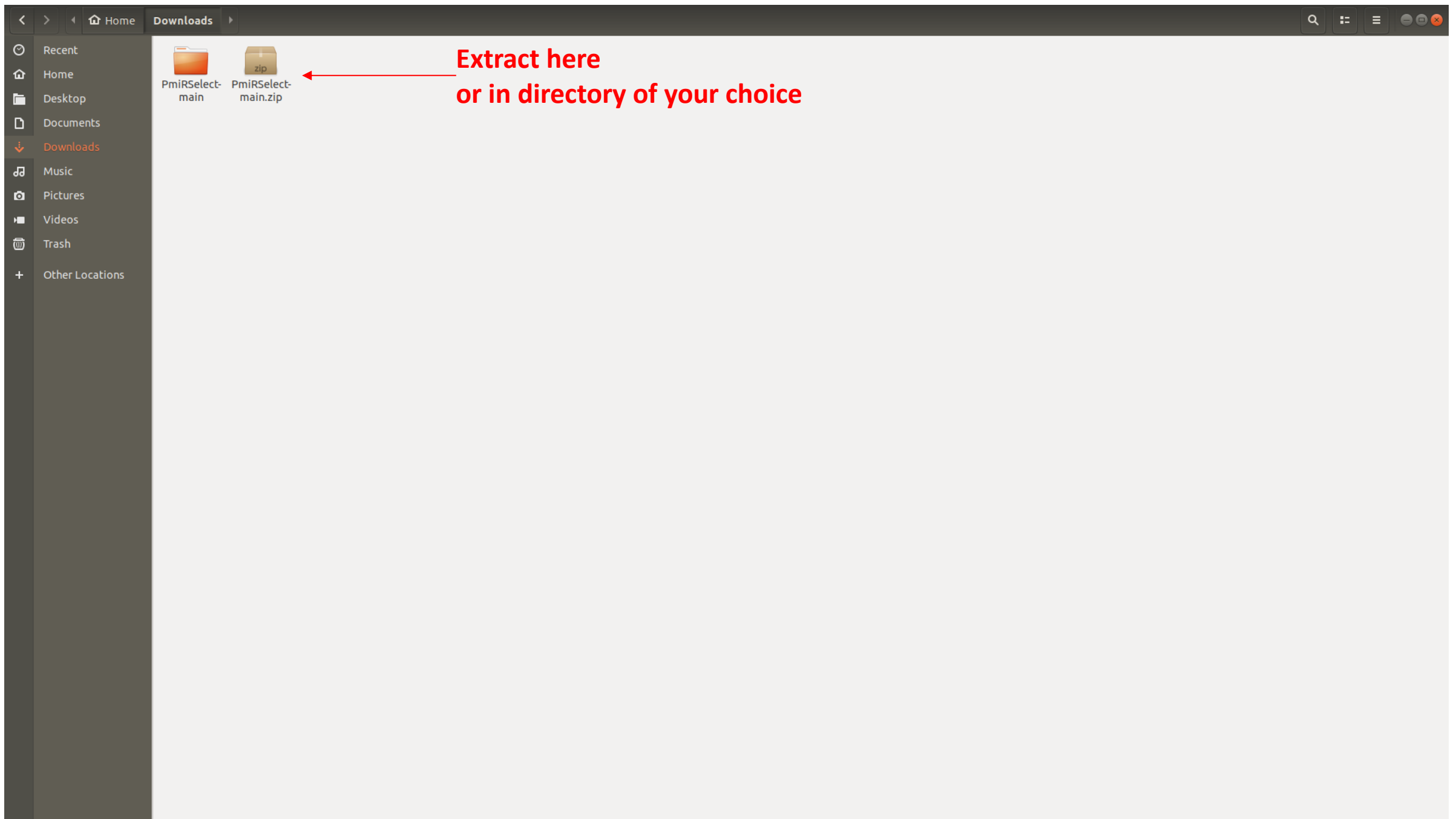
No releases published

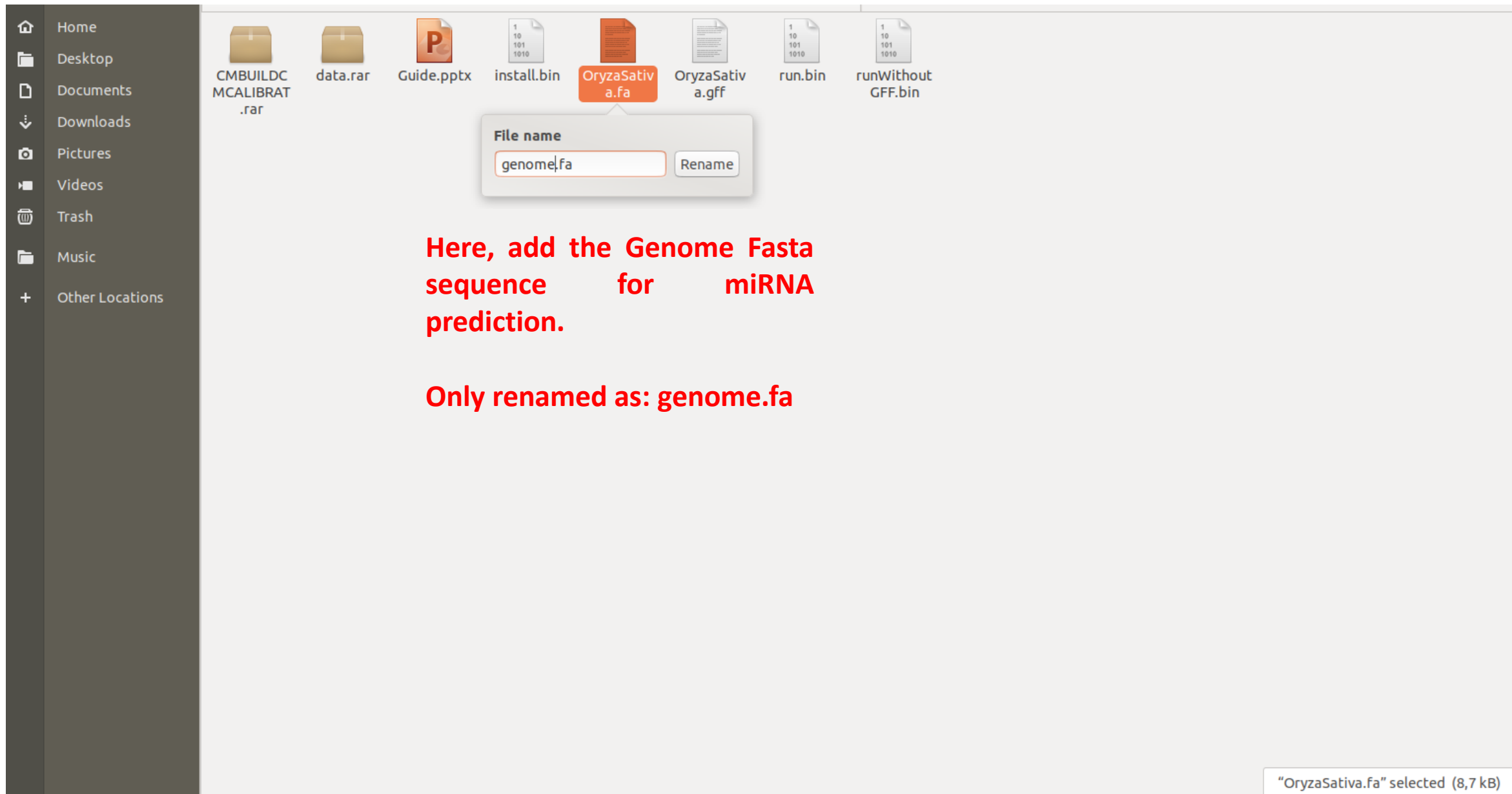
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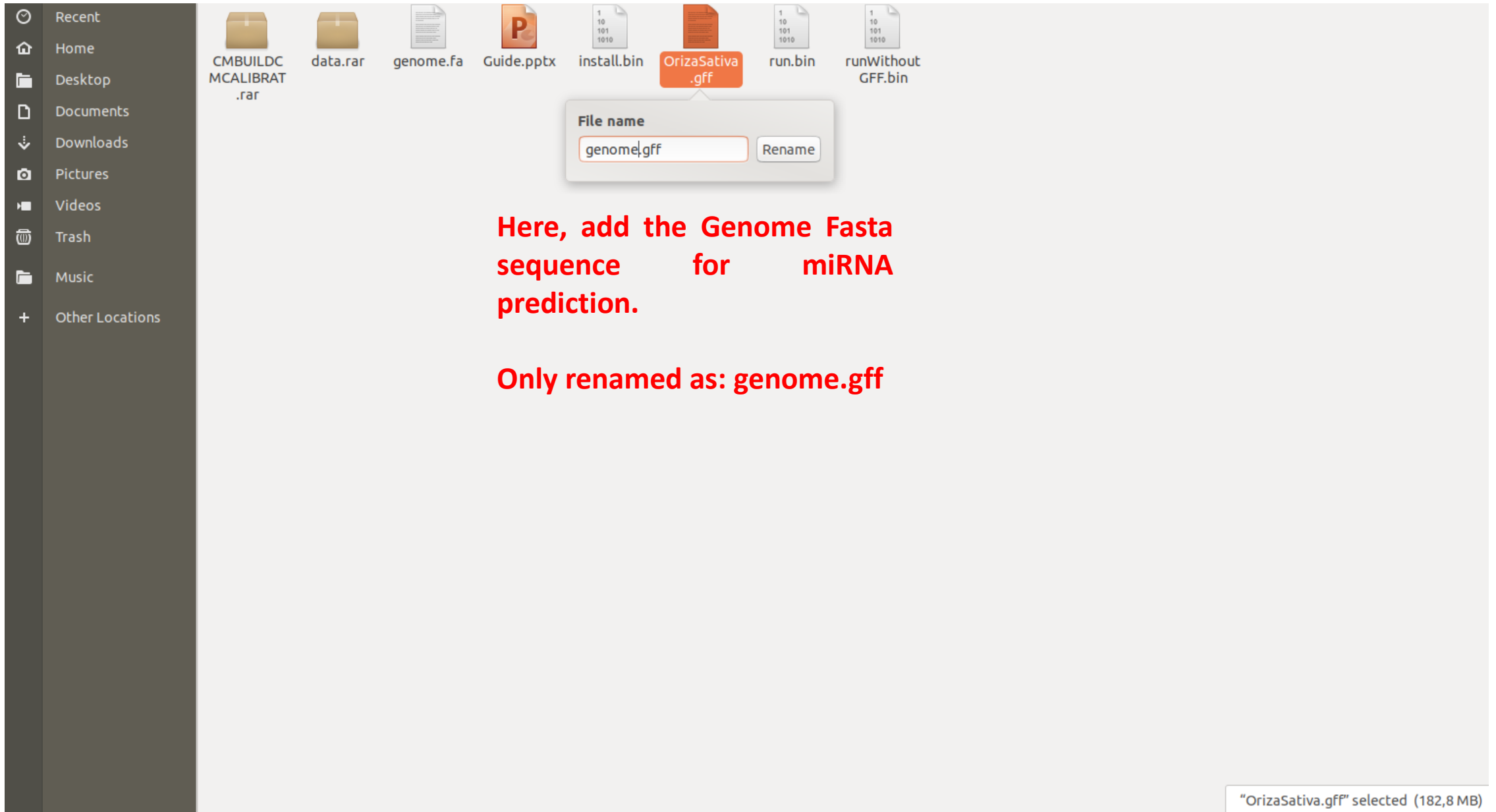
Packages

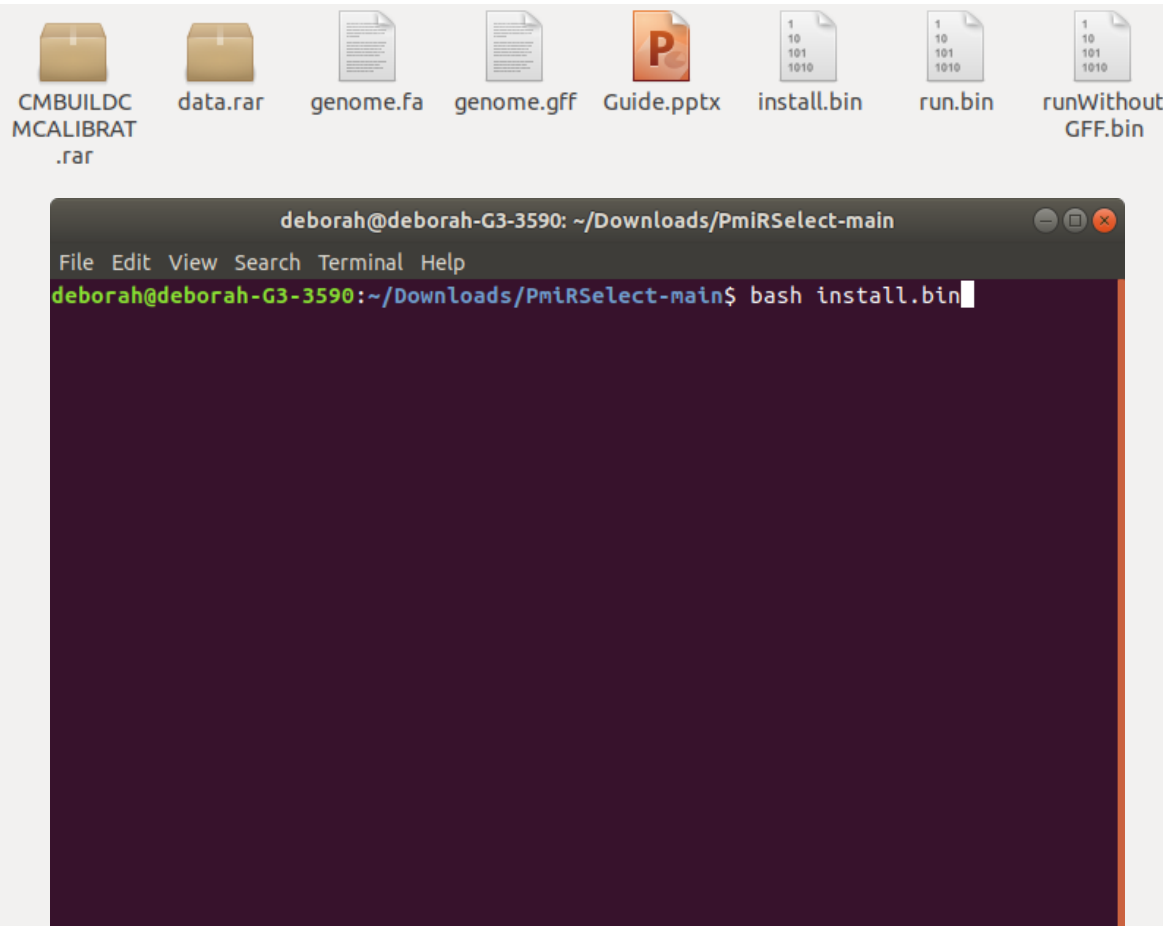
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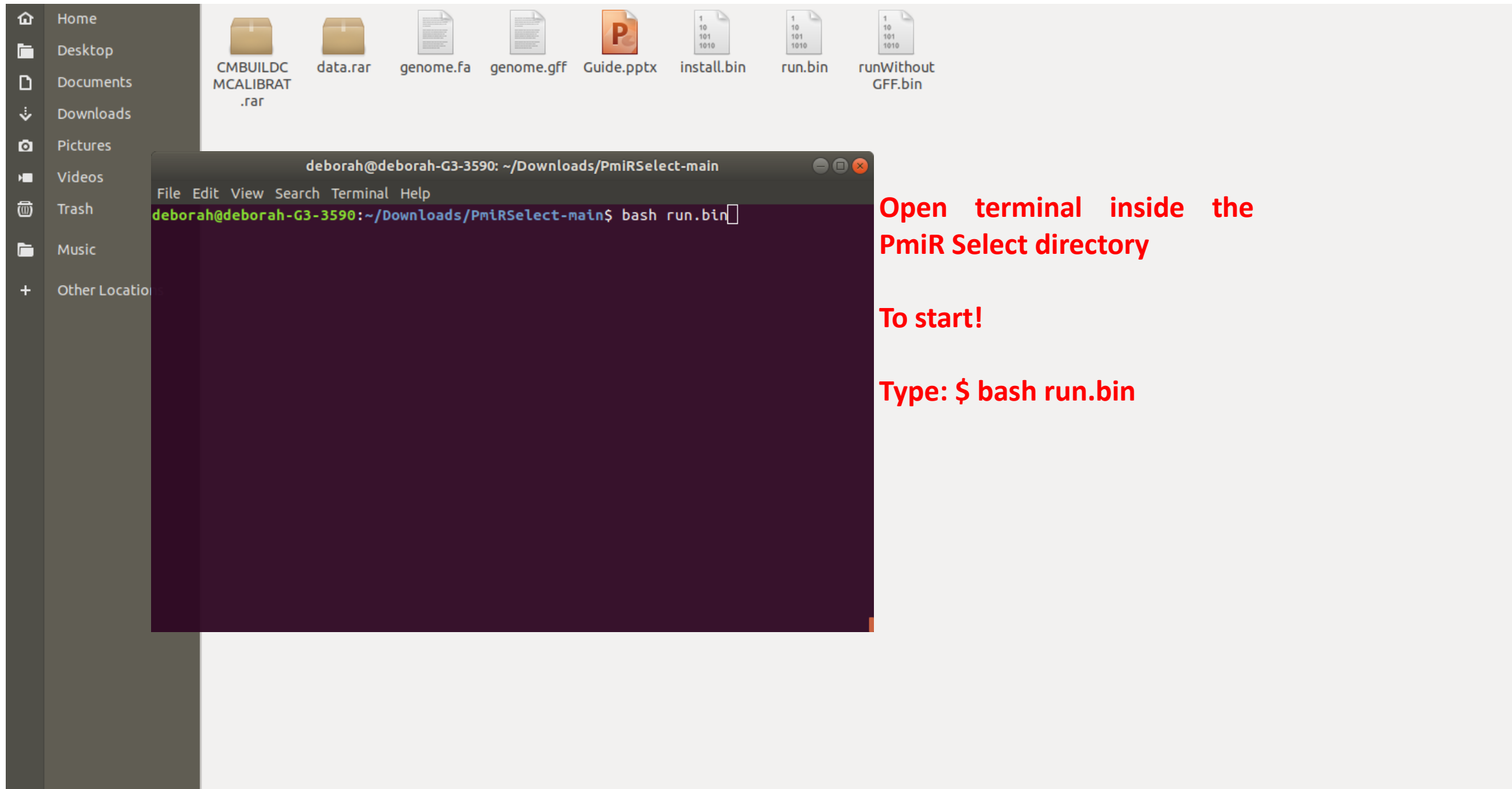
**Open terminal inside the PmiR Select directory**

**To Install dependences (for Ubuntu)**

**Type: \$ bash install.bin**

**If your operating system is another install accordingly:**

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

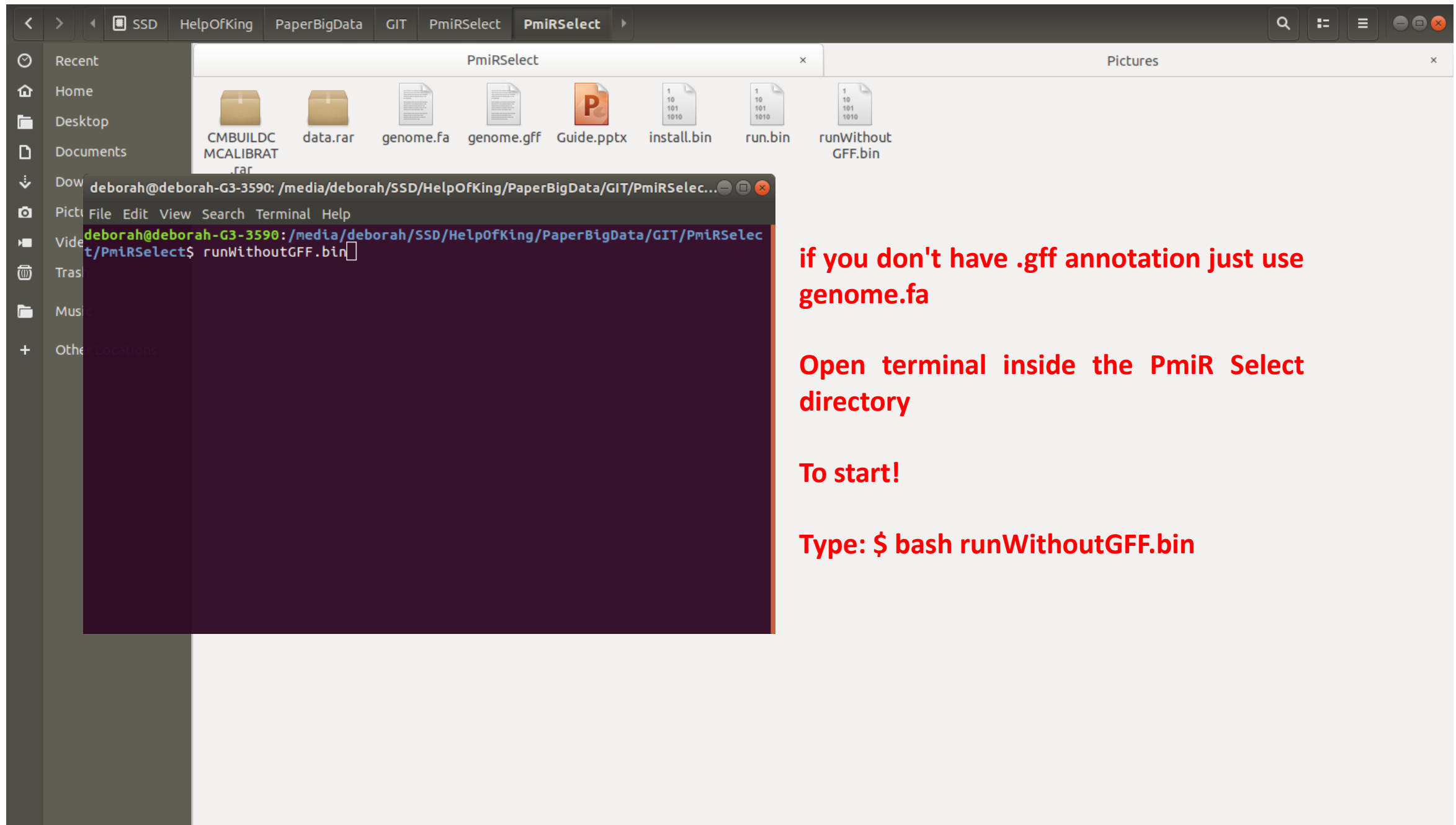


**Open terminal inside the  
PmiR Select directory**

**To start!**

**Type: \$ bash run.bin**





if you don't have .gff annotation just use genome.fa

Open terminal inside the PmiR Select directory

To start!

Type: `$ bash runWithoutGFF.bin`

```
deborah@deborah-G3-3590: /media/deborah/SSD/HelpOfKing/PaperBigData/GIT/PmiRSelec...
File Edit View Search Terminal Help
Extracting CMBUILDCMCALIBRAT/MIR9780.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9781.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9782.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9783.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9863.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9897.cm OK
All OK

UNRAR 5.50 freeware      Copyright (c) 1993-2017 Alexander Roshal

Extracting from data.rar

Creating    data                                OK
Extracting  data/PlantHairpin.fa                OK
Extracting  data/PlantHairpinBlast.nhr          OK
Extracting  data/PlantHairpinBlast.nin          OK
Extracting  data/PlantHairpinBlast.nsq          OK
Extracting  data/PlantMature.fa                 OK
Extracting  data/PlantMatureBlast.nhr           OK
Extracting  data/PlantMatureBlast.nin           OK
Extracting  data/PlantMatureBlast.nsq           OK
All OK
```

**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: /media/deborah/SSD/HelpOfKing/PaperBigData/GIT/PmiRSelec...
File Edit View Search Terminal Help
Curated/MIR12161
Curated/MIR12162
Curated/MIR12163
Curated/MIR12164
Curated/MIR12165
Curated/MIR12166
Curated/MIR12167
Curated/MIR12168
Curated/MIR12169
Curated/MIR1217
Curated/MIR12170
Curated/MIR12171
Curated/MIR12172
Curated/MIR12173
Curated/MIR12174
Curated/MIR12175
Curated/MIR12176
Curated/MIR12177
Curated/MIR1218
Curated/MIR1219
Curated/MIR1220
Curated/MIR1221
deborah@deborah-G3-3590: /media/deborah/SSD/HelpOfKing/PaperBigData/GIT/PmiRSelec
t-main$
```

**Finish!**

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

