Docker image build

Objective:

This purpose of this task is for the applicant to modify an existing Dockerfile to add additional software to the image, then build the docker image and run a container from that image. You will need a system with a working docker installation to perform this task.

Input Data:

A Dockerfile

Process:

Modify the Dockerfile per the instructions in the task(s) below. Build a docker image. Run an interactive container using that image. Run the command(s) indicated.

Output:

The modified Dockerfile should build an image successfully, and you should be able to run a container using the docker image. Please provide:

1. The modified Dockerfile
2. The build command for the task(s)
3. The run command for an interactive container for the task(s). There is no need to mount any local files or docker volumes, or use any other docker run options

Task 1:

Modify the provided Dockerfile to include an installation of bedtools 2.27.1. The source files for this software may be found at:
https://github.com/arq5x/bedtools2/releases/download/v2.27.1/bedtools-2.27.1.tar.gz

- Building the provided Dockerfile to an image and running a container produces the following output when attempting to run bedtools:

```
root@082e351b259b:/# bedtools
bash: bedtools: command not found
```

- After you modify the Dockerfile, build the image, and run a container, the output should be as follows:

```
root@9374573b5798:/# bedtools | head -4
bedtools is a powerful toolset for genome arithmetic.

Version:   v2.27.1
```

About: developed in the `quinlanlab.org` and by many contributors worldwide.

Dockerfile is attached:

Solution: found commands on net and made changes.

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1. Addition to the Dockerfile:
    ```
    RUN cd /tmp && \
        wget https://github.com/arq5x/bedtools2/releases/download/v2.29.1/bedtools-2.29.1.tar.gz && \
        tar -zxvf bedtools-2.29.1.tar.gz && \
        cd bedtools2 && \
        make && \
        cp ./bin/* /usr/local/bin && \
        rm -rf /tmp/{bedtools2,bedtools-2.29.1.tar.gz}
    ```

2. Commands:

    ```
    To build docker image

    sudo docker build -t rna-preprocessing .

    to test the setup

    sudo docker run -it rna-preprocessing:latest

    this takes the user into docker
    ```

Reference: https://docs.docker.com/compose/gettingstarted/

```
inf-container
(base) sunee@sunee-System-Product-Name:~/Downloads/Docker/Task_D
Unable to find image '6db2e9d6fdf0:latest' locally
docker: Error response from daemon: pull access denied for 6db2e
See 'docker run --help'.
(base) sunee@sunee-System-Product-Name:~/Downloads/Docker/Task_D
[sudo] password for sunee:
sudo: run: command not found
(base) sunee@sunee-System-Product-Name:~/Downloads/Docker/Task_D
root@1a5be47161c2:/# bedtools -h
bedtools is a powerful toolset for genome arithmetic.

Version:    v2.29.1
About:      developed in the quinlanlab.org and by many contribu
Docs:       http://bedtools.readthedocs.io/
Code:       https://github.com/arq5x/bedtools2
Mail:       https://groups.google.com/forum/#!forum/bedtools-dis

Usage:      bedtools <subcommand> [options]

The bedtools sub-commands include:

[ Genome arithmetic ]
    intersect      Find overlapping intervals in various ways.
    window         Find overlapping intervals within a window an
```

[Miscellaneous tools]
    overlap   Computes the amount of overlap from two interval
    igv   Create an IGV snapshot batch script.
    links   Create a HTML page of links to UCSC locations.
    makewindows   Make interval "windows" across a genome.
    groupby   Group by common cols. & summarize oth. cols. (~
    expand   Replicate lines based on lists of values in colu
    split   Split a file into multiple files with equal reco
    summary   Statistical summary of intervals in a file.

[General help]
    --help   Print this help menu.
    --version   What version of bedtools are you using?.
    --contact   Feature requests, bugs, mailing lists, etc.

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