PanGraphRNA User Manual

(version 1.0)

- PanGraphRNA is an efficient, flexible and web-based Galaxy platform that can be easily used to construct graph pangenomes from genetic variations at individual, subpopulation, and population levels. It can assist researchers to select appropriate graph pangenomes using various performance metrics for both real and simulation experiments.
- Currently, PanGraphRNA is composed of four functional modules: **Graph Pangenome Preparation Module, Construction Module, Evaluation Module, and Application Moudule**.
- PanGraphRNA was powered with an advanced packaging technology, which enables compatibility and portability.
- PanGraphRNA project is hosted on https://github.com/cma2015/PanGraphRNA
- PanGraphRNA docker image is available at https://hub.docker.com/r/malab/pangraphrna

PanGraphRNA installation

- **Step 1**: Docker installation

  i) Docker installation and start (Official installation tutorial)

  For **Windows (Only available for Windows 10 Prefessional and Enterprise version):**

  - Download [Docker](https://download.docker.com/win/stable/Docker for Windows Installer.exe) for windows;
  - Double click the EXE file to open it;
  - Follow the wizard instruction and complete installation;
  - Search docker, select **Docker for Windows** in the search results and click it.

  For **Mac OS X (Test on macOS Sierra version 10.12.6 and macOS High Sierra version 10.13.3):**

  - Download Docker for Mac OS;

  - Double click the DMG file to open it;

  - Drag the docker into Applications and complete installation;

- Start docker from Launchpad by click it.

For **Ubuntu (Test on Ubuntu 18.04 LTS):**

- Go to [Docker](#), choose your Ubuntu version, browse to **pool/stable** and choose **amd64, armhf, ppc64el or s390x**. Download the **DEB** file for the Docker version you want to install;

- Install Docker, supposing that the DEB file is download into following path:**"/home/docker-ce~ubuntu_amd64.deb"**

```
$ sudo dpkg -i /home/docker-ce<version-XXX>~ubuntu_amd64.deb
$ sudo apt-get install -f
```

ii) Verify if Docker is installed correctly

Once Docker installation is completed, we can run `hello-world` image to verify if Docker is installed correctly. Open terminal in Mac OS X and Linux operating system and open CMD for Windows operating system, then type the following command:

```
$ docker run hello-world
```

Note: root permission is required for Linux operating system.

- **Step 2**: PanGraphRNA installation from Docker Hub

```
# pull latest PanGraphRNA Docker image from docker hub
$ docker pull malab/pangraphrna
```

- **Step 3**: Launch PanGraphRNA local server

```
$ docker run -it -p 880:8080 malab/pangraphrna bash
$ bash /home/galaxy/run.sh
```

Then, PanGraphRNA local server can be accessed via http://localhost:8080

Tools

search tools

⬆ **Upload Data**

Graph Pangenome Preparation Module

Graph Pangenome Construction Module and Alignment

Graph Pangenome Evaluation Module

Graph Pangenome Application Module

Additional tools

Built-in Converters

WORKFLOWS

All workflows

Welcome to PanGraphRNA
An Efficient and Flexible Bioinformatics Platform for Graph Pangenome-based RNA-seq Data Analysis

About

- PanGraphRNA is an efficient, flexible and web-based Galaxy platform that can be easily used to construct graph pangenomes from genetic variations at individual, subpopulation, and population levels. It can assist researchers to select appropriate graph pangenomes using various performance metrics for both real and simulation experiments.

- Currently, PanGraphRNA is composed of four functional modules: Graph Pangenome Preparation Module, Construction Module, Evaluation Module, and Application Moudule.

- PanGraphRNA was powered with an advanced packaging technology, which enables compatibility and portability.

- PanGraphRNA project is hosted on https://github.com/cma2015/PanGraphRNA.

- PanGraphRNA docker image is available at https://hub.docker.com/r/malab/pangraphrna.

History

search datasets

Unnamed history

226 MB   ♥ 0   🗑 3   ⟳

ⓘ This history is empty.
You can load your own data or get data from an external source.