

# **Tutorial of potential of mean force by MolAICal**

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## 1. Introduction

The potential of mean force (PMF) can be used to calculate the free energy landscape with principal components. The PMF along the coordinate is computed from the average distribution function (see below equation).

$$\Delta G = -k_B T \ln \rho(x, y)$$

Where  $T$  and  $k_B$  is the temperature and Boltzmann constant, respectively. The  $x$  and  $y$  represent two principal components. In this tutorial, the molecular dynamics (MD) simulated results of glucagon receptor (GCGR) are selected for this example (Front Chem. 2019 Dec 17;7:851.)<sup>1</sup>. Here, MolAICal (<https://molaical.github.io>) is employed for this tutorial.

## 2. Materials

### 2.1. Software requirement

1) MolAICal: <https://molaical.github.io>

### 2.2. Example files

1) All the necessary tutorial files are downloaded from:  
<https://github.com/MolAICal/tutorials/tree/master/007-PMF>

## 3. Procedure

This tutorial can be run on Linux and Windows systems. In the Linux system, it may happen errors as follows:

*Exception in thread "main" java.lang.UnsatisfiedLinkError: /home/feng/MolAICal-linux64-v1.1/libdislin\_d.so.11: libXm.so.4: cannot open shared object file: No such file or directory*

**Solution:** It is lack of openmotif. Users can install it by root account:

```
sudo apt-get update -y  
sudo apt-get install -y libmotif-common  
sudo apt-get install libmotif-dev
```

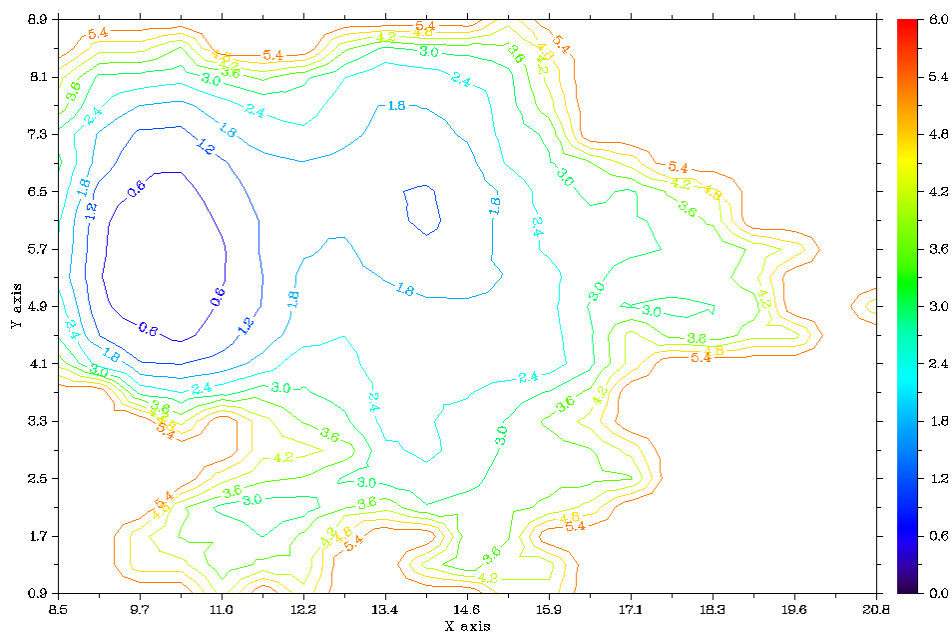
### 3.1. Plot energy contour by MolAICal

```
#> cd 007-PMF
```

Open “rmsd-dis.dat”, the 1st column is RMSD values, 2nd column is the distance. You can replace these data with your appointed principal components. Then, run the command:

```
#> molaical.exe -pmf -i rmsd-dis.dat
```

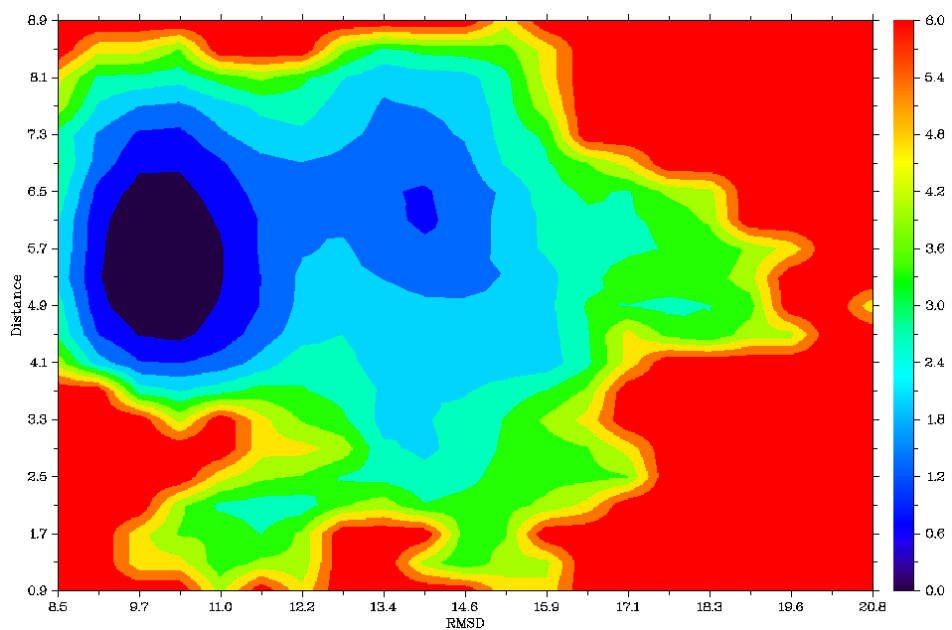
The plotted results show in Figure 1



**Figure 1. PMF contour.**

Running command as below. It plots the figure with another shape (see Figure 2).

```
#> molaical.exe -pmf -i D:/pmf/rmsd-dis.dat -g 20 -l 10 -m conshd -b none -x "RMSD" -y "Distance"
```



**Figure 2. PMF contour.**

### 3.2. Advance tutorial

The part just produces a beautiful figure by OriginLab software. If you do not care about it, you can skip this part. The demo version of OriginLab can be downloaded from <https://www.originlab.com>.

Running command as below:

```
#> molaical.exe -pmf -i rmsd-dis.dat > plot.dat
```

The file “plot.dat” can be used to reproduce the contour of free energy.

1) Import “plot.dat” (see Figure 3)

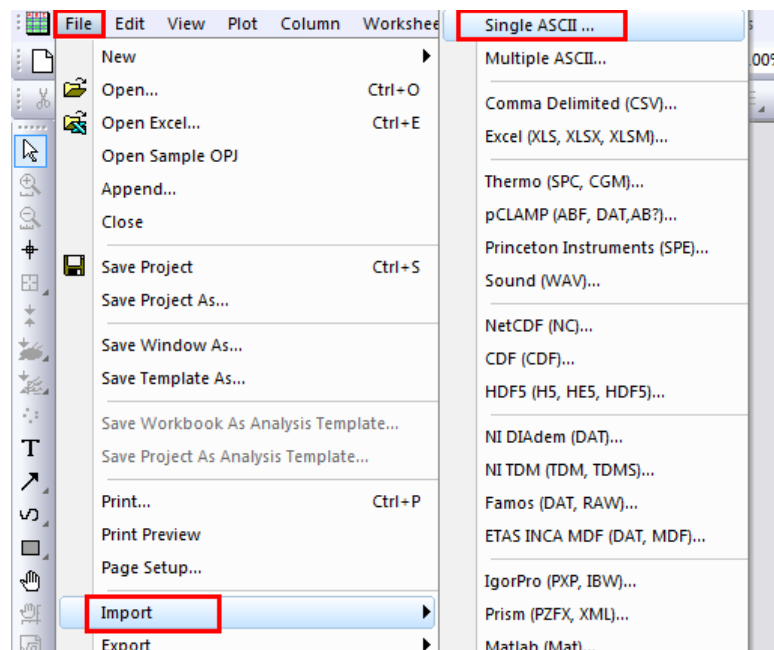


Figure 3. Import data

2) Double click selected column C(Y) and change C(Y) to Z (see Figure 4)

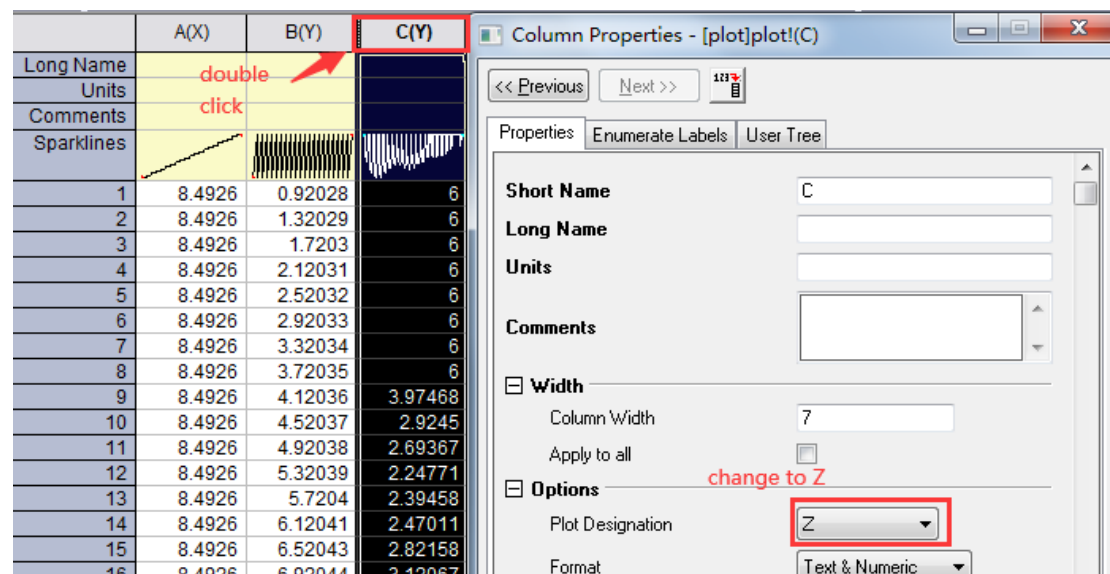


Figure 4. set parameters for plotting

3) Select all data columns and plot the contour (see Figure 5)

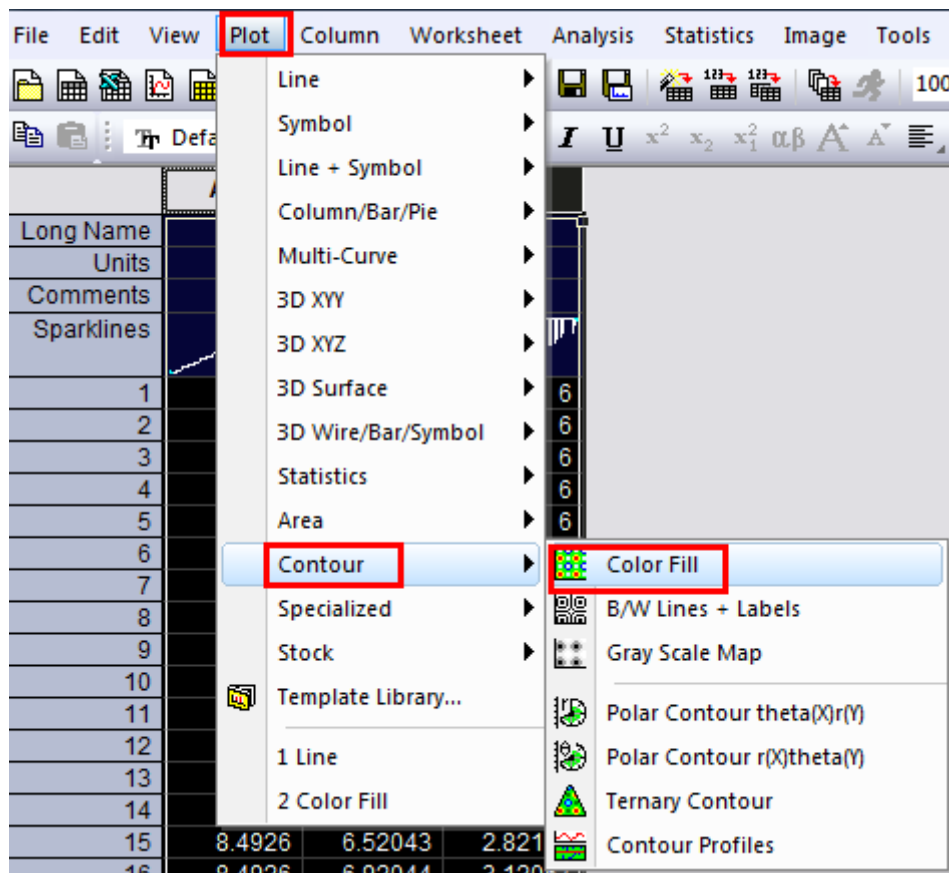


Figure 5. Plot contour

- 4) It may show “Speed Mode is On”. You can double click the contour, click “Layer1”, choose “Size/Speed”, and cancel the term in the red box in Figure 6. If you do not want to cancel “Speed Mode”, you can skip this step.

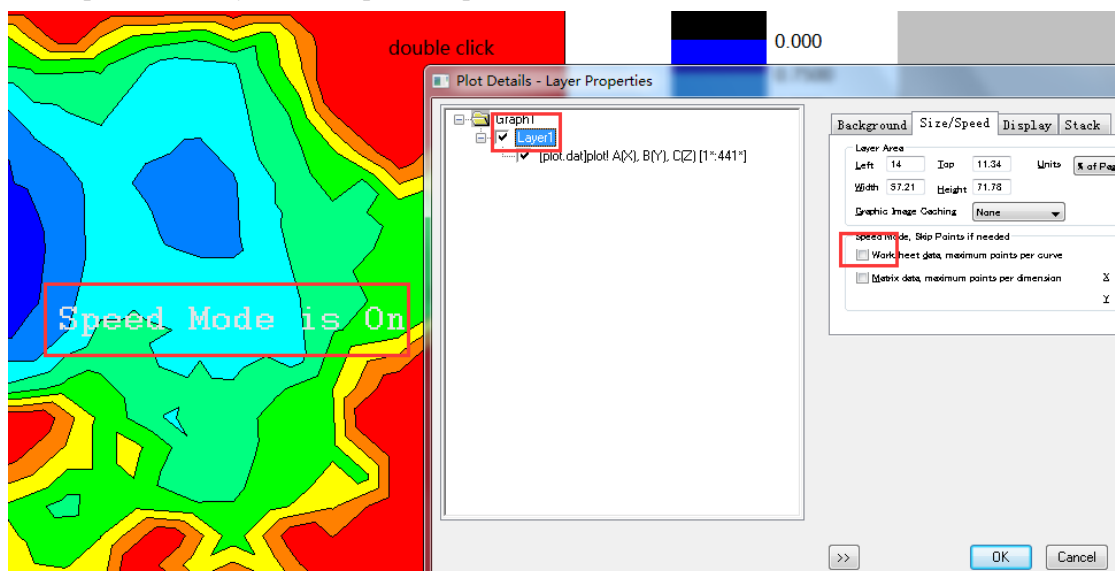
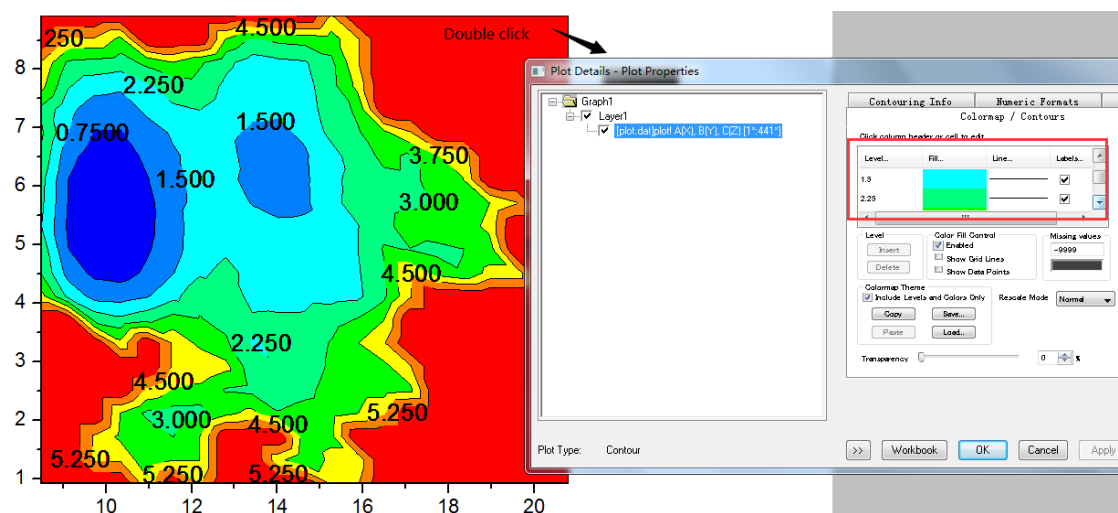


Figure 6. Cancel “Speed Mode”

- 5) If you want to show values on the contour lines, you can double click mouse on the contour and select the terms as shown in Figure 7.



**Figure 7.** Plotting contour

## References

- 1 Bai, Q. *et al.* Conformation Transition of Intracellular Part of Glucagon Receptor in Complex With Agonist Glucagon by Conventional and Accelerated Molecular Dynamics Simulations. *Front Chem* **7**, 851 (2019).