

SGLT

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Note: This example is discussed in detail by [Gawthrop and Pan \[2020\]](#) available [here](#).

Note: this is the `SGLT.ipynb` notebook. The PDF version “Sodium Glucose Symporter” is available [here](#).

1 Introduction

The Sodium-Glucose Transport Protein 1 (SGLT1) (also known as the Na^+ -glucose symporter [Keener and Sneyd, 2009, § 2.4.2]) was studied experimentally by Parent et al. [1992a] and explained by a biophysical model [Parent et al., 1992b]; further experiments and modelling were conducted by Chen et al. [1995]. Eskandari et al. [2005] examined the kinetics of the reverse mode using similar experiments and analysis to Parent et al. [1992a,b] but with reverse transport and currents.

This note looks at a bond graph based model of SGLT1 based on the model of Eskandari et al. [2005].

The model of Figure 6B of Eskandari et al. [2005] is based on the six-state biomolecular cycle of Figure 2 of Parent et al. [1992b]. When operating normally, sugar is transported from the outside to the inside of the membrane driven against a possibly adverse gradient by the concentration gradient of Na^+ .

A similar situation is analysed in §~1.1 of the book by Hill [1989] and the corresponding bond graph of the biomolecular cycle is described by Gawthrop and Crampin [2017].

```
[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
import svgBondGraph as sbg

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

quiet = True

## Data file
import json

## Save the figure
SaveFig = False

```

```

[2]: ## Load data from Eskandari et. al. Fig 3A
      ## Digitised using https://apps.automeris.io/wpd/

```

```

def loadData():

    with open('SGLT_data.json') as f:
        Dict = json.load(f)

    List = Dict['datasetColl'][0]['data']

    X = []
    Y = []
    for item in List:
        xy = item['value']
        X.append(xy[0])
        Y.append(xy[1])

    return X,Y

print(loadData())

```

```

([-149.08132530120483, -128.50492880613362, -108.26396495071195,
-88.92935377875138, -68.92045454545456, -49.776150054764514,
-29.841182913472096, -9.930859802847777, 11.341730558597988, 30.71741511500545],
[1.3909090909090907, 1.8090909090909086, 3.409090909090909, 3.6636363636363636,
4.236363636363636, 4.9818181818181815, 5.2272727272727275, 5.363636363636363,
4.863636363636363, 5.3])

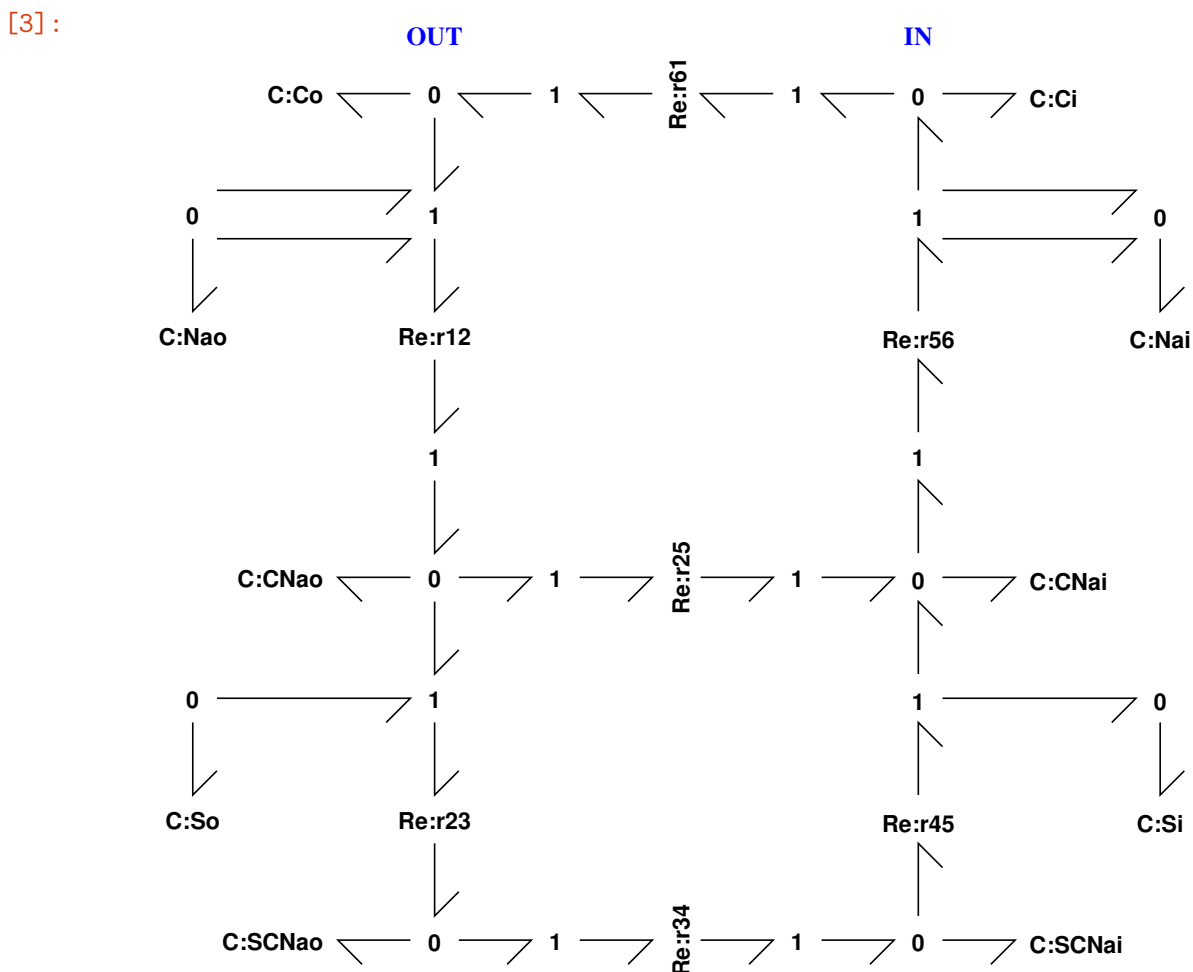
```

2 Sodium-Glucose Symporter - zero membrane potential.

This non-electrogenic version is used to compute species and reaction parameters from the published model values.

2.1 Bond graph

```
[3]: ## Sodium-Glucose transporter - no E
sbgl.model('SGLT_abg.svg')
import SGLT_abg
disp.SVG('SGLT_abg.svg')
```



2.2 Stoichiometry

```
[4]: ## Stoichiometry
s0 = st.stoich(SGLT_abg.model(), quiet=quiet)
chemostats = ['Nai', 'Nao', 'Si', 'So']
sc0 = st.statify(s0, chemostats=chemostats)
#print(s['species'])
#disp.Latex(st.sprint(s0, 'K'))
```

```
#print(st.sprints(s))
```

2.3 Convert parameters

The model of [Eskandari et al. \[2005\]](#) is based on rate constants. The following code converts this into the parameters required for the bond graph model.

```
[5]: def Keq2K(K_eq,N,K,tol=1e-6):  
    ## Compute BG C parameters K_c from equilibrium constants K_eq.  
    ## NB K_eq must be thermodynamically consistent.  
  
    logK_eq = np.log(K_eq)  
    #print(K_eq)  
    #print(logK_eq)  
  
    if len(K) != 0:  
        ##First check that Keq is thermodynamically consistent.  
        check = np.linalg.norm(K.T*logK_eq)/np.linalg.norm(logK_eq)  
        print(check)  
  
    ## Transformation of mu to affinities  
    NN = -N.T  
  
    ## Pseudo inverse  
    pNN = np.linalg.pinv(NN)  
  
    ## BG C constants  
    K_c = np.exp(pNN*logK_eq)  
  
    return K_c
```

```
[6]: ## Set non-unit parameters using data from EskWriLoo05  
def setPar(s,tol=1e-6):  
  
    ## Extract stoichiometry  
    N = s['N']  
    Nf = s['Nf']  
    Nr = s['Nr']  
    K = s['K']  
  
    n_V = s['n_V']  
  
    ## Rate constants from Fig 6.  
    kf = {}  
    kr = {}  
  
    ## Rate constants from Fig 6.  
    kf['r12'] = 8e4;  
    kr['r12'] = 500;
```

```

kf['r23'] = 1e5;
kr['r23'] = 20;

kf['r34'] = 50;
kr['r34'] = 50;

kf['r45'] = 800;
kr['r45'] = 12190;

kf['r56'] = 10;
kr['r56'] = 4500;

kf['r61'] = 3;
kr['r61'] = 350;

kf['r25'] = 0.3;
kr['r25'] = 9.1e-4;

## Equilibrium constants.
K_eq = np.zeros(n_V)
k_f = np.zeros(n_V)
k_r = np.zeros(n_V)
for i, reac in enumerate(s['reaction']):
    K_eq[i] = kf[reac]/kr[reac]
    k_f[i] = kf[reac]
    k_r[i] = kr[reac]

## Compute Ce constants from equilibrium constants
K_c = Keq2K(K_eq, N, K)

#     print(K_eq)
#     print(s['n_X'], K_c.shape)

# Forward rates induced by Cs
k_f0 = np.exp(Nf.T@np.log(K_c))

## Rate constants kappa (Amps)
kappa = (k_f/k_f0)*st.F()

## Sanity check
k_r0 = np.exp(Nr.T@np.log(K_c))
kappa_r = (k_r/k_r0)*st.F()
check = np.linalg.norm(kappa-kappa_r)

if check>tol:
    print(f'Error in kappa: {check:.2}')
```

Parameters
parameter = {}

```

## Ce constants
for i,spec in enumerate(s['species']):
    print(f'K_{spec} = {K_c[i]:.4f}')
    parameter['K_'+spec] = K_c[i]

## Re constants
for i,react in enumerate(s['reaction']):
    print(f'{react} K_eq = {K_eq[i]:.4f}; kappa = {kappa[i]:.4f}')
    parameter['kappa_'+react] = kappa[i]

return parameter

par = setPar(s0)
#print(par)

```

```

Error in kappa: 1.2e-05
K_CNai = 0.149
K_CNao = 49.12
K_Ci = 0.3457
K_Co = 40.33
K_Nai = 13.93
K_Nao = 13.96
K_SCNai = 0.099
K_SCNao = 0.099
K_Si = 10.12
K_So = 10.08
r12 K_eq = 160.0000; kappa = 982183.7246
r23 K_eq = 5000.0000; kappa = 19492291.8173
r25 K_eq = 329.6703; kappa = 589.3102
r34 K_eq = 1.0000; kappa = 48730729.5432
r45 K_eq = 0.0656; kappa = 779691672.6910
r56 K_eq = 0.0022; kappa = 6475936.6454
r61 K_eq = 0.0086; kappa = 837303.6199

```

3 Electrogenic Sodium-Glucose Symporter

3.1 Bond graph

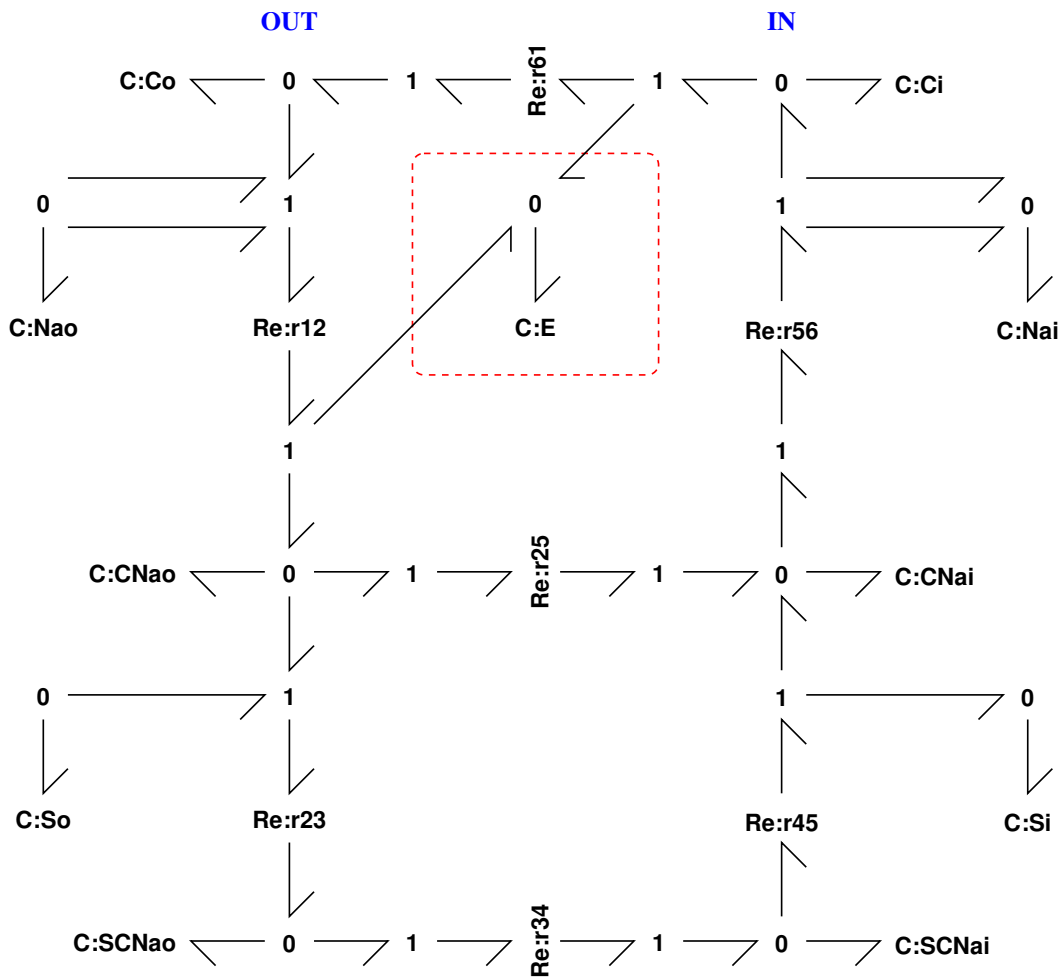
The component C:E is added to express the effect of the charged Na^+ ion crossing the membrane.

```

[7]: ## Sodium-Glucose transporter - electrogenic
      sbg.model('ESGLT_abg.svg')
      import ESGLT_abg
      disp.SVG('ESGLT_abg.svg')

```

[7]:



3.2 Stoichiometry

```
[8]: ## Stoichiometry
s = st.stoich(ESGLT_abg.model(),linear=['E'], quiet=quiet)
chemostats = ['Nai','Nao','Si','So','E']
sc = st.statify(s,chemostats=chemostats)

disp.Latex(st.sprint(sc,'K'))
```

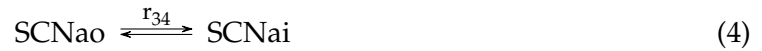
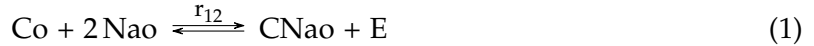
```
K:
[[ 0  1]
 [ 1  0]
 [-1  1]
 [ 1  0]
 [ 1  0]
 [ 0  1]
 [ 0  1]]
```

```
[8]: <IPython.core.display.Latex object>
```

3.3 Reactions and flows

```
[9]: ## Reactions
disp.Latex(st.sprintrl(s,chemformula=True,all=True))
```

[9]:



```
[10]: ## Flows
disp.Latex(st.sprintvl(s))
```

[10]:

$$v_{r12} = \kappa_{r12} \left(-K_{\text{CNao}} x_{\text{CNao}} e^{\frac{K_E x_E}{V_N}} + K_{\text{Co}} K_{\text{NaO}}^2 x_{\text{Co}} x_{\text{NaO}}^2 \right) \quad (8)$$

$$v_{r23} = \kappa_{r23} (K_{\text{CNao}} K_{\text{So}} x_{\text{CNao}} x_{\text{So}} - K_{\text{SCNao}} x_{\text{SCNao}}) \quad (9)$$

$$v_{r25} = \kappa_{r25} (-K_{\text{CNai}} x_{\text{CNai}} + K_{\text{CNao}} x_{\text{CNao}}) \quad (10)$$

$$v_{r34} = \kappa_{r34} (-K_{\text{SCNai}} x_{\text{SCNai}} + K_{\text{SCNao}} x_{\text{SCNao}}) \quad (11)$$

$$v_{r45} = \kappa_{r45} (-K_{\text{CNai}} K_{\text{Si}} x_{\text{CNai}} x_{\text{Si}} + K_{\text{SCNai}} x_{\text{SCNai}}) \quad (12)$$

$$v_{r56} = \kappa_{r56} (K_{\text{CNai}} x_{\text{CNai}} - K_{\text{Ci}} K_{\text{Nai}}^2 x_{\text{Ci}} x_{\text{Nai}}^2) \quad (13)$$

$$v_{r61} = \kappa_{r61} \left(K_{\text{Ci}} x_{\text{Ci}} e^{-\frac{K_E x_E}{V_N}} - K_{\text{Co}} x_{\text{Co}} \right) \quad (14)$$

3.4 Sdet up initial conditions for simulation

```
[11]: def setX(s):

    sp = s['species']
    X0 = np.zeros(s['n_X'])
    X0[sp.index('So')] = 1e-6
    X0[sp.index('Si')] = 1e-3
    X0[sp.index('NaO')] = 1e-2
    X0[sp.index('Nai')] = 0.5

    #    X0 *= st.F()

    ## Normalised value
    C_T = 1
    others = ['Co', 'CNao', 'SCNao', 'Ci', 'CNai', 'SCNai']
    for spec in others:
        X0[sp.index(spec)] = C_T/len(others)
```



```

#N_C = 3e6
N_C = 7.5e7
N_avo = 6.022e23
C_T_0 = N_C/N_avo

I_0_pA = 1e12*C_T_0/C_T

print(f'N_C = {N_C}; i_0 = {I_0_pA}pA')

#X0 *= st.F()

return X0,I_0_pA

#print(setX(s))

```

4 Comparison with experimental data

```

[12]: ## Vary E
E0 = -170/1000
E1 = 50/1000
#E1 = 200/1000
X_chemo = {'E':str(E0)}

## Simulation
t = np.linspace(0,1e3,100)
parameter = setPar(s0)
X0,I_0_pA = setX(s)
dat = st.sim(s,sc=sc,t=t,parameter=parameter,X_chemo=X_chemo,X0=X0)

## Extract data
spec = s['species']
reac = s['reaction']
X_ss = dat['X'][-1,:]
print(X_ss[spec.index('E')])

x_E = f'{E0} + {(E1-E0)/max(t)}*t'
print(x_E)
X_chemo = {'E':x_E}

dat = st.sim(s,sc=sc,t=t,parameter=parameter,X0=X_ss,X_chemo=X_chemo)
f_E = dat['dX'][:,spec.index('E')]
E = dat['X'][:,spec.index('E')]

print(E[0],E[-1])

X,Y = loadData()
plt.plot(1000*E,-f_E*I_0_pA, label='Model')

```

```

plt.scatter(X,Y,label='Experimental')
plt.legend()
plt.grid()
plt.xlabel('$E$ mV')
plt.ylabel('$-f$ pA')
if SaveFig:
    plt.savefig('Figs/splt.pdf')
plt.show()

```

Error in kappa: 1.2e-05

K_CNai = 0.149

K_CNao = 49.12

K_Ci = 0.3457

K_Co = 40.33

K_Nai = 13.93

K_Nao = 13.96

K_SCNai = 0.099

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K_Si = 10.12

K_So = 10.08

r12 K_eq = 160.0000; kappa = 982183.7246

r23 K_eq = 5000.0000; kappa = 19492291.8173

r25 K_eq = 329.6703; kappa = 589.3102

r34 K_eq = 1.0000; kappa = 48730729.5432

r45 K_eq = 0.0656; kappa = 779691672.6910

r56 K_eq = 0.0022; kappa = 6475936.6454

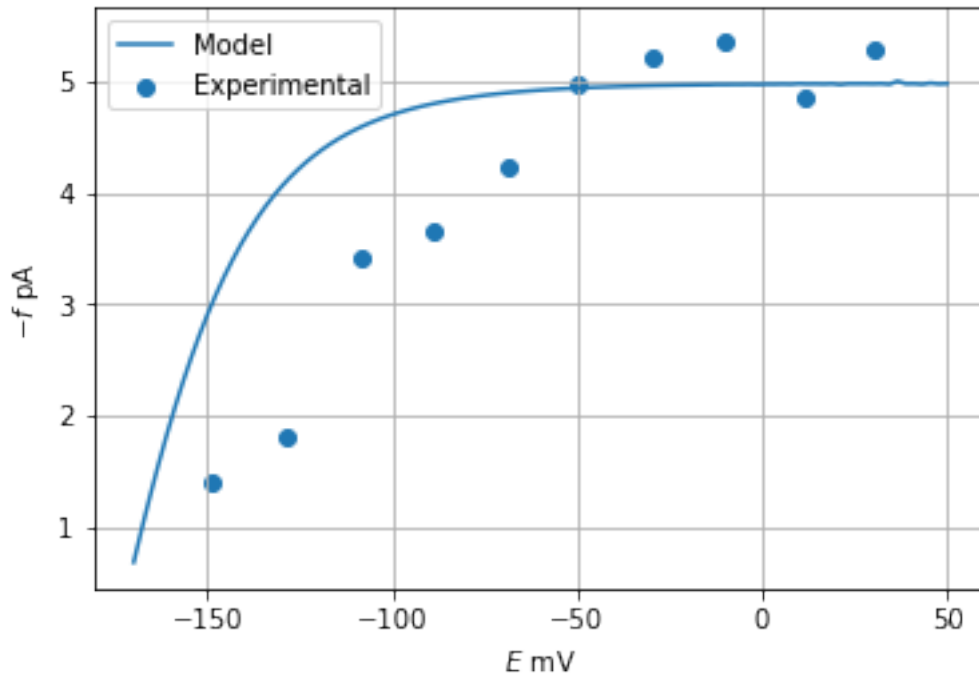
r61 K_eq = 0.0086; kappa = 837303.6199

N_C = 75000000.0; i_0 = 0.00012454334108269677pA

-0.17

-0.17 + 0.00022000000000000003*t

-0.17 0.050000000000000002



[]:

References

- Xing-Zhen Chen, Michael J Coady, Francis Jackson, Alfred Berteloot, and Jean-Yves Lapointe. Thermodynamic determination of the Na⁺: glucose coupling ratio for the human SGLT1 cotransporter. *Biophysical Journal*, 69(6):2405, 1995. doi: 10.1016/S0006-3495(95)80110-4.
- S. Eskandari, E. M. Wright, and D. D. F. Loo. Kinetics of the Reverse Mode of the Na⁺/Glucose Cotransporter. *J Membr Biol*, 204(1):23–32, Mar 2005. ISSN 0022-2631. doi: 10.1007/s00232-005-0743-x. 16007500[pmid].
- 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.
- Peter J. Gawthrop and Michael Pan. Network thermodynamical modelling of bioelectrical systems: A bond graph approach. Available at arXiv:2009.02217, 2020.
- Terrell L Hill. *Free energy transduction and biochemical cycle kinetics*. Springer-Verlag, New York, 1989.
- James P Keener and James Sneyd. *Mathematical Physiology: I: Cellular Physiology*, volume 1. Springer, New York, 2nd edition, 2009.
- Lucie Parent, Stéphane Supplisson, Donald D. F. Loo, and Ernest M. Wright. Electrogenic properties of the cloned Na⁺/glucose cotransporter: I. voltage-clamp studies. *The Journal of Membrane Biology*, 125(1):49–62, 1992a. ISSN 1432-1424. doi: 10.1007/BF00235797.

Lucie Parent, Stéphane Supplisson, Donald D. F. Loo, and Ernest M. Wright. Electrogenic properties of the cloned Na⁺/glucose cotransporter: II. a transport model under nonrapid equilibrium conditions. *The Journal of Membrane Biology*, 125(1):63–79, 1992b. ISSN 1432-1424. doi: 10.1007/BF00235798.