Simplified models of vibrational energy transfer in proteins

Steven Lade

Supervisor: Yuri Kivshar

Nonlinear Physics Centre

The Australian National University, Canberra

http://wwwrsphysse.anu.edu.au/nonlinear/

ARC Centre for Complex Systems
School of ITEE | The University of Queensland | ST LUCIA QLD 4069 | AUSTRALIA

T: +61 7 3365 1003 | F: +61 7 3365 1533 | E: outreach@accs.edu.au

Outline

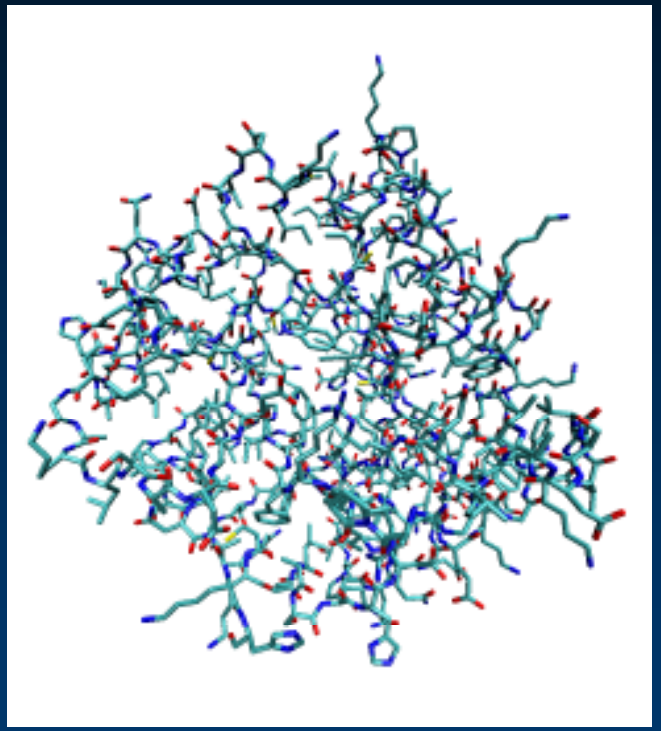
- What is vibrational energy transfer in proteins?
- Previous molecular dynamics study
- Parametric resonance and analogy to nonlinear optics
- Simplified model

Goal:

To develop a *simplified* model for vibrational energy transfer in proteins

Proteins

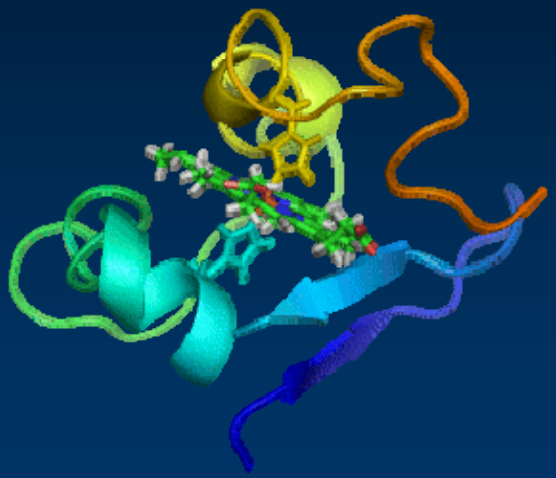
- Complex macromolecules: series of amino acids linked into a chain and folded into a specific 3D structure
- Fundamental importance: enzymes, structure, mechanics, transport, signalling



The protein triose-phosphate isomerase
Wikipedia

Vibrational energy transfer

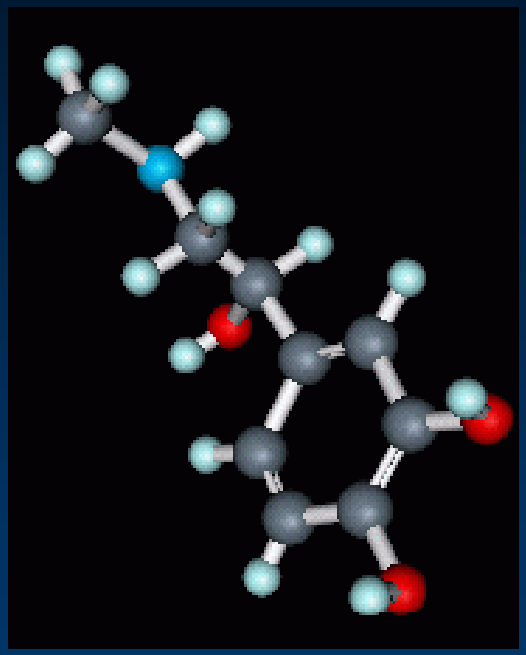
- Not static: vibrating all the time
- One key to the behaviour and function of proteins is the transfer of this vibrational energy
- Especially interesting following some perturbation



Cytochrome C
Wikipedia

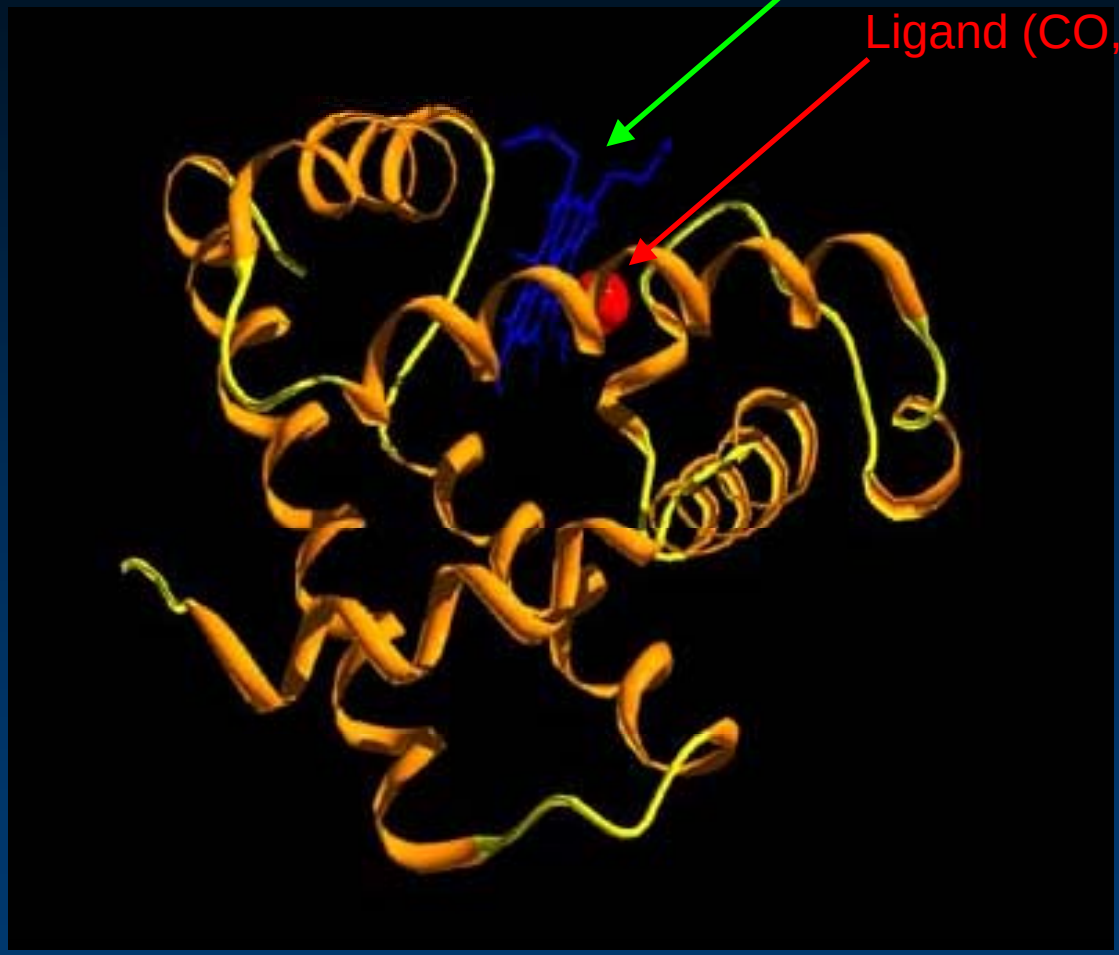
Normal modes

- Normal modes: independent patterns of oscillation
- Small coupling nonlinearity allows the normal modes to exchange vibrational energy
- Normal mode picture is valid for proteins provided they maintain the same configuration, e.g. low temperature



Adrenaline
http://www2.chemie.uni-erlangen.de/projects/ChemVis/motm/adrenir.html

Myoglobin



http://www.biophysik.uni-freiburg.de/Spectroscopy/Protein Folding/Prot_fold.html

Why myoglobin?

- Relatively simple and well-known structure
- *Ligand dissociation can be triggered optically*

Myoglobin

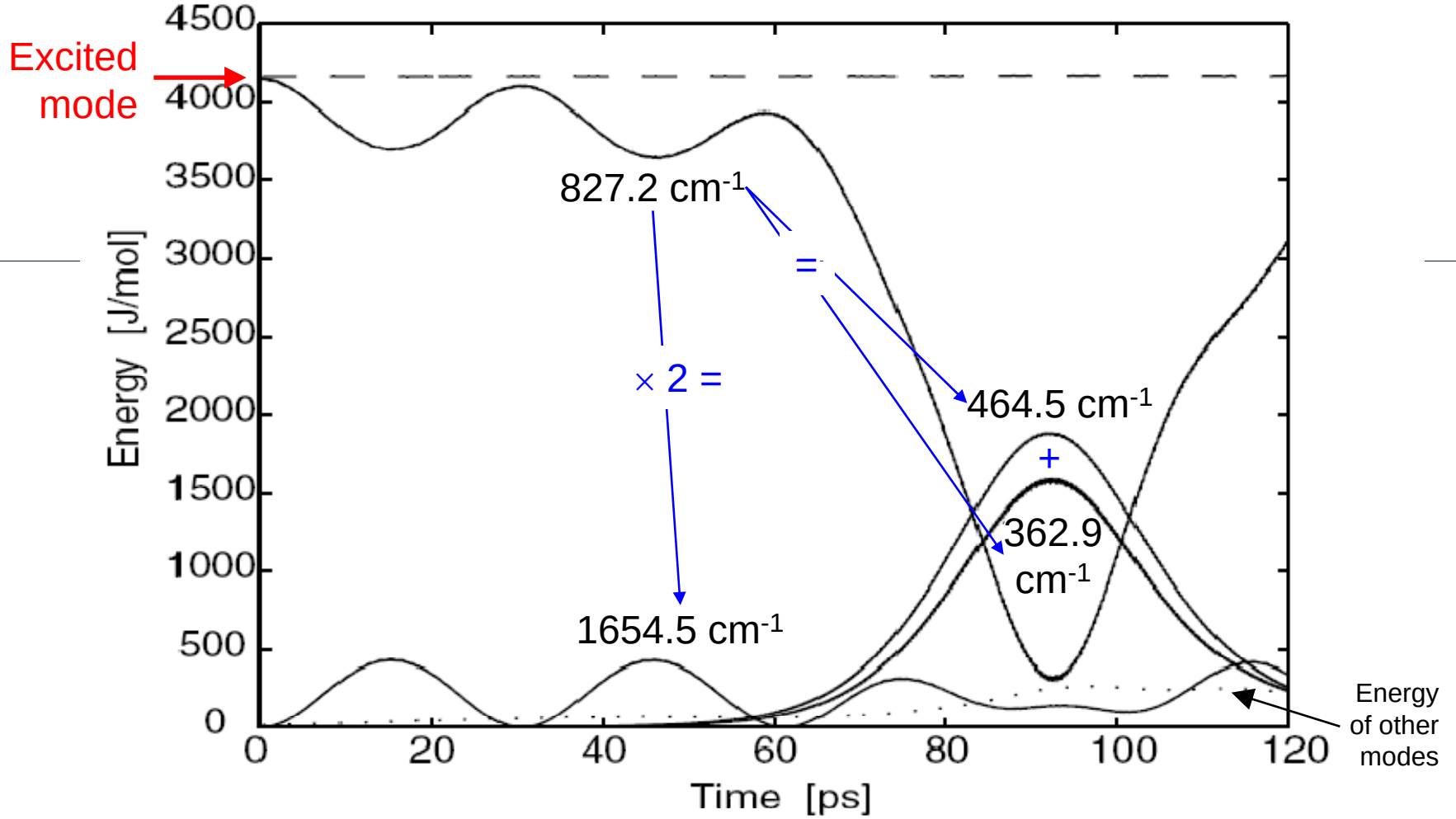
VOLUME 85, NUMBER 18 PHYSICAL REVIEW LETTERS 30 OCTOBER 2000

Vibrational Energy Transfer in a Protein Molecule

Kei Moritsugu, Osamu Miyashita, and Akinori Kidera
Department of Chemistry, Graduate School of Science, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan
(Received 6 April 2000)

- Take structure of deoxymyoglobin from Protein Data Bank
- Empirical interaction potentials from standard model AMBER
- Identify normal modes (7419 for myoglobin)
- Assign excess energy to one mode
- Evolve equations with standard package PRESTO, at low temperature
- At each step project state of protein onto normal modes, get energy in each normal mode

Moritsugu *et al*: results



Parametric resonance: Nonlinear optics

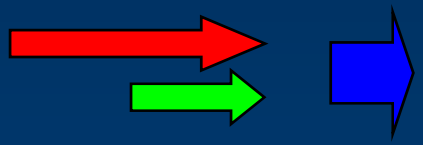
- With a medium that responds nonlinearly to an applied electric field, it is possible to mix light of different frequencies

Second harmonic generation

$2\omega_1 \rightarrow \omega_2$

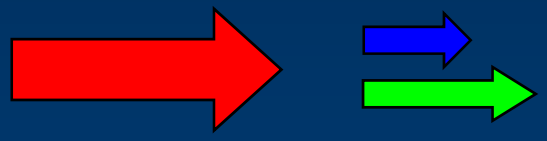
Sum frequency generation

$\omega_1 + \omega_2 \rightarrow \omega_3$



Difference frequency generation

$\omega_1 - \omega_2 \rightarrow \omega_3$



Optical parametric oscillation

$\omega_1 \rightarrow \omega_2 + \omega_3$

Boyd (2003), *Nonlinear Optics*, 2nd ed., Academic Press, San Diego

Parametric resonance: General

$$L = \underbrace{\sum_{j=1}^{4} \tfrac{1}{2}\dot{q}_j^2}_{\text{kinetic}} - \underbrace{\sum_{j=1}^{4} \tfrac{1}{2}\omega_j^2 q_j^2}_{\text{potential energy}} - \underbrace{\alpha q_1 q_2 q_3 - \beta q_1^2 q_4}_{\text{weak coupling (nonlinearity)}}$$

q_j = normal mode co-ordinates

$$\omega_1 \leftrightarrow \omega_2 + \omega_3$$

$$2\omega_1 \leftrightarrow \omega_4$$

- Physically, in proteins the nonlinear response comes from the nonlinear interaction between atoms

Slow amplitude equations

$$\dot{\psi}_1 = \frac{i\alpha}{2\omega_1}\psi_2\psi_3 e^{-i\Delta_\alpha t} + \frac{2i\beta}{2\omega_1}\psi_1^*\psi_4 e^{-i\Delta_\beta t}$$

$$\dot{\psi}_2 = \frac{i\alpha}{2\omega_2}\psi_1\psi_3^* e^{i\Delta_\alpha t}$$

$$\dot{\psi}_3 = \frac{i\alpha}{2\omega_3}\psi_1\psi_2^* e^{i\Delta_\alpha t}$$

$$\dot{\psi}_4 = \frac{i\beta}{2\omega_4}\psi_1^2 e^{i\Delta_\beta t}$$

ψ_j = complex slow amplitudes

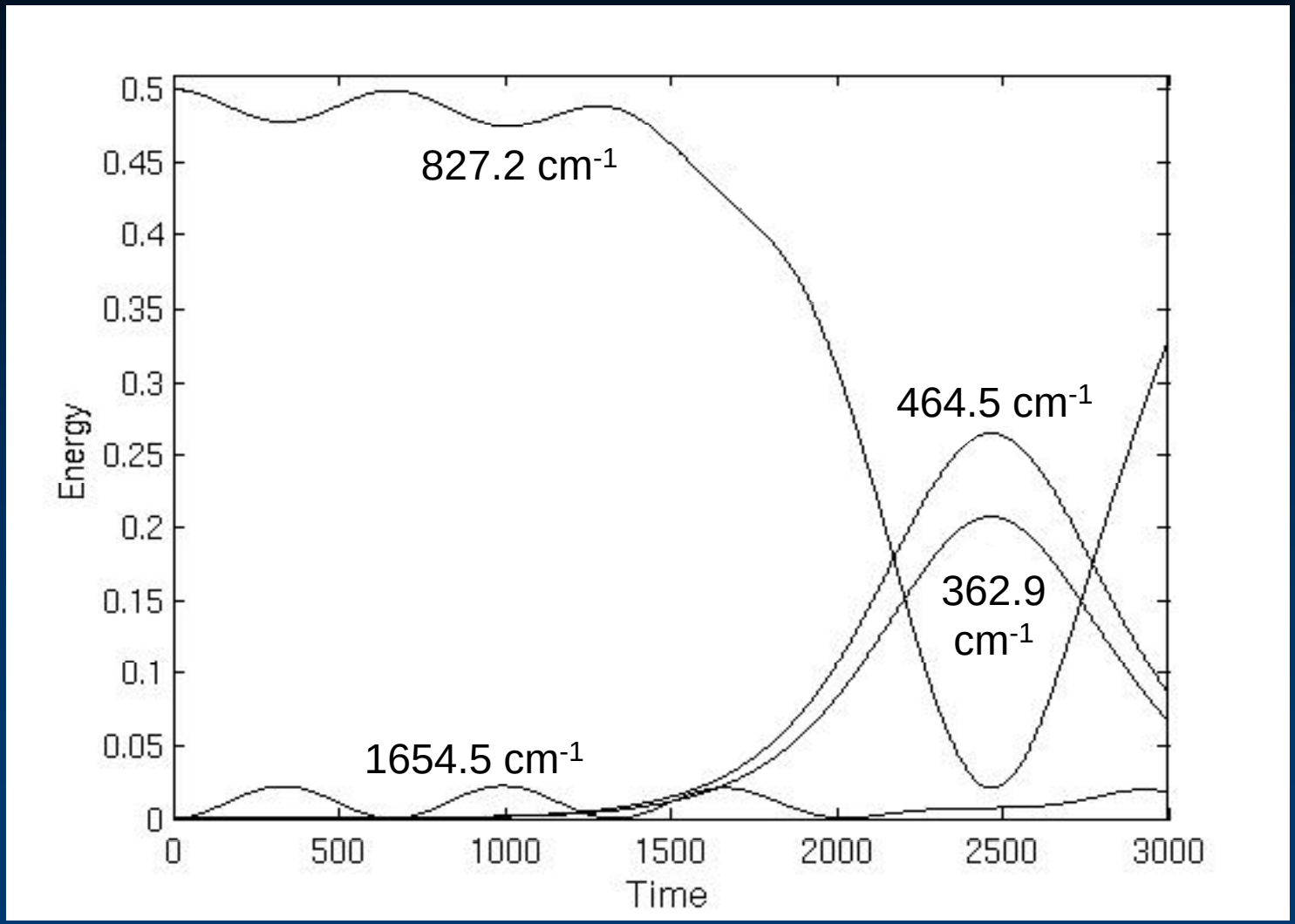
$$[q_j(t) = \psi_j(t)\, e^{i\omega_j t} + c.c.]$$

α, β = coupling coefficients

$\Delta_\alpha = \omega_1 - \omega_2 - \omega_3$

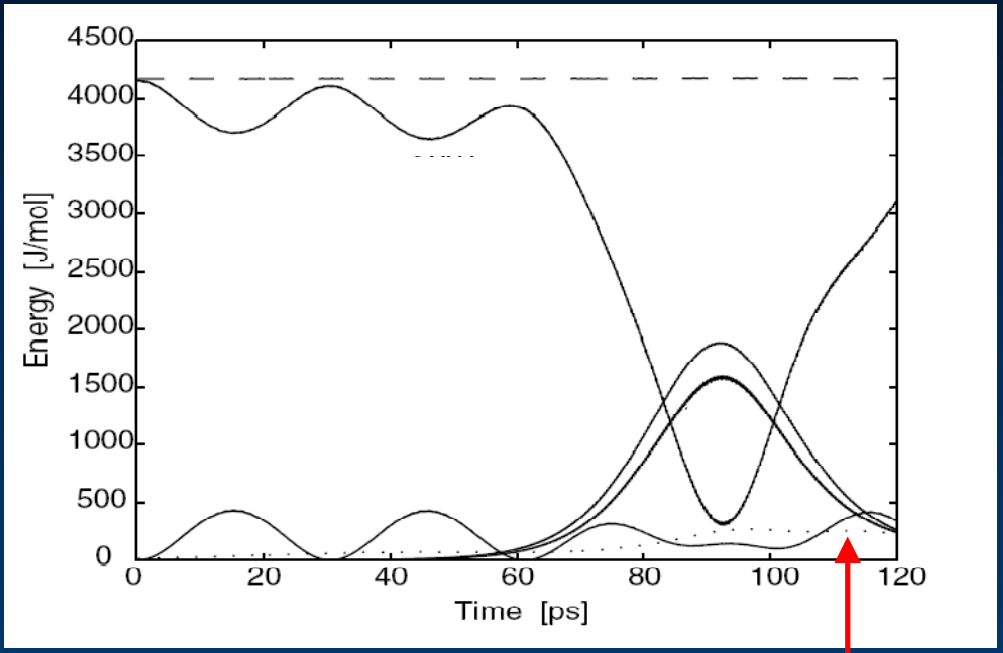
$\Delta_\beta = 2\omega_1 - \omega_4$

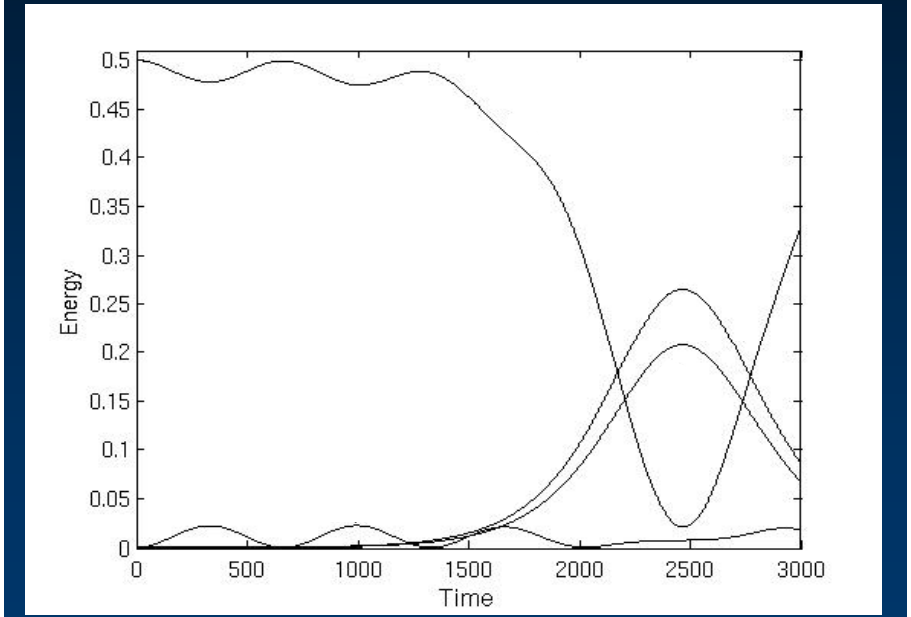
Results of simplified model



Frequencies and coupling coefficients from data of Moritsugu *et al.*

Comparison





Moritsugu *et al.*

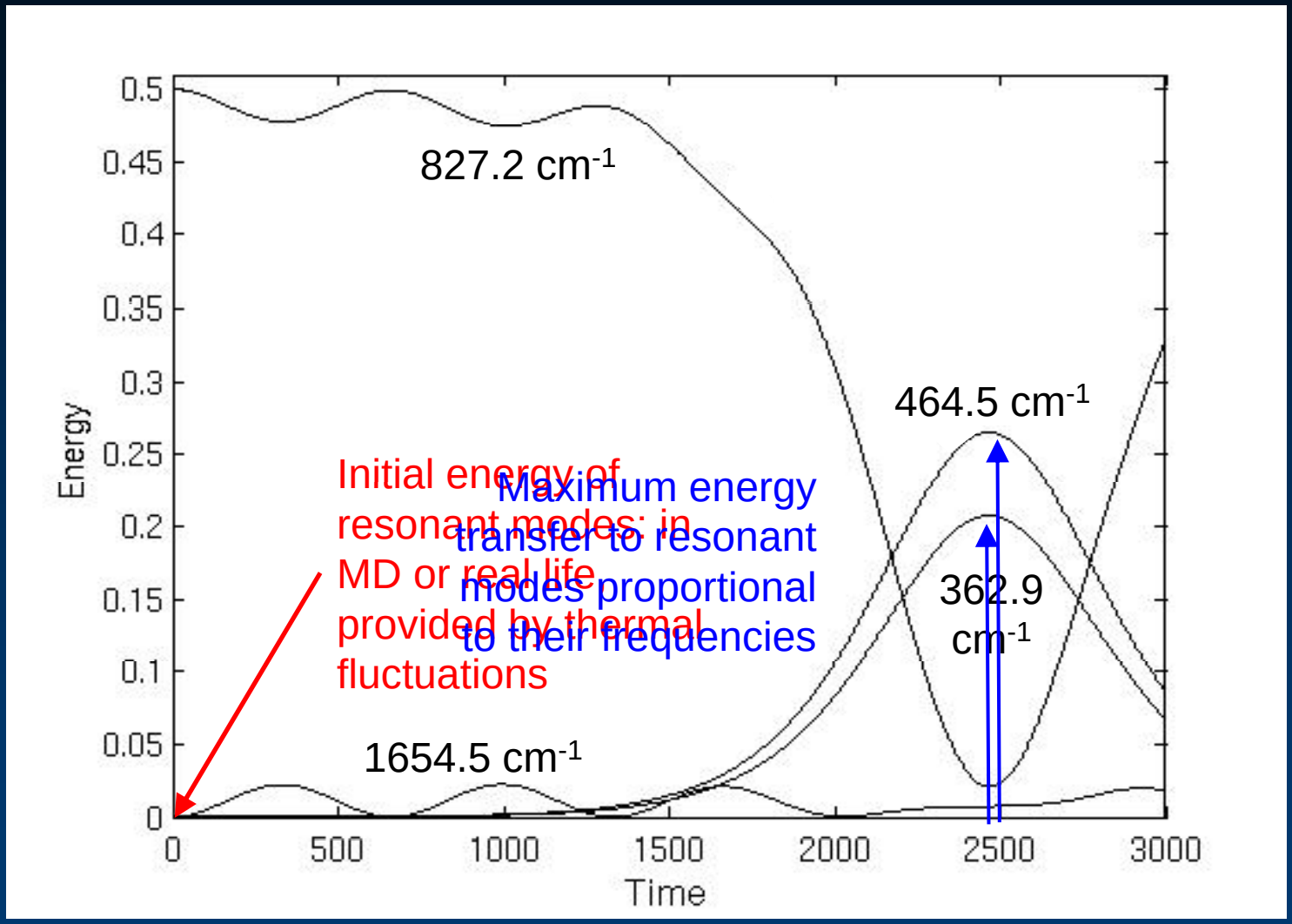
Energy of other modes

Simplified model

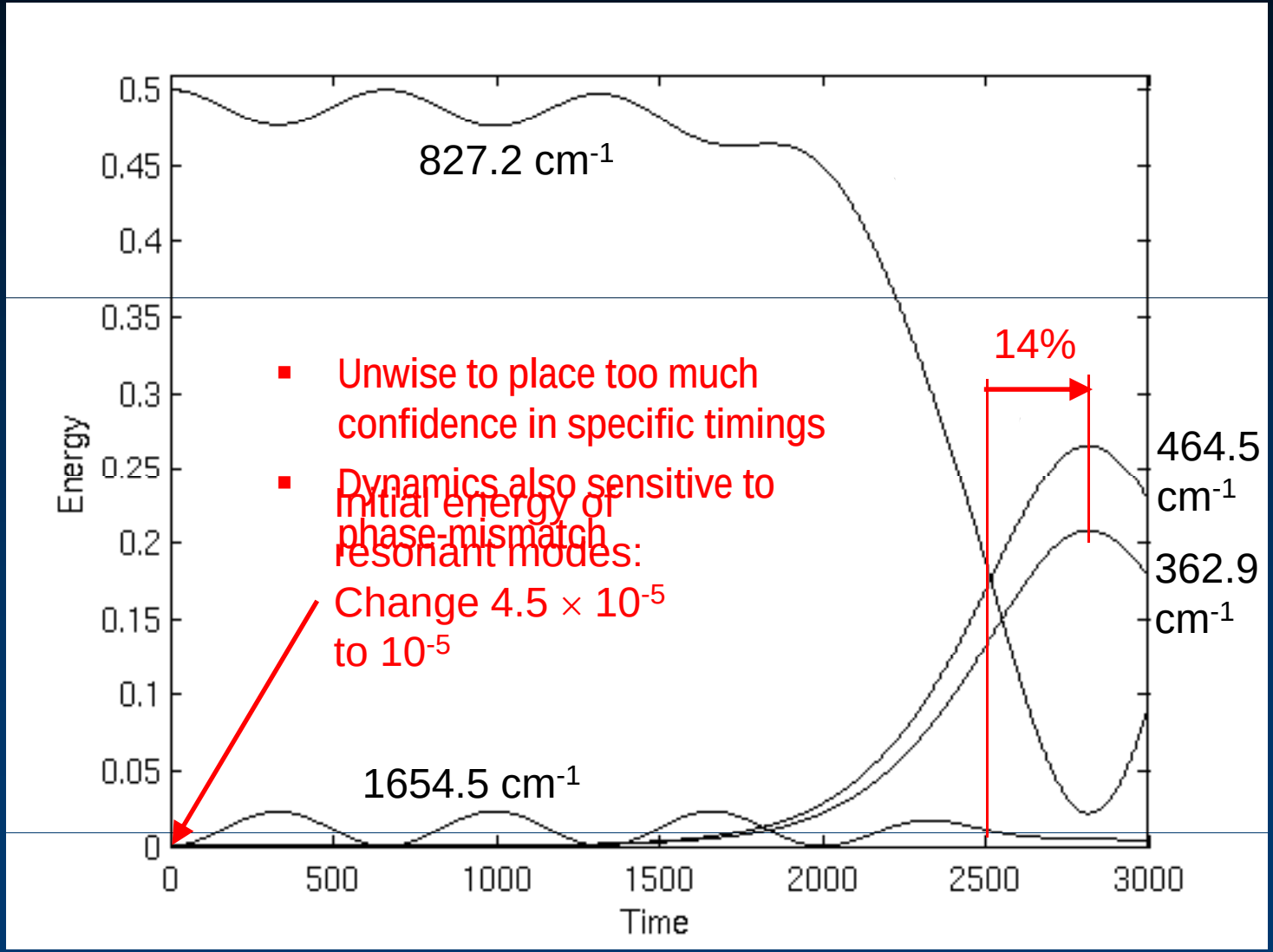
Simplified model

- It was *not* necessary to simulate all 7419 modes
- Just use protein structure calculations to identify normal modes and coupling coefficients
- Then use simplified model to solve for dynamics

Results of simplified model



Results of simplified model

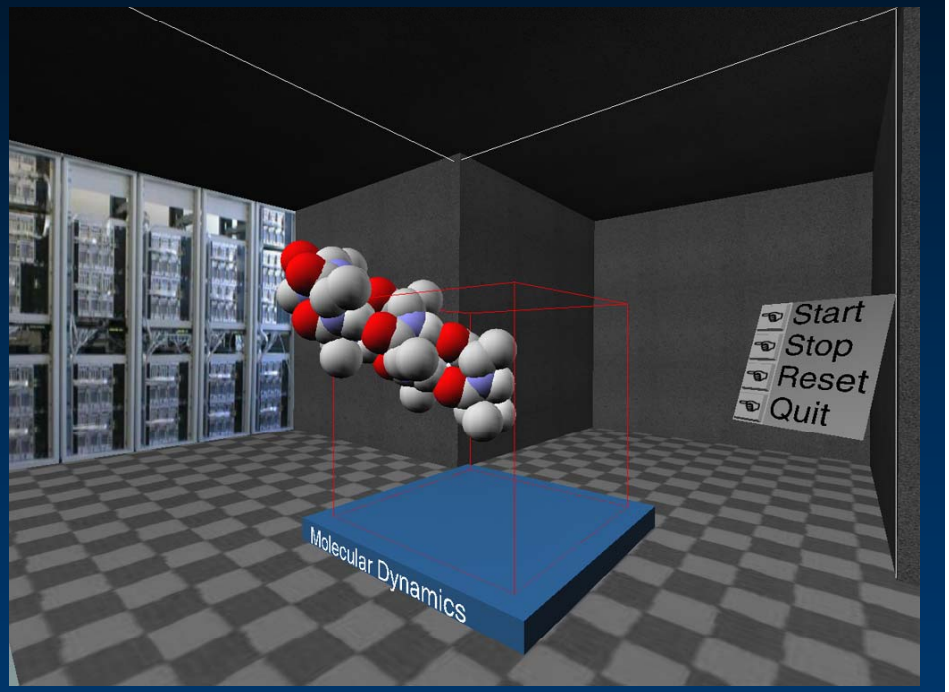


Summary and conclusions

- Vibrational energy transfer through parametric resonance in proteins
- Simplified model that reproduces molecular dynamics simulations to high accuracy
- Also demonstrated predictive capability
- Future work: extend model, also interested in nonlinear dynamics in other areas of biophysics

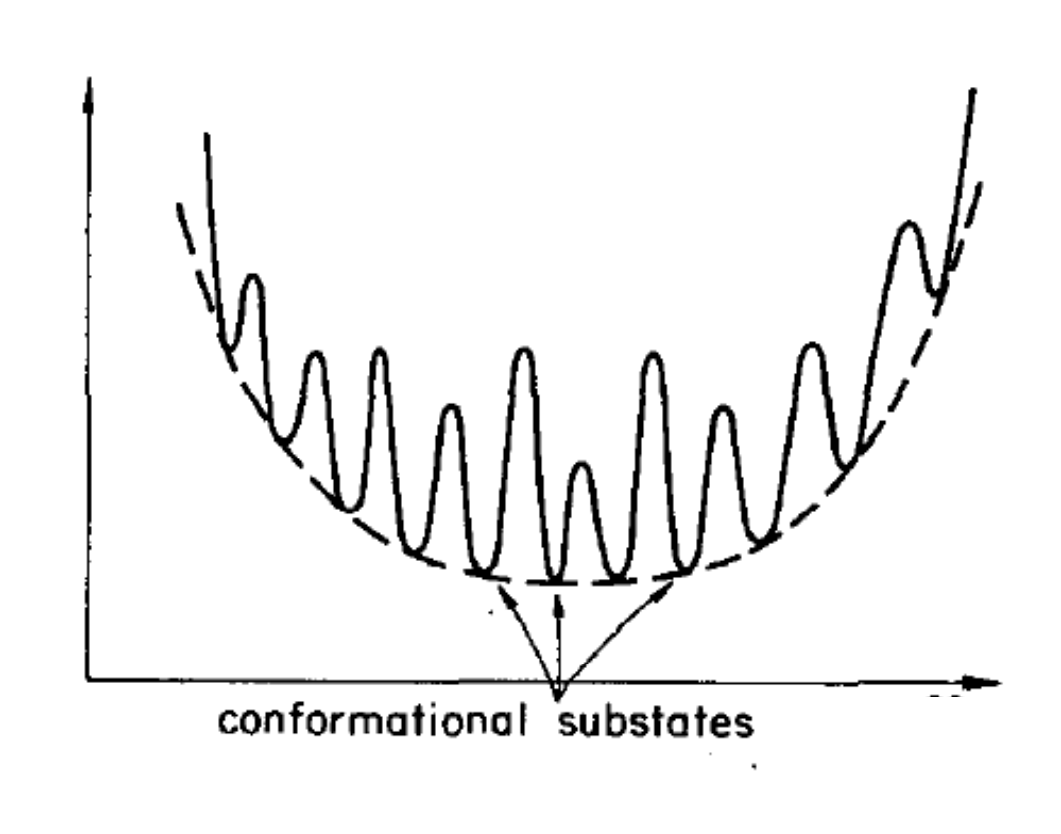
Investigating vibrational energy transfer

- Experimentally: time-resolved spectroscopy
- Numerically: Molecular dynamics simulations



A molecular dynamics simulator!
http://www.cs.vu.nl/~renambot/vr/photos/lab1.jpg

Fraunfelder's energy landscape



Fraunfelder, Parak & Young (1988), *Ann. Rev. Biophys. Biophys. Chem.* 17:451-79