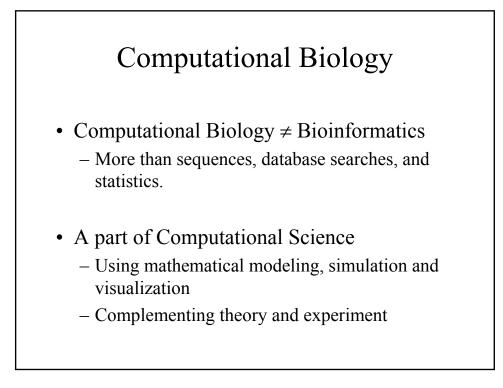
Modeling Metabolic Pathways-Glycolysis: a few reactions

^{By} Raquell M. Holmes, Ph.D. BioQUEST March, 2005



Today's journey

- Bioinformatics
 - From protein sequence
 - Metabolic pathway databases
- Metabolic behaviors
- Computer modeling glycolysis

Bioinformatics

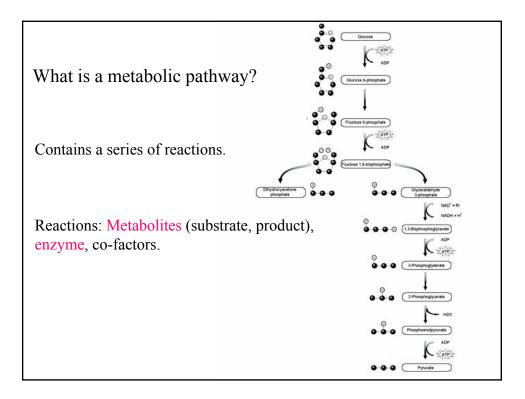
Common starting point

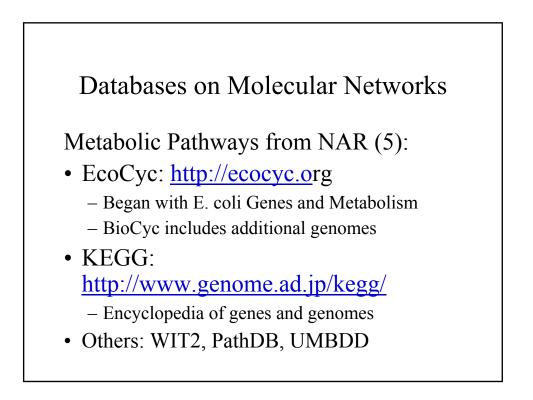
Generic Protein Seq. Record

- <u>Sequence</u>: hexokinase
- <u>E.C. #:</u> 2.7.1.1
- Publication: Stachelek et al 1986
- Organism: Yeast
- <u>Function</u>: main glucose phosphorylating enzyme
- Links: other databases or tools
- <u>Pre-determined Properties</u>: – families, folds...
- <u>Swissprot</u> example for enzyme.

What we learn from protein sequence?

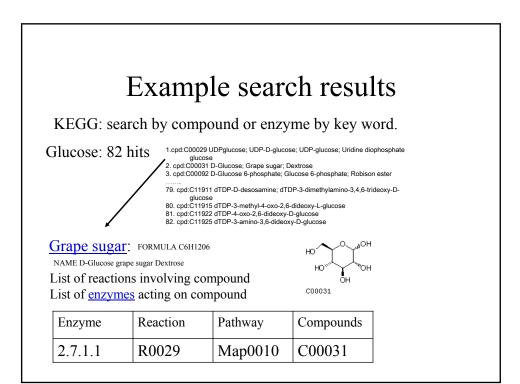
- Similarity searches :
 - Homology with other proteins
 - Conserved domains
 - Active sites
- How do we find the related pathway?
- Are there metabolism databases?





Starting out...

- Metabolism pathway databases
 - Search by name or sequence
 - Compounds, Reactions, Pathway, Genes
 - Associated information
 - Formulas, Names, Synonyms, Links to other databases



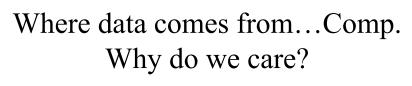
Database Content

Over 11 Data Categories

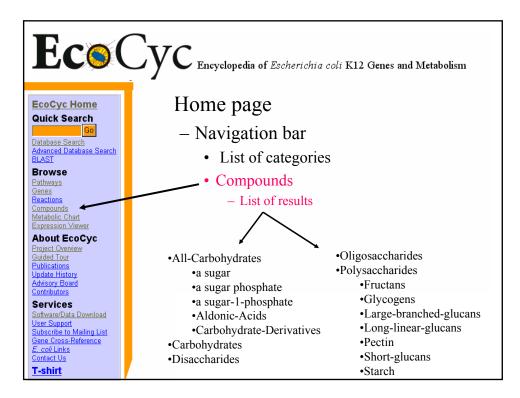
- Sequence: DNA, RNA, protein
- Structure: genomics, protein, carbohydrate
- Networks: metabolic enzymes and pathways (signaling)
- Organisms: human/vertebrate, human genes and diseases
- Expression: mircroarry and gene expression, proteomics
- Nucleic Acid Research
 - Dedicated to review of databases (548-'04, 386-'03)
 - http://nar.oupsjournal.org
- Most discussion focus on sequence databases.

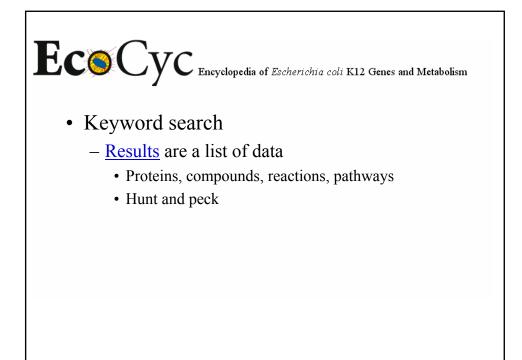
Where data comes from...Exp. Why do we care?

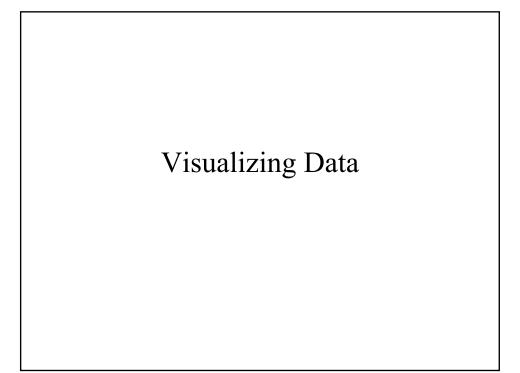
- Experiments
 - <u>Sequencing data:</u> Gene or protein identity
 - Enzymatic assays: Biochemical properties
 - <u>Expression studies</u>:Localization, putative cellular function, regulation patterns
 - Protein interactions: complexes and networks

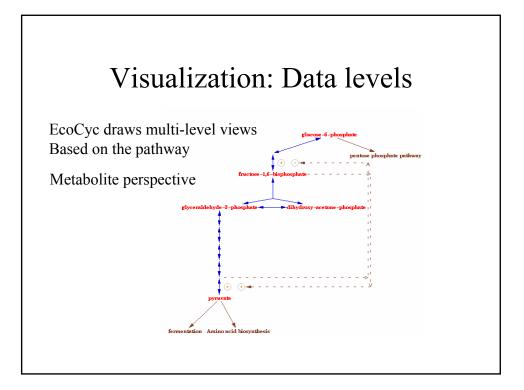


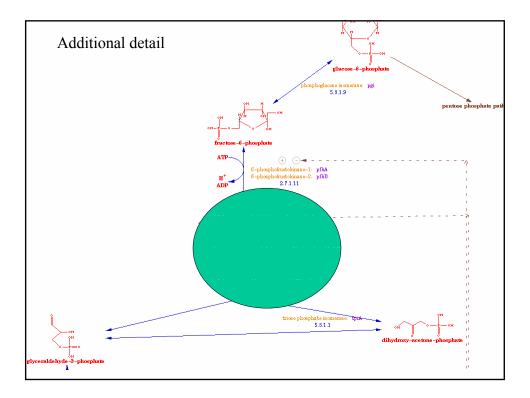
- Annotated sequences
 - Align sequences (full/partial)
 - · Homology to other genes, Identity
 - Pattern recognition, property predictions
 - Biochemical properties
 - Motifs, profiles, families
 - Enzyme activity and structure prediction
 - Pathways
 - Homologous function

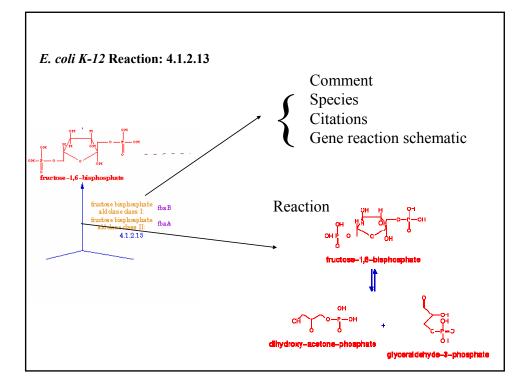


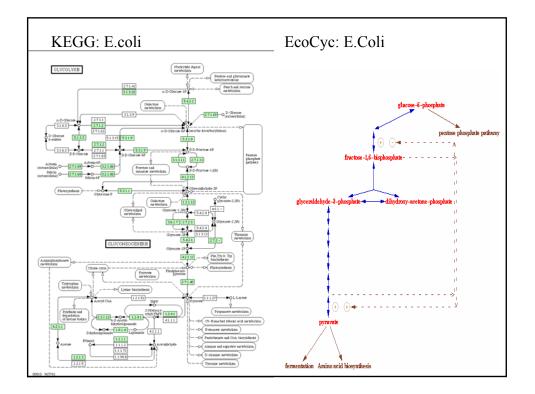








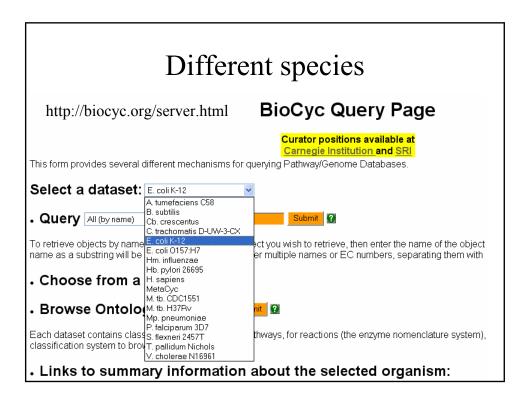


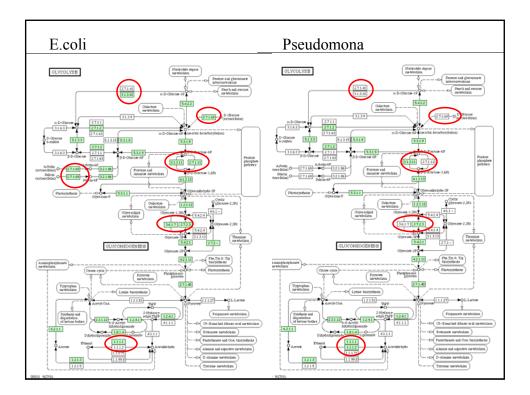


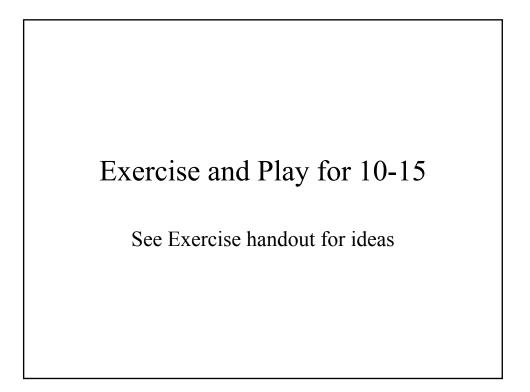
Summary I

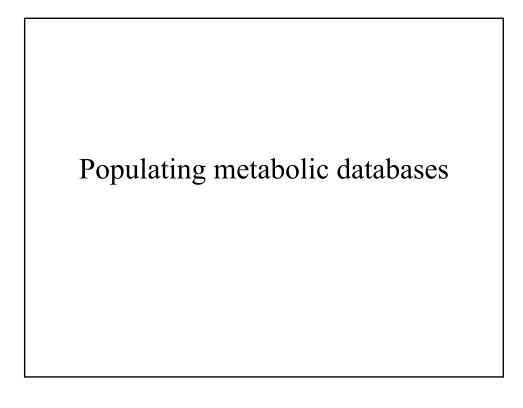
• Protein ->enzyme->pathway database

- Pathway Database Content:
 - Species specific (BioCyc), general (KEGG)
 - Known and proposed enzymes, co-factors, metabolites.
 - Searches return similar results (compounds, reactions...) with different appearance.









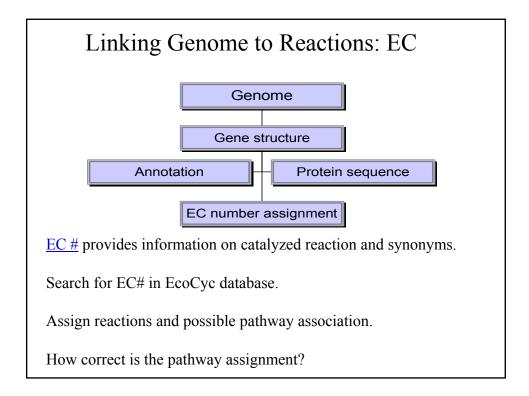
Where do the pathways come from?

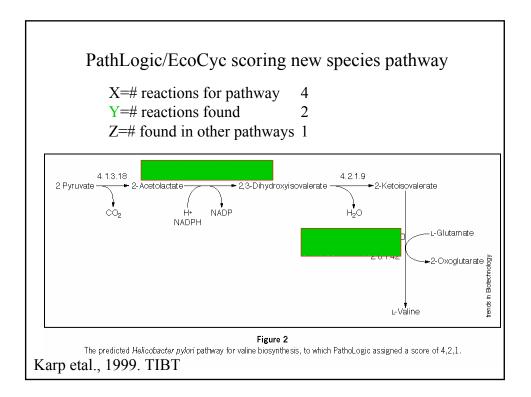
Databases: KEGG, WIT, BioCyc

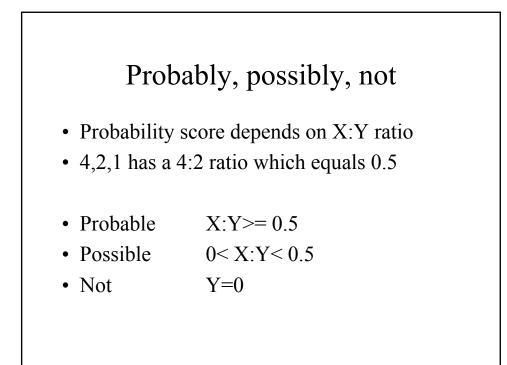
Resources:

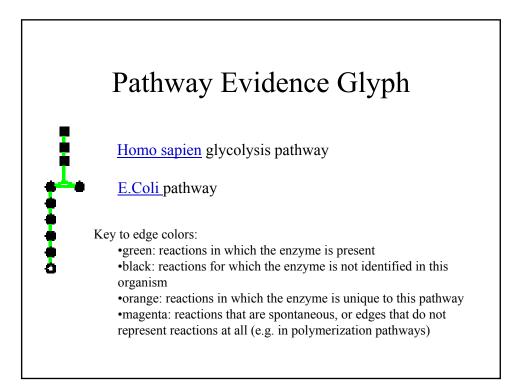
Experimental data based on literature Genomic data from other databases

Determination of metabolic pathway Comparison to known pathways.









Summary II

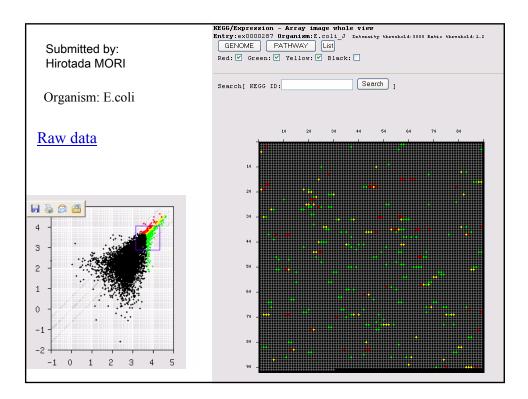
- Genomes used to create database of reactions
- EC# link gene product to enzyme in reactions
- Pathways in the database vary in degrees of probability.

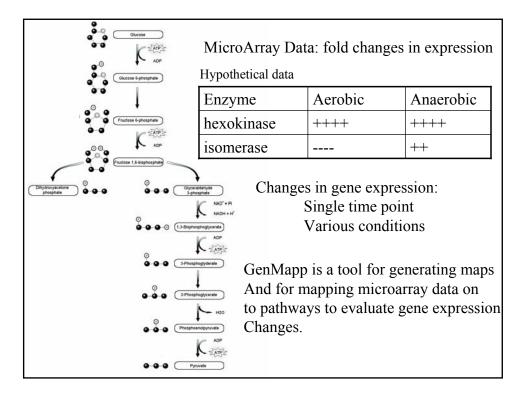
From Data to Dynamics

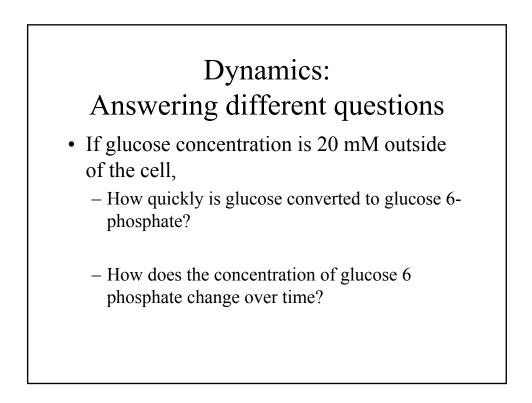
- Static Data
- What is the behavior of the pathway?
 - Expression data
 - Dynamics

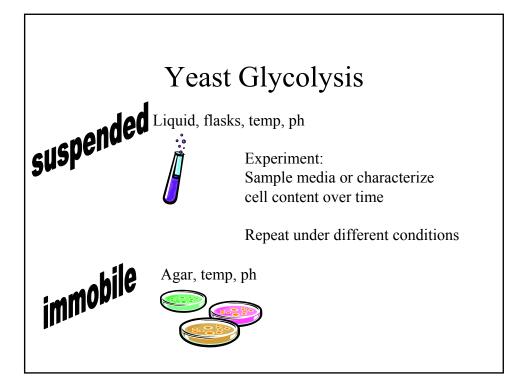
Expression data

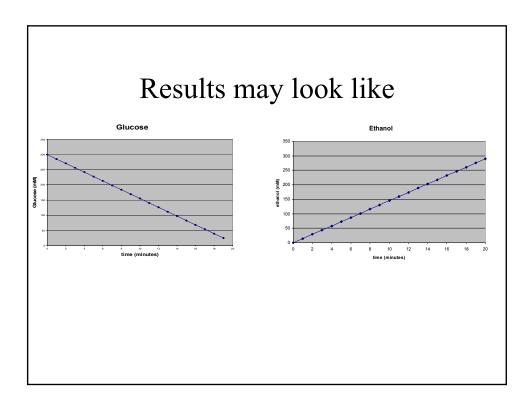
- KEGG:
 - retrievable expression data sets
- EcoCyc:
 - input expression data to view in relation to metabolic data.
- Expression data is one way of viewing the behavior of a system.











Computer Modeling

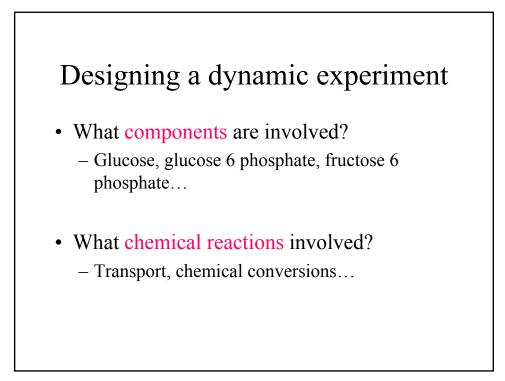
•Method for analyzing what we know about a biological process

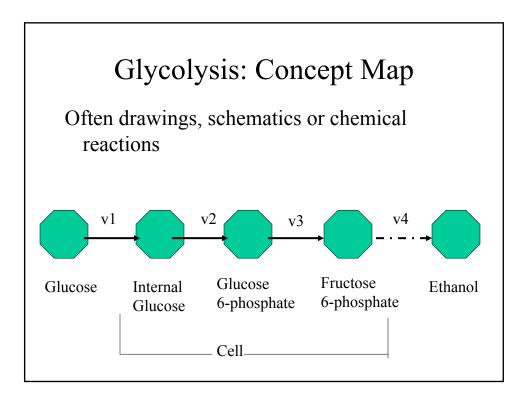
•Used to describe mechanisms behind changes

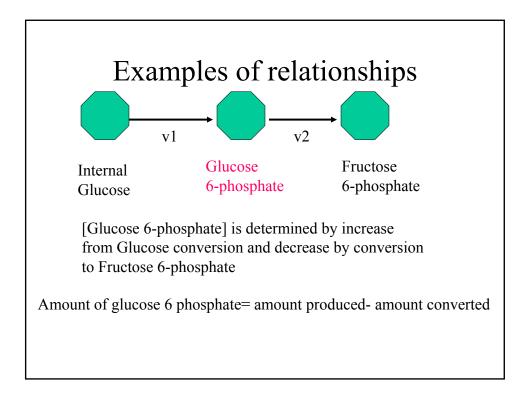
•Determines what can be seen or predicted

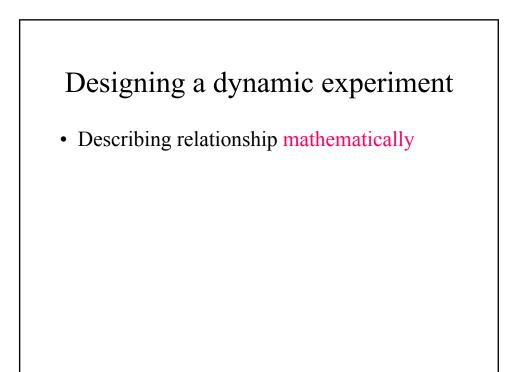
Walking through a Computational Model

- Concept Map
- Factors and relationships between factors
- Describe relationships mathematically
- Solve equations: using computer tools
- View and interpret results









Relationship in terms of rates of change

The rate of change of Glucose-6-phosphate (S₂) is the rate of Glucose conversion (v1) minus the rate of conversion (v2) to Fructose-6-phosphate.

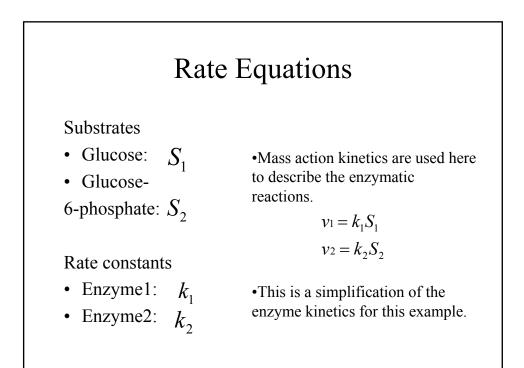
$$\frac{dS_2}{dt} = v_1 - v_2$$

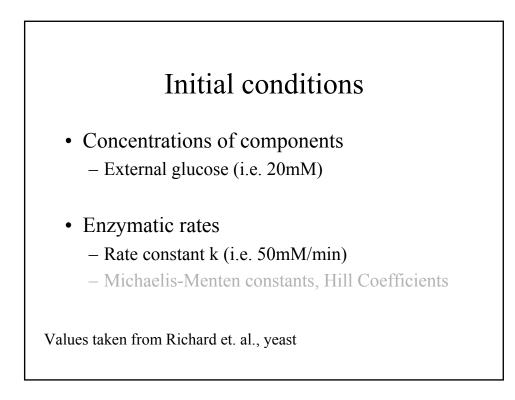
Describing a dynamic experiment Describing relationship mathematically What rate laws are known to describe the enzymatic reaction? Types of rate laws/kinetic models Constant, mass action, michaelis menten...

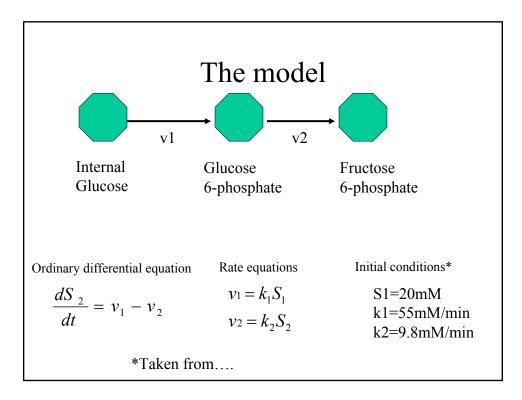
Simplify

• Glucose transport (v1) • Facilitated diffusion

$$v = V^{+} \frac{\frac{Glc_{out} - Glc_{in}}{K_{Glc}}}{1 + \frac{Glc_{out}}{K_{Glc}} + \frac{Glc_{in}}{K_{Glc}} + K_{i} \frac{Glc_{out}Glc_{in}}{K_{Glc}}}{K_{Glc}}$$

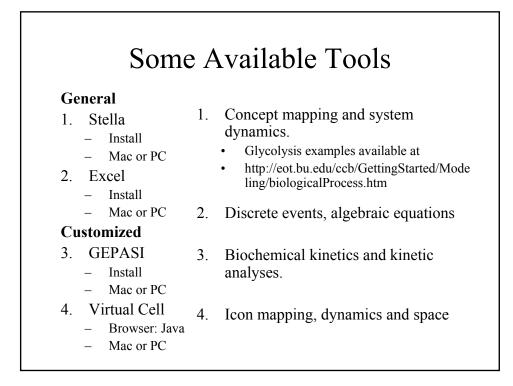


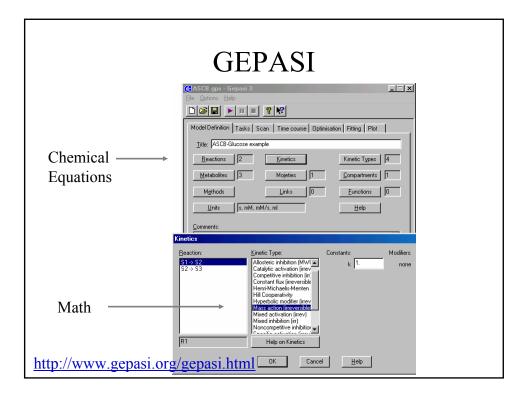


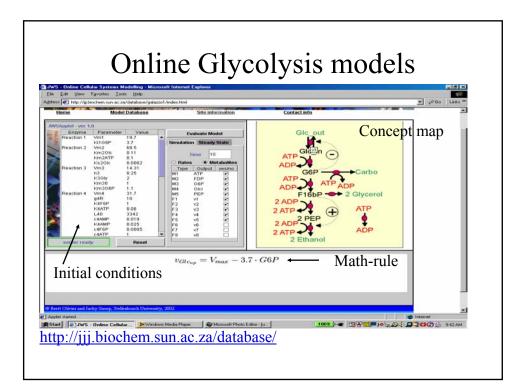


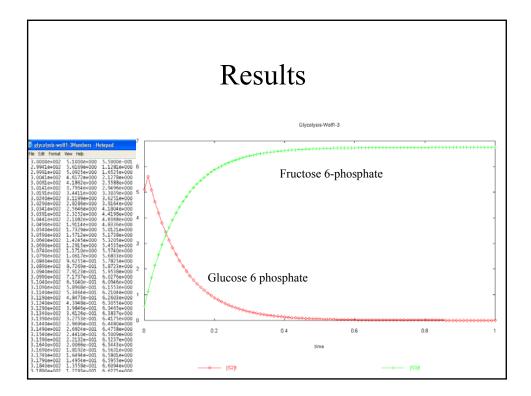
Walking through a Computational Model

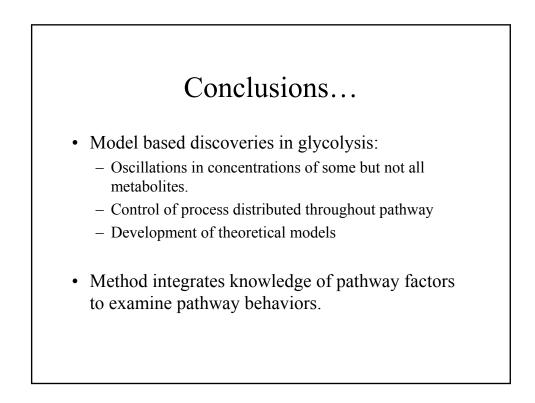
- Concept Map
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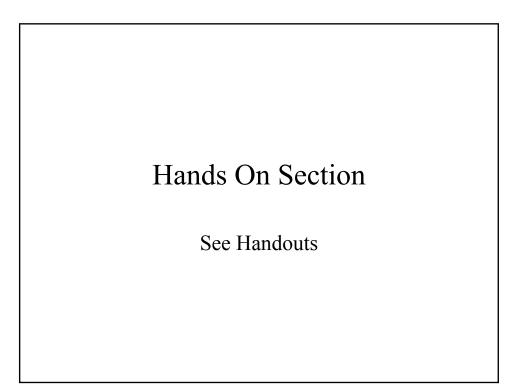






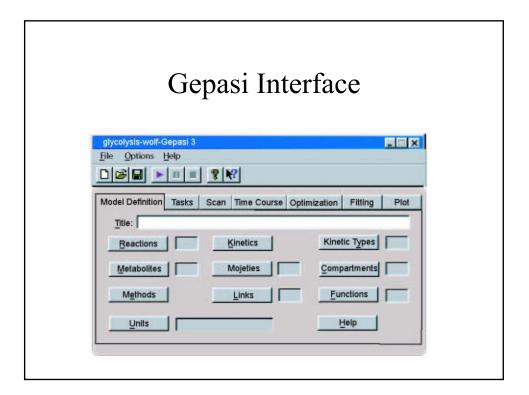
Modeling

- Requires formalizing assumptions
 - Rate equations
 - Inclusion or exclusion from model
- Worst case scenario
 - See what you believe
- Best case scenario
 - See something unexplainable
 - Create new laboratory experiments



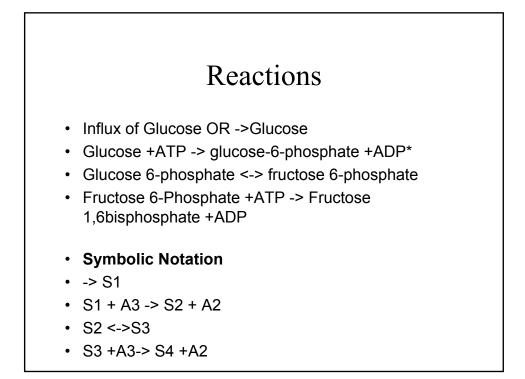
Modeling Glycolysis What part of glycolysis do you want to model?

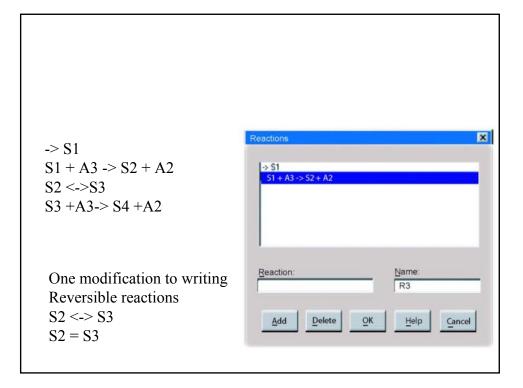
- Draw out a concept map
- Write out the biochemical reactions
 - Glucose +ATP->Glucose 6-phosphate +ADP
- Create a legend of symbols to molecule names
 - Try to use standard biochemical notation, but this is not required.

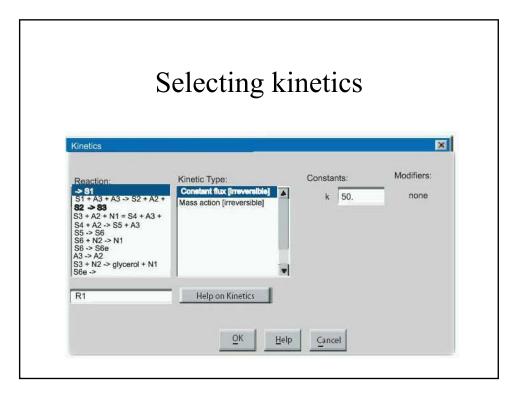


Write your reactions in Gepasi

- Gepasi uses standard biochemical notation for entering Reactions.
 - Table of reactions provided are a reference for a simplified glycolytic model.
- Enter Kinetics for reactions
- Enter Metabolite concentrations
- Select Tasks to be performed







Kinetics			X
Reaction:	Kinetic Type:	Constants:	Modifiers:
-> S1 S1 + A3 + A3 -> S2 + A2 + S2 -> S3 S3 + A2 + N1 = S4 + A3 + S4 + A2 -> S5 + A3 S5 -> S6 S6 + N2 -> N1 S6 -> S6 A3 -> A2 S3 + N2 -> glycerol + N1 S6e ->	Allosteric activation [MWC] Allosteric inhibition [MWC] Catalytic activation [reversib Competitive inhibition [rrever Constant flux [rreversible] Henri-Michaelis-Menten Hill Cooperativity Hyperbolic modifier [rreversi Mixed activation [rrev] Mixed activation [rrev]	k 1.	none
R3	Help on Kinetics		

		olites	3		
	Metabolites				
4	Name	Initial Conc.	Fixed	I Compartment	ОК
	S1	1.09		compartment	Help
	S2	5.1	Г	compartment	Cance
	S3	0.55		compartment 💌	
	A2	1.e-005		compartment	
	S4	8.3100000		compartment	
	A3	2.19		compartment	Add
	N2	0.41		compartment	
	S5	8.3100000		compartment	
	S6	8.e-002		compartment	
	N1	1.e-005		compartment	More.

	Methods				
	wiethous				
1	umerical Methods	i di K			×
	Derivation factor: +/- 0.01	%	BDF order:	5	
	SS. resolution: 1e-009		Adams order:	12	
	Newton iterations: 50		Abs. tolerance:	1e-012	
	Scaled MCA		Rel. tolerance:	1e-006	
	Time course elasticities				
	Strategy for steady-state solu				
	C Newton+integration	10.00			
	C Backward integration	Ва	ckward integratio	n ir all eise fails	
	ОК	Can	icel	Help	

Tasks @glycolysis-wolf.gps - Gepasi 3 File Options Help	_:X
Model Definition Tasks Scan Time course Optimisation Fitting PI Time course Time course Edit [S1]t Scan Scan Scan Scan Fitting PI Time course Time course Edit [S2]t Scan <	ot Bun Stop Help
Steady state File: simresults.ss Edit Up Col. width Separator 12 Space Titles Quotes	Set []i
For Help, press F1	

