

Additional material for: Network Thermodynamics of Biological Systems: A Bond Graph Approach

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Contents

1	Introduction	2
1.1	Some useful imports	2
2	Basic reactions	2
2.1	$A \Leftrightarrow B$	2
2.1.1	Graphical bond graph representation	2
2.1.2	Convert graphical representation to BondGraphTools representation . . .	3
2.1.3	Stoichiometric analysis and reactions	3
3	Reactions with connections	3
3.1	$A + B \Leftrightarrow C + D$	3
3.1.1	Graphical bond graph representation	3
3.1.2	Convert graphical representation to BondGraphTools representation . . .	4
3.1.3	Stoichiometric analysis and reactions	4
3.2	$A \Leftrightarrow B \Leftrightarrow C$	4
3.2.1	Graphical bond graph representation	4
3.2.2	Convert graphical representation to BondGraphTools representation . . .	4
3.2.3	Stoichiometric analysis and reactions	4
4	Multiple stoichiometry	5
4.1	$A+2B \Leftrightarrow 3C+4D$	5
4.1.1	Graphical bond graph representation	5
4.1.2	Convert graphical representation to BondGraphTools representation . . .	5
4.1.3	Stoichiometric analysis and reactions	5
5	One-port Re component	5
5.1	$A+2B \Leftrightarrow 3C+4D$	5
5.1.1	Graphical bond graph representation	5
5.1.2	Convert graphical representation to BondGraphTools representation . . .	6
5.1.3	Stoichiometric analysis and reactions	6

1 Introduction

- This document contains additional material for the paper: *Network Thermodynamics of Biological Systems: A Bond Graph Approach* by Peter Gawthrop and Michael Pan.
- It illustrates how the Python package [BondGraphTools](#) can be used to create and analyse chemical reaction networks.
- It provides background to Section 3, Chemical Reactions.
- This document is **Reactions.pdf** (see also **Chloroplast.pdf**).
- The document is available as the Jupyter notebook **Reactions.ipynb**.

1.1 Some useful imports

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

## Stoichiometric analysis
import stoich as st

## SVG bg representation conversion
import svgBondGraph as sbg

## Modular bond graphs
import modularBondGraph as mbg

## Display (eg disp.SVG(), disp.
import IPython.display as disp

## Data
import phiData
import redoxData

import importlib as imp

## Some switches
chemformula = True
quiet = True
```

2 Basic reactions

2.1 $A \rightleftharpoons B$

2.1.1 Graphical bond graph representation

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

[2]:



2.1.2 Convert graphical representation to BondGraphTools representation

```
[3]: # imp.reload(sbg)
sbg.model('ABbasic_abg.svg',quiet=quiet)
import ABbasic_abg
# imp.reload(ABbasic_abg)
```

2.1.3 Stoichiometric analysis and reactions

```
[4]: ## Stoichiometry
sABbasic = st.stoich(ABbasic_abg.model(),quiet=quiet)
disp.Latex(st.sprintrl(sABbasic,chemformula=chemformula))
```

[4]:



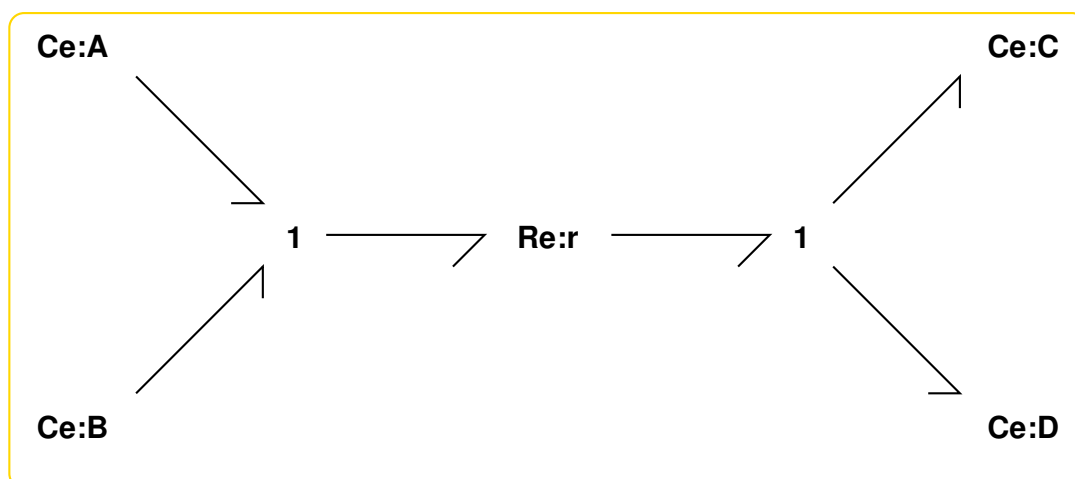
3 Reactions with connections

3.1 A + B ⇌ C + D

3.1.1 Graphical bond graph representation

```
[5]: disp.SVG('ABCDbasic_abg.svg')
```

[5]:



3.1.2 Convert graphical representation to BondGraphTools representation

```
[6]: # imp.reload(sbg)
      sbg.model('ABCDbasic_abg.svg',quiet=quiet)
      import ABCDbasic_abg
      # imp.reload(ABCDbasic_abg)
```

3.1.3 Stoichiometric analysis and reactions

```
[7]: ## Stoichiometry
      sABCDbasic = st.stoich(ABCDbasic_abg.model(),quiet=quiet)
      disp.Latex(st.sprintrl(sABCDbasic,chemformula=chemformula))
```

[7]:

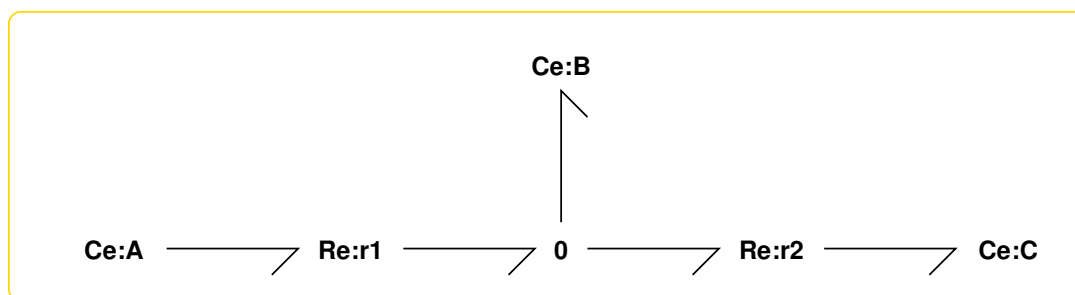


3.2 $A \Leftrightarrow B \Leftrightarrow C$

3.2.1 Graphical bond graph representation

```
[8]: disp.SVG('ABCbasic_abg.svg')
```

[8]:



3.2.2 Convert graphical representation to BondGraphTools representation

```
[9]: # imp.reload(sbg)
      sbg.model('ABCbasic_abg.svg',quiet=quiet)
      import ABCbasic_abg
      # imp.reload(ABCbasic_abg)
```

3.2.3 Stoichiometric analysis and reactions

```
[10]: ## Stoichiometry
       sABCbasic = st.stoich(ABCbasic_abg.model(),quiet=quiet)
       disp.Latex(st.sprintrl(sABCbasic,chemformula=chemformula))
```

[10]:



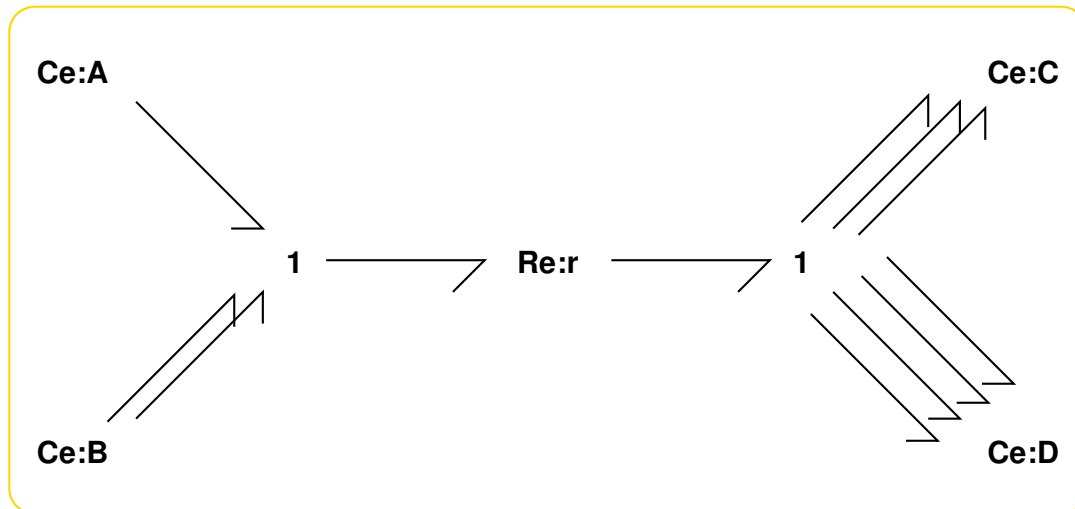
4 Multiple stoichiometry

4.1 $A+2B \rightleftharpoons 3C+4D$

4.1.1 Graphical bond graph representation

```
[11]: disp.SVG('ABCDmult_abg.svg')
```

[11]:



4.1.2 Convert graphical representation to BondGraphTools representation

```
[12]: # imp.reload(sbg)
      sbg.model('ABCDmult_abg.svg', convertCe=True, quiet=quiet)
      import ABCDmult_abg
      # imp.reload(ABCDmult_abg)
```

4.1.3 Stoichiometric analysis and reactions

```
[13]: ## Stoichiometry
      sABCDmult = st.stoich(ABCDmult_abg.model(), quiet=quiet)
      disp.Latex(st.sprintrl(sABCDmult, chemformula=chemformula))
```

[13]:



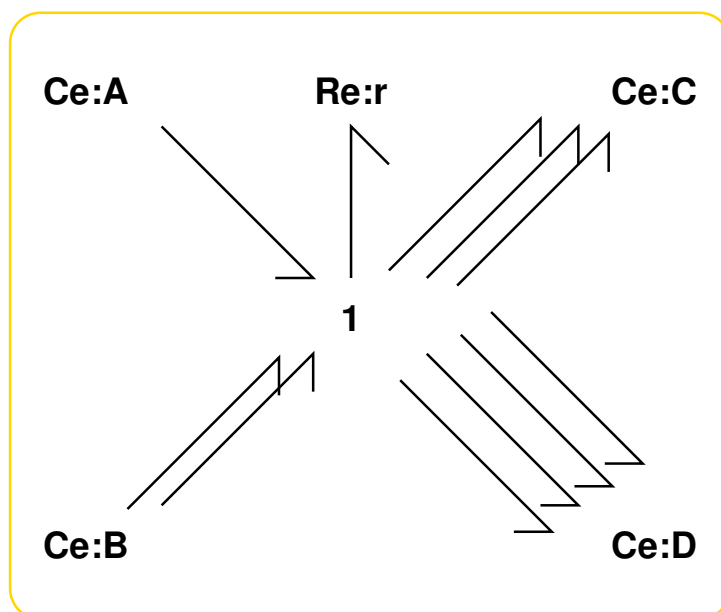
5 One-port Re component

5.1 $A+2B \rightleftharpoons 3C+4D$

5.1.1 Graphical bond graph representation

```
[14]: disp.SVG('ABCDone_abg.svg')
```

[14]:



5.1.2 Convert graphical representation to BondGraphTools representation

```
[15]: # imp.reload(sbg)
      sbg.model('ABCDone_abg.svg',convertCe=True,convertR=True,quiet=quiet)
      import ABCDone_abg
      # imp.reload(ABCDone_abg)
```

5.1.3 Stoichiometric analysis and reactions

```
[16]: ## Stoichiometry
      sABCDone = st.stoich(ABCDone_abg.model(),quiet=quiet)
      disp.Latex(st.sprintrl(sABCDone,chemformula=chemformula))
```

[16]:

