# 12-Files

## Unknown Author

August 20, 2013

# 1 Python: File operations

Materials by: John Blischak and other Software Carpentry instructors (Joshua R. Smith, Milad Fatenejad, Katy Huff, Tommy Guy and many more)In this lesson we will cover how to read and write files. Currently, this material is mostly a repeat of what was in Loops.

# 2 Reading from a file

Note: "less" here is an ipython "line magic." It's not part of regular python. It displays the contents of a file.

```
In [1]:  less example.txt
```

```
In [2]:  my_file = open("example.txt")
         for line in my_file:
             print line.strip()
         my_file.close()

         This is line 1.
         This is line 2.
         This is line 3.
         This is line 4.
         This is line 5.
```

# 3 Writing to a file

```
In [3]:  new_file = open("example2.txt", "w")
         dwight = ['bears', 'beets', 'Battlestar Galactica']
         for i in dwight:
             new_file.write(i + '\n')
         new_file.close()
```

```
In [4]:  less example2.txt
```

## 3.1 More genetics examples

The file genos.txt has a column of genotypes. Read in the data and convert the genotypes as above. Hint: You'll need to use the built-in string method strip to remove the new-line characters (See the example of reading in a file above. We will cover string methods in the next section).

```
In [5]:  # Store the genotypes from genos.txt in this list
         genos_from_file = []
```

Check your work:

```
In [6]:  genos_from_file[:15] == [2, 2, 1, 1, 0, 0, 2, 2, 2, 0, 'NA', 1, 0, 0, 2]
```

```
Out [6]:
         False
```