**INSTALLATION**

1. If needed, please download Python 2.7.5 and install the following packages: *getopt, re, argparse, xlwt, scipy,* and *statsmodels*.
2. Download Bowtie 1.0.1 and the human genome version GRCh38 index to run with the Bowtie aligner. This can all be done from <http://bowtie-bio.sourceforge.net/index.shtml>. Ensure that you download the correct version depending on your operating system.
3. Download the most recent version of the BAIMS pipeline code. Please keep all of the scripts together in the “BAIMS\_Pipeline” directory.
4. In the BAIMS\_Pipeline directory, there is a bash script called “BAIMS\_pipeline.sh”. You will need to open this file in a text editor, such as Sublime, and make the following edits:
   1. Find the variable name “bowtie\_Path” at the top of the script. Above the variable name, you should see the following comment: “#NEED TO COMPLETE THIS WITH THE PATH TO THE FOLDER THAT HOLDS THE BOWTIE-1.0.1 EXECUTABLE; DO NOT INCLUDE "/" FOLLOWING THE NAME OF THE FOLDER”. You need to change “bowtie\_Path” so that it holds the path to the Bowtie 1.0.1 aligner executable. Do not include a backslash (“/”) after the name of the directory that contains the Bowtie aligner executable.
   2. Find the variable name “bowtie\_index\_Path” at the top of the script. Above the variable name, you should see the following comment: “#NEED TO COMPLETE THIS WITH THE PATH TO THE BOWTIE INDEX TO USE FOR ALIGNMENT, AS SPECIFIED IN THE BOWTIE MANUAL”. You need to change “bowtie\_index\_Path” so that it holds the path to the GRCh38 index files for Bowtie and ends with the basename for index files. This is the same path and basename that you must normally provide to the Bowtie aligner to perform any sort of alignment. This path should follow the following structure: “path\_to\_GRCH38\_index\_directory/basename\_for\_index\_files”.
   3. Find the variable name “pipeline\_Path” at the top of the script. Above the variable name, you should see the following comment: “#NEED TO COMPLETE THIS WITH THE PATH TO THE "BAIMS\_Pipeline" FOLDER; DO NOT INCLUDE "/" FOLLOWING THE NAME OF THE FOLDER”. You need to change “pipeline\_Path” so that it holds the path to the directory that contains the scripts for the BAIMS pipeline. Do not include a backslash (“/”) after the name of the directory that contains the scripts for the BAIMS pipeline.
   4. Save and close the “BAIMS\_pipeline.sh” file.
5. Once these steps have been taken, the pipeline should be fully functional and can be run from any directory on your machine.

**USAGE**

1. To run the pipeline, you must execute the “BAIMS\_pipeline.sh” script, as such:
   1. USAGE: *Path\_to\_BAIMS\_pipeline\_directory/BAIMS\_pipeline.sh -c <path\_to\_control\_fastq\_file> -s <path\_to\_selected\_fastq\_file>*
   2. The “-c <path\_to\_control\_fastq\_file>” and “-s <path\_to\_selected\_fastq\_file>” parameters are required even though they use the optional parameters format. This format is used for easy parsing of the parameters.
   3. The “-n <basename\_for\_output\_files>” parameter is optional and can be used to specify a basename for the output files from the BAIMS pipeline.
   4. The “--binSize <integer>” parameter is optional and can be used to specify the bin size used in the BAIMS pipeline.