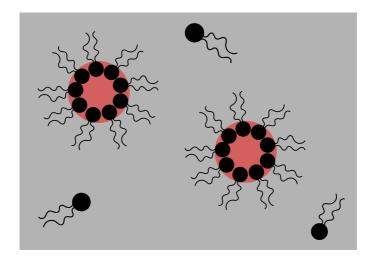
Molecular dynamics simulation of reverse micelles: problems after 25 years of investigations

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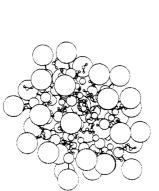
Reverse micelles

Reverse micelles form in nonpolar solutions of definite surfactants



Reverse micelles: first simulation...

...was carried out in 1988 (Brown and Clarke):



36 surfactant molecules

72 water molecules

1079 nonpolar solvent molecules

1403 atoms

 $1.6 \cdot 10^{-10}$ seconds — time scale

22 hours — calculating time

Today, 1 hour and 1 CPU are required for similar simulation

205 CPUs

Modern supercomputers

 10^5-10^7 atoms (1000 times more than in 1988)

 10^{-7} - 10^{-6} seconds of time scale (3000 times more than in 1988)

 10^3 – 10^5 CPU/GPU cores (app. 50 times more than in 1988)



Evident question

Is it possible to completely investigate all properties of reverse micelles: shape, structure, distribution of components, energy profiles, etc — by molecular dynamics simulation at some modern supercomputer during several days/weeks?

Evident question

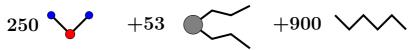
Is it possible to completely investigate all properties of reverse micelles: shape, structure, distribution of components, energy profiles, etc — by molecular dynamics simulation at some modern supercomputer during several days/weeks?

There are some problems,

and increased calculation power of modern supercomputers is not sufficient to solve these problems

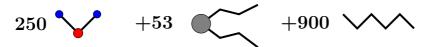
Prepare to MD: Initial geometry

Step 1. Choice of constant number of particles N:

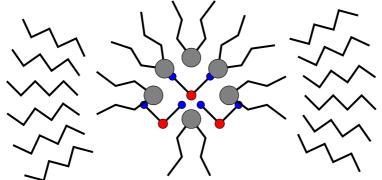


Prepare to MD: Initial geometry

Step 1. Choice of constant number of particles N:



Step 2. Choice of spatial arrangement of these molecules:



Initial geometry for proteins

First question: how many molecules?

Simple answer: 1 main molecule

Second question: how to distribute this molecule?

Answer: There are two possible ways

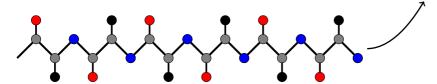
Initial geometry for proteins

Way 1. Use X-Ray structural analysis:

Protein data bank gives tertiary structure

 ${\bf http://www.rcsb.org/pdb/home/home.do}$

Way 2. Try to use protein primary structure:



Primary structure becomes tertiary structure during MD if we have quite appropriate simulation technique

First question: how many molecules?

Two types of main molecules — water and surfactant

 \boldsymbol{x} water and \boldsymbol{y} surfactant molecules

 \boldsymbol{x} and \boldsymbol{y} are independent

Second question: how to distribute these molecules?

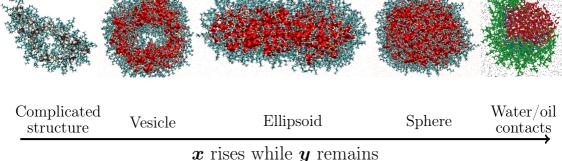
There are two possible ways

- 1. Preassembled micelle
- 2. Random distributed molecules

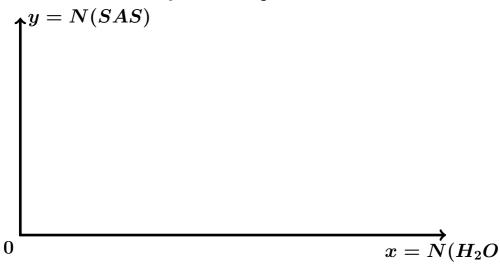
How to choose \boldsymbol{x} waters and \boldsymbol{y} surfactants?

- 1. Try to use information from experiment
- 2. Try to guess \boldsymbol{x} and \boldsymbol{y}
- We should remember that experiment information is available only for widely investigated reverse micelles
- Accuracy of \boldsymbol{x} and \boldsymbol{y} is not sufficient even if reverse micelles are widely studied

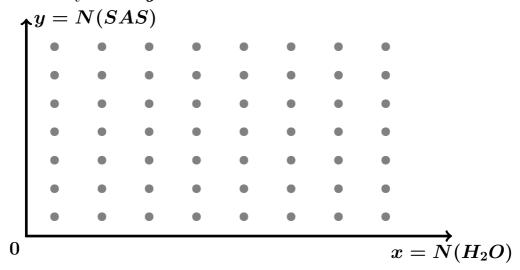
Single aggregate will form at any \boldsymbol{x} and \boldsymbol{y} There are 5 structures at different \boldsymbol{x} and \boldsymbol{y}



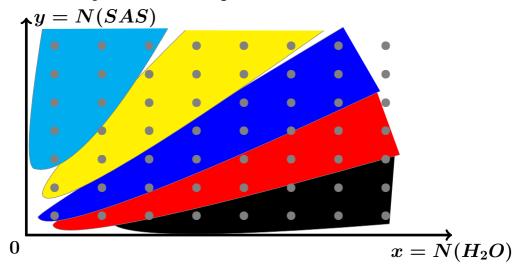
Because of the accuracy of \boldsymbol{x} and \boldsymbol{y} is not sufficient:



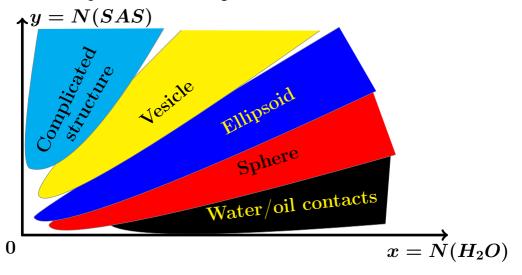
Choose any \boldsymbol{x} and \boldsymbol{y} :



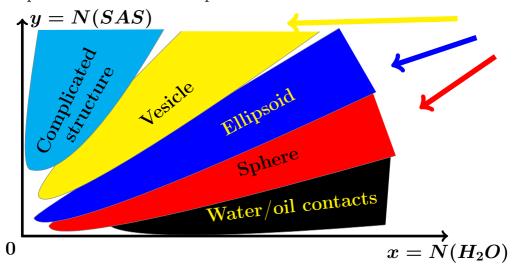
Structure depends of \boldsymbol{x} and \boldsymbol{y} :



Structure depends on \boldsymbol{x} and \boldsymbol{y} :



Compare structure with experiment:

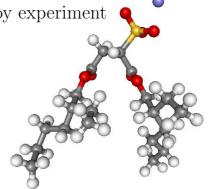


Reverse micelles of Aerosol OT

Reverse micelles of Aerosol OT:

1. are the most widely investigated by experiment

2. have spherical shape



Reverse micelles of Aerosol OT

Cell size: 12–15 nanometers

30000-300000 atoms

Preassembled micelle as initial geometry

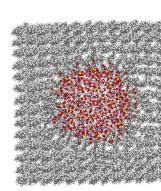
Time scale -20-50 nanoseconds

Cores of CPU: 8

(at Institute of Problems of Chemical Physics, RAS)

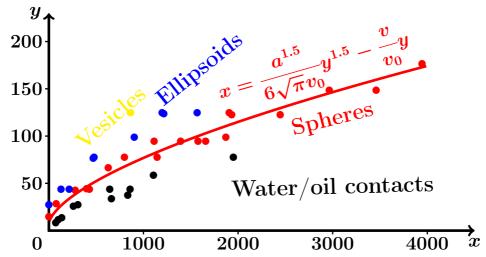


Number of calculations: 20–50



Reverse micelles of Aerosol OT

Save the micelles with spherical shape:



Thank you for attention!