

iggy

User Guide

version 0.6

Sven Thiele

1 What is iggy?

iggy is a tool for consistency based analysis of influence graphs and observed systems behavior. For many biological systems knowledge bases are available that describe the interaction of its components usually in terms of causal networks and influence graphs. In particular signed influence graphs where edges indicate either positive or negative effect of one node upon another. Building upon a notion of consistency between biochemical/genetic regulations and high-throughput profiles of cell activity **iggy** implements methods to check the consistency of large-scale data sets and provides explanations for inconsistencies. In practice, this can be used to identify unreliable data or to indicate missing reactions. Further, **iggy** addresses the problem of repairing networks and corresponding yet often discrepant measurements in order to re-establish their mutual consistency and predict unobserved variations even under inconsistency

2 Installation

You can install the **iggy** package by running:

```
$ pip install --user iggy
```

On Linux the executable scripts can then be found in `./local/bin`
and on Mac OS the scripts are under `/Users/YOURUSERNAME/Library/Python/2.7/bin`.

3 Usage

Typical usage is:

```
$ iggy.py network.sif observation.obs --show_labelings 10 --show_predictions
```

For more options you can ask for help as follows:

```
$ iggy.py -h
usage: iggy.py [-h] [--no_zero_constraints]
               [--propagate_unambiguous_influences] [--no_founded_constraint]
               [--autoinputs] [--scenfit] [--show_labelings SHOW_LABELINGS]
               [--show_predictions]
               networkfile observationfile

positional arguments:
  networkfile           influence graph in SIF format
  observationfile       observations in bioquali format

optional arguments:
  -h, --help            show this help message and exit
  --no_zero_constraints
                        turn constraints on zero variations OFF, default is ON
  --propagate_unambiguous_influences
                        turn constraints ON that if all predecessor of a node
                        have the same influence this must have an effect,
                        default is ON
  --no_founded_constraint
                        turn constraints OFF that every variation must be
                        explained by an input, default is ON
  --autoinputs          compute possible inputs of the network (nodes with
                        indegree 0)
  --scenfit             compute scenfit of the data, default is mcos
  --show_labelings SHOW_LABELINGS
                        number of labelings to print, default is OFF, 0=all
  --show_predictions    show predictions
```

4 Input

iggy works with two kinds of data. The first is network data representing an influence graph model. The second is the experimental data, representing experimental condition and observed behavior.

4.1 Network data

The network data is represented as a file in simple interaction format SIF as shown below. Lines in the SIF file specify a source node, a relationship type (or edge type), and one target node. For our influence graph models we have the edge types 1 for *increases* and -1 for *decreases*. The first line in the example below therefore states that **depor** has an *activating* (1) influence on **shp2_ph**. The last line states that **shp2_ph** has an *inhibiting* (-1) influence on **plcg**. Duplicate entries are ignored. Multiple edges between the same nodes must have different edge types. Other edge types than 1 and -1 will lead to a parsing error.

```
1 depor_p      1      shp2_ph
2 gab1_mem_p   1      shp2_ph
3 shp2_ph      -1     pi3k
4 gab1_mem_p   1      pi3k
5 pi3k         1      gab1_mem_p
6 shp2_ph      -1     plcg
```

4.2 Experimental data

The experimental data is given in the file format shown below. Nodes which are perturbed in the experimental condition are denoted as **input**. The first line of the example below states that **depor** has been perturbed in the experiment. This means **depor** has been under the control of the experimentalist and its behavior must therefore not be explained. The behavior of a node can be either +, -, 0, **notPlus**, **notMinus**. Line 2 states that an *increase* (+) was observed in **depor**, as it is declared an **input** this behavior has been caused by the experimentalist. Line 3 states that **stat5ab.py** has *decreased* (-) and line 4 states that **ras** has *not changed* (0). Line 5 states that an *uncertain decrease* (**notPlus**) has been observed in **plcg** and line 6 states that an *uncertain increase* (**notMinus**) has been observed in **mtorc1**.

```
1 depor        = input
2 depor        = +
3 stat5ab.py   = -
4 ras          = 0
5 plcg         = notPlus
6 mtorc1       = notMinus
```

5 Output

iggy presents the results of its analysis as text output. The output of **iggy** can be redirected into a file using the > operator. For example to write the results shown below into the file **myfile.txt** type:

```
$ iggy.py network.sif observation.obs --show_labelings 10 --show_predictions > myfile.txt
```

In the following we will dissect the output generated by **iggy**. The first 3 lines of the output state the constraints that have been used to analyze network and data. For our example it is the default setting with the following constraints. For a deeper understanding of these constraints see [2].

```
1 all observed changes must be explained by an predecessor
2 no-change observations must be explained
3 all observed changes must be explained by an input
```

Next follow some statistics on the input data. Line 4-5 tells us that the influence graph model given as **network.sif** consists of 96 nodes, with 116 edges with activating influence and 16 edges with inhibiting influence and 0 edges with Dual or ambiguous influence. Line 9 tells that the experimental data given as **observation.obs** in itself is **consistent**, which means it does not contain contradictory observations. Line 11 tells that the experimental conditions consists of 14 perturbations marked as **input** nodes, that 12 nodes were observed as increased +, 10 nodes *decreased* (-), 20 nodes did *not change* (0), 5 nodes were observed with an *uncertain decrease* (**notPlus**), 4 nodes were observed with an *uncertain increase* (**notMinus**), 74 nodes were **unobserved** and the experimental data contained 0 observations of things that are not in the given influence graph model.

```
4 Reading network network.sif ... done.
5   Nodes: 96  Activations: 116  Inhibitions: 16  Dual: 0
6
7 Reading observations observation.obs ... done.
8
9 Checking observations observation.obs ... done.
```

```

10 Observations are consistent.
11 inputs: 14 observed +: 12 observed -: 10 observed 0: 20 observed notPlus: 5
12 observed notMinus: 4 unobserved: 74 not in model: 0

```

Then follow the results of the consistency analysis. Line 14 tells us that network and data are inconsistent and that the size of a *minimal correction set* (**mcos**) is 1. This means that at least 1 influence needs to be added to restore consistency. For a deeper understanding of mcos see [1]. Further the output contains at most 10 consistent labeling including correction set. This is because we choose to set the flag **--show_labelings** 10. In our example we have only 2 possible labelings. Each labeling represents a consistent behavior of the model (given mcos the corrections). **Labeling 1**, tells it is possible that **STAT3_n** and **PAK1** *increase* (+), **IGF1_act** does *not change* (0) and that **KS6A5/KS6A4** and **TNR1A/TNR1B** *decrease* (-). Line 26 tells us that this is a consistent behavior if **MTOR** would receive a positive influence, which is currently not included in the model. **Labeling 2**, represents an alternative behavior, here **PAK1** and **KS6A5/KS6A4** do *not change* (0). Please note that in this example both labelings are consistent under the same correction set. In another example more than one minimal correction set could exists.

```

13 Computing mcos of network and data ... done.
14   The network and data are inconsistent: mcos = 1.
15
16 Compute mcos labelings ... done.
17 Labeling 1:
18   gen("STAT3_n") = +
19   gen("PAK1") = +
20   gen("IGF1_act") = 0
21   gen("KS6A5/KS6A4") = -
22   gen("TNR1A/TNR1B") = -
23
24   labeled +: 2   labeled -: 2   labeled 0: 1
25
26   new_influence("observation.obs",gen("MTOR"),1)
27
28 Labeling 2:
29   gen("STAT3_n") = +
30   gen("PAK1") = 0
31   gen("IGF1_act") = 0
32   gen("KS6A5/KS6A4") = 0
33   gen("TNR1A/TNR1B") = -
34
35   labeled +: 1   labeled -: 1   labeled 0: 3
36
37   new_influence("observation.obs",gen("MTOR"),1)

```

Finally the prediction results are listed. A prediction is a statement that hold under all labeling under all minimal repairs. For a formal definition of predictions see [2]. Here the predictions say that **STAT3_n** *always increases* (+), **PAK1** *never decreases* (NOT -), **IGF1_act** always stays *unchanged* (0), **KS6A5/KS6A4** *never increases* (NOT +), and that **TNR1A/TNR1B** *always decreases* (-).

```

38 Compute predictions under mcos ... done.
39   gen("STAT3_n") = +
40   gen("PAK1") = NOT -
41   gen("IGF1_act") = 0
42   gen("KS6A5/KS6A4") = NOT +
43   gen("TNR1A/TNR1B") = -
44
45   predicted +: 1   predicted -: 1   predicted 0: 1   predicted NOT +: 1
46   predicted NOT -: 1   predicted CHANGE: 0

```

References

- [1] Ioannis N. Melas, Regina Samaga, Leonidas G. Alexopoulos, and Steffen Klamt. Detecting and Removing Inconsistencies between Experimental Data and Signaling Network Topologies Using Integer Linear Programming on Interaction Graphs. *PLoS Computational Biology*, 9(9):e1003204, 09 2013.
- [2] Sven Thiele, Luca Cerone, Julio Saez-Rodriguez, Anne Siegel, Carito Guziolowski, and Steffen Klamt. Extended notions of sign consistency to relate experimental data to regulatory network topologies. 2015.