

Guide HySISAT

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This document assumes that the program is already installed. For installation instructions see <https://github.com/joostzwart/ThesisSARXSAT>. To start the program run gui.py. A graphical user interface will popup.



On the left side parameters can be specified. Starting on the top-left, the order of the input and output can be prescribed in addition to the bound on the error. Checking the checkbox next to split large datasets will tell the program to split the dataset into smaller pieces. When this checkbox is ticked, an input field will appear where the number of pieces can be chosen.

This close-up view of the 'Parameters' panel shows the following settings: 'Order of the output' is 1, 'Order of the input' is 1, and 'Bound on the error' is 0.0010. The 'Split Large Datasets' checkbox is checked, which has revealed an additional input field for 'Number of blocks' set to 3. The 'SARX' radio button is selected.

Next, the user has to decide to identify a SARX model or a PWARX model. When identifying a SARX model the minimum dwell time can be specified.

This close-up view shows the model selection section. The 'SARX' radio button is selected, and the 'Minimum dwell time' is specified as 10. The 'PWARX' option is unselected.

On the other hand for a PWARX model the number of switches can be specified.

☒ PWARX

Maximum number of switches:

The final choice that has to be made is to either identify a dataset, or to generate a new model for identification. When generating a new model the following properties should be defined: The simulation time (length of dataset that is generated), The number of submodels, the bound on the noise, the number of inputs and outputs, the type of input and finally a seed.

☒ Generate random system

Length of the dataset:

Number of models:

Bound on the noise:

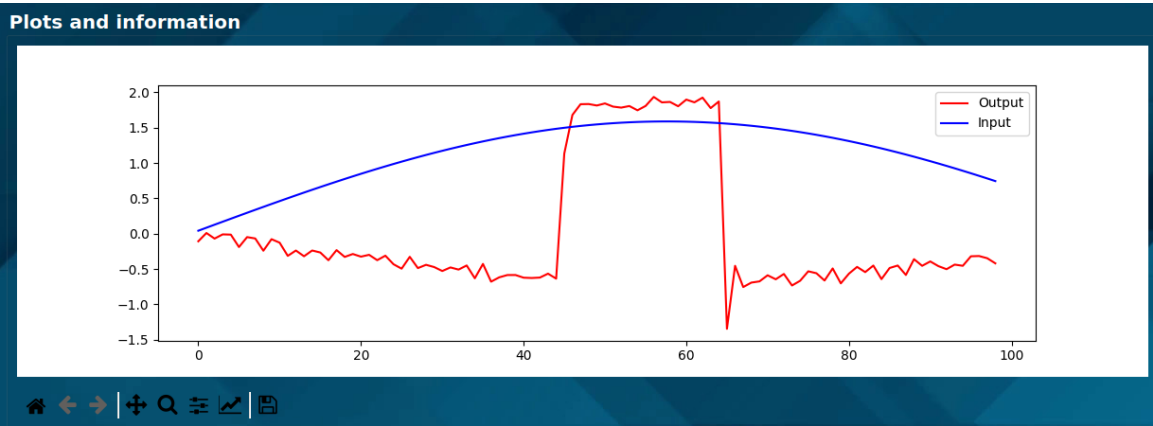
Number of inputs:

Number of outputs:

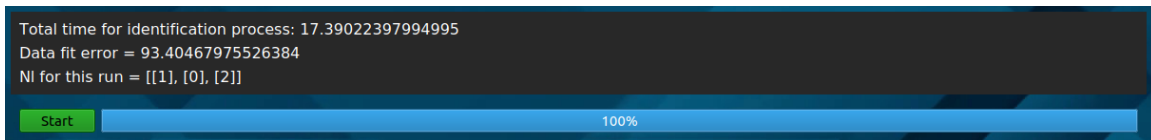
Seed for randomness. 0 for a random seed

Type of input:

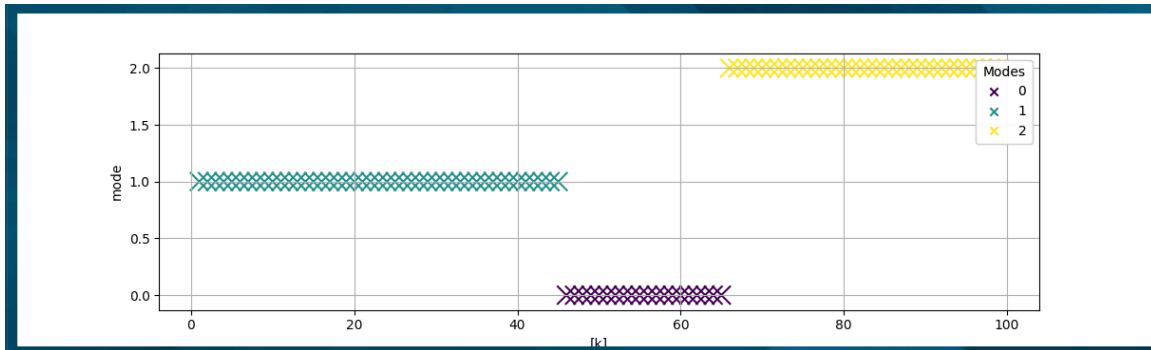
When identification from an existing dataset is conducted, the input and output should both be provided as comma separated textfiles. When both are provided the input and output can be seen on the top right.



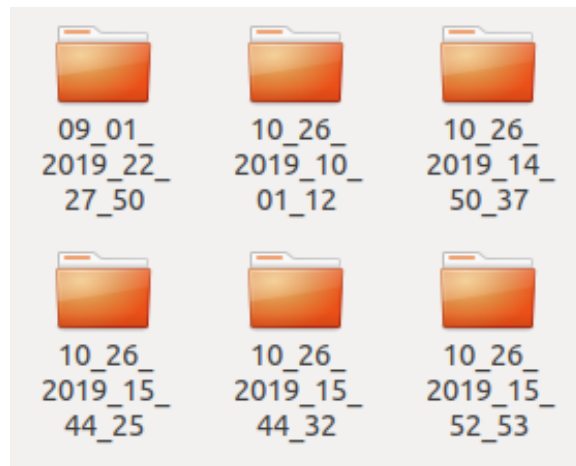
Everything is setup now and identification can start by pressing the green start button. The progress bar in the bottom of the screen will keep track of the progress and the information screen will keep the user informed.



After the identification process is finished, the resulting switching sequence is displayed.



The program can now be closed. After every successful identification procedure a folder will be created containing the results.



This folder contains information about the resulting switching sequence, models, input, output, regressor, and finally the partition of the regressor space in case a PWARX model was identified.

