How to Use Mi-GARDEN

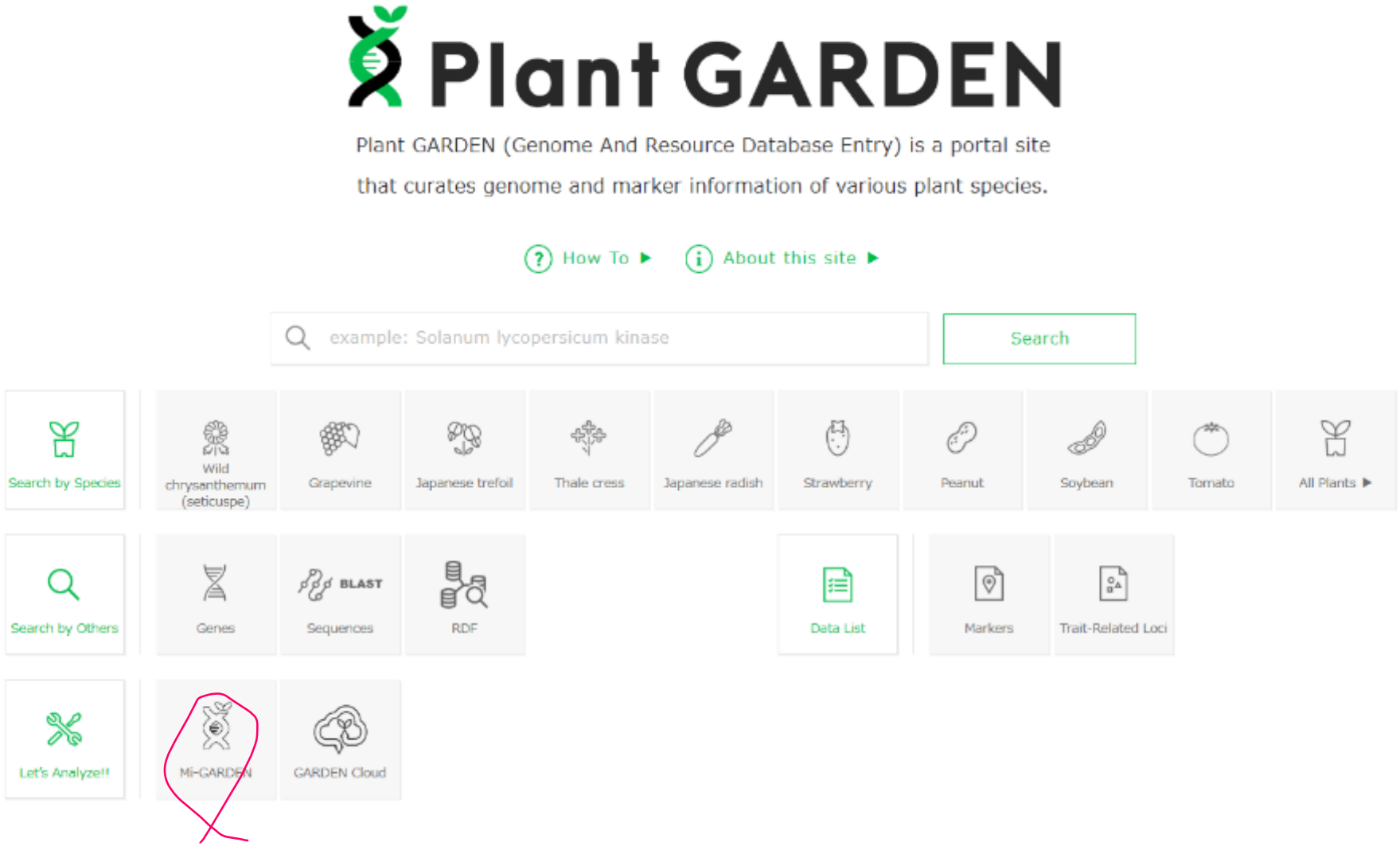
Get started Mi-GARDEN

- ✓ Install Docker
- ✓ Download Mi-GARDEN
- ✓ Run Docker Desktop
- ✓ Install Mi-GARDEN
- ✓ Input Data Preparation
- ✓ Run Mi-GARDEN

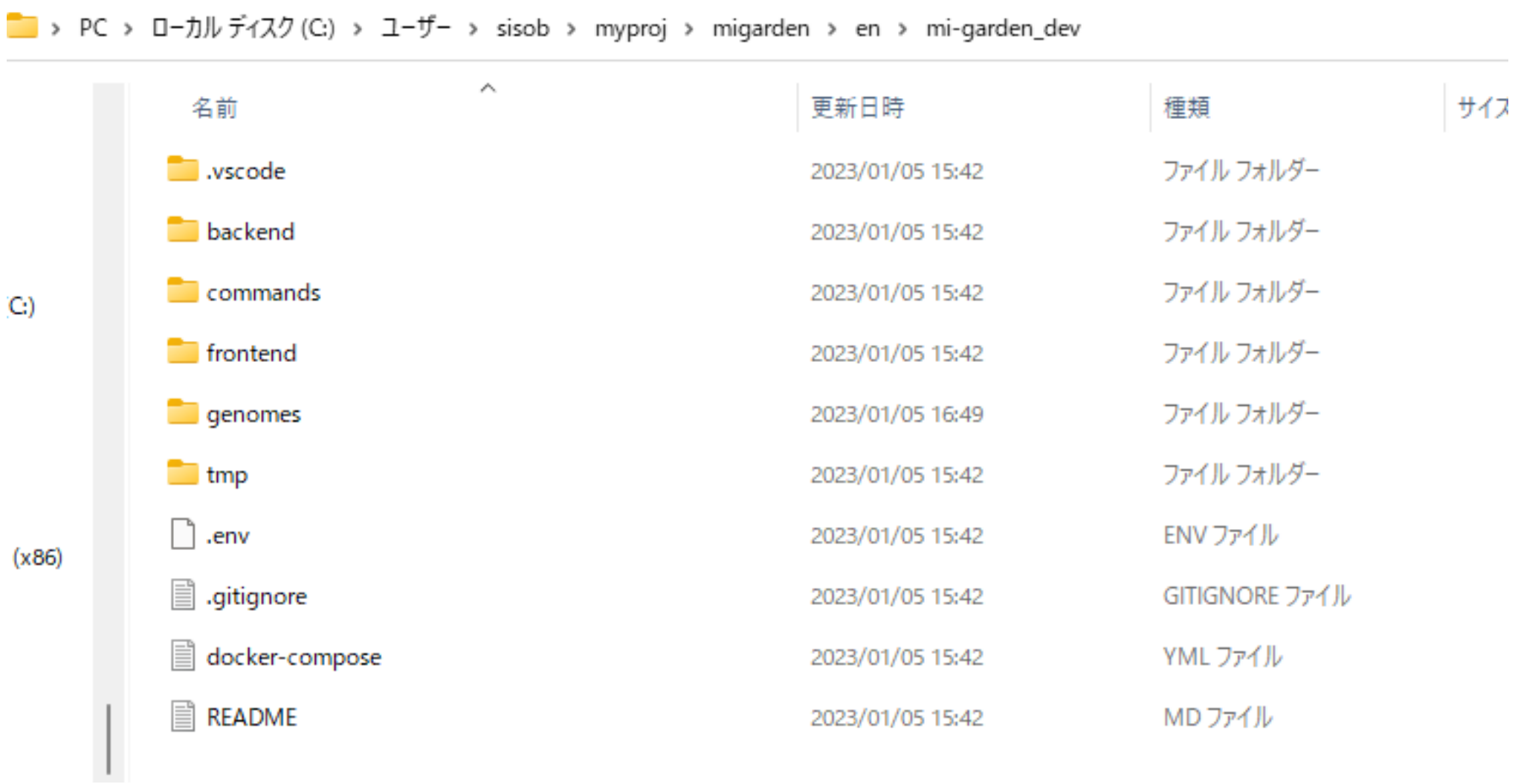
Docker Install

https://www.docker.com/

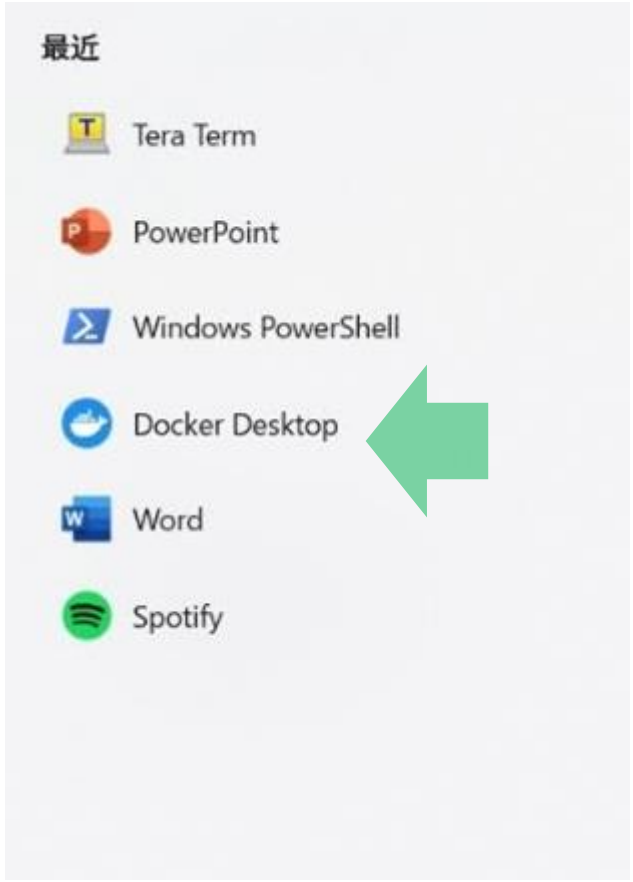
Download Mi-GARDEN



Unzip and put the files on an any folder

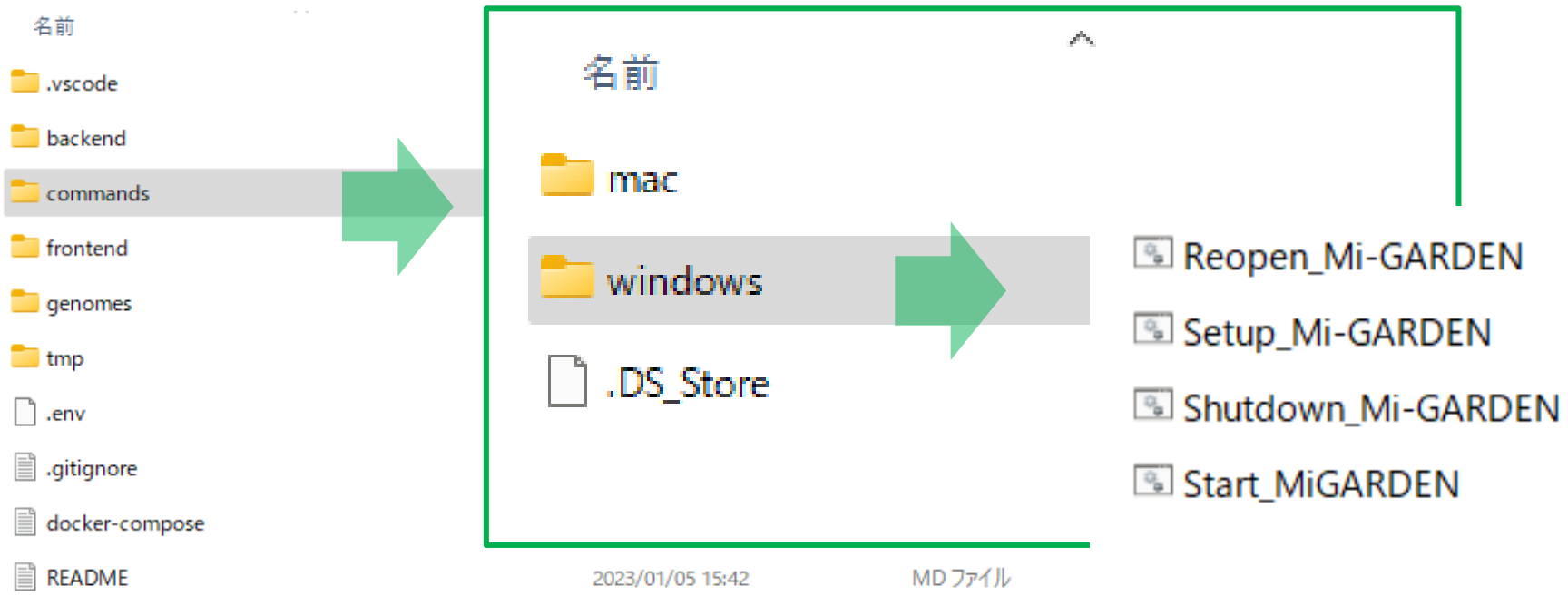


Run Docker Desktop



Run Docker Desktop

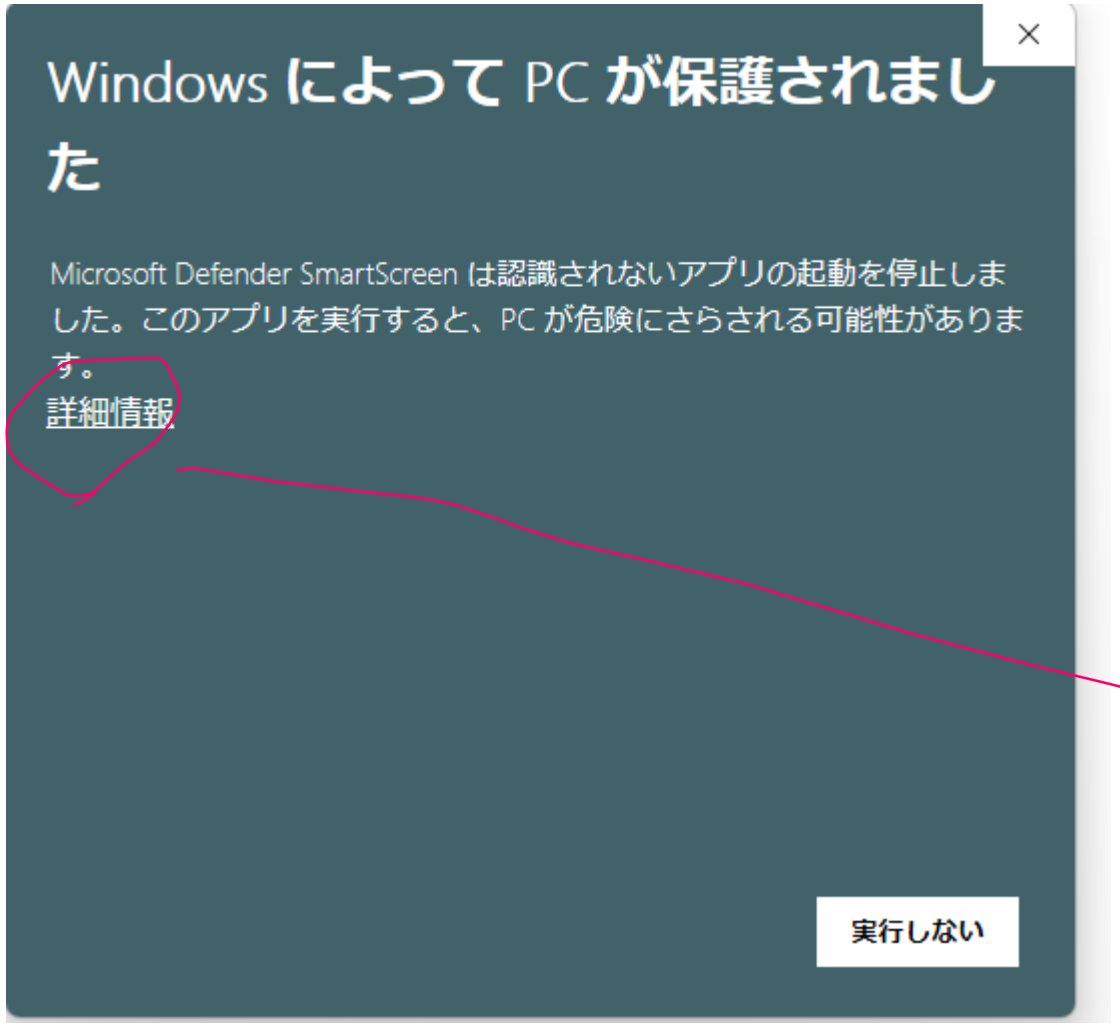
Open Commands folder commands/mac or commands/windows

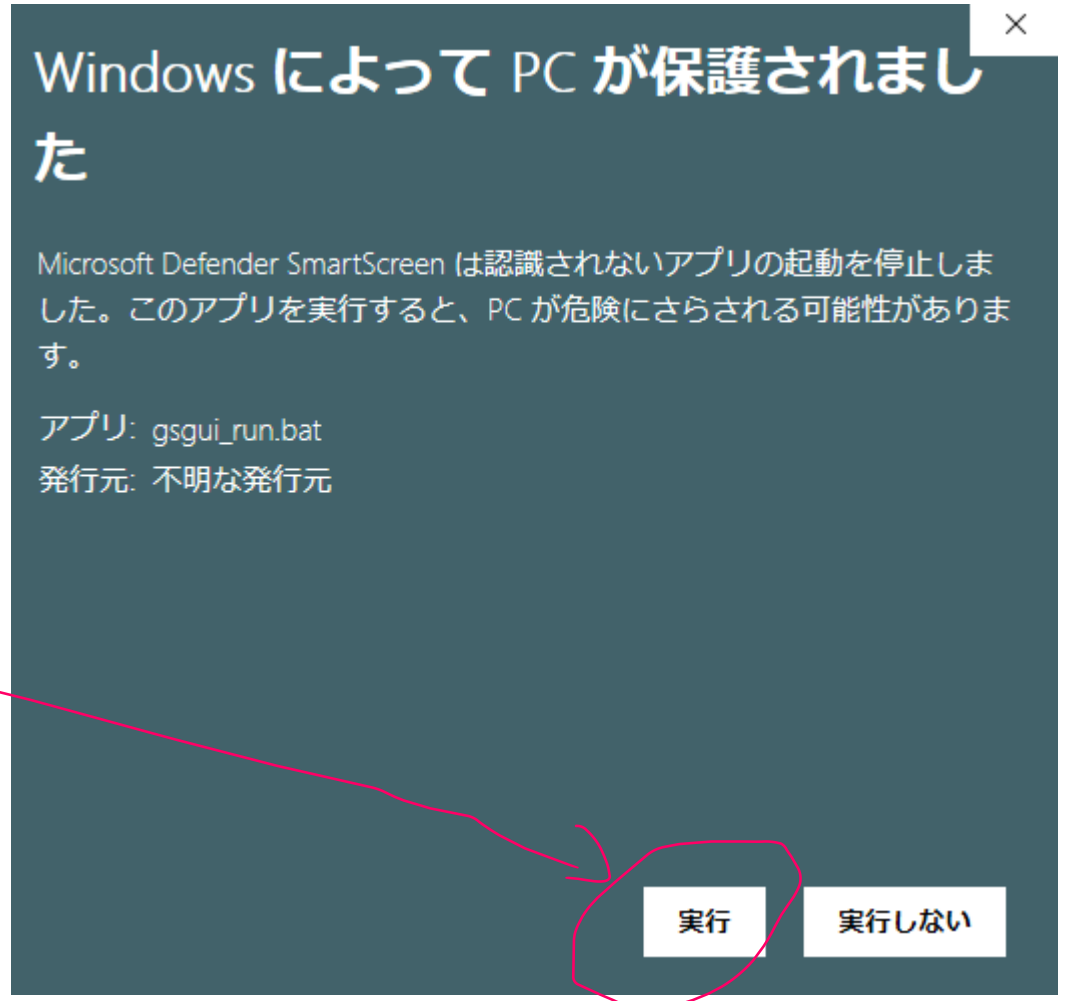


Click Setup_Mi-GARDEN

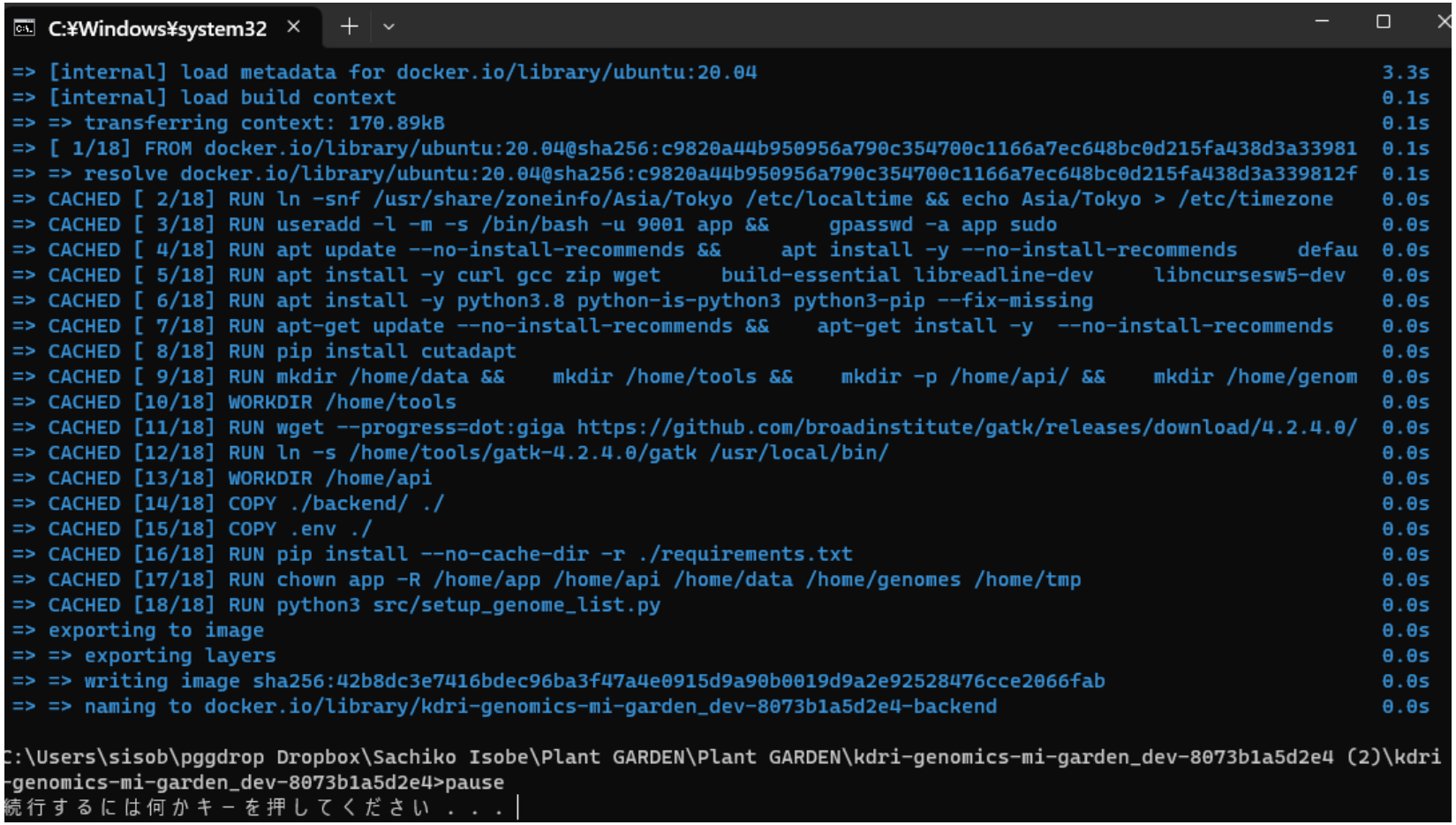
This process is for installation of Mi-GARDEN, and done only once.

Security Alert





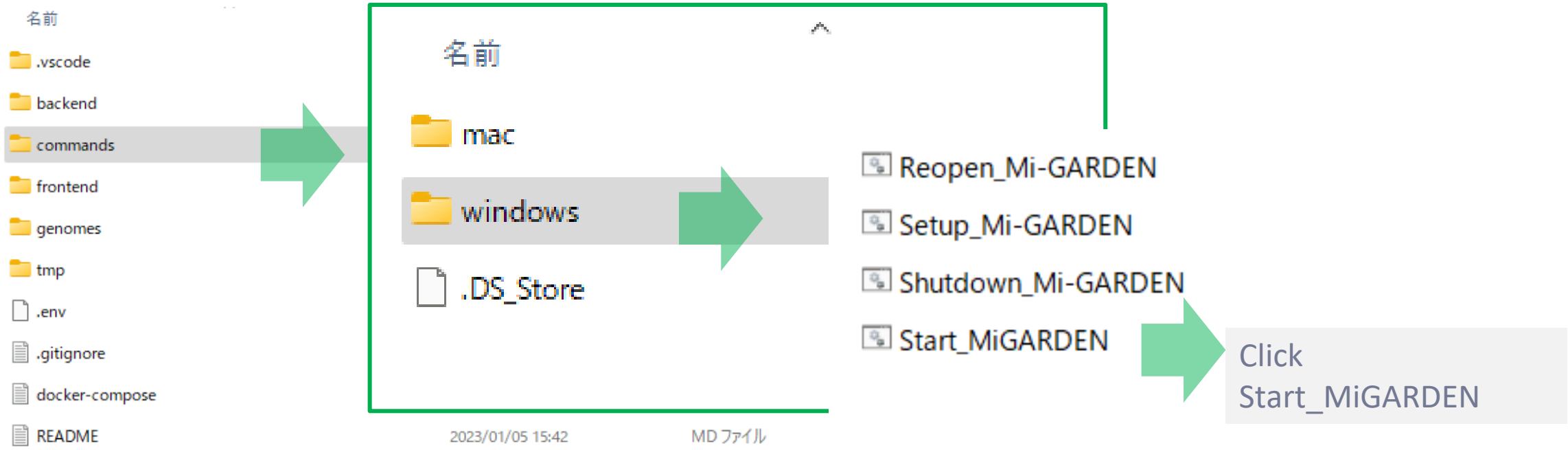
Start installing



The command prompt will automatically start up again, wait a moment.

When ‘Press any key to continue’ is displayed, the process is finished.

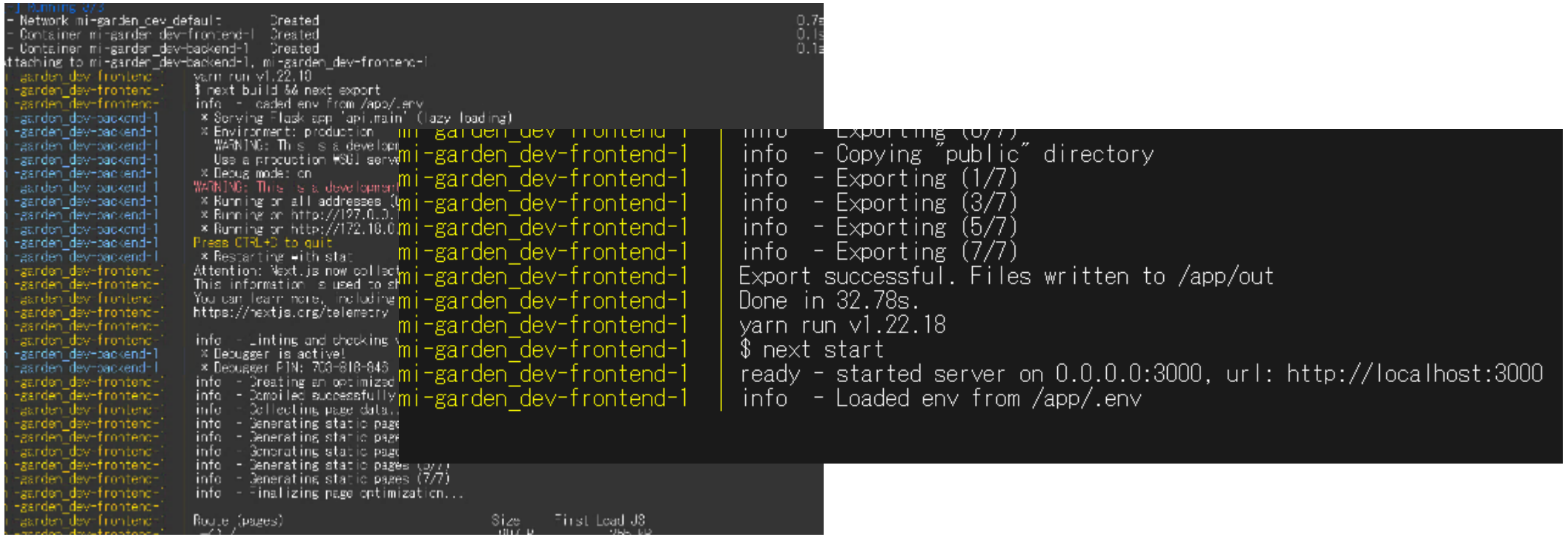
Run Mi-GARDEN



This action corresponds to <run> in the programme.After you have done the Build work, you can launch the docker desktop and then click docker_up for the usual operation. You can also make a shortcut and put on the desktop (windows).

Run Mi-GARDEN

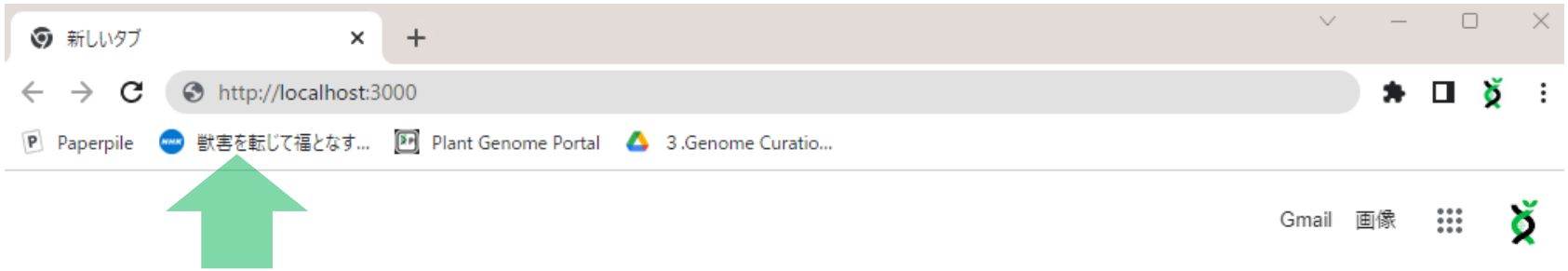
The command prompt will automatically start up again, wait a moment.

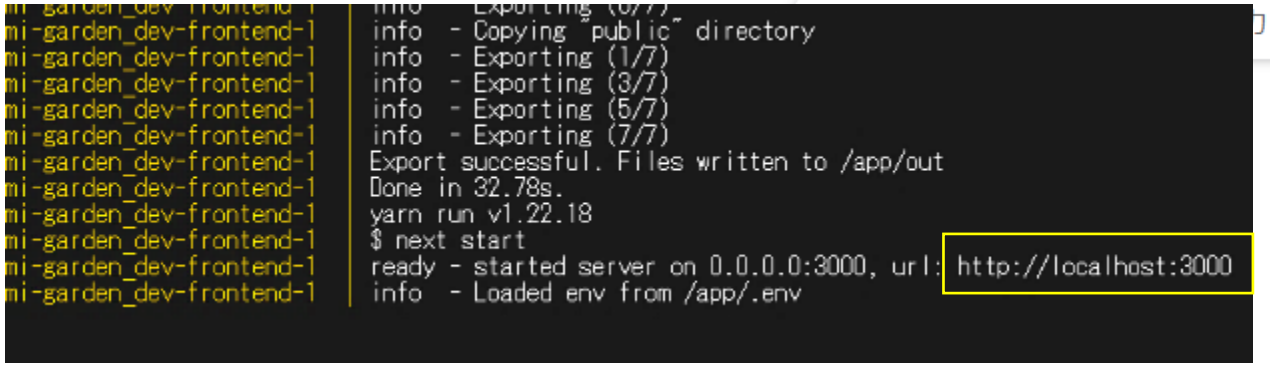


When ‘Press any key to continue’ is displayed, the process is finished.

Open a web browser and put ‘http://localhost:3000’

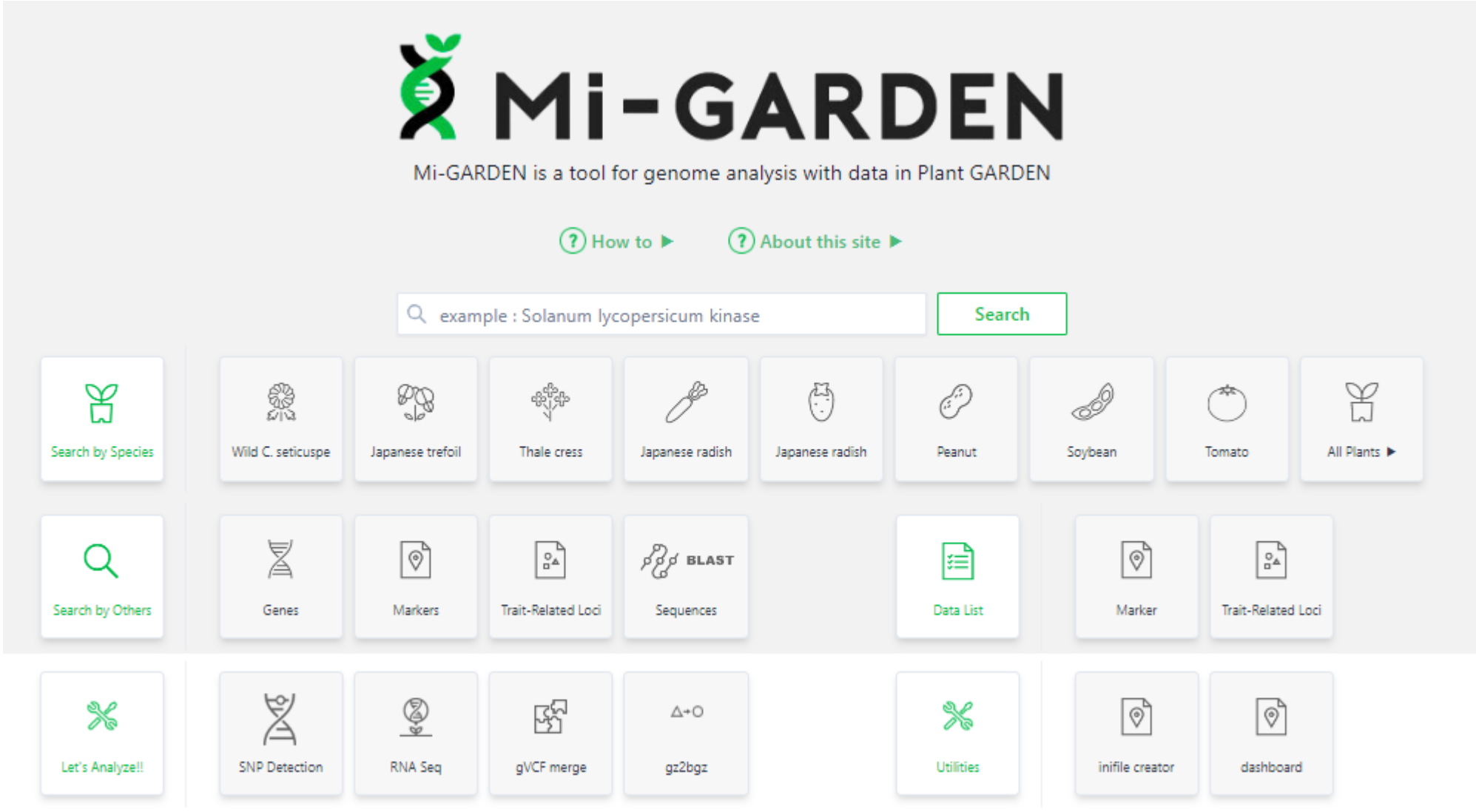
Web Browser is automatically open, but if not, please type http://localhost:3000





Or Ctr + enter(win)

Mi-GARDEN is Opened



Select Your analysis

Select Reference

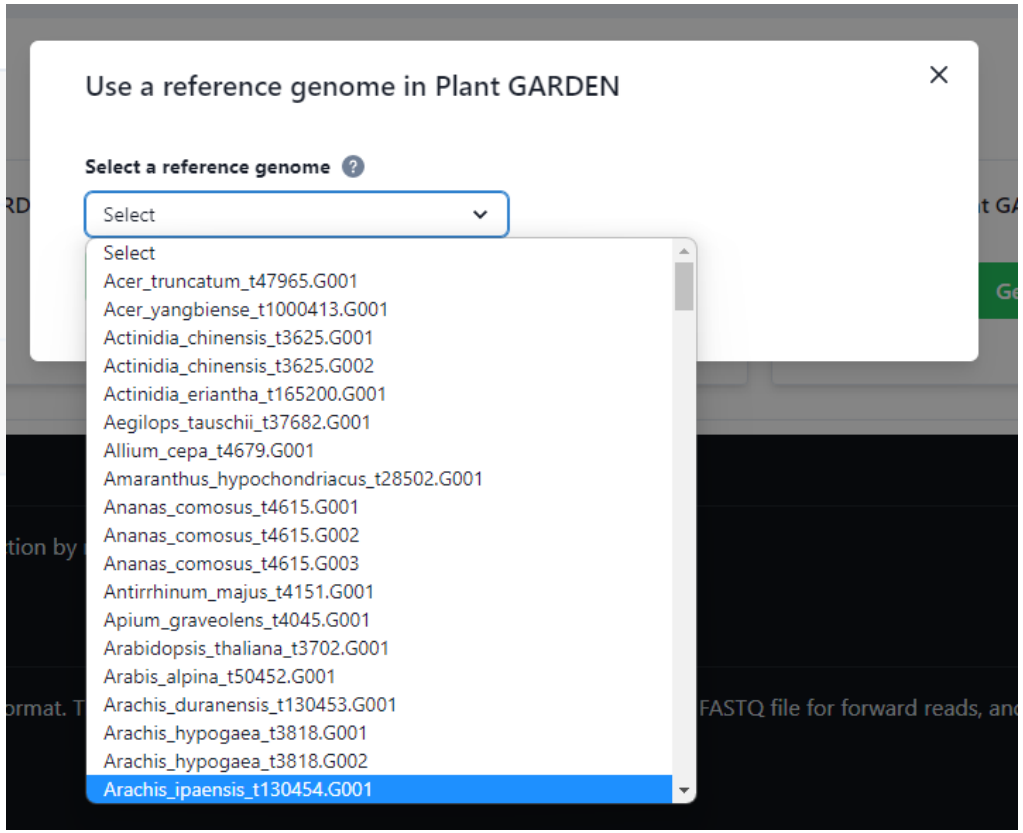
SNP Detection

A Tool for read QC, trimming and SNP detection by mapping short reads onto a reference sequence.

Use a reference genome in Plant GARDEN

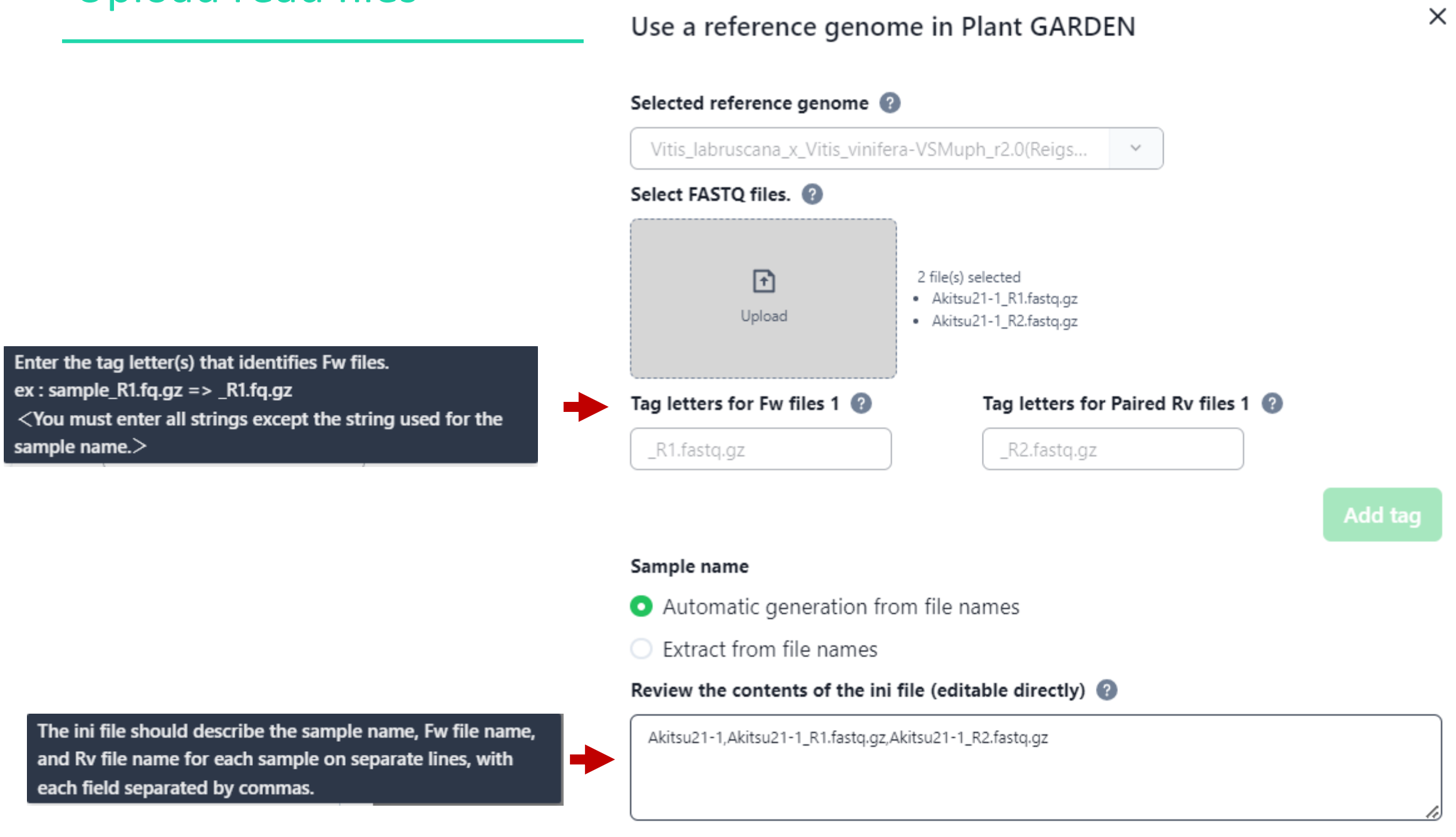
Use your own reference genome

Update the Plant GARDEN genome sequence list



In the genome sequence list of Plant GARDEN, only the genome sequences for which gff files have been created for RNA-Seq analysis are displayed.

Upload read files



Select Analysis

quality check

No Yes

adapter trim

No Yes

adapter5

No Yes

adapter5

AGATCGGAAGAGC

adapter3

No Yes

adapter3

AGATCGGAAGAGC

quality control

No Yes

Set the quality threshold for quality control in cutadapt.

30

mapping

No Yes

variant call

No Yes

vcf

No Yes

gvcf

No Yes

multi-sample vcf

No Yes

Run Analysis

Run

Use a reference genome in Plant GARDEN

You can close the cat, and check the status on the dashboard

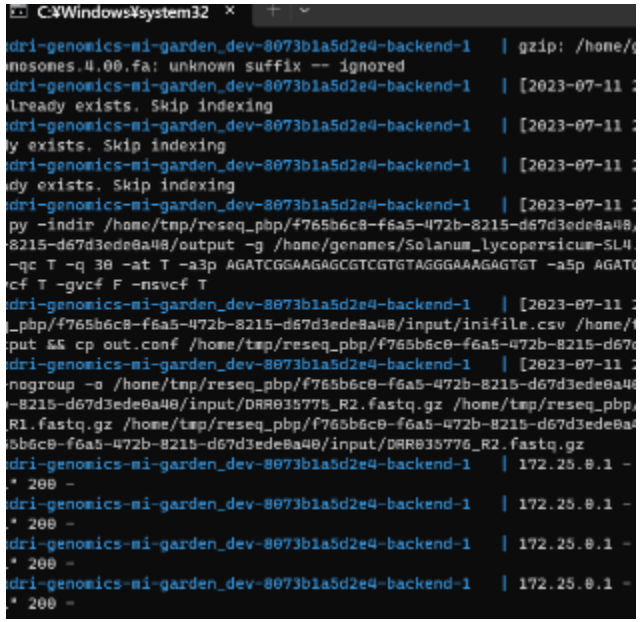
Confirm the status

Dashboard

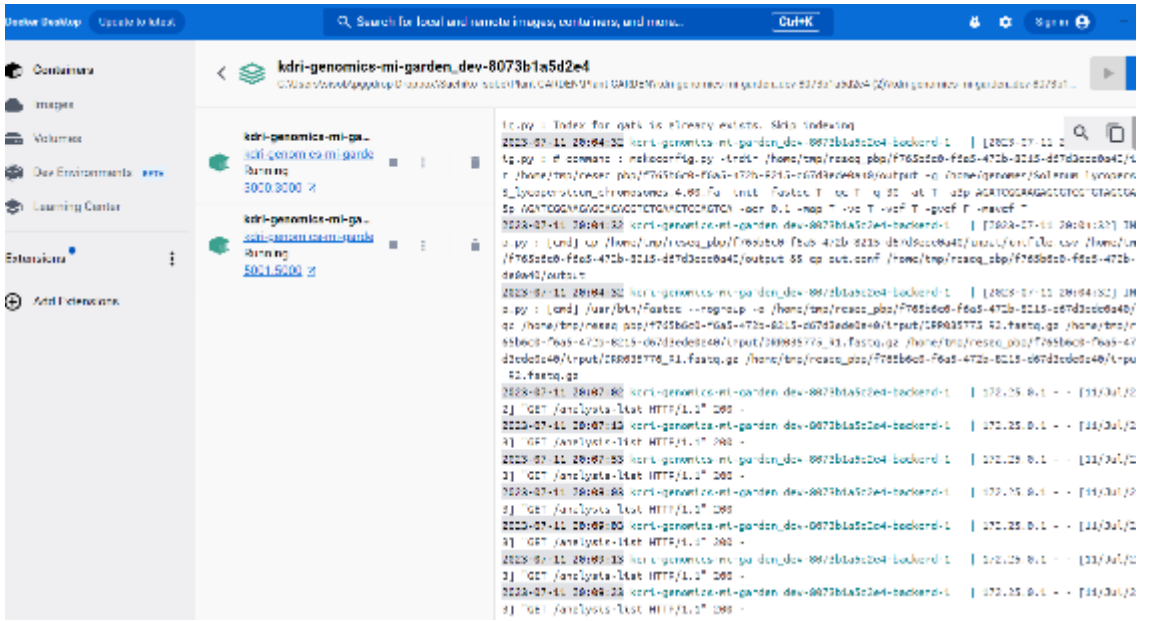
delete all tracks

Analysis Name	Reference Name	Started at	Finished at	Options	Status	Show deleted tracks
SNP Detection	Solanum_lycopersicum-SL4.0	2023/7/11 20:04:32	-		Analyzing	

Command prompt

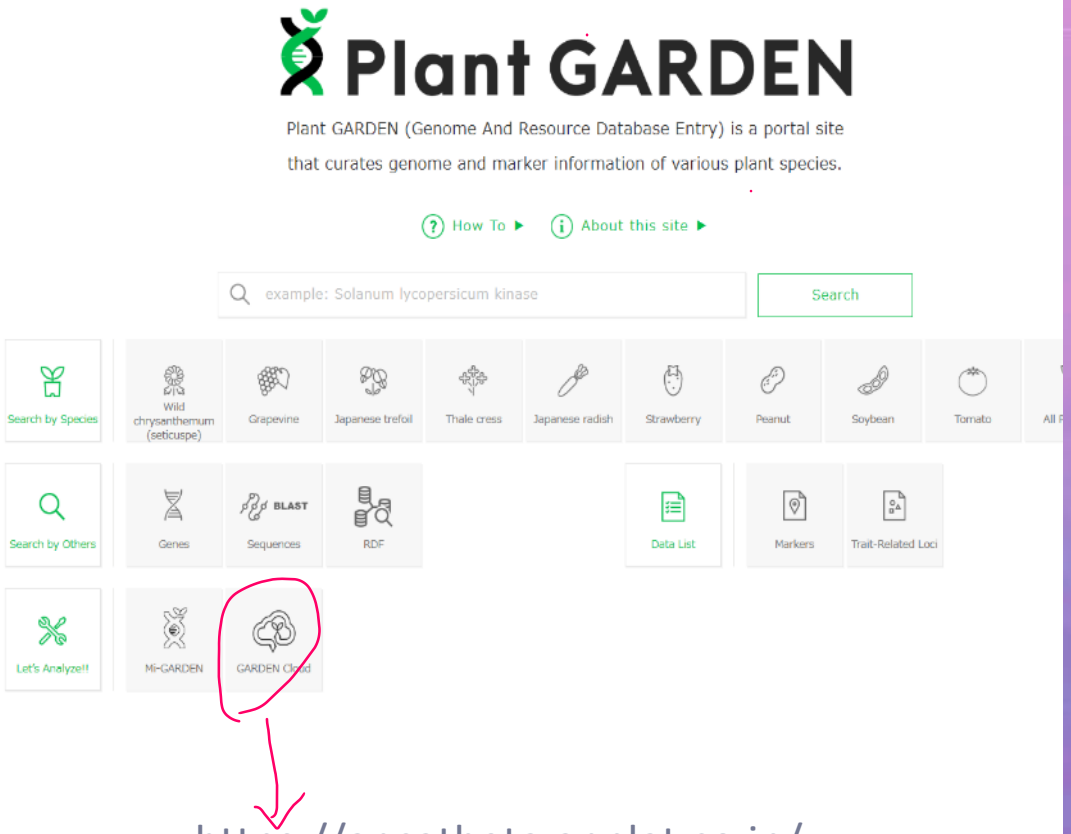


Docker desktop

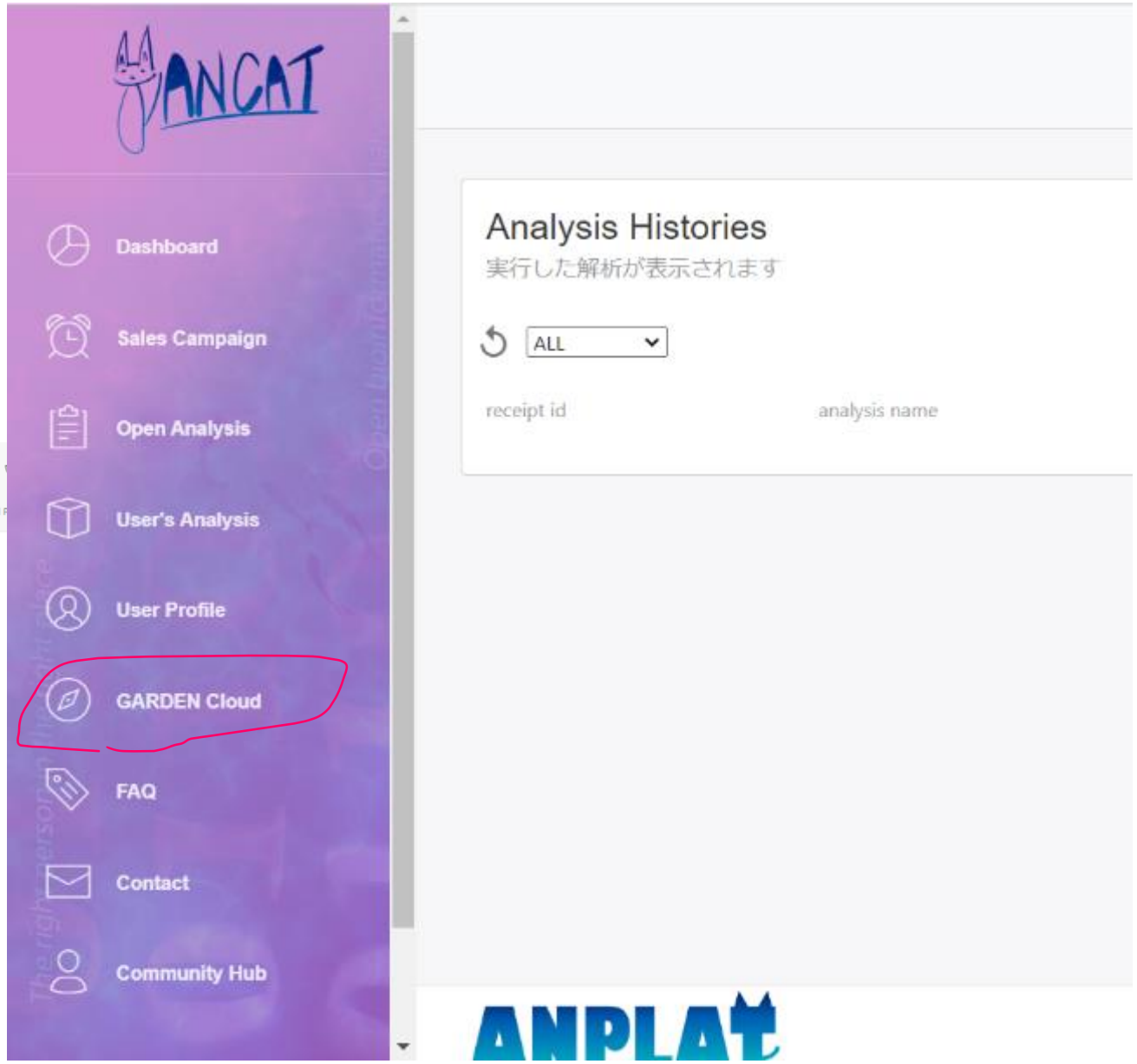


GARDEN Cloud

If the analysis takes too long on your own PC, you can also use paid cloud services.



https://ancatbeta.anplat.co.jp/



GARDEN Cloud

Price for SNP Detection

SNPWorkflow

Price list

upload data size	prices include tax	run time prediction
~ 10GB	¥5500	~ 1 day
~ 10GB with BAM	¥6050	~ 1 day
~ 50GB	¥33000	~ 3 days
~ 50GB with BAM	¥38500	~ 3 days
~ 100GB	¥88000	~ 7 days
~ 100GB with BAM	¥98600	~ 7 days
more than 100GB	Please consult with us separately.	-

If the analysis is taking longer than expected run time, the analysis may have failed, so please contact us via chat.