System requirements:

* Windows, Linux or Mac Operating System
* Java Virtual Machine (You can download and install it [here](http://www.java.com/en/download/index.jsp))

How to run the program:

* You can open the program’s Jar file when using Windows and the program will start running
* You can run the program with the following command on Linux operating systems
  + java –jar filename (Replace the filename with the program’s Jar filename)

Project structure:

This program is Project based. Different projects can be made and used in the program. Each project can also have some libraries and some Data Tables. The graphical structure of the program is as below.

Files you will need:

* SAM files which is the output of the Burrow Wheeler Aligner. This file is used to create libraries.
  + This file can be created using the program (only if you are using Linux operating system, for more information see BWA tab in the program)
* Gene annotation files. These files are to create the Data tables.
  + These files can be downloaded from the [NCBI ftp server](ftp://ftp.ncbi.nih.gov/genomes/Bacteria/). (you can use the program to download the files automatically)
  + IMG files downloaded from the [IMG server](http://img.jgi.doe.gov/) can be used in this program.

Brief explanation of the program functionalities:

1. When the program is started, a project needs to be selected in the “Create/Open Projects” windows.
2. After selecting a project, “Sequence Length” and Gene annotation file should be provided for the program (if not already provided). This can be done in the “Main” tab of the program. All other tabs are disabled until both Sequence length and the annotation file is provided.
3. Under “Manage Libraries” tab, a new library can be added to the project. To create a new library a SAM file is needed. (SAM files can be created under “BWA” tab of the program when using Linux operating system)
4. Under “Manage Libraries” tab, you can also plot the distribution of the number of unique insertions per window for a specific library.
5. Under “Manage Data Tables” tab, a new table can be created. This will use the gene annotation file to create a formatted data table for the program.
6. For adding new essentially indices to the data tables, there is a button provided under the “Manage Data Tables” tab. First a particular data table needs to be selected and after clicking on the button, a new window will appear and you can add more data to the selected table.
7. A data table can also be opened in a spreadsheet application using the “Open as spreadsheet” button under the “Manage Data Tabled” tab. After clicking on this button all the functionalities of the program is temporarily disabled until the spreadsheet application is closed and one of the “Replace” or “Cancel” buttons are clicked. If any changes are made to the table using the spreadsheet application, it needs to be saved as a tab delimited file. If the changes need to be applied in the program, the “Replace” button should be clicked. If the changes need to be ignored, the “Cancel” button needs to be clicked.
8. When using the “BWA” tab, the “[bwa](http://bio-bwa.sourceforge.net/)” program can be installed using the program. For this purpose the program will need the root user password. This program can also be installed manually by the user.
9. After installing the bwa program, a SAM file can be created using FNA and FASTQ files.