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kvdlab/puma ☆0

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Papillomavirus genome annotation tool.

IMAGE

Pulls 139

Overview Tags

PuMA 1.2.1 (7/28/2020)

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How to use the Docker app

Be sure you have Docker installed on your machine. Do the following to pull the image locally:

```
docker pull kvdlab/puma:1.2.1
```

Now you should be able to run the image and see the following output:

```
$ docker run --rm -it kvdlab/puma:1.2.1
usage: run_puma.py [-h] -i FILE [-f FORMAT] [-d DIR] [-o DIR] [-e FLOAT]
                   [-m NUM] [-D STR] [-L FILE]
run_puma.py: error: the following arguments are required: -i/--input
```

To run Puma on your data, you will need to mount your local input and output directories. For instance, from within this "docker" directory, we can run the program like so:

```
$ docker run --rm \
    -v `pwd`/../data_dir:/data \           <1>
    -v `pwd`/../input_and_output:/in_out \ <2>
    kvdlab/puma:1.2.1 \                    <3>
    run_puma.py -i /in_out/BPV2_new.fa -o /in_out/puma_out -d /data <4>
```

1. The "data_dir" dir will be mounted as "/data"
2. The "input_and_output" dir will be mounted as "/in_out"
3. This is the tag of the Docker image to run
4. This is the command to execute Puma with the input and output arguments

When running PuMA through Docker, the output argument needs to be specified ('-o'). In the above example the "input_and_output" folder represents where the input file and the "puma_out" directory are. The output directory is "puma_out" since part of the command is "-o /in_out/puma_out".

Formatting Input FASTA File

```
>Short name|Full Name
Sequence
```

Short name is the abbreviation or accession number you want for output files (e.g. HPV16)

Full name is what will be printed to the screen (e.g. Human papillomavirus 16)

For a multi genome file, follow the same naming convention as above.

Docker Pull Command

```
docker pull kvdlab/puma
```

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