Instructions to install phenomics workflow on a new computer

Installation of *JupyterLab*

Note: If you are viewing these instructions in *JupyterLab*, this is already complete.

1. Install *Anaconda*
2. Install *JupyterLab* by the command:
   ```
   conda install -c conda-forge jupyterlab<\code>
   ```

3. Install the bash kernel for *JupyterLab* by the command:
   ```
   conda install -c conda-forge bash_kernel
   ```

4. Open *JupyterLab* using the command: jupyter lab

Installation of GMOdetector

1. Clone gmodetector_py from Github using the command:
   ```
   git clone https://github.com/naglemi/gmodetector_py.git
   ```

1. Create a conda environment that already has most dependencies using this command:
   conda create -q -n test-environment python=$TRAVIS_PYTHON_VERSION pytest codecov numpy pandas
   matplotlib tzlocal h5py pytables

2. Activate the new conda environment
   source activate test-environment

3. Install additional packages through conda:
   Install *rpy* to allow loading of R packages in Python
   conda install -c conda-forge rpy2
   Install *GNU parallel* to allow parallelization
   conda install -c conda-forge parallel

4. Install *Spectral Python* from the *pypi* repository
   pip install spectral

5. Launch R and install scales from the R console via:
   install.packages('scales', repos = 'http://cran.us.r-project.org')

6. Install gmodetector_py and test dependencies:
   pip install ".[test]"

Installation of segmentation tools

Install all dependencies for deeplab in a new conda environment

```
conda create --name deeplab

conda activate deeplab

conda install -c anaconda scipy

conda install -c conda-forge opencv

conda install -c conda-forge tensorflow=1.14
conda install -c anaconda yaml  # Not needed
pip install pyyaml

conda install -c anaconda pillow
```

Copy or clone the appropriate deeplab repo with pretrained model (not yet all in one place on Github at time of writing; currently in deeplab folder on OSU server steed)

Installation of tools for classifying missing/contaminated explants

Follow instructions on repo https://github.com/Contamination-Classification/DenseNet (https://github.com/Contamination-Classification/DenseNet) and note that tensorflow v1.14 can be used if there is an issue installing v1.13

Installation of image alignment

```
git clone https://github.com/NSF-Image-alignment/ImageAlignment.git
```

```
cd ImageAlignment
```

Create the environment and install dependencies available through pip

```
conda create -n alignment python=3.7
conda activate alignment
pip3 install pillow scikit-image numpy matplotlib easydict opencv-python pandas argparse xlrd
```

Install some additional dependencies through conda

```
 conda install -y -c anaconda xlrd
conda install -y numpy
conda install -y -c conda-forge opencv
conda install -y -c conda-forge easydict
conda install -y scikit-image
conda install -y -c anaconda pandas
```

Installation of GMOlabeler

1. Create and activate a new environment

```
 conda create -n gmolabeler
conda activate gmolabeler
```

1. Install R. Instructions can be found here: https://cloud.r-project.org/ (https://cloud.r-project.org/)
   Alternatively, R may be installed through conda, either by installing R itself alone or by installing R as a dependency for rpy2 as shown below.

```
conda install -c conda-forge rpy2
```

1. Launch the R console and install required R packages from the R console:

```
install.packages("optparse")

install.packages("data.table")

install.packages("stringr")
```

1. Install Python (and R) dependencies

```
# Python dependencies
conda install -y -c anaconda pillow
conda install -y -c anaconda pandas
conda install -c anaconda pytables

# One R dependency installed by conda for randomcoloR R package
conda install -c conda-forge libv8
```

Install R package dependencies from within R

R

```
 install.packages("scales")
install.packages("readxl")
install.packages("ggplot2")
install.packages("randomcoloR")
install.packages("tidyr")
```