

Bioinformatics II

VISUALISIERUNG (VU) – 13.MAY.2015

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Visualizing biological pathways

- ▶ Introduction:
 - ▶ pathway models for biological processes
 - ▶ significant broad impacts
 - ▶ for products in biotech applications and drug discovery
 - ▶ Goal: to try to convey complex global functionality
- ▶ Scientists are skeptical about the biological value of this way visualizations.

Problem

- ▶ There is not yet standardized language for describing the pathways
- ▶ ‘pathway’ is the user-defined network of the biological interactions
- ▶ Categories:
 - ▶ metabolic pathways
 - ▶ gene regulation/transcription pathways
 - ▶ signal transduction pathways

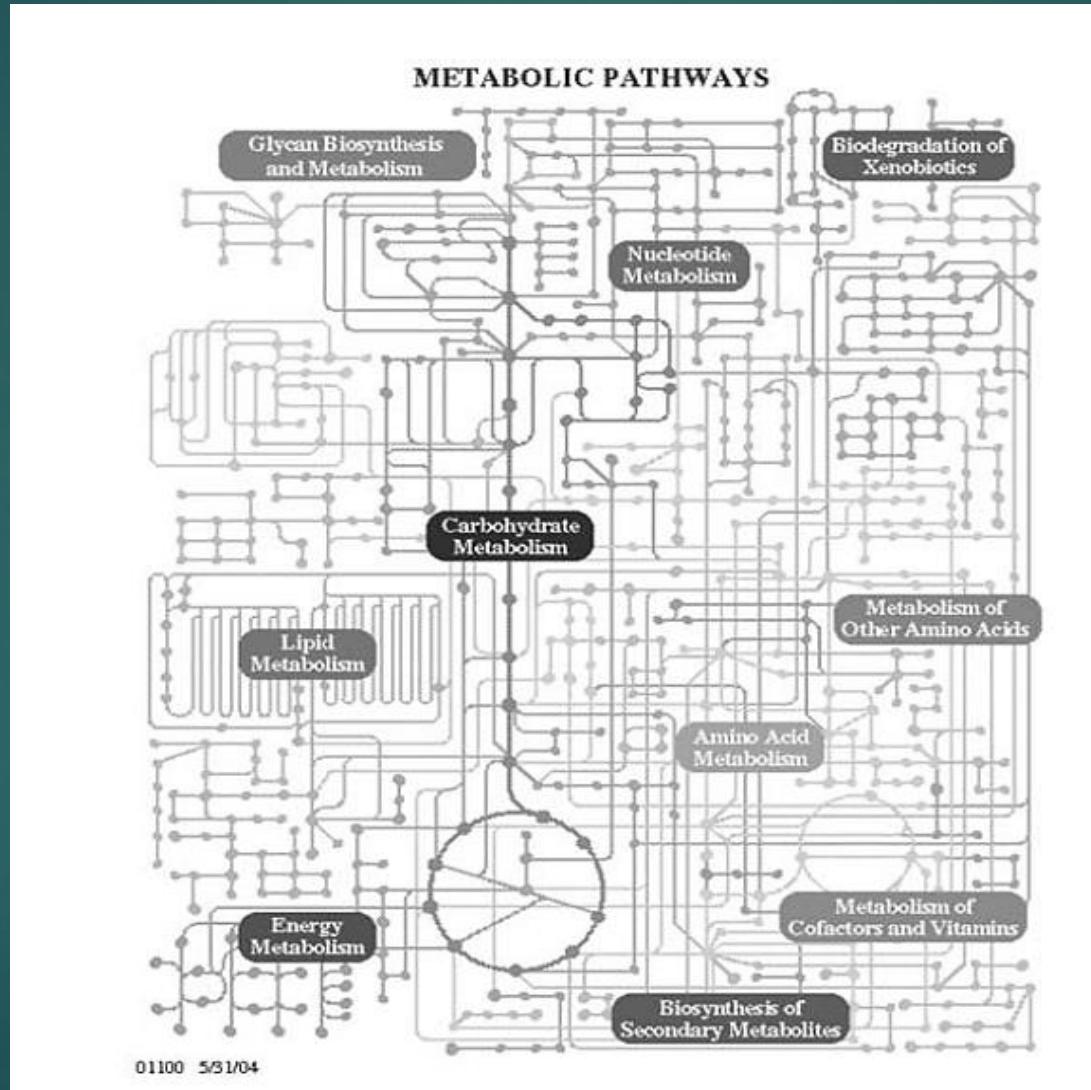
Summary

Table 1 Summary of requirements for pathway visualization systems

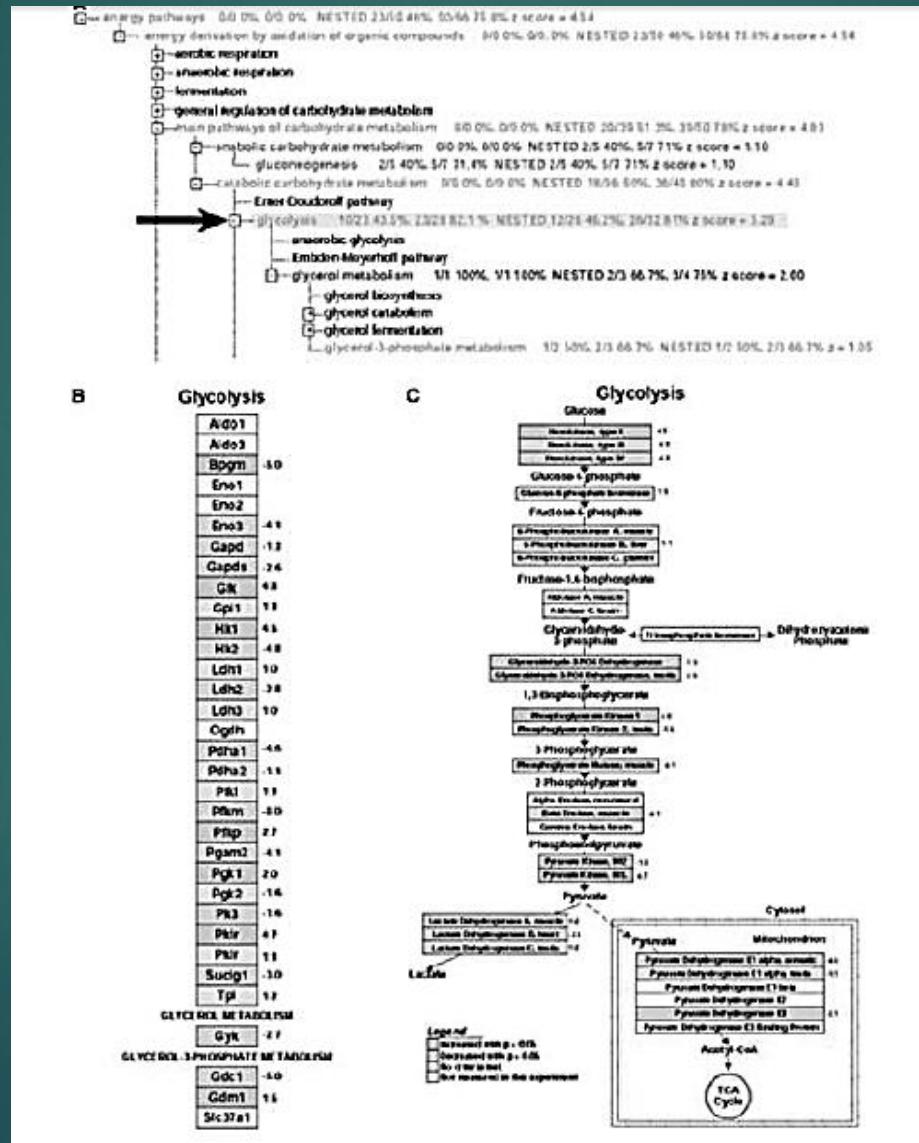
Categories	Requirements	Tasks
Pathway assembly	1. Construct and Update 2. Context 3. Uncertainty 4. Collaboration	Collect and link pathways from multiple resources Provide information about pathways Maintain alternate hypotheses and information reliability Enable group work
Information overlay	5. Node and edge representation 6. Source 7. Spatial information 8. Temporal information 9. High-throughput data	Details about network entities and interactions Details about source resources Physical locations of pathway entities in the cell Time-related properties Expression data from high-throughput experiments
Pathway analysis	10. Overview 11. Inter-connectivity 12. Multi-scale 13. Notebook	Comprehend large or multiple pathways Intra- and inter-pathway effects of entities on each other Relate networks at different levels of abstraction Track accumulated research information

The requirements are grouped into three main categories: pathway assembly, information overlay, and pathway analysis.

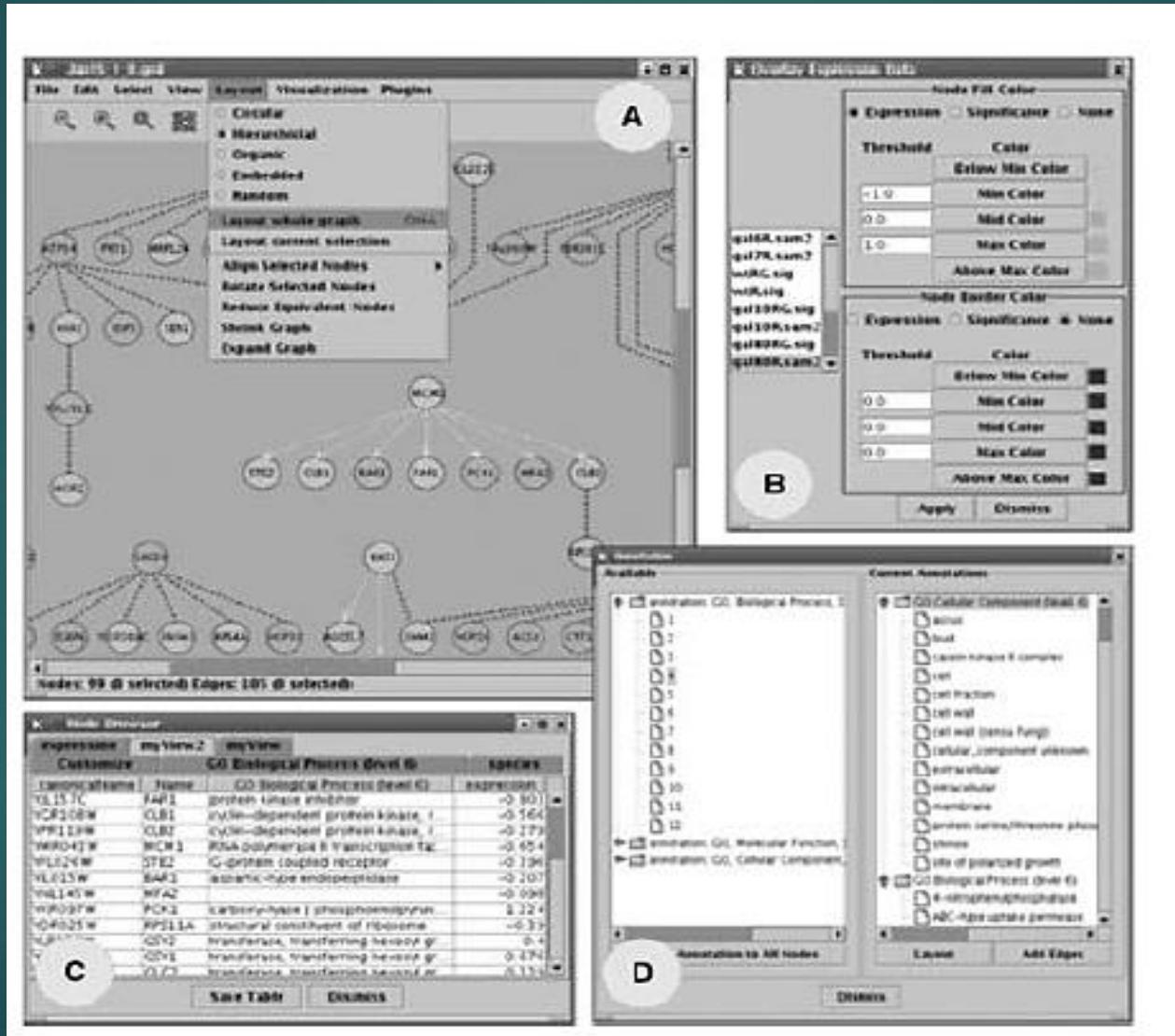
Metabolic pathways



GenMapp – Statistical Analysis

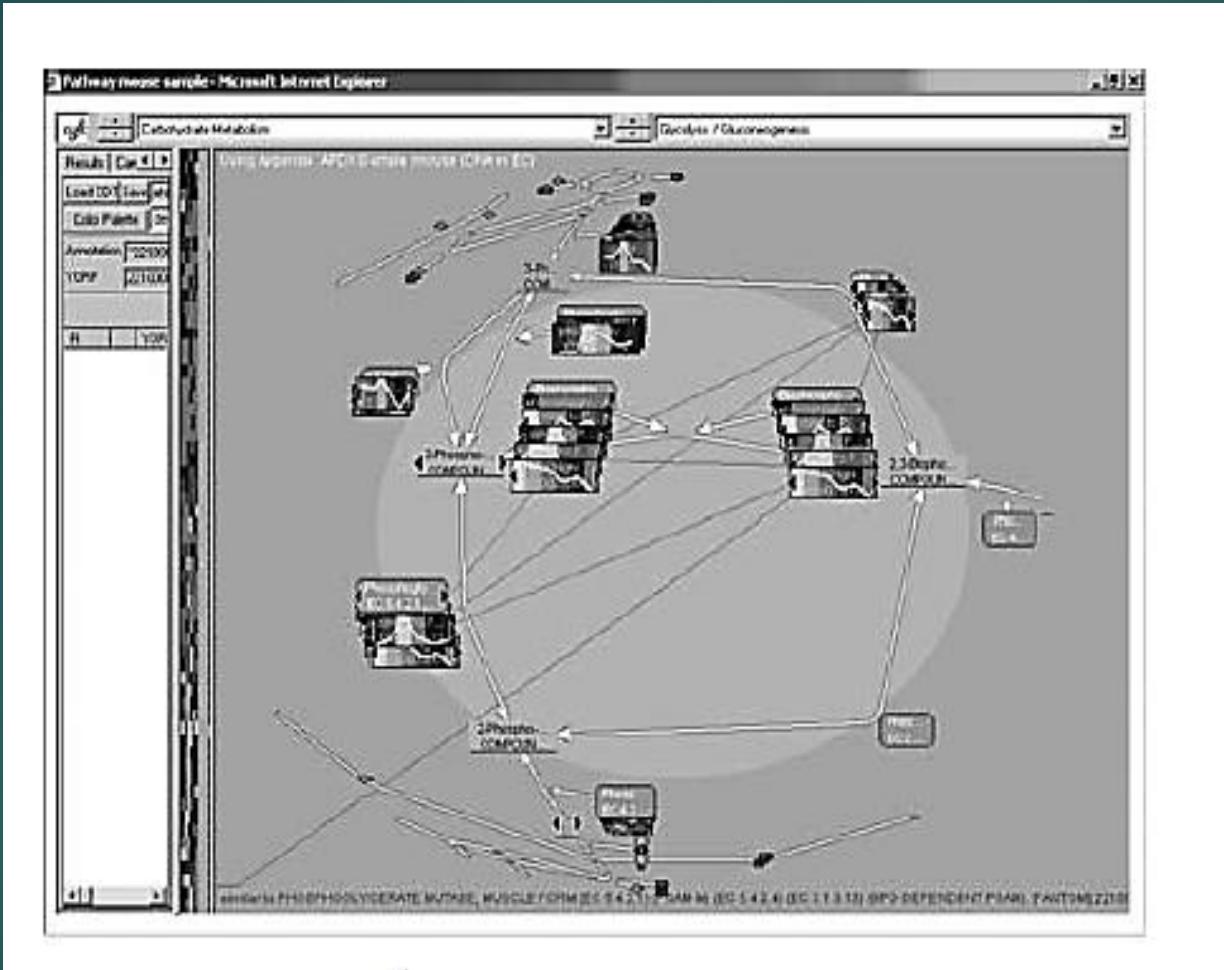


Cytoscape



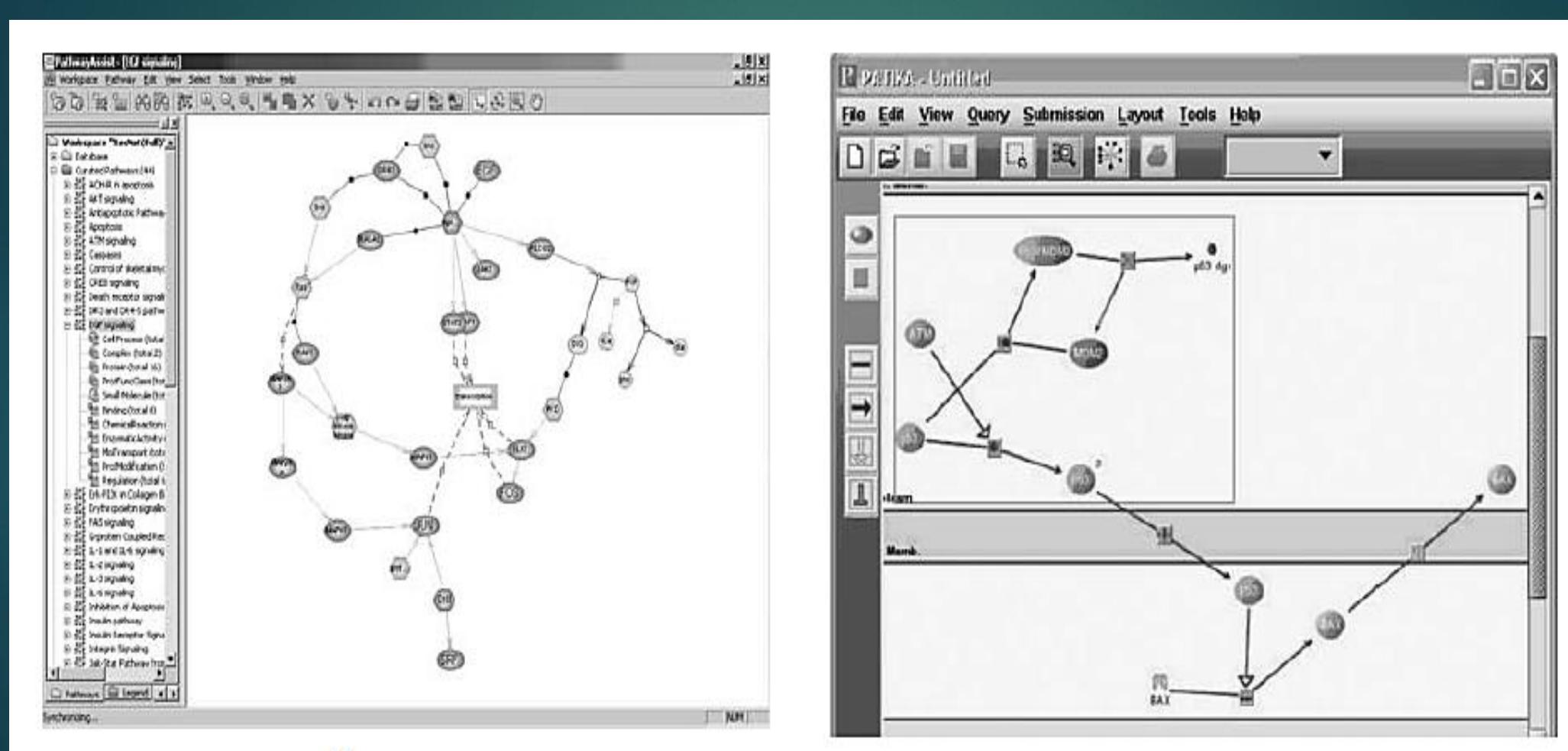
GScope

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VISSS14

PathwayAssist and Patika



Shortcomings

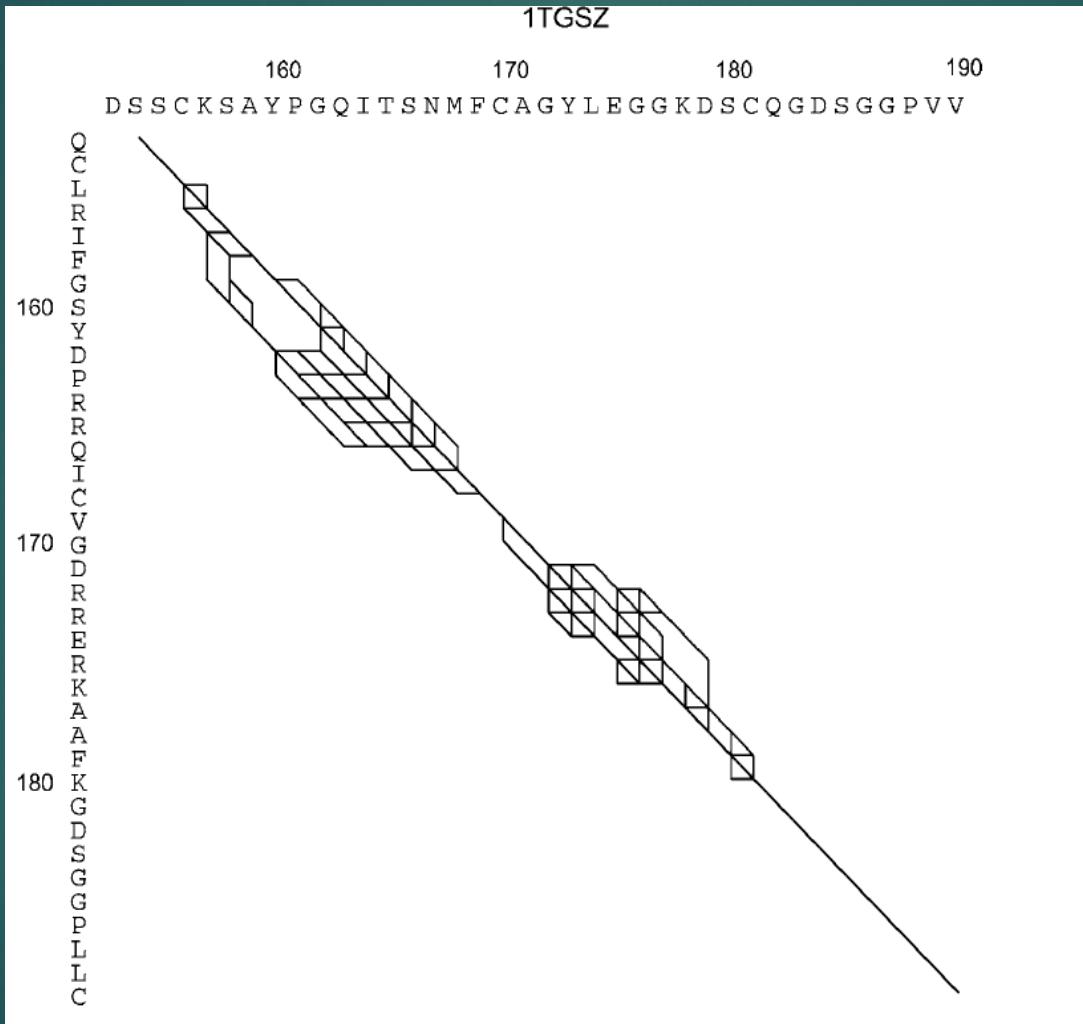
- ▶ they do not provide adequate domain-specific biological context
- ▶ Users must perform many tedious operations to search for and extract relevant information
- ▶ Tools does not provide users with rapid biologically relevant insight
- ▶ Tools for exploring large complex biological systems of many integrated pathways are still needed!

A system for visualizing and analyzing near-optimal protein sequence alignments

- ▶ two alternative methods for displaying large sets of protein alignment solutions:
 - ▶ Optimal
 - ▶ near-optimal

	10	20	30	40	50		
1AU8A	-----IIGGRESRPHSRPYMAYLQIQSPAGQSRCGGFLVREDFVLTAAHCWGSNINVTL						
	...:	..::	...:	...::::	...:::	
1TGSZ	VDDDDKIVGGYTCGANTVPY---QVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRL						
	10	20	30	40	50		
	60	70	80	90	100	110	
1AU8A	GAHNIQRRENTQQHITARRAIRHPQYNQRTIQNDIMLLQLSRRVRRNRNVNPVALPRAQE						
	: :	...::	...:	...::::	...::	
1TGSZ	GEDNINVVEGNEQFISASKSIVHPSYNSNTLNNDIMLIKLKSAASLNSRVASISLPTSCA						
	60	70	80	90	100	110	
	120	130	140	150	160	170	
1AU8A	GLRPGLCTVAGWG--RVSMRRGTDTLREVQLRVQRDRQCLRIFGSYDPRRQICVGDRRE						
	. :	...::	..:	...:	...:	...:	
1TGSZ	S--AGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEG						
	120	130	140	150	160	170	
	180	190	200	210	220		
1AU8A	RKA AFKG DSGG PLLCN NVAH GIVSY GKSS GVP--PEVF TRVSS FLPW IR TT MRS-						
	:::	...::	..:	...::	...::	
1TGSZ	GKDSCQGD SGGP VVCS GKLQG I VSWG SGCA QK NKP G VY TKVC NYV SWIK QT ASN						
	180	190	200	210	220		

Path graphs



System goals

- ▶ to aid understanding of the relationship between two proteins
- ▶ to facilitate understanding of the alignment generation algorithms.

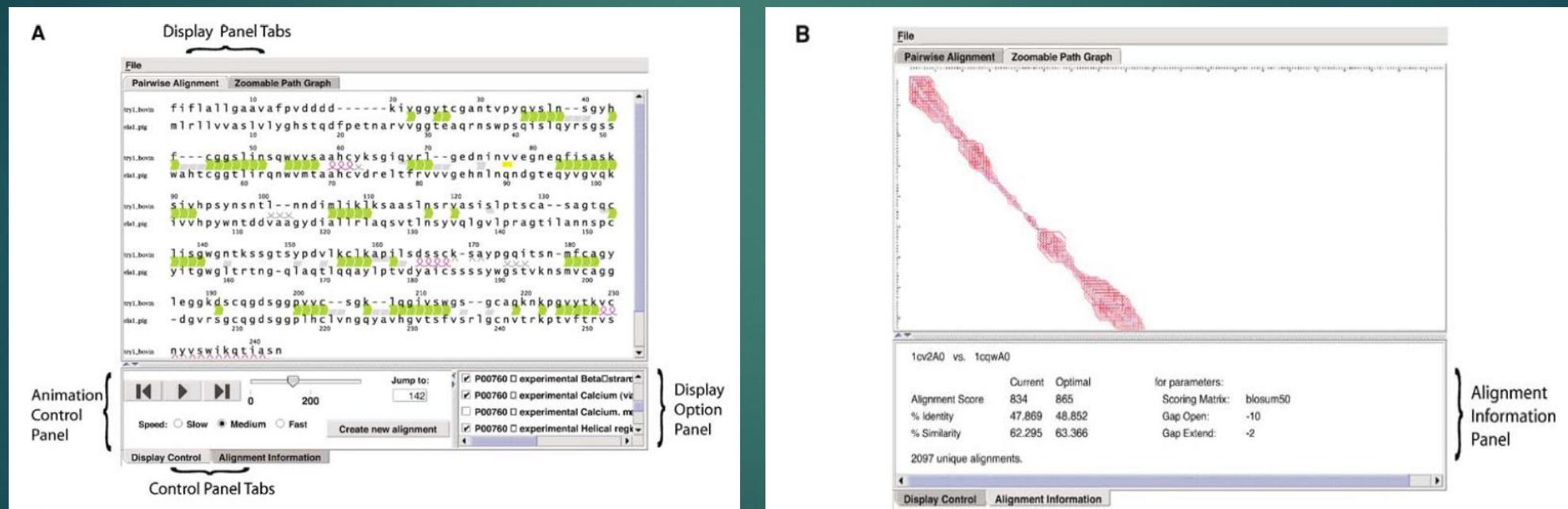
System screenshots

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VIS SSS 14

animated pairwise alignment

partial path graph alignment



Conclusion 1.1

- ▶ a system that improves the understanding of relationship between two proteins
- ▶ The ability for users to exploit and use expert knowledge is facilitated by the application of highlights, filters and the ability to directly create and edit alignments.

Conclusion 1.2

- ▶ not a replacement
- ▶ supplement to existing sequence analysis techniques
- ▶ the system could be used to construct high-quality homology models

Thank you for your attention!

References

1. **Visualizing Biological Pathways: Requirements Analysis, Systems Evaluation and Research Agenda**, Purvi Saraiya, Chris North and Karen Duca, 2005
2. **A System for Visualizing and Analyzing Near-Optimal Protein Sequence Alignments**, Michael E. Smoot, Ellen J. Bass, Stephanie A. Guerlain and William R. Pearson, 2005