

# **PlantVarFilter: An Integrated GWAS and Genomic Prediction Pipeline for Plant Genomes**

## **Documentation:**

### **How to run it on Linux with MiniFrog and Mamba**

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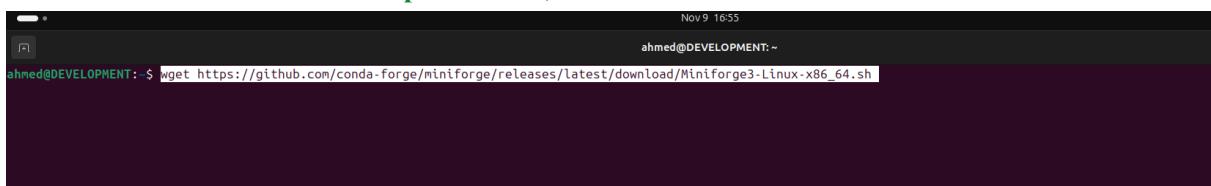
## **Installing steps in Ubuntu:**

### **Uses the Commands:**

#### **Open the Ubuntu terminal and use the commands one by one:**

1. `sudo apt update && sudo apt upgrade -y`
2. Install the minifrog version from conda by these commands: pull the conda from the GitHub repository “`wget`  
[https://github.com/conda-forge/miniforge/releases/latest/download/Miniforge3-Linux-x86\\_64.sh](https://github.com/conda-forge/miniforge/releases/latest/download/Miniforge3-Linux-x86_64.sh)

**Put the link in the terminal and press Enter, and wait for the installation.**



```
Nov 9 16:55
ahmed@DEVELOPMENT:~$ wget https://github.com/conda-forge/miniforge/releases/latest/download/Miniforge3-Linux-x86_64.sh
```

**Now you save a minifrog on your device**

```

ahmed@DEVELOPMENT:~$ wget https://github.com/conda-forge/miniforge/releases/latest/download/Miniforge3-Linux-x86_64.sh
--2025-11-09 16:56:43- https://github.com/conda-forge/miniforge/releases/latest/download/Miniforge3-Linux-x86_64.sh
Resolving github.com (github.com)... 140.82.121.3
Connecting to github.com (github.com)|140.82.121.3|:443... connected.
HTTP request sent, awaiting response... 302 Found
Location: https://github.com/conda-forge/miniforge/releases/download/25.9.1.0/Miniforge3-Linux-x86_64.sh [following]
--2025-11-09 16:56:44- https://github.com/conda-forge/miniforge/releases/download/25.9.1.0/Miniforge3-Linux-x86_64.sh
Reusing existing connection to github.com:443.
HTTP request sent, awaiting response... 302 Found
Location: https://github-production-release-asset/221584277/57d0f57-d33b-407d-a2cb-9736b144dc37?pr_r=8&v=2018-11-09&r=b&sp=https&s=2025-11-09T15X3A32%3A132&scd=attachment%3Bfilename%3DMiniforge3-Linux-x86_64.sh&srct=application%2Foctet-stream&kid=96c2d410-5711-43a1-aedd-ab1947aa7ab08skid=398a6654-997b-47e9-b12b-9515b96b4de&skt=2025-11-09T14X3A318%3A56Z&skv=2025-11-09&sig=VA5X9q02AH76FD6E00DA35e1rb159SYce0mDVhsKj308jw=eyJ0eXAiOiJKV1QiLCJhbGciOiJlZiUzIiNlJ39.eyJpc3MiAiRodWlu29titiwYXVkJjgicnVszWFzZ1h3NLmHuZl0ahVldNlcnvbnlbQuy29tIwlazv5j0ia2VSMSisImV4cC16Tc2MjcwJAWNCwlbmJnijoXzYnAwMjA0LcJwXR0iJoicmVsZWFzZv0cHvh2Vjd1vLwib69LmNjUud2luZ093cy5uXQfTQ-3tWmVEecksY9t9tQ.3tWmVEeCrSY9t9NQ1t8wAfYLcnHt3ymLpbyQKmVtd4&response-content-disposition=attachment%3Bfilename%3DMiniforge3-Linux-x86_64.sh&response-content-type=application%2Foctet-stream [followin
]
--2025-11-09 16:56:45- https://release-assets.githubusercontent.com/github-production-release-asset/221584277/57d0f57-d33b-407d-a2cb-9736b144dc37?pr_r=8&v=2018-11-09&r=b&sp=https&s=2025-11-09T15X3A32%3A132&scd=attachment%3Bfilename%3DMiniforge3-Linux-x86_64.sh&srct=application%2Foctet-stream&kid=96c2d410-5711-43a1-aedd-ab1947aa7ab08skid=398a6654-997b-47e9-b12b-9515b96b4de&skt=2025-11-09T14X3A318%3A56Z&skv=2025-11-09&sig=VA5X9q02AH76FD6E00DA35e1rb159SYce0mDVhsKj308jw=eyJ0eXAiOiJKV1QiLCJhbGciOiJlZiUzIiNlJ39.eyJpc3MiAiRodWlu29titiwYXVkJjgicnVszWFzZ1h3NLmHuZl0ahVldNlcnvbnlbQuy29tIwlazv5j0ia2VSMSisImV4cC16Tc2MjcwJAWNCwlbmJnijoXzYnAwMjA0LcJwXR0iJoicmVsZWFzZv0cHvh2Vjd1vLwib69LmNjUud2luZ093cy5uXQfTQ-3tWmVEecksY9t9tQ.3tWmVEeCrSY9t9NQ1t8wAfYLcnHt3ymLpbyQKmVtd4&response-content-disposition=attachment%3Bfilename%3DMiniforge3-Linux-x86_64.sh&response-content-type=application%2Foctet-stream [f
]
Resolving release-assets.githubusercontent.com (release-assets.githubusercontent.com)... 185.199.109.133, 185.199.110.133, 185.199.111.133.
Connecting to release-assets.githubusercontent.com (release-assets.githubusercontent.com)|185.199.109.133|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 82862660 (79M) [application/octet-stream]
Saving to: "Miniforge3-Linux-x86_64.sh"

Miniforge3-Linux-x86_64.sh: 100%[=====] 79.02M 3.30MB/s in 24s

2025-11-09 16:57:09 (3.27 MB/s) - 'Miniforge3-Linux-x86_64.sh' saved [82862660/82862660]

```

**Now we are installing the minifro from this command:  
“bash Miniforge3-Linux-x86\_64.sh”**

**Then press “Enter,” then Yes to create licenses and Enter to install**

```

the GNU General Public License and can be found in pkgs/<pkg-name>/info/licenses
Folders.

Miniforge installer comes with a bootstrapping executable that is used
when installing miniforge and is deleted after miniforge is installed.
The bootstrapping executable uses micromamba, cl11, cpp-filesystem,
curl, c-ares, krb5, libarchive, libev, lz4, nghttp2, openssl, libsvl,
nljohnmann-json, reproc and zstd which are licensed under BSD-3-Clause,
MIT and OpenSSL licenses. Licenses and copyright notices of these
projects can be found at the following URL.
https://github.com/conda-forge/micromamba-feedstock/tree/master/recipe.

=====
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Do you accept the license terms? [yes|no]
>>> yes

```

**When you finish the minifrog install, put the command in the terminal**

```

ahmed@DEVELOPMENT:~$ source ~/.bashrc
ahmed@DEVELOPMENT:~$ 

```

**3- Create the plantvarfilter environment to install:**

**Use this command:**

**“mamba create -n pvf -c conda-forge -c bioconda python=3.11 samtools bcftools bowtie2 minimap2 plink”**

```

ahmed@DEVELOPMENT: $ mamba create -n pvf -c conda-forge -c bioconda python=3.11 samtools bcftools bowtie2 minimap2 plink
Found conda-prefix at '/home/ahmed/miniforge3/envs/pvf'. Overwrite?: [y/N] y
warning libmamba 'repo.anaconda.com', a commercial channel hosted by Anaconda.com, is used.
warning libmamba Please make sure you understand Anaconda Terms of Services.
warning libmamba See: https://legal.anaconda.com/policies/en/
[+] 4.6s
conda-forge/linux-64 ━━━━━━━━
conda-forge/noarch ━━━━━━
bioconda/linux-64 ━━━━━━
bioconda/noarch ━━━━
pkgs/main/linux-64 ━━━━
4.0MB / 48.6MB @ 883.8kB/s 4.6s
2.9MB / 23.2MB @ 629.8kB/s 4.6s
2.6MB / 5.3MB @ 573.2kB/s 4.6s
2.8MB / 5.0MB @ 608.3kB/s 4.6s
2.2MB / 9.0MB @ 475.1kB/s 4.6s

```

#### 4- When finished, activate mamba env

**“mamba activate pvf”**

**Note:**

The “PVF”, our env name, you can put any name.

```

ahmed@DEVELOPMENT:~$ mamba activate pvf
(pvf) ahmed@DEVELOPMENT:~$ █

```

#### 5- Now Install the Plantvarfilter package, Command:

**“pip install plantvarfilter”**

```

(pvf) ahmed@DEVELOPMENT:~$ pip install plantvarfilter
Collecting plantvarfilter
  Using cached plantvarfilter-0.2.4-py3-none-any.whl.metadata (13 kB)
Collecting numpy>=1.26 (from plantvarfilter)
  Using cached numpy-2.3.4-cp311-cp311-manylinux_2_27_x86_64.manylinux_2_28_x86_64.whl.metadata (62 kB)
Collecting pandas>=2.0 (from plantvarfilter)
  Using cached pandas-2.3.3-cp311-cp311-manylinux_2_24_x86_64.manylinux_2_28_x86_64.whl.metadata (91 kB)
Collecting scipy>=1.11 (from plantvarfilter)
  Using cached scipy-1.16.3-cp311-cp311-manylinux2014_x86_64.manylinux_2_17_x86_64.whl.metadata (62 kB)
Collecting matplotlib>=3.7 (from plantvarfilter)
  Using cached matplotlib-3.10.7-cp311-cp311-manylinux2014_x86_64.manylinux_2_17_x86_64.whl.metadata (11 kB)
Collecting scikit-learn>=1.3 (from plantvarfilter)

```

Then install fastlmm, geneview, xgboost

**“pip install fastlmm”**

**“pip install geneview”**

**“pip install xgboost”**

**From this command, you can turn on the package:**

**“plantvarfilter”**

