Rstudio on GitPod

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Introduction: Running a Docker Containerized RStudio RNA-seq Experiment

In recent years, Docker has emerged as a powerful tool for creating lightweight, portable, and reproducible software environments. Docker containers encapsulate applications and their dependencies, enabling seamless deployment across different computing platforms. Leveraging Docker containers for bioinformatics analyses, such as RNA-seq experiments, offers numerous advantages, including simplified software installation, environment consistency, and scalability.

Why Docker for Bioinformatics?

Traditional bioinformatics analyses often require complex software installations and dependencies management, posing challenges in reproducibility and scalability. Docker addresses these issues by providing a standardized environment where software packages and dependencies are encapsulated within isolated containers. This ensures that analyses run consistently across different computing environments, regardless of underlying system configurations.

Running a Docker Containerized RStudio RNA-seq Experiment

Build image

Build Image:

```
docker build --progress=plain -f
rocker/Dockerfile_tidyverse_verse_dockering --tag rocker_verse_rna-seq .
```

Explanation:

docker build: This command is used to build a Docker image from a Dockerfile.

--progress=plain: This option specifies the format for the progress output during the build process. Setting it to plain ensures that only plain text progress is displayed, which can be helpful for scripting or automation.

-f rocker/Dockerfile_tidyverse_verse_dockering: This option specifies the path to the Dockerfile to use for building the image. In this case, it points to a Dockerfile named Dockerfile_tidyverse_verse_dockering located in the rocker/ directory.

--tag rocker_verse_rna-seq: This option assigns a tag to the built image, allowing it to be easily referenced and identified. Here, the tag rocker_verse_rna-seq is assigned to the image.

Run Image:

```
docker run --rm -ti -e PASSWORD=password -p 127.0.0.1:8787:8787 -v
$(pwd):/home/rstudio -it rocker_verse_rna-seq
```

Explanation:

docker run: This command is used to run a Docker container based on a specified image.

--rm: This option specifies that the container should be removed automatically after it exits. This helps to clean up resources and avoid cluttering the system with unused containers.

-ti: These options allocate a pseudo-TTY and keep STDIN open even if not attached, allowing interactive terminal access to the container.

-e PASSWORD=password: This option sets the environment variable PASSWORD inside the container to the value password. This is used to set the password for accessing RStudio within the container.

-p 127.0.0.1:8787:8787: This option maps port 8787 on the host machine to port 8787 inside the container. This enables access to RStudio Server running within the container via a web browser on http://localhost:8787.

-v $(pwd):/home/rstudio: This option mounts the current working directory (pwd) on the host machine to the /home/rstudio directory inside the container. This allows files and data from the host to be accessed and manipulated within the container.

-it: These options allocate an interactive terminal session with the container.

rocker_verse_rna-seq: This is the name of the Docker image to run as a container. It refers to the image built in the previous step.

Launch Rstudio

This URL corresponds to the localhost (or loopback) address on Gitpod, and port 8787 is the port to which RStudio Server is mapped inside the Docker container. Now go to VSC tab port and click on the network http 8787 port and a new web browser will open with Rstudio.

Logging in to RStudio:

Once you access the URL localhost:8787 or 127.0.0.1:8787, you will be prompted with the RStudio login page. Enter the username root in the Username field. Enter the password that you previously set during the Docker container setup. If you followed the previous example, the password is password.

Setting Home Directory in RStudio and open Practical

After logging into RStudio, you should select open File and set the home directory to a specific path by following these steps. Locate and click on the three dots (...) icon in the Files pane of RStudio. This icon is

typically located at the top-right corner of the Files pane. A dialog box will pop up, prompting you to specify the directory path. Enter `/home/rstudio/` in the input field. Once you have entered the path, click on the desired Rmarkdown.