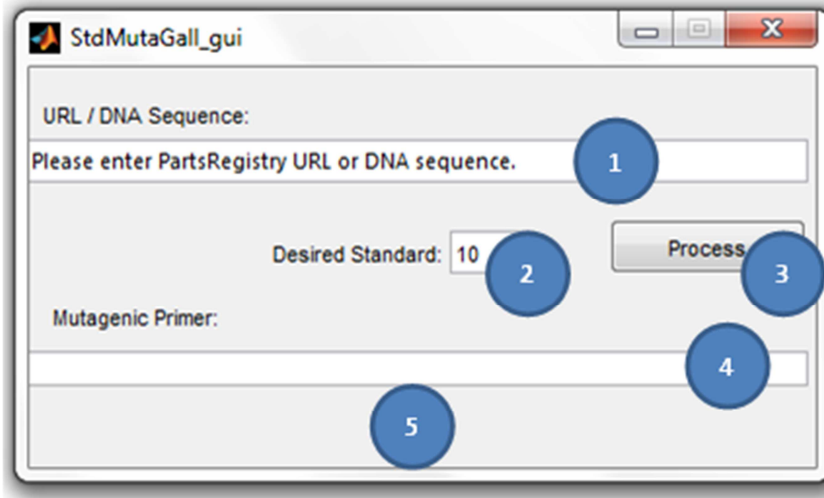


## S<sup>2</sup>MT Tutorial

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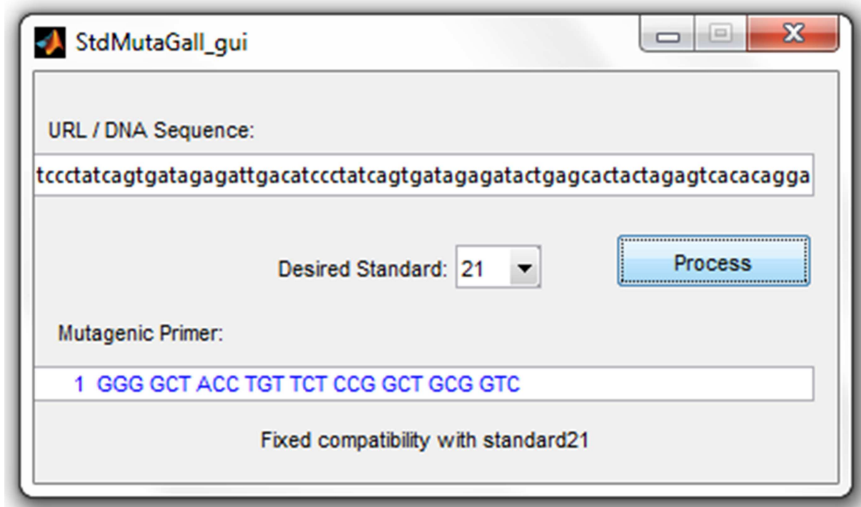


(S<sup>2</sup>MT) GUI parts:

- 1. URL/DNA Sequence textbox: This is the main input.
- 2. Standard selection: We can select the desired standard and the program will check the compatibility with it.
- 3. Process button: After giving the inputs, analyze the sequence.
- 4. Primer textbox: Here we get the output.
- 5. Notification area: The script's feedback.

Some points to take in consideration:

- The primer's starting positions will appear in the MATLAB's console.
- The sequence box can either get an URL from the Parts Registry pointing to a specific Part or a DNA sequence (the textbox is case insensitive).
- Some PartsRegistry Devices does not have it corresponding DNA Sequence on it.
- Be sure that the DNA Sequence you put in the box does not contain any other letter than 'a', 't', 'g' and 'c'.
- Some sequence's incompatibility can't be fixed.



(S<sup>2</sup>MT) successfully fixing the incompatibility of the given DNA sequence with the standard 21.

To download the script go to: [https://github.com/igemsoftware/UTP\\_Software\\_2012](https://github.com/igemsoftware/UTP_Software_2012) and get all three files.

Files descriptions:

- S2MT.m: Does all the sequence analysis process.
- S2MT\_G.m: Code for the graphical interface. (Run this)
- S2MT\_G.fig: Binary file for the graphical interface.

Note that (S<sup>2</sup>MT) relies on the Bioinformatics Toolbox of MATLAB (both supplied by iGEM) to make its computations, so you need the toolbox to be able to run the script.