Bond Graph Representation of Complexes: Bringing Graph Theory to Bond Graphs

Peter Gawthrop. *peter.gawthrop@unimelb.edu.au*

May 21, 2024

Contents

Note: this is the Complexes.ipynb notebook. The PDF version "Bond Graph Representation of Complexes: Bringing Graph Theory to Bond Graphs" is available here.

1 Introduction

Chemical Reaction Network theory Feinberg (1972); Feinberg and Horn (1974); Horn and Jackson (1972); van der Schaft et al. (2013, 2016, 2015) uses the formal concept of *complexes*. Complexes are the combination of chemical species forming the substrate and products of the network reactions. In particular, the stoichiometric matrix N can be decomposed as: $N = ZD$ where Z relates complexes to species and D is the *incidence matrix* of the directed graph formed by taking the complexes to be vertices and the reactions to be edges. This digraph can then be analysed using standard graph theory.

This notion can be given a bond graph interpretation Gawthrop and Crampin (2018). This notebook illustrates complexes using examples from this paper; please see the paper for further explanation.

As noted by Gawthrop and Crampin (2018) the digraphs for systems with and without chemostats are very different and so both are shown in the following examples. The digraphs associated with chemostats are related to bond graph pathway analysis Gawthrop and Crampin (2017); for each of the three examples the corresponding pathways are given.

1.1 Import some python code

The bond graph analysis uses a number of Python modules:

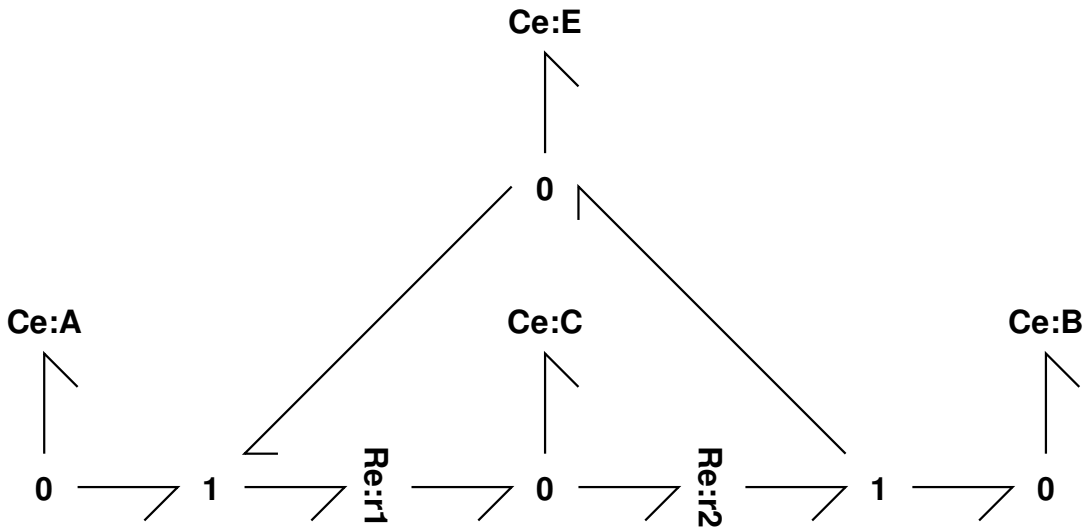
[1]:
```
## Some useful imports
import BondGraphTools as bgt
import numpy as np
import sympy as sp
import matplotlib.pyplot as plt
import IPython.display as disp

## Stoichiometric analysis
import stoich as st

## SVG bg representation conversion
import svgBondGraph as sbg

## Set quiet=False for verbose output
quiet = True

## Chemformula output
chemformula = False
```

2 Example 1: enzyme-catalysed reaction

The bond graph representation of the (reversible) enzyme-catalysed reaction is Gawthrop and Crampin (2018):

[2]:
```
disp.SVG('RE_abg.svg')
```

[2]:



This graphical representation may be converted to bond-graph tools format using

[3]:
```
sbg.model('RE_abg.svg')
import RE_abg
```

```
{}
```

2.1 Reactions

The reactions corresponding to this system are:

[4]:
```
s = st.stoich(RE_abg.model(),quiet=quiet)
disp.Latex(st.sprintrl(s,chemformula=chemformula))
```

[4]:

$$A + E \Leftrightarrow C \tag{1}$$
$$C \Leftrightarrow B + E \tag{2}$$

2.2 Stoichiometric matrix and its decomposition

[5]:
```
disp.Latex(st.sprintl(s,'species'))
```

[5]:

$$X = \begin{pmatrix} X_A \\ X_B \\ X_C \\ X_E \end{pmatrix} \tag{3}$$

[6]:
```
disp.Latex(st.sprintl(s,'reaction'))
```

[6]:

$$V = \begin{pmatrix} V_{r1} \\ V_{r2} \end{pmatrix} \tag{4}$$

[7]:
```
disp.Latex(st.sprintl(s,'N'))
```

[7]:

$$N = \begin{pmatrix} -1 & 0 \\ 0 & 1 \\ 1 & -1 \\ -1 & 1 \end{pmatrix} \tag{5}$$

[8]:
```
disp.Latex(st.sprintl(s,'Z'))
```

[8]:

$$Z = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 0 & 1 \\ 0 & 1 & 0 \\ 1 & 0 & 1 \end{pmatrix} \tag{6}$$

[9]:
```
disp.Latex(st.sprintl(s,'D'))
```

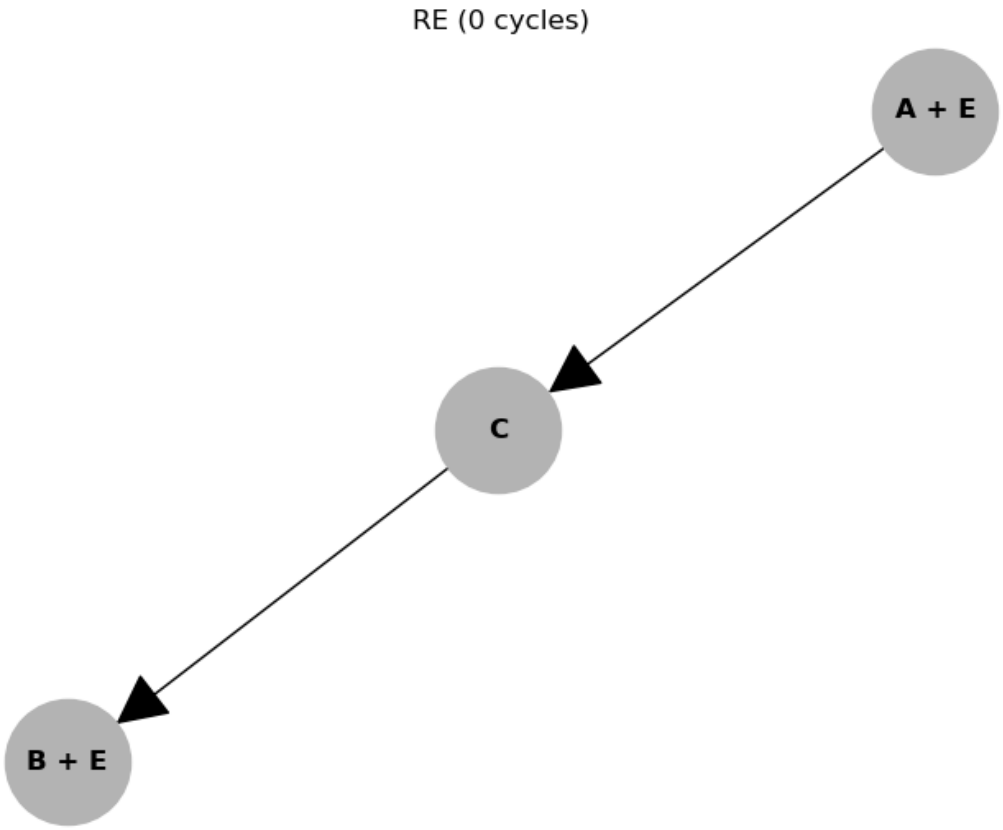
[9]:

$$D = \begin{pmatrix} -1 & 0 \\ 1 & -1 \\ 0 & 1 \end{pmatrix} \tag{7}$$

2.3 System digraph

[10]:
```
st.draw(s)
```

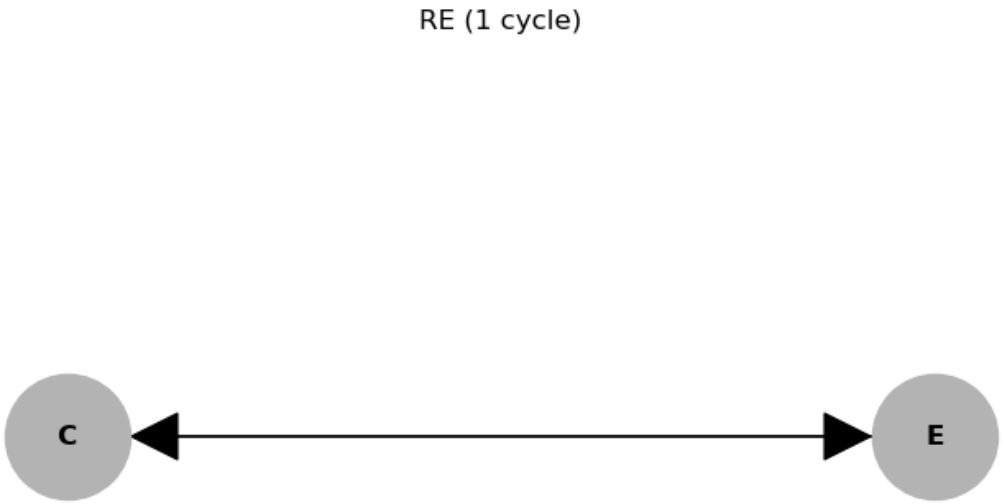
```
Complexes: ['A + E', 'C', 'B + E']
```



2.4 System digraph (with chemostats)

[11]:
```
chemostats = ['A','B']
sc = st.statify(s,chemostats=chemostats)
st.draw(sc)
```

```
Complexes: ['E', 'C']
```



2.5 Pathway analysis

[12]:
```
sp = st.path(s,sc)
print(st.sprintp(sc))
disp.Latex(st.sprintrl(sp,chemformula=chemformula))
```

```
1 pathways
0:  + r1 + r2
```

[12]:

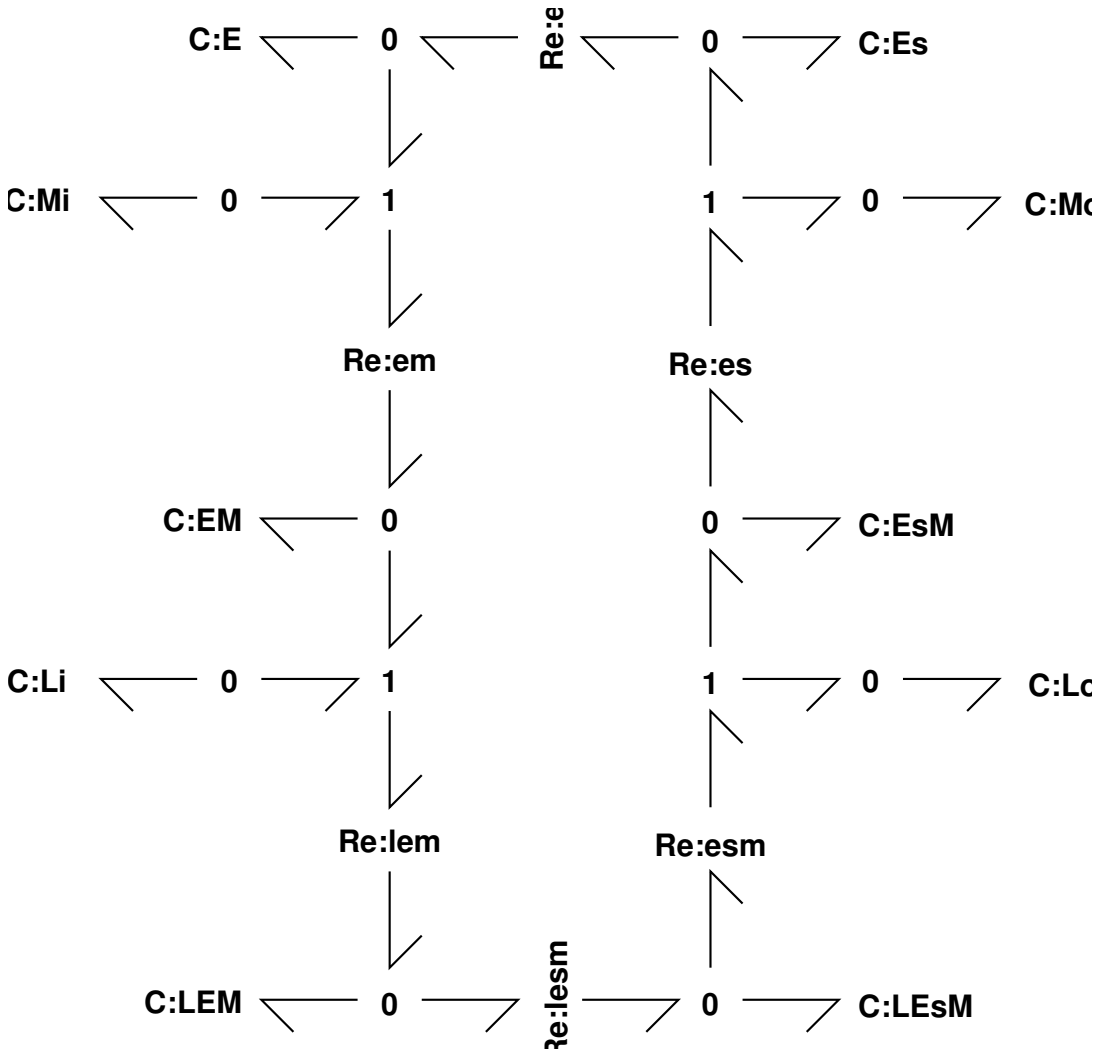
$$A \Leftrightarrow B \tag{8}$$

3 Example 2: Transporter

This example looks at bond graph representation of a membrane transporter which is discussed in detail by Gawthrop and Crampin (2017) and analysed by Gawthrop and Crampin (2018).

[13]:
```
disp.SVG('Hill_abg.svg')
```

[13]:



This graphical representation may be converted to bond-graph tools format using

[14]:
```
sbg.model('Hill_abg.svg')
import Hill_abg
```

{}

3.1 Reactions

The reactions corresponding to this system are:

[15]:
```
s = st.stoich(Hill_abg.model(),quiet=quiet)
disp.Latex(st.sprintrl(s,chemformula=chemformula))
```

[15]:

$$Es \Leftrightarrow E \tag{9}$$
$$E + Mi \Leftrightarrow EM \tag{10}$$
$$EsM \Leftrightarrow Es + Mo \tag{11}$$
$$LEsM \Leftrightarrow EsM + Lo \tag{12}$$
$$EM + Li \Leftrightarrow LEM \tag{13}$$
$$LEM \Leftrightarrow LEsM \tag{14}$$

3.2 Stoichiometric matrix and its decomposition

[16]:
```
disp.Latex(st.sprintl(s,'species'))
```

[16]:

$$X = \begin{pmatrix} X_{E} \\ X_{EM} \\ X_{Es} \\ X_{EsM} \\ X_{LEM} \\ X_{LEsM} \\ X_{Li} \\ X_{Lo} \\ X_{Mi} \\ X_{Mo} \end{pmatrix} \tag{15}$$

[17]:
```
disp.Latex(st.sprintl(s,'reaction'))
```

[17]:

$$V = \begin{pmatrix} V_{e} \\ V_{em} \\ V_{es} \\ V_{esm} \\ V_{lem} \\ V_{lesm} \end{pmatrix} \tag{16}$$

[18]:
```
disp.Latex(st.sprintl(s,'N'))
```

[18]:

$$N = \begin{pmatrix} 1 & -1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & -1 & 0 \\ -1 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & -1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & -1 \\ 0 & 0 & 0 & -1 & 0 & 1 \\ 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \end{pmatrix} \tag{17}$$

[19]:
```
disp.Latex(st.sprintl(s,'Z'))
```

[19]:

$$Z = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{pmatrix} \tag{18}$$

[20]:
```
disp.Latex(st.sprintl(s,'D'))
```

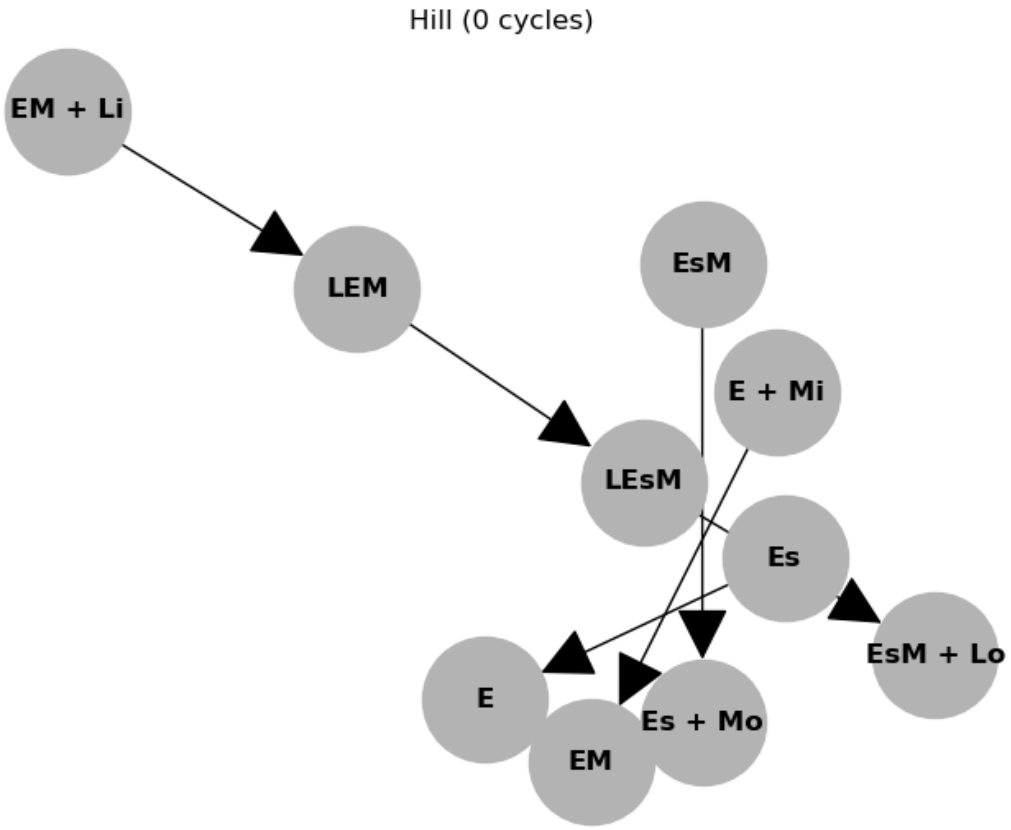
[20]:

$$D = \begin{pmatrix} -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 1 \\ 0 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 1 & -1 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \end{pmatrix} \tag{19}$$

3.3 System digraph

[21]:
```
st.draw(s)
```

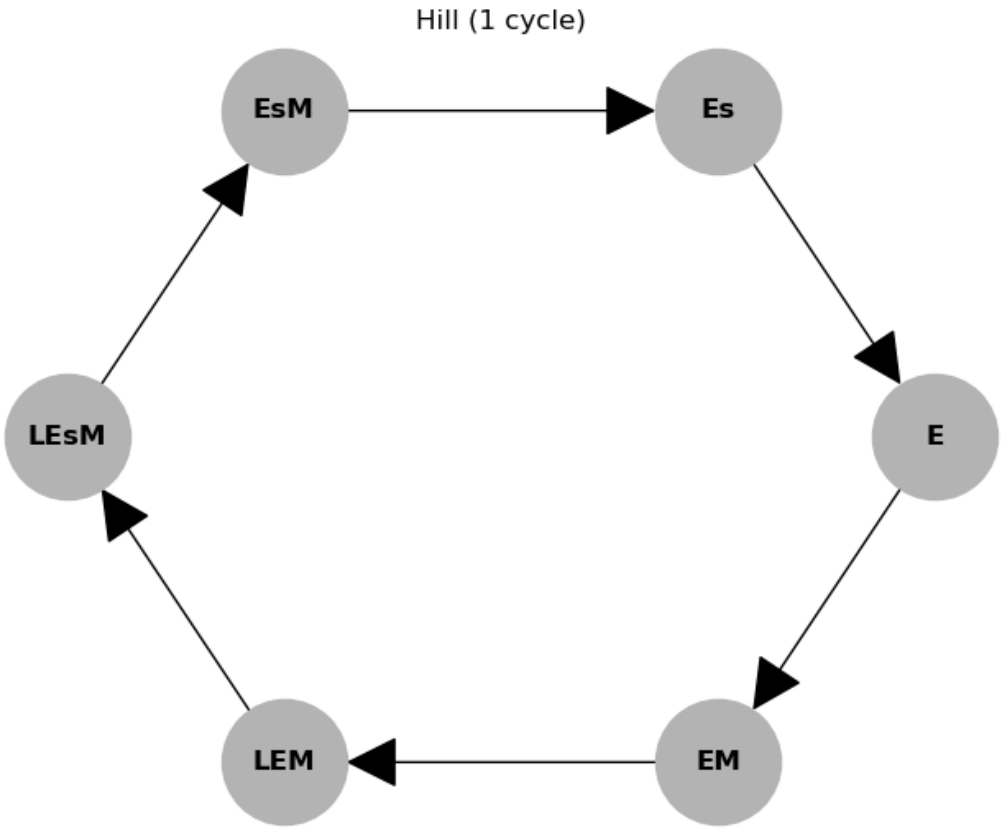
```
Complexes: ['Es', 'E + Mi', 'EsM', 'LEsM', 'EM + Li', 'LEM', 'E', 'EM', 'Es +
Mo', 'EsM + Lo']
```



3.4 System digraph (with chemostats)

[22]:
```
chemostats = ['Mi','Mo','Li','Lo']
sc = st.statify(s,chemostats=chemostats)
st.draw(sc)
```

```
Complexes: ['Es', 'E', 'EsM', 'LEsM', 'EM', 'LEM']
```



3.5 Pathway analysis

[23]:
```
sp = st.path(s,sc)
print(st.sprintp(sc))
disp.Latex(st.sprintrl(sp,chemformula=chemformula))
```

```
1 pathways
0:  + e + em + es + esm + lem + lesm
```

[23]:

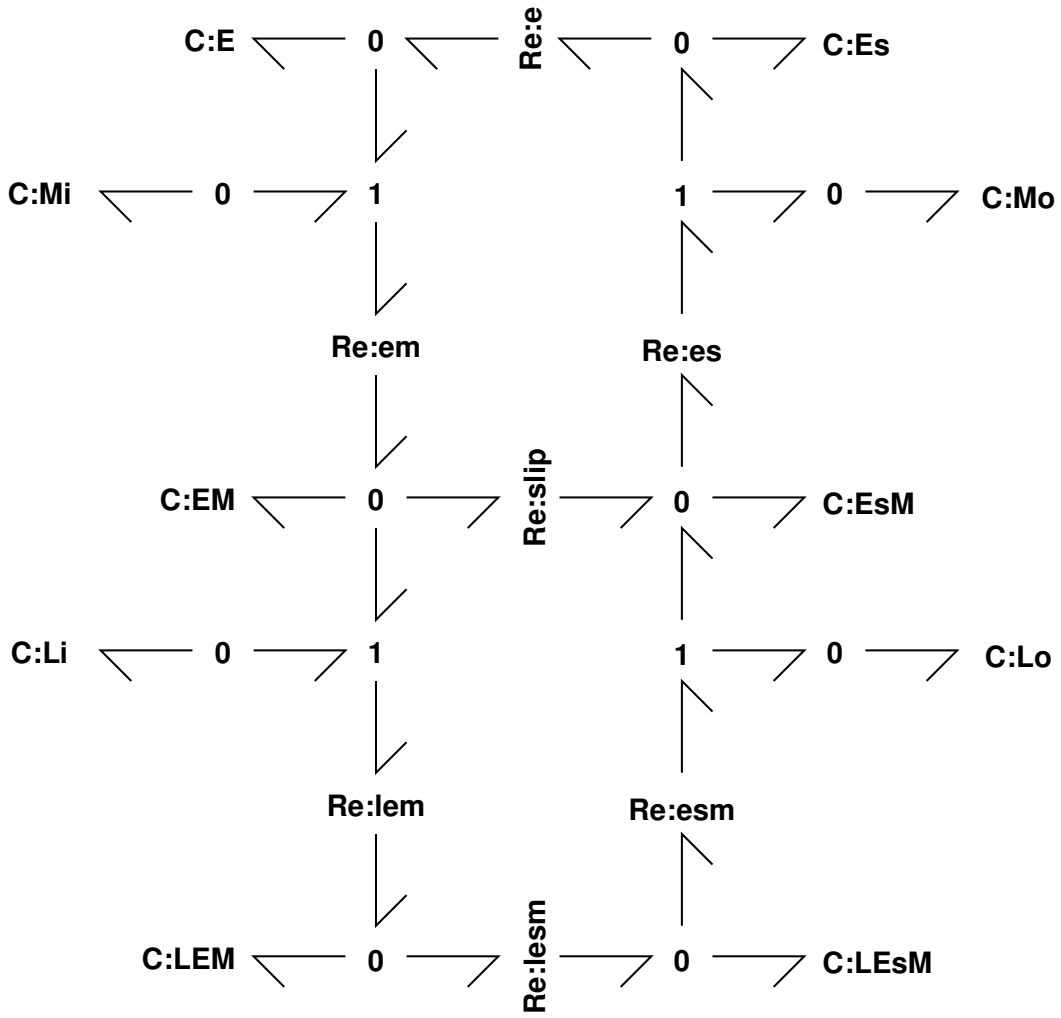
$$Li + Mi \Leftrightarrow Lo + Mo \tag{20}$$

4 Example 3: Transporter with slippage

[24]:
```
sbg.model('Hills_abg.svg')
import Hills_abg
disp.SVG('Hills_abg.svg')
```

```
{}
```

[24]:



4.1 Reactions

The reactions corresponding to this system are:

[25]:
```
s = st.stoich(Hills_abg.model(),quiet=quiet)
disp.Latex(st.sprintrl(s,chemformula=chemformula))
```

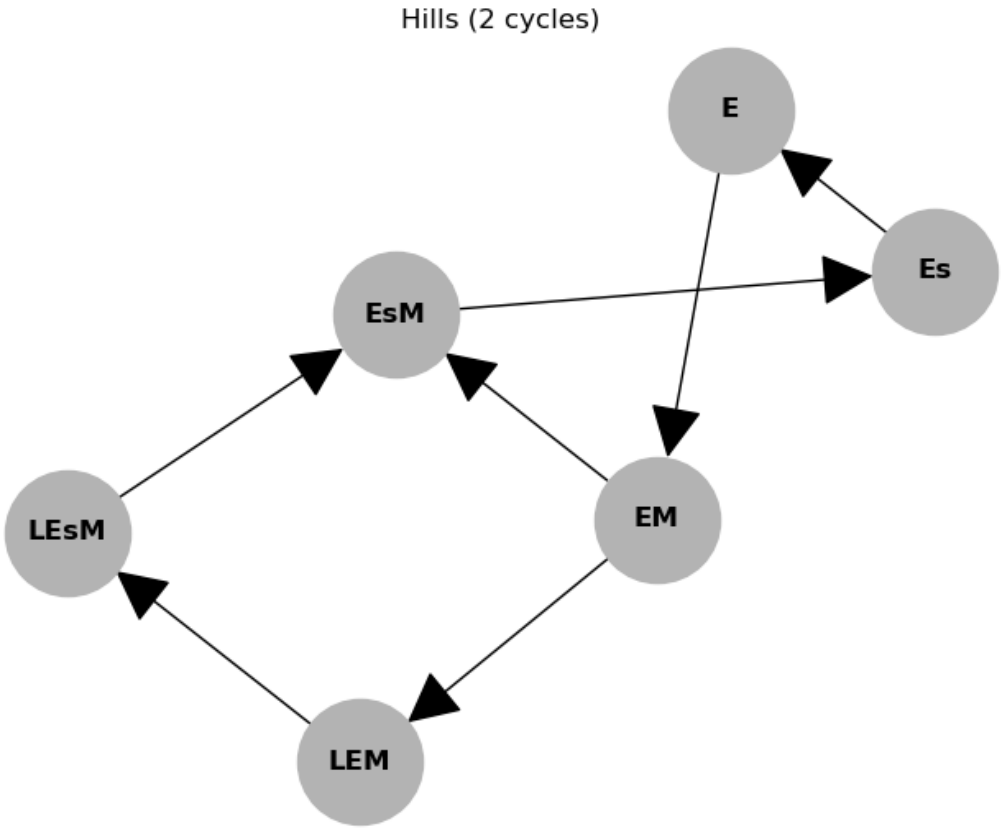
[25]:

$$Es \Leftrightarrow E \tag{21}$$
$$E + Mi \Leftrightarrow EM \tag{22}$$
$$EsM \Leftrightarrow Es + Mo \tag{23}$$
$$LEsM \Leftrightarrow EsM + Lo \tag{24}$$
$$EM + Li \Leftrightarrow LEM \tag{25}$$
$$LEM \Leftrightarrow LEsM \tag{26}$$
$$EM \Leftrightarrow EsM \tag{27}$$

4.2 System digraph (with chemostats)

[26]:
```
chemostats = ['Mi','Mo','Li','Lo']
sc = st.statify(s,chemostats=chemostats)
st.draw(sc)
```

```
Complexes: ['Es', 'E', 'EsM', 'LEsM', 'EM', 'LEM']
```



4.3 Pathway analysis

[27]:
```
sp = st.path(s,sc)
print(st.sprintp(sc))
disp.Latex(st.sprintrl(sp,chemformula=chemformula))
```

```
2 pathways
0:  + e + em + es + esm + lem + lesm
1:  + e + em + es + slip
```

[27]:

$$Li + Mi \Leftrightarrow Lo + Mo \tag{28}$$

$$Mi \Leftrightarrow Mo \tag{29}$$

[ ]:

References

Martin Feinberg. On chemical kinetics of a certain class. *Archive for Rational Mechanics and Analysis*, 46(1):1–41, 1972. ISSN 0003-9527. doi: 10.1007/BF00251866.

Martin Feinberg and Friedrich J.M. Horn. Dynamics of open chemical systems and the algebraic structure of the underlying reaction network. *Chemical Engineering Science*, 29(3):775 – 787, 1974. ISSN 0009-2509. doi: 10.1016/0009-2509(74)80195-8.

P. Gawthrop and E. J. Crampin. Bond graph representation of chemical reaction networks. *IEEE Transactions on NanoBioscience*, 17(4):449–455, October 2018. ISSN 1536-1241. doi: 10.1109/TNB.2018.2876391. Available at arXiv:1809.00449.

Peter J. Gawthrop and Edmund J. Crampin. Energy-based analysis of biomolecular pathways. *Proceedings of the Royal Society of London A: Mathematical, Physical and Engineering Sciences*, 473(2202), 2017. ISSN 1364-5021. doi: 10.1098/rspa.2016.0825. Available at arXiv:1611.02332.

F. Horn and R. Jackson. General mass action kinetics. *Archive for Rational Mechanics and Analysis*, 47(2):81–116, Jan 1972. ISSN 1432-0673. doi: 10.1007/BF00251225.

A. van der Schaft, S. Rao, and B. Jayawardhana. On the mathematical structure of balanced chemical reaction networks governed by mass action kinetics. *SIAM Journal on Applied Mathematics*, 73(2):953–973, 2013. doi: 10.1137/11085431X.

A. J. van der Schaft, S. Rao, and B. Jayawardhana. A network dynamics approach to chemical reaction networks. *International Journal of Control*, 89(4):731–745, 2016. doi: 10.1080/00207179.2015.1095353.

Arjan van der Schaft, Shodhan Rao, and Bayu Jayawardhana. Complex and detailed balancing of chemical reaction networks revisited. *Journal of Mathematical Chemistry*, 53(6):1445–1458, Jun 2015. ISSN 1572-8897. doi: 10.1007/s10910-015-0498-2.