Overview of time in Levitt Lab (‘93-’96) & subsequent work with the extended "Levitt Legacy," in 3 themes

(Theme I) Macromolecular motions, simulation & packing
(Postdoc experiences & following on research with Mike & Jerry)

• The volume of atoms on the protein surface: calculated from simulation, using Voronoi polyhedra.
  MG, J Tsai, M Levitt (‘95) JMB

• Simulating water & the molecules of life.
  MG, M Levitt (‘98). Sci Am. [Fig]

• The packing density in proteins: standard radii & volumes. J Tsai... MG (‘99) JMB

• ...DB of Macromolecular Motions... at the decade mark. S Flores... MG (‘06). NAR

• Relating protein conformational changes to packing efficiency....
  N Bhardwaj, MG (‘09). Prot Sci. [Fig]
(Theme II) Molecular networks & how they're impacted by mutations: Connectivity associated with constraint

(How Brandon taught an old dog new tricks!)

- Analyzing cellular biochemistry in terms of molecular networks.  
  Y Xia, MG ('04). *Ann Rev Biochem*
- ...prediction of the helical membrane protein interactome... Y Xia, L Lu, MG ('06). *JMB*
- ...Assessment of genomic correlates of protein evolutionary rate.  
  Y Xia, E Franzosa, MG ('09). *PLoS CB* [Fig]

![Diagram of molecular network with hubs and bottlenecks](image)
Relating 3D structures to protein networks provides evolutionary insights. P Kim, L Lu, Y Xia, MG. Science ('06)
(Theme III) Big Data in a Big Crowd: Annotating the Human Genome, with comparative approaches & (sometimes) networks (Connecting with Steven over the phone!)

- Integrative analysis of the C. elegans genome by the modENCODE project.
  MG, Z Lu... [129 authors]... R Waterston. Science ('10)

- Architecture of the human regulatory network derived from ENCODE data.
  MG... [51 au.]... M Snyder. Nature ('12)

- **Comparative analysis of the transcriptome** across distant species.
  MG, J Rozowsky, K Yan, D Wang... [5 au.]... J Li... [82 au]... S Brenner... [3 au.]... R Waterston. Nature ('14) [Fig]
Key Result from Brenner-MG ENCODE collaboration:
Conserved gene-expression modules, enriched in important "hourglass" genes, contain most info. for aligning developmental timecourses

- Simultaneous clustering of 585 RNAseq expt. in human, worm & fly
- 16 conserved modules (containing many ncRNAs)
- 12 enriched in "hourglass" genes
- Alignment of the worm & fly timecourses driven by "hourglass" modules