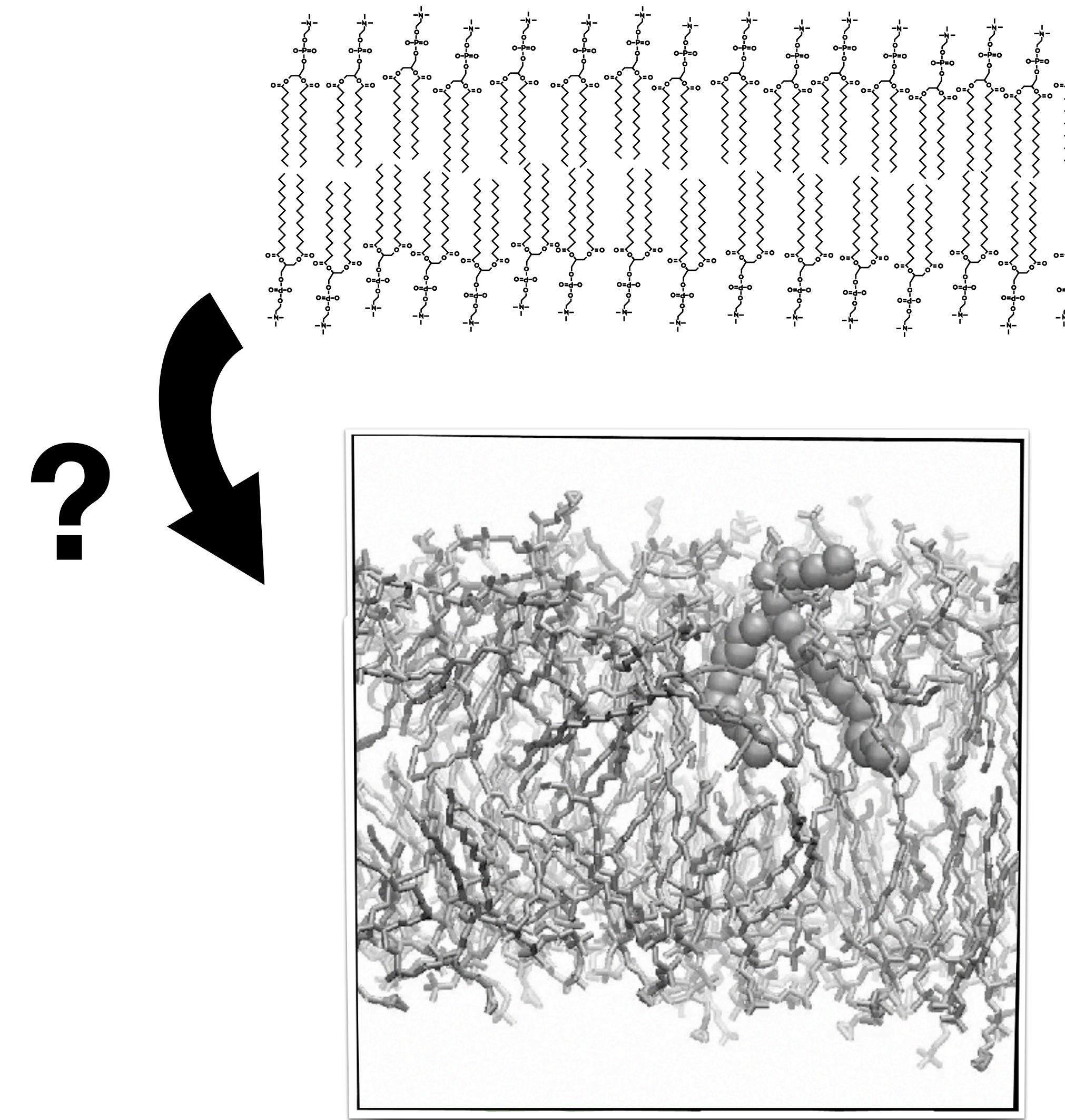


# Introduction to lipid bilayer MD simulations and applications

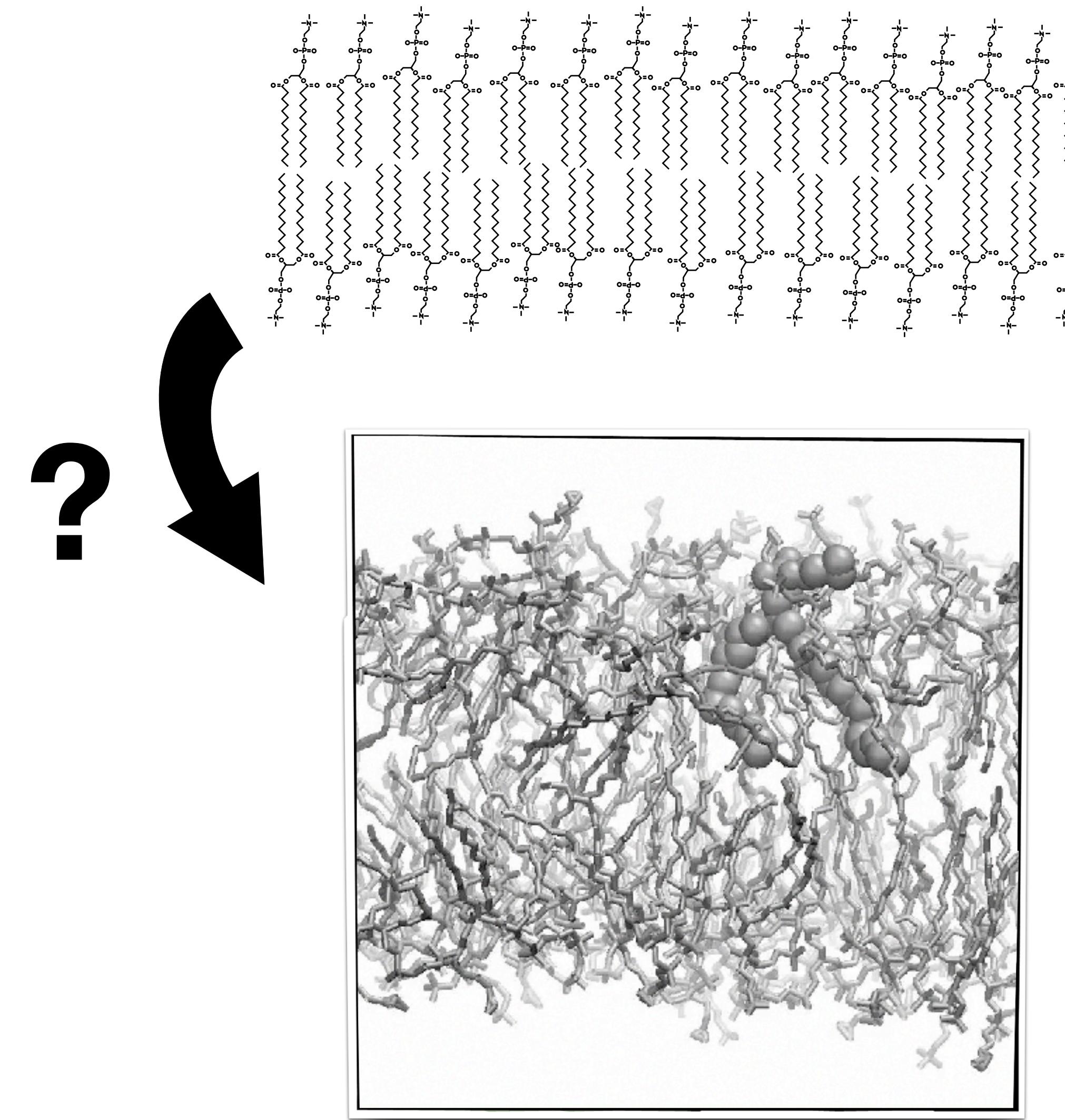
markus.miettinen@uib.no

NMRlipids summer school  
Helsinki, June 1<sup>st</sup> 2022

# Simulating biomolecular systems

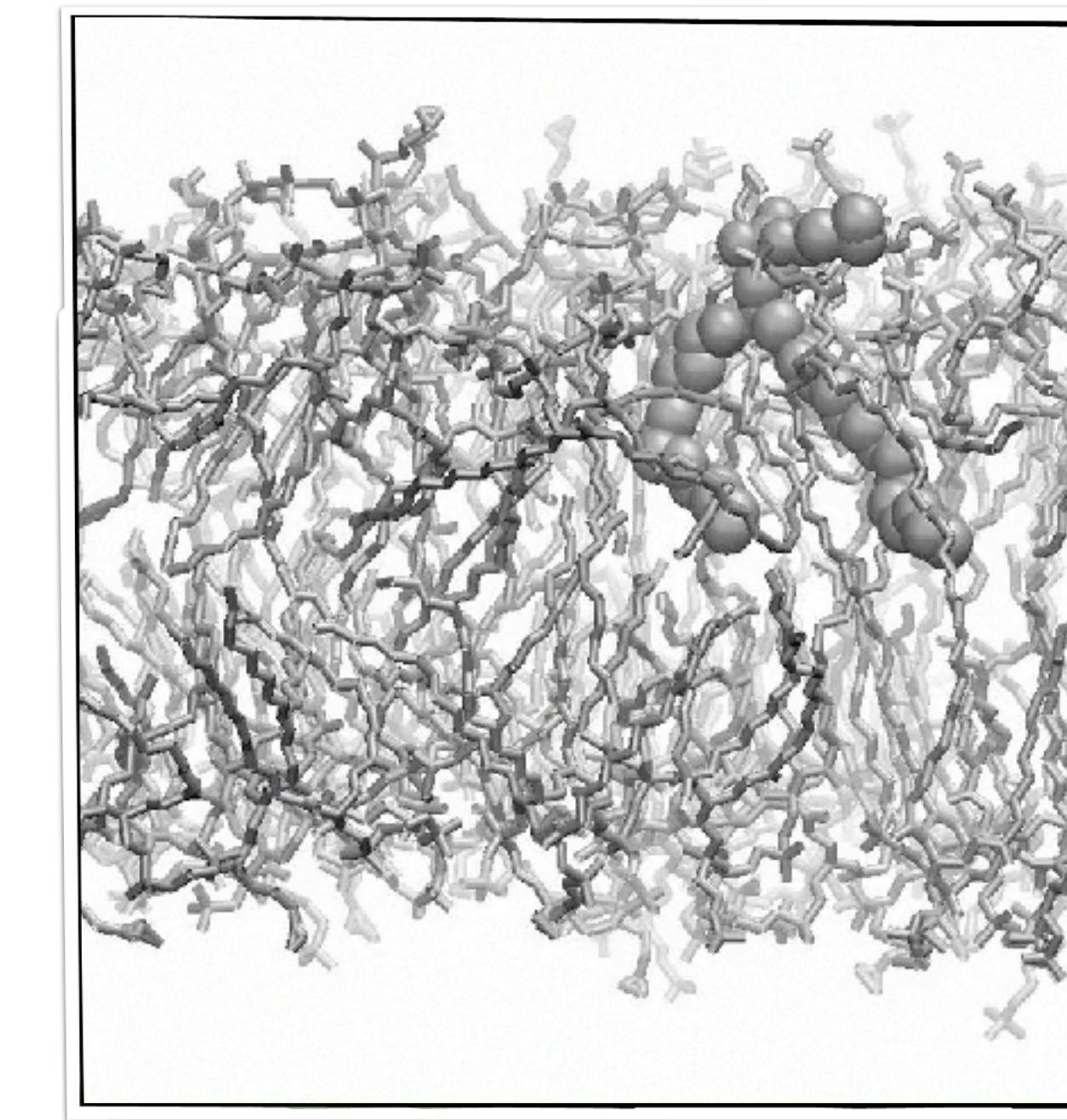
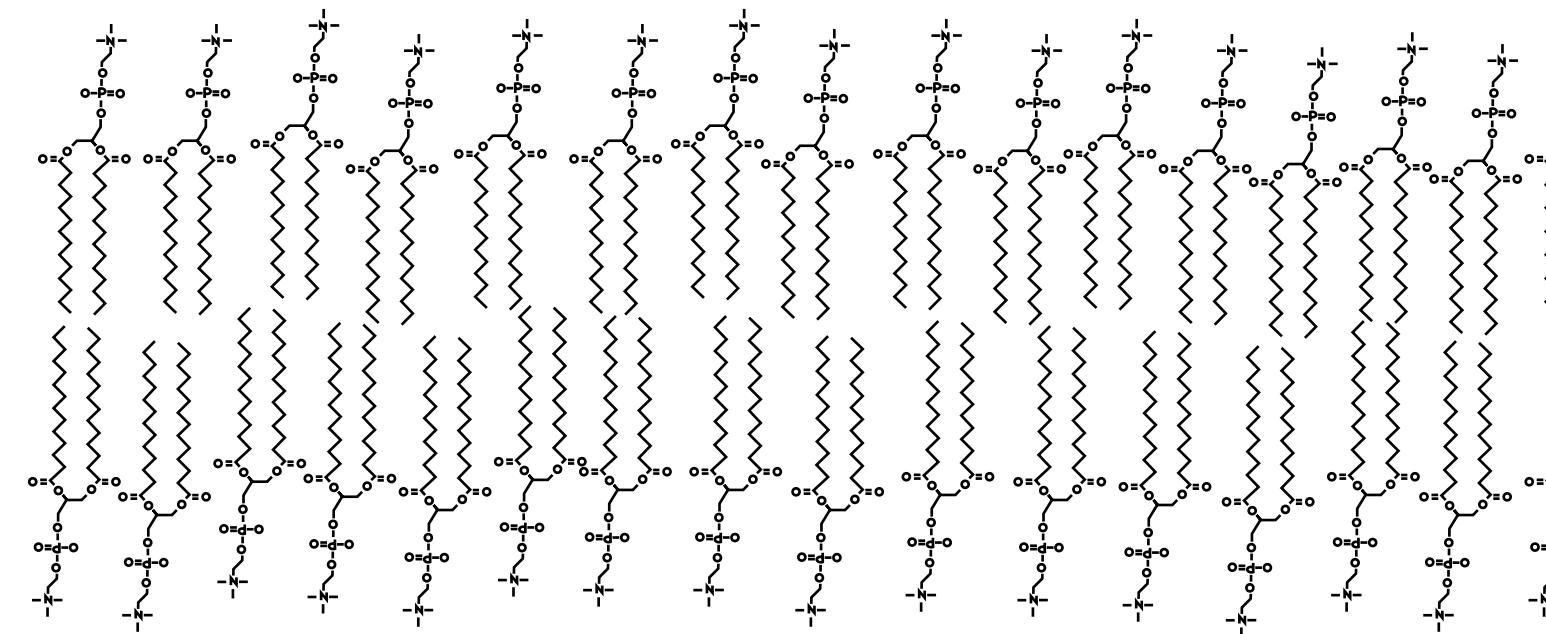


# Simulating biomolecular systems

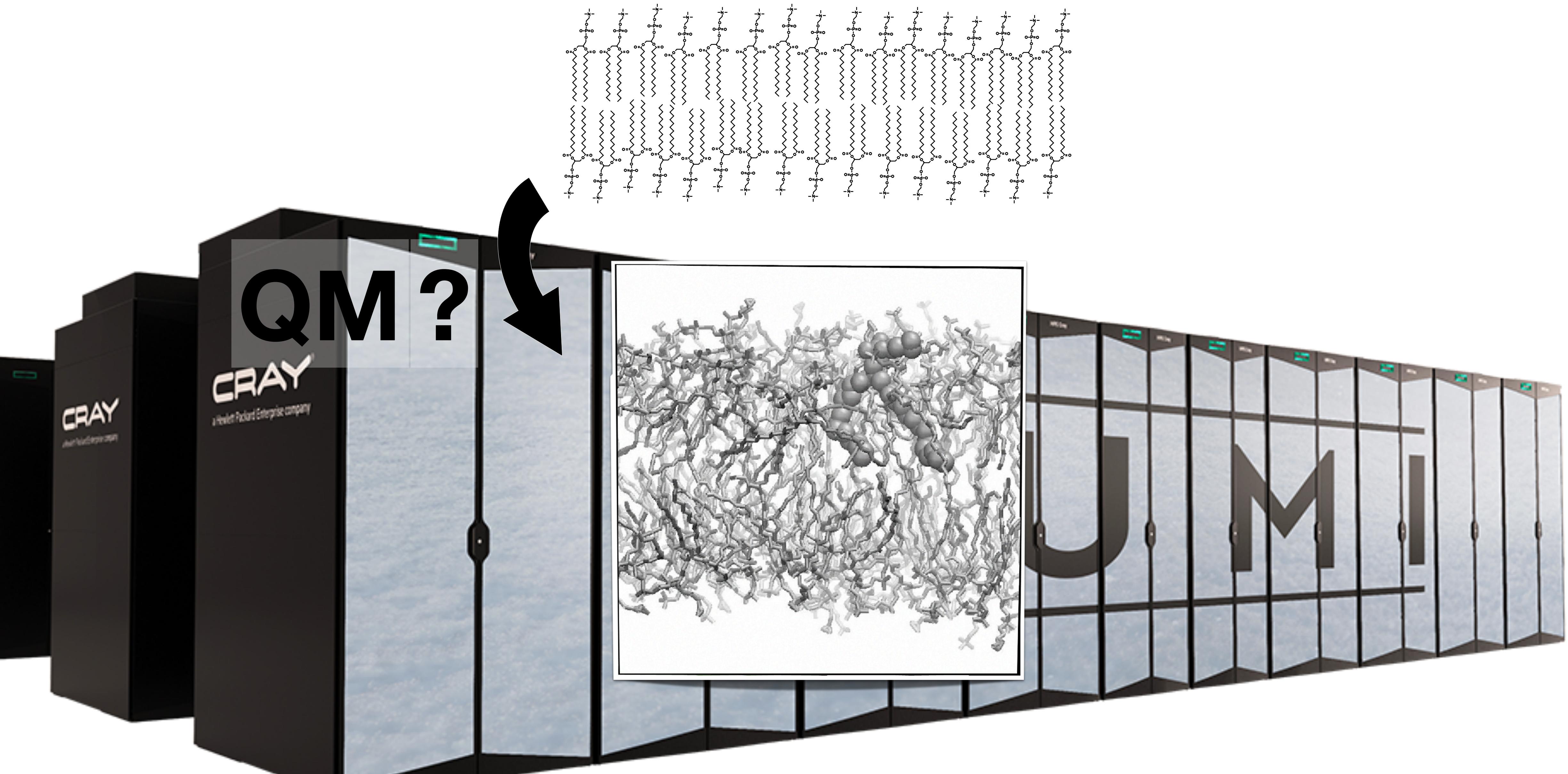


# Simulating biomolecular systems

QM ? ↘

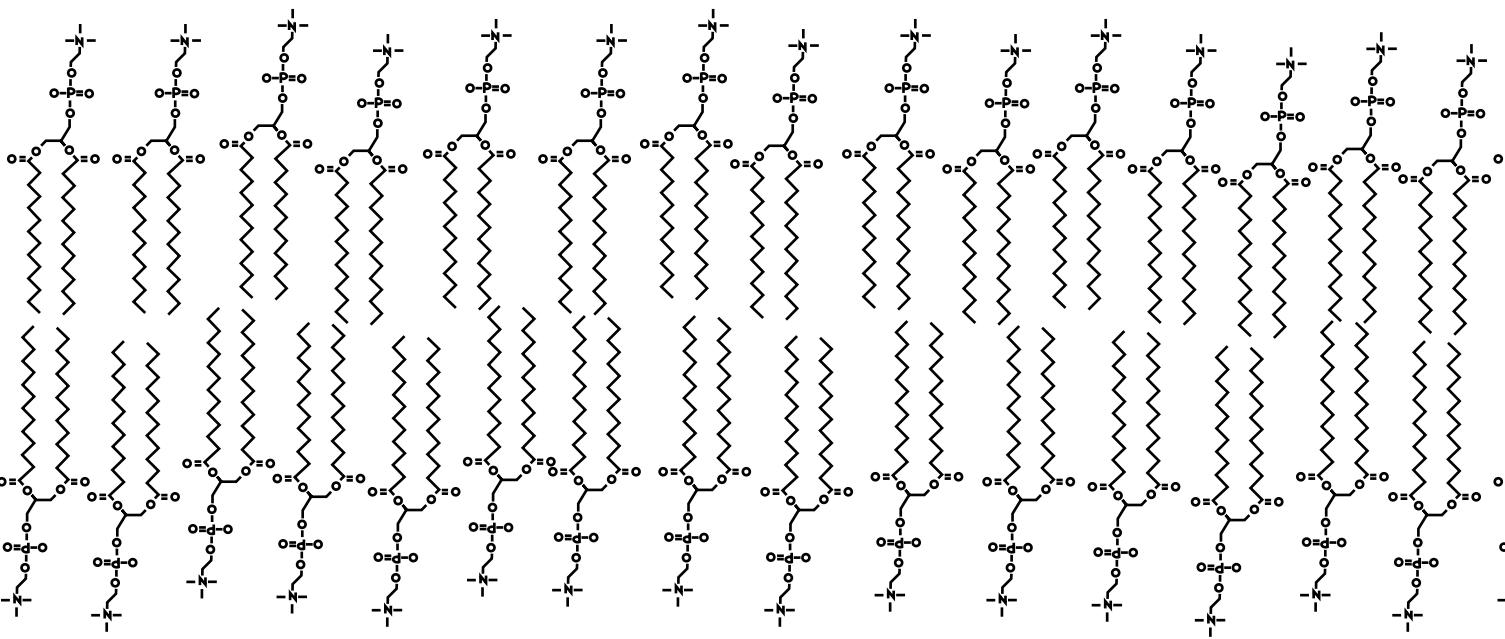


# Simulating biomolecular systems

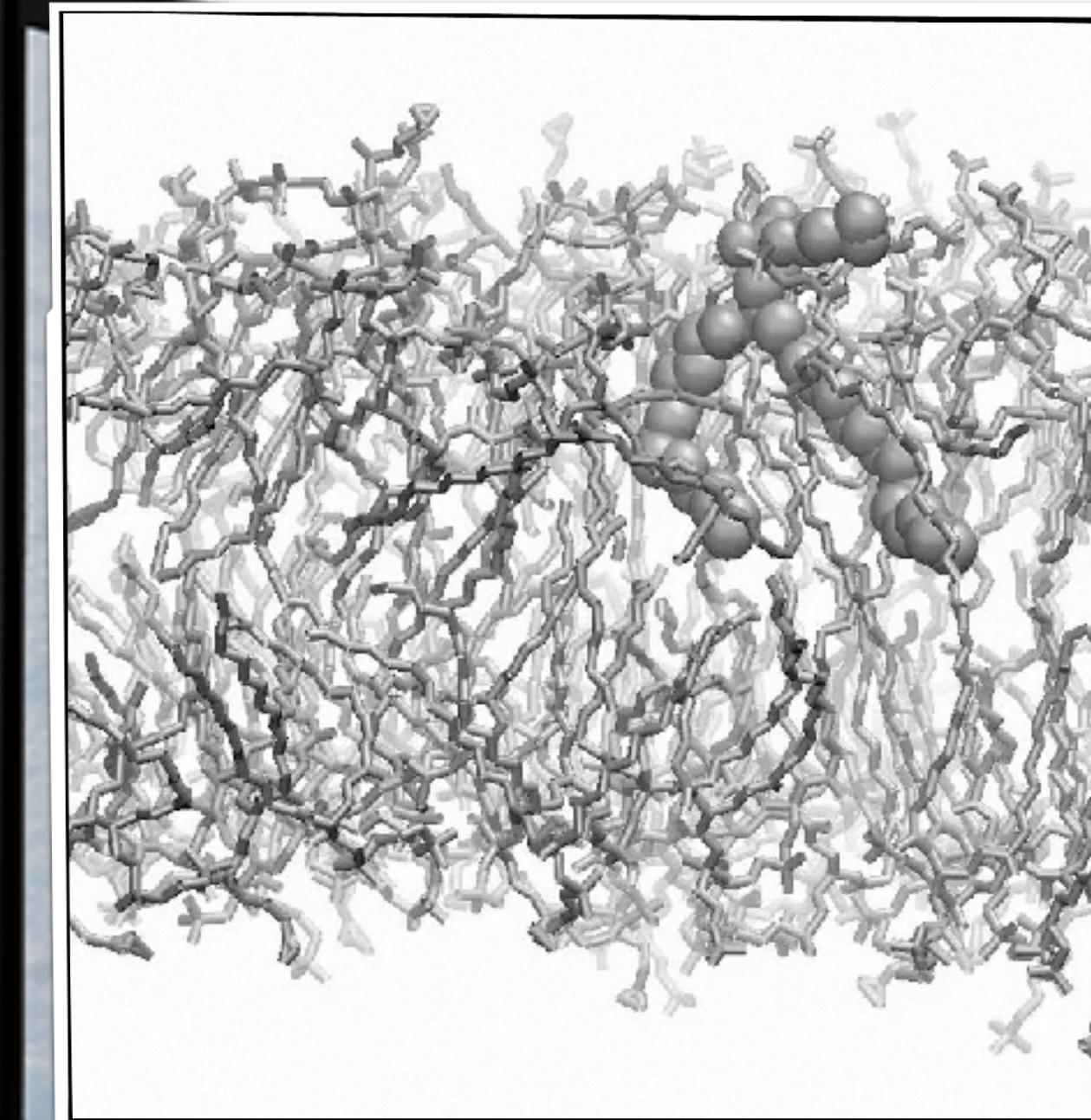


# Simulating biomolecular systems

1

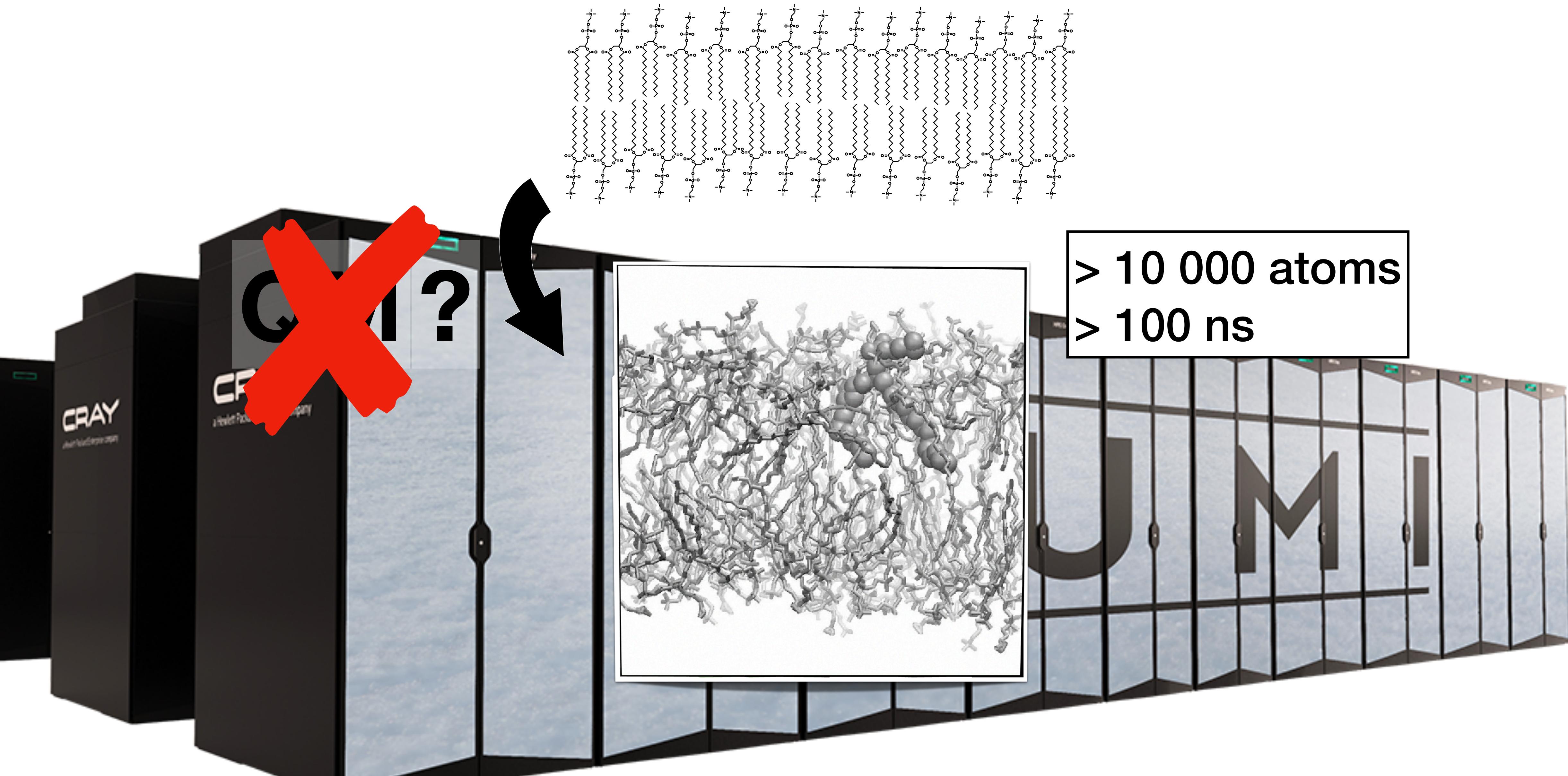


# QM?

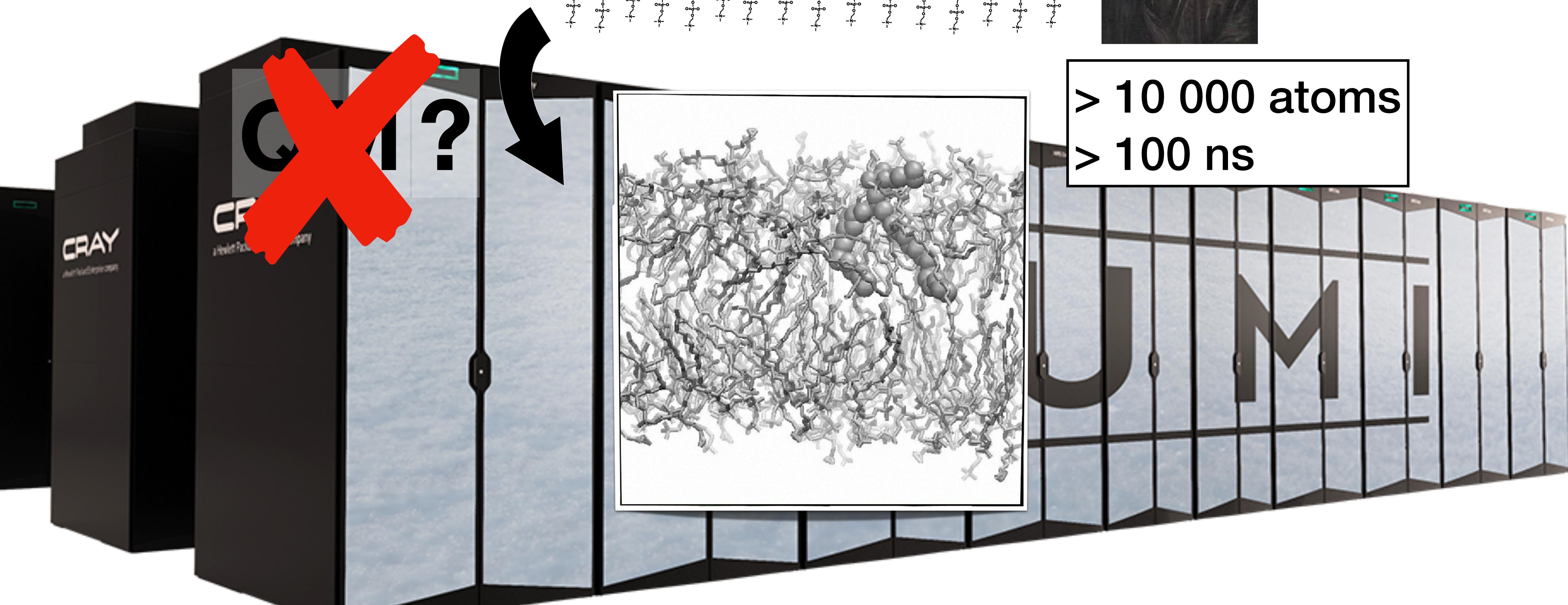


$\nabla > 10\ 000$  atoms  
 $\nabla > 100$  ns

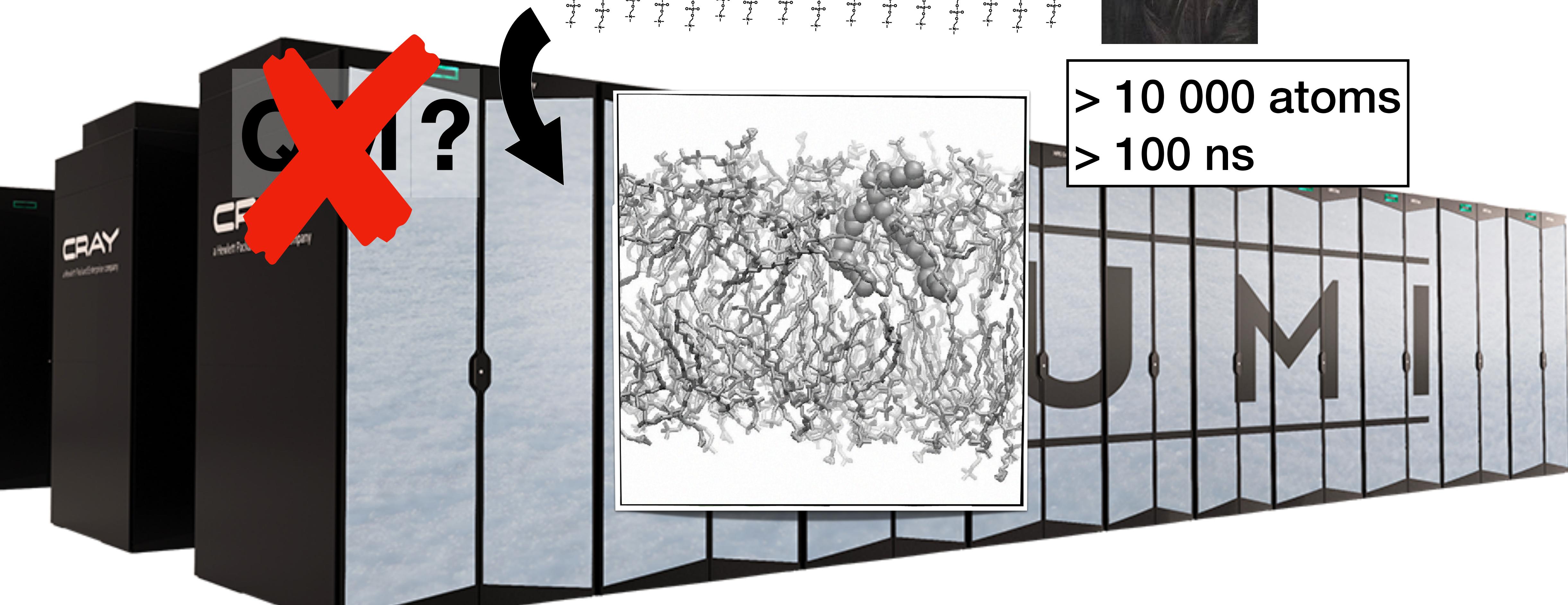
# Simulating biomolecular systems



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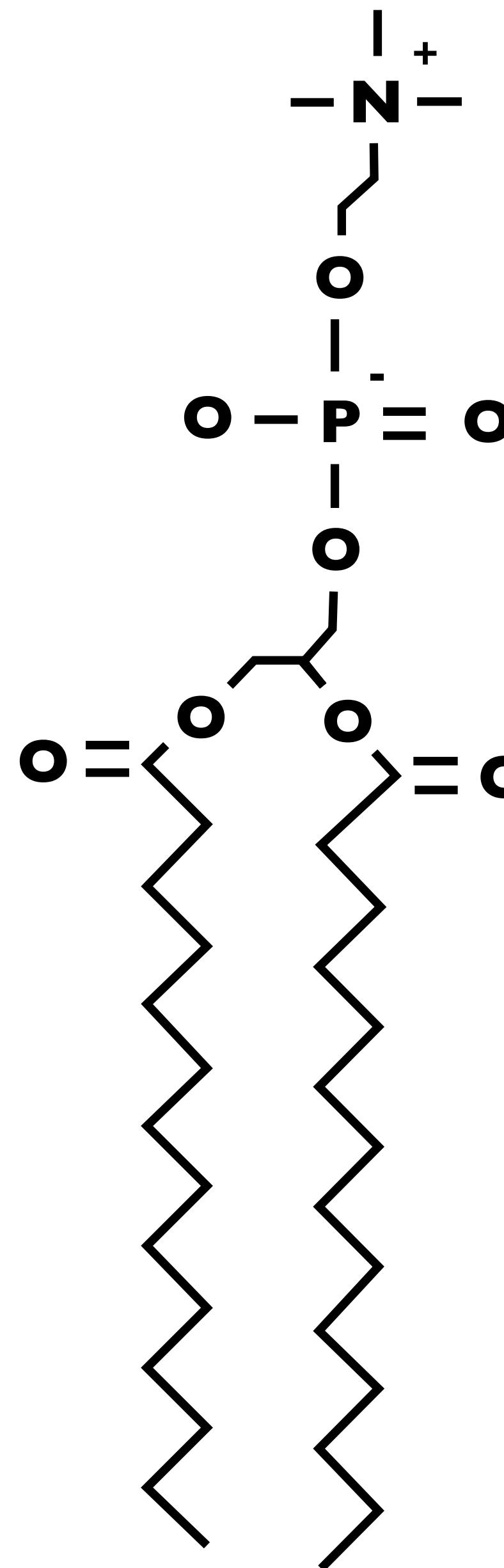
# Simulating biomolecular systems



# Molecular Dynamics simulations

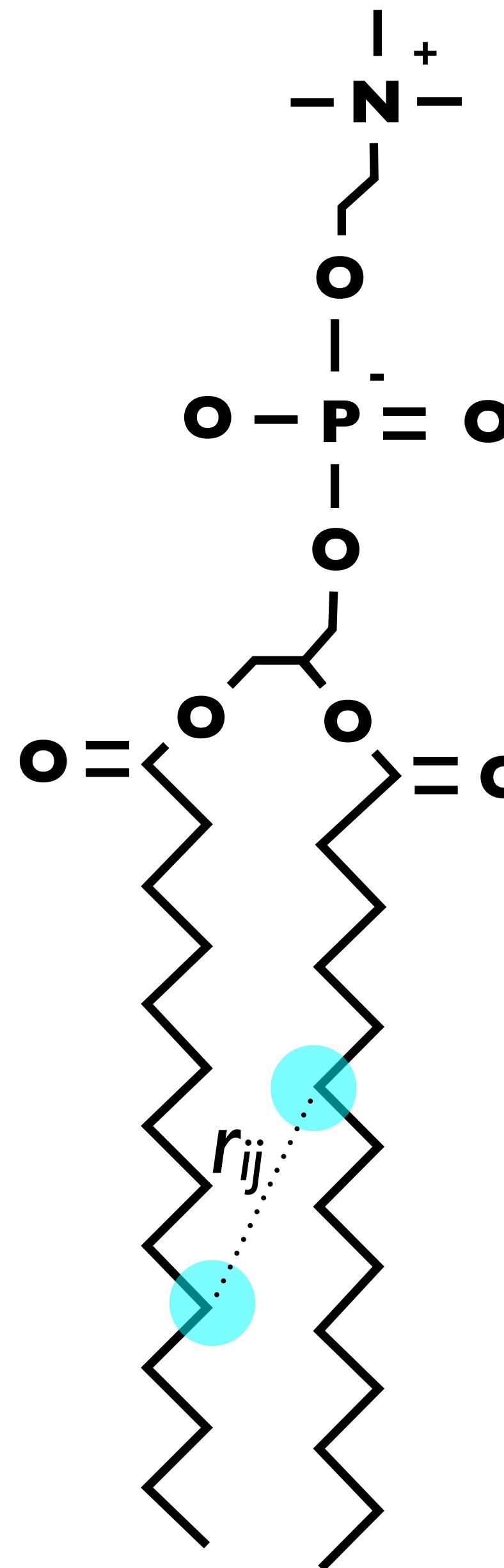
The (inherently quantum mechanical) interactions of atoms are approximated by classical position-dependent potentials:

# Molecular Dynamics simulations



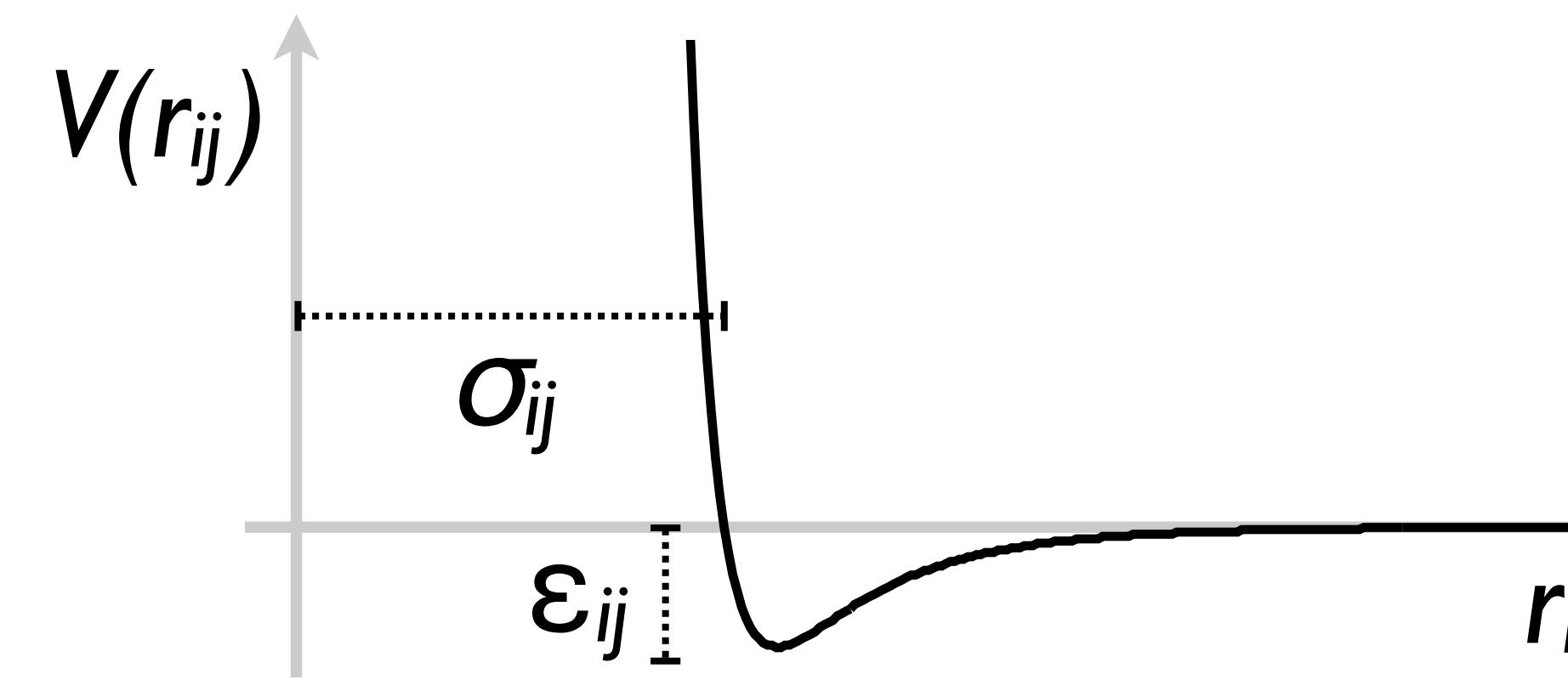
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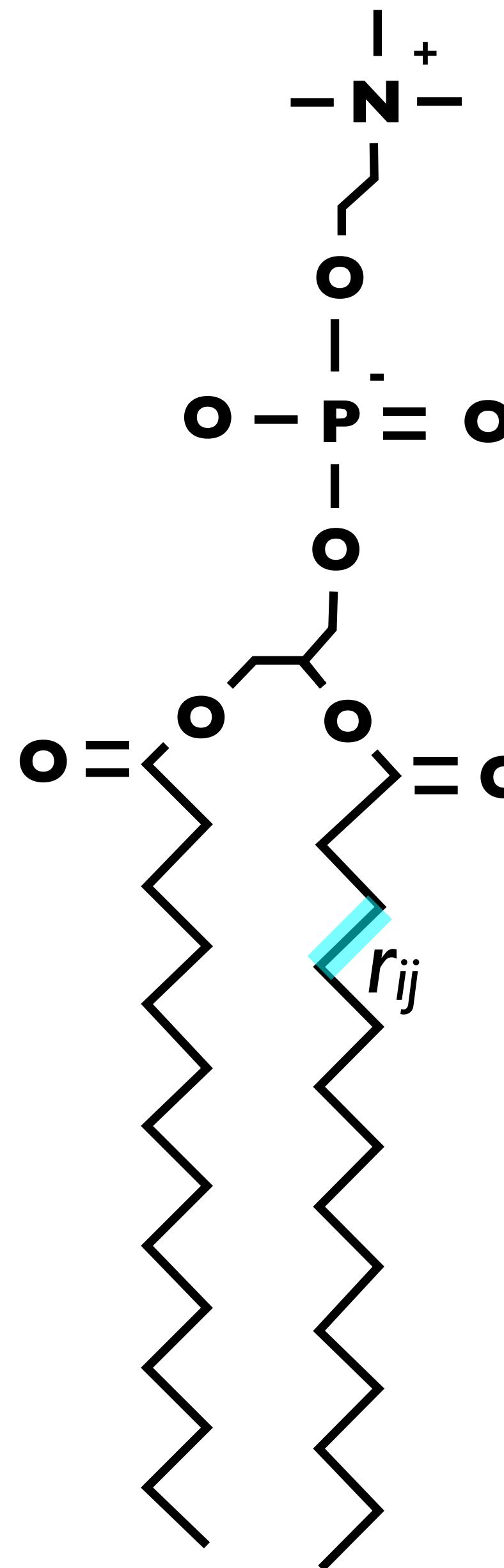


The (inherently quantum mechanical) interactions of atoms are approximated by classical position-dependent potentials:

I) non-bonded interactions

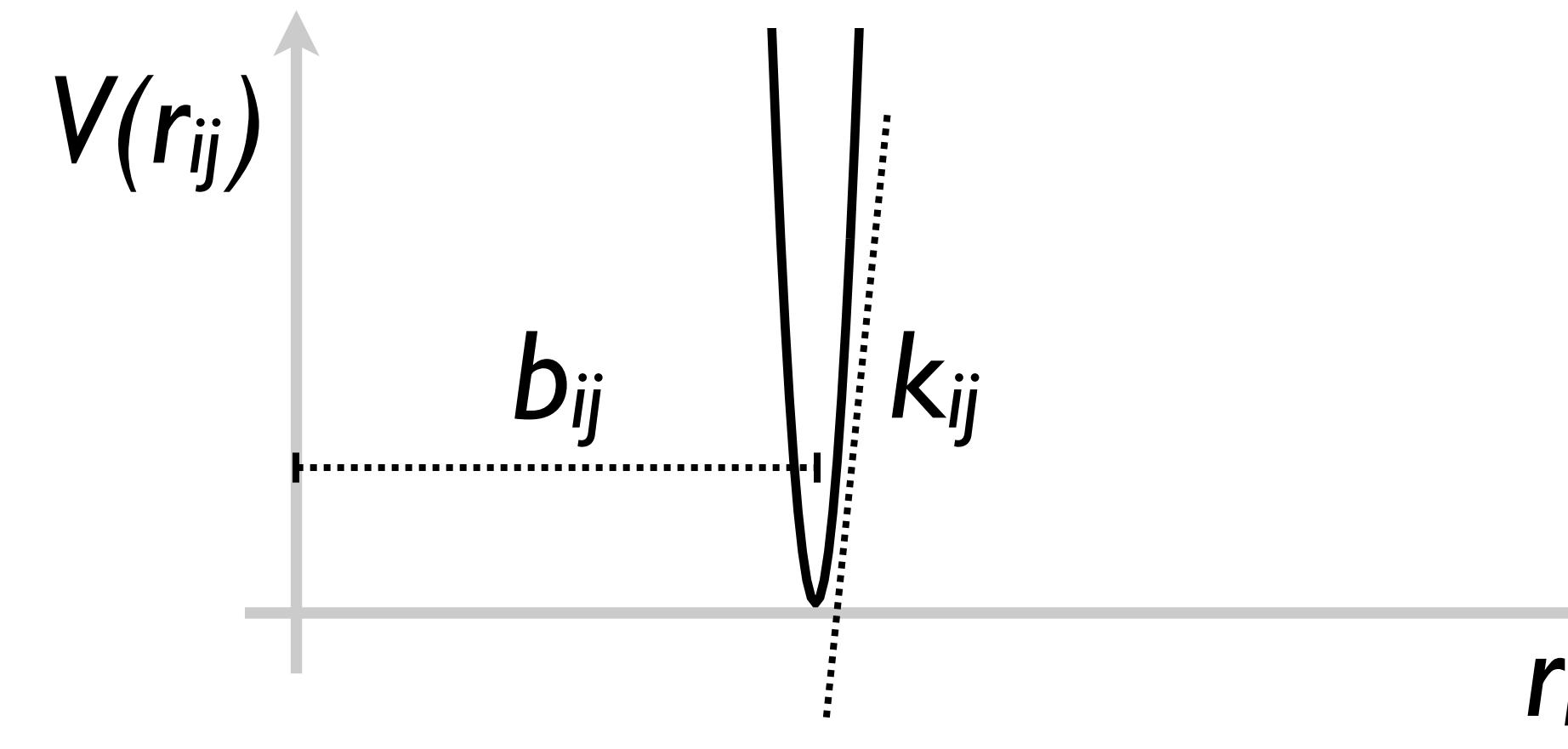


# Molecular Dynamics simulations

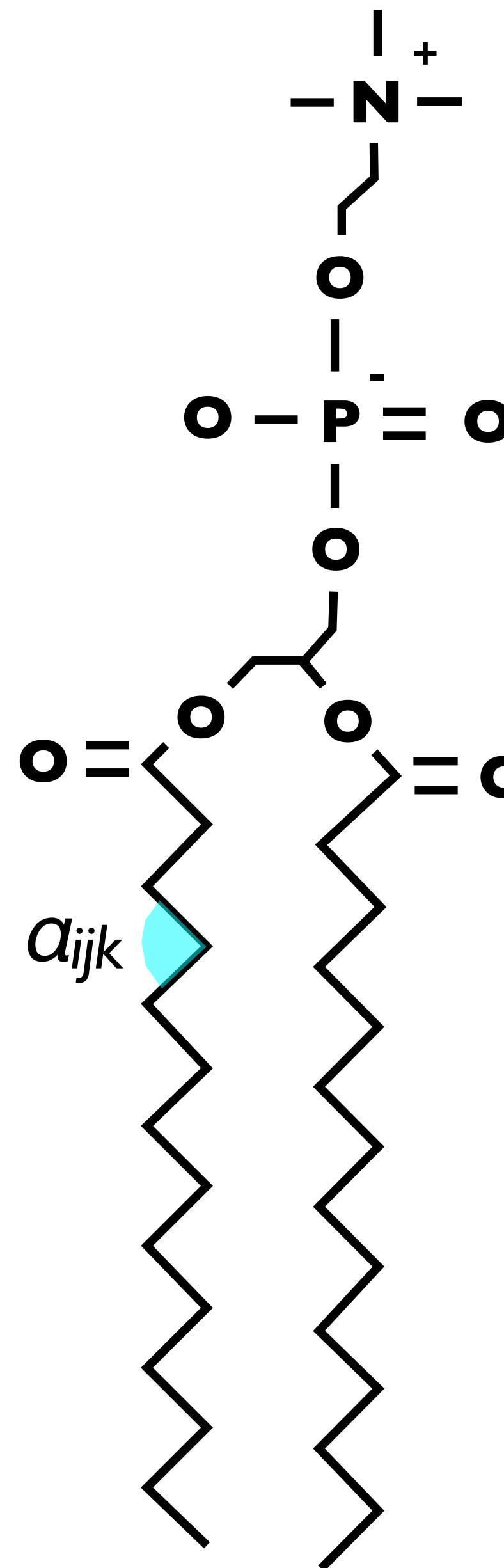


The (inherently quantum mechanical) interactions of atoms are approximated by classical position-dependent potentials:

- 1) non-bonded interactions
- 2) bonds

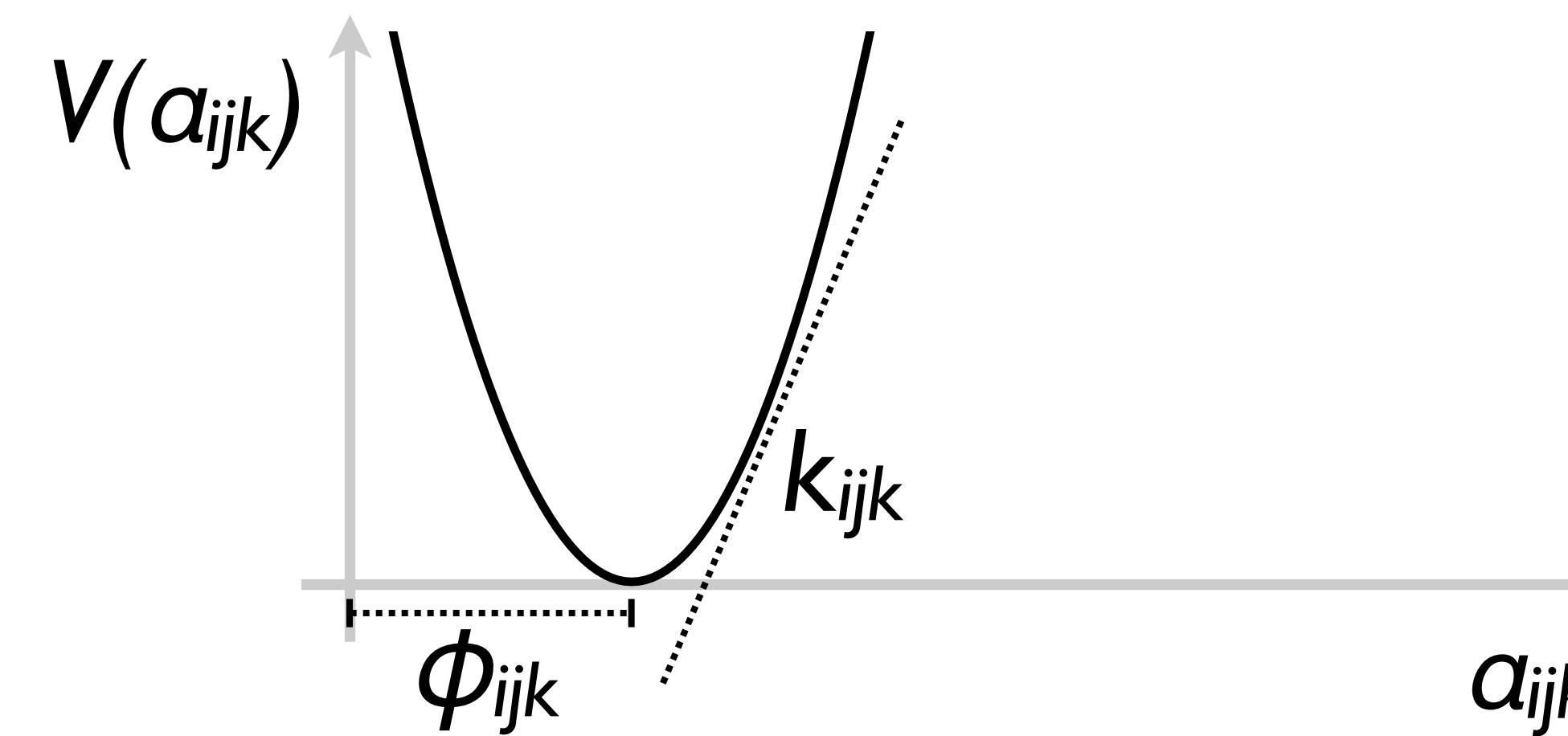


# Molecular Dynamics simulations

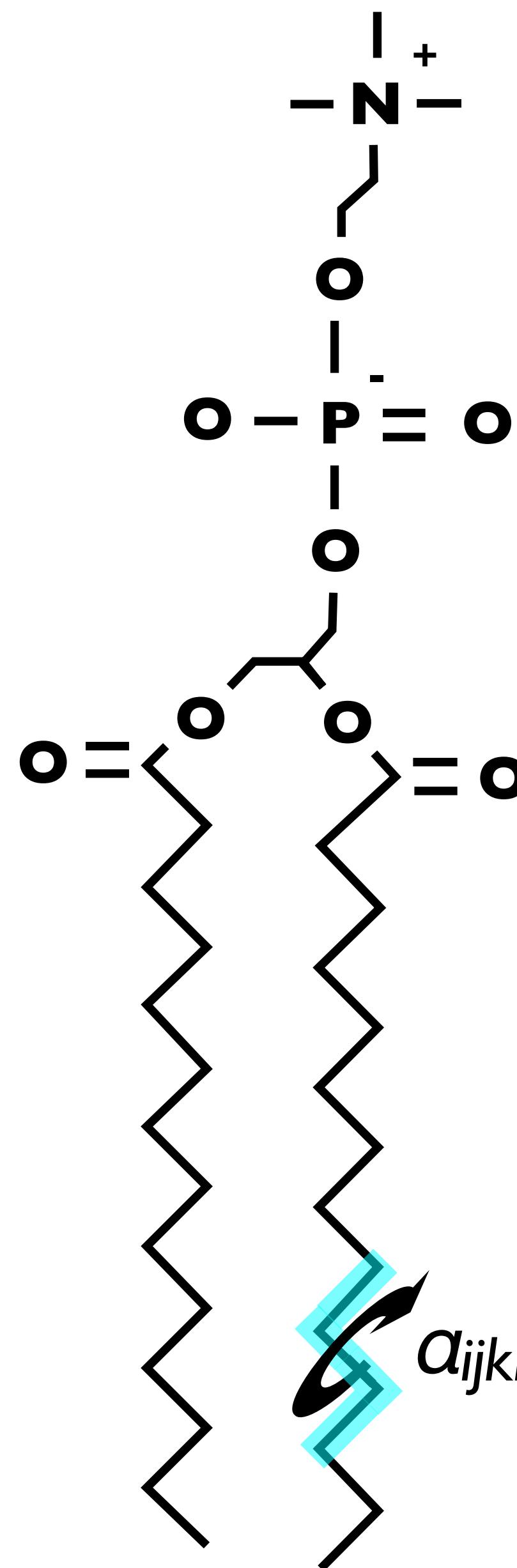


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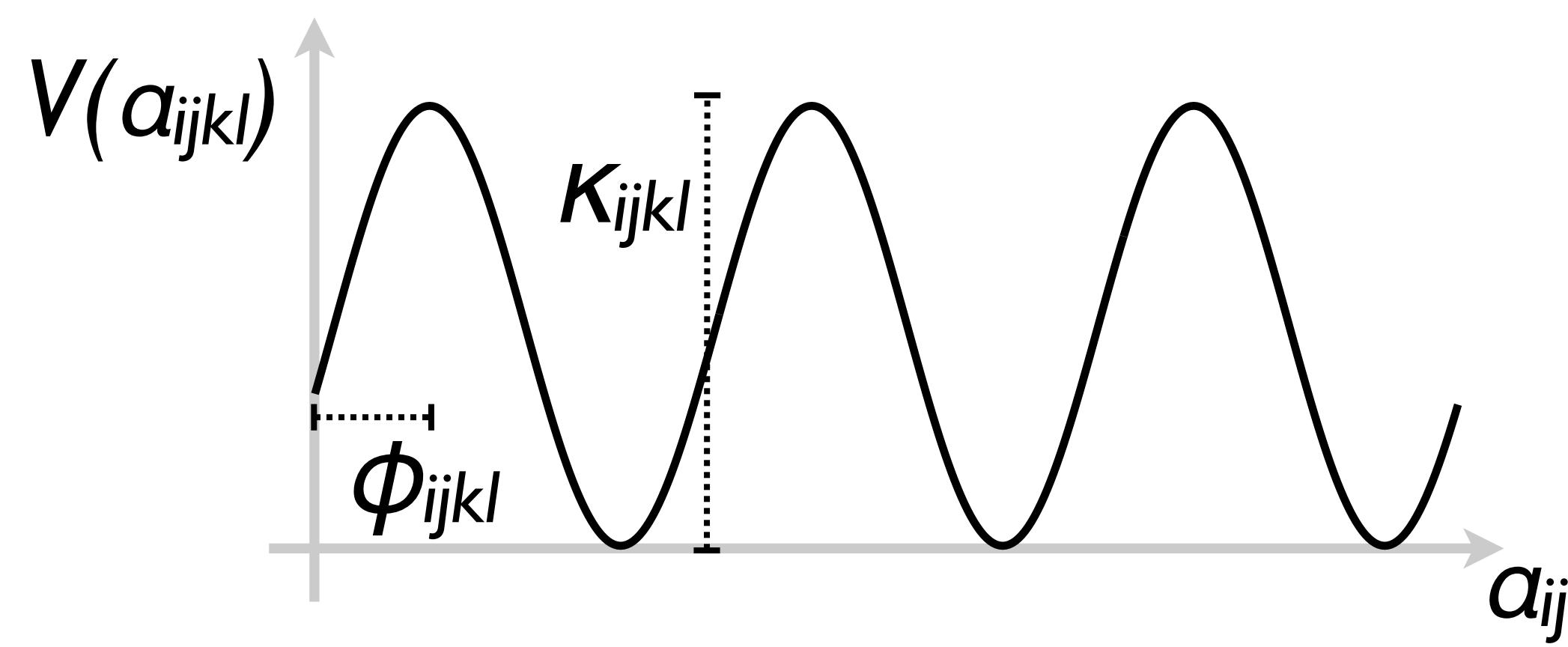


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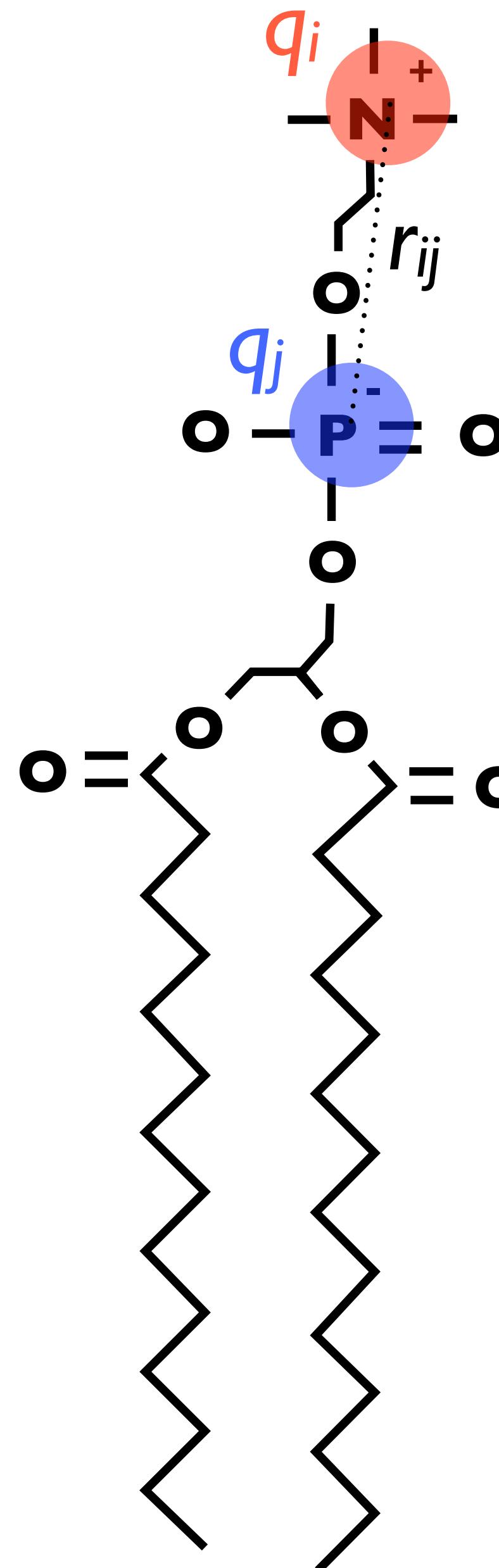


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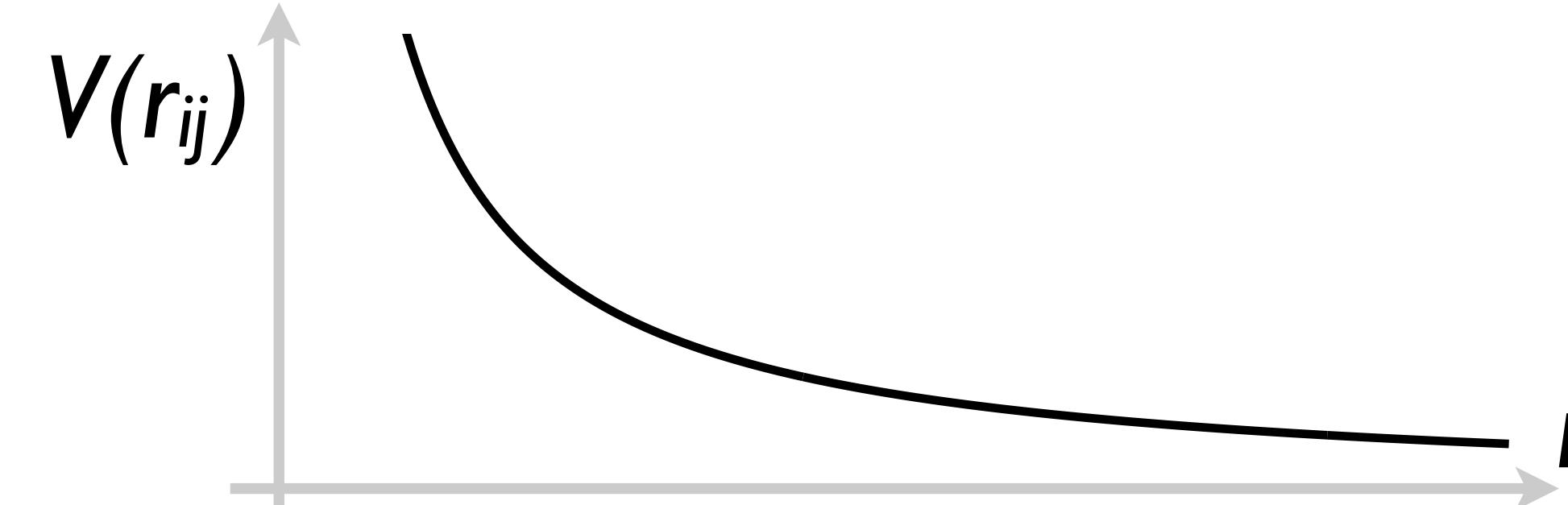


# Molecular Dynamics simulations

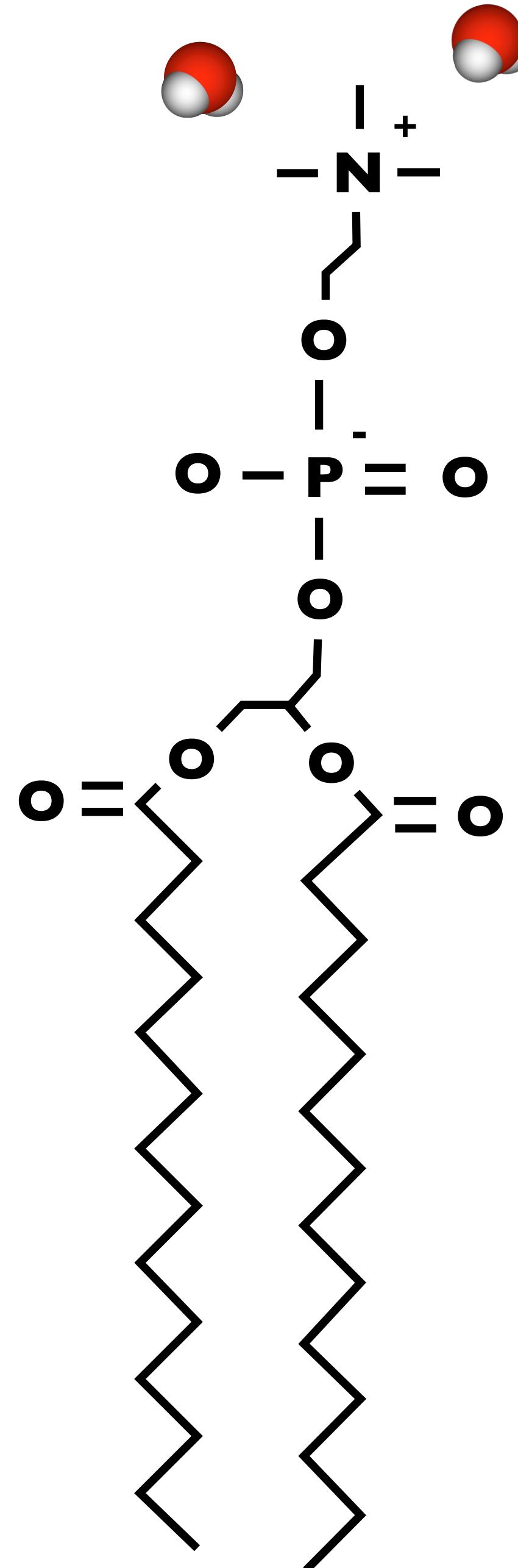


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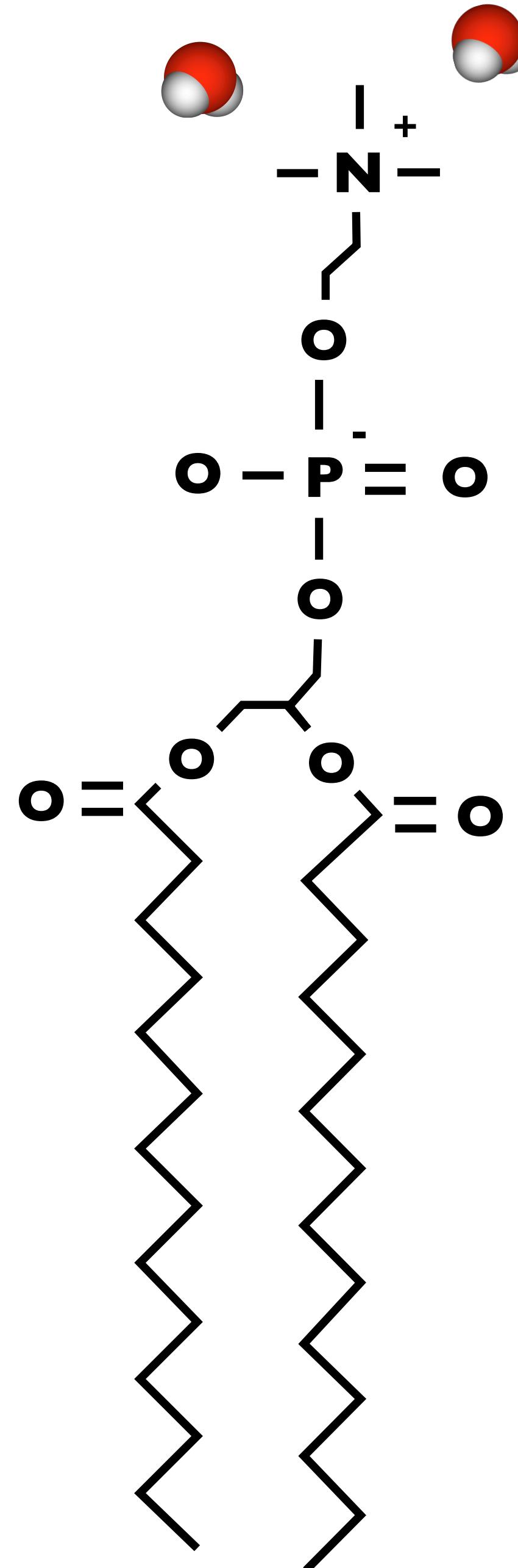
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**‘Force field’**  
(> 100 parameters)

# Three commonly known facts about **force fields**:

1

They determine all the molecular detail.

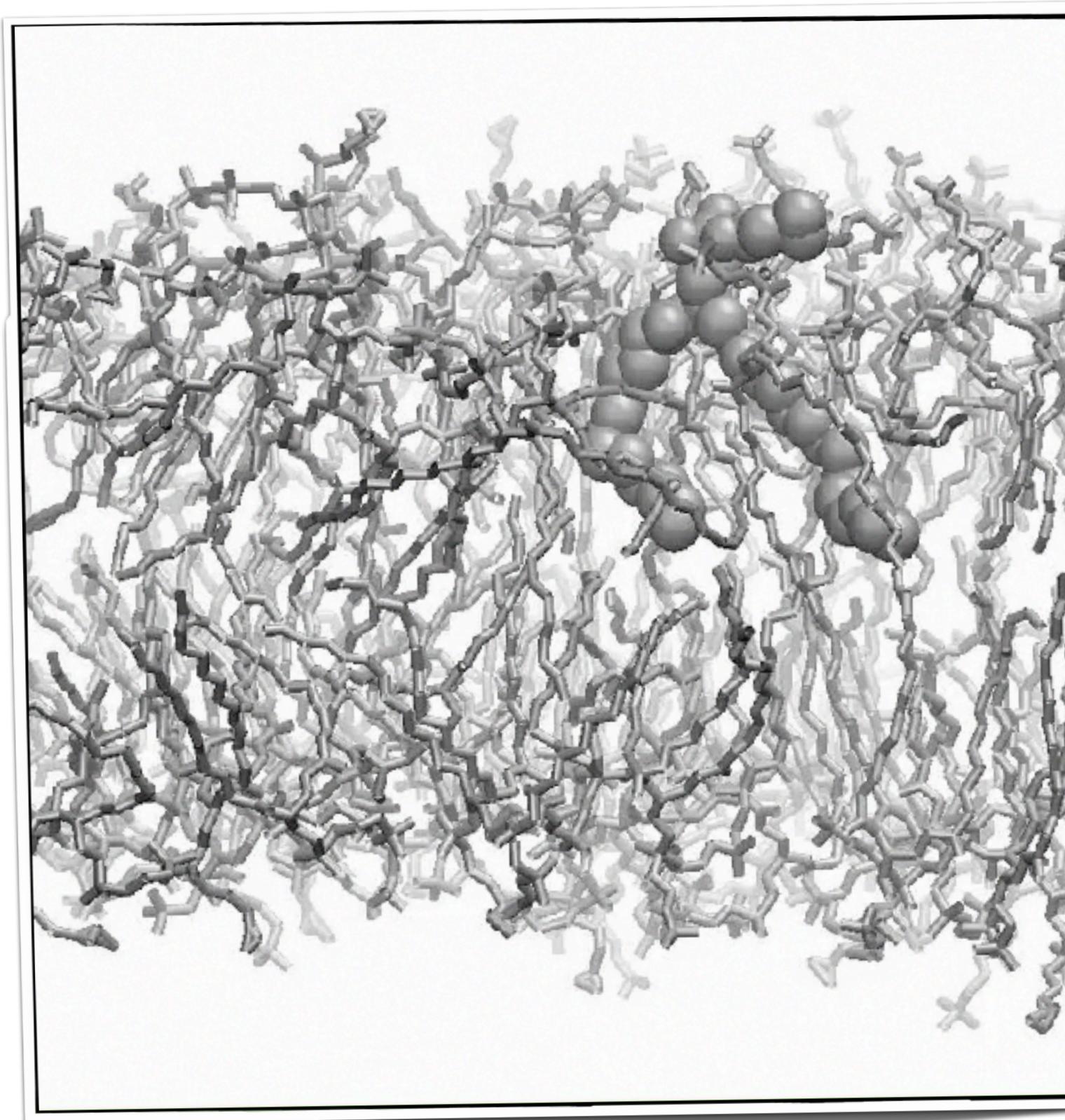
2

None of them is perfect.

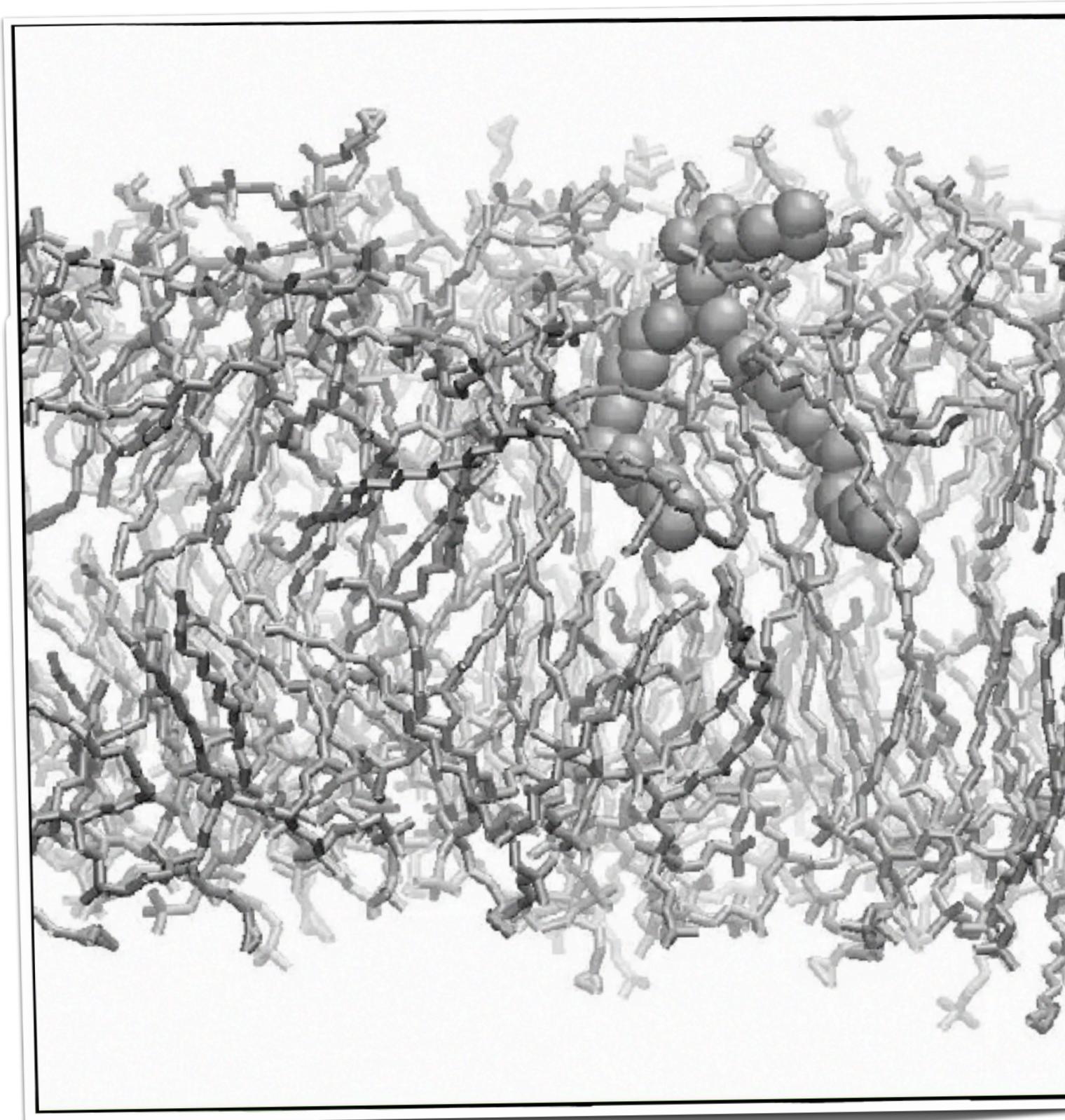
3

Testing and developing them is hard work —  
and hard to fund.

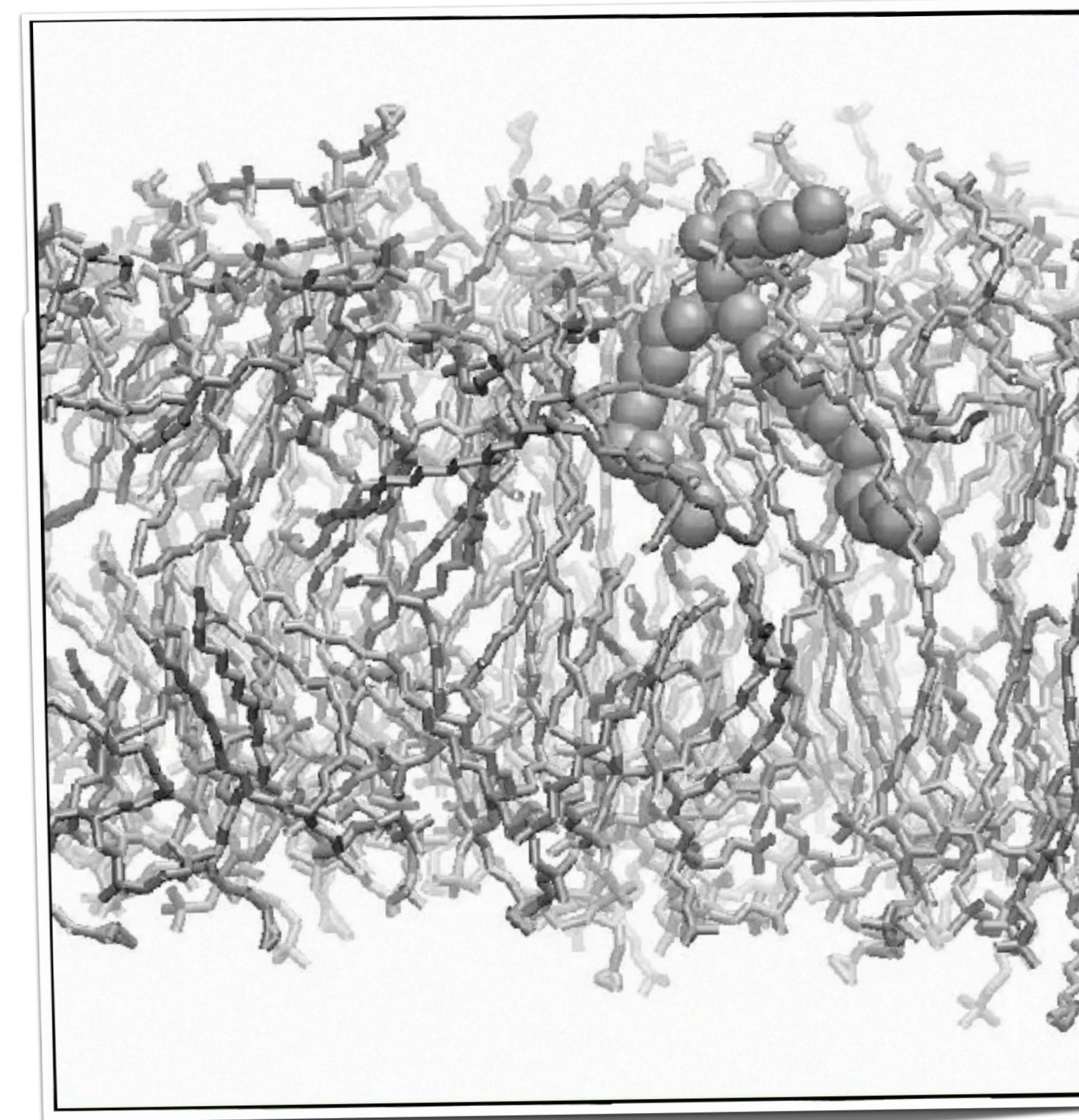
# So you do get this:



# So you do get this:

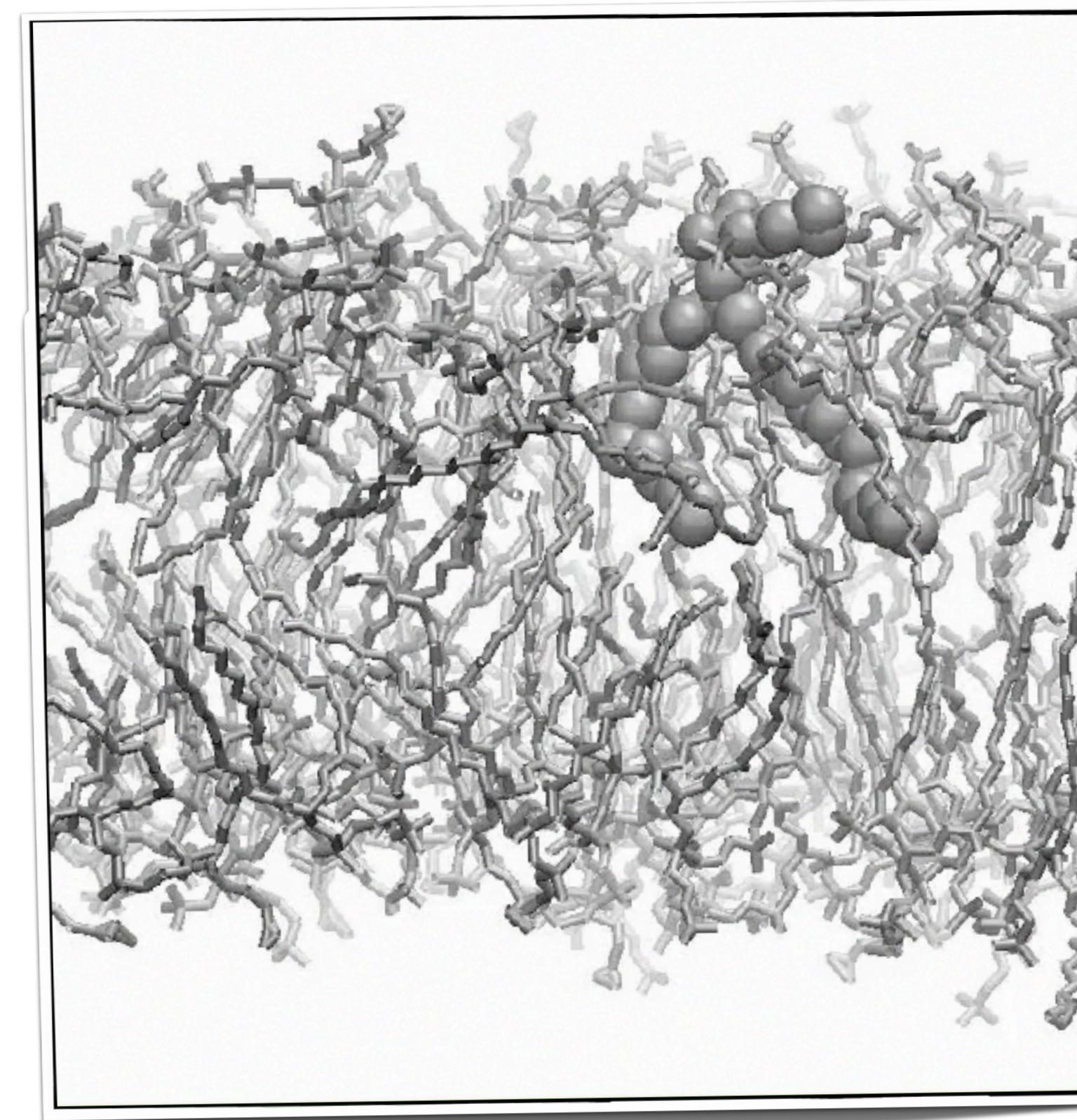


So you do get this:



But is it what actually happens?

So you do get this:



But is it what actually happens?  
No, not quite. But more on this at 16:30.

# Time integration, or “How do you make them move?”

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**First guess: Would just a Taylor expansion in time work?**

$$x(t+\Delta) = x(t) + x'(t)\Delta + (x''(t)/2)\Delta^2$$

# Time integration, or “How do you make them move?”

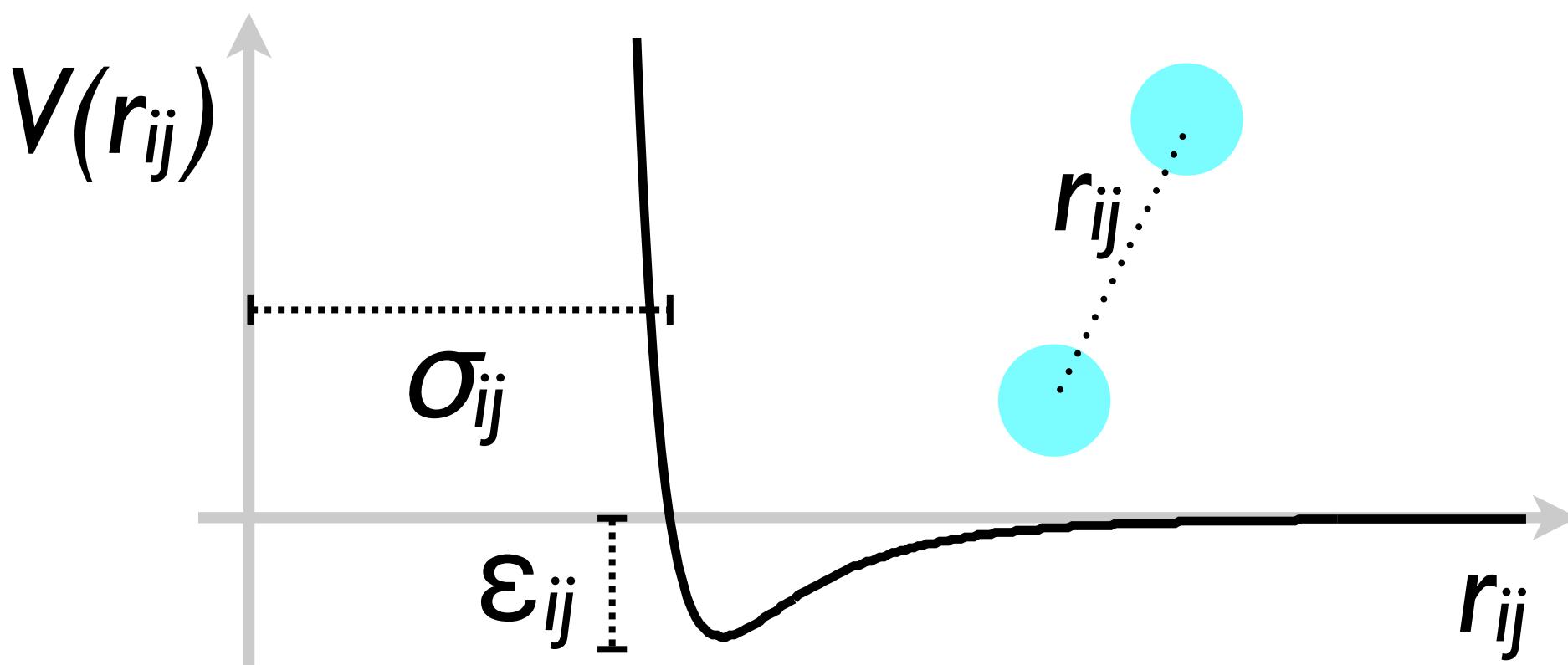
**First guess: Would just a Taylor expansion in time work?**

$$\begin{aligned}x(t+\Delta) &= x(t) + x'(t)\Delta + (x''(t)/2)\Delta^2 \\&= x(t) + v(t)\Delta + (F(t)/2m)\Delta^2\end{aligned}$$

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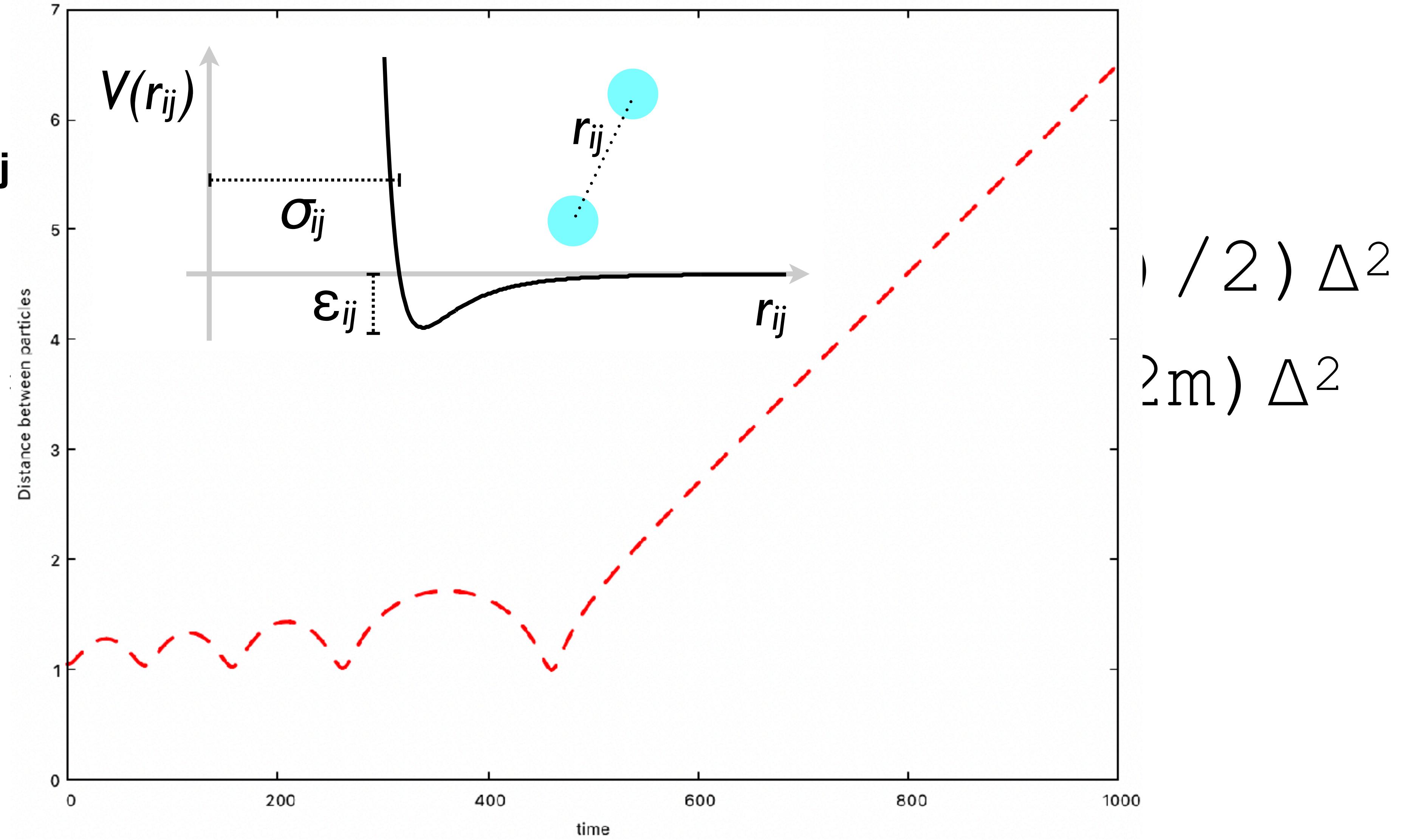
$$\begin{aligned}
 x(t+\Delta) &= & (x''(t)/2)\Delta^2 \\
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 \end{aligned}$$



# Time integration, or “How do you make them move?”

**First guess: Would j**

$x(t + \Delta)$



# Time integration, or “How do you make them move?”

First guess: Would just a Taylor expansion in time work?

$$\begin{aligned}x(t+\Delta) &= x(t) + \cancel{x'(t)} \Delta + (x''(t)/2) \Delta^2 \\&= x(t) + \cancel{\tau} \Delta + (F(t)/2m) \Delta^2\end{aligned}$$

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**Second guess:**

$$\begin{aligned}x(t+\Delta) &= x(t) + v(t) \Delta + (F(t)/2m) \Delta^2 \\x(t-\Delta) &= x(t) - v(t) \Delta + (F(t)/2m) \Delta^2\end{aligned}$$

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# Time integration. or

**“How**

**First guess:** Would just

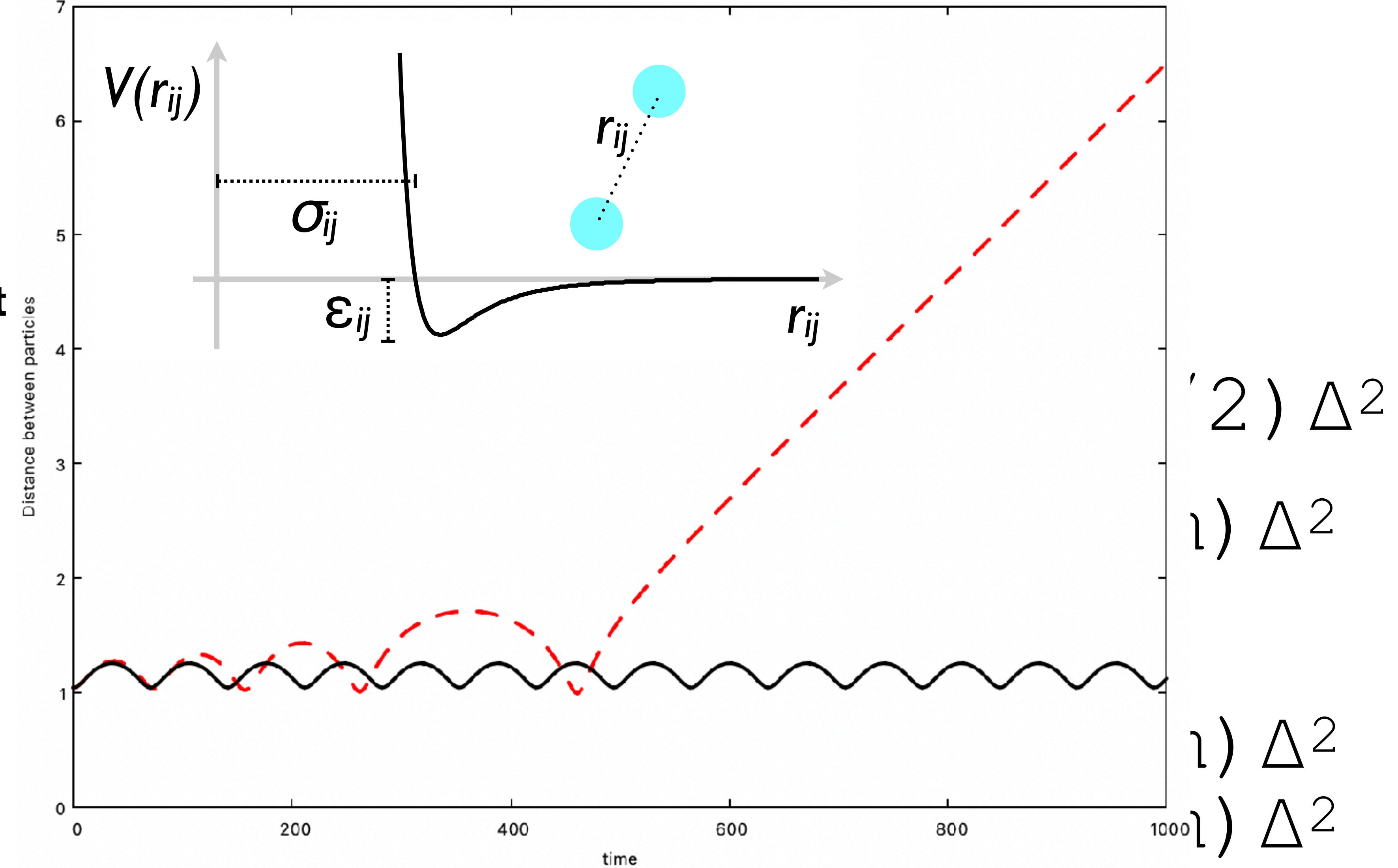
$$x(t+\Delta) =$$

$$=$$

**Second guess:**

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$$+ x(t-\Delta) =$$



---

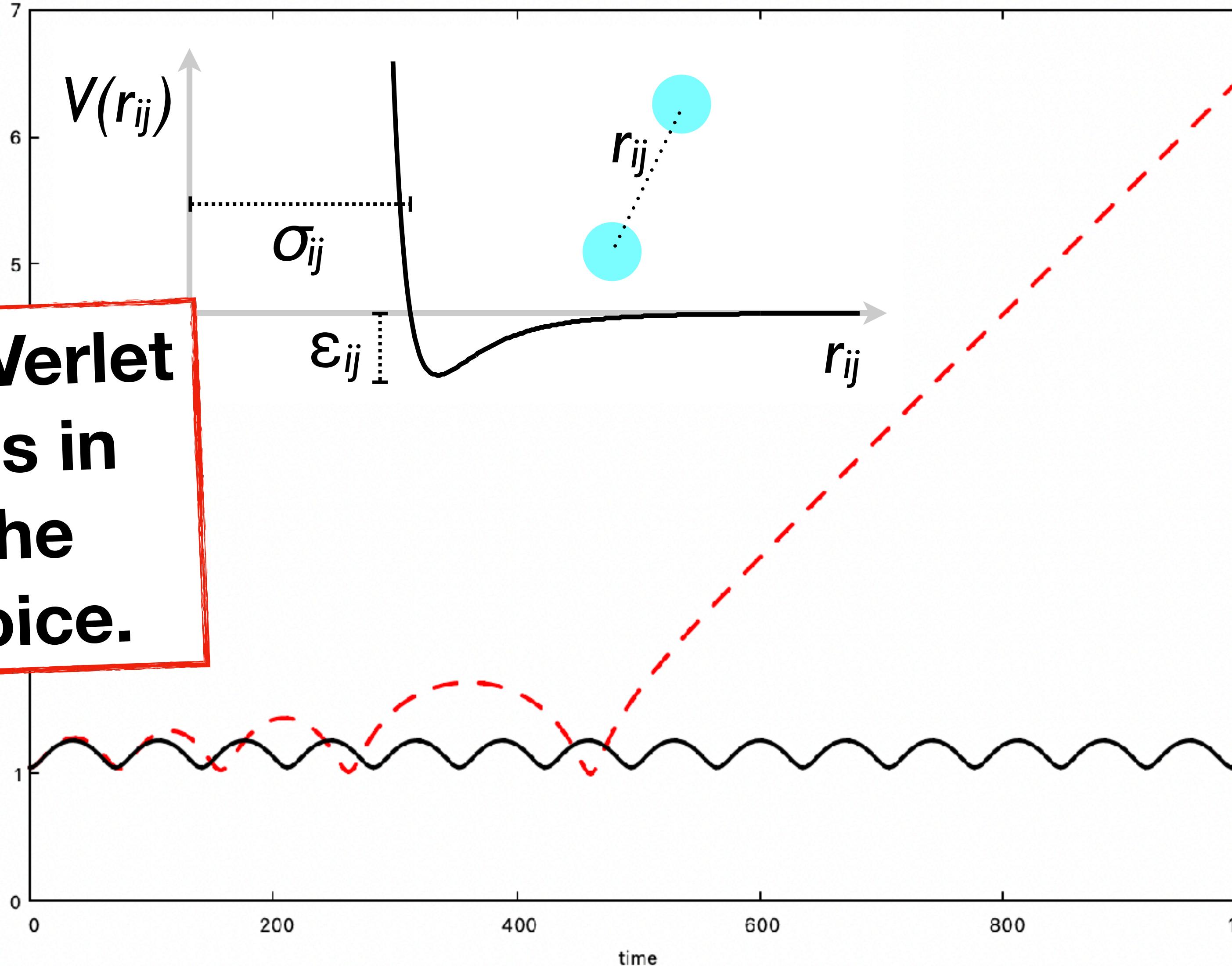

$$x(t+\Delta) = 2x(t) - x(t-\Delta) + (F(t)/m) \Delta^2$$

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First

This simple ‘Verlet algorithm’ is in practice the optimal choice.



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---


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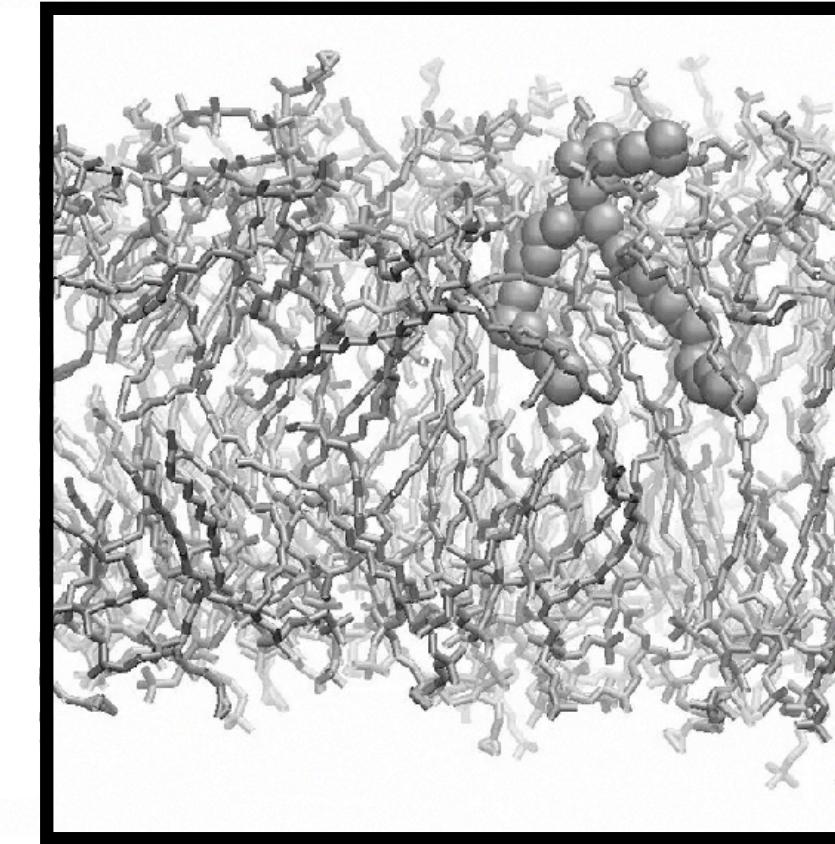
‘2)  $\Delta^2$

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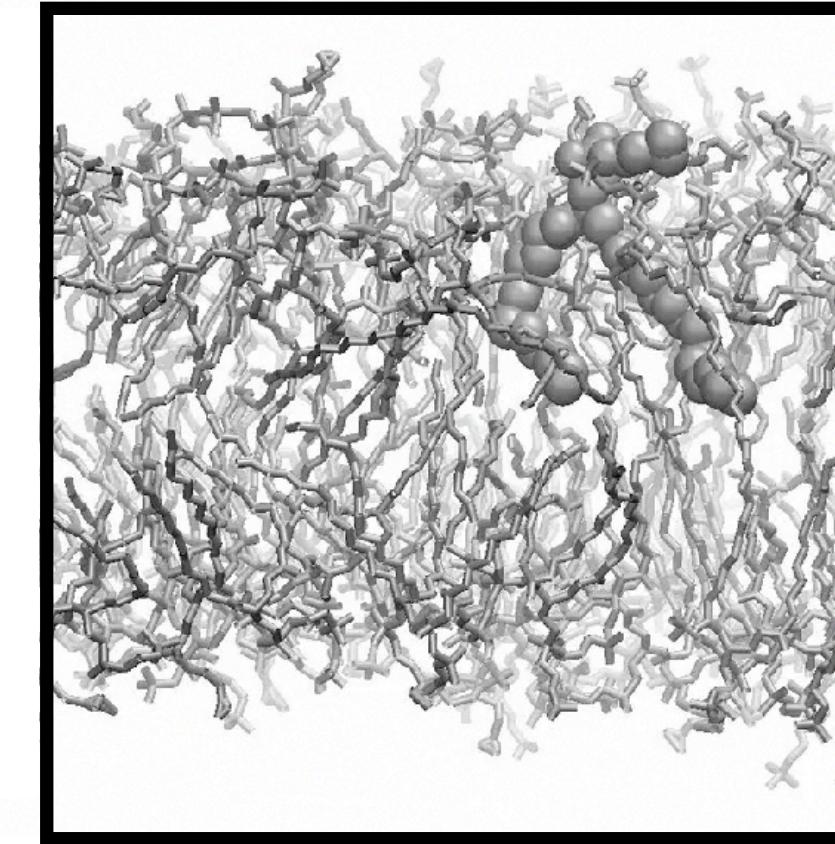
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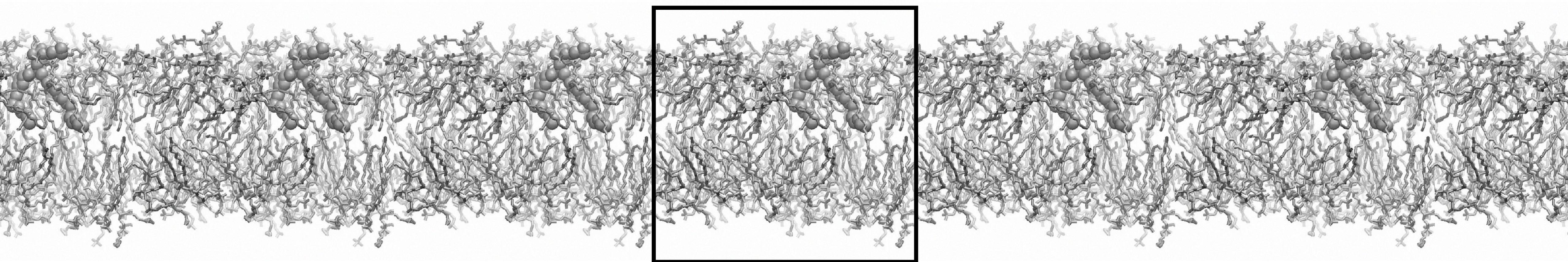
# Periodic Boundary Conditions



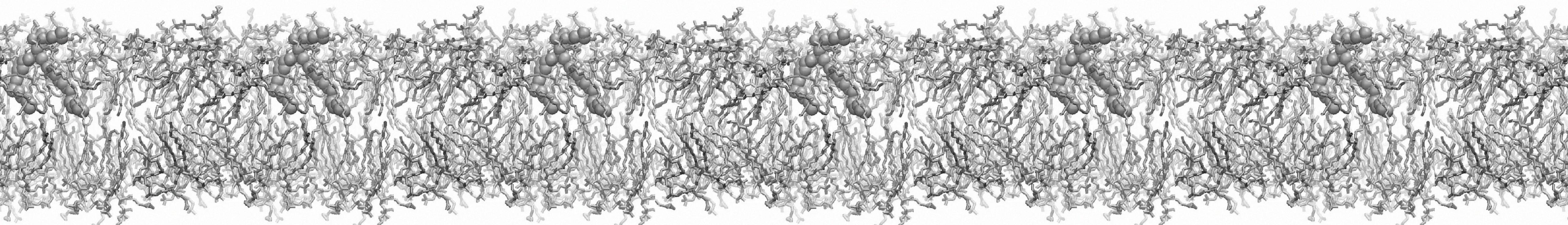
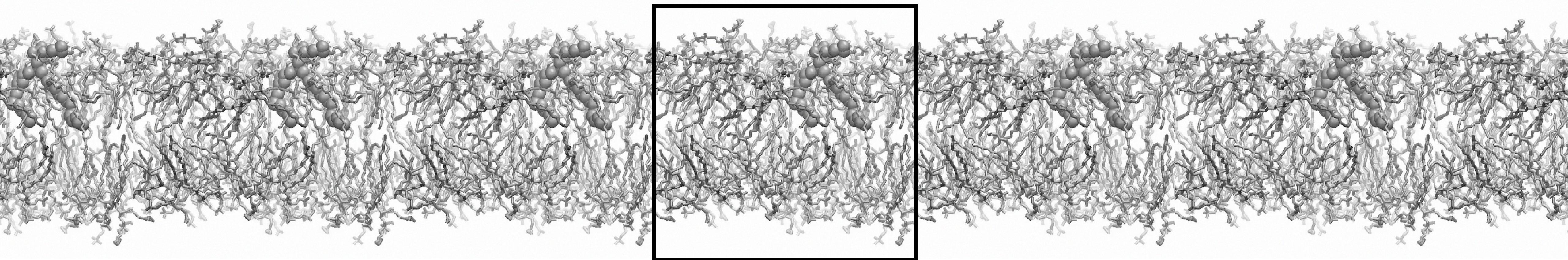
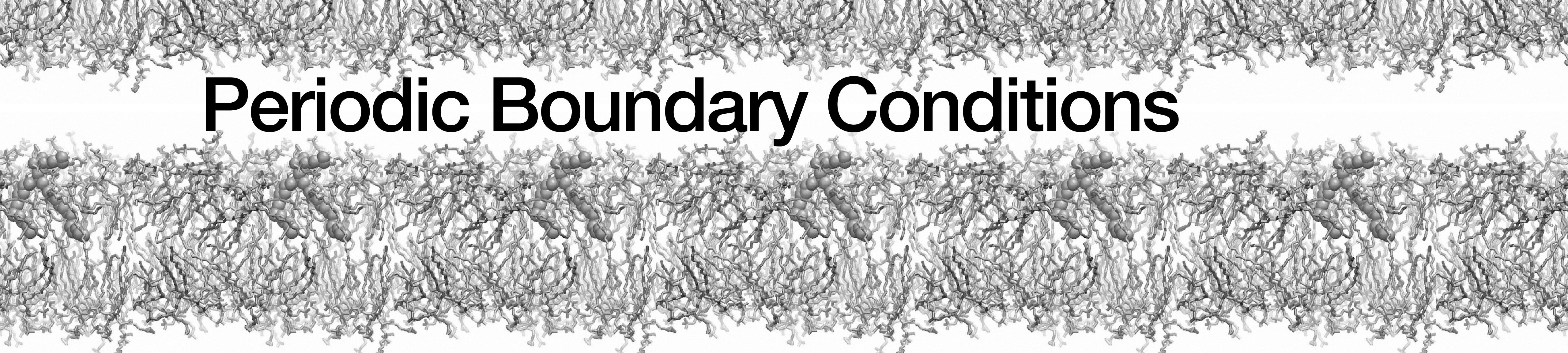
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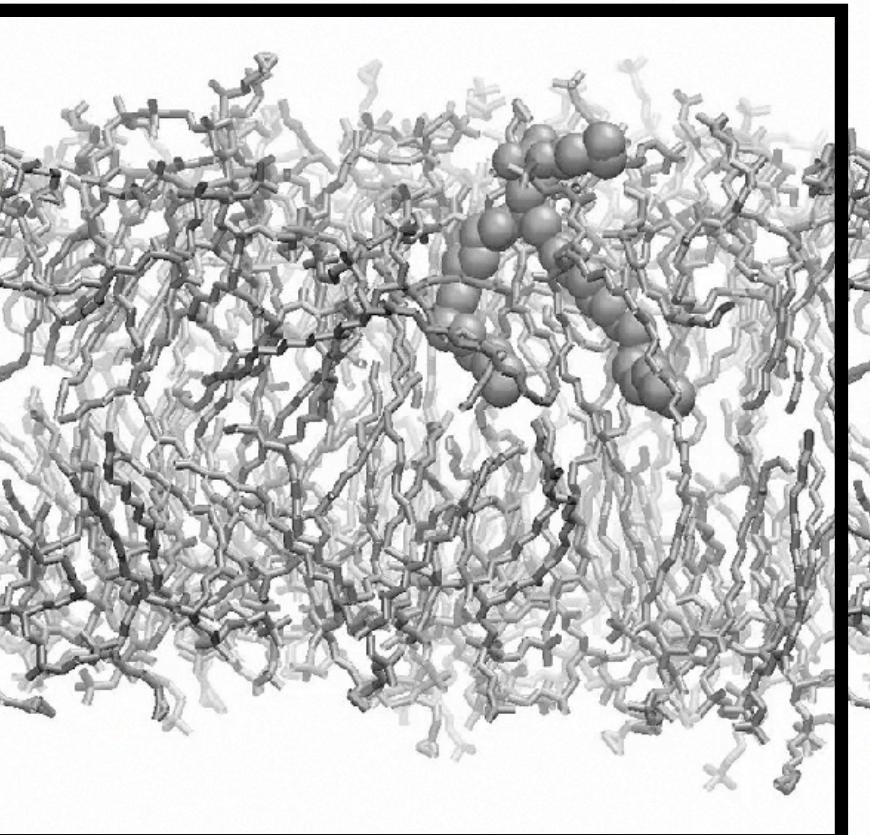
# Periodic Boundary Conditions



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## Advantages

- no surface effects
- no tracking of  
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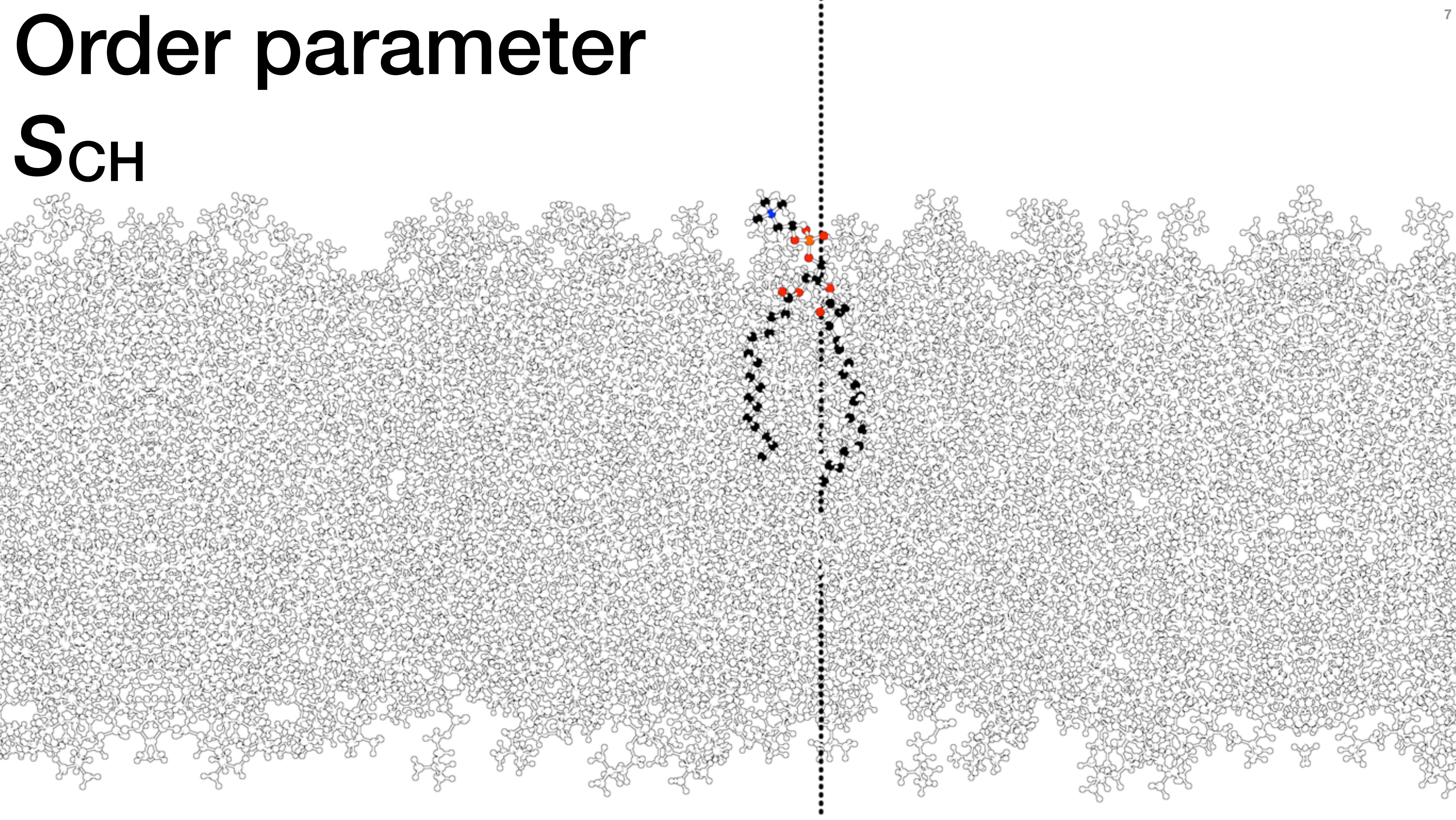
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**Note: Location of the ‘central box’ has no physical meaning.**

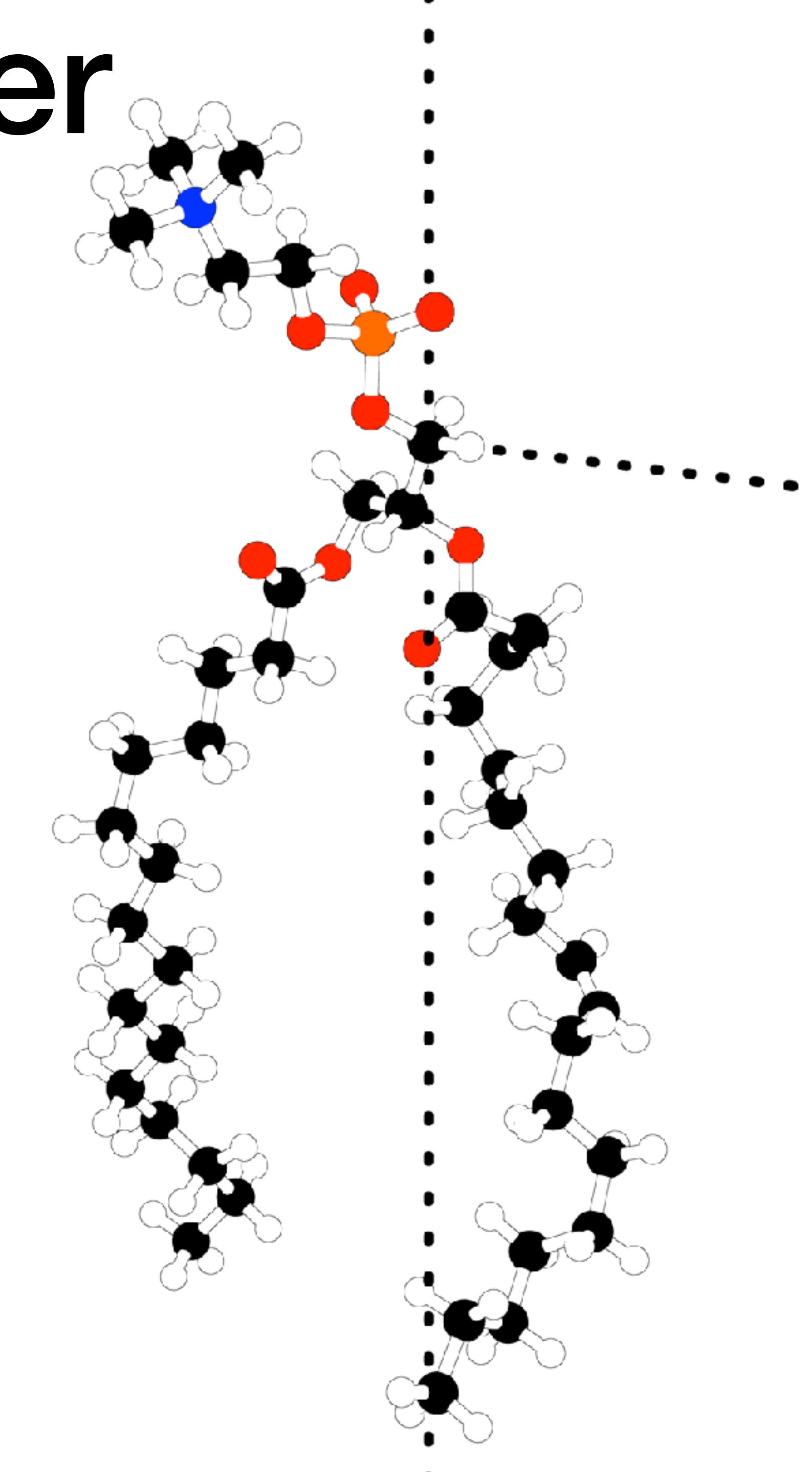
# Applications: How one measures from MD:

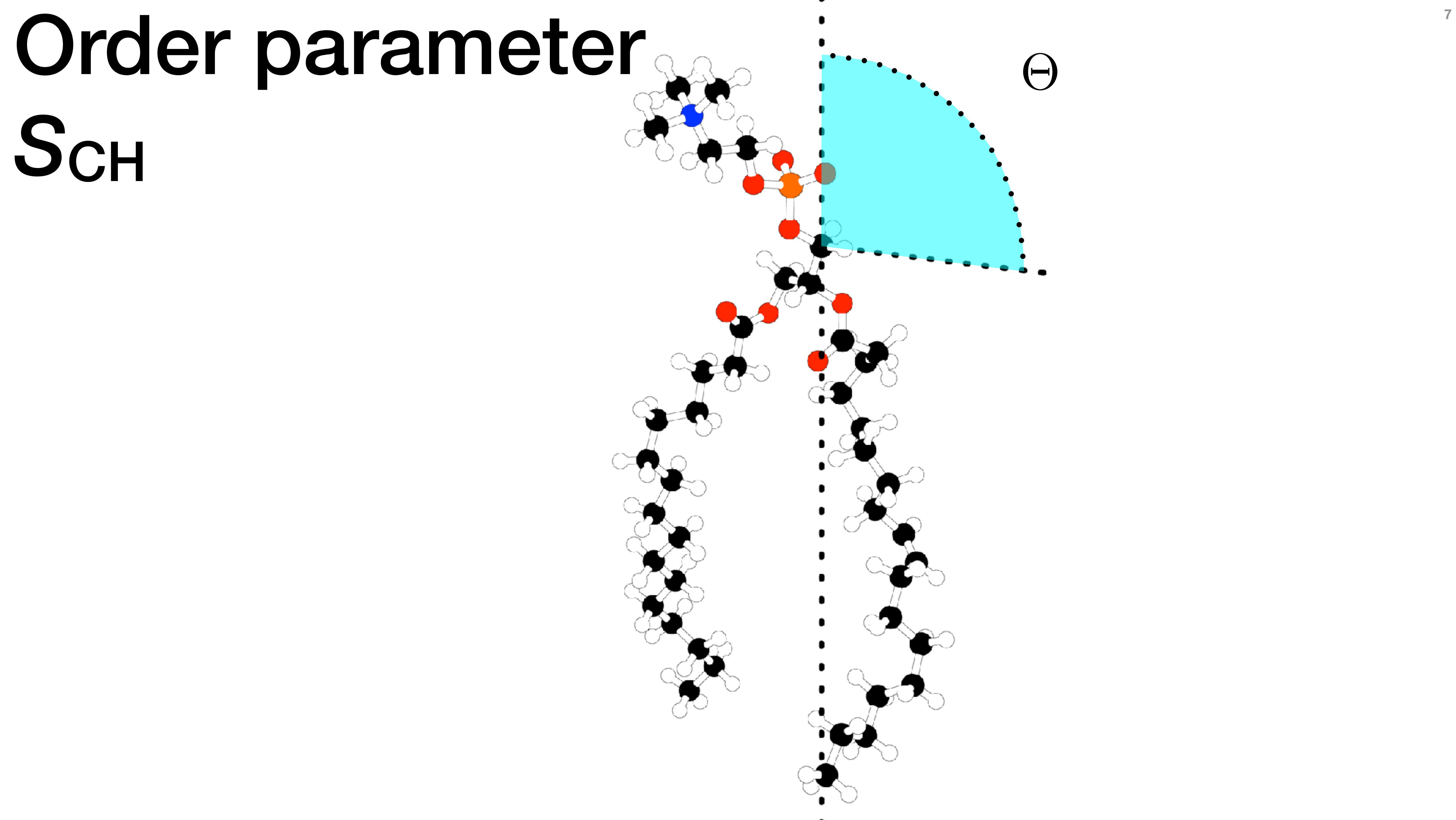
- 1) C-H bond order parameters  $S_{\text{CH}}$
- 2) C-H bond effective correlation times  $\tau_e$
- 3) X-ray scattering form factors  $F(q)$

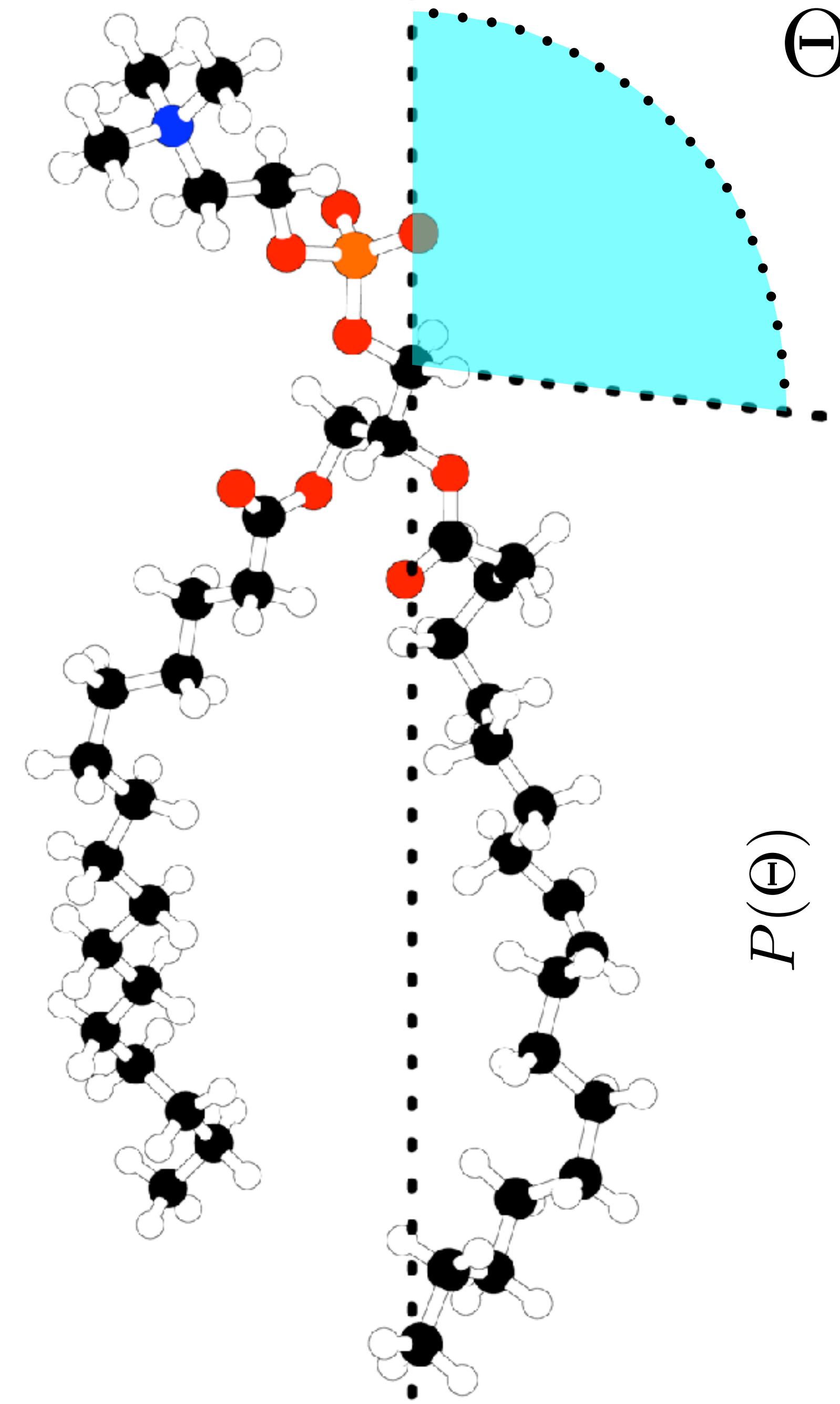


# Order parameter

$S_{\text{CH}}$

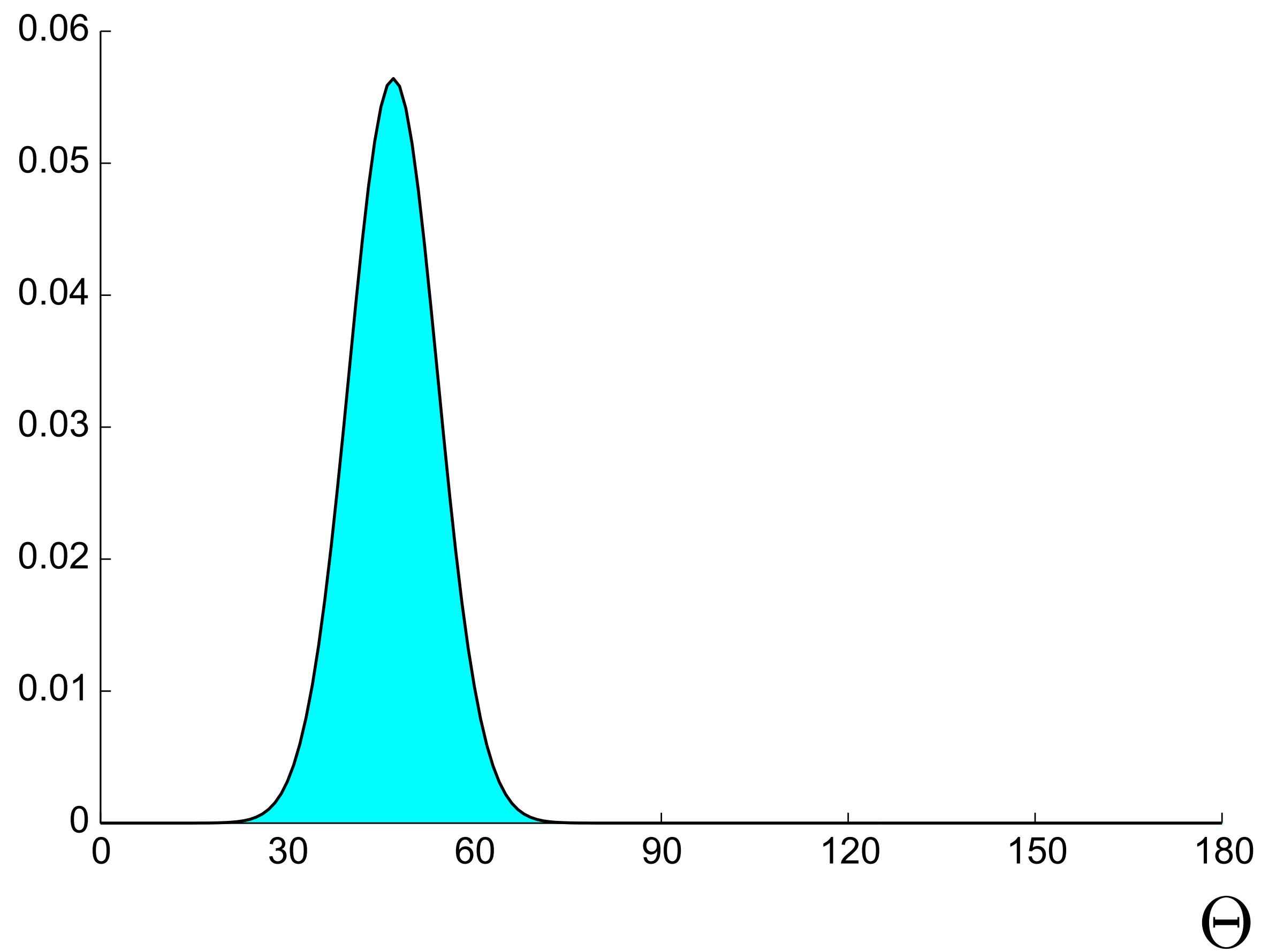




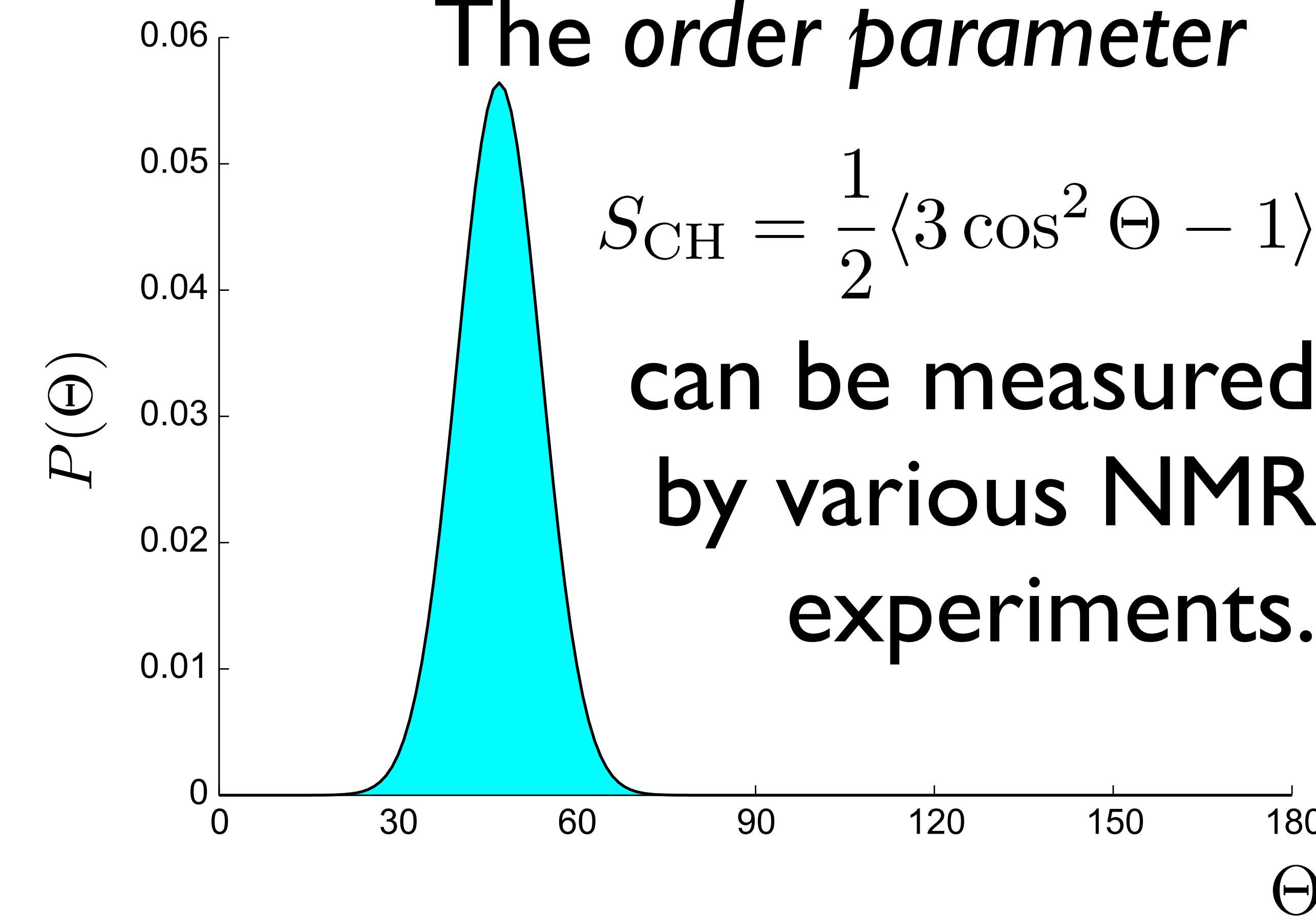
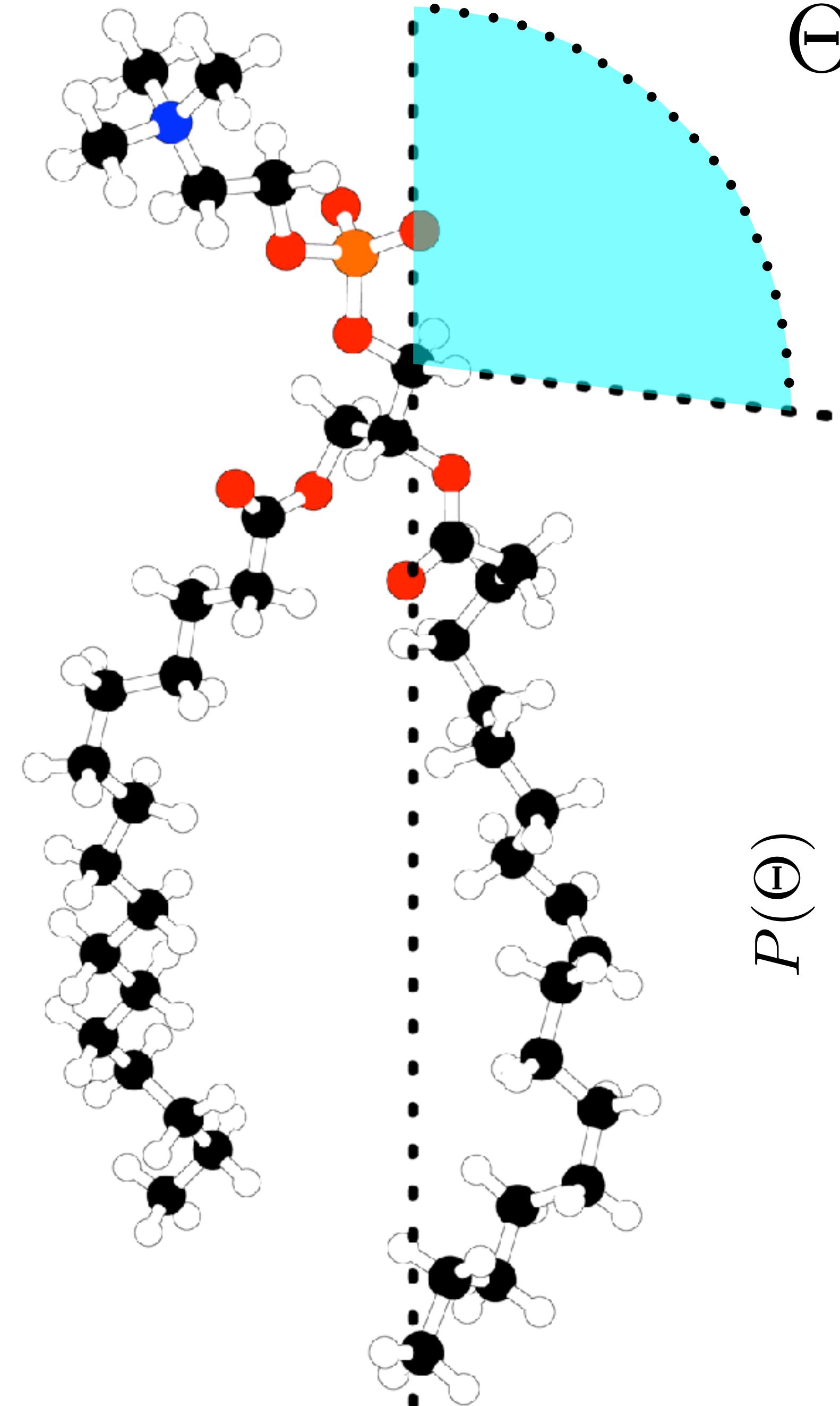


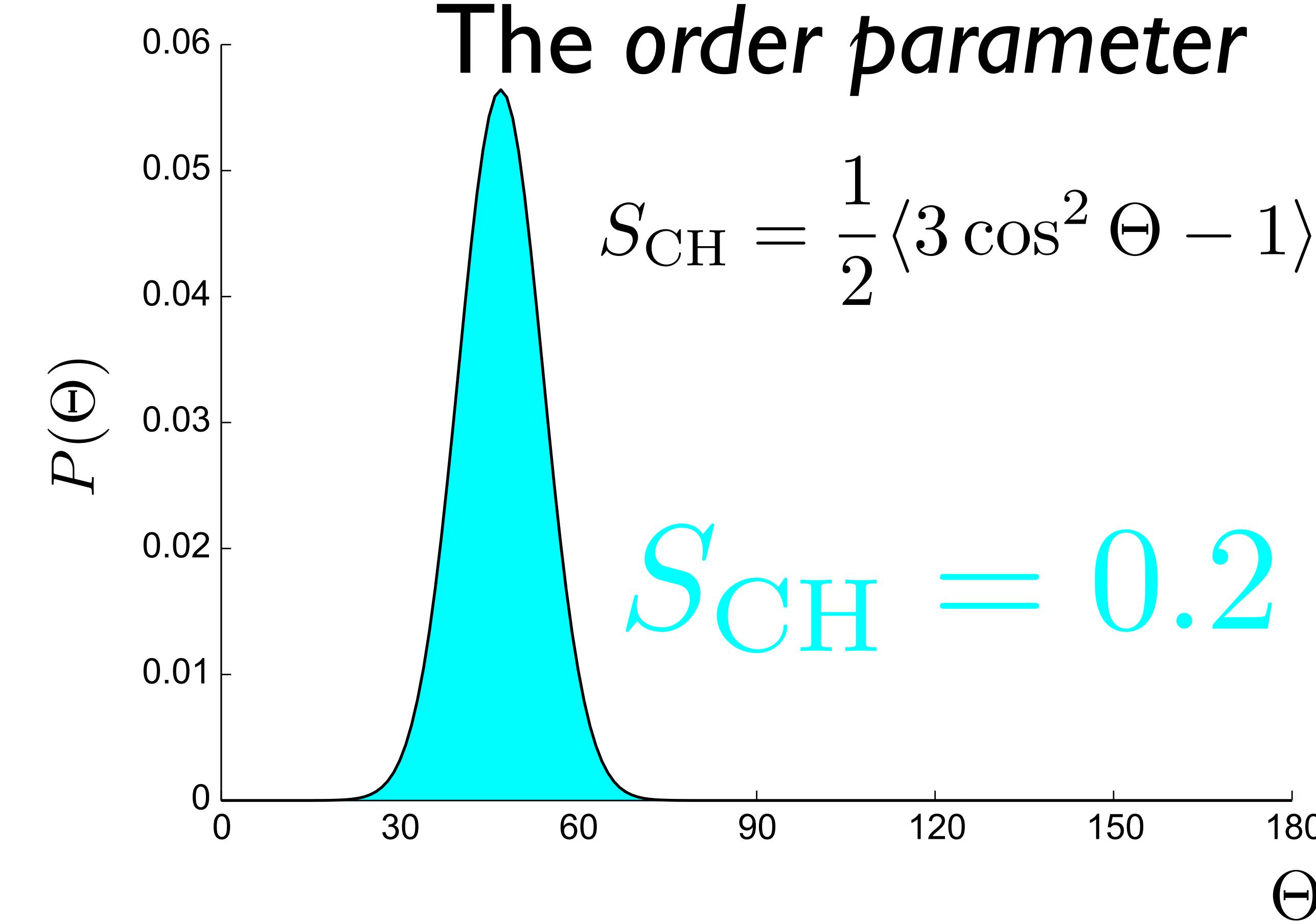
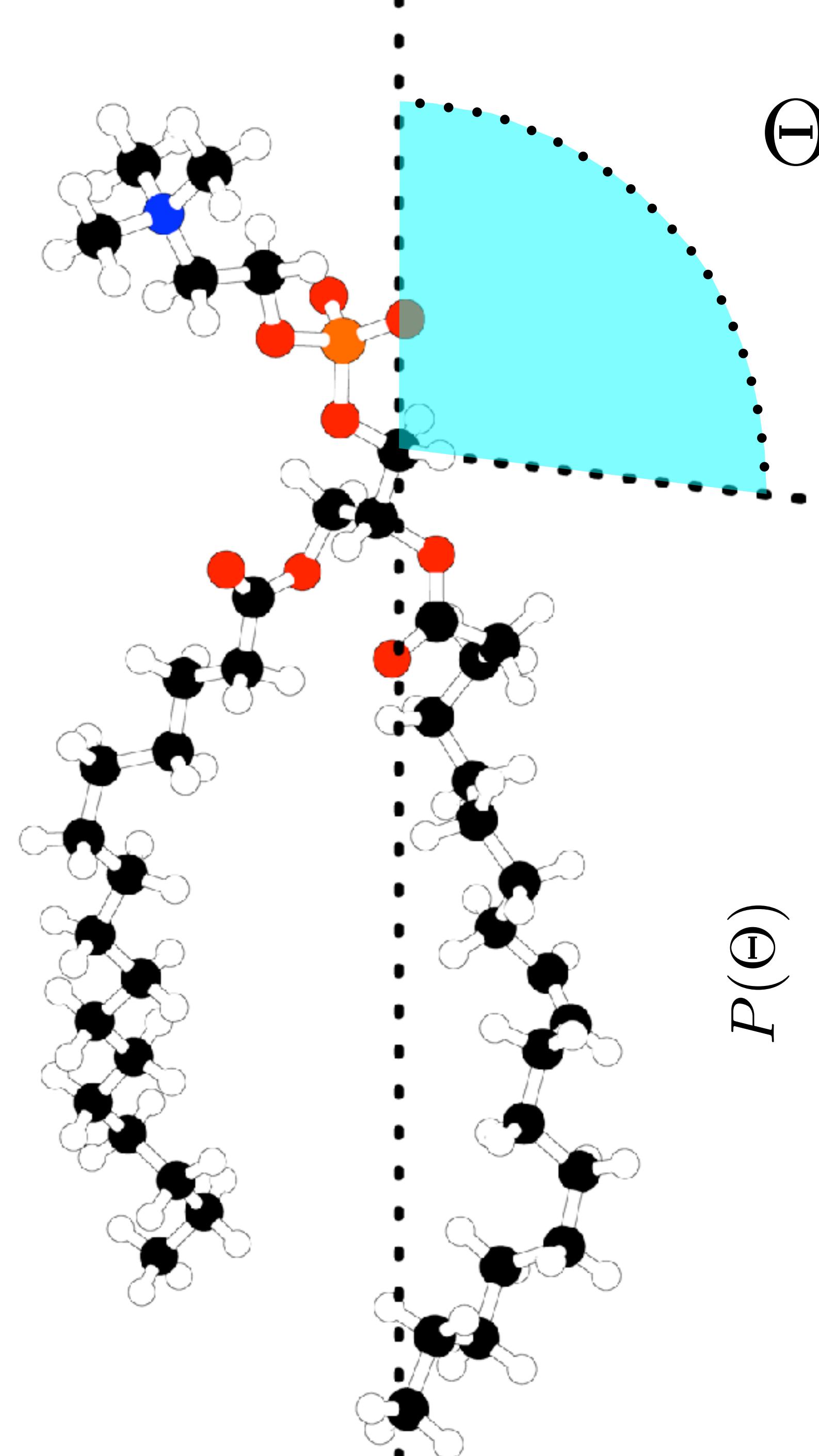
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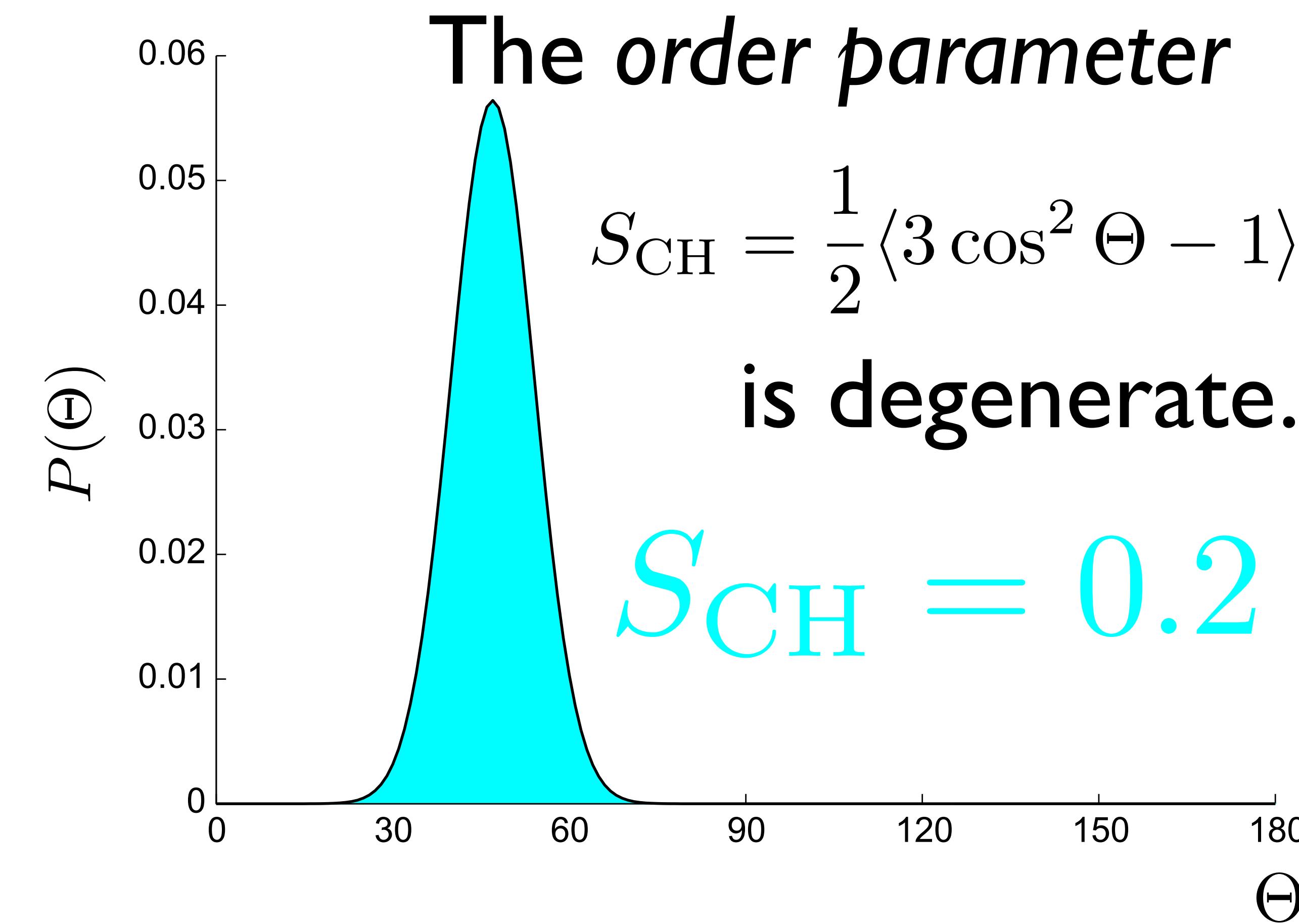
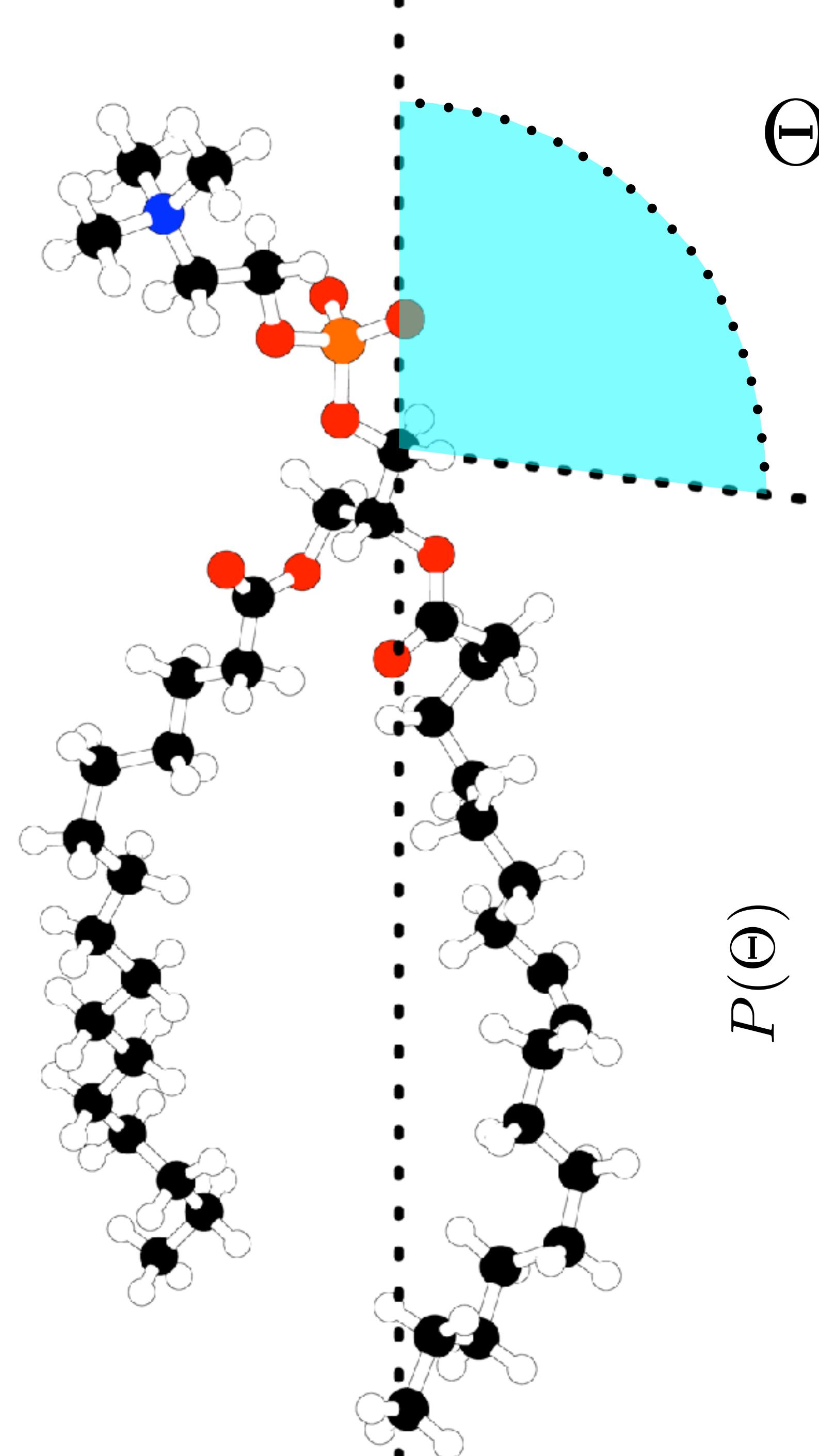
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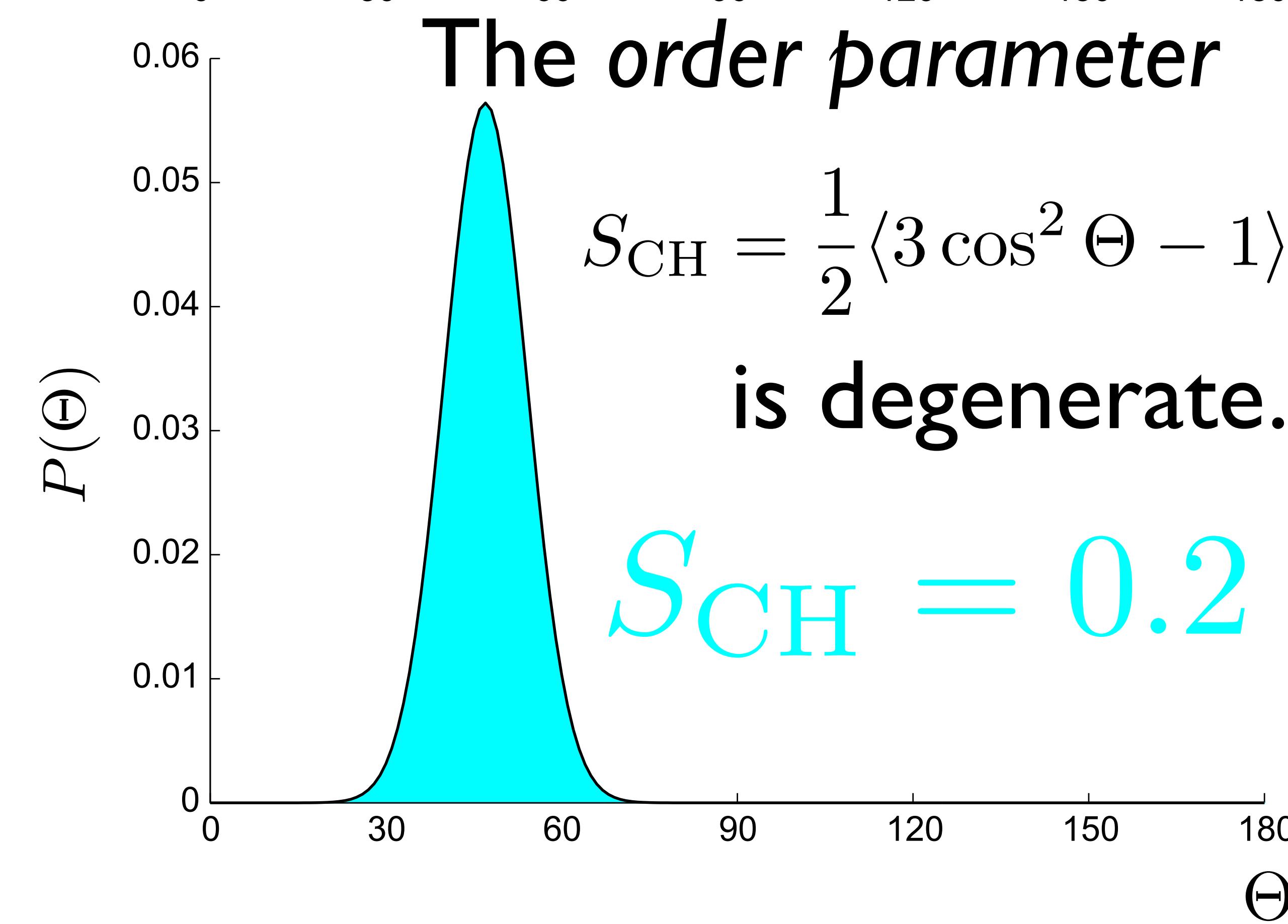
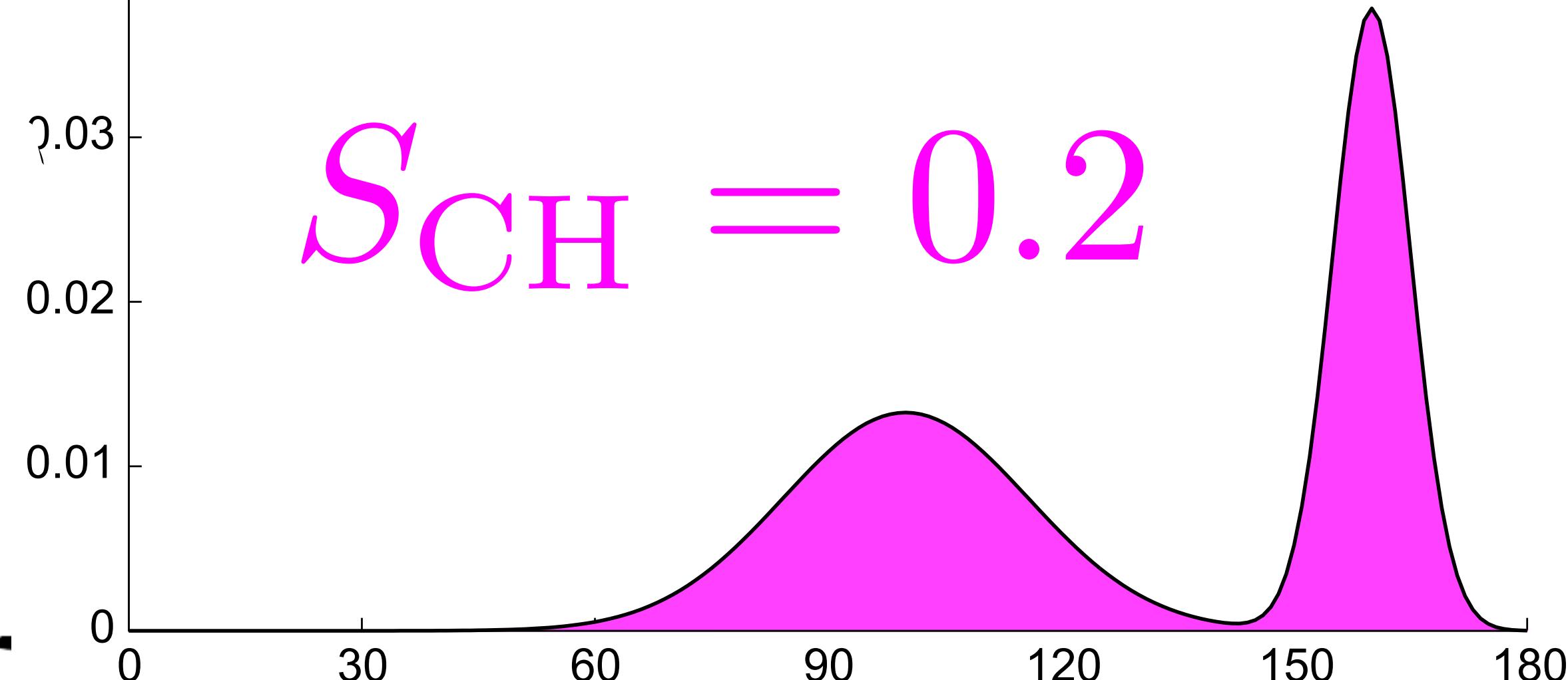
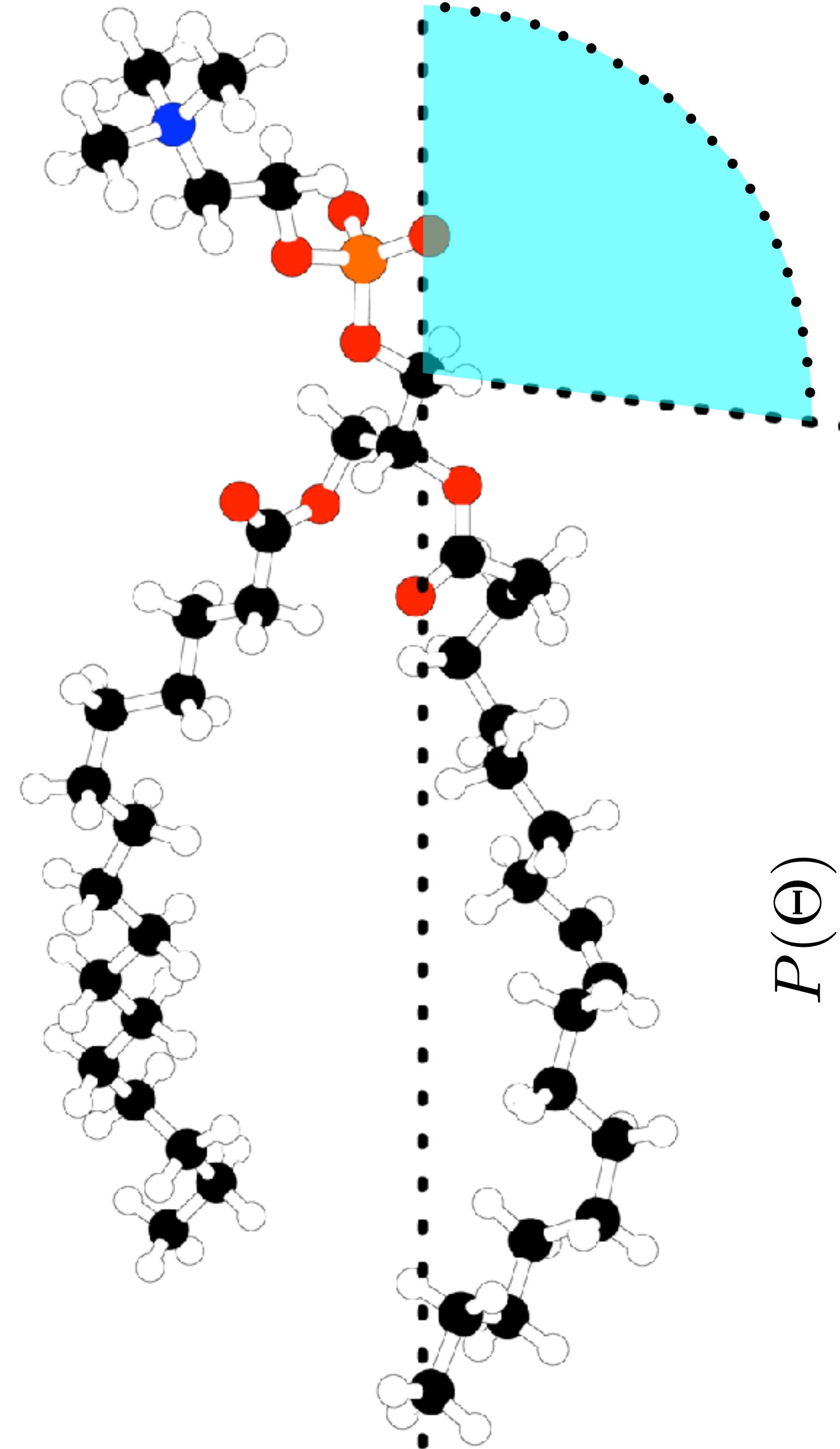


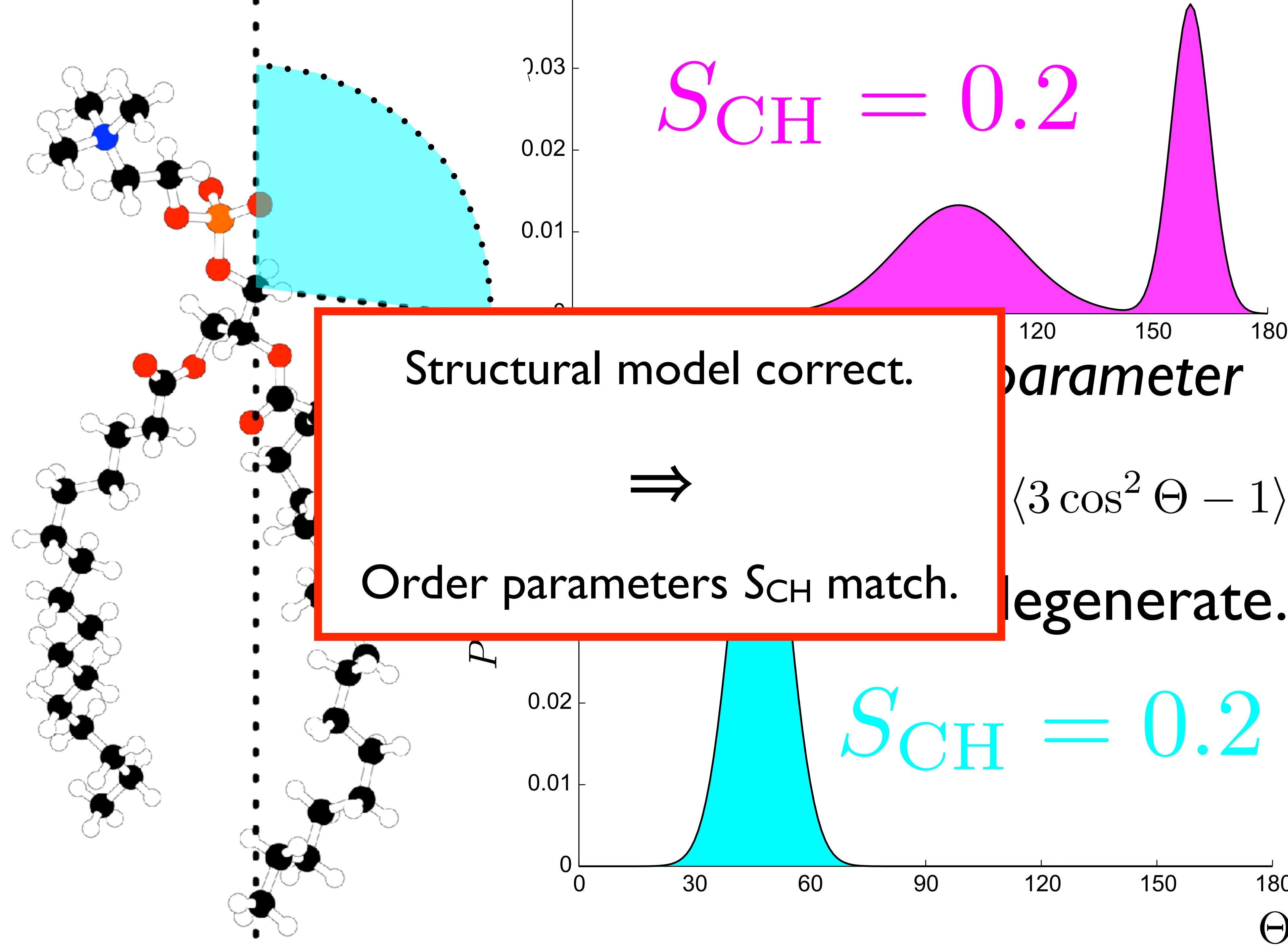
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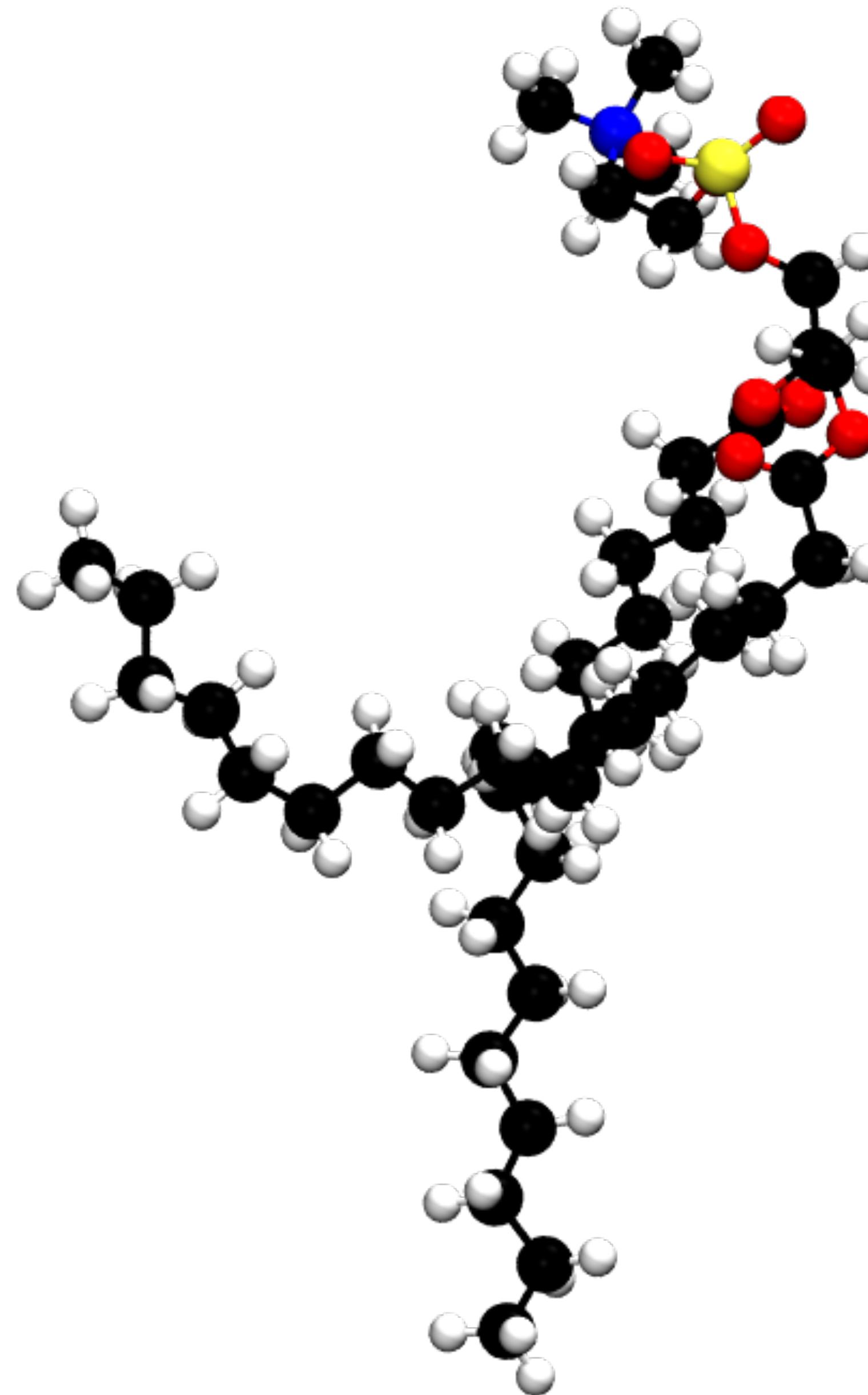




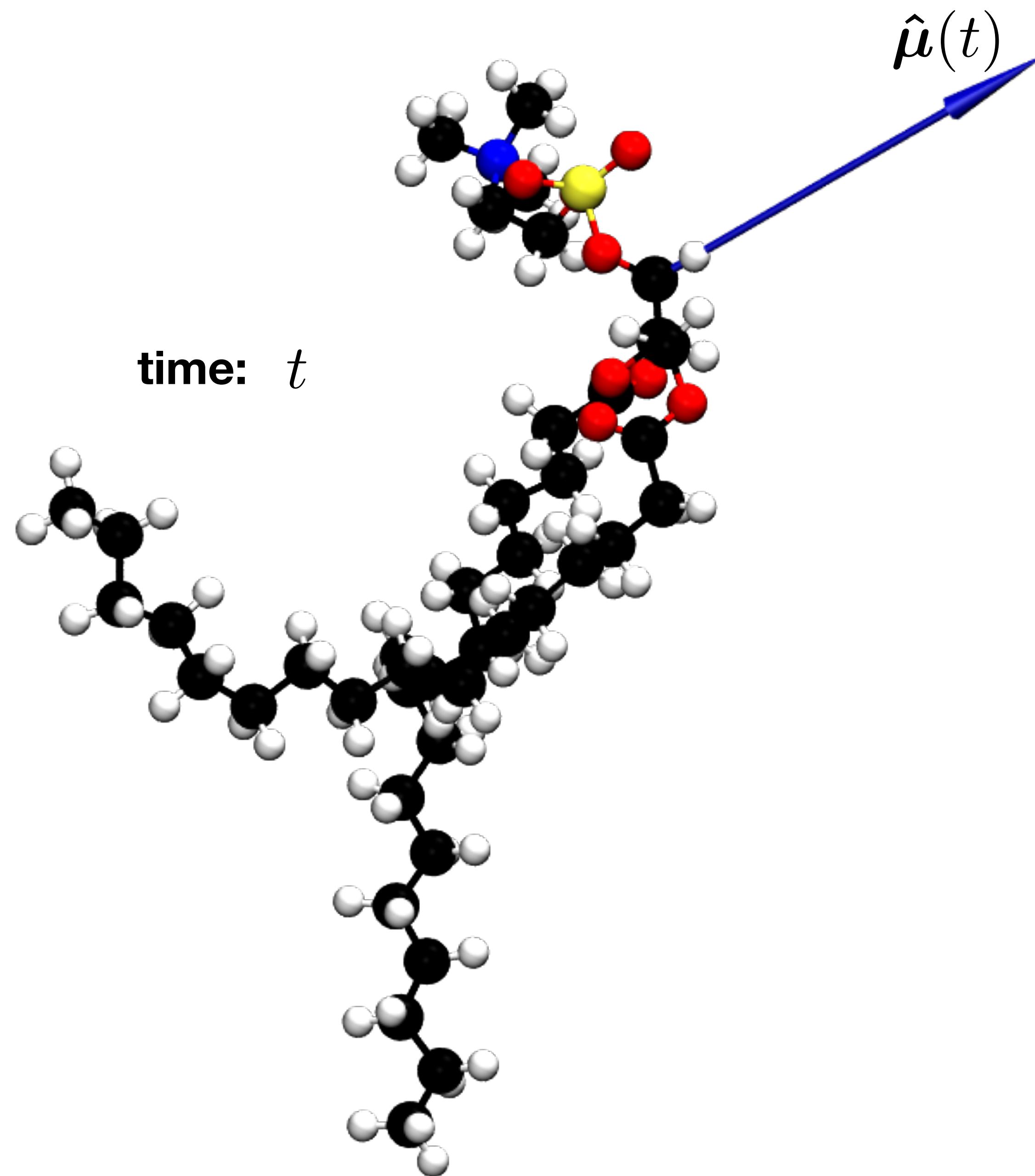




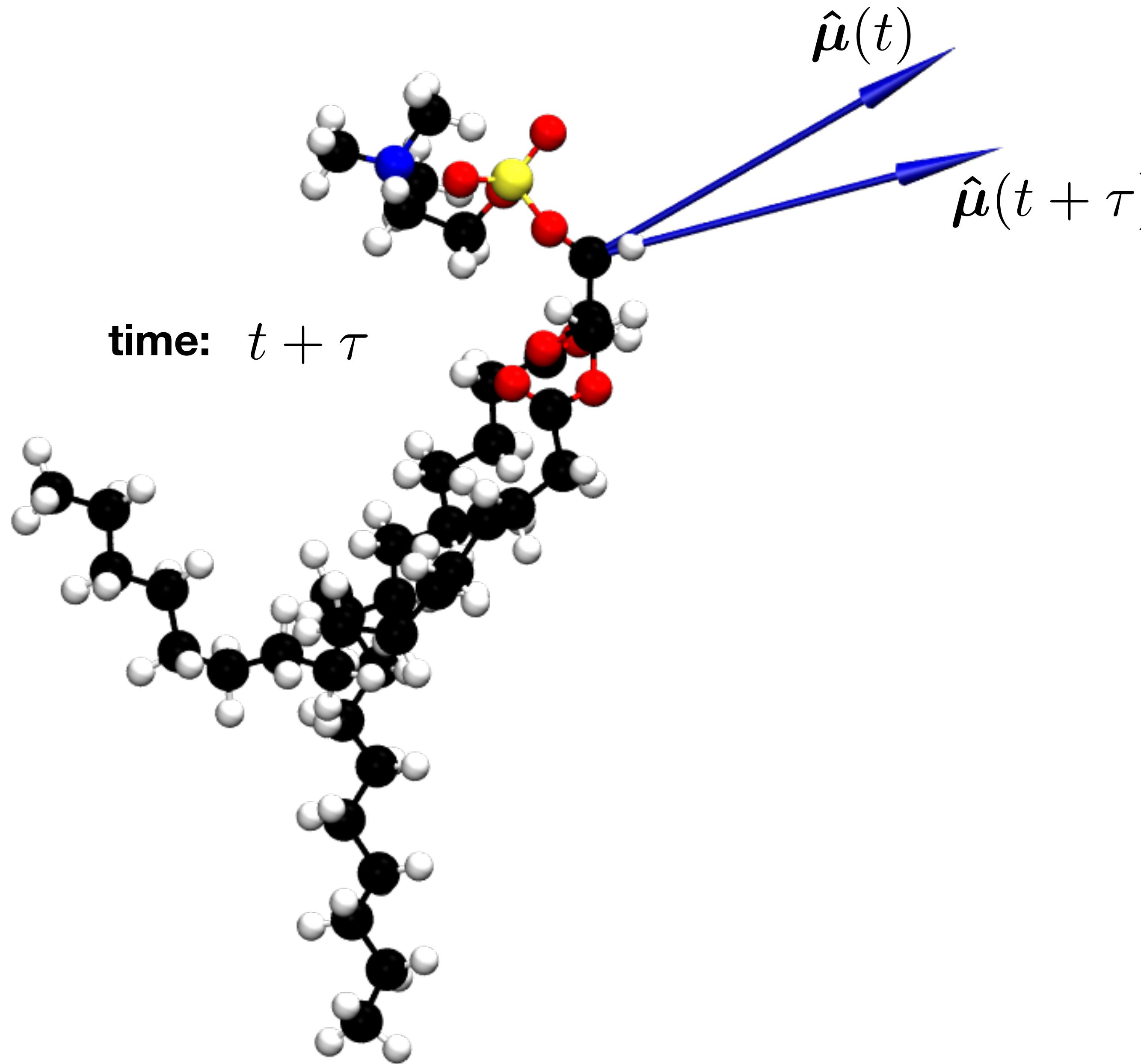
# Effective correlation time $\tau_e$



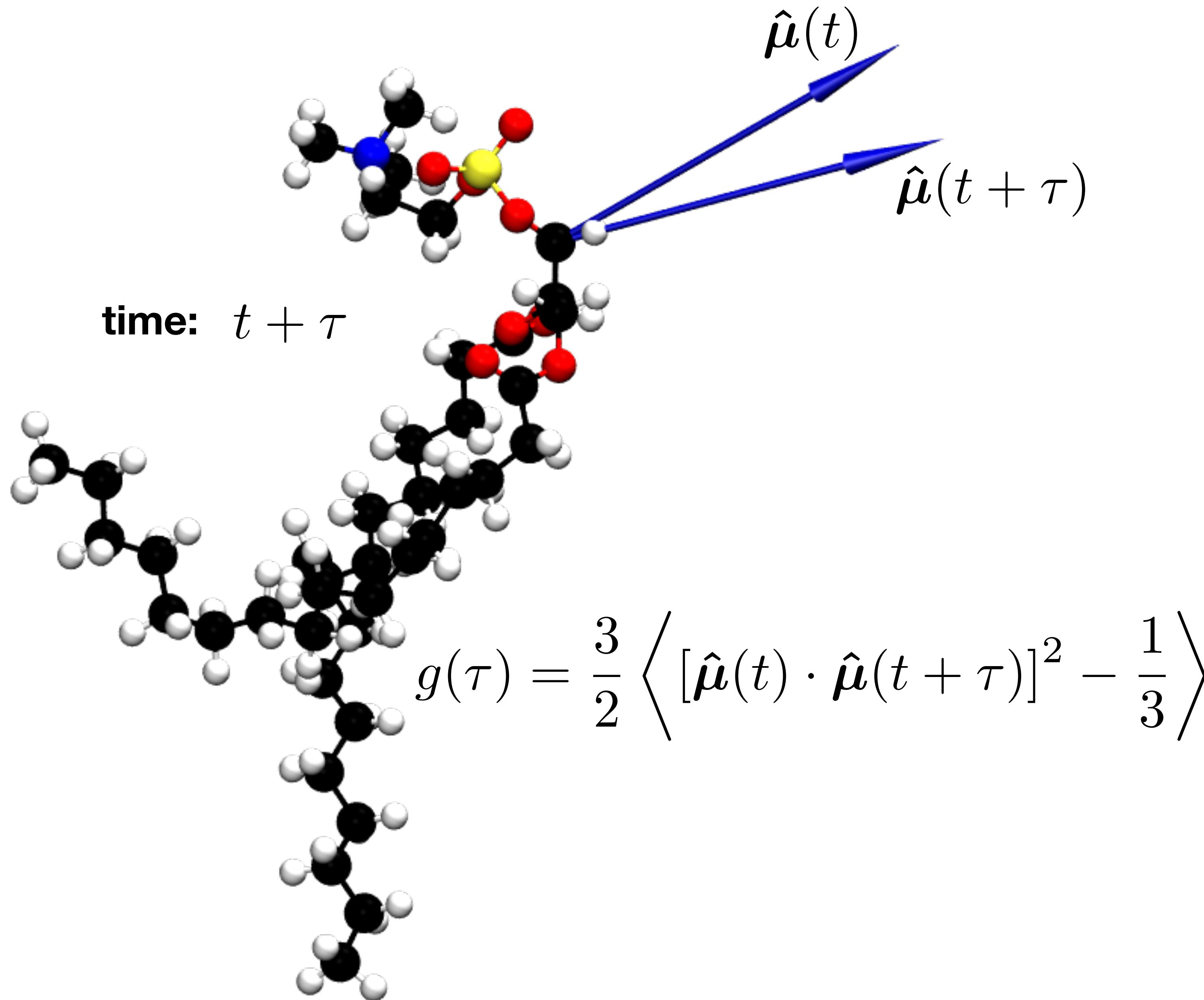
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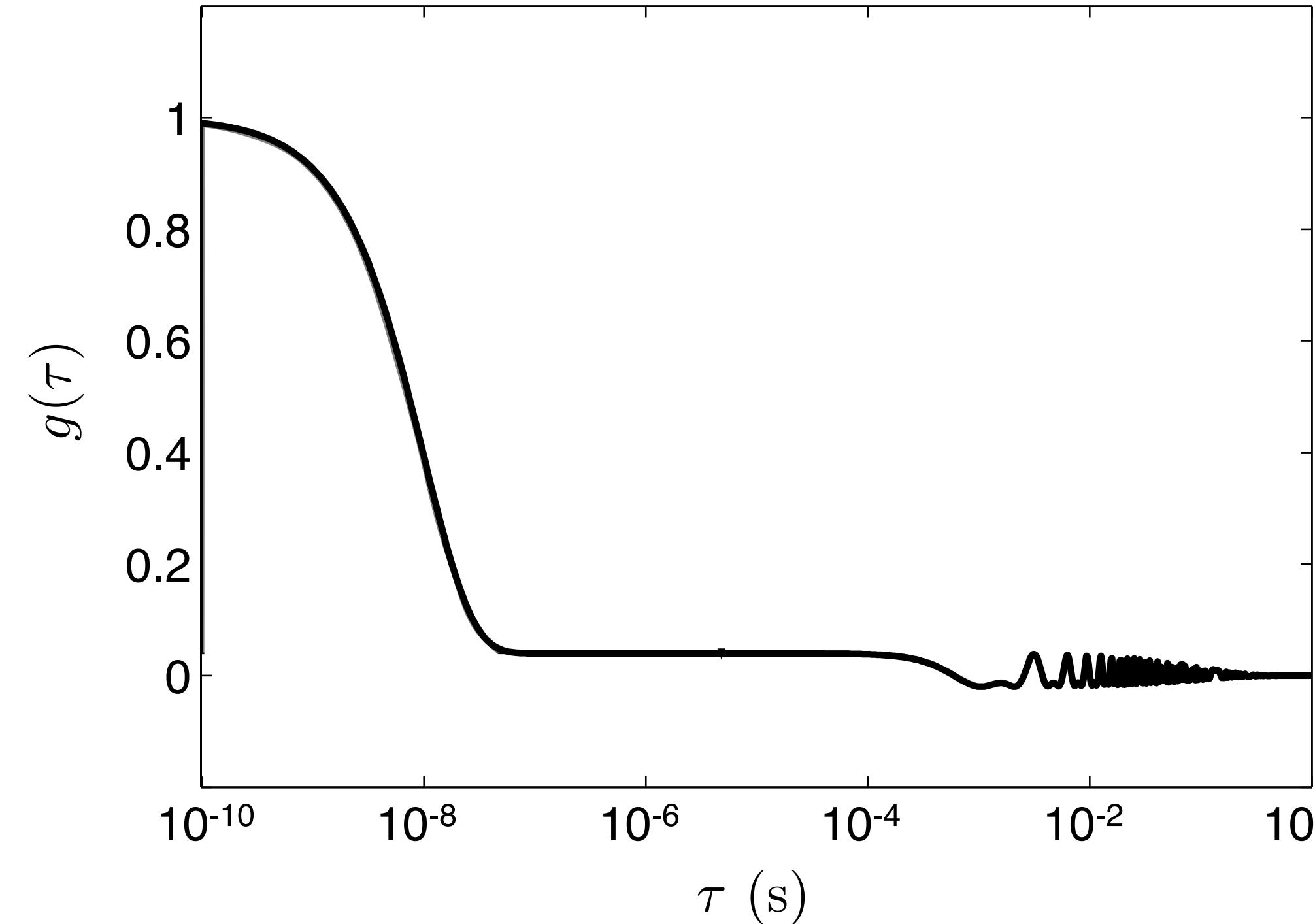
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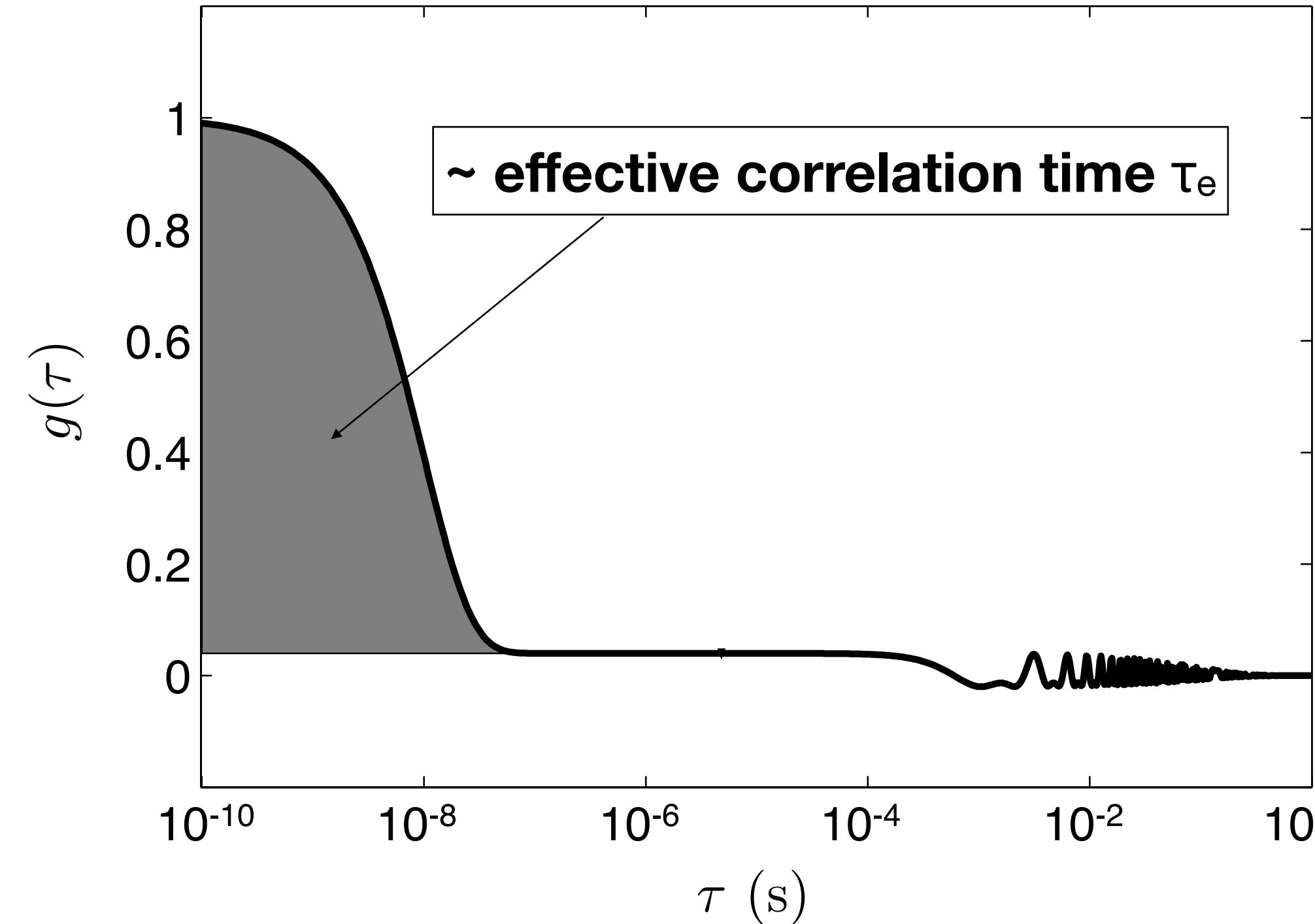


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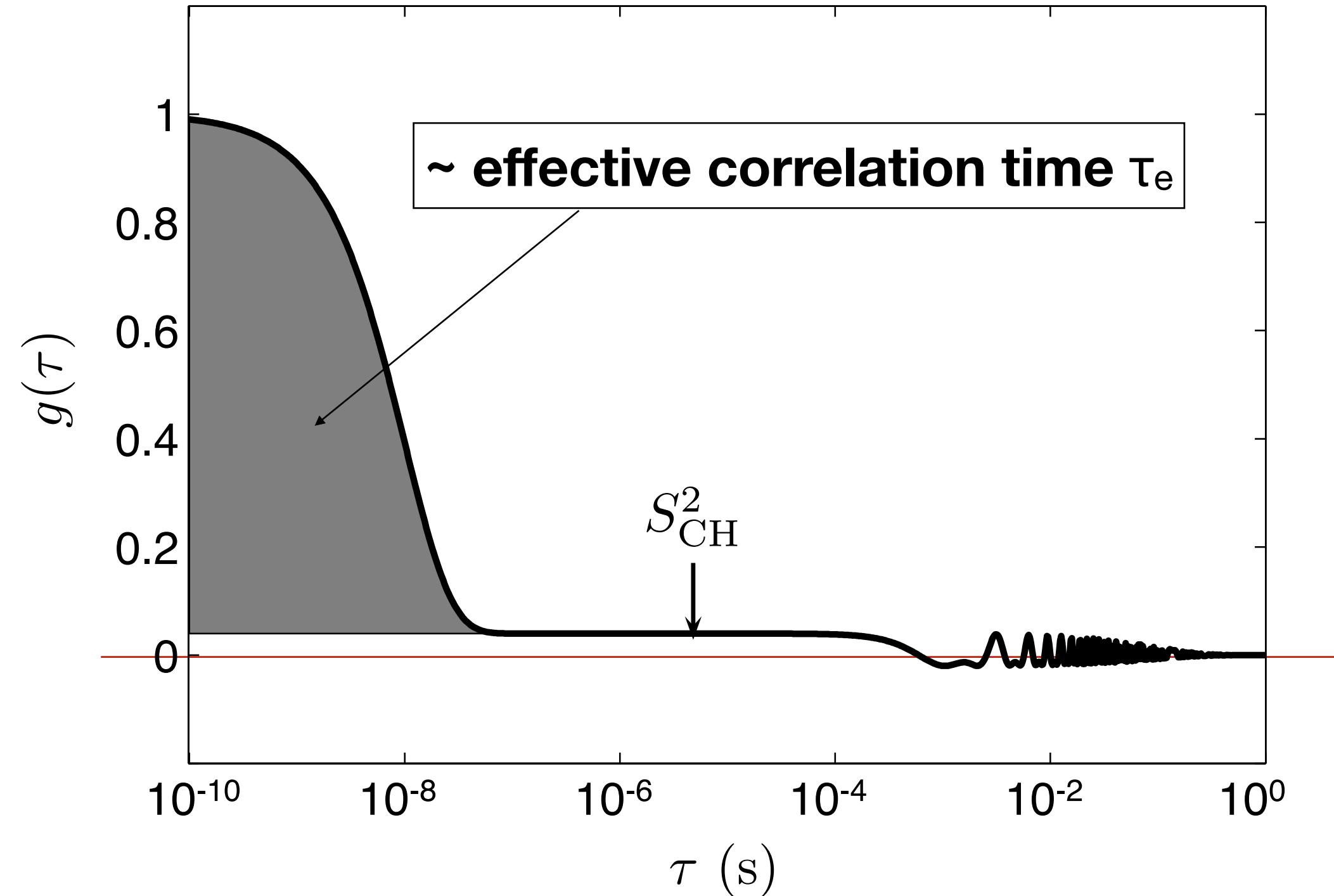
$$g(\tau) = \frac{3}{2} \left\langle [\hat{\mu}(t) \cdot \hat{\mu}(t + \tau)]^2 - \frac{1}{3} \right\rangle$$

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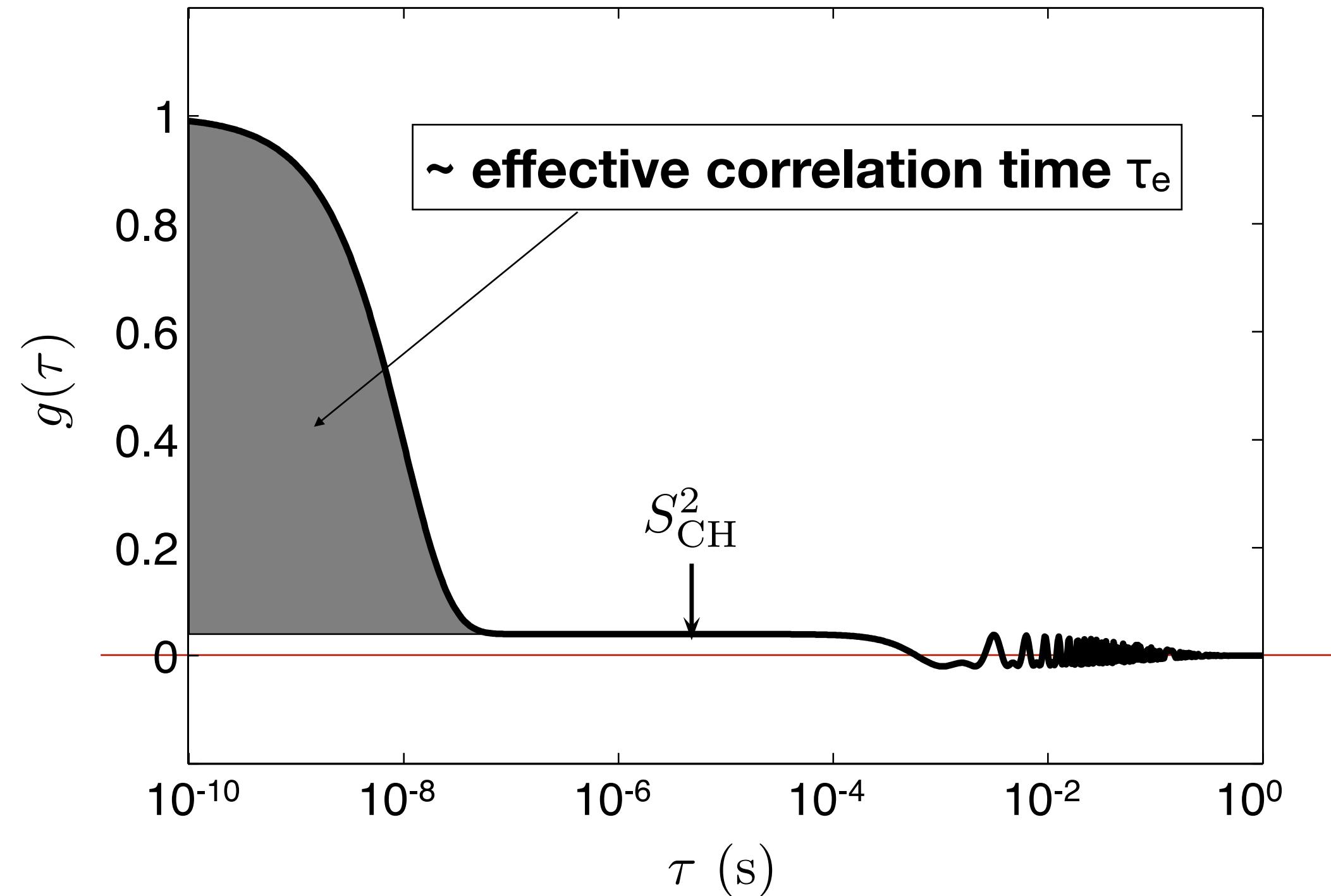
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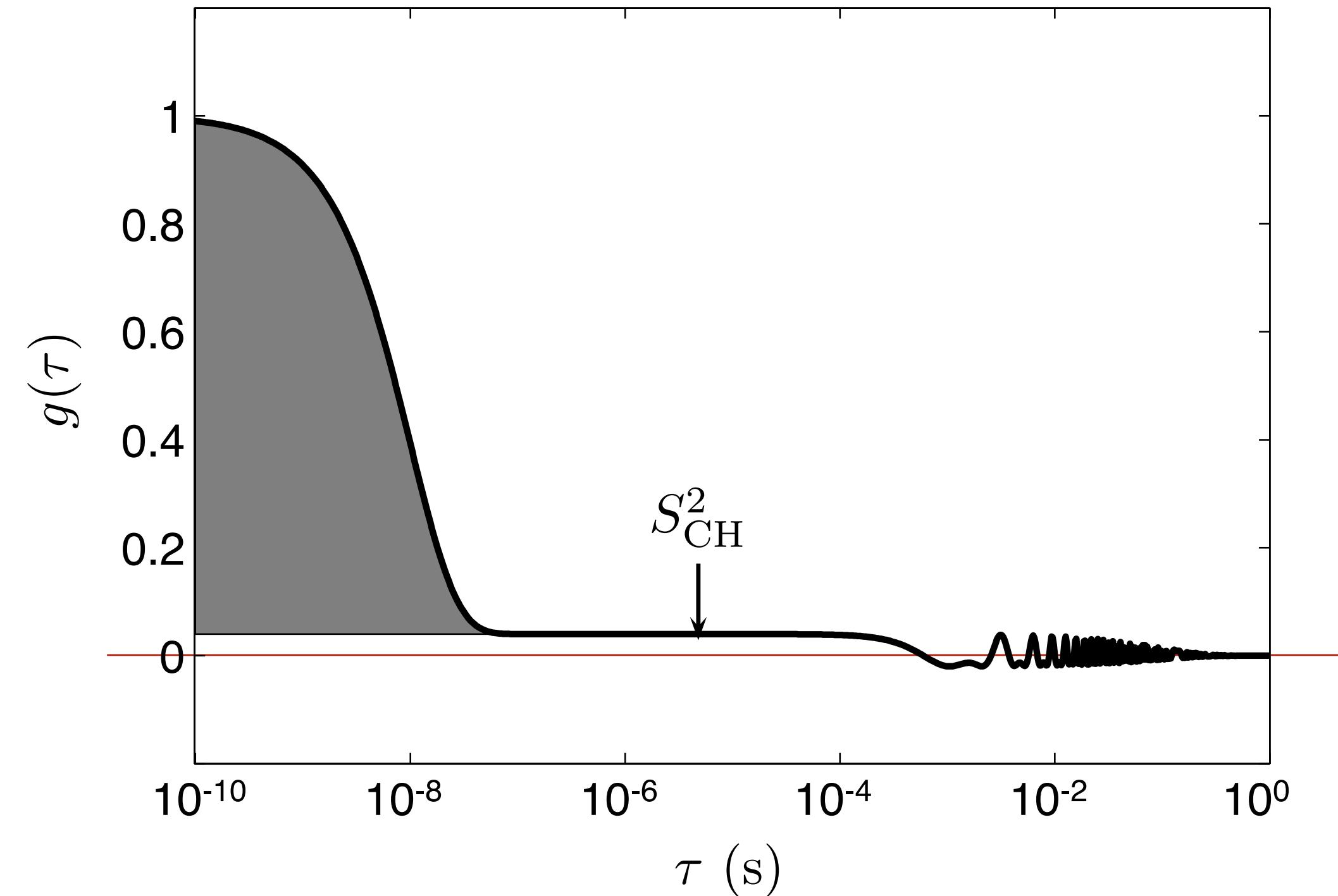
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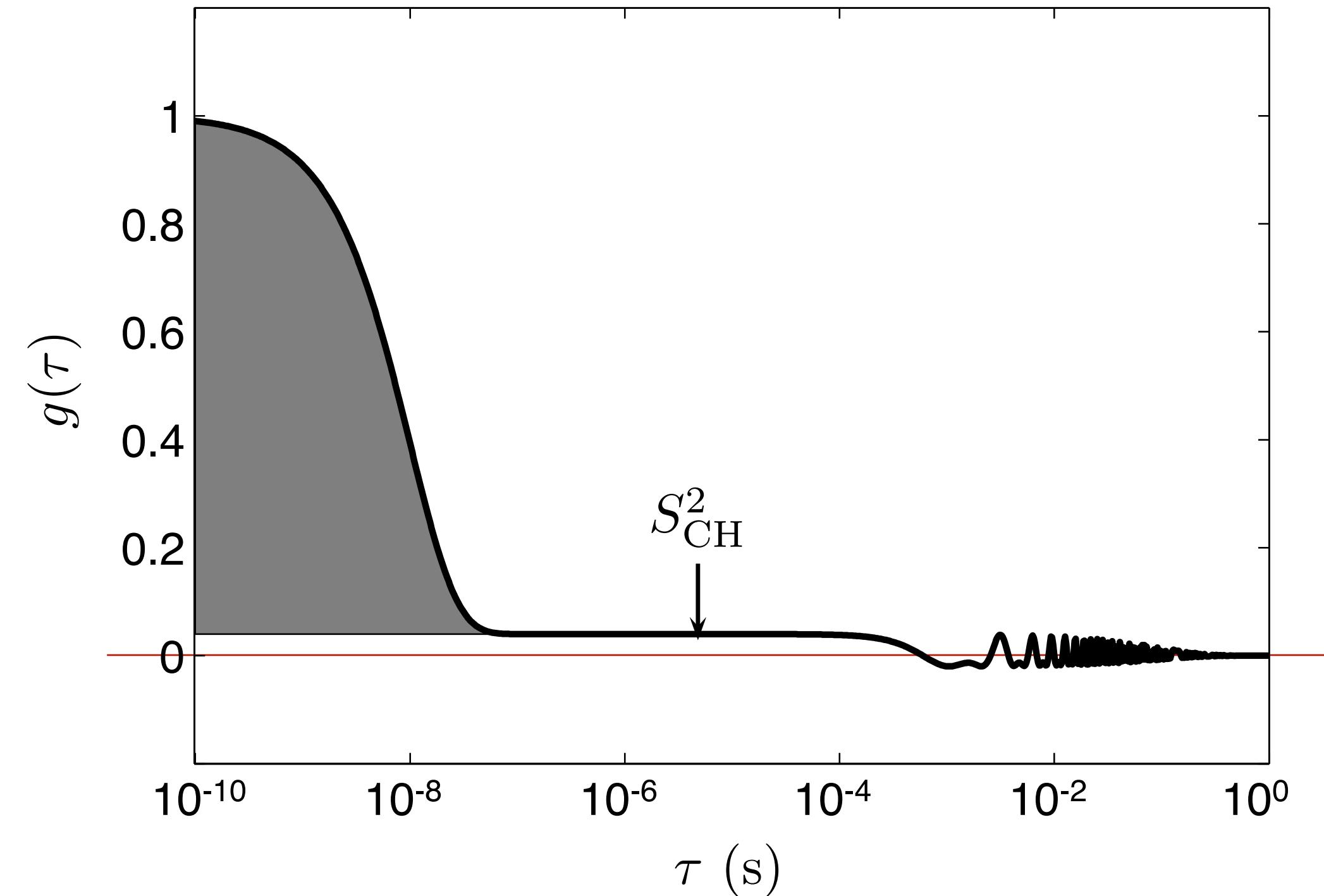
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# MD gives only a lower bound for $\tau_e$ !



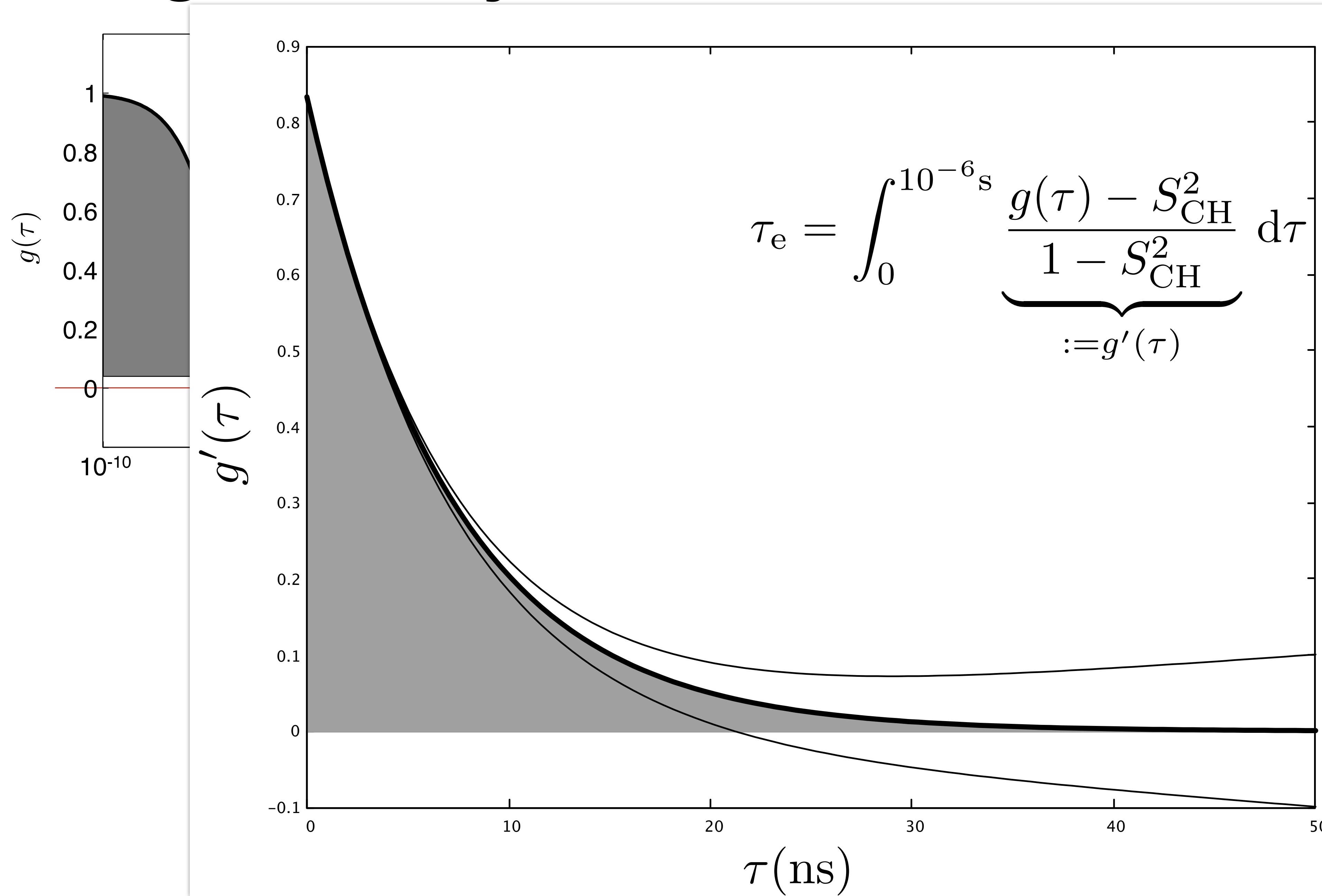
$$\tau_e = \int_0^{10^{-6}\text{s}} \frac{g(\tau) - S_{\text{CH}}^2}{1 - S_{\text{CH}}^2} d\tau$$

# MD gives only a lower bound for $\tau_e$ !

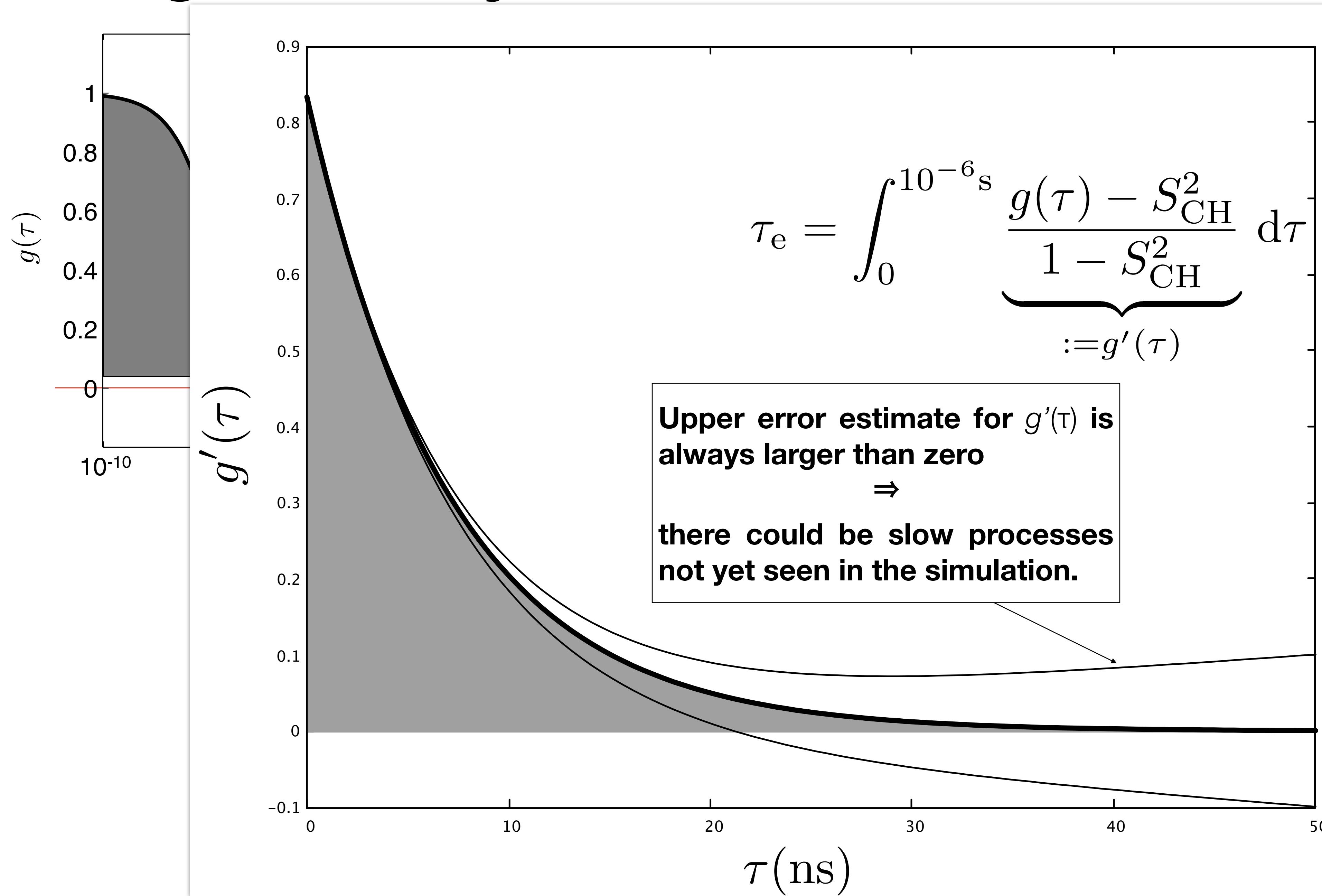


$$\tau_e = \int_0^{10^{-6}\text{s}} \underbrace{\frac{g(\tau) - S_{\text{CH}}^2}{1 - S_{\text{CH}}^2} d\tau}_{:=g'(\tau)}$$

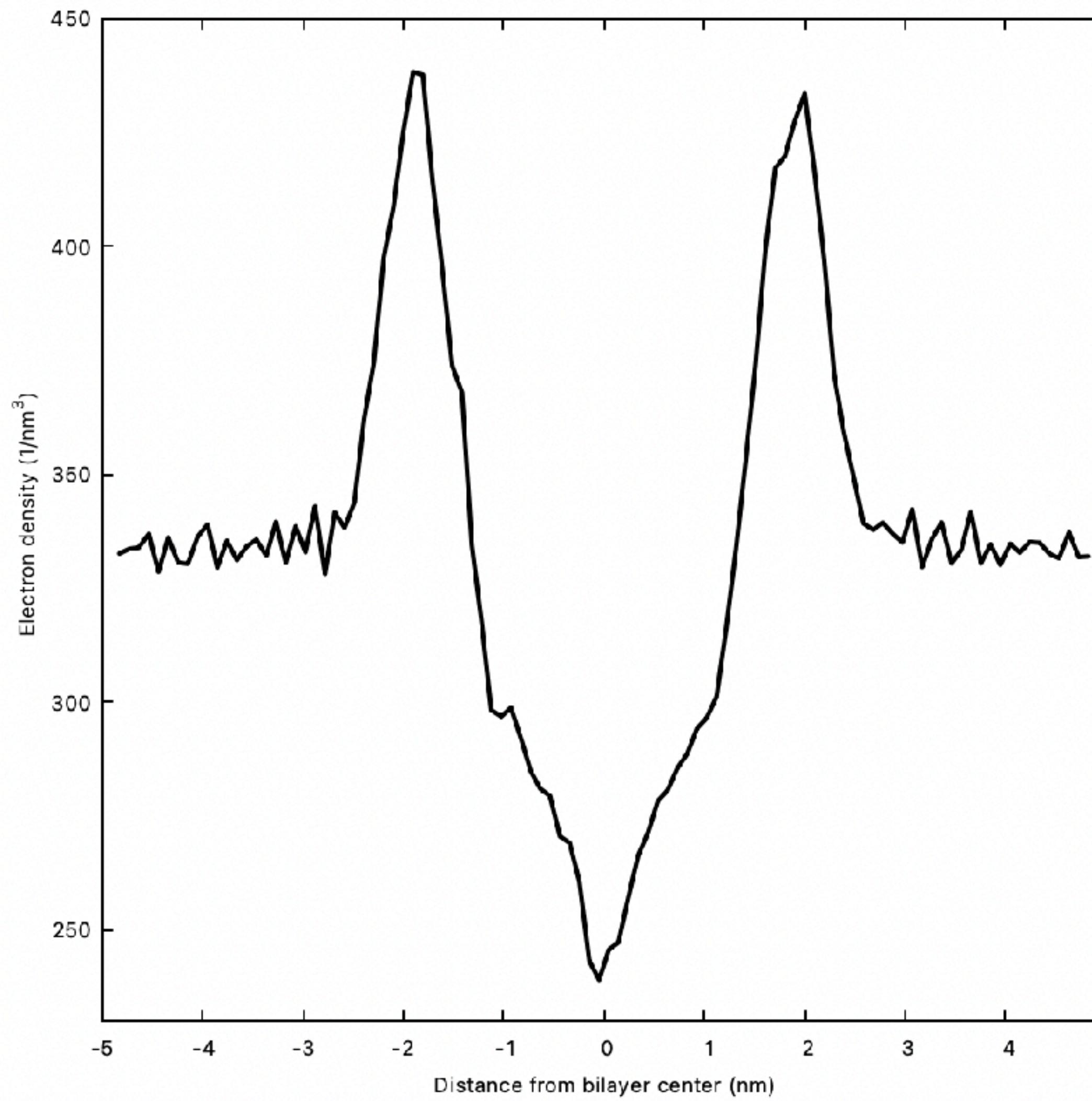
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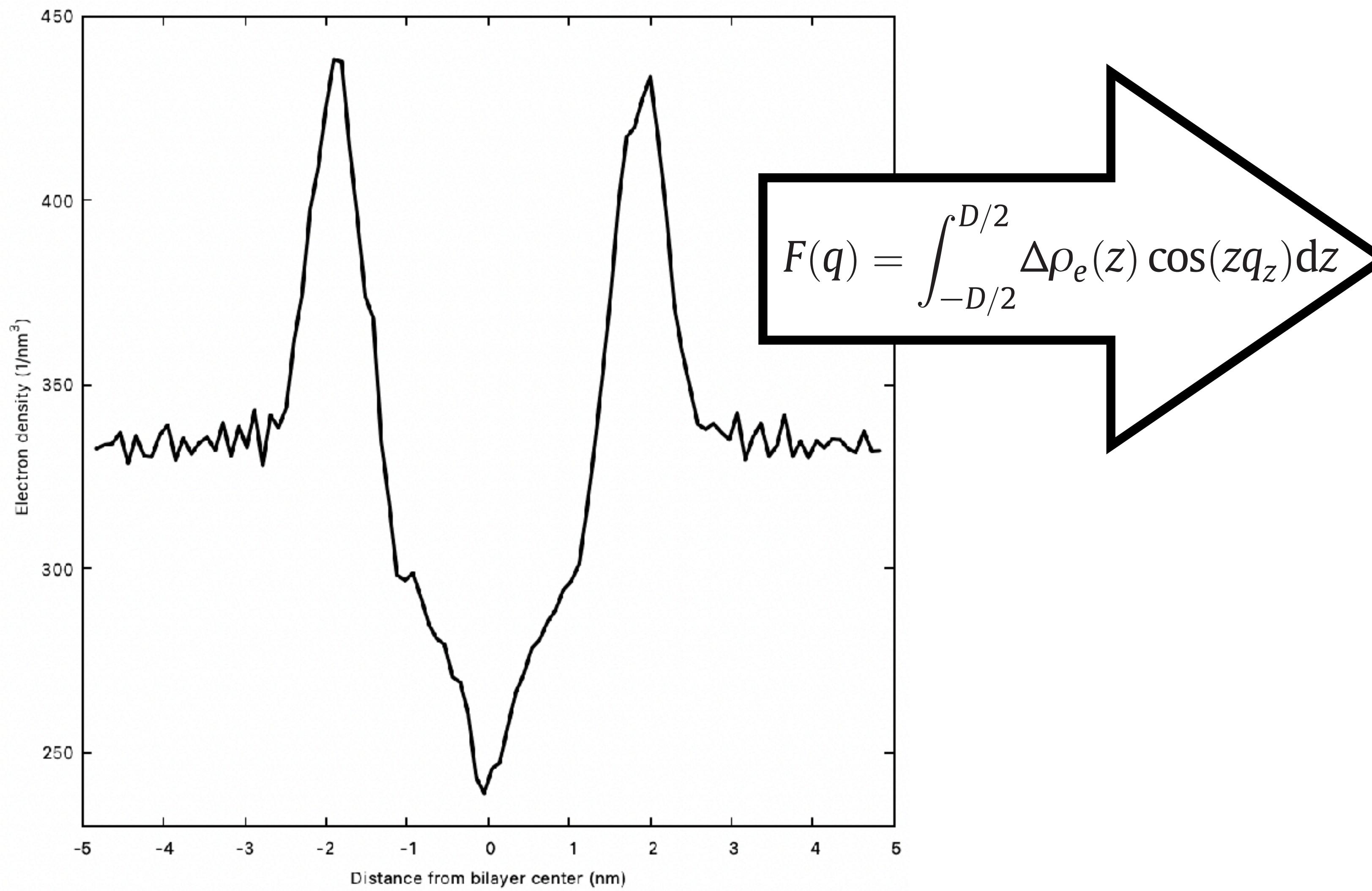
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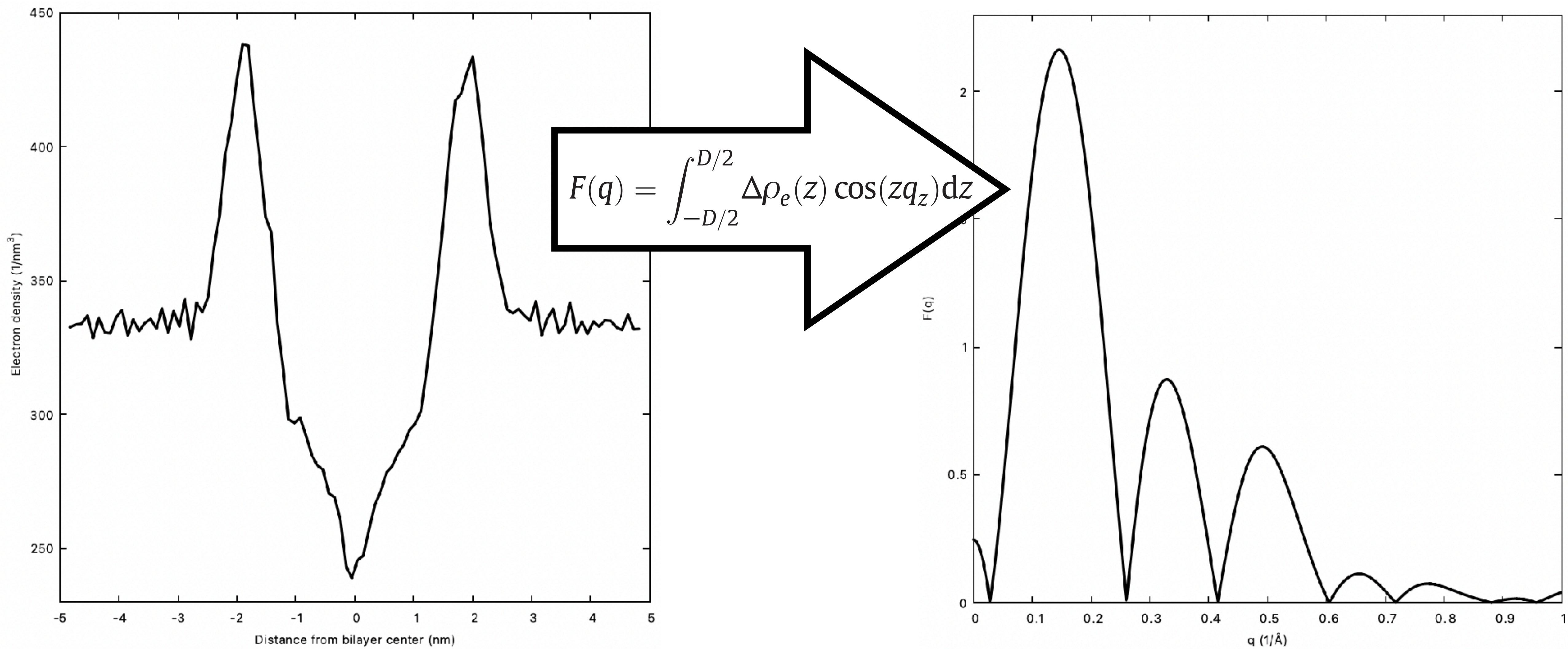
# Scattering form factor $F(q)$



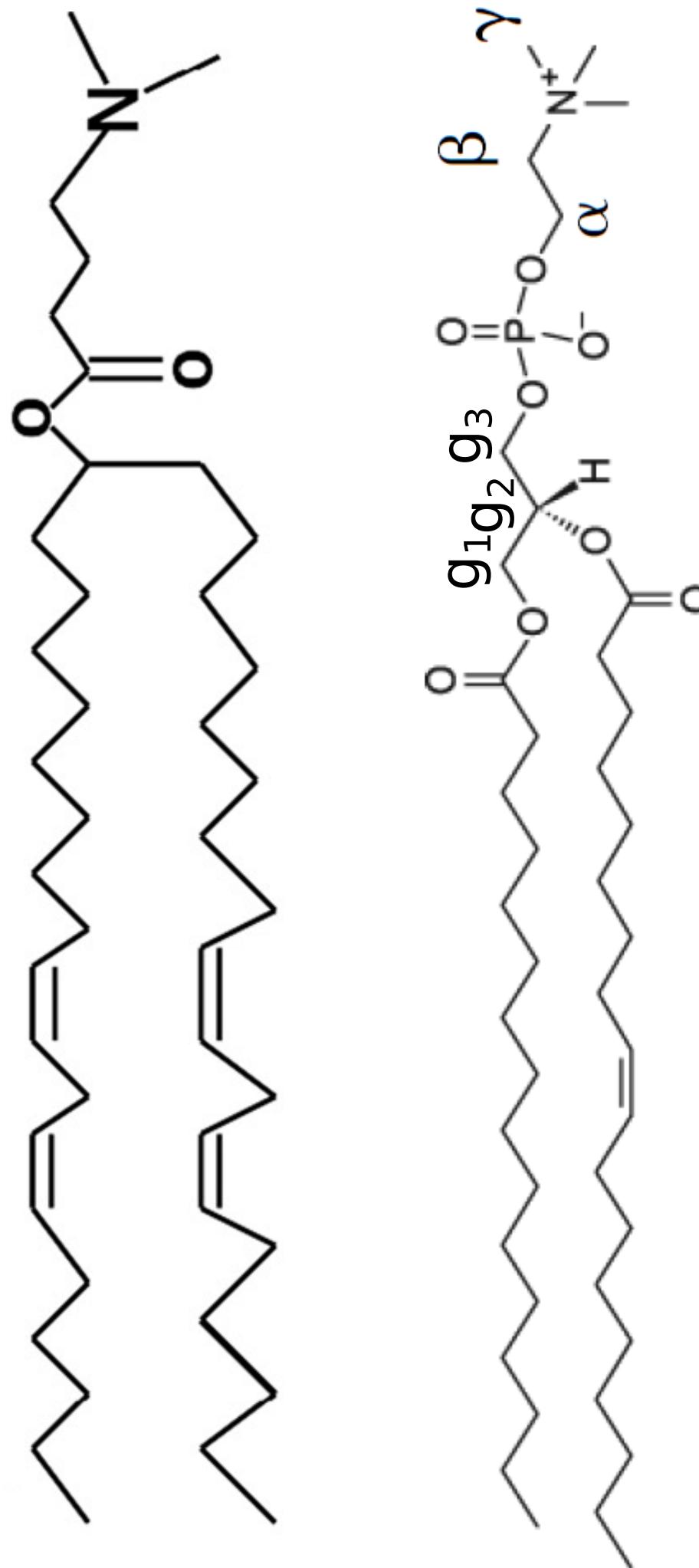
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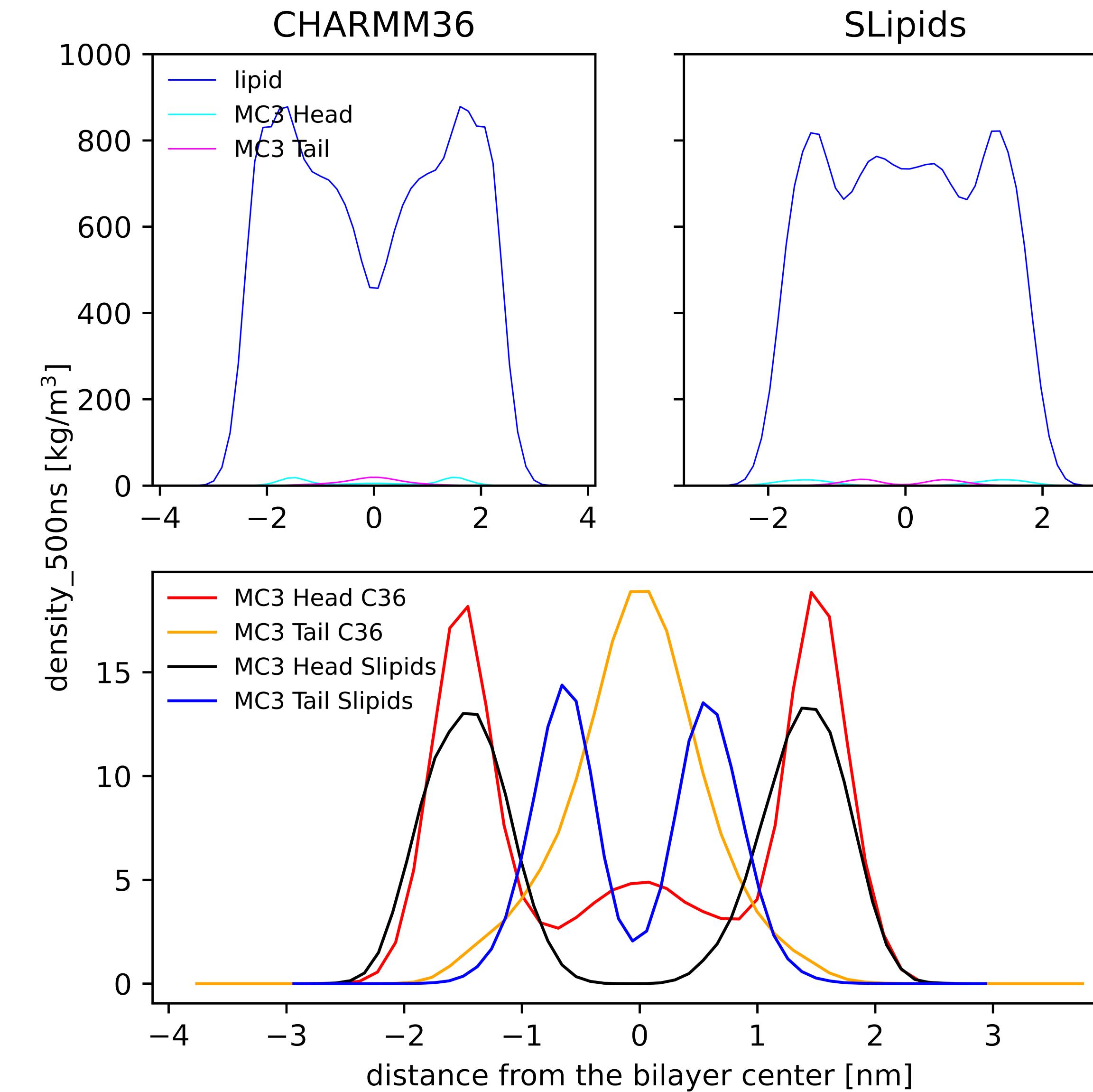
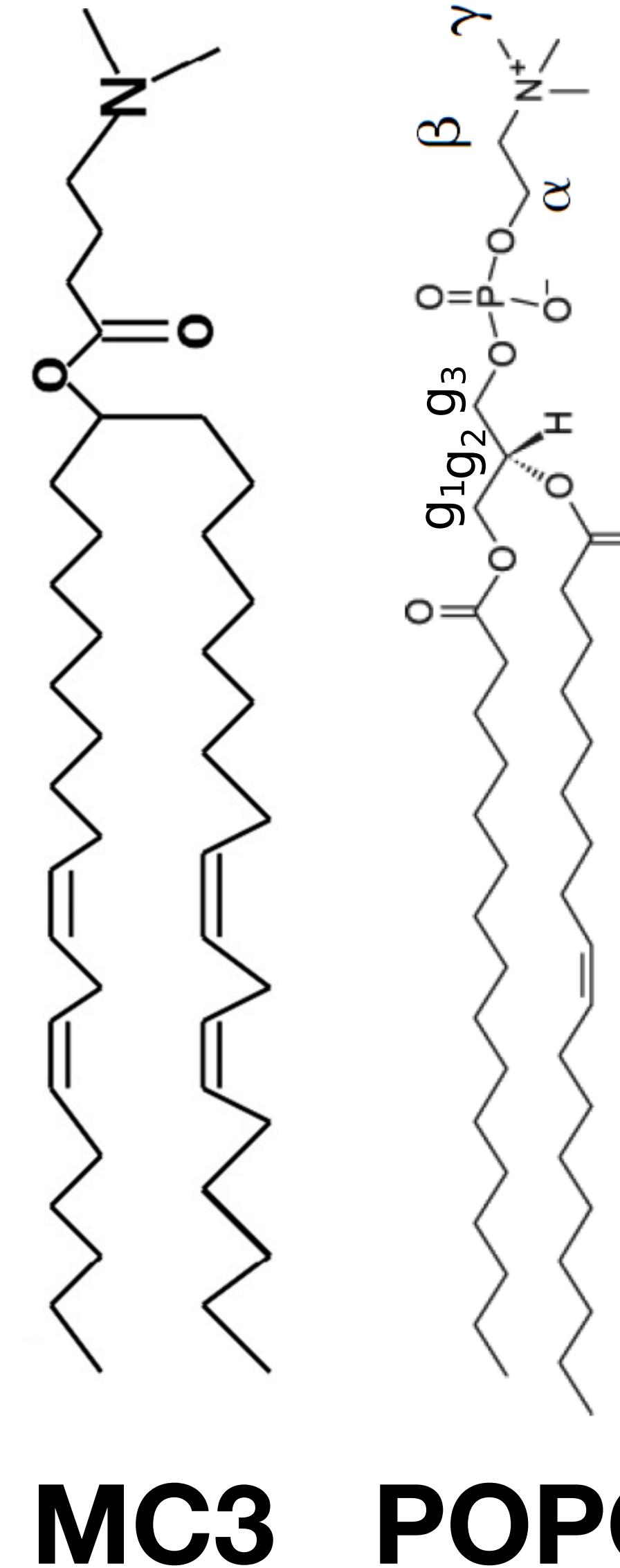
# Application: lipid nanoparticle simulations (Batu)



**MC3    POPC**

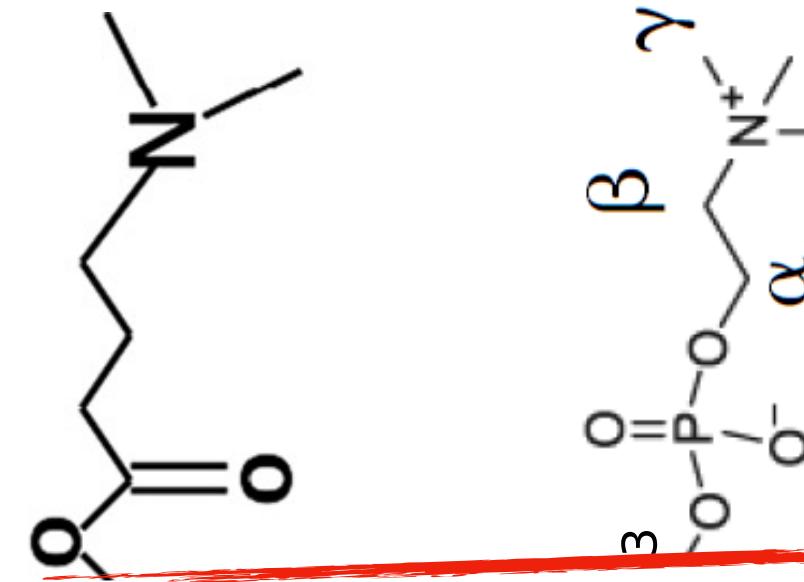
# Application: lipid nanoparticle simulations (Batu)

15% MC3 85% POPC

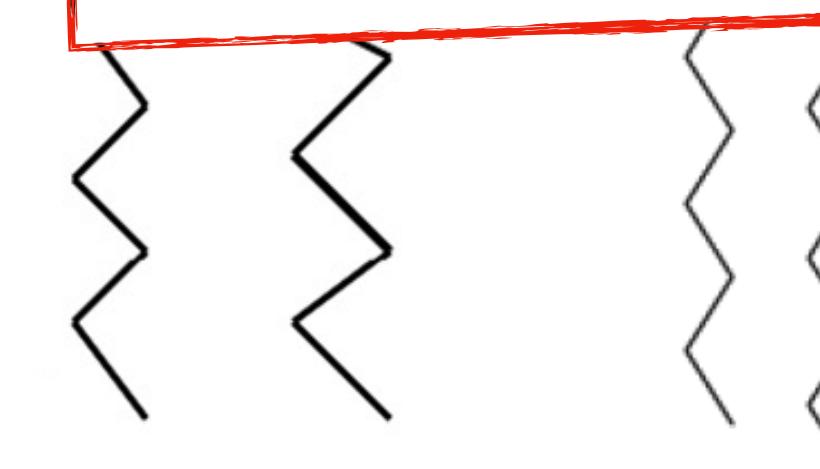


# Application: lipid nanoparticle simulations (Batu)

15% MC3 85% POPC



**Take home:**  
Force field can  
qualitatively  
change what you  
see.



**MC3    POPC**

