

concvar

Software Manual

Version 1.0

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website: <http://sobereva.com/soft/concvar>

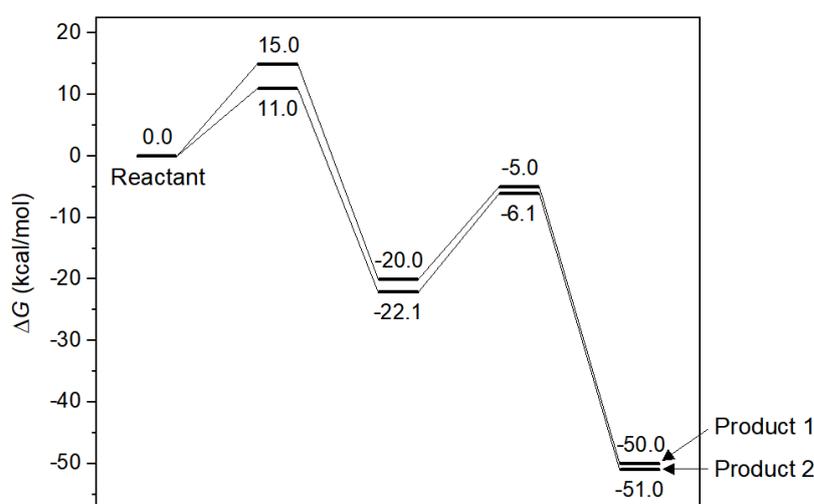
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1 Overview

A complex chemical reaction consists of multiple elementary reactions, and there are multiple minima on the overall energy profile, which correspond to various chemical substances. It is not only theoretically interesting, but also of great practical significance, to investigate how concentration of various substances change over reaction time. For example, in the following energy profile, there are two reaction paths from the reactant, which finally lead to two different products, which one is the major product at a given reaction condition? This is an important and frequently encountered problem in practical research, however the answer is not obvious. If one numerically simulates the change in concentration over time according to reaction rate constants that estimated according to free energy barriers, the results will be clear.



Concvar is a program aiming at studying variation of concentration of various substances (minima) over reaction time by numerically solving reaction kinetics equations. The answer to the above problem can be readily obtained via concvar; that is, setting concentration of the reactant to a certain value, after simulating the above reaction long enough at actual reaction temperature, checking the concentrations of the two products, then the main product and ratio of the products will be directly known.

Features of concvar

Concvar has the following features:

- Input file is very convenient to manually create, and output information is very easy to understand
- Arbitrary number of minima and transition states can be defined
- Each minimum can connect arbitrary number of reaction paths
- Reaction rate constants can be manually set or automatically derived by transition state theory
- Rate of generation and consumption of any minimum can be defined
- Concentrations of minima can change spontaneously or be fixed at specific values
- Criterion of concentration for any minimum can be set to stop the simulation at the right time
- Boltzmann redistribution among specific minima can be conducted at every simulation step

- Both unimolecular and bimolecular elementary reactions can be included

Citation of concvar

If concvar is employed in your study, **please cite** it in your paper as follows:

Tian Lu, Concvar: A computer program for simulating concentration variation of complex chemical reaction, *ChemRxiv* (2022) DOI: 10.26434/chemrxiv-2022-r6rh8-v2

Seeking for help

If you encountered any problem in using concvar, please feel free to contact me via E-mail (sobereva@sina.com). You can also post your question on quantum chemistry board of computational chemistry commune forum (<http://bbs.keinsci.com/forum-103-1.html>), I will always timely reply you.

2 Theory behind concvar

During the simulation of concvar program, concentration (c) of a minimum, for example system i , changes according to the following equation at each simulation step:

$$c_i(t + \Delta t) = c_i(t) + [r_i^{\text{react}}(t) + r_i^{\text{gen}} - r_i^{\text{sink}}] \Delta t \quad (1)$$

where Δt is simulation step size, t and $t + \Delta t$ correspond to time of current and next step, respectively. The initial concentration $c(0)$ of each minimum is defined in input file.

The r_i in above equation is rate of concentration variation of substance i . Three types of sources are considered by concvar. The first one comes from occurrence of relevant elementary reactions (unimolecular reaction is assumed here)

$$r_i^{\text{react}}(t) = \sum_j [k_{j \rightarrow i} c_j(t) - k_{i \rightarrow j} c_i(t)] \quad (2)$$

where j loops over all minima connected to minimum i . $k_{j \rightarrow i}$ corresponds to reaction rate constant from other adjacent substance j to i , which increases concentration of i , while $k_{i \rightarrow j}$ corresponds to reaction rate constant from i to other adjacent substance j , which decreases concentration of i .

The k in Eq. 2 is normally obtained via transition state theory (TST) based on free energy barrier (ΔG^{\ddagger}) at standard state, and it is strongly dependent of reaction temperature (T). For reactions in liquid phase, the standard state concentration is 1 M, and expression of TST in this case is

$$k = \kappa \sigma \frac{k_B T}{h} \exp \left[\frac{-\Delta G^{\ddagger}(T)}{RT} \right] \quad (3)$$

where σ is degeneracy of reaction path and κ is transmission factor due to tunneling effect, they are not explicitly considered by concvar (to take them into account, users should directly specify the k values containing the two factors in input file).

The r_i^{gen} and r_i^{sink} in Eq. 1 correspond to generation and consumption rates of minimum i due to external reasons, respectively, they can be manually defined in input file. Introduction of r_i^{sink} term may lead to unphysical negative concentration according to Eq. 1, so, concentration is automatically set to zero by concvar when it is detected to be negative during simulation.

concvar performs simulation according to Eq. 1, in which the concentration of each minima changes continuously during simulation, until maximum number of steps is reached or one of predefined concentration criteria is satisfied. There are also artificial schemes controlling concentrations in concvar, including concentration fixing and concentration Boltzmann redistribution.

3 Usage of concvar

3.1 Files in concvar package

- *concvar.exe*: Executable file of concvar in Windows
- *concvar*: Executable file of concvar in Linux
- *concvar_manual.pdf*: Manual
- "examples" folder: Containing example input and output files involved in Section 4

3.2 Running concvar

concvar does not need installation. Under Windows, you just need to double-click the *concvar.exe* to boot up it. Under Linux, after adding executable permission for *concvar* file, then it can be directly run.

After booting up, you will be asked to input path of input file. Then various information of current simulation will be printed on screen, please carefully check. During simulation, the progress is shown on screen, and meantime result is continuously outputted to *conc.txt* in current folder. You can monitor this file during simulation. If maximum number of steps is reached, or any stop criteria of concentration is satisfied, the simulation will be stopped, then you can examine concentration variation of various substances in the *conc.txt*, and you may use *e.g.* Origin, Grace and Gnuplot to plot how concentrations vary over simulation time.

Unless otherwise specified, all concentrations involved in concvar and this manual are M (mol/L), all energies are kcal/mol.

3.3 Input file

The following content is a typical input file of concvar. The meaning of each part will be described next. As can be seen there are many options and many fields starting from \$ symbol. Between two fields there must be a blank line, and there must be a blank line at end of input file.

```
temper= 298.15
stepsize= 1E-6
nstep= 500000
outfreq= 1000
ioutfmt= 1
```

```
$G
```

```
0
```

```
15
```

```
-20
```

```
-5
```

```
-50
```

```
$link
```

```
1,2,3
```

```
3,4,5
```

`$cinit`

`1 1.0`

`$gen`

`$sink`

`$conccrit`

Options

- `temper`: Temperature of simulation in K
- `stepsize`: Step size of simulation in s, which corresponds to Δt of Eq. 1 in Section 2. In principle, at given k values, the smaller the step size, the more accurate the simulated concentration variation.

- `nstep`: Maximum number of simulation. Product of `nstep` and `stepsize` corresponds to maximum simulation time. Obviously, simulation cost is positively proportional to simulated steps. Note that the simulation may be stopped before reaching `nstep` if you have set concentration criteria via `$conccrit` field, see later.

Hint on choice of step size: The suitable `stepsize` depends on maximum value of all k involved in the simulation (k_{\max}), the larger the k_{\max} , the smaller the `stepsize` is needed. If only unimolecular elementary reactions are involved, a rule of thumb is that `stepsize` should be less than $0.1/k_{\max}$, corresponding to the case that concentration variation of each step is less than 10% of current concentration (because $\Delta t < 0.1/k_{\max}$ is equivalent to $\Delta t * c * k_{\max} < 0.1c$, where c is current concentration, and the left side of the equation corresponds to change in concentration at current step). For example, after loading input file, assume that the maximum k shown on screen is $5.4E4 \text{ s}^{-1}$, then a `stepsize` less than $1.8E-6 \text{ s}$ should be used.

Because `concvr` automatically sets negative concentrations to zero, occurrence of unreasonably large concentration change due to overlage step size may result in drift of total concentration (assumed that `$gen` and `$sink` are not set), therefore break of conservation of total concentration (can be found in `conc.txt`) is a direct signal of too large step size.

- `outfreq`: Frequency of outputting current concentrations to `conc.txt`. Product of `outfreq` and `stepsize` corresponds to time interval of outputting.

- `ioutfmt`: Output format of concentrations in `concvr.txt`. 1 and 2 correspond to scientific and decimal forms, respectively.

\$G field

This field defines Gibbs free energy (kcal/mol) at liquid standard state concentration (1 M), namely G° , for all stationary points (minima and transition states) considered in current simulation. The G° in this context actually corresponds to relative G° , while the reference is arbitrary, since only free energy barriers are utilized in the simulation.

For example, the following content in `$G` field define G° of systems 1, 2 and 3 as 0, 15.2 and -20.64 kcal/mol, respectively.

`0`

`15.2`

`-20.64`

It should be note that G° is dependent of temperature, namely if `temper` parameter is set to x , then the provided G° should also be calculated at temperature x . Evaluating G° at different temperatures is very easy via my Shermo code (<http://sobereva.com/soft/shermo/>). Also note that

dependency of free energy barriers on temperature is often not strong, therefore if you only hope to roughly examine influence of temperature effect, calculating G° values at different temperatures may not be absolutely necessary.

Slink field

This field provides linking relationship between different minima and transition states. You can write multiple lines to define multiple linking relations.

For example, if you write the following line under *Slink* field

1, 2, 3

then systems 1 (minimum) will link to systems 3 (minimum) by passing system 2 (transition state).

The case of bimolecular reactants and products can also be defined in *Slink*. For example, the following content defines that systems 1 and 2 link to system 4 by passing system 3.

1&2, 3, 4

The following content defines that system 3 links to systems 5 and 8 by passing system 4

3, 4, 5&8

The following content defines that systems 3 and 4 link to systems 6 and 11 by passing system 5

3&4, 5, 6&11

Each linking relation is automatically converted by concvar to two reactions, namely a forward and a reverse elementary reaction. By default, concvar automatically calculates free energy barrier of the elementary reactions according to the data provided in *\$G* field, and converts them to k values via standard transition state theory, see Eq. 3.

You can also manually specify k of forward and reverse elementary reactions at the end of each line. For example, if you write

1, 2, 3 0.329 5.3E-9

then $k_{1\rightarrow 3}$ and $k_{3\rightarrow 1}$ will be set to 0.329 and 5.3E-9 s⁻¹, respectively. If you write

1&2, 3, 4 0.89 6.36E-5

then $k_{1\&2\rightarrow 4}$ and $k_{4\rightarrow 1\&2}$ will be set to 0.89 (M·s)⁻¹ and 6.36E-5 s⁻¹, respectively.

Notice that if a bimolecular elementary reaction considered in the simulation occurs under gas phase, because the formula to evaluate k is different to Eq. 3 in Section 2, you must manually specify the k in above form, you can easily estimate the k via TSTcalculator (<http://sobereva.com/310>).

Scinit field

By default, all initial concentrations are 0. By using this field, you can set initial concentration (M) for specific minima. Defining initial concentration for transition state is obviously meaningless. For example, the following content under this field defines initial concentration of systems 1 and 3 as 0.35 and 0.1 M, respectively.

1 0.35

3 0.1

Sgen field

This field defines rate of generation (M/s) for specific minima, namely the r^{gen} term in Eq. 1. You can write one or multiple lines. By default, r^{gen} for all minima is zero. This field may be ignored or left blank if you do not hope to define any r^{gen} .

For example, the following content under this field sets r^{gen} of system 1 to 0.25 M/s.

1 0.25

\$sink field

This field defines rate of consumption (M/s) for specific minima, namely the r^{sink} term in Eq. 1. You can write one or multiple lines. By default, r^{sink} for all minima is zero. This field may be ignored or left blank if you do not hope to define any r^{sink} .

For example, the following content under this fields sets r^{sink} of system 3 to 0.15 M/s.

```
3 0.15
```

\$conccrit field

This field sets concentration criteria for stopping simulation. You can write one or multiple lines, in each line you should set system index, judgment symbol (> or <) and concentration. Conccvar monitors related concentrations during simulation, if any criterion is satisfied, the simulation will be stopped, even if maximum number of simulation steps set by *nsteps* has not reached. This field should be ignored or left blank if you do not hope to set any concentration criterion.

For example, the following content under this field requests conccvar to stop simulation if concentration of system 1 is detected to be less than 0.5 M or that of system 3 is detected to be higher than 0.35 M.

```
1 < 0.5
```

```
3 > 0.35
```

\$Boltzmann field

Concentrations of the minima specified in each line of this field are reset every step according to Boltzmann distribution at present temperature, in other words, their total concentration is redistributed among these systems. You can write one or multiple lines. This field should be ignored or left blank if you do not hope to set.

For example, the following content under this field requests conccvar to redistribute concentration among systems 1, 3 and 5 (all of them are minima) every step.

```
1,3,5
```

See example in Section 4.4 on when *\$Boltzmann* field should be used.

\$fix field

Usually, concentrations of minima are allowed to change spontaneously, however via *\$fix* field, concentrations of some minima could be fixed at specific values. You can write one or multiple lines. This field should be ignored or left blank if you do not hope to set.

For example, the following content under this field requires that the concentration of systems 3 and 7 be fixed at 0.1 M and 0.5 M, respectively.

```
3 0.1
```

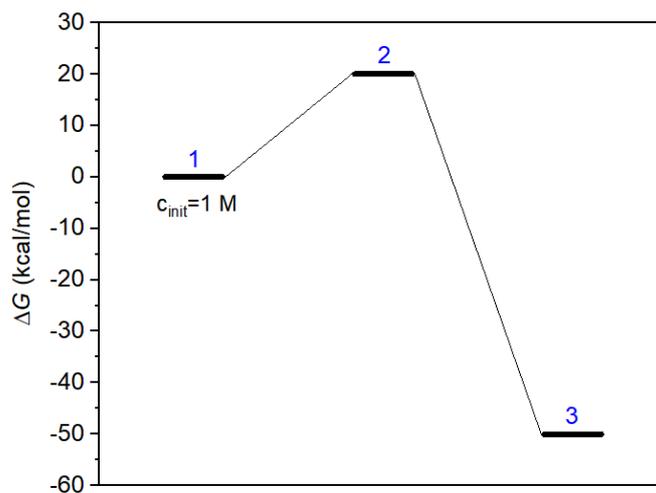
```
7 0.5
```

4 Examples

In this section several examples are given, by following the examples one by one you will easily understand how to utilize concvar to solve practical problems.

4.1 Example 1: Elementary reaction

The first example is very simple, namely an elementary reaction. As illustrated below, there are two minima and one transition state. The G° of the three systems at 298.15 K are 0, 20 and -50 kcal/mol, respectively. Clearly, reverse reaction is negligible compared to forward reaction when temperature is not extremely high.



Now we use concvar to simulate how concentrations vary within 200 s at 298.15 K. The c_{init} of system 1 (reactant) is set to 1.0 M, while that of system 3 (product) is zero. Create concvar input file with the following content. The file has been provided as *examples\Example1.txt*.

```
temper= 298.15
stepsize= 1E-4
nstep= 2000000
outfreq= 1000
ioutfmt= 2
```

```
$G
0
20
-50
```

```
$link
1,2,3
```

```
$cinit
1 1.0
```

Boot up concvar, then input the path of the input file (in Windows system you can also directly drag the icon of the input file into the concvar window), after pressing ENTER button, simulation details will be printed on screen, as shown below, and then the simulation starts. Since we did not explicitly specify k , the k values shown below are directly calculated by transition state theory according to free energy barriers (G barr). It can be seen that the forward k is a modest value ($1.358867 \cdot 10^{-2} \text{ s}^{-1}$), while the reverse k is fully negligible at current temperature. Concvar also mentions that step size should be smaller than 7.36 s for present case, since the step size employed by us is $1\text{E-}4$ s, therefore the accuracy of present simulation is fully guaranteed.

```

Temperature: 298.150 K
Simulation stepsize: 1.000E-04 s
Number of simulation steps: 2000000
Total simulation time: 200.000000 s ( 3.333333 min)
Output frequency: per 1000 steps ( 0.100000 s)

Number of systems: 3
Number of minima: 2
  1 # System index: 1, G: 0.00 kcal/mol, c(init): 1.000000 M
  2 # System index: 3, G: -50.00 kcal/mol, c(init): 0.000000 M

Number of reactions: 2
  1 # System 1 to 3, G barr: 20.00 kcal/mol, k: 1.358867E-02 s^-1
  2 # System 3 to 1, G barr: 70.00 kcal/mol, k: 3.040630E-39 s^-1
Maximum k is 1.358867E-02 s^-1
Stepsize is suggested to be smaller than 7.36E+00 s for present situation

```

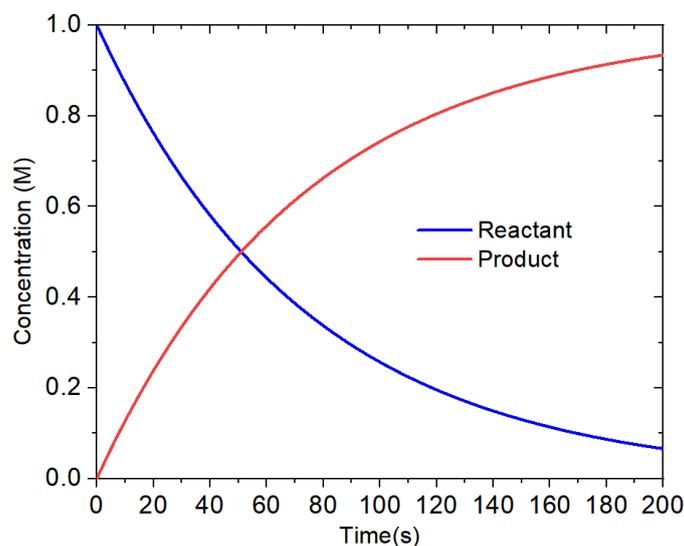
During simulation, you can open the generated *conc.txt* in current folder any time to monitor the simulation progress. After calculation has completed, from the *conc.txt* you can see the following information, the data is printed every 1000 steps (0.1 s), as requested by the *outfreq* parameter. This file has also been provided as *examples\conc_Example1.txt*.

Step	Time(s)	1	3	Total
0	0.0000E+00	1.0000000	0.0000000	1.0000000
1000	1.0000E-01	0.9986421	0.0013579	1.0000000
2000	2.0000E-01	0.9972860	0.0027140	1.0000000
3000	3.0000E-01	0.9959317	0.0040683	1.0000000
...ignored				
1997000	1.9970E+02	0.0662937	0.9337063	1.0000000
1998000	1.9980E+02	0.0662037	0.9337963	1.0000000
1999000	1.9990E+02	0.0661138	0.9338862	1.0000000
2000000	2.0000E+02	0.0660240	0.9339760	1.0000000

It can be seen that at 200 s, the concentration of reactant is 0.066 M and that of product is 0.934 M. The total concentration is always 1.0 M since we did not set generation and consumption terms

in this example.

Based on the *conc.txt*, you can plot variation of concentrations of reactant and product via e.g. Origin, see the map below.



Next, let us study half-life of the reaction using concvar. Add the following content to the input file, meaning if concentration of system 1 (reactant) is lower than 0.5 M (half of initial concentration), the simulation will be stopped. The modified file has been provided as *examples\Example1_2.txt*.

```
$conccrit  
1 < 0.5
```

Use concvar to run this new input file, you can see the simulation is stopped at step 510092 (see below), which corresponds to $510092 \times 10^{-4} = 51.0092$ s.

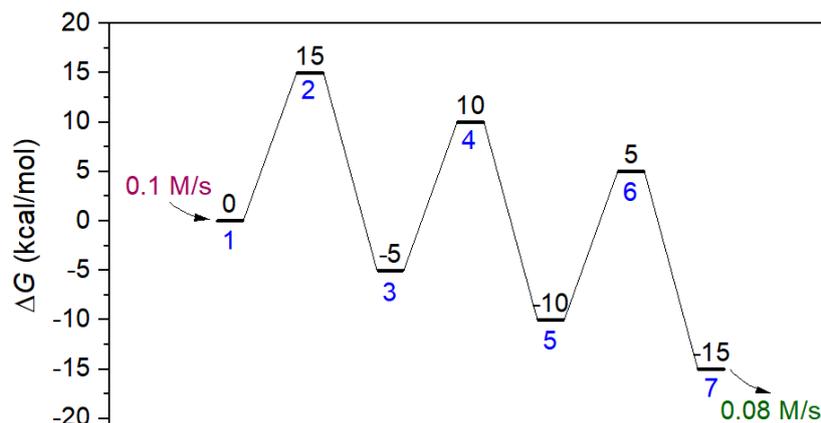
```
Simulating and meantime writing conc.txt, please wait...  
Progress: [#####] 100.00 % /  
Simulation is stopped because concentration of 1 < 0.500000 M has been satisfied at step 510092 ( 51.00920000 s). Current concentration: 5.0000E-01 M
```

Is the half-life simulated by concvar reasonable? The analytic equation for evaluating half-life time of unimolecular reaction is $\ln(2)/k$ (assume that reverse reaction is negligible). As mentioned above, the forward k of current reaction is $1.358867 \times 10^{-2} \text{ s}^{-1}$, therefore the exact half-life time is $\ln(2)/1.358867 \times 10^{-2} = 51.0092$ s, which is completely in agreement with our simulation!

In the current example we use *stepsize* of 1×10^{-4} s, it completely does not matter even if we use an evidently larger value such as 1×10^{-3} s, in this case the numerically simulated half-life time is 51.009 s, which is still fairly accurate.

4.2 Example 2: Complex reaction consisting of multiple elementary steps

In this example, we study concentration variation of a complex reaction consisting of multiple elementary steps, as shown below.



From the above illustration it can be seen that systems 1 and 7 are reactant and product, respectively. Systems 2, 4 and 6 are transition states (TSs), while systems 3 and 5 are intermediates (IMs). Forward and reverse barriers of all elementary steps are all 15 kcal/mol and 20 kcal/mol, respectively. In our simulation, all substances have initial concentration of zero, the reactant (system 1) has a generation rate of 0.1 M/s, while product (system 7) has a consumption rate of 0.08 M/s. We will conduct simulation at 250 K for 50 s. The input file of this simulation is *examples\Example2.txt*, the content is shown below. The values in the \$G field are G° value of all systems relative to reactant.

```
temper= 250
stepsize= 1E-4
nstep= 500000
outfreq= 100
ioutfmt= 2
```

```
$G
0
15
-5
10
-10
5
-15
```

```
$link
1,2,3
3,4,5
5,6,7
```

```
$gen
1 0.1
```

```
$sink
```

7 0.08

Now use concvar to run the input file, then the following information is shown on screen

```
Number of systems:    7
Number of minima:    4
  1 # System index:   1, G:    0.00 kcal/mol, c(init):  0.000000 M
  2 # System index:   3, G:   -5.00 kcal/mol, c(init):  0.000000 M
  3 # System index:   5, G:  -10.00 kcal/mol, c(init):  0.000000 M
  4 # System index:   7, G:  -15.00 kcal/mol, c(init):  0.000000 M

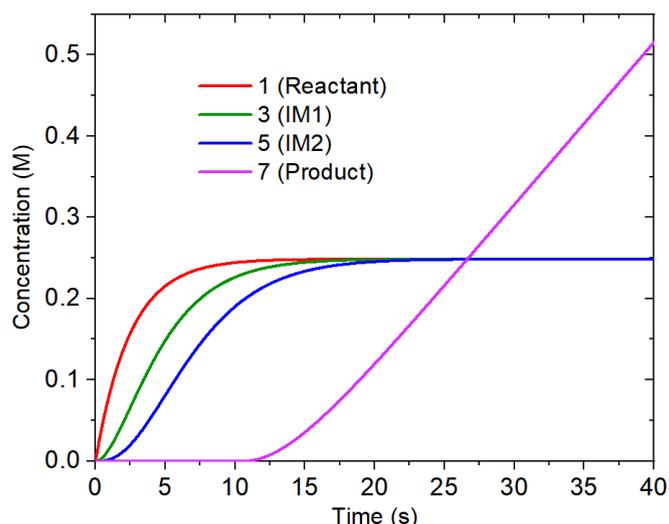
Generation and consumption rates:
  1 # System index:   1, gen.:  0.100000 M/s,  consump.:  0.000000 M/s
  2 # System index:   3, gen.:  0.000000 M/s,  consump.:  0.000000 M/s
  3 # System index:   5, gen.:  0.000000 M/s,  consump.:  0.000000 M/s
  4 # System index:   7, gen.:  0.000000 M/s,  consump.:  0.080000 M/s

Number of reactions:    6
  1 # System    1 to    3, G barr:  15.00 kcal/mol, k:  4.018411E-01 s^-1
  2 # System    3 to    1, G barr:  20.00 kcal/mol, k:  1.710605E-05 s^-1
  3 # System    3 to    5, G barr:  15.00 kcal/mol, k:  4.018411E-01 s^-1
  4 # System    5 to    3, G barr:  20.00 kcal/mol, k:  1.710605E-05 s^-1
  5 # System    5 to    7, G barr:  15.00 kcal/mol, k:  4.018411E-01 s^-1
  6 # System    7 to    5, G barr:  20.00 kcal/mol, k:  1.710605E-05 s^-1
Maximum k is  4.018411E-01 s^-1
Stepsize is suggested to be smaller than 2.49E-01 s for present situation
```

The output file of this task is provided as *examples\conc_Example2.txt*, you can find how concentration of each minimum varies along with simulation:

```
Step    Time(s)    1    3    5    7    Total
  0  0.0000E+00  0.0000000  0.0000000  0.0000000  0.0000000  0.0000000
 100  1.0000E-02  0.0009980  0.0000020  0.0000000  0.0000000  0.0010000
 200  2.0000E-02  0.0019920  0.0000080  0.0000000  0.0000000  0.0020000
 300  3.0000E-02  0.0029820  0.0000179  0.0000001  0.0000000  0.0030000
ignored...
```

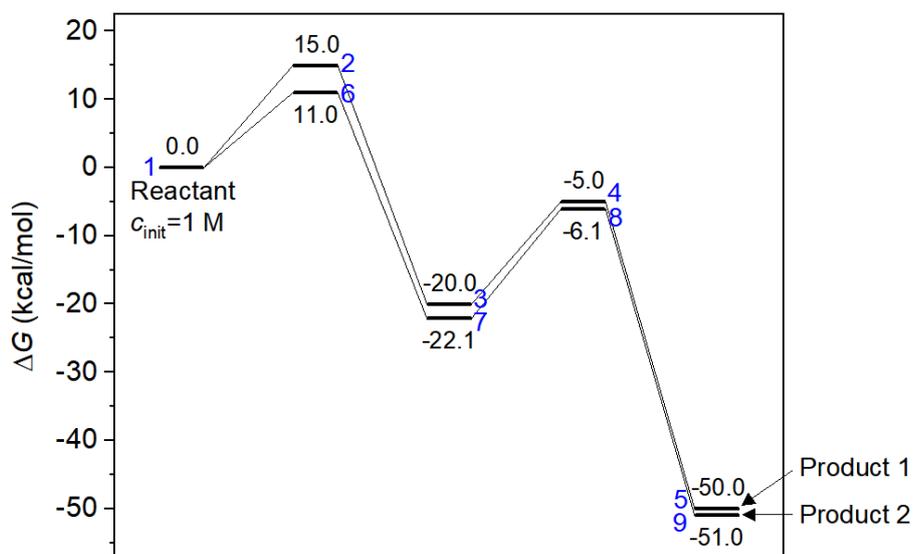
To intuitively understand concentration variation, we plot the data in the outputted *conc.txt* as curves, as shown below



Due to the continuous external input of reactant (0.1 M/s), it can be seen that concentration of system 1 (reactant), system 3 (IM1) and system 5 (IM2) accumulate gradually in sequence, then their concentrations reach the same maximum value (0.249 M) and keep unchanged since 20 s. According the data in *conc.txt* and as can be viewed from the above map, concentration of product is exactly zero until 10.7 s, because its consumption rate is set to be 0.08 M/s, while before 10.7 s its production rate due to reaction from system 5 (IM2) is lower than this value. After about simulation time of 20 s, concentration of product increases linearly with rate of 0.02 M/s, this is because reactant, IM1 and IM2 have reached steady state (concentration no longer changes), while generation rate of reactant is higher than consumption rate of product by 0.02 M/s.

4.3 Example 3: Complex reaction containing competitive paths

In this example, we consider the situation shown in the following energy profile map. There are two competitive reaction paths from reactant, in order to determine the major product, we will perform simulation via *concvr*.



The input file of this example is *examples\Example3.txt*, the content is shown as follows. We perform simulation for $1000000 \times 1\text{E-}6 = 1$ s at 298.15 K. Initial concentration of reactant is 1 M. As can be seen in the *\$link* field, reactant (system 1) connects to both systems 1 and 7, which respectively correspond to the intermediate of the two reaction paths.

```
temper= 298.15
stepsize= 1E-6
nstep= 1000000
outfreq= 1000
ioutfmt= 2
```

```
$G
0
15
-20
-5
-50
11
-22.1
-6.1
-51
```

```
$link
1,2,3
3,4,5
1,6,7
7,8,9
```

```
$cinit
1 1.0
```

The outputted *conc.txt* has been provided as *examples\conc_Example3.txt*, the content is

Step	Time(s)	1	3	5	7	9	Total
0	0.0000E+00	1.0000000	0.0000000	0.0000000	0.0000000	0.0000000	1.0000000
1000	1.0000E-03	0.0000000	0.0010982	0.0000699	0.9875062	0.0113257	1.0000000
2000	2.0000E-03	0.0000000	0.0010313	0.0001367	0.9760981	0.0227339	1.0000000
3000	3.0000E-03	0.0000000	0.0009685	0.0001996	0.9648217	0.0340102	1.0000000
ignored...							
997000	9.9700E-01	0.0000000	0.0000000	0.0011681	0.0000093	0.9988226	1.0000000
998000	9.9800E-01	0.0000000	0.0000000	0.0011681	0.0000092	0.9988227	1.0000000
999000	9.9900E-01	0.0000000	0.0000000	0.0011681	0.0000091	0.9988228	1.0000000
1000000	1.0000E+00	0.0000000	0.0000000	0.0011681	0.0000090	0.9988229	1.0000000

Systems 5 and 9 correspond to the two products. It can be seen that after simulation of 1 s, almost all 1 M reactant has transformed to the product of the second reaction path (0.9988 M), while

product of the first reaction path is negligible (about 0.0012 M). Also note that the reaction has proceeded sufficiently, because the concentrations of the reactant (system 1) and intermediates (systems 3 and 7) are basically zero. Therefore, we can draw conclusion that major product is product 1, and the reaction is highly selective.

Note that in this example a relative small stepsize 1E-6 s is used. This is because highest k is relatively large. After loading the input file, you can find following information from screen

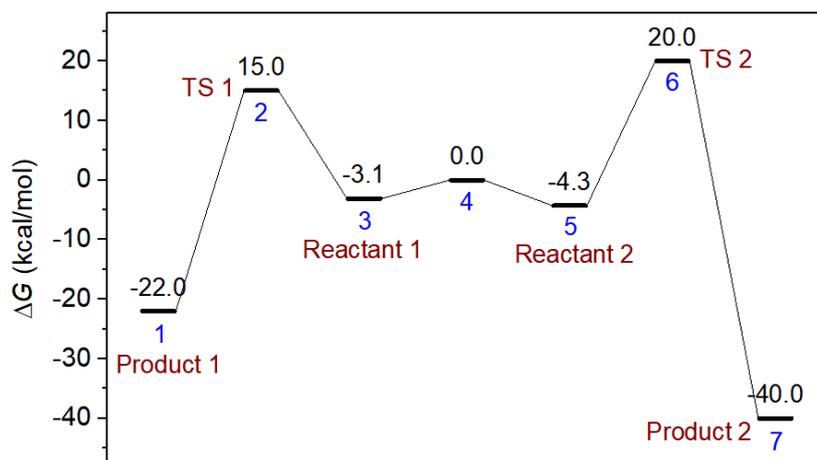
Maximum k is 5.372984E+04 s⁻¹

As mentioned in Section 3.3, the safe *stepsize* should be smaller than $0.1/5.37E4 = 1.86E-6$ s.

4.4 Example 4: Verifying Curtin–Hammett principle

Curtin–Hammett principle is a well-known principle in chemical kinetics, it states that for a reaction that has a pair of reactants that undergo rapid interconversion, and meantime each one can irreversibly transform to a product, the product distribution is determined by the energy difference between the two rate-determining transition states.

The energy profile shown below is a representative case where Curtin–Hammett principle is well suited. The systems 3 and 5 are two reactants, since the barrier between them is very low, their interconversion is quite fast and thus thermodynamics equilibrium between them is always satisfied at ambient condition. Because both the two reverse barriers (15+22=37 and 20+40=60 kcal/mol) are relatively high, possibility of reverse reactions is negligible. According to Curtin–Hammett principle, since TS 1 is notably lower than TS 2, after the reaction is fully completed, concentration of product 1 should be significantly higher than that of product 2, despite that reactant 2 has a lower energy and thus possesses higher concentration than reactant 1 during the reaction, and despite that product 2 has a much lower energy than product 1 and thus it is much more thermodynamically favourable.



Next, let us use concvar to numerically simulate the above reaction and check if the major product predicted by Curtin–Hammett principle is really true or not at 298.15 K. According to the above map, we create a concvar input file with the following content, which has also been provided as *examples/Example4.txt*. Notice that in this example, we do not add 3,4,5 in *\$link* field, but add 3,5 in the *\$Boltzmann* field to require that the concentration ratio of these two reactants always satisfies Boltzmann distribution, this is a very important point. Because $k_{3 \rightarrow 5}$ and $k_{5 \rightarrow 3}$ are larger than other k in this simulation by many orders of magnitude, if we explicitly consider them as usual,

then extremely small step size (about $1\text{E-}12$ s) is needed, and in this case the number of steps needed for long enough simulation to study product distribution (*e.g.* several hundreds of seconds) will be too large to be acceptable. Because interconversion between systems 3 and 5 is by far faster than any other elementary reaction, assumption of their thermodynamic equilibrium status is fully valid. In this simulation, we request the total concentration of the two reactants to be 1 M, to this aim, in *\$cinit* you only need to make the sum of the concentrations of the two reactants equals to 1.0. For example, you can make both of their concentrations to 0.5 M, or you can set either of them to 1.0 M.

```
temper= 298.15
stepsize= 1E-3
nstep= 500000
outfreq= 100
ioutfmt= 2
```

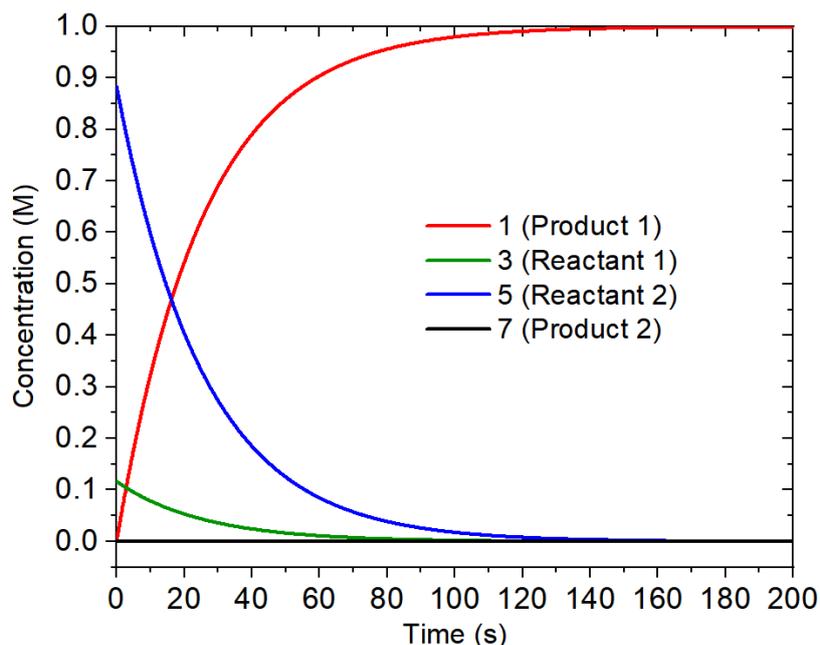
```
$G
-22
15
-3.1
0
-4.3
20
-40
```

```
$link
1,2,3
5,6,7
```

```
$Boltzmann
3,5
```

```
$cinit
3 0.5
5 0.5
```

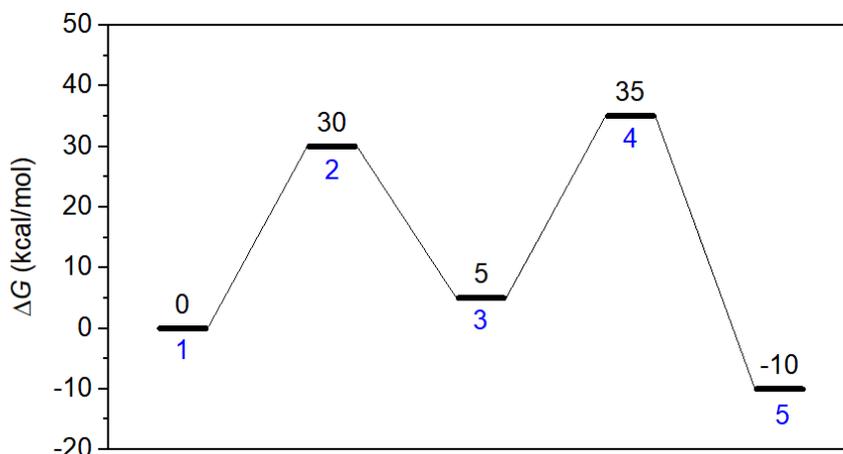
Now we use the above input file to conduct simulation via *concvr*, the simulation time is $500000 \times 1\text{E-}3 = 500$ s. From the outputted *conc.txt* (provided as *examples\conc_Example4.txt*) we can find that all concentrations basically keep unchanged after 200 s, so only concentration variation for the first 200 s is plotted below.



From the above map it can be seen that concentration of the two reactants gradually decreases, and their ratio is fixed throughout the simulation (0.131:1). Concentration of product 2 is always nearly zero, while that of product 1 accumulates rapidly, clearly product 1 is the dominant product. This observation is fully in line with the estimation due to the Curtin–Hammett principle.

4.5 Example 5: Finding rate-determining transition state

Rate-determining transition state (RDTS) refers to the transition state whose energy (more specifically, Gibbs free energy) plays most crucial role on determining overall reaction rate. Slight decrease of energy of RDTS makes reaction rate increase markedly. Concvar can also be used to determine RDTS by examining sensitivity of rate of product generation on energy of various transition states, I will show how to realize this with the following energy profile. As you can see, there are two elementary steps, and forward barrier of both steps is 30 kcal/mol. Systems 2 and 4 are the respective transition state, which one determines overall reaction rate most?



We create an input file with the following content (*examples\Example5.txt*) to conduct

simulation as usual, reaction temperature is assumed to be 350 K and initial concentration of reactant is set to 1 M. The *nstep* is fairly large since the forward *k* is quite small.

Note that if you run the task, from screen you can find step size is suggested to be smaller than 55.9 s. We use an evidently smaller step size (10 s) in this run because we will then decrease energy of transition state, at that time the maximally acceptable step size will be smaller.

```
temper= 350
stepsize= 10
nstep= 10000000
outfreq= 10000
ioutfmt= 1
```

```
$G
0
30
5
35
-10
```

```
$link
1,2,3
3,4,5
```

```
$cinit
1 1.0
```

Run this task, from the outputted *conc.txt* (provided as *examples\conc_Example5.txt*) shown below you can see that after 1E8 s simulation, product (system 5) has a concentration of 0.096783 M.

Step	Time(s)	1	3	5	Total
0.0000E+00	0.0000E+00	1.0000E+00	0.0000E+00	0.0000E+00	1.0000E+00
1.0000E+04	1.0000E+05	9.9915E-01	7.5375E-04	1.0122E-04	1.0000E+00
...	ignored				
1.0000E+07	1.0000E+08	9.0254E-01	6.8087E-04	9.6783E-02	1.0000E+00

Then, we decrease energy of the first transition (system 2) by 1 kcal/mol (to 29 kcal/mol), and rerun the simulation. The corresponding input and output files are *Example5-2.txt* and *conc_Example5-2.txt* in “examples” folder, respectively. After the simulation, you can find product has a concentration of 0.096836 M, obviously the reaction rate has little sensitivity to energy of the first transition.

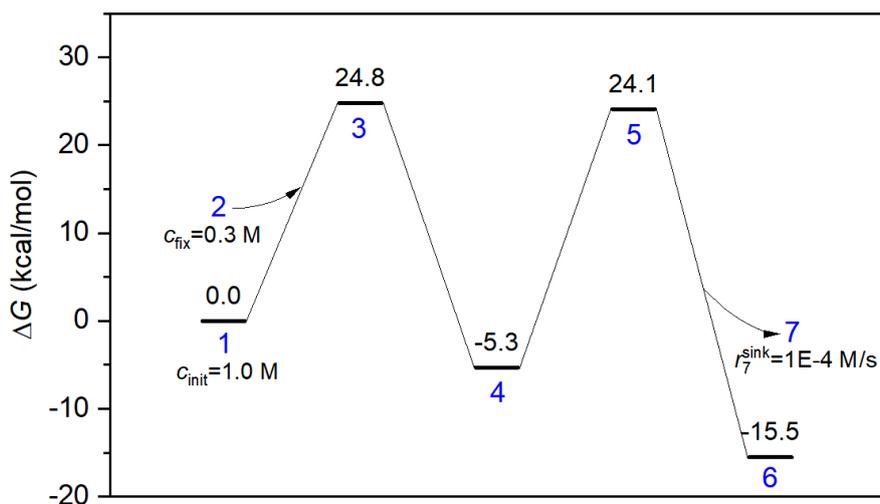
We restore the energy of the first transition to 30 kcal/mol, but decrease energy of the second transition (system 4) by 1 kcal/mol (to 34 kcal/mol) and conduct the simulation again. The corresponding input and output files are *Example5-3.txt* and *conc_Example5-3.txt* in “examples” folder, respectively. After the simulation, you can find the product has a concentration of 0.34796

M. Because the generation rate of product in this case becomes evidently higher than before, we can unambiguously identify the second transition state as the RDTS.

4.6 Example 6: Complex reaction containing bimolecular elementary steps

All examples in previous sections are completely unimolecular elementary reactions. Concar also supports inclusion of bimolecular elementary steps in the studied complex reaction, in this section I will illustrate this feature. (I remind the user again that if the simulation involves bimolecular reactions in the gas phase, the k of those reactions must be directly provided in $\$link$ field, as already mentioned in Section 3.3)

The energy profile in this example is shown below. The first elementary step has bimolecular reactants, while the second elementary step has bimolecular products. Systems 2 is regarded as adding molecule, while system 7 is viewed as leaving molecule, they are treated normally as minima in concvar. Note that only energy barriers affect result, it is customary to set G° of adding and leaving molecules to zero. So, in the following energy profile, energy of system 3 is higher than the sum of energies of systems 1 and 2 by $24.8 - 0.0 = 24.8$ kcal/mol, energy of system 5 is higher than the sum of energies of systems 6 and 7 by $24.1 + 15.5 = 39.6$ kcal/mol.



In our simulation, we will set initial concentration of system 1 to 1.0 M, and assume concentration of adding molecule to be constant at 0.3 M. As seen from the following input file, $\$fix$ field is used to realize concentration fixing. In addition, we assume that the concentration of the leaving molecule is gradually lost at a maximal rate of 0.0001 M/s. The input file of this simulation is shown below and has been provided as *examples\Example5.txt*, note that $\&$ symbol is used in $\$link$ field to indicate bimolecular situation.

```

temper= 400
stepsize= 1E-2
nstep= 1000000
outfreq= 1000
ioutfmt= 2

```

```

$G
0
0
24.8
-5.3
24.1
-15.5
0

$link
1&2,3,4
4,5,6&7

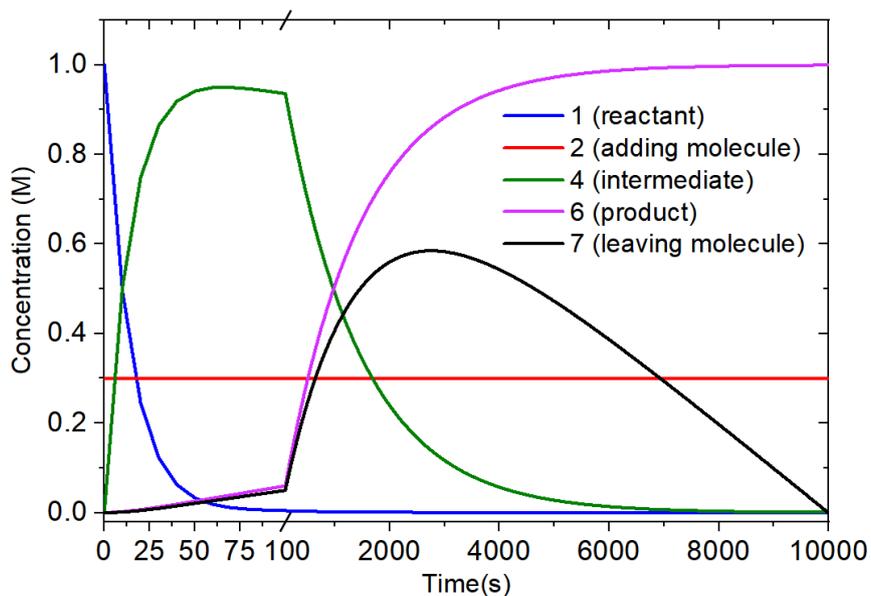
$cinit
1 1.0

$fix
2 0.3

$sink
7 1E-4

```

The concentration variations of various substances during the 10000 s simulation at 400 K are plotted below, the output file has been provided as *examples\conc_Example6.txt*. Since concentration of reactant and intermediate varies sharply at the beginning of the reaction, a break is set on the horizontal axis of the map so that you can clearly examine their concentration variations.



As can be seen from the above figure, after tens of seconds of the reaction, the reactant almost fully became intermediate. The concentration of adding molecules is always constant at 0.3 M due

to fixing setting. With the further progress of the reaction, the concentration of the intermediate gradually decreased and the product was formed. After 10000 s, the original 1 M reactant all turned into the product. The concentration of leaving molecules peaked at about 2800 s, since its generation is slower than consumption after this time point, leaving molecule is fully consumed at the end of the entire simulation.