Report:

To run CellProfiler on VM through command line you have to run the following commands:

1. sudo apt-get update

2. sudo apt-get install -y git python-h5py python-zmq python-matplotlib cython openjdk-7-jdk python-wxgtk2.8 python-scipy python-mysqldb python-vigra --fix-missing

3. export JAVA_HOME=/usr/lib/jvm/java-7-openjdk-amd64

4. export LD_LIBRARY_PATH=/usr/lib/jvm/java-7-openjdk-amd64/jre/lib/amd64/server:/usr/lib/jvm/java-7-openjdk-amd64:/usr/lib/jvm/java-7-openjdk-amd64/include

5. git clone https://github.com/CellProfiler/CellProfiler.git

6. cd CellProfiler/

7. git checkout 2.1.1

8. python CellProfiler.py

Then you have to install the following libraries:

➔ sudo apt-get install python-keystoneclient

➔ sudo apt-get install python-pip

➔ sudo pip install Flask

➔ sudo apt-get install rabbitmq-server

➔ sudo pip install python-swiftclient

➔ sudo pip install celery

Then we have to start a rabbitmq-server (check if there are already some running server's then do kill them)

➔ ps aux | grep erl (for killing the already running rabbitmq server)

    To start the rabbitmq server:
➔ sudo rabbitmq-server

Start a celery worker in a new windows:

➔ celery –loglevel=INFO worker -A celery_tasks (name of the celery file)

Note: Do sourcing of your smog cloud document for every new terminal window you create.

We pasted the **Export** commands inside our **nano .profile**, by running:

$ nano .profile

 And then used **source .profile** for the current window.

To check to see if it works: echo $JAVA_HOME