**Major comments:**

**Reviewer’s comment 1**

I tested to install the software from pip and that worked fine, I also started the GUI. Then I imported some file and tried to simulate it both with RK4 and SSA, but I could not see anything happening. Probably I am using it in the wrong way. You should provide README documentations, tutorials and how-to guides (with pictures) for how to use the software in practice.

**Answer:**

“I could not see anything happening”

We would like to know the details of the problem. You may be trying to run a huge system that takes too long to compute (might have very stiff regions in the trajectory) or maybe there is a runtime error. We would like to know the exact system you were running and OS you are using.

We also suggest to try using BioSANS as a python import. There you can have stuffs printed and see if the run is working. Our GUI support is basically for small to medium size problems.

provide README documentations

tutorials

how-to guides

**Reviewer’s comment 2**

The code quality needs to be improved. I have checked selected files, and there is virtually no doc-strings. You should document the SDK and provide SDK documentation using one of the autodocs systems (e.g. Sphinx). You should also try to comply to the PEP8 standard, this helps library users work with your code. An IDE like PyCharm can help you with that.

**Answer:**

To ensure compliance with PEP8 standards, we manually edit each module with the help of the following python libraries; pylint, pycodestyle, and autopep8. Now, all of the BioSANS modules and functions have doc-strings with pylint score of around 9.51 and no pycodestyle error. The tabulation of each individual score are shown in the following table.

|  |  |  |  |
| --- | --- | --- | --- |
| **Table 1. Pylint scores of python files in BioSANS2020 package** | | | |
| Python Files | Pylint score | Python Files | Pylint score |
| sample\_points.py | 10.00 | mytauleap.py | 9.58 |
| prepare\_canvas.py | 10.00 | analytical\_sol.py | 9.53 |
| scrollable\_text.py | 10.00 | my\_mcem.py | 9.42 |
| new\_file.py | 10.00 | law\_of\_localization.py | 9.42 |
| topology\_view.py | 10.00 | runge\_kutta4.py | 9.41 |
| mglobals.py | 10.00 | param\_slider.py | 9.40 |
| proc\_global.py | 10.00 | plot\_traj.py | 9.40 |
| \_\_main\_\_.py | 10.00 | mystiffcle.py | 9.38 |
| transform\_data.py | 9.87 | process.py | 9.36 |
| processes\_hub.py | 9.85 | euler\_mod.py | 9.31 |
| convtopotosbml.py | 9.84 | BioSANS.py | 9.28 |
| ode\_extract.py | 9.80 | lna\_approx.py | 9.27 |
| draw\_figure.py | 9.76 | tau\_leaping2.py | 9.25 |
| ssl\_calls.py | 9.73 | lna\_function\_of\_time.py | 9.19 |
| lna\_approx2.py | 9.72 | ode\_int.py | 9.19 |
| create\_wxmaxima\_command.py | 9.72 | gillespie\_ssa.py | 9.09 |
| param\_estimate.py | 9.69 | recalculate\_globals.py | 9.04 |
| sbml\_math.py | 9.68 | BioSSL.py | 8.99 |
| process\_sbml.py | 9.63 | propensity.py | 8.87 |
| tau\_leaping.py | 9.62 | RunBioSANS.py | 7.27 |

We created documentation using pydoc and sphinx and published it in GitHub. It can be accessed in <https://efajiculay.github.io/SysBioSoft/>. We also provide a detailed documentation in the supplementary material.

4. The functional tests and comparisons to other software are extensive, this is very good. However, in particular for discrete stochastic simulations (SSA etc) and parameter inference, performance is of utmost importance. You should include some performance tests / comparisons. Be sure to specify the hardware setup for your experiments.

**Minor comments:**

1. StochKit 2 is no longer maintained, a more relevant comparison is to gillespy2 in the StochSS suite of tools.  
2. You should discuss how the software compares to pysb.  
3. The pip bundling is a bit awkward. You should make it so that install is simply "pip install biosans".