

Get started Mi-GARDEN

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

Docker Install

<https://www.docker.com/>

Download Mi-GARDEN



Plant GARDEN (Genome And Resource Database Entry) is a portal site that curates genome and marker information of various plant species.

[? How To ▶](#) [i About this site ▶](#)

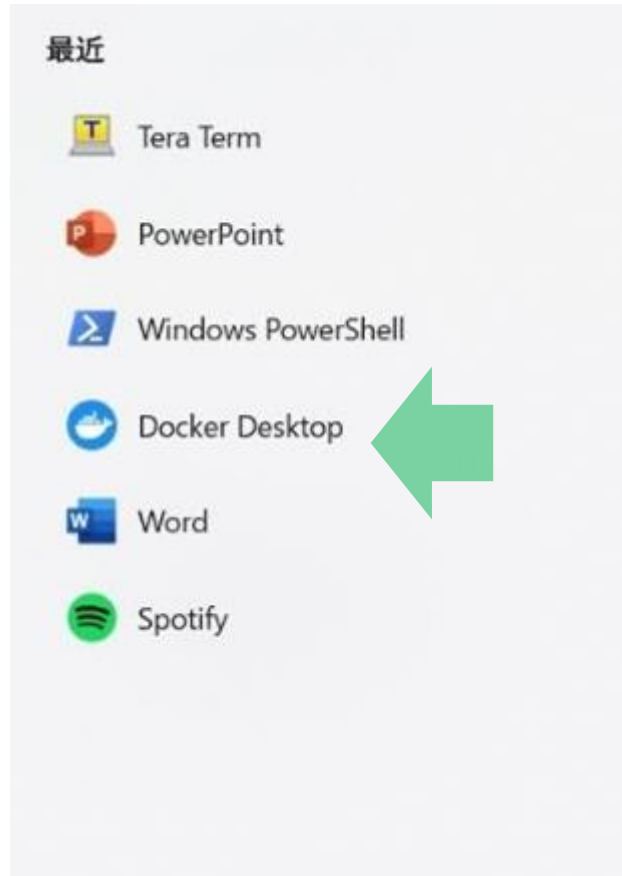
Search by Species	Wild chrysanthemum (seticuspe)	Grapevine	Japanese trefoil	Thale cress	Japanese radish	Strawberry	Peanut	Soybean	Tomato	All Plants ▶
Search by Others	Genes	Sequences	RDF	Data List			Markers	Trait-Related Loci		
Let's Analyze!!	Mi-GARDEN	GARDEN Cloud								

Unzip and put the files on an any folder

PC > ローカルディスク (C:) > ユーザー > sisob > myproj > migarden > en > mi-garden_dev

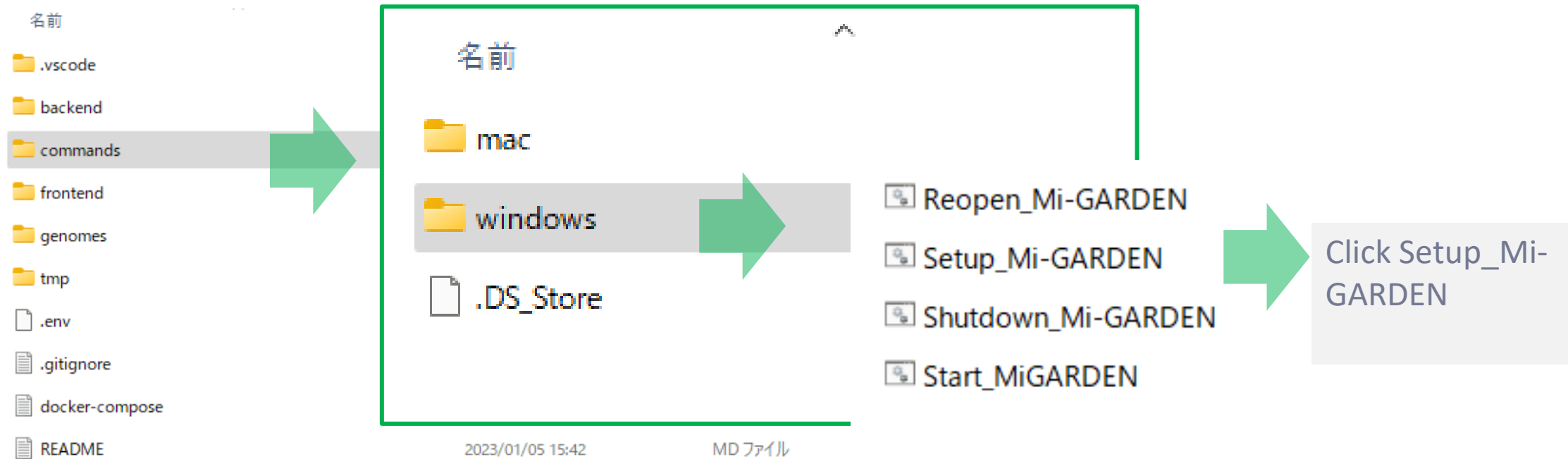
名前	更新日時	種類	サイズ
フォルダ .vscode	2023/01/05 15:42	ファイル フォルダー	
フォルダ backend	2023/01/05 15:42	ファイル フォルダー	
フォルダ commands	2023/01/05 15:42	ファイル フォルダー	
フォルダ frontend	2023/01/05 15:42	ファイル フォルダー	
フォルダ genomes	2023/01/05 16:49	ファイル フォルダー	
フォルダ tmp	2023/01/05 15:42	ファイル フォルダー	
ファイル .env	2023/01/05 15:42	ENV ファイル	
ファイル .gitignore	2023/01/05 15:42	GITIGNORE ファイル	
ファイル docker-compose	2023/01/05 15:42	YML ファイル	
ファイル README	2023/01/05 15:42	MD ファイル	

Run Docker Desktop



Run Docker Desktop

Open Commands folder `commands/mac` or `commands/windows`



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

Security Alert

Windows によって PC が保護されました

Microsoft Defender SmartScreen は認識されないアプリの起動を停止しました。このアプリを実行すると、PC が危険にさらされる可能性があります。

詳細情報

実行しない

Windows によって PC が保護されました

Microsoft Defender SmartScreen は認識されないアプリの起動を停止しました。このアプリを実行すると、PC が危険にさらされる可能性があります。

アプリ: gsgui_run.bat
発行元: 不明な発行元

実行 実行しない

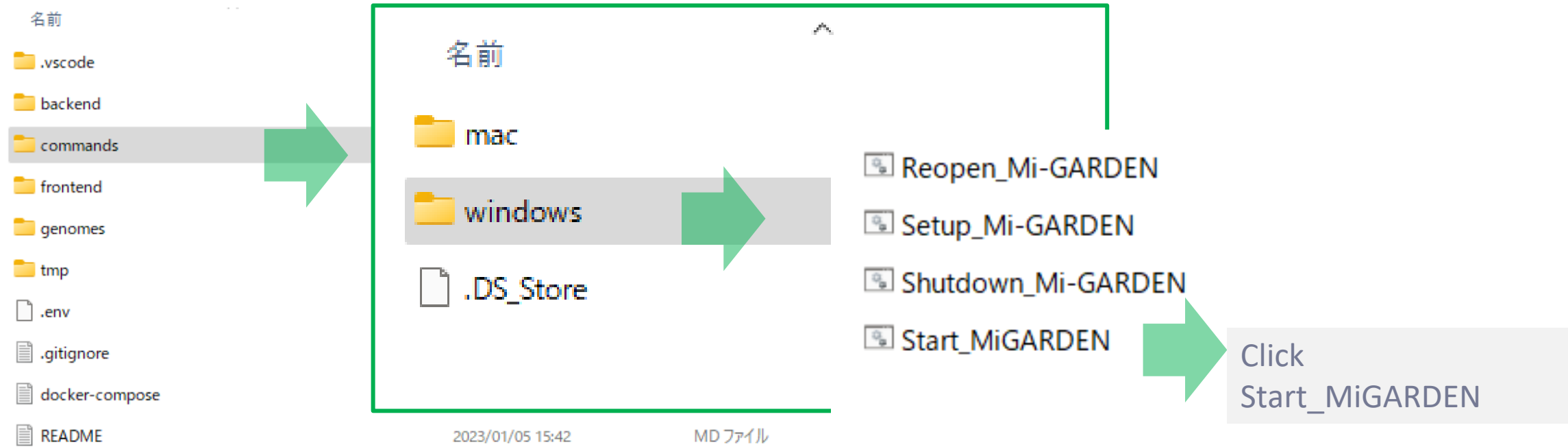
Start installing

```
C:\Windows\system32 x + v
=> [internal] load metadata for docker.io/library/ubuntu:20.04 3.3s
=> [internal] load build context 0.1s
=> => transferring context: 170.89kB 0.1s
=> [ 1/18] FROM docker.io/library/ubuntu:20.04@sha256:c9820a44b950956a790c354700c1166a7ec648bc0d215fa438d3a33981 0.1s
=> => resolve docker.io/library/ubuntu:20.04@sha256:c9820a44b950956a790c354700c1166a7ec648bc0d215fa438d3a339812f 0.1s
=> CACHED [ 2/18] RUN ln -snf /usr/share/zoneinfo/Asia/Tokyo /etc/localtime && echo Asia/Tokyo > /etc/timezone 0.0s
=> CACHED [ 3/18] RUN useradd -l -m -s /bin/bash -u 9001 app && gpasswd -a app sudo 0.0s
=> CACHED [ 4/18] RUN apt update --no-install-recommends && apt install -y --no-install-recommends defau 0.0s
=> CACHED [ 5/18] RUN apt install -y curl gcc zip wget build-essential libreadline-dev libncursesw5-dev 0.0s
=> CACHED [ 6/18] RUN apt install -y python3.8 python-is-python3 python3-pip --fix-missing 0.0s
=> CACHED [ 7/18] RUN apt-get update --no-install-recommends && apt-get install -y --no-install-recommends 0.0s
=> CACHED [ 8/18] RUN pip install cutadapt 0.0s
=> CACHED [ 9/18] RUN mkdir /home/data && mkdir /home/tools && mkdir -p /home/api/ && mkdir /home/genom 0.0s
=> CACHED [10/18] WORKDIR /home/tools 0.0s
=> CACHED [11/18] RUN wget --progress=dot:giga https://github.com/broadinstitute/gatk/releases/download/4.2.4.0/ 0.0s
=> CACHED [12/18] RUN ln -s /home/tools/gatk-4.2.4.0/gatk /usr/local/bin/ 0.0s
=> CACHED [13/18] WORKDIR /home/api 0.0s
=> CACHED [14/18] COPY ./backend/ ./ 0.0s
=> CACHED [15/18] COPY .env ./ 0.0s
=> CACHED [16/18] RUN pip install --no-cache-dir -r ./requirements.txt 0.0s
=> CACHED [17/18] RUN chown app -R /home/app /home/api /home/data /home/genomes /home/tmp 0.0s
=> CACHED [18/18] RUN python3 src/setup_genome_list.py 0.0s
=> exporting to image 0.0s
=> => exporting layers 0.0s
=> => writing image sha256:42b8dc3e7416bdec96ba3f47a4e0915d9a90b0019d9a2e92528476cce2066fab 0.0s
=> => naming to docker.io/library/kdri-genomics-mi-garden_dev-8073b1a5d2e4-backend 0.0s
C:\Users\sisob\pggdrop Dropbox\Sachiko Isobe\Plant GARDEN\Plant GARDEN\kdri-genomics-mi-garden_dev-8073b1a5d2e4 (2)\kdri
-genomics-mi-garden_dev-8073b1a5d2e4>pause
続行するには何かキーを押してください . . . |
```

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

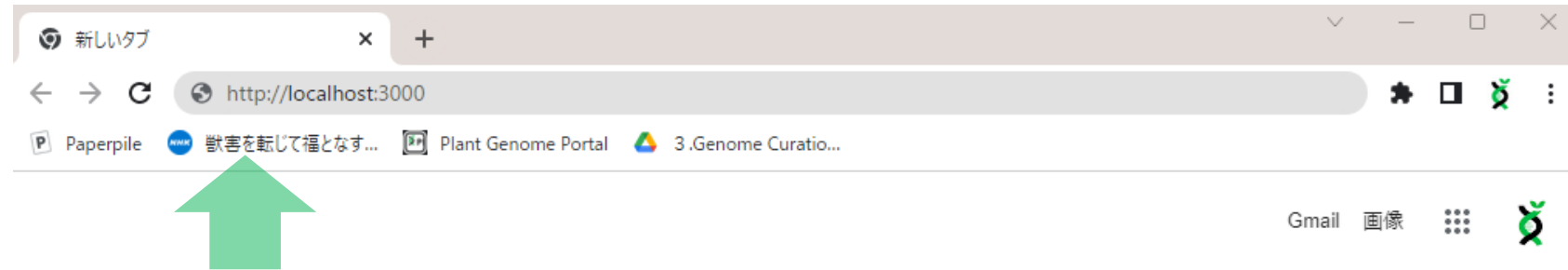
The command prompt will automatically start up again, wait a moment.

```
Running 0/2
- Network mi-garden_dev default      Created          0.7s
- Container mi-garden_dev-frontend-1 Created          0.1s
- Container mi-garden_dev-backend-1  Created          0.1s
Attaching to mi-garden_dev-backend-1, mi-garden_dev-frontend-1
mi-garden_dev-frontend-1 | yarn run v1.22.18
mi-garden_dev-frontend-1 | info - next build && next export
mi-garden_dev-frontend-1 | info - Loaded env from /app/.env
mi-garden_dev-backend-1 | * Serving Flask app "api.main" (lazy loading)
mi-garden_dev-backend-1 | * Environment: production
mi-garden_dev-frontend-1 | info - Exporting (0/7)
mi-garden_dev-backend-1 | WARNING: This is a development server.
mi-garden_dev-frontend-1 | info - Copying "public" directory
mi-garden_dev-backend-1 | Use a production HTTP server instead.
mi-garden_dev-frontend-1 | info - Exporting (1/7)
mi-garden_dev-backend-1 | * Debug mode: on
mi-garden_dev-frontend-1 | info - Exporting (3/7)
mi-garden_dev-backend-1 | WARNING: This is a development server.
mi-garden_dev-frontend-1 | info - Exporting (5/7)
mi-garden_dev-backend-1 | * Running on all addresses (0.0.0.0)
mi-garden_dev-frontend-1 | info - Exporting (7/7)
mi-garden_dev-backend-1 | * Running on http://127.0.0.1:5000
mi-garden_dev-frontend-1 | Export successful. Files written to /app/out
mi-garden_dev-backend-1 | * Restarting with stat
mi-garden_dev-frontend-1 | Done in 32.78s.
mi-garden_dev-backend-1 | Attention: Next.js now collects anonymous telemetry
mi-garden_dev-frontend-1 | yarn run v1.22.18
mi-garden_dev-backend-1 | You can learn more, including how to opt-out,
mi-garden_dev-frontend-1 | info - Linting and checking validity of types
mi-garden_dev-backend-1 | * Debugger is active!
mi-garden_dev-frontend-1 | info - Compiled successfully
mi-garden_dev-backend-1 | * Debugger PIN: 703-818-843
mi-garden_dev-frontend-1 | info - Collecting page data...
mi-garden_dev-backend-1 | info - Creating an optimized production build
mi-garden_dev-frontend-1 | info - Generating static page (1/7)
mi-garden_dev-backend-1 | info - Generating static page (1/7)
mi-garden_dev-frontend-1 | info - Generating static page (2/7)
mi-garden_dev-backend-1 | info - Generating static page (2/7)
mi-garden_dev-frontend-1 | info - Generating static page (3/7)
mi-garden_dev-backend-1 | info - Generating static page (3/7)
mi-garden_dev-frontend-1 | info - Generating static page (4/7)
mi-garden_dev-backend-1 | info - Generating static page (4/7)
mi-garden_dev-frontend-1 | info - Generating static page (5/7)
mi-garden_dev-backend-1 | info - Generating static page (5/7)
mi-garden_dev-frontend-1 | info - Generating static page (6/7)
mi-garden_dev-backend-1 | info - Generating static page (6/7)
mi-garden_dev-frontend-1 | info - Generating static page (7/7)
mi-garden_dev-backend-1 | info - Generating static page (7/7)
mi-garden_dev-frontend-1 | info - Finalizing page optimization...
mi-garden_dev-frontend-1 |
mi-garden_dev-frontend-1 | Route (pages) | Size | First Load JS
mi-garden_dev-frontend-1 | --- | --- | ---
mi-garden_dev-frontend-1 | /_next/static/chunks/pages/_error.js | 1.18 KB | 1.18 KB
```

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



Google

```
mi-garden_dev-frontend-1 | info - Exporting (6/7)
mi-garden_dev-frontend-1 | info - Copying "public" directory
mi-garden_dev-frontend-1 | info - Exporting (1/7)
mi-garden_dev-frontend-1 | info - Exporting (3/7)
mi-garden_dev-frontend-1 | info - Exporting (5/7)
mi-garden_dev-frontend-1 | info - Exporting (7/7)
mi-garden_dev-frontend-1 | Export successful. Files written to /app/out
mi-garden_dev-frontend-1 | Done in 32.78s.
mi-garden_dev-frontend-1 | yarn run v1.22.18
mi-garden_dev-frontend-1 | $ next start
mi-garden_dev-frontend-1 | ready - started server on 0.0.0.0:3000, url: http://localhost:3000
mi-garden_dev-frontend-1 | info - Loaded env from /app/.env
```

Or Ctr + enter(win)

Mi-GARDEN is Opened

The screenshot displays the Mi-GARDEN website interface. At the top center is the logo, which consists of a green DNA double helix with a plant sprout growing from it, followed by the text "Mi-GARDEN" in a bold, black, sans-serif font. Below the logo is the tagline "Mi-GARDEN is a tool for genome analysis with data in Plant GARDEN".

Below the tagline are two links: "? How to ►" and "? About this site ►". A search bar is positioned below these links, containing the text "example : Solanum lycopersicum kinase" and a "Search" button to its right.

The main content area is organized into three rows of buttons, each with an icon and a label:

- Row 1:** "Search by Species" (plant icon), "Wild C. seticuspe" (flower icon), "Japanese trefoil" (flower icon), "Thale cress" (flower icon), "Japanese radish" (radish icon), "Japanese radish" (radish icon), "Peanut" (peanut icon), "Soybean" (soybean icon), "Tomato" (tomato icon), and "All Plants ►" (plant icon).
- Row 2:** "Search by Others" (magnifying glass icon), "Genes" (DNA helix icon), "Markers" (location pin icon), "Trait-Related Loci" (document icon), "Sequences" (DNA helix icon with "BLAST" text), "Data List" (document icon with list), "Marker" (location pin icon), and "Trait-Related Loci" (document icon).
- Row 3:** "Let's Analyze!!" (scissors icon), "SNP Detection" (DNA helix icon), "RNA Seq" (microscope icon), "gVCF merge" (puzzle pieces icon), "gz2bgz" (triangle and circle icon), "Utilities" (scissors icon), "infile creator" (location pin icon), and "dashboard" (location pin icon).

← Select Your analysis

Select Reference

SNP Detection

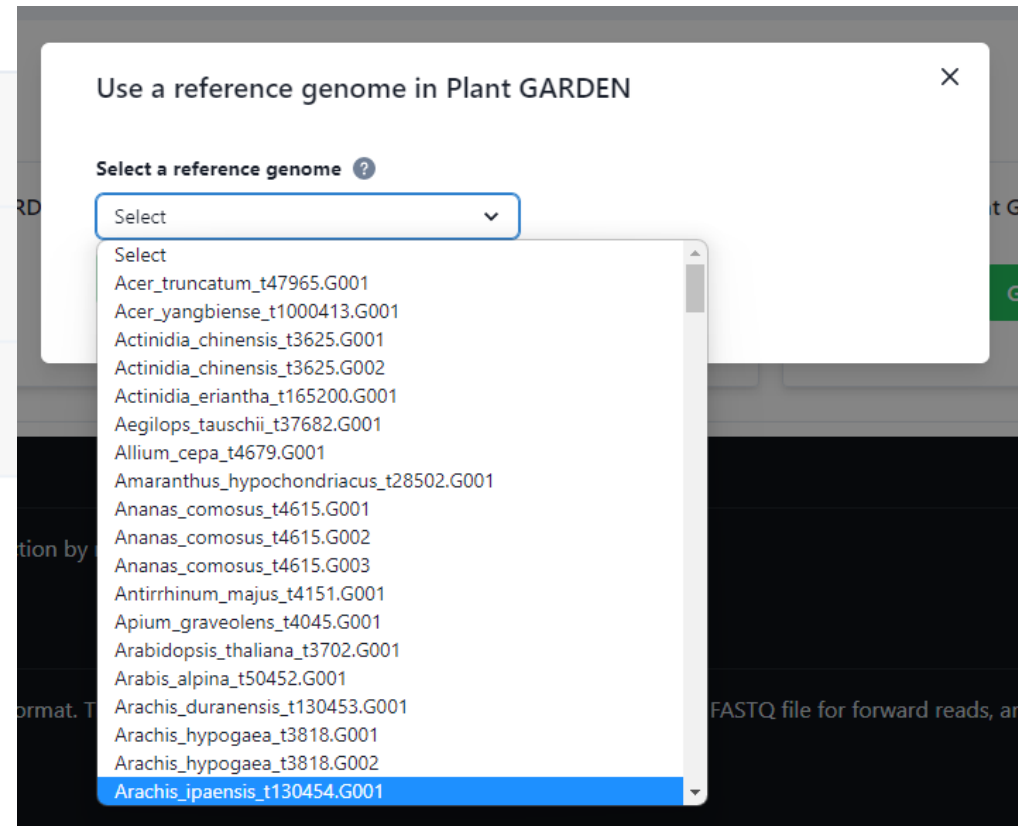
A Tool for read QC, trimming and SNP detection by mapping short reads onto a reference sequence.

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

Enter the tag letter(s) that identifies Fw files.
ex : sample_R1.fastq.gz => _R1.fastq.gz
<You must enter all strings except the string used for the sample name.>



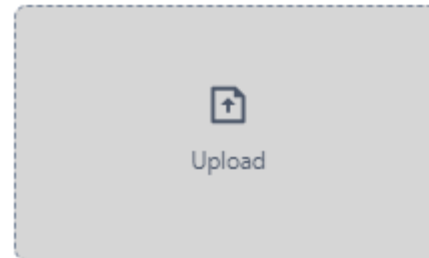
Use a reference genome in Plant GARDEN



Selected reference genome ?

Vitis_labruscana_x_Vitis_vinifera-VSMuph_r2.0(Reigs... ▾

Select FASTQ files. ?



2 file(s) selected

- Akitsu21-1_R1.fastq.gz
- Akitsu21-1_R2.fastq.gz

Tag letters for Fw files 1 ?

_R1.fastq.gz

Tag letters for Paired Rv files 1 ?

_R2.fastq.gz

Add tag

Sample name

- Automatic generation from file names
- Extract from file names

Review the contents of the ini file (editable directly) ?

Akitsu21-1,Akitsu21-1_R1.fastq.gz,Akitsu21-1_R2.fastq.gz



The ini file should describe the sample name, Fw file name, and Rv file name for each sample on separate lines, with each field separated by commas.

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



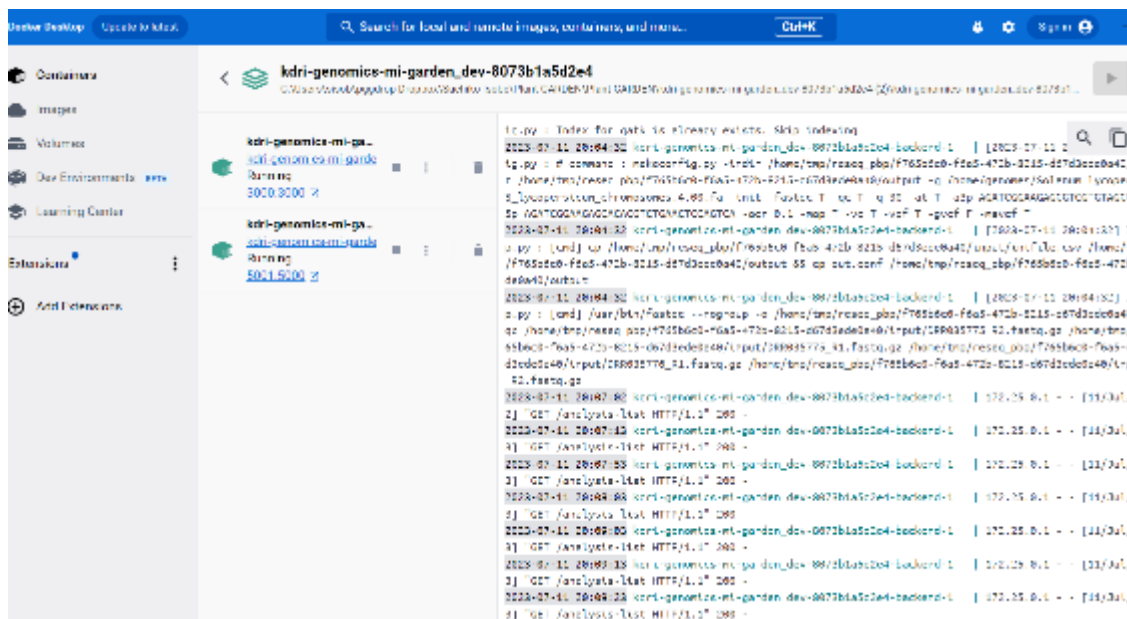
delete all tracks

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	<input type="checkbox"/>

Command prompt

```
C:\Windows\system32
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | gzip: /home/...
osomes.4.00.fa: unknown suffix -- ignored
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | [2023-07-11 20:04:32]
already exists. Skip indexing
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | [2023-07-11 20:04:32]
already exists. Skip indexing
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | [2023-07-11 20:04:32]
already exists. Skip indexing
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | [2023-07-11 20:04:32]
py -indir /home/tmp/reseq_pbp/f765b6c8-f6a5-472b-8215-d67d3ede8a48/
8215-d67d3ede8a48/output -g /home/genomes/Solanum_lycopersicum-SL4.0
-qc T -q 30 -at T -a3p AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT -a5p AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT
cf T -gvcf F -msvcf T
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | [2023-07-11 20:04:32]
_pbp/f765b6c8-f6a5-472b-8215-d67d3ede8a48/input/inifile.csv /home/...
put && cp out.conf /home/tmp/reseq_pbp/f765b6c8-f6a5-472b-8215-d67d3ede8a48/
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | [2023-07-11 20:04:32]
nogroup -o /home/tmp/reseq_pbp/f765b6c8-f6a5-472b-8215-d67d3ede8a48/
8215-d67d3ede8a48/input/DRR835775_R2.fastq.gz /home/tmp/reseq_pbp/
R1.fastq.gz /home/tmp/reseq_pbp/f765b6c8-f6a5-472b-8215-d67d3ede8a48/
b6c8-f6a5-472b-8215-d67d3ede8a48/input/DRR835775_R2.fastq.gz
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | 172.25.0.1 -
* 200 -
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | 172.25.0.1 -
* 200 -
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | 172.25.0.1 -
* 200 -
kndri-genomics-mi-garden_dev-8073b1a5d2e4-backend-1 | 172.25.0.1 -
* 200 -
```

Docker desktop



The image shows a composite of three parts: the main website interface, a navigation sidebar, and a user interface for analysis histories.

Plant GARDEN Main Page: The top section features the logo "Plant GARDEN" with a green DNA helix icon. Below it, a description reads: "Plant GARDEN (Genome And Resource Database Entry) is a portal site that curates genome and marker information of various plant species." There are links for "How To" and "About this site". A search bar contains the text "example: Solanum lycopersicum kinase" and a "Search" button. Below the search bar are several categories of search options:

- Search by Species:** Wild chrysanthemum (seticuspe), Grapevine, Japanese trefoil, Thale cress, Japanese radish, Strawberry, Peanut, Soybean, Tomato.
- Search by Others:** Genes, Sequences, RDF, Data List, Markers, Trait-Related Loci.
- Let's Analyze!!:** MI-GARDEN, GARDEN Cloud (circled in red).

Navigation Sidebar (ANCAT): A vertical purple sidebar on the right contains the following menu items: Dashboard, Sales Campaign, Open Analysis, User's Analysis, User Profile, GARDEN Cloud (circled in red), FAQ, Contact, and Community Hub.

Analysis Histories UI: A white panel on the right titled "Analysis Histories" with the subtitle "実行した解析が表示されます". It includes a refresh icon and a dropdown menu set to "ALL". Below this is a table header with columns for "receipt id" and "analysis name".

URL: A red arrow points from the "GARDEN Cloud" icon in the sidebar to the URL <https://ancatbeta.anplat.co.jp/>.

ANPLAT Logo: The ANPLAT logo is visible in the bottom right corner.



GARDEN Cloud 利用規約

本解析手法は、株式会社アンプラット（以下「アンプラット社」という。）が運営する生命科学データ解析プラットフォームサービス「ANCAT MarketPlace」（以下「本リーpis」という。）を使用して提供される、公益財団法人かずさDNA研究所が権利を有する解析手法です。公益財団法人かずさDNA研究所（以下「当所」という。）は、本解析手法の利用を希望するユーザーに対し、以下の条件で利用を許諾します。ユーザーは、本ライセンスに同意したうえで、本解析手法の利用を申し込むものとします。

- 第1条（解析手法の利用） ユーザーは、本解析手法を次の各号に定める範囲において利用することができます。
 - (1) 解析手法の名称、目的、内容その他当所が指定する項目の閲覧
 - (2) 次条に定める解析実行
- 第2条（解析実行）

Disagree Agree



A workflow for SNP detection using cutadapt for quality control, bwa for mapping and gatk for SNP detection. Use a reference genome sequences registered in Plant GARDEN as references.

クオリティコントロールにcutadapt、mappingにbwa、変異検出にgatkを用いてSNP検出を行うワークフロー。Plant GARDENに登録されているゲノムをリファレンスとして変異解析が可能。

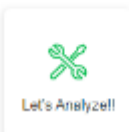
¥5500~



A tool to merge multiple gVCF files created for genome sequences registered in Plant GARDEN. Multiple VCF files created on an identical genome sequence can also be merged.

Plant GARDENに登録されているゲノム配列に対して作成した複数のgVCFファイルを1つに統合する。同一のゲノム配列上に対して作成された複数のVCFファイルの統合も行うことができる。

¥1100~



Link to download page for analysis tool used in local PC such as Mi-GARDEN

Plant GARDENで配布されているLocalで解析を行うツール群のダウンロードページ。Mi-GARDENなどのダウンロードが可能。

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.