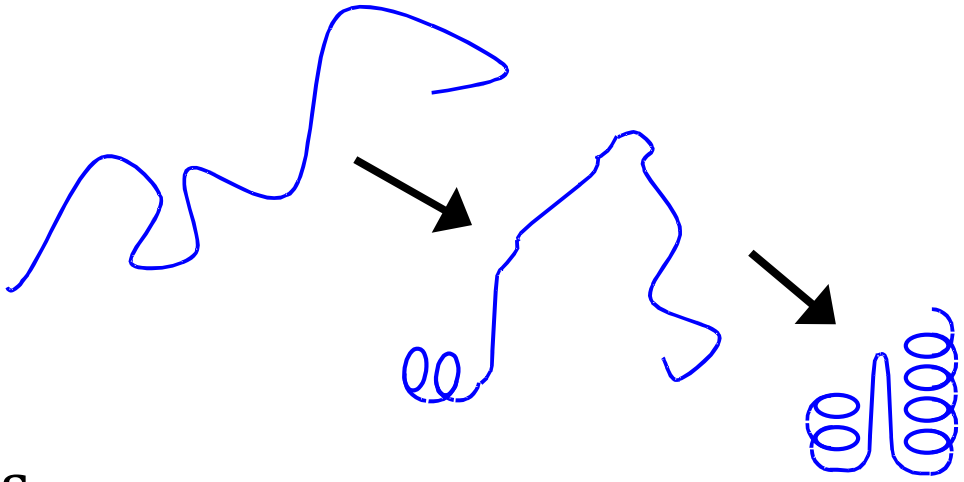
Protein folding

How does a protein do this ?



Ideas

- kinetic vs thermodynamic structures
- experimental methods for following protein folding
- pathways for folding
- entropic barriers

Background / stories

From biochemistry Übungen (protein folding – easy)

- take lysozyme / ribonuclease...
- put in 8M urea (unfolds)
- remove urea (refolds)

Conclusion ?

- the protein sequence is all you need to fold a protein
- is this true ? Not always

Alternative (logical reasoning)

- protein folding should be impossible…

Protein folding should be difficult

Levinthal's paradox

- each amino acid has 2 or 3 or n conformations
  - for a protein of m residues, it should visit n^m
- if it spends 10^{-15}s at each conformation ?

- time to find one conformation for n=3 and 100 residues
  - $3^{100} \times 10^{-15}$ s $\approx 1.6 \times 10^{25}$ years

Consequence

- proteins cannot be exploring space randomly
- historic idea of "folding pathway"

Who cares about protein folding ? Faith..

If we could understand folding we could

- predict structure
- design proteins that fold better (more stable)
- identify essential residues for folding (not suitable for mutagenesis)

Issues / Questions

- Kinetic versus thermodynamic
- What order do events happen in ? (collapse *vs* secondary struct)
- Is unfolding the same as folding ?
- Is folding in a test tube the same as nature ?

Are proteins in energy minima ?

Anfinsen story..

- proteins can be unfolded and refolded alone
- all the information is in the sequence
- native conformations are the (free) energy minimum
- thermodynamic belief

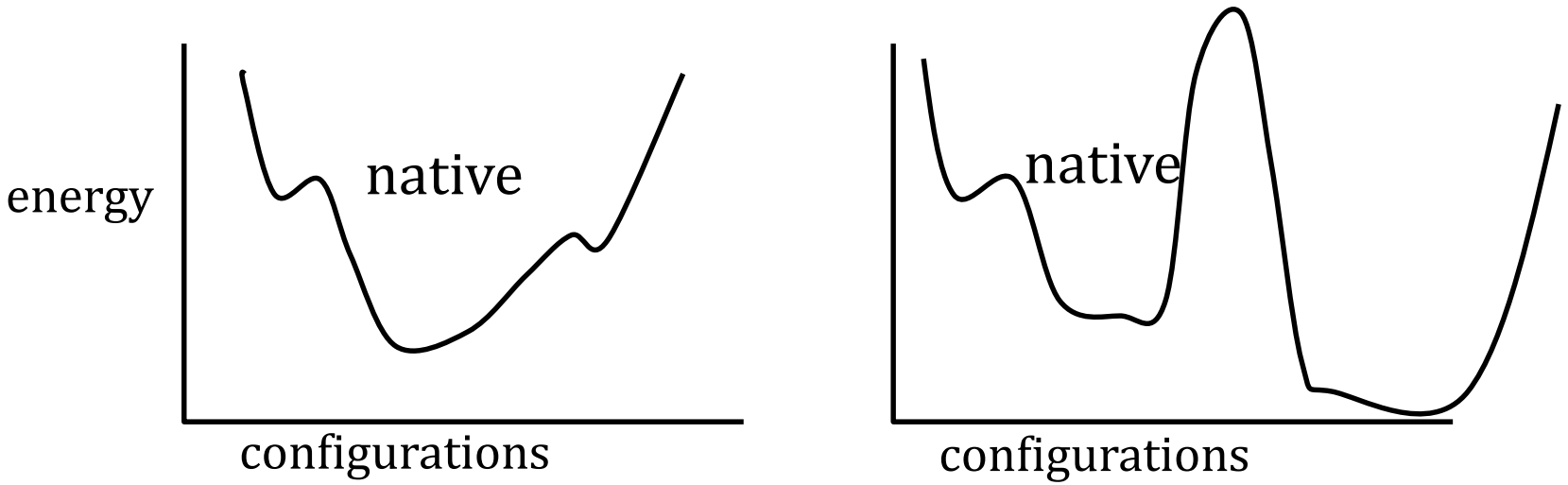
More modern

- many many proteins cannot be refolded in the lab
  - consequence .. maybe they need something else
  - maybe they are not always in free energy minimum

Kinetically trapped proteins..

Kinetic versus thermodynamic

- If proteins fold spontaneously and remain folded, they are thermodynamically determined
- If you leave a protein long enough and it unfolds, it was not in an energy minimum



thermodynamic

kinetically trapped

Consequences

Thermodynamic

- protein structure prediction
  - just a matter of modelling the real world

Kinetically trapped

- we cannot predict structure from sequence just by energies

Consequences

Can we see which is the case ?

- leave a protein for 10 minutes
  - see if it finds another state
- leave it for 10 years ?
- depends on barriers

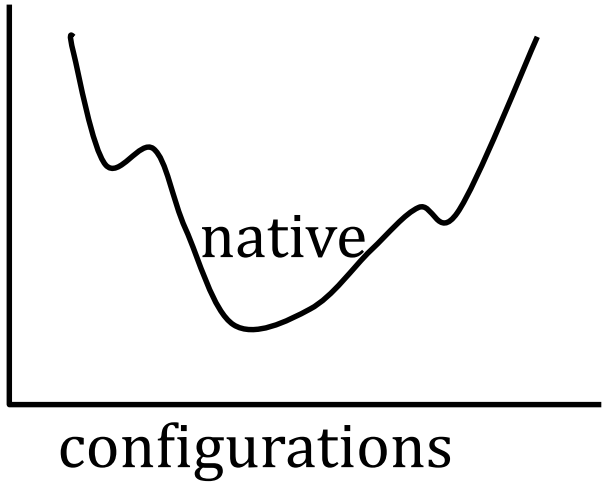
Empirically

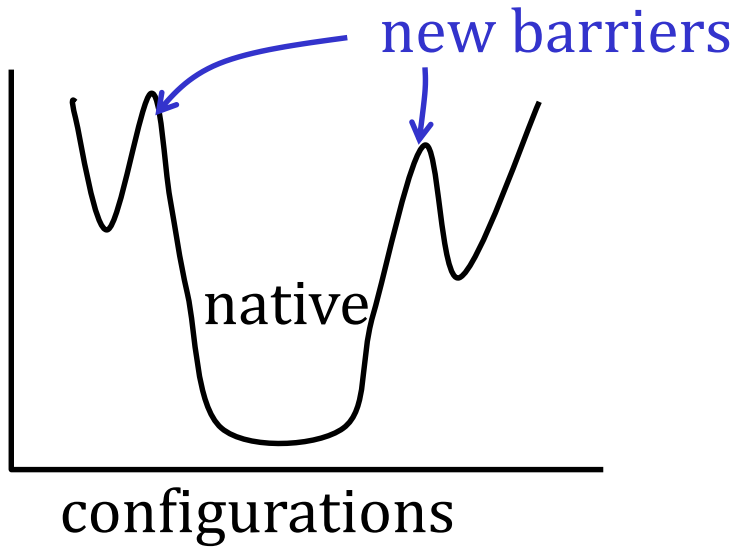
- some evidence of kinetic trapping
- some proteins do have other states
  - β-fibrils, Alzheimers, mad cow disease

Evolution / design consequences

Imagine I can predict structure and stability

- I design a better / more stable protein





- my new protein may be more stable
- it may never fold
- evolutionary implications
  - protein sequences may evolve for folding (+ structure and function)

Change of direction

- enough background on folding
- brief overview of experiments
- simulation

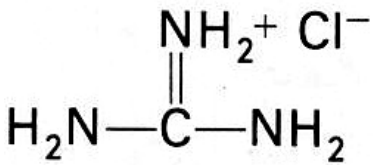
Experiments

Timescales

- maybe 10^{-6} s for folding
- maybe orders of magnitude slower or faster

Experimental approaches

- force protein to unfold
  - chemistry (guanidinium HCL, 8M urea)
  - temperature (heat, cold)
  - change conditions and watch
- try to measure very fast
- try to change timescale
- try to measure unfolding



Experiments - problems

Very difficult to measure on the μs / ms time scale

- temperature jump
- stop - flow
- fluorescence
- NMR
- circular dichroism (CD)

Are experiments relevant ?

- Technical difficulties (obvious)
- Tradeoff
  - fast methods – less information
  - more information – too slow
- How real is it ?
- Imaginary technique :
  - I can take any protein in denaturant
  - suddenly bring back native conditions
  - follow every detail
  - is this what happens in nature ?...

How real is experiment ?

Our bodies – about 150 mM salt, regulated pH, temperature, ...

Denature a protein with high salt

- is the partially folded state natural ?
  - it comes from disrupting a very special set of ionic interactions

How real is experiment ?

Heat the protein

- guaranteed to visit high energy states which are not natural

Hope ..

- the strongest interactions are formed first – last to be broken

Do proteins fold like this in nature ?

- proteins made from N to C terminus
- N terminus gets a chance to find structure, before rest of protein is there
- would permit very specific paths / kinetic trapping

Next ... simulation and theory...

Monster Simulations

Months of cpu time

- very hard to fold
  - 1 copy
  - 1 protein

2011 record holder Shaw Research

- some ms simulations, small proteins

more feasible

- simulate unfolding

Klepeis,J.L. Lindorff-Larsen, K, Dror,R.O., Shaw, D.E., 2009, Curr. Opin. Struct Biol, 209, 19, 120-127,
Long-timescale molecular dynamics simulations of protein structure and function
Shaw, D.E., Maragaikis, P., Lindorff-Larsen, K., Piana, S.... Shan, Y., Wriggers, W. 2010, Science, 330, 341-346

Simulating unfolding

Atomistic simulation of real protein too slow

- take native structure at 300 K
- gradually heat up
- watch it fall apart
- what breaks first ?
  - secondary structure ?
  - overall fold ?
  - everything ?

Reasons to believe

- the last interactions to form (folding) may be first to break (unfolding)

Problems simulating unfolding

Problems

- the system is visiting high energy states which may not really exist
- force fields are parameterised for 300 K
- property of unfolded state(s)
  - statistics may be dominated by huge number of partially folded states (more later)
  - cannot visit these states in realistic time

Forgetting atomistic detail

- What are questions we can ask ?
- What can we guess without any calculations ?
- Questions
  - is there such a thing as a folding pathway ?
  - how should we look at folding ?
    - secondary structure forms first and is rearranged
    - hydrophobic residues come together and then secondary structure forms ?
    - a few important contacts are formed, then structure forms

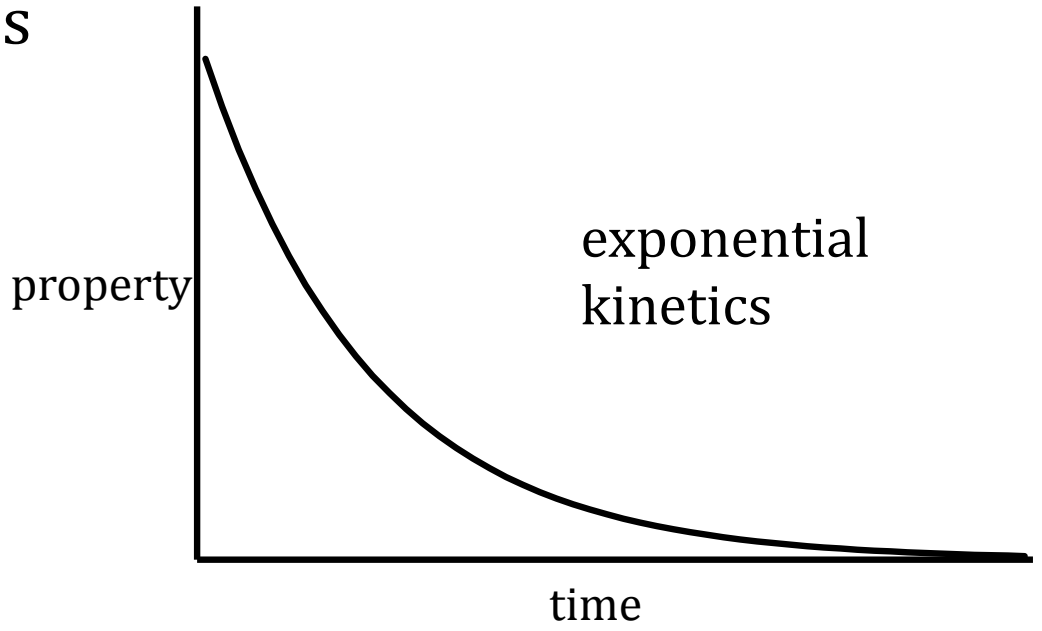
General kinetics

What have we seen so far ?

- most properties have something like exponential decay
- property = $a\ e^{-\alpha t}$
- rate of change proportional to quantity present

A model should explain at least this

- later by ensemble view..
  where are barriers ?



What do we know

Possibilities

- Proteins form secondary structure first
- helices and sheets then arrange themselves

OR

Hydrophobic collapse

- hydrophobic residues find each other
- backbone rearranges and secondary structure is fixed

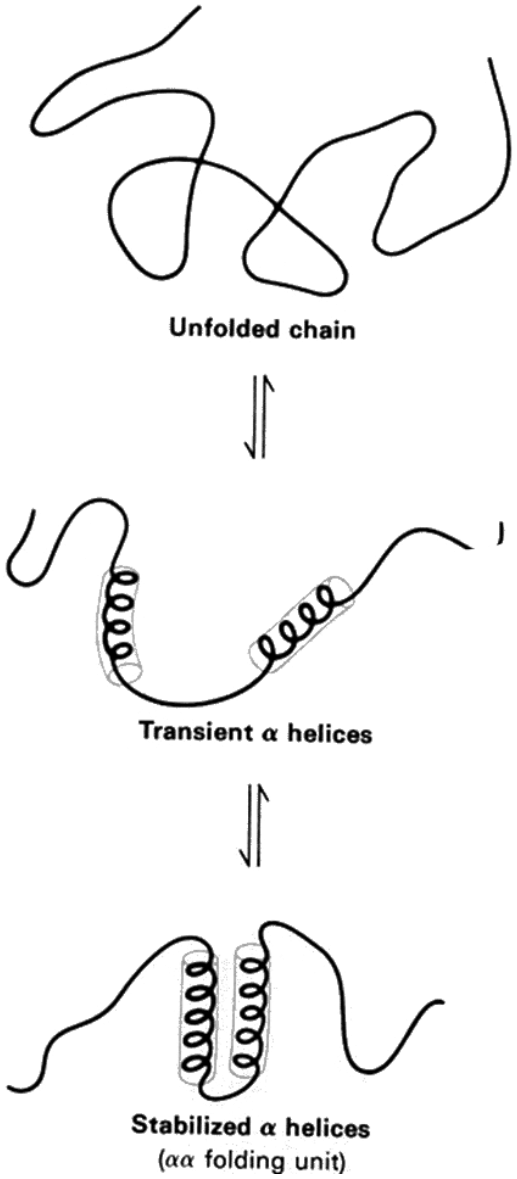
Side chain vs backbone driven

Old textbook

- local secondary structure forms, then reorganises
- secondary structure depends largely on backbone

Alternative

- sidechains are very important



Stryer, L. Biochemistry, 1981, WH Freeman, "Biochemistry", page 36

Sidechains might be important

- backbone view does not predict collapse of protein
- α-helix and β-strand propensity is weak
  - isolated peptides are not stable
  - β-strands often depend on long-range H bonds
- helix / strand formation depends on environment / solvent and is not known in open structure
- fold is largely predictable / characterised by pattern of HP (sidechains)
- proteins are most sensitive to mutations in core
  (they are important for stability)

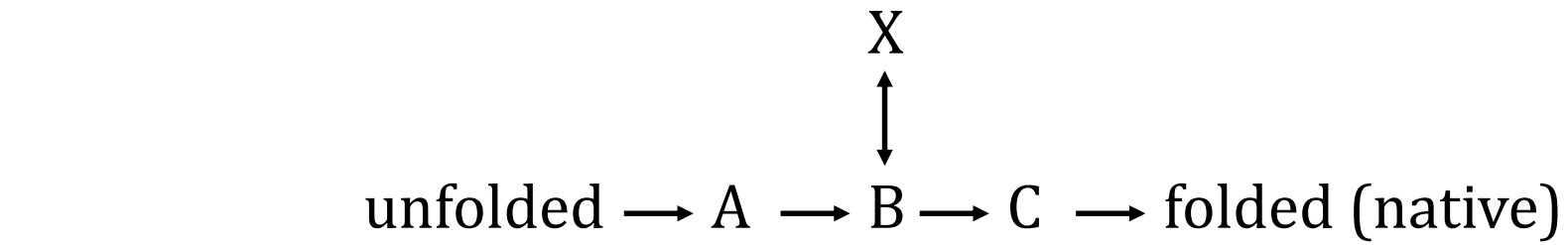
from Dill, K.A., Protein Sci., 8, 1166-1180, 1999, Polymer principles and protein folding

Types of pathway

From classical chemistry we would like a path

unfolded → A→ B→C→ folded (native)

Slightly more complicated – detours and sideproducts (X) allowed



Basic idea

- molecules may get sidetracked, but
  - every molecule sees A, B, C...
- where does it come from ?
  - Levinthal's answer to paradox
    - there must be a preferred pathway
- old view / microstate pathway approach

Consequence of simple pathway

Two state kinetics

- A → B or B → C might be part of transition barrier
- pathway with detours explains multi-state kinetics (if necessary)

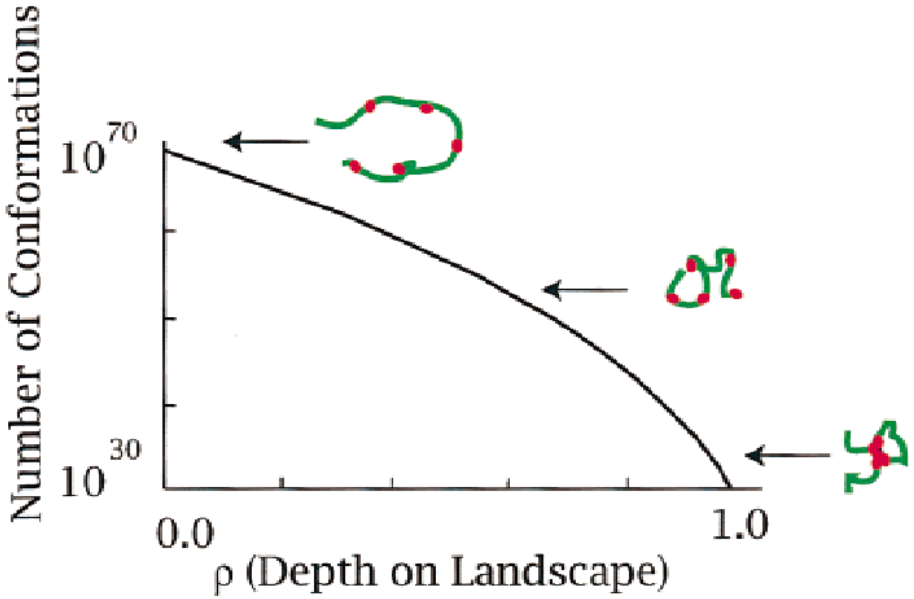
Does it sound intuitively reasonable ?

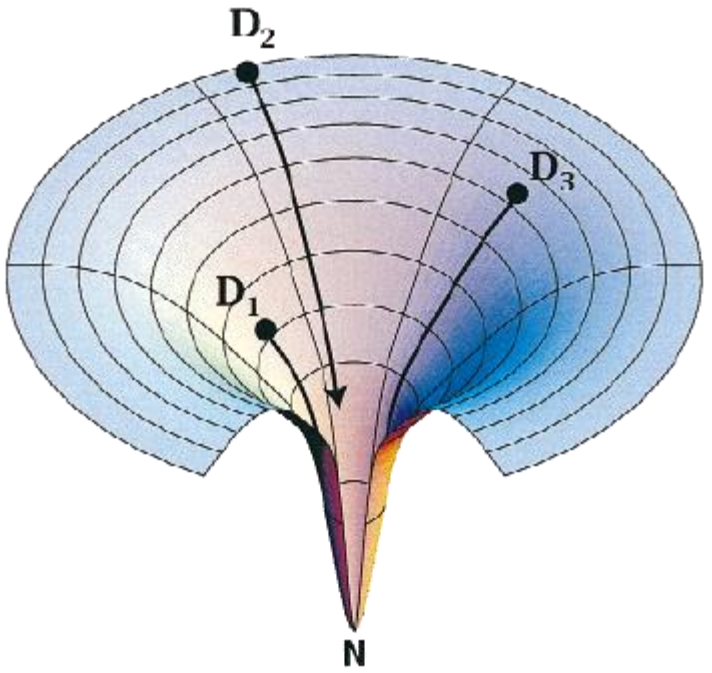
- what if a mutation perturbs A or B or C ?
  - whole pathway might break
  - maybe OK (this is why some mutants do not fold)

Do you need conventional pathway to explain barriers ?

Ensemble view

- conformation space is huge
- will a protein be able to find a neat path through it ?
- should we even look for paths ?
- consider a multitude of paths...
- is this merely a cute picture ?
- first implication...
  - entropy vs energy





Dill, K.A., Protein Sci., 8, 1166-1180, 1999
Polymer principles and protein folding

Consequence of ensemble view

As a protein folds

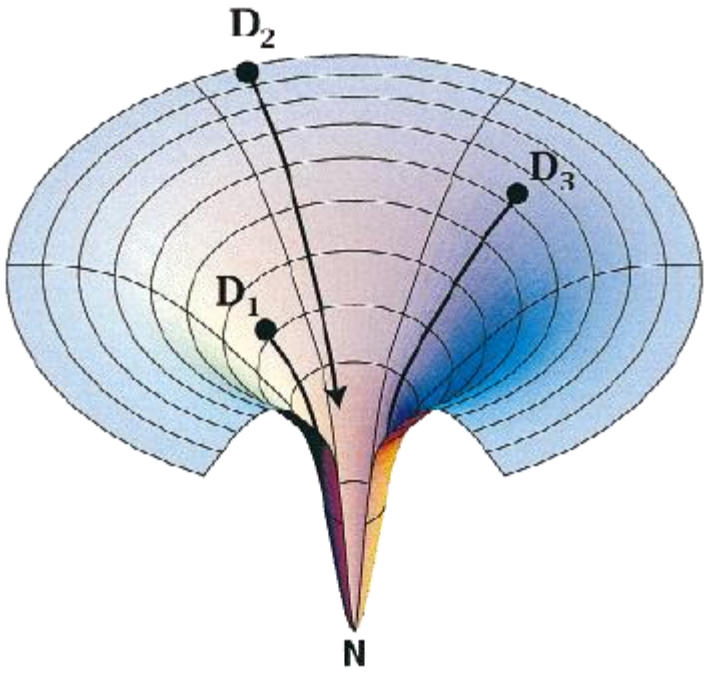
- potential energy goes down (happy)
- number of possible states goes down
- entropy goes down (unhappy)

Interpretation in chemical terms

- do we have a off-pathway intermediate ?

Do we have a reaction coordinate ?

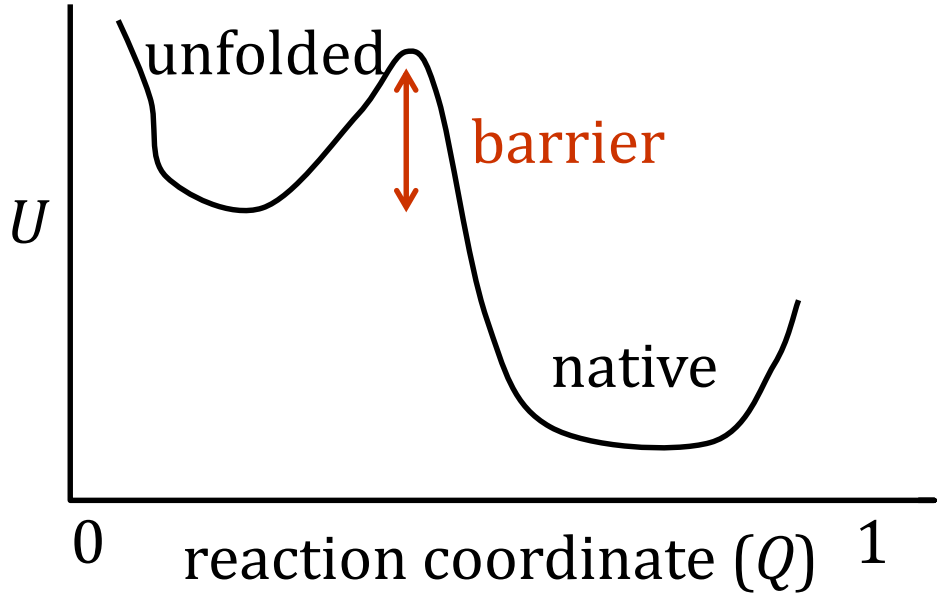
- not a classic one
- can we invent one ? yes
  - if two atoms are in contact in the final structure
    - native contact
  - Q = fraction of contacts which are correct



Reaction path

Is this like a chemical reaction ?

- no
- many molecules have same Q, but different conformations



We want at least two state kinetics

- where does barrier come from ?

Entropic barriers

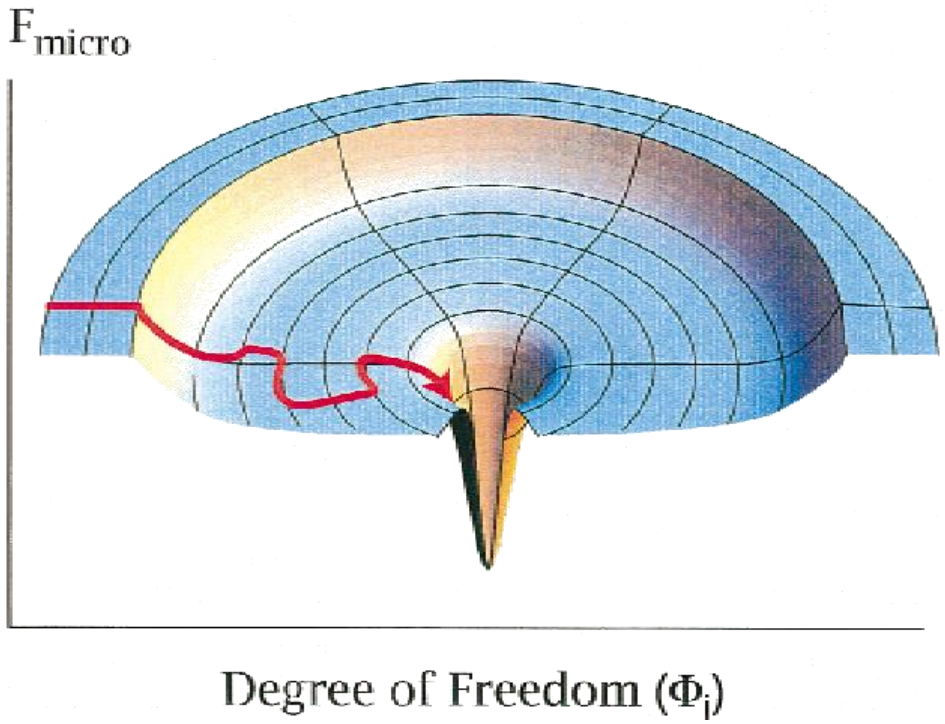
Nature cares about free energies

$$\Delta G = U - T\Delta S$$

If a molecule walks around

- it takes a long time
- looks the same as an energy barrier

- Are these pictures useful ?
- Do they agree with calculation ?



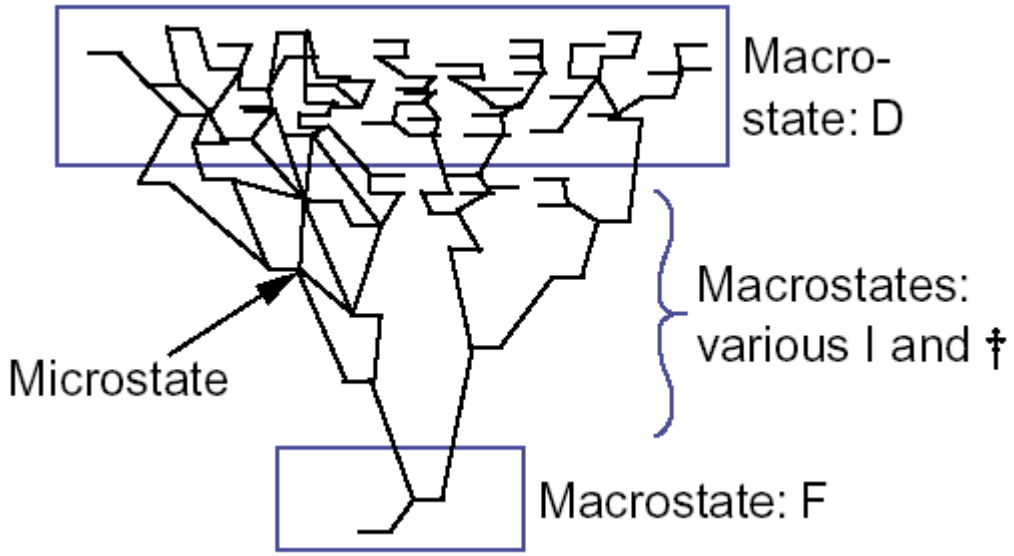
Dill, K.A., Protein Sci., 8, 1166-1180, 1999, Polymer principles and protein folding

Interpretation of landscape

Does this disagree with conventional pathway ?

$A \rightarrow B \rightarrow C$?

- mostly at early stages
- there is a multiplicity of "A"
- when near native, there are relatively few conformations, so there may be something more like a pathway



Gruebele, M, Curr. Opin. Struct. Biol. 12, 161-168, 2002, Protein folding: the free energy surface

Agreement with other ideas

Agreement with experiment ?

- experiment says most about average properties
  - these are the same in landscape picture
  - should we expect to find well defined, early intermediates ?

Agreement with MD simulation ?

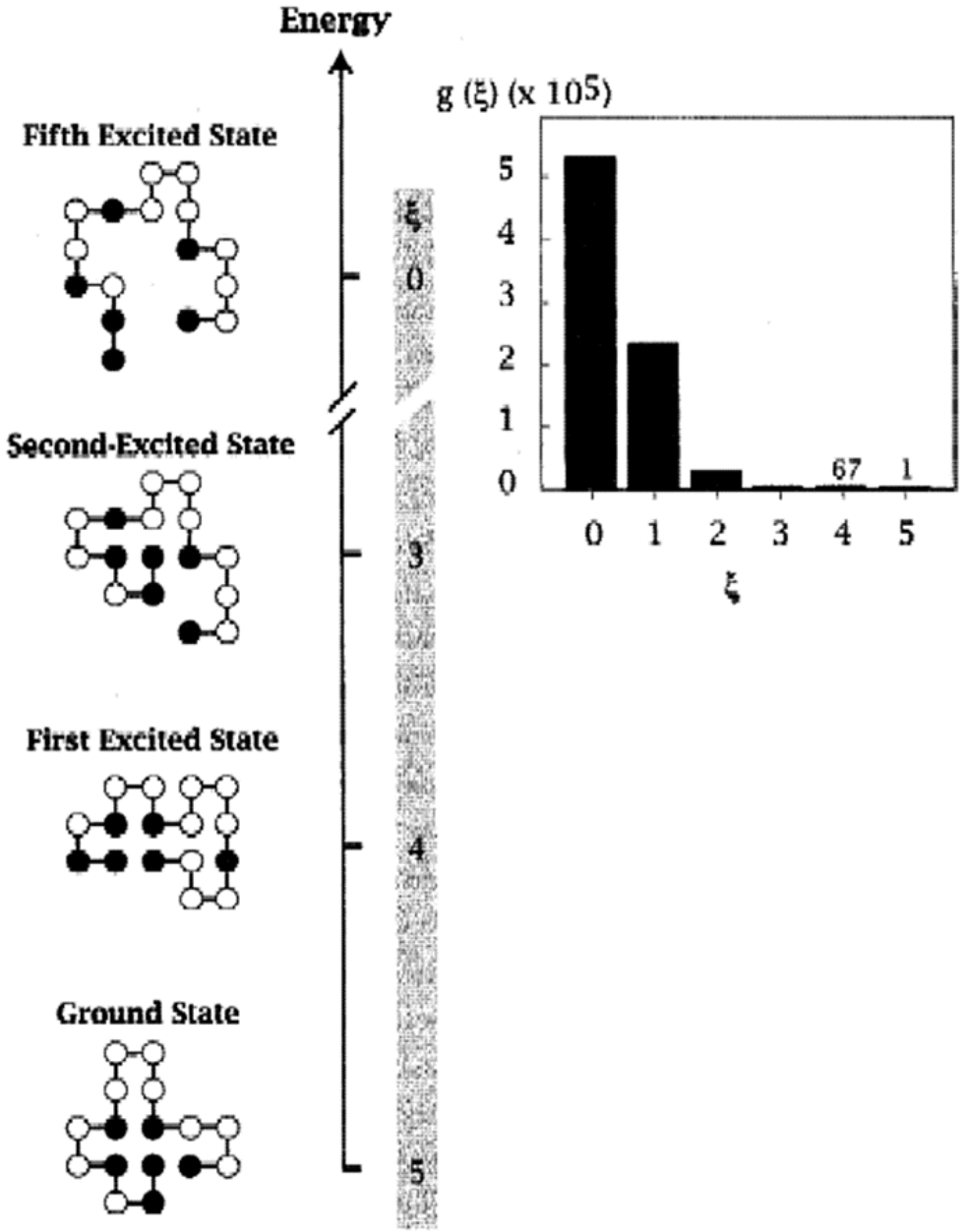
- peptide results – argue that they correspond to near native view

Simple models

Return of HP models

- g(ξ) is density of states
- how many conformations have ξ correct contacts

A bigger calculation

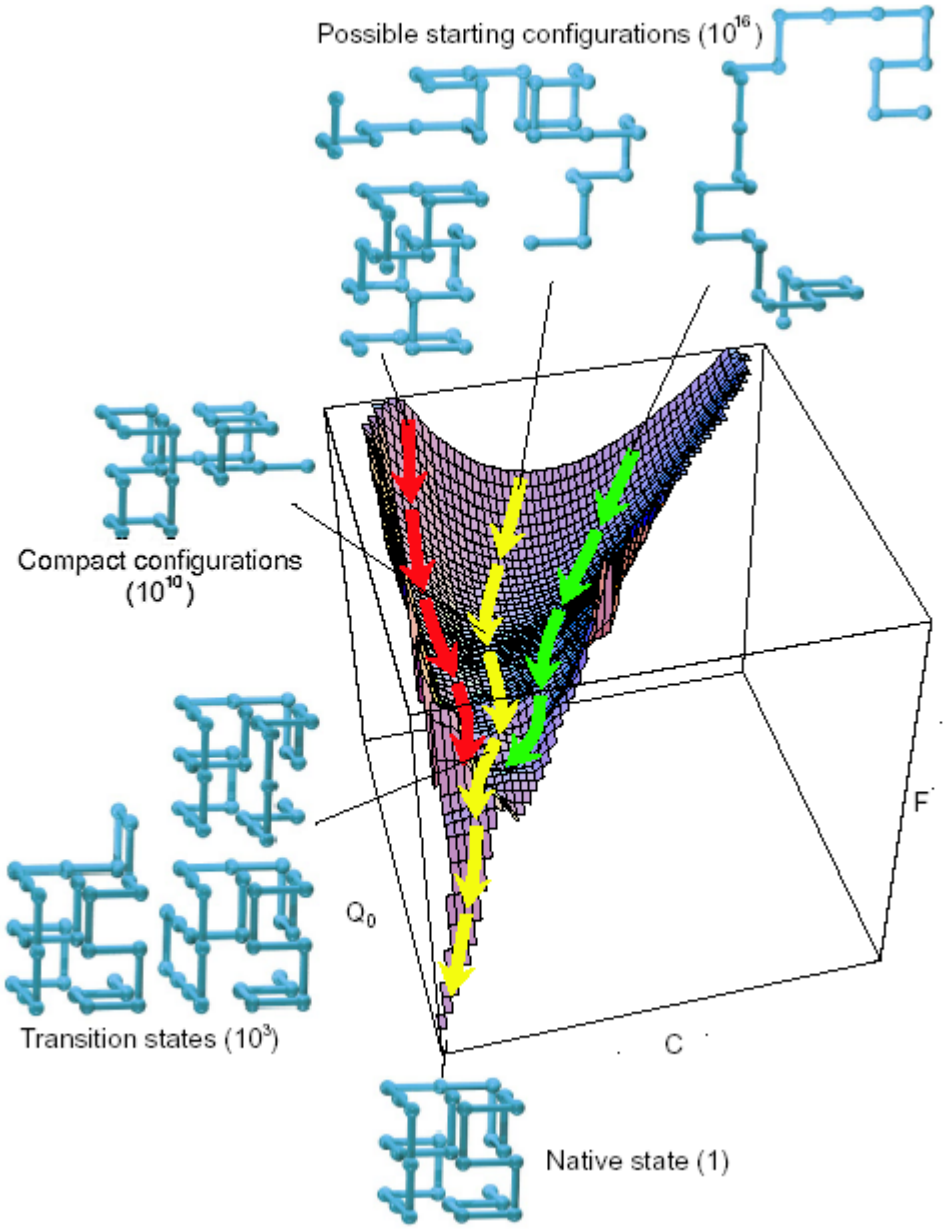


from Dill, K.A., Protein Sci., 8, 1166-1180, 1999, Polymer principles and protein folding

A larger calculation

27 residue

- simple lattice model
- estimations by sampling
  - not exhaustive
  - Q_0 correct contacts
  - C total contacts
  - F free energy



from Dinner, A.R., Šali, A., Smith, L.J. Dobson, C.M., Karplus, M, Trends Biochem Sci. 25, 331-339, 2000, Understanding protein folding ...

Summary

- Experiment vs. theory
  - experiment usually gives us averages
  - most calculations look at details
- Very different views on folding may be hard to distinguish – are predictions different ?
- Folding may be guided by sidechains (not hierarchical)
- Early folding may be best modelled by very crude models (so space can be sampled)
- Any useful model should predict exponential kinetics (or more complicated)