**Docker image modification Task**

**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 is supplied in the same shared Box folder as this document.

**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.