

# “Feedback loop and self-loop detection in an ODE”

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## Introduction

A biological system can be mathematically represented as a system of ordinary differential equations (ODEs). The Jacobian matrix of a system of ODEs is the matrix of the partial derivatives. The Jacobian matrix can be represented as a graph where each species is a node and an entry unequal to zero in the matrix is an edge in the graph. With directed path detection in the graph it is possible to determine if a species is affecting itself either directly (self-loop) or via other species (loop). The loop detection package can calculate self-loops and loops and shows if these are positive or negative. The output is a data frame which can easily be filtered for different parameters (e.g. loop length, loops containing a certain edge). The packages NetworkX, Numpy and Pandas have to be installed to use loop detection.

## Calculate Jacobian matrix

The following code shows how to calculate the Jacobian matrix of a user-defined ODE.

A file defining the function of the ODE system (*NEGm4*) and the parameters (*param\_NEGm4*) will be opened. Here we use an example of a chain model with negative feedback. To calculate the Jacobian, we need the package Numdifftools and the function *numdifftools.Jacobian*. It is important that the function in the file returns a *numpy* array. :

```
import numdifftools as nd
import numpy as np
exec(open("NEGm4_func.py").read())
jac = nd.Jacobian(NEGm4)
jacobian = jac(np.array([1,0.1,1,1]),t=0,parameters=param_NEGm4)
jacobian
array([[ -1.6 ,  0.   ,  0.   ,  0.75],
       [ 1.5 , -2.   ,  0.   , -0.75],
       [ 0.   ,  1.   , -3.   ,  0.   ],
       [ 0.   ,  0.   ,  2.   , -3.   ]])
```

The Jacobian can then be used in the function *get\_all\_loops*. If the user already calculated the Jacobian, it is also possible to use this in the function. The input has to be a *numpy* array.

## Find all loops

To find all loops for the given Jacobian matrix the function *get\_all\_loops* creates a directed graph from the matrix with the function *networkx.DiGraph*. To find all cycles in the graph, the function uses *networkx.simple\_cycles*. :

```
exec(open("loop_detection.py").read())
loops = get_all_loops(jacobian=jacobian)
loops
```

	loop	length	sign
0	[0, 1, 2, 3, 0]	4	1
1	[0, 0]	1	-1
2	[1, 2, 3, 1]	3	-1
3	[1, 1]	1	-1
4	[2, 2]	1	-1
5	[3, 3]	1	-1

The output is a *pandas* data frame with three columns: loop, length and sign. So each row in the data frame shows the loop, the respective length and sign (1=positive loop, -1=negative loop). In the example ODE we found six loops. The first one is a path with the nodes and edges 0-> 1-> 2-> 3-> 0, which is positive and has length four. The third one is a path with the nodes and edges 1-> 2-> 3-> 1, which is negative and has length three. The other four loops are negative self loops.

## Helpful functions to get an overview about the results

Within the *pandas* data frame it is easy to sort (e.g. for length). The following example shows how to sort for length in ascending order with the inbuilt function *sort\_values*. :

```
loops.sort_values("length")
```

	loop	length	sign
1	[0, 0]	1	-1
3	[1, 1]	1	-1
4	[2, 2]	1	-1
5	[3, 3]	1	-1
2	[1, 2, 3, 1]	3	-1
0	[0, 1, 2, 3, 0]	4	1

With the inbuilt function *value\_count* it is also possible to get an overview how many negative and positive loops or how many loops with a certain length were found. :

```
loops.sign.value_counts()
-1    5
 1    1
Name: sign, dtype: int64

loops.length.value_counts()
1    4
3    1
4    1
Name: length, dtype: int64
```

## Extract and read in the results

To store the results in a .tsv file for example, we can use the *pandas* function *to\_csv* and specify the file as tab-delimited. To read in such a file afterwards, we can use the *pandas.read\_csv* function. :

```
loops.to_csv("loops_NEGm4.tsv",sep='\t')
loops = pandas.read_csv("loops_NEGm4.tsv",delimiter='\t')
```