

Lattice Models

classify models by detail

detail	type	properties
high	quantum mechanical atomistic	very physical some approximations, mostly physical terms
low	coarse grain	crude functions, approximations, often non-physical terms

Another important property

- continuous vs discrete

Continuous versus discrete

Continuous models

- coordinates (and other properties) take on any value
- typical properties
 - can take derivative with respect to coordinates
 - energy defined almost everywhere

Discrete

- coordinates (maybe more) are limited to certain values
 - think real/float versus integers
- examples
 - weather forecasts, oceanography, wind tunnels
 - finite element methods (engineering)
 - statistical mechanics (Ising model)

Aim

- Simulations so far
 - long simulations necessary to sample conformational space
 - to get average properties

$$A_{obs} = \frac{1}{N_{obs}} \sum_{i=1}^{N_{obs}} A_i \quad \text{or} \quad A_{obs} = \frac{1}{b-a} \int_a^b A_i dt$$

- with drastic simplifications either
 1. increase N_{obs} or
 2. visit all possible (exhaustive enumeration) ..

Exhaustive enumeration

- real world properties – average over all states
- probabilities depend on all states
- previously, we had " N_{obs} "

$$p_i = \frac{e^{\frac{-E_i}{kT}}}{Z} \quad \text{and} \quad Z = \sum_i e^{\frac{-E_i}{kT}}$$

- in a simple system, one can visit all i states
= exhaustive enumeration

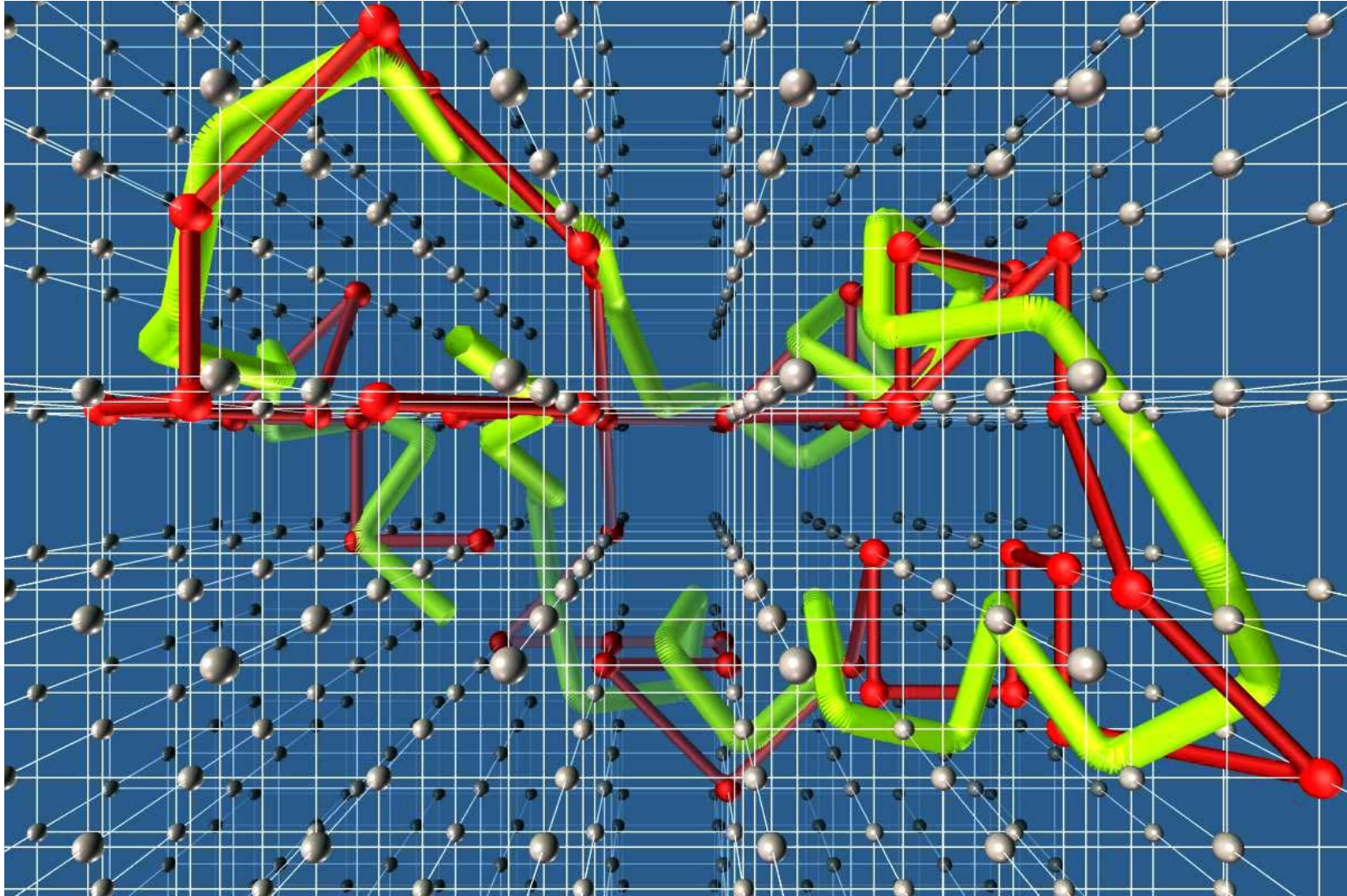
Discrete proteins

How do we make proteins discrete ?

- most common
 - lattices, grids, (Gitter)
- sometimes picture of real world
 - more common – a very simple model to analyse some property

Putting a protein on a lattice

- Put down a protein and find nearest grid point



Lattices, errors

What would the error be on a lattice ?

- for 1 Å, should be $\frac{1}{2}$ Å
- can be made arbitrarily small
- what if two continuous residues map to one point ?
- not the only (or best) criterion
 - first, what would our energy look like ?

Energy functions

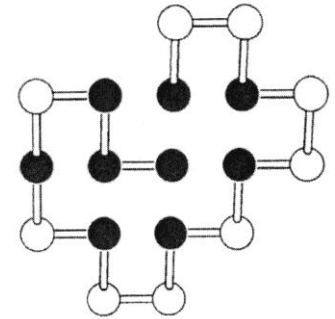
Two philosophies

1. mimic approximation to real energies

- earlier picture

2. simpler approach

- continuous space for realistic simulations, real proteins
- use simple model for some topic of interest



$$U = \sum_{i < j} c_{ij} \Delta(\vec{r}_i, \vec{r}_j)$$

- c_{ij} is some parameterisation constant for types i and j
- switching function

$$\Delta(\vec{r}_i, \vec{r}_j) = \begin{cases} 1 & \text{if } i - j \neq 1 \text{ and } |\vec{r}_i - \vec{r}_j| = 1 \\ 0 & \text{otherwise} \end{cases}$$

Why simple energy functions ?

Simple functions (contact terms)

- some residues like to interact with each other
- will be happiest when the most favourable contacts are made (like a real protein)
- can reproduce very specific structures
 - interactions can be anything you want
- gross properties like hydrophobic packing

Reduced alphabets

Typical question – we want to guess

- how does folding time depend on size ?
- how much hydrophobic area is exposed for some sequence ?

Do we need 20 amino acids ?

- general principle, consider 5 or 6 residue types
 - charged - (asp, glu)
 - charged + (lys, arg)
 - polar (thr, ser, gln, asn)
 - hydrophobic aromatic (tyr, phe, his, trp)
 - hydrophobic aliphatic (ala, leu, val, ile, met, cys)
 - special (gly, pro)

Reduced alphabets - HP model

- history of protein structure
 - most proteins have a hydrophobic core
 - can this explain much of protein structure ?
- minimalist version
 - two residue types (hydrophobic / polar, HP)
- Say that protein structure is dominated by hydrophobic collapse
 - two residue types are really enough for many calculations

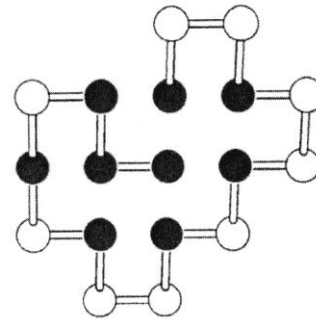
Reduced dimensions

Do I care about specific real proteins ?

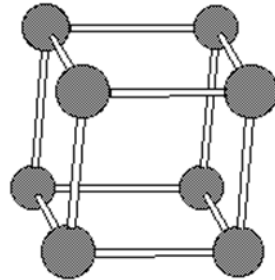
- not always

Is there a simple system which looks like a protein ?

- two dimensional protein
- very very simple protein ?
- 2-D, HP model

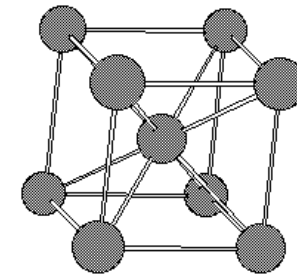


Different types of lattice

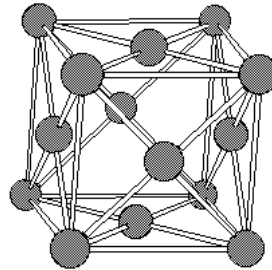


- simple cubic lattice

- body centred cubic



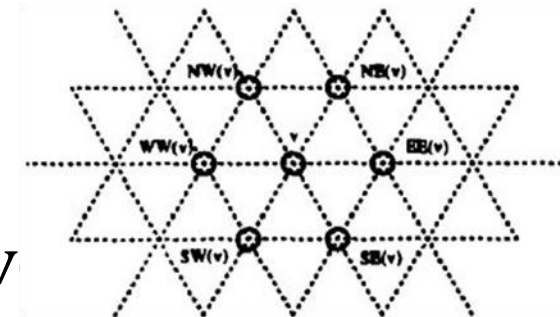
- face centred cubic



- triangular 2D / 3D

most important difference ?

- score functions count contacts
- how many neighbours does each hav



Why are lattice calculations so fast ?

- normal code
 - for each particle
 - for each other particle
 - is it a neighbour ? calculate energy $O(n^2)$
- lattice code
 - for each particle
 - set up list of neighbour cells (often 6, 8, ..)
 - look if neighbour is occupied $O(n)$
- what if we have a very realistic system ?
 - all distances can be precalculated
 - 1 unit is 3.8 Å or 0.5 Å or ...
 - no more square roots $x^{1/2}$, cutoffs, ...

Calculations

We have some machinery, what kinds of calculations ?

- simulation (brief now, more later)
- others

Simulating on a lattice

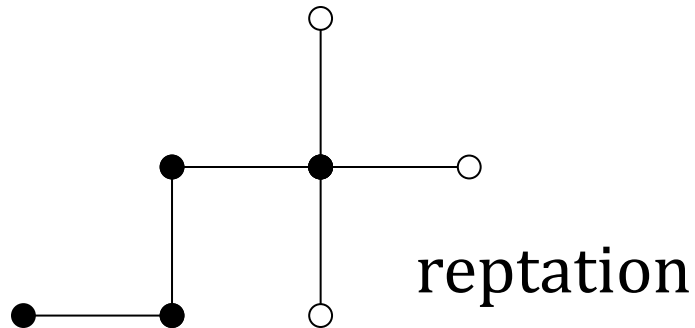
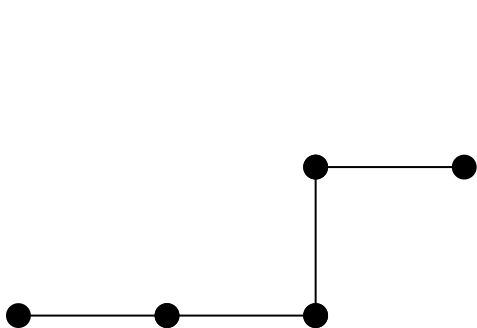
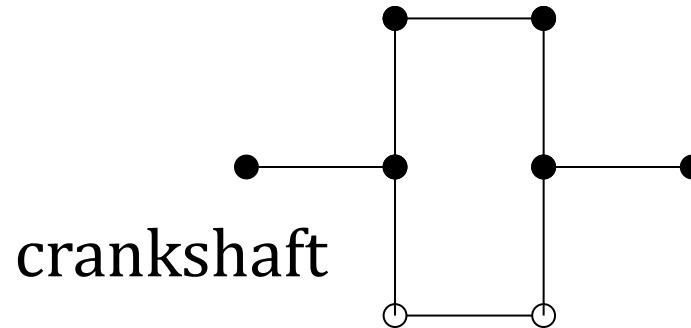
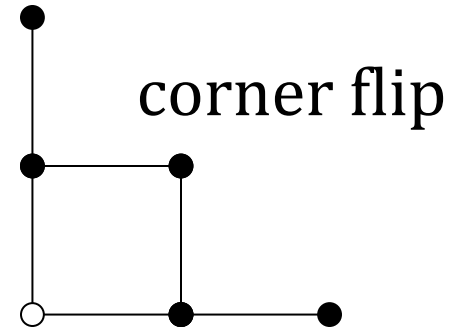
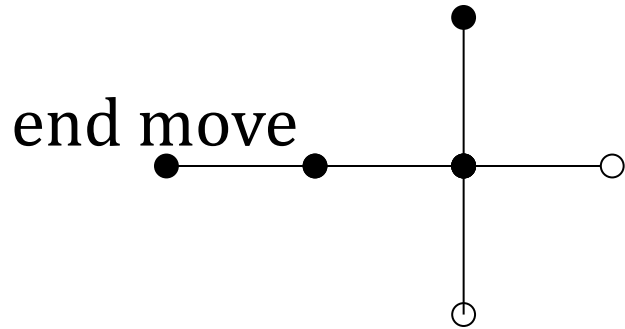
- we do not have gradients of our energy terms (not much help if we do)
- we do know the energy of a configuration
- calls for Monte Carlo

Lattice simulations

Monte Carlo

- apply normal conventions
- take a step
- calculate energy
 - accept / reject according to Metropolis criterion
- what would our moves look like ?
 - anything reasonable
 - from one starting point, should (eventually) be able to reach any other
 - typical moves ..

Move sets



What can we get from simulating

- Take a system usually < 100 residues
- start from
 - random configurations
 - extended configurations
 - misfolded configurations
- run for 10^6 or as many steps as you can afford
 - does a simulation always find a similar minimum energy ?
 - what is the energy spread of misfolded structures ?
 - are there many similar low energy structures ?
 - are there a large number of different low energy structures ?

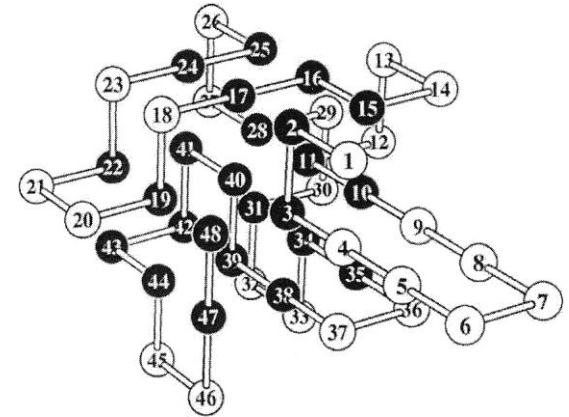
Results from simulations

From a 3D HP model, typical structure

- features ?
 - hydrophobic residues in middle

Compare with MD simulation

- biggest simulation in literature
 - 36 residues
 - months of cpu time
 - does not find global minimum



More on simulations later...

Unique possibilities

Big problem with atomistic systems

- for any system more than about handful of residues
 - nearly impossible to visit all conformations
- for more than about 10 residues (maybe 15 or 20)
 - little evidence that the global minimum can be found

Lattices

- exhaustive enumeration (visit all possibilities)
 - configuration
 - sequence
- location of optimal structure

Exhaustive enumeration of conformations

Why bother ?

- define almost all the stat mech properties of a system
- remember partition function
- summation over all conformations

$$Z = \sum_i e^{\frac{-E_i}{kT}}$$

We can find things like

- free energies
- distribution of energies

How many configurations are there ? 2D HP model

- 16 residues in 2D is no problem
- in 3D, about $3 \times 3 \times 3$ feasible

length	num configurations
14	110 188
16	802 075

Exhaustive enumeration of sequences

20 amino acids

- too hard

5 or 6 amino acids

- quite realistic, but difficult

HP model ?

- 16 residues is easy (65 536 sequences)
- with this machinery, what can we do ?

Example question

- folding
 - what are driving forces ? (hydrophobic collapse, HP)
 - what is first to form (local or long range ?)
 - how smooth is the folding pathway
 - more later
- evolution
 - more later
- do all protein sequences fold ?
- sequence vs structure space ?

Do all proteins fold ?

If I take a random amino acid sequence, is it a protein ?

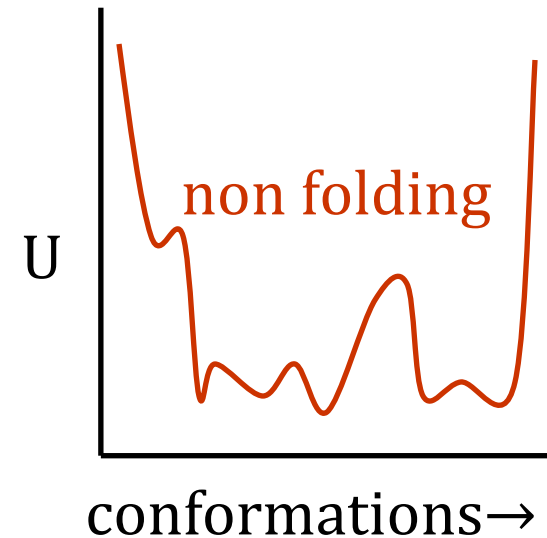
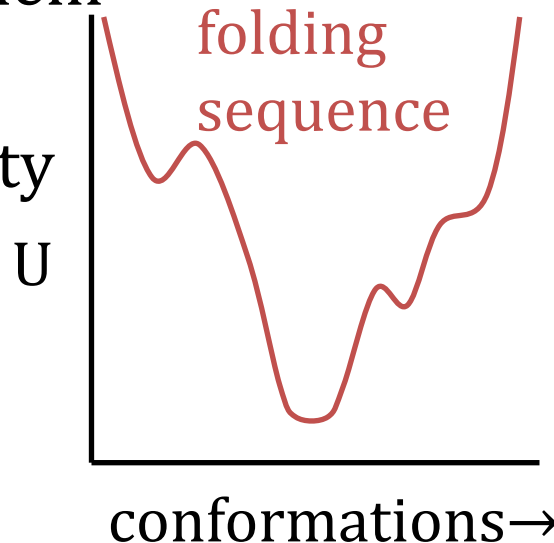
- experiment ? less than 1 in 100 fold
- test by MD simulation ?
 - cannot even fold one protein

Lattice models

- well studied problem

Definition

- important property
 - folding vs non-folding



Folding versus non-folding

Non-folding in a lattice model

- find a sequence
 - visit all conformations
 - rank energies
- how many different conformations have the lowest energy ?
- how many have energy within kT (could be visited at T) ?

Answers ?

- most random sequences do not fold
- intuitive example
 - a very very hydrophobic sequence is happy as long as it is compact
 - there are many ways to make it compact
- agrees with experiment

Sequence versus structure space

From earlier lectures

- different sequences may fold to nearly same structure
 - large number of different sequences known for
 - globins, β -sandwiches, ...
- different structures ? usually have unrelated sequences

Can we see this from MD ? No.

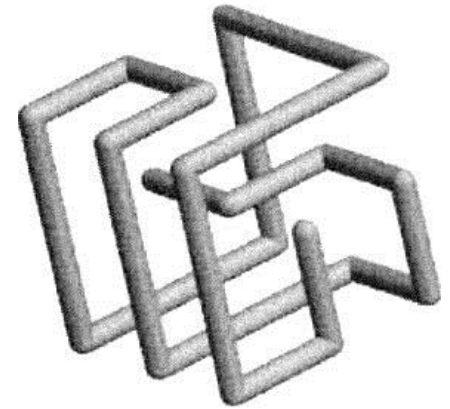
From lattice

- for each configuration
 - try every sequence and see if it is an energy minimum
- see how many sequences like each structure

Favourite structures

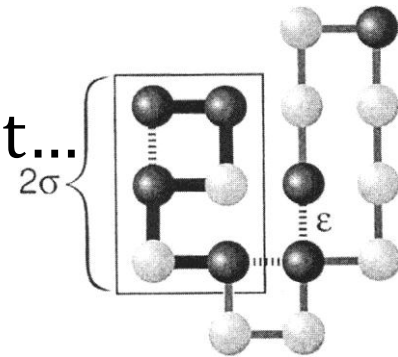
Some structures are the minimum energy for many sequences

- in a $3 \times 3 \times 3$ HP model, there are 100's of sequences which like this structure
- some structures are popular, some much less so
- in principle, totally agrees with nature
 - exact numbers have no meaning



Problems and limitation of lattices

- statistical mechanics are completely valid, but...
- loss of detail
 - resolution is obvious
 - interpreting in physical (or structural) requires faith
 - example of α -helix in 2D
 - whole structural properties may be lost
 - chirality ? chirality of a helix
- discretisation
 - energies and configurations are discrete
 - if a property depends on number of states, results will be model-dependent



Relating lattices to the real world

- simple models and reduced alphabets
 - only trends are believable
 - some trends can be tested
 - how do results change with 2 versus 3 amino acids ?
- for detailed models,
 - dependence on lattice type and resolution

Artefacts

Susceptibility to artefacts ? Examples

- dependence on alphabet size
 - how popular is a structure may depend on alphabet size
 - in simple alphabets and energies, there are less foldable structure
 - more complicated models make lowest energy more unique
- properties depend on kind of lattice
 - extreme example !
 - a triangular lattice has more foldable structures

Are we finished with lattices ?