Non_paternity Manual

Setting up environment

Packages this code uses:
- Networkx
- [NumPy](#)
- Argparse
- Pandas

This code can be run on command prompt or terminal. Python and numpy installed. A guide on how to install python can be found [here](#).

Packages can be installed by using pip. Typing "pip install numpy" will start the installation for numpy. The same might be needed for pandas.

```
pip install numpy
```

Download the [repository](#) file and unzip it in the desired file location. Set it as the working directory by changing the directory typing
cd "pathwaytofolder".

```
cd Desktop/myScript/non_paternity
```

Running code with sample data

Some sample data is provided in the repository. In order to run the code we need to provide the family edge list and the file containing the individual's id. We use the flags -f to designate our "test_fam.nx" file with our edge list and the -p flag to set the "test_fam_profile.txt" for our profile ids. The line should look like this

```
python run_non_paternity.py -f test_fam.nx -p test_fam_profile.txt
```

python run_non_paternity.py -f test_fam.nx -p test_fam_profile.txt

This will create a file named "test_fam_non_paternity.nx". This will contain an updated list of parent-child relationships

There some optional parameters we can use as well

Output
-o allows you to name the output file

```
python run_non_paternity.py -f testfam.nx -p test_fam_profile.txt -o fam1
```

python run_non_paternity.py -f test_fam.nx -p test_fam_profile.txt -o fam1

This will create the updated edge list and name the file "fam1.nx"

Probability
-c will alter the chance of a non-paternity for each individual. By default the probability is set to 1%

```
python run_non_paternity.py -f testfam.nx -p test_fam_profile.txt -o fam1 -c .25
```

python run_non_paternity.py -f test_fam.nx -p test_fam_profile.txt -o fam1 -c .25

This will give each individual a 25% chance for a non-paternity event