**How to run analooper on MacOS**

This process has several dependencies; check to ensure the following are installed on your computer: java, python 2.7, pip, numpy, scipy, pandas, biopython

1. Java is required for this process. If you do not have Java, install using homebrew via terminal

Install homebrew if needed:

ruby -e "$(curl –fsSL https://raw.githubusercontent.com/Homebrew/install/master/install)"

Install java if needed:

brew cask install java

1. Install python 2.7 if needed:

brew install python

1. Install pip if needed:

sudo easy\_install pip

1. Install the following dependencies if needed:

pip install numpy

pip install scipy

pip install pandas

pip install bipython

Note: if biopython fails to install due to lack of permissions to python site-packages folder, then:

sudo chown -R $USER /Library/Python/2.7

pip install biopython

**To run analooper:**

Run the script: …/analooper.sh [options] OutputFolder R1read R2read

Optional Arguments  
-b <int> specify the barcode length (default = 14)

-c <int> specify the codon length used during LOOPER (default = 5)

-l <int> specify the length of the sequenced duplex post-sequencing adapter trimming (default = 114)

-s <int> specify spacer length of invariant sequence on barcoding adapter (default = 5)

output folder will contain *fidelity.txt*

column 1: pentanucleotide (5’🡪3’)

column 2: codon (3’🡪5’)

column 3: instances of codon

column 4: instances of misincorporation

columns 5-n: misincorporated pentanucleotides

**Note: Ensure that no directory paths have spaces in their name.**