

# Water models / solvation

Andrew Torda, May 2008, 00.912

Biggest effects of water

- electrostatic
- dynamic

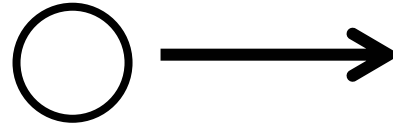
Model types

- explicit
- implicit

Dynamic effects of water

# Dynamic effects of water

one lonely moving particle



- initial velocity  $\dot{x}_t$
- future velocity easy  $\dot{x}_{t+\delta t} = \dot{x}_t$
- energy ? constant  $\frac{m\dot{x}^2}{2}$

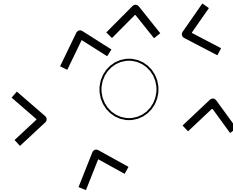
two particles ? interacting ?

- future velocity a bit more difficult
- easily bounded – cannot be more than  $\frac{m_1\dot{x}_1^2 + m_2\dot{x}_2^2}{2}$

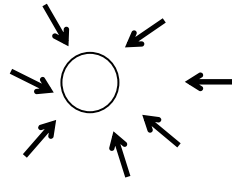
one particle in water...

# Velocities of particles in water

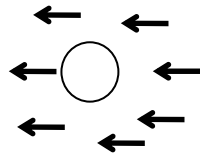
- lots of random interactions



- a small velocity ?



- a big velocity ?

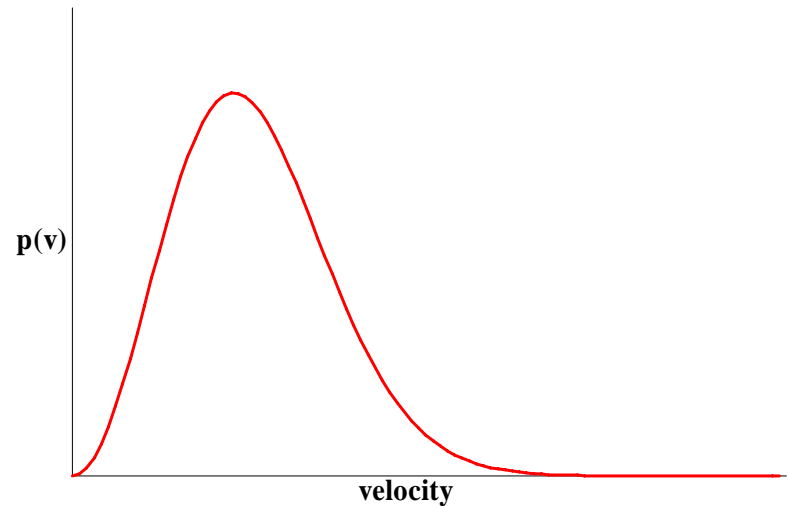


- a probability distribution

+

- how does  $\dot{x}_t$  tell us about  $\dot{x}_{t+\delta t}$  ?

- much less



# Modelling dynamic effects

## Summary

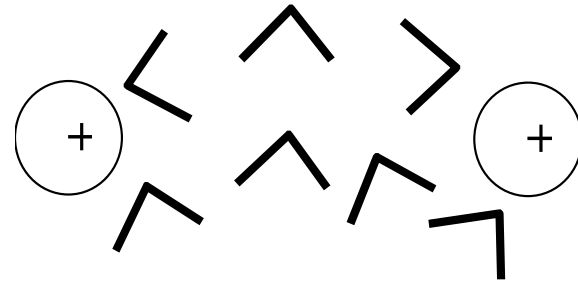
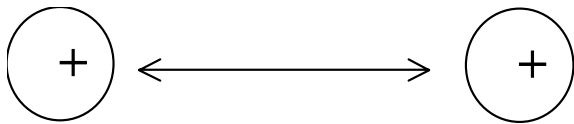
- solvent will add fluctuations
- makes us forget velocity faster

Can this be modelled ?

- yes (in molecular dynamics simulations)
- not really a force field / energy topic
- add random fluctuations to velocities
- can be made to look like water

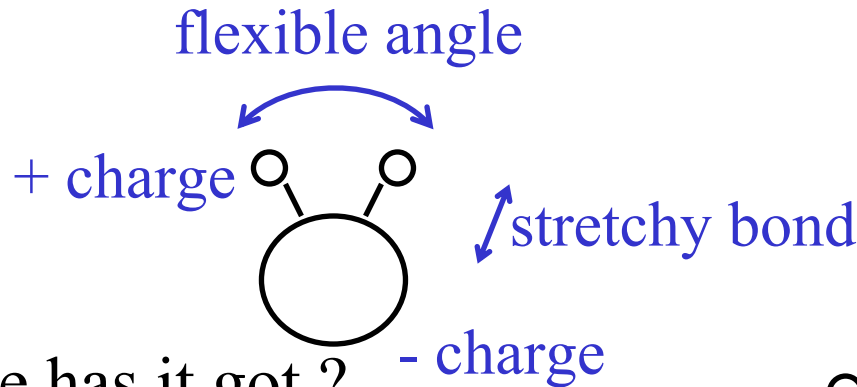
# Electrostatic effects of water

- water molecules
  - not charged
  - polar
- interaction between charges very different if water in between
- details soon

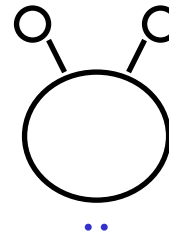


# Explicit water

- earlier descriptions of proteins
  - a set of connected atoms
- extend to include water
- what does water look like ?



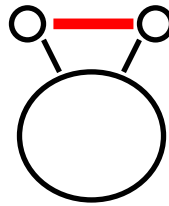
- what else has it got ?
  - think about electron pair on “O”
- what is really important ?



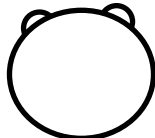
# Important features of a water model

Do we care about water internal dynamics ?

- usually not
- make bonds rigid
- make angle rigid
  - treat as a bond

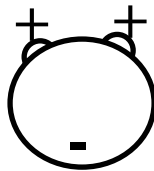


Dimensions

- protons are really small
- does water geometry matter ? 
  - usually not

Charge

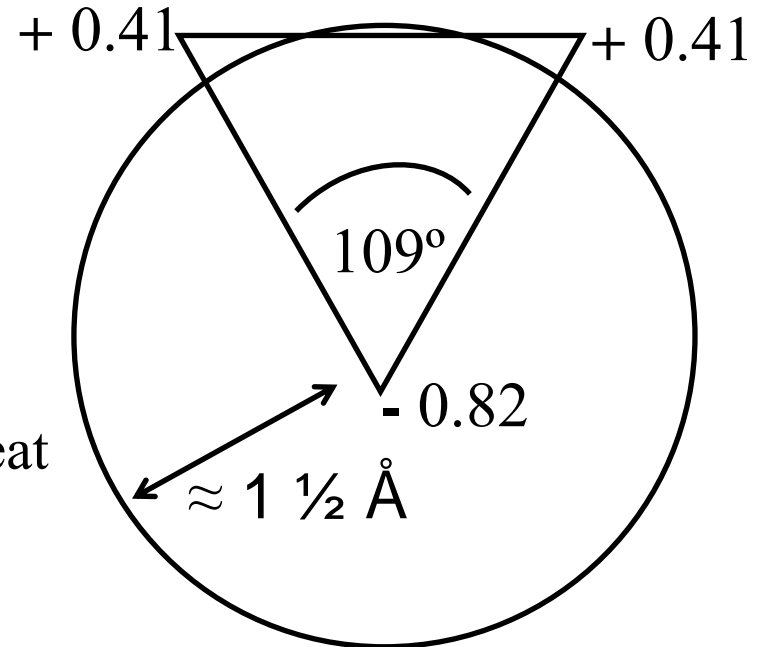
- most important



Final result..

# A useful explicit water model

- 3 charges
- 1 Lennard-Jones radius
- 3 masses - why ?
  - only for molecular dynamics
- 3 bonds (completely rigid)
- has a name – “SPC”
- what can it do ?
  - diffusion, density, compressibility, heat capacity
  - dielectric constant
  - solvation energies ?
- perfect ?
  - no
    - add polarisation, bonds, bond angles, offset charge from mass





# Explicit water + protein

## Protein water interactions

- via charge
- via Lennard-Jones term ( $r^{-12}$  and  $r^{-6}$ )

Only average properties are interesting

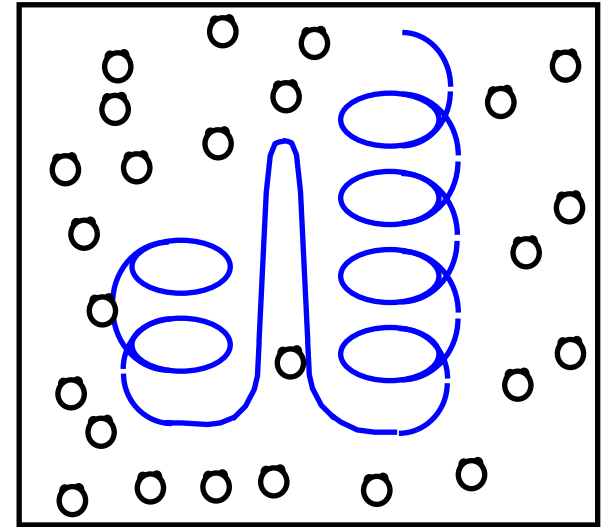
- useful only in simulations (MC, MD)

What is neat

- automatically incorporates
  - dynamic effects
  - electrostatics

Problems

- very very expensive
- typical simulation  $10^3$  protein atoms
- $10^4$  solvent atoms



# worst case for proteins + water

Imagine a world with no cutoffs for interactions

- scales as  $O(n^2)$  \*
- adding water takes 5 or 10 times as many atoms
- takes 25 or 100 times as much CPU time

What to do ?

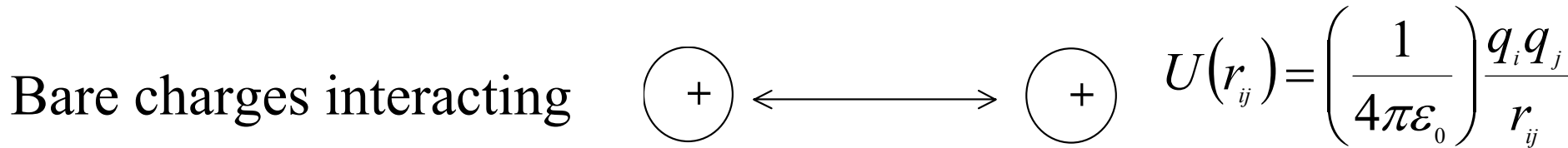
- look for cheaper model

\* not really true

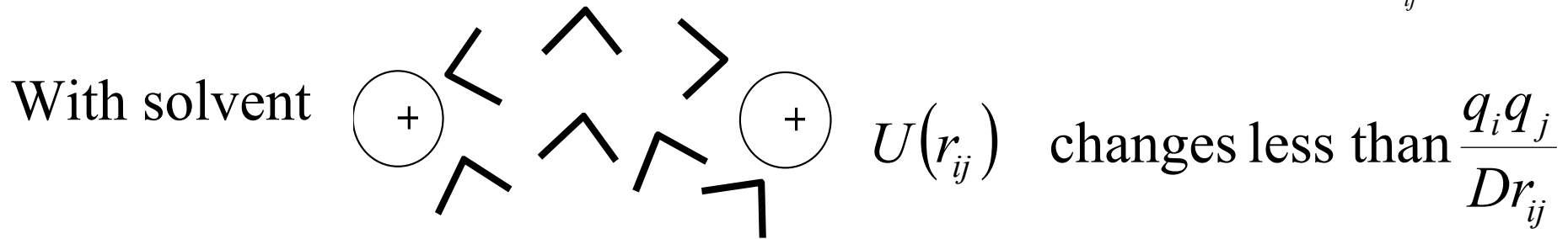
# Cheaper water models

- Do we really need dynamic effects of water ?
  - maybe not
    - only want energies
    - only care about structures
  - or
    - model with a random force
- then look for model which gets most essential aspects of water
  - electrostatics
    - distance dependent dielectric
    - reaction field
    - surface area methods

# Distance dependent idea



$$\equiv \frac{q_i q_j}{Dr_{ij}}$$



Net effect ?

- water is very polar and tends to orient itself around charges
- as if the water "screened" the charges (makes them smaller)

# Distance dependent dielectric implementation

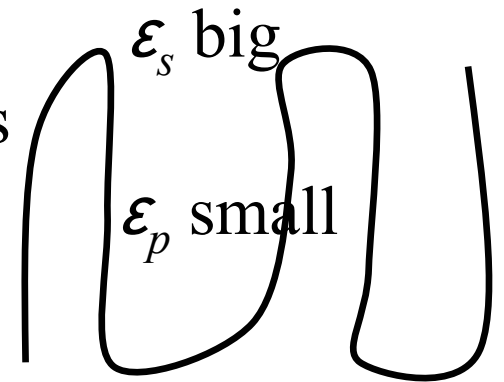
- invent approximation  $D_{eff}=r_{ij}$  then  $U(r_{ij}) \approx \frac{q_i q_j}{D_{eff} r_{ij}} \approx \frac{q_i q_j}{r_{ij}^2}$
- is this physics ?
  - no
- does it work ?
  - a bit (ugly)
  - little real physical basis
- water does not behave so simply
- fundamental problem...

# Fundamental problem with distance dependent D

- if we rely on distance dependent dielectric constant
  - assume one 'fix' works everywhere (not true)

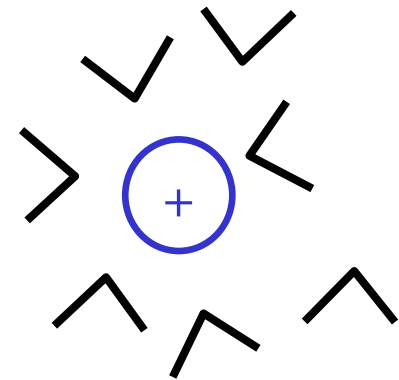
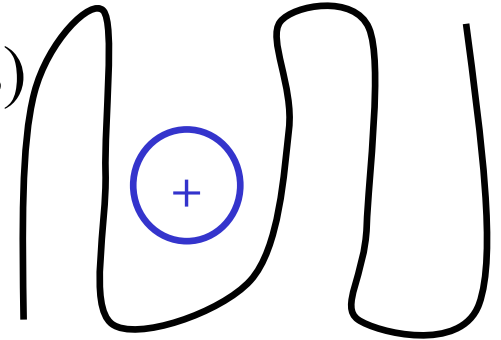
- think of formula  $U(r_{ij}) = \frac{q_i q_j}{4\pi\epsilon_0 r_{ij}}$

- model will differ on big and small proteins



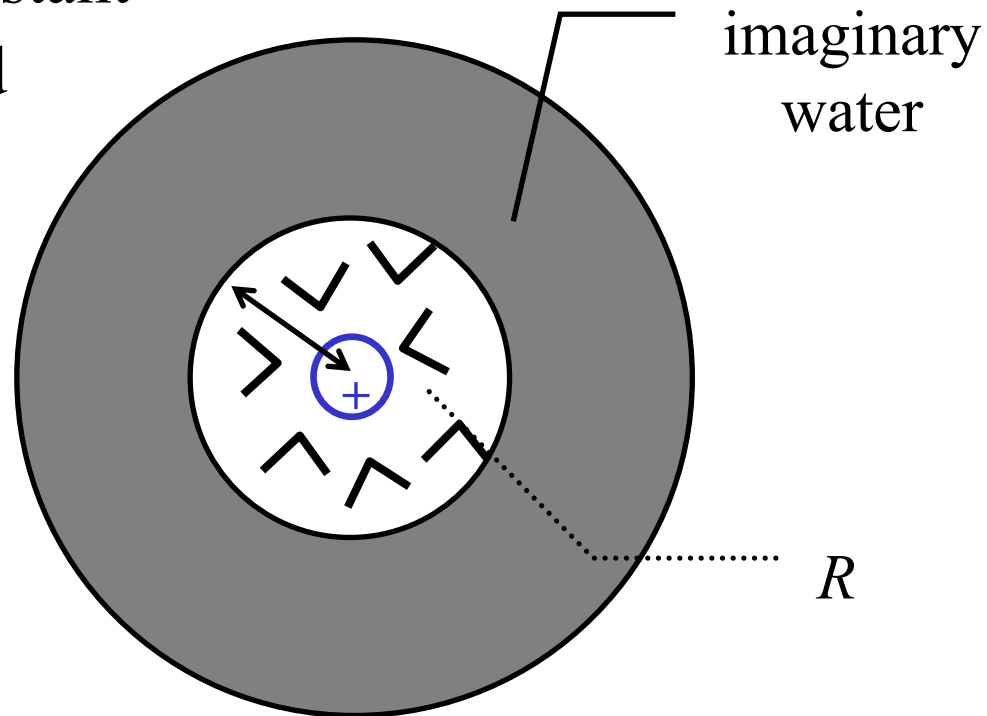
# Reaction field idea

- different problem to before
- charge in a protein (lots of neutral CH groups)
  - not much happens
- particle in water
  - what does the water do ?
  - tends to orient
  - lots of  $q^+q^-$  interactions
    - much better energy
  - is this like a force ?
    - yes, think  $-dU / dr$
  - can this be modelled ?



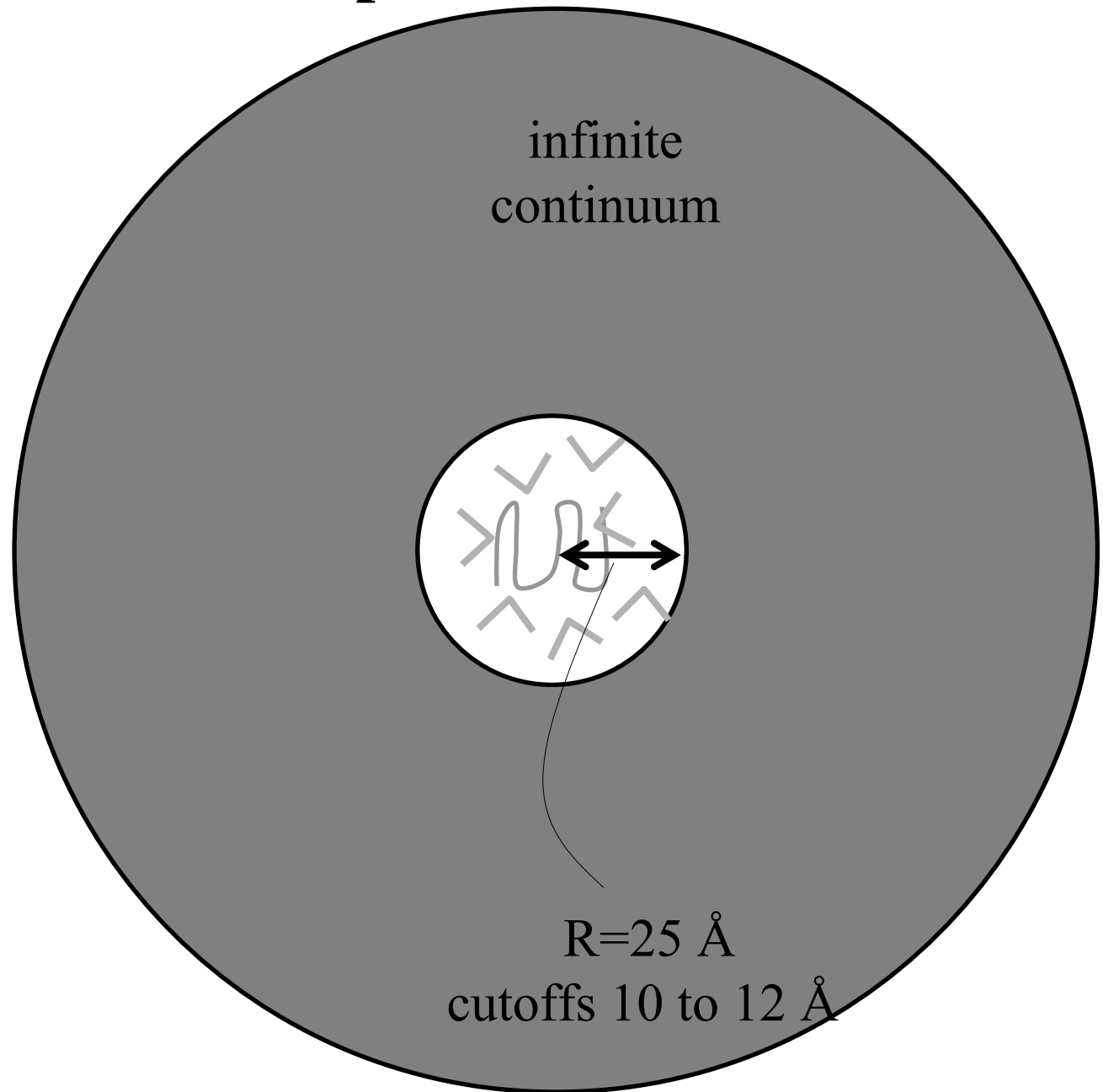
# interaction with imaginary solvent

- think of particle interacting with distant water molecules
- our charge interacts with them all but
  - if they are far away (big  $R$ ) less important
  - depends on dielectric constant
  - inside white region  $\epsilon_r$  and
  - grey region  $\epsilon_s$
- within white region
  - treat atoms with a correction
- grey region
  - treat as continuum





# Realistic picture



# Reaction field / image charge formula

- as if we interact with an "image" charge

- size 
$$q_{im} = -\frac{(\epsilon_s - \epsilon_r) q_i R}{(\epsilon_s + \epsilon_r) r_i}$$

- location 
$$\left(\frac{R}{r_i}\right)^2 \vec{r}_i$$

- near middle

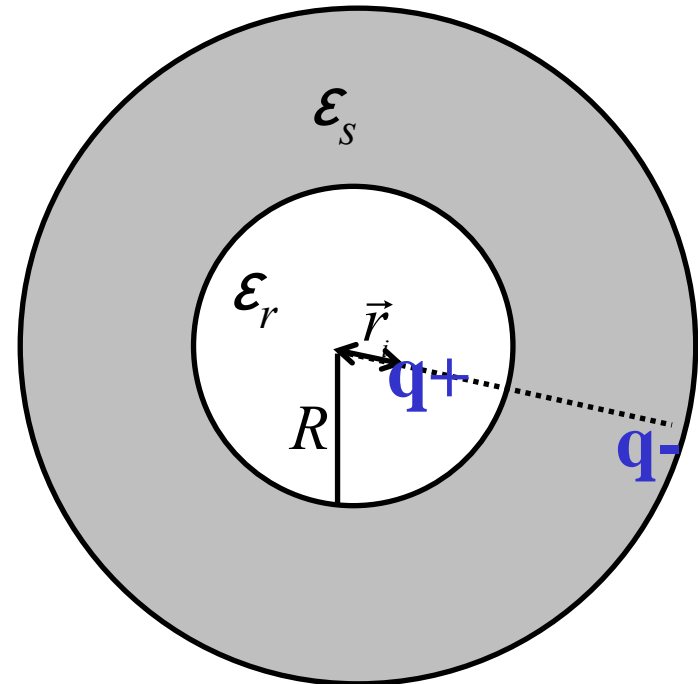
- $R \gg r_i$
- image far away

- near boundary

- imaginary solvent important
- strong (favourable) interaction

- important result

- we have modelled the happiness of a charge in solution
- charges happiest on outside of protein



# Reaction fields and pairs

- charge  $q_i$  interacts with water
- water responds
- $q_j$  feels effect of water

- no longer 
$$U(r_{ij}) = \frac{q_i q_j}{4\pi\epsilon_0 r_{ij}}$$

- instead, 
$$U(r_{ij}) = \frac{q_i q_j}{4\pi\epsilon_0 r_{ij}} \cdot f(q_i, q_j, \text{distances to center, ...})$$

# Simpler ways to model solvent

## Problem with real physics

- if you use this model, you are obliged to use
  - real charges, real coordinates...
- parameters not perfect
- hard to rationalise repairs

## Many effects simultaneously

- charges interacting with water dipoles
- loss of water – water interactions
- change of solvent entropy
- change of solute entropy ?

## Different approach

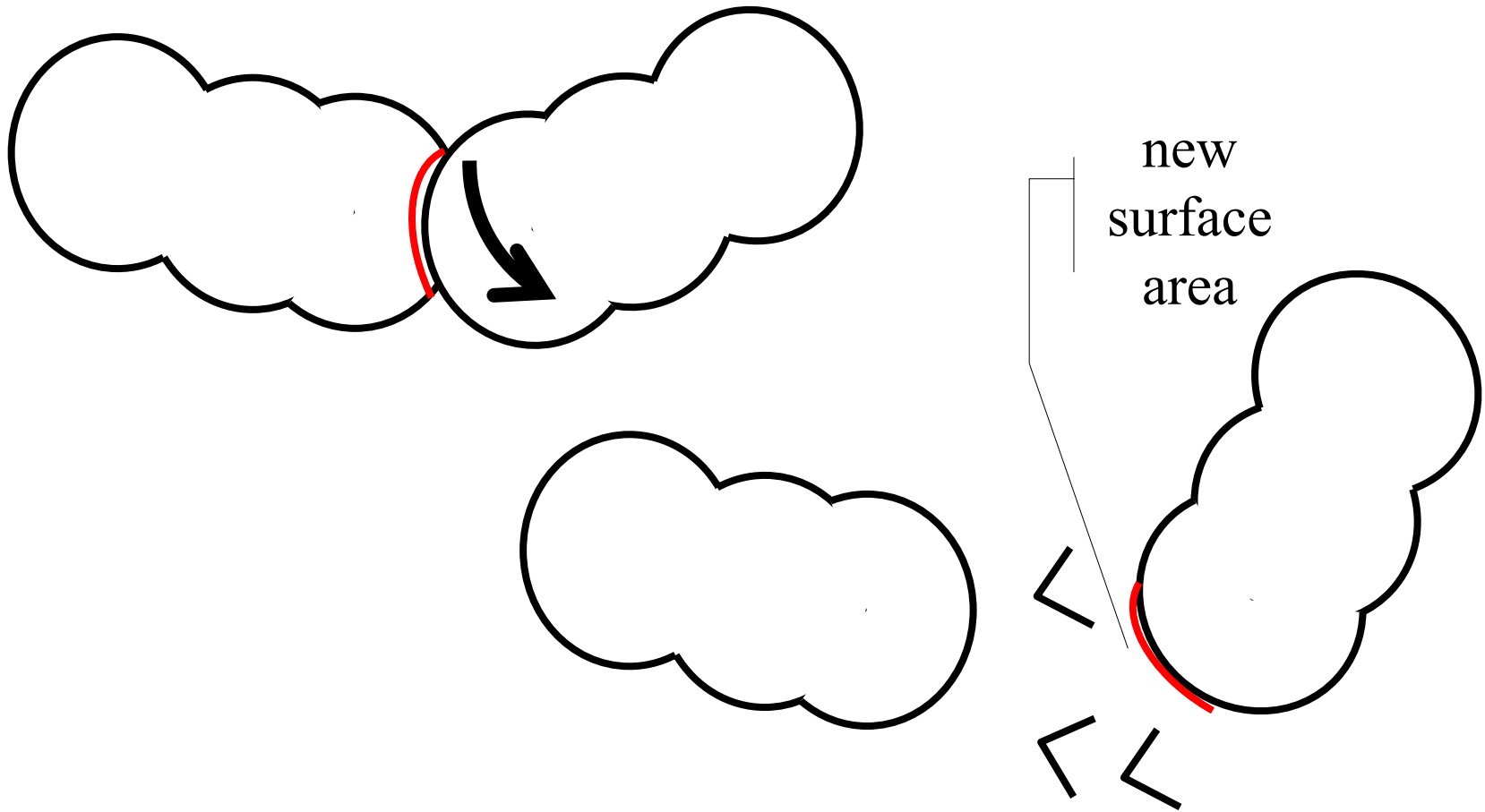
- less rigorous models

# Basis of quick water model

## Philosophy

- I can not model water properly
- find a very general way to incorporate effects
- Water makes some atoms happy
- Others do not care too much
- Find some very general way to include water effects
  - whether they are favourable / unfavourable
- what is easiest way to think about water influence ?

# Atom surface area



- simple model
  - for each atom, energy depends on surface area

# Formalising SASA model

- Solvent accessible surface area (SASA)
- for every atom,  $i$   $G_i^{solv}(\vec{r}_i) = \gamma_i A_i(\vec{r}_i)$
- $G$  because we no longer have a pure potential energy
- $G_i^{solv}(\vec{r}_i)$  because the energy term depends on coordinates
- $\gamma_i$  is a specific parameter for each kind of atom
  - for O, N will be negative
  - for CH, CH<sub>2</sub>, CH<sub>3</sub> will be positive or near zero
- area,  $A_i$ , has to be calculated

## Problems

- $A_i$  is difficult to calculate
  - use approximation
- $\gamma_i$  not easy to estimate

# Example SASA calculation<sup>1</sup>

- classical atomistic force field
- distance dependent dielectric
- two  $\gamma_i$  parameters,  $\gamma_{C,S} = 0.012$  and  $\gamma_{O,N} = -0.060$  kcal mol<sup>-1</sup>

## Results

- better than *in vacuo*
  - deviation from known structure during simulation
  - not too many H-bonds formed
  - radius of gyration ? (how big is protein)
- why do they appear OK ? why only two  $\gamma_i$  ?
  - not tested in detail
  - worst problems fixed

<sup>1</sup>Ferrara, P, Apostolakis, J and Caflisch, A. 2002, Proteins, 46, 24-33



# summary

- Explicit water is best, but expensive
- We have not discussed dynamic effects
- distance dependent dielectric +
  - SASA style models
  - complementary
- many variations
  - surface accessible volume
  - more  $V_i$  parameters
  - add in reaction field for better long range electrostatics
- changes and flaws in one parameter are hidden by others