**INSTALLING AND RUNNING JAVA, FASTQC AND MULTIQC**

There are three (3) tools that you will learn and use for the exercises in this session:

1. **FastQC** will be used to assess the quality of raw reads (fastq files).
2. **MultiQC** will be used for aggregation of multiple fastqc reports into a single report.
3. CGI assembler will be used to assemble raw reads.

The GCI assembler is a web-based tool used for genome assembly and does not need to be installed locally. You can visit CGI assembly webpage by typing clicking the link below or typing it into your web browser: <https://cge.cbs.dtu.dk/services/Assembler/>

The following describes step-by-step process for the installation of FastQC and MultiQC, both of which require Java to be installed. Please follow the instructions below to install these software **before** Day 2 of the course module. If you have any problems with the installation, do not despair; installation is one of the hardest tasks in bioinformatics. Just send a message on the Slack channel and help will be provided as needed.

**HOW TO INSTALL JAVA**

1. Java is freely available for download and installation
2. You need to first determine if you have java installed on your device or not.
3. If you're not sure whether you have java installed then you can test this from a command prompt.
   1. To get a command prompt try:
   2. Windows: Select Start > Run, and type 'cmd' (no quotes) in the box which appears, press OK
   3. MaxOSX: Run Applications > Utilities > Terminal
4. At the command prompt type 'java -version' and press enter. You should see something like:
   1. *java version "1.8.0\_60"*
   2. *Java(TM) SE Runtime Environment (build 1.8.0\_60-b27)*
   3. *Java HotSpot(TM) 64-Bit Server VM (build 25.60-b23, mixed mode)*
5. If you get an error, then you don't have java installed. If the version listed on the first line is less than 1.6 then you might have problems running FastQC. In which case you will have to re-install/upgrade java.

If you have verified that you don’t have java installed on your machine, please follow these steps to install java:

Windows/Linux: Go to <https://java.com/en/download/>

1. Java should automatically detect your OS and whether it is 64-bit or 32-bit
2. Click on the large red button “Agree and Start Free Download”
3. Allow the programme to download completely.
4. If this does not work, - DON'T click the large red button again, but take the following steps
   1. choose the smaller link almost at the bottom of the page "See all java downloads".
   2. Find your operating system and select the appropriate offline installer. If you are using a 64-bit operating system (and nearly everyone is these days), then make sure you select the 64-bit version of the installer.
   3. Once you have downloaded the appropriate java file
   4. Locate the file on your machine (will usually be found in “Downloads” for most machines).
   5. Double click on the java file to open it
   6. A window will appear with two options - “run” “don’t run”, click on “run”
   7. Another window will appear asking if you want this app to make changes to your device, click on “YES”
   8. Another window will appear “welcome to java updated terms”, click on install
   9. Wait for java to finish installation. Once installation is complete, a window will appear saying “you have successfully installed java”, close this window and re-start your device.

OSX: On newer versions of OSX you need to install the Java Development Kit. The normal Java runtime environment IS NOT enough.

1. To get this go to <https://java.com/en/download/>
2. then IGNORE the big red button, and select "See all java downloads",
3. on the next screen select "Looking for the JDK?" from the left hand menu and select the link to "JDK downloads" in the first paragraph.
4. You can then click the "Download" button underneath JDK in the page you are taken to.
5. Once you have java installed (you can verify by typing “java -version” into your terminal or cmd for Mac/Linux and Windows respectively), please go on to install Fastqc
6. You may need to follow the suggestions in Java Help Center <https://www.java.com/en/download/help/index.html> ). Or fastqc documentation page (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/INSTALL.txt>)
7. If you are lucky to be using a 64-bit windows machine, you will find a 64-bit Java on “Software” on the Google Drive that you can install
8. Of course, you can interact with instructors on Gather, Slack or even send a mail.

**HOW TO INSTALL FASTQC (WINDOWS)**

1. Download and install FastQC from <https://www.bioinformatics.babraham.ac.uk/projects/download.html#fastqc>
2. Unzip/Extract the fastqc folder using Winrar, Winzip, or similar programmes.
3. Double-click the extracted folder (it will be in the folder you downloaded the fastqc zip folder).
4. Double-click the sub-folder (FastQC) and double-click “run\_fastqc” file
5. FastQC is now displayed in an interactive graphical mode.

**HOW TO INSTALL FASTQC (LINUX/OSX)**

1. Download and install FastQC Disk Image (.dmg) from <https://www.bioinformatics.babraham.ac.uk/projects/download.html#fastqc>
2. Double-click on the dmg and it will become executable
3. Unzip the fastqc file, and open the folder

***You will FastQC Windows/Linux zip file for Windows/Linux and a Mac DMG image file for Mac on “Software” on the Google Drive that you can install. This should make your installation experience simpler!***

**HOW TO INSTALL MULTIQC**

1. Multiqc was designed to take input from fastqc (fastqc.report) and aggregate mutiples fastqc reports into a single mutiqc report. You will find tutorials and demonstrations here: <https://multiqc.info/>
2. Multiqc documentations (<https://multiqc.info/docs/> ) says that “MultiQ is primarily been designed for Windows. However, it *should* work on Unix systems (Linux, Mac OSX) too. Indeed, automated [continuous integration tests](https://github.com/ewels/MultiQC/actions) run using GitHub Actions to check compatibility (see test config [here](https://github.com/ewels/MultiQC/blob/master/.github/workflows/multiqc_windows.yml)). Note that support for using the base multiqc command was improved in MultiQC version 1.8.”
3. To install MultiQC,
   1. Simply run “pip install multiqc” on the command line.
   2. If you use conda, you can run “conda install -c bioconda multiqc” instead.
   3. For Git, use “git install <https://github.com/ewels/MultiQC.git>”

**HOW TO RUN FASTQC**

1. Open the extracted FastQC sub\_folder and double-click ‘run\_fastqc”
2. This will pop-up an interactive FastQC window (Windows and Linux)
3. For Mac just double-click the DMG image and this will pop-up an interactive
4. You will find examples reports for various sequencing platforms here: <https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>