Seq2C Getting Started Guide

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# Source Location

The Seq2C source code is located at <https://github.com/AstraZeneca-NGS/Seq2CJava>.

To load the project, execute the following command:

git clone --recursive https://github.com/AstraZeneca-NGS/Seq2CJava.git

# Build Instruction

The following prerequisites are necessary to build the Seq2C project:

* JDK1.7 (or higher)
* Internet access

The project uses Gradle (<http://gradle.org/>) and already includes a gradlew script.

To build the project, in the root folder of the project, run the following command:  
./gradlew clean installDist

To build the project as a distribution archive, in the build/distributions folder, run the following command:

./gradlew clean distZip

This command builds the project and creates an archive of the distribution package in the folder.

## Distribution Package Structure

When the build command completes successfully, the build/install/Seq2C folder contains the distribution package.

The distribution package has the following structure:

bin/ - contains the launch scripts

lib/ - has the jar file that contains the compiled project code and the jar files of the third-party libraries that the project uses.

You can move the distribution package (the content of the build/install/Seq2C folder) to any convenient location.

## Third-Party Libraries

Currently, the project uses the following third-party libraries:

* **Commons CLI** (<http://commons.apache.org/proper/commons-cli>, Apache License) – a library for parsing the command line.
* **HTSJDK** (<http://smtools.github.io/htsjdk/>) is an implementation of a unified Java library for accessing common file formats, such as SAM and VCF.
* **Commons Math** (<https://commons.apache.org/proper/commons-math>) - a library of lightweight, self-contained mathematics and statistics components.

# Launch Instruction

The following prerequisites are necessary to launch the program:

* Java 1.7 (or higher)

To launch Seq2C:

* Run the command <distribution package path>/bin/Seq2C or
* Run just Seq2C if <distribution package path>/bin/ is in path

The work of the program is identical to the function of the original Perl script and thus can replace it.

For example, the original launch command (from the ***readme*** file of the perl version) is:

seq2c.sh sample2bam.txt Illumina\_TruSeq\_Exome.bed

The same command in Seq2CJava is as follows:

<distribution package path>/bin/Seq2C sample2bam.txt Illumina\_TruSeq\_Exome.bed cov.txt

The program uses the same parameters as the Perl version. The Java version contains an additional parameter: -i. This parameter manages the number of threads that do the work. If this parameter is missing, then the mode is one-thread. If you add the -i parameter, the number of threads equals to the number of processor cores. The parameter -i threads sets the number of threads explicitly.

For launching the separate parts of code an additional parameter –r is used. For launching the first part of code option –r 1 (analogue to seq2cov.pl script to Perl) is used. For launching the second part of code option –r 2 (analogue to bam2reads.pl, cov2lr.pl and lr2gene.pl scripts in Perl). When Seq2c is launched without option –r all code will run from start to end.