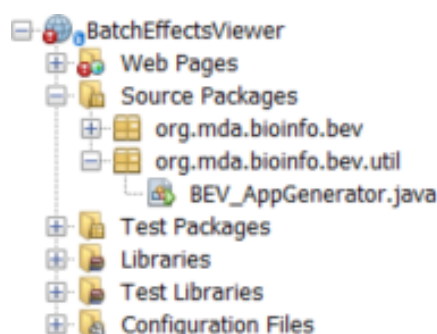


1. Building the Stand-Alone Batch Effects Viewer

The Batch Effects Viewer supports building a stand-alone version of the application to run offline. The stand-alone application contains all the front-end resources (JavaScript, CSS, HTML, and images) gathered into a single HTML file. Instead of receiving data from a web server, the user feeds local data to the application via a zip archive.

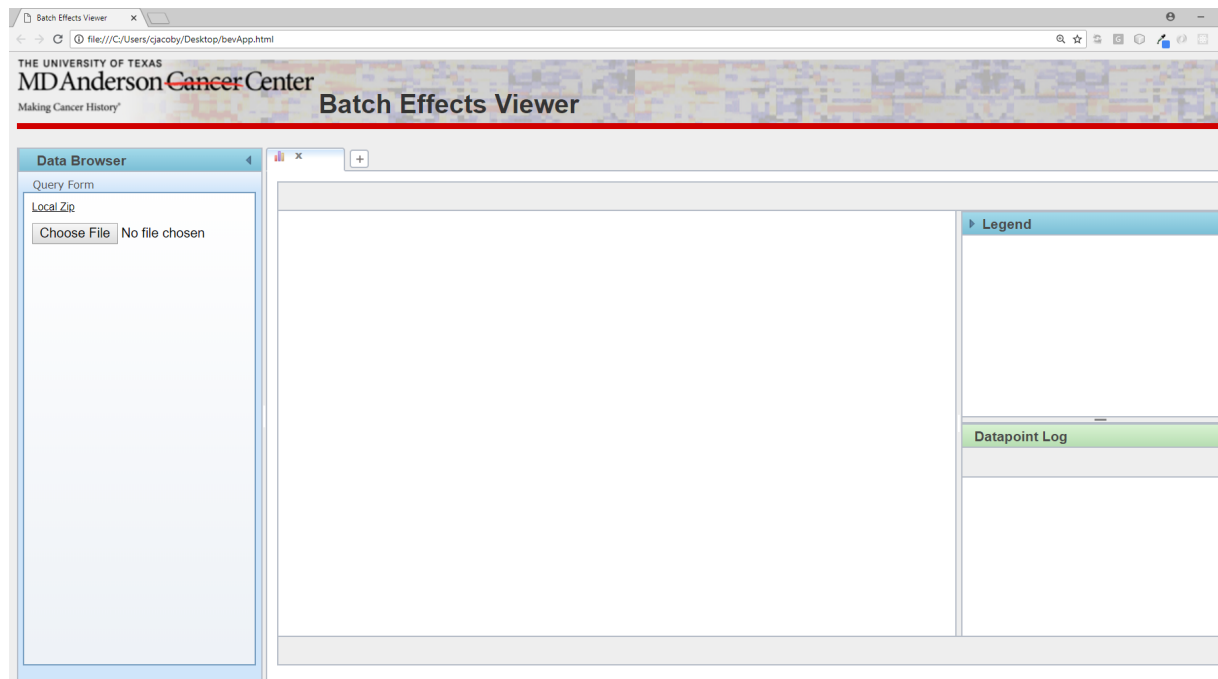


To build a stand-alone version of the application, locate the java utility program `BEV_AppGenerator.java`, found in the package `org.mda.bioinfo.bev.util`.

`BEV_AppGenerator.java` is a command line utility that takes two arguments. The first argument is the path to the Batch Effects Viewer web directory. The second argument is the name of the generated stand-alone HTML file. When successfully ran, the stand-alone HTML file will automatically be created in the Batch Effects Viewer web directory.

2. Using the Stand-Alone Batch Effects Viewer

After generating a stand-alone Batch Effects Viewer HTML file, open the file with any modern internet browser (Internet Explorer not supported). A file prompt will appear asking for a zip archive.



The zip archive will be an output from MD Anderson's MBatch R package. A zip archive can be obtained by configuring and running an MBatch analysis with the Batch Effects Interface application, or by using the MBatch R package directly from the command line. Once a zip archive is obtained, the application will automatically build out all user selection options within the Query Form, and render the default diagram.