README for Using the Singularity Container for CPGView

Last updated: 2022/08/17

Dear Users:

Thank you for your interests in using CPGView. We provide a singularity container for CPGVIew. The details for using the container can be found below.

Step 1. install conda;
Step 2: install singularity;
Step 3: download CPGView container;
Step 4: download the test data;
Step 5: run the container;
Step 6: check the result

Detailed instructions are provided below:
      "$" indicates the command lines

####**Step 1. install conda**
The detailed instructions can be found from here:
https://engineeringfordatascience.com/posts/install_miniconda_from_the_command_line/

The instruction is reproduced below.
```
$ mkdir -p ~/miniconda3
$ wget
https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_64.sh -O ~/miniconda3/miniconda.sh
$ bash ~/miniconda3/miniconda.sh -b -u -p ~/miniconda3
$ rm -rf ~/miniconda3/miniconda.sh
$ ~/miniconda3/bin/conda init bash
$ ~/miniconda3/bin/conda init zsh
```

####**Step 2. install singularity with conda**
The detailed instructions can be found from here:
https://anaconda.org/conda-forge/singularity
```
$ conda create -n singularity
$ conda activate singularity
$ conda install -c conda-forge singularity
```

####**Step 3. find and download the CPGView**
```
$ singularity search cpgview
```

```
$ singularity pull library://cliu/default/cpgview
$ ls
```

Step 4. Download the test data

```
$ wget http://47.96.249.172:16085/tmp/sample_files/sami.gb
```

Step 5. Run the CPGView pipeline through the container

```
### use NCBI accession number
$ singularity exec cpgview_latest runCPGView 100 /tmp/dir_100
gb:NC_034787.1

### use genbank file
singularity exec cpgview_latest runCPGView 1007 /tmp/d1007 sami.gb
```

Step 6. Check the analysis results

The output file is /tmp/dir_100.

Three annotation results could be found in the result file.

Questioins and Comments:

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