**Genome Flow**

**Documentation of observations, changes and comments**

**Files to consider**

* · JmolPanel.java….. StartJmol
* · Jmol-resources.property.= Menu options
* · Token.java – link the menu option to functions
* · ScriptEvaluator

**Starting point**

When you debug/run…. Viewer function is the first stop

**Notable changes made by Tuan (Search for Tuan)**

**1. Adding to the Menu bar**

Changes made in two files

GuiMap.java and org.openscience.jmol.Properties.Jmol-resources.properties

The one in Jmol-resources.properties is a placeholder, actual name to show on the menu bar is made inside GuiMap.java

**2. Placing the Panel interface (\*)**

org.openscience.jmol.app.jmolpanel.JmolPanel.java

You need the JmolPanel.java, interface to accept action event

**3. Link the Menu bar button and** the functions (\*\*)

Link the command and the code right here:

org**/jmol/script/Scriptevaluator.java and org/jmol/script/Token.java**

Set the Token with Token.java

Get the constant variables defined in JmolPanel.java above

ScriptEvaluator, **write code for the algorithms here, model structure and output the result**

**To the output folder specified**

Link the function in scriptEvaluator.java **(switch statement**) and link the button command with Token.java

**scriptEvaluator.java**: **contains the functions , changes to method can be found here**

The JmolPanel code can be linked with the Token.java code

script = "pdb2GSS"; in Jmol

"pdb2GSS", new Token(pdb2gss), in Token.Java

**4. JmolViewer**

The class for the set property. Accept input from the user . Used in JmolPanel.java

Set the variable input accepted from the User in JmolPanel, store in Constant varibles

Also set the script, defined in Token.

**Include the abstract path**

Change Jmolviewer in path, used for 3Dmax Modeller:

Org.jmol.api.Jmolviewer