Bioinformatics Docker Images Project

Phenotypic Evolution Group – IBMC/i3S



https://pegi3s.github.io/dockerfiles/

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Motivation

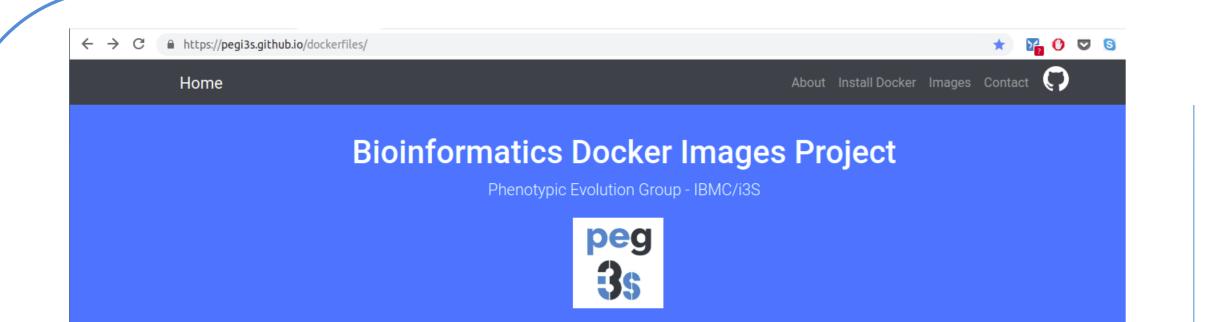
Nowadays bioinformatics is one of the most important areas in modern biology. Nevertheless, the use of scientific software is not always easy for researchers without an informatics background. This is mainly due to:

Docker Images Advantages

1) Easy to use since it only requires the installation of Docker;

- 1) Availability of the software for Linux operating systems only, since most researchers working on the life sciences use Windows or Macintosh operating systems;
- 2) The **complexity of the installation**, since scientific software often have many dependencies and some may be non-trivial to install;
- 3) The lack of knowledge regarding alternatives that mitigate the previous drawbacks, and how to use them.

Website https://pegi3s.github.io/dockerfiles/



2) Portable between computers and immutable;

3) Can be deposited in public databases such as **Docker Hub**;

4) Can be downloaded when needed and erased when no longer needed;

5) Presents a user friendly interface – **Portainer.io** – that allows users to build and manage Docker environments easily;

6) The installed scientific software is ready to run;



Feel free to contact us: pegi3sdocker@gmail.com

7) Software invoked through the command line can be directly run in **Linux** and Windows platforms;

8) Docker images can be used in pipelines;

9) All Docker images can be run using a VirtualBox Ubuntu image with Docker previously installed.

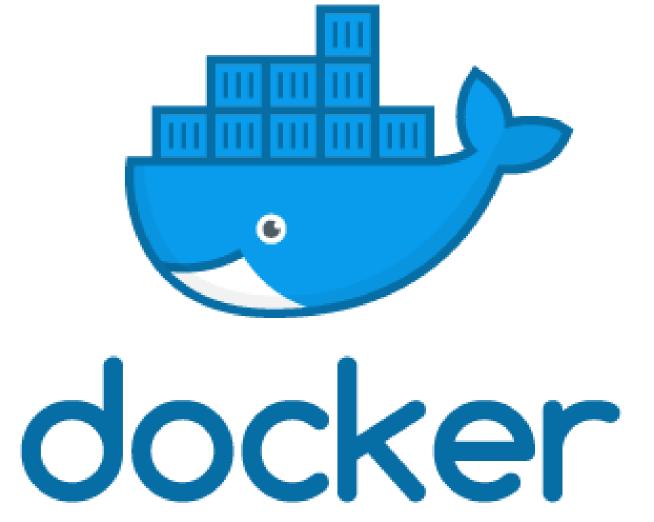
ubunt



Images

List of available images:

- abyss [doc] de novo sequence assembler
- adops [doc] Philogenetics and detection of positively selected sites
- aftergc [doc] Sequence read quality assessment
- alter [doc] File conversion
- autoaugustus [doc] Gene annotation
- bdbm [doc] Sequence database manager



1098 pulls

About this page

This website contains information about the Docker images maintained by the Phenotypic Evolution Group (pegi3s) at the Instituto de Biologia Molecular e Celular (IBMC) / Instituto de Investigação e Inovação em Saúde da Universidade do Porto (i3S). All images are available through our Docker Hub repository.

In addition, this repository also contains tutorials to serve as guidance on the usage of existing Docker images (e.g. Trinity for RNA-Seq).

Windows

Docker first.

Linux

Install Docker

information can be found here).

To install Docker in Windows, please download the official installer Docker for Windows Installer.exe. If your system does not meet the requirements to run Docker for Windows (available here), please install Docker Toolbox instead.

In order to use the Docker images maintained by pegi3s, users need to install

To install Docker in Linux, please follow the steps provided here (additional

VirtualBox

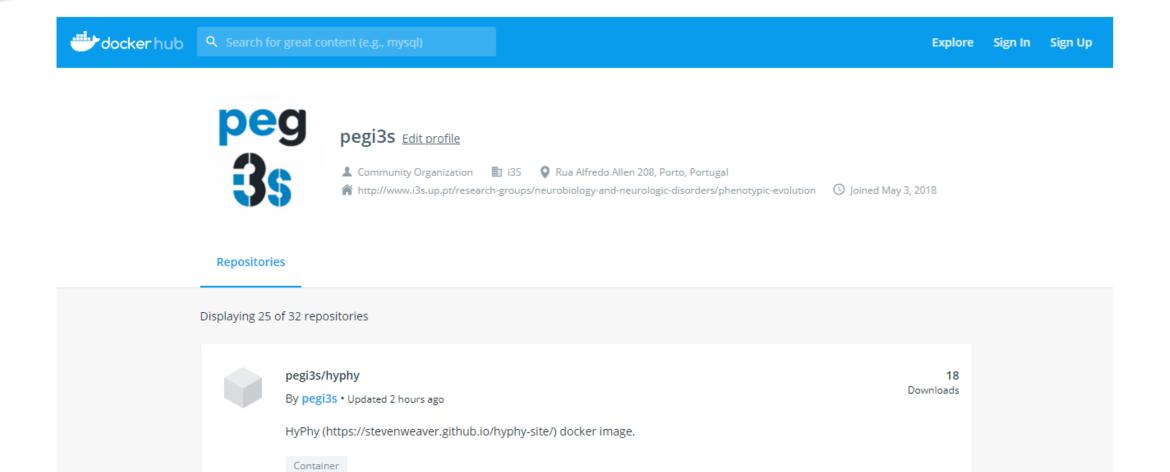
As an alternative and for practical purposes, we provide an Ubuntu 18.04 LTS (Linux) virtual image with 11.8 GB, with Docker and Portainer already installed. Please note that this virtual image is limited to 100 GB. In order to run it, first download VirtualBox here. After installing VirtualBox, users just need to import the OVA file here provided. To import an existing virtual machine into VirtualBox, please follow the steps described here. The administrator's user and password is pegi3s.

The username and password for Portainer is pegi3sdocker.



- blast [doc] Sequence alignment
- clustalomega [doc] Sequence alignment
- coral [doc] Sequence read correction
- cutadapt [doc] Sequence read trimming
- edena [doc] de novo sequence assembler
- emboss [doc] General utilities
- fastqc [doc] Sequence read quality assessment
- fasttree [doc] Philogenetics inferences
- flash [doc] Sequence read overlap
- hyphy [doc] Philogenetics inferences
- mauve [doc] Genome alignment
- mrbayes [doc] Philogenetics inferences
- omegamap [doc] Detection of positively selected sites
- phipack [doc] Recombination tests
- popart [doc] Population genetics software
- raxml [doc] Philogenetics inferences
- sapp [doc] Genomic tools
- seda [doc] Sequence dataset builder

Clear instru	ctions
Clear most to on how to	use!!
	Docker Hub



	pegi3	s/seda	☆		
By pegi3s • Updated 2 months ago					
	SEDA (www Container	DA (www.sing-group.org/seda) docker image.		nage.	Docker Pull Command
					docker pull pegi3s/seda
Overview	Tags	Dockerfile	Builds	3	Pulls 45
Using the SEDA image in Linux					
Please note that the following instructions must be executed in Linux environments only.					
You should adapt and run the following command: docker runrm -ti -e USERID=\$UID -e USER=\$USER -e					
DISPLAY=\$DISPLAY -v /var/db:/var/db:Z -v /tmp/.X11-unix:/tmp/.X11-unix -v					
SHOME/.Xauthority:/home/developer/.Xauthority -v "/your/data/dir:/data" pegi3s/seda					
If the above command fails, try running xhost + first. In this command, you should replace:					

SEDA Docker Image (GUI)

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		 /your/data/dir to point to the directory that you want to have available at SEDA.
pegi3s/mrbayes By pegi3s • Updated 12 hours ago	39 Downloads	Running this command opens the SEDA Graphical User Interface. Your data directory will be available through the file browser at /data.

In memory processing Output directory: /	
Process selected files Process clipboard content	

Hyphy Docker Image (Command Line Ubuntu 16.04 LTS)	 We provide Docker images for more than 30 scientific softwares, commonly used in genomics, transcriptomics, sequence analysis, and philogenetics, and new images are constantly being added; 	INSTITUTO DE INVESTIGAÇÃO E INOVAÇÃO EM SAÚDE UNIVERSIDADE
 (1) Selection Analyses (2) Evolutionary Hypothesis Testing (3) Relative evolutionary rate inference (4) Coevolutionary analysis (5) Basic Analyses (6) Codon Selection Analyses (7) Compartmentalization (8) Data File Tools (9) Miscellaneous (10) Model Comparison (11) Kernel Analysis Tools (12) Molecular Clock (13) Phylogeny Reconstruction 	 Clear instructions on how to use the images and when appropriate providing test cases. Links to the scientific software developer's manuals; We provide a VirtualBox Ubuntu image with Docker installed for those users not familiar with Linux operating systems; 	DO PORTO Rua Alfredo Allen, 208 4200-135 Porto Portugal
<pre>(13) Phytogeny Reconstruction (14) Positive Selection (15) Recombination (16) Selection/Recombination (17) Relative Rate (18) Relative Ratio (19) Substitution Rates</pre>	 <u>Main difference to BioContainers</u>: detailed information that is given allowing researchers without a background in informatics to easily use these Docker images; 	+351 220 408 800
Please select type of analyses you want to list (or press ENTER to process custom batch file):1	 More than 1K Docker images already downloaded! 	www.i3s.up.pt

