The file types available for downloading are: **.bel** and **.xgmml** files

* The **.bel files** can be easily opened with any text editor.
* And to visualize the BEL model in Cytoscape you can open the **.xgmml file** with the Cytoscape; please follow these steps:
* Download and install the Cytoscape (works fine with version 2.8.3 onwards)
* Open Cytoscape
* Please go to the file menu and select import Network (multiple file types) option.
* Please browse through the downloaded network file (in .xgmml format).
* Then select the network file and you will see the network in your Cytoscape window.

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* **Advanced plugins provided by Selventa** (developer of OpenBEL language; <http://www.openbel.org/tools> ):
  + To Install the OpenBEL framework and tools please follow this link: <http://wiki.openbel.org/display/OP/Installation+Overview+-+BEL+Framework+and+Related+Tools>
  + If you need to have more options in visualizing the BEL models using KAM navigator, please follow: <https://github.com/openbel/Cytoscape-Plugins/wiki>

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***Note: Custom Namespaces for SNPs:***

*We have used Custom Namespaces to represent SNPs. Before compilation of your .bel files please make sure that you change the path in the definition section to the namespace folder of SNP.belns: file:///[path to BEL compilation]/Namespaces/SNP.belns and also in the index.xml file in Namespace folder.*

*If you have any questions, please feel free to contact: Alpha Tom Kodamullil*

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