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**vscode-bngl**

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This is a VS Code extension for BioNetGen language. It can be found in VS Code marketplace.



## INSTALLATION

There are three ways to use this VS Code extension

- Using the [marketplace](#)
- Cloning the [repository](#) and placing it under your VSCode extensions folder
- Cloning the [repository](#) and using the extension in debug mode

To use the extension in debug mode:

1. Download and install VS Code from <https://code.visualstudio.com>
2. Open VS Code and open a new terminal \* Terminal -> New Terminal, or
  - `CTRL/CMD + ~`
3. In the terminal, run this line: `git clone https://github.com/RuleWorld/BNG_vscode_extension.git``  
to clone the repository in the desired directory
4. File -> Open to open the repository folder (BNG\_vscode\_extension)
5. To run the extension,
  - Run -> Start Debugging, or
  - `F5`

which will open up a new window running the extension 6. Open an existing `.bnl`` file or create a new file with `.bnl`` extension





BioNetGen modelling language is a language for writing rule-based models of biochemical systems, including signal transduction, metabolic, and genetic regulatory networks, see [here](#) for more information.

This VS Code extension is designed to help write BNGL models by adding syntax highlighting and snippet support, do rapid tests of the model as you write with the help of a built-in run button and basic plotting features.

## 2.1 Syntax highlighting and snippets

Once the extension is installed you can create a new file with `.bngl`. This file extension will be automatically detected and you should see a run button at the top right corner of the file if the extension is running correctly. This extension will also do syntax highlighting on files with `.net` extension.

Next you can start writing your model. This VS Code extension supports a large list of snippets that can help you write your model. For a full list, see [here](#), we will update this with a snippet guide in the future.

## 2.2 Using the correct theme

If you notice that there is no highlighting on certain parts of the model or if the colors don't match with the figures presented here, please make sure you have the `dark-bngl` theme activated (see [here](#) to learn how to select color themes). Currently only a dark theme is supported, we will include a light version in the future.

## 2.3 Running a model

Once you finished writing the model, you can try running it. For the run button to work, the default terminal window VS Code opens should have access to [Perl](#), [Python3](#) (preferably [anaconda python](#)) and the [PyBioNetGen library](#). See [here](#) for more instructions on how to install the library. You can test if you have the library correctly installed by [opening a new terminal](#) and running `bionetgen -h`.

Once you press the run button (or use the shortcut `CTRL/CMD+SHIFT+F1`), the extension should create a new folder with the same name as the model. A time stamped folder will also be created and the current model will be copied under there and the extension will use the terminal and the [PyBioNetGen library](#) to run the model. Once the run completes, if the run created a `.gdat` file, it should open automatically.

## 2.4 Plotting results

Once you have some `gdat/cdat/scan` files to look at, you can open one and you should see two new buttons instead of the run button. The white and red button on the right should plot your file into a png with some basic defaults (options to change these options will be provided in future releases).

The blue button on the left should open a new window with an interactive plot (thanks to [plotly.js](#)). You can also use the `CTRL/CMD+SHIFT+F1` shortcut. The plotly window also allows you to save the image as a png as well as a svg file and has [interactive features](#). You can also change the plotting type to markers or lines+markers and use one of the selection tools to sub-select time series. If you select a region on the plot with no data points, every time series in the original dataset will be shown again.

## INDICES AND TABLES

- genindex
- modindex
- search