

# The Whole-Cell Network of *Mycoplasma genitalium*

- ▶ Paulo Burke – ICT – Unifesp  
[paulo.burke@unifesp.br](mailto:paulo.burke@unifesp.br)
- ▶ Advisor: Marcos G. Quiles

# Complex Networks

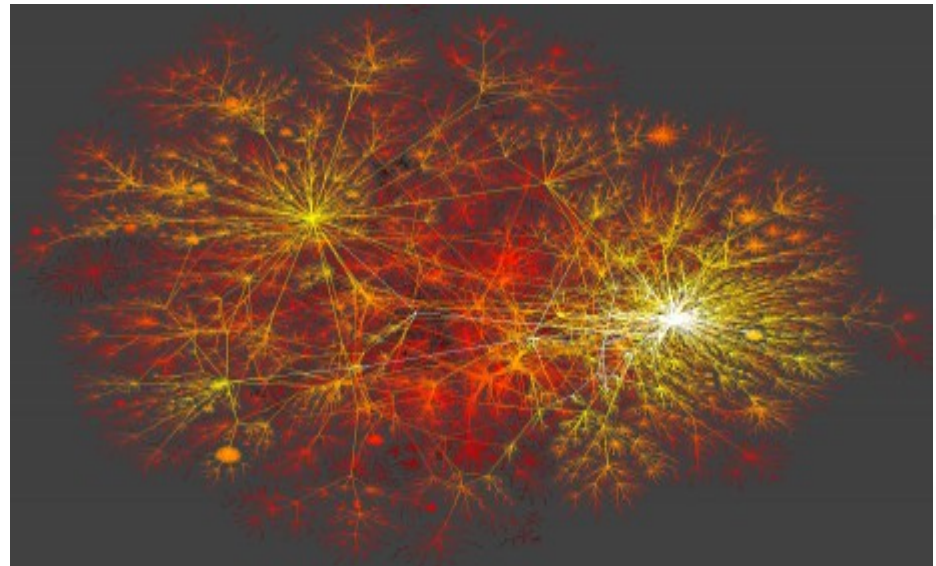
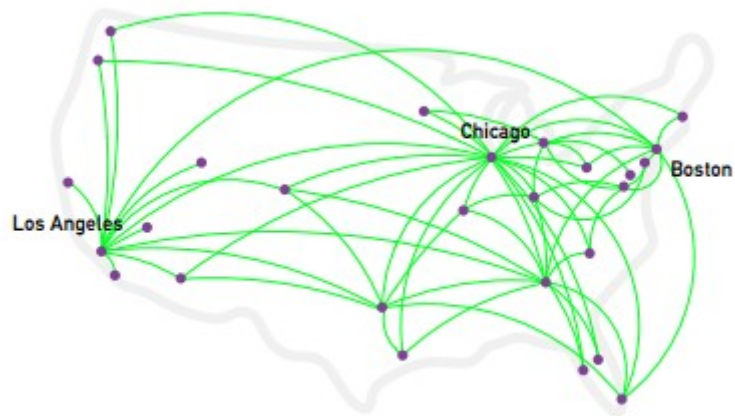
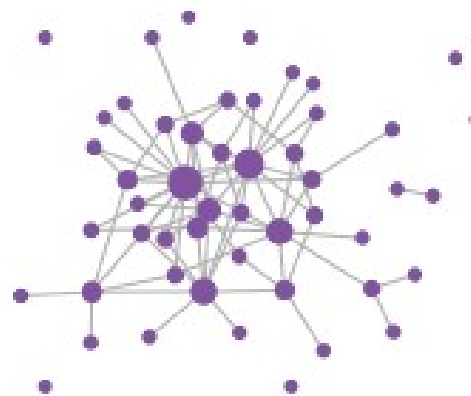
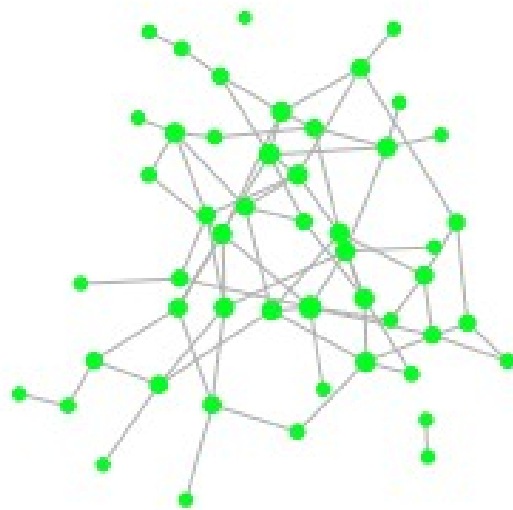
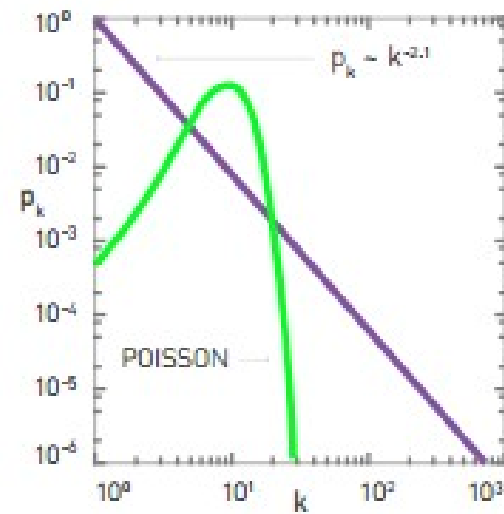
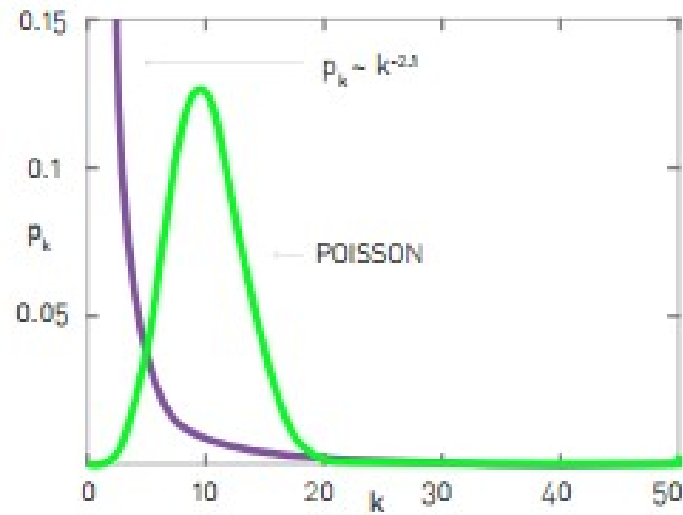


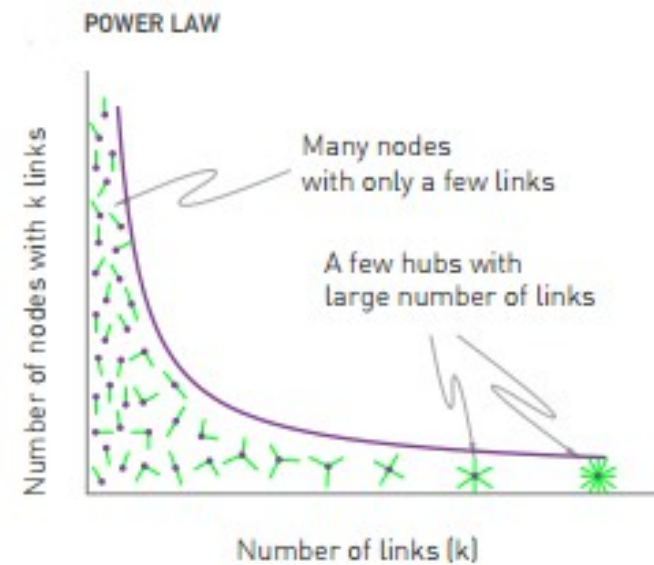
Image: ALBERT-LÁSZLÓ BARABÁSI, NETWORK SCIENCE, chapters 1 and 4

# Scale-Free Networks

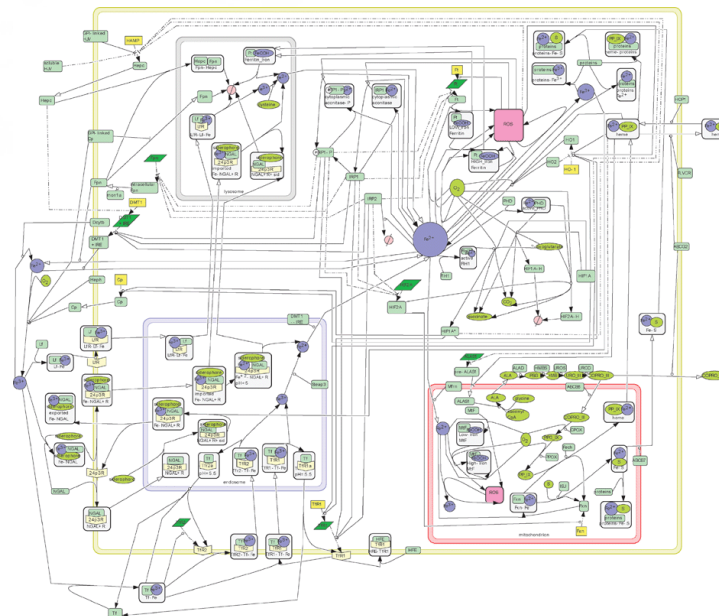
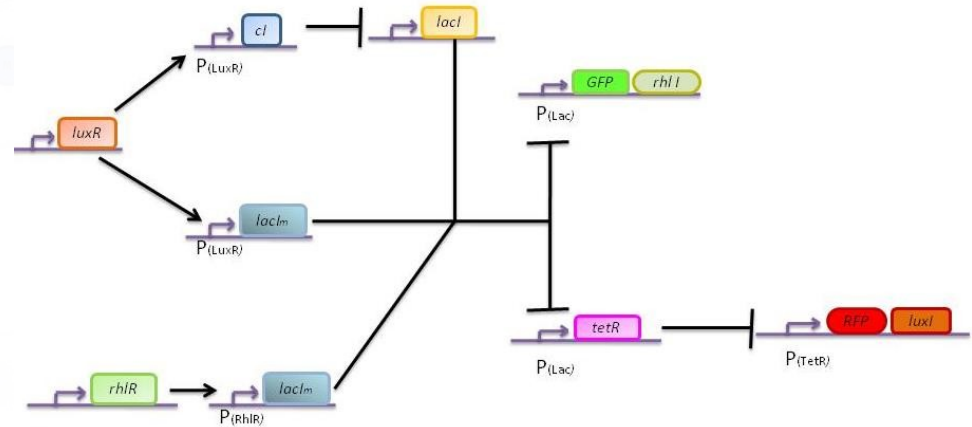
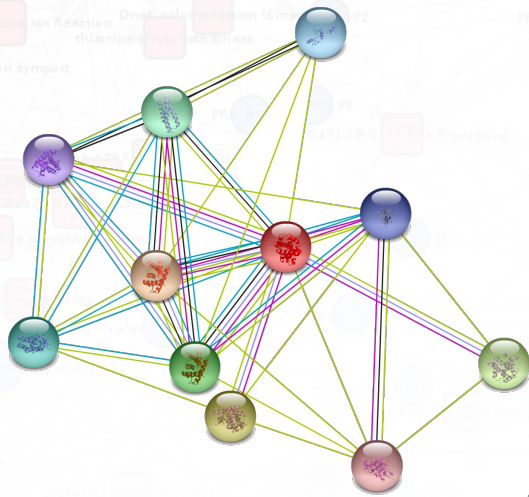


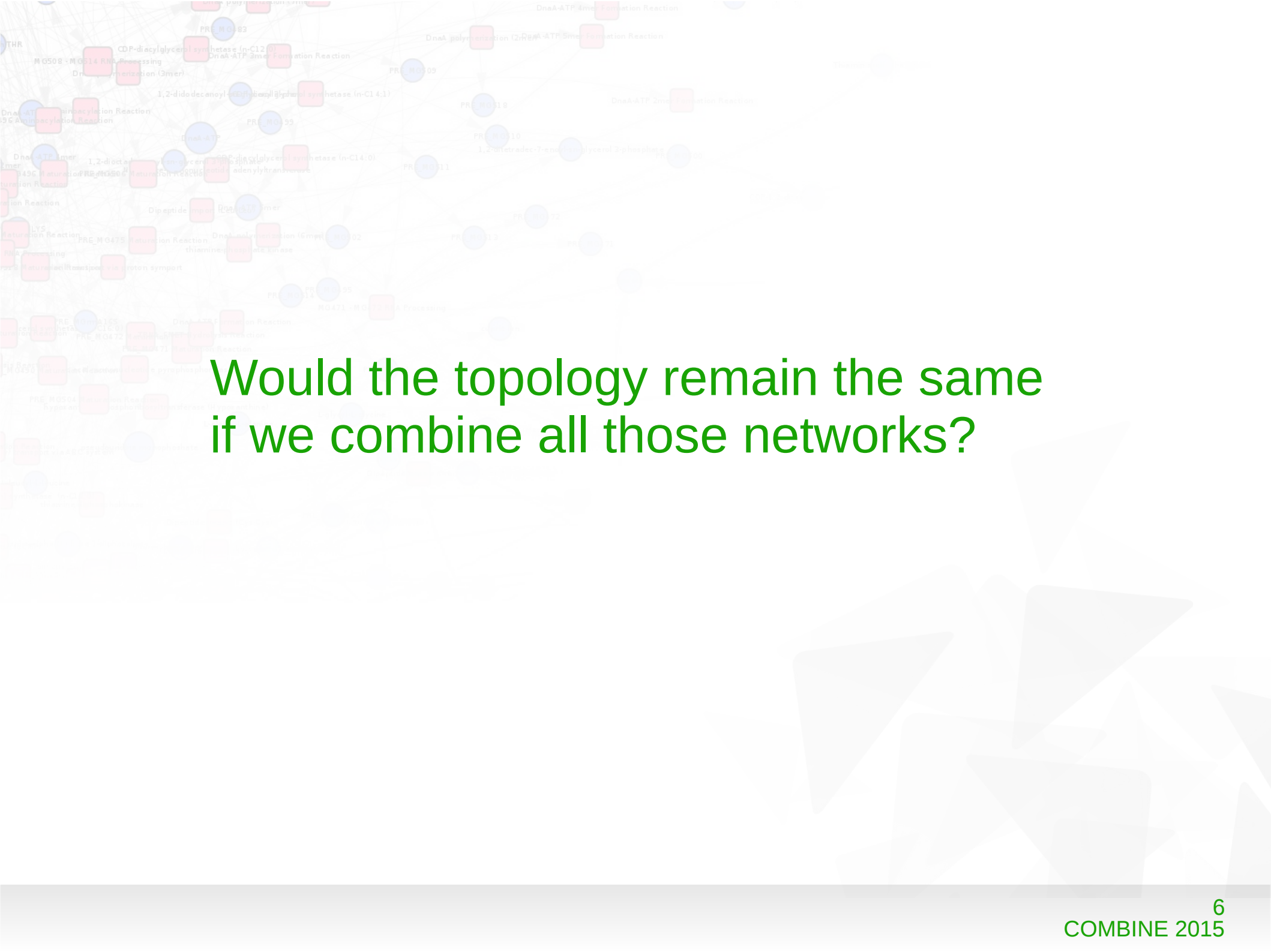


# USA Airport Network



# Scale-Free Topology of Biological Networks





Would the topology remain the same  
if we combine all those networks?

# Whole-Cell Network set of rules

- Each molecule or structure in the cell should be represented by a unique molecule node;
- Each different state of a molecule (e.g., active and inactive protein) should be represented by a different molecule node;
- Each molecular interaction should be represented by a single reaction node;
- Multi-step reactions (e.g., polymerization, degradation) should be condensed into single reaction nodes;
- Edges should only run between different types of nodes;
- The incoming edges of the reaction nodes can be of two types: reactant edges, which link molecule nodes that are consumed during the reactions, and modifier edges, which link molecule nodes representing catalysts or molecules that do not change during the reactions;
- The outgoing edges of the reaction nodes target the molecule nodes produced by interactions;
- The weight of each edge determines its stoichiometry in the interaction.



# Biological Model

## *Mycoplasma genitalium*

- Pathogenic bacteria
- Smallest known genome (580 kb)
- 525 genes

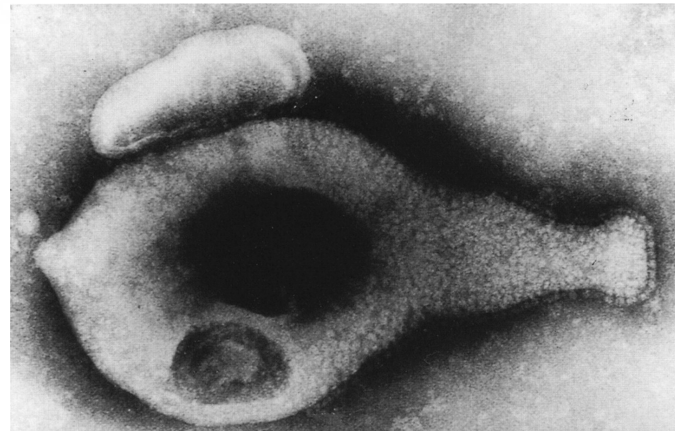
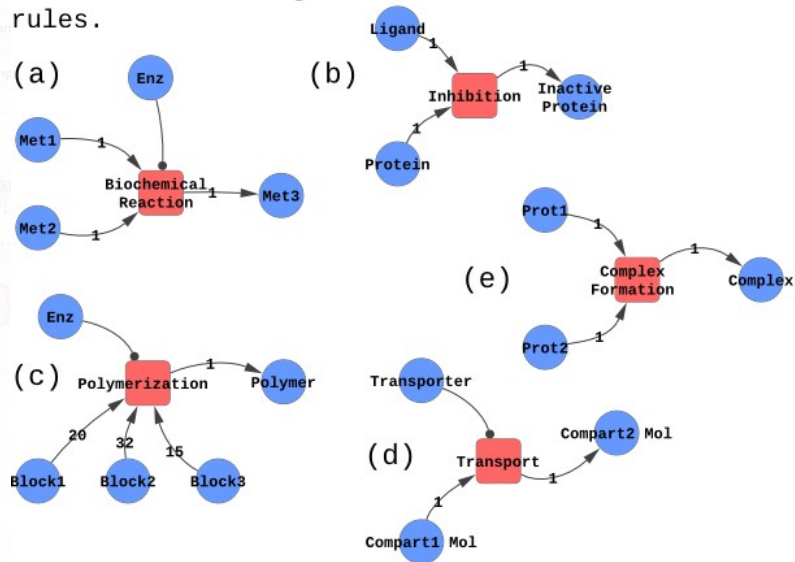


Image: Taylor-Robinson, D., & Jensen, J. S. (2011). *Mycoplasma genitalium*: From chrysalis to multicolored butterfly. *Clinical Microbiology Reviews*, 24, 498–514. doi:10.1128/CMR.00006-11



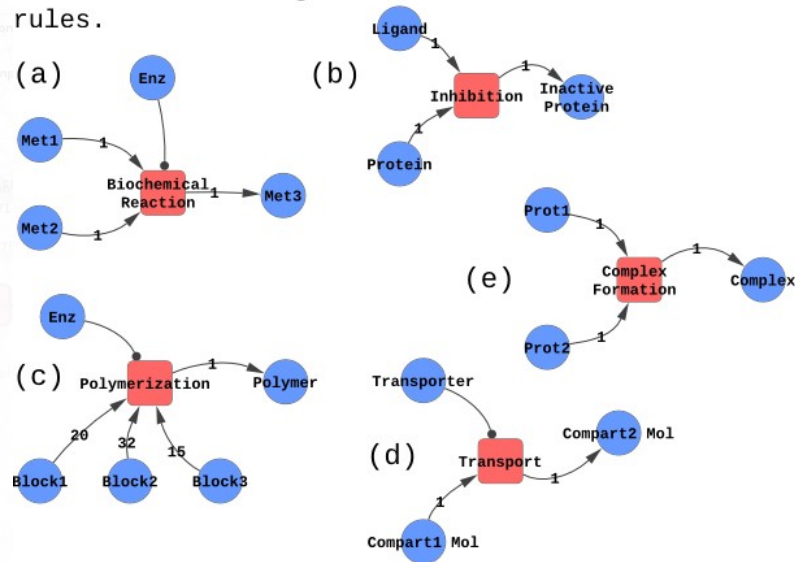
# Modeling

**I.** Model molecular interactions with the whole-cell modeling rules.

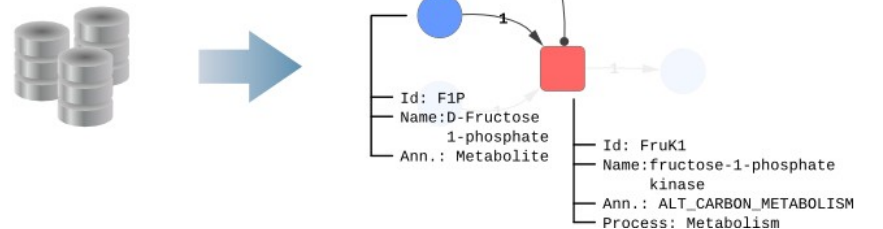


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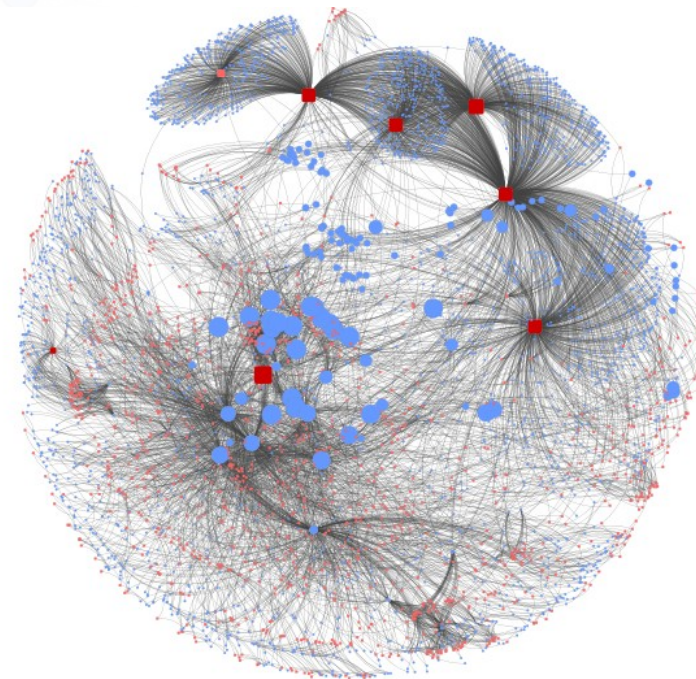
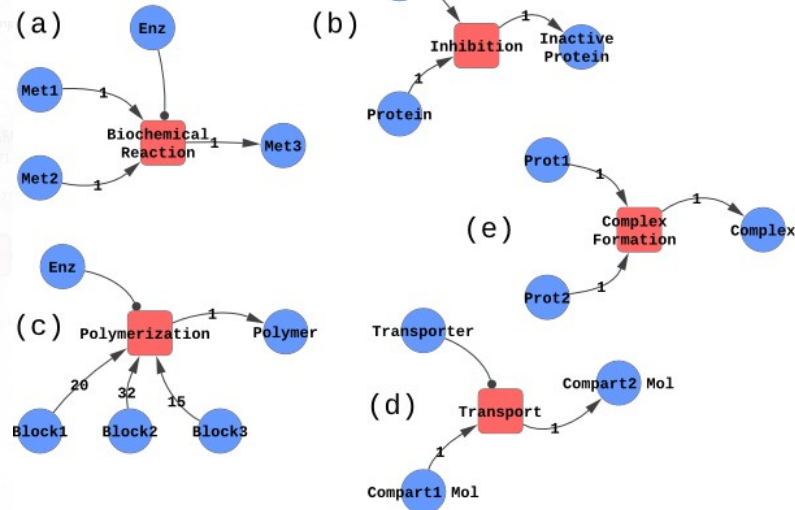


**II.** Feed model with large-scale data regarding a desired organism.



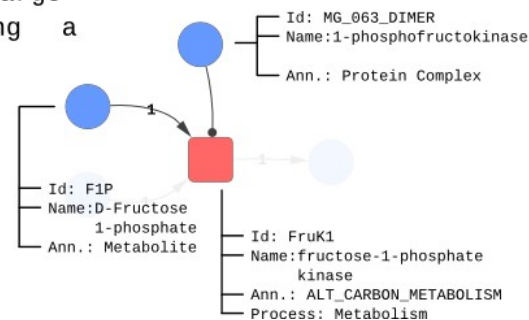
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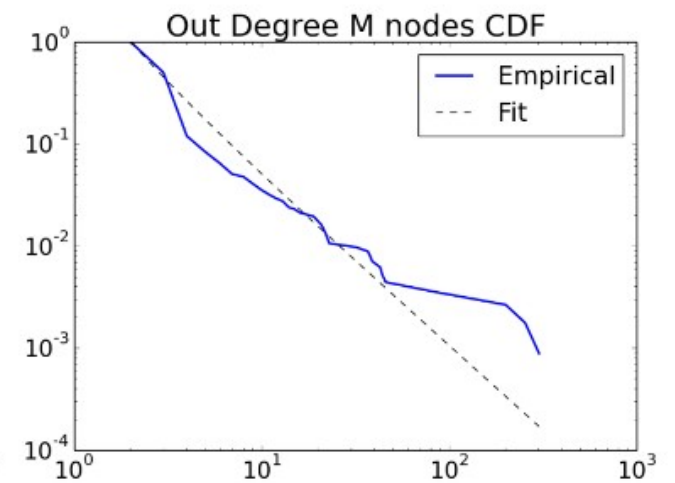
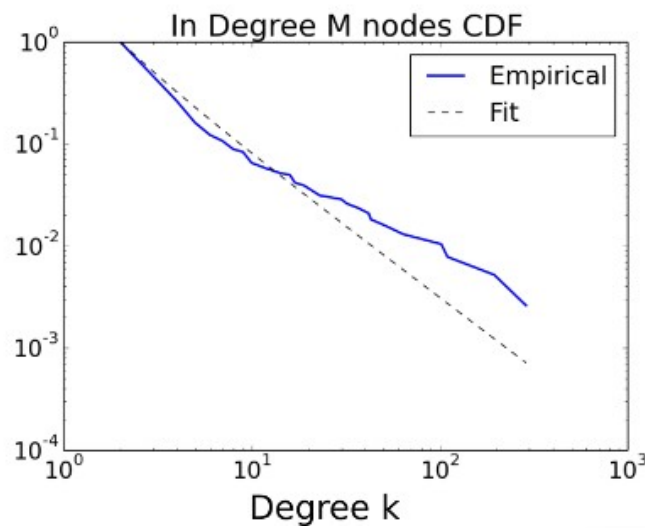
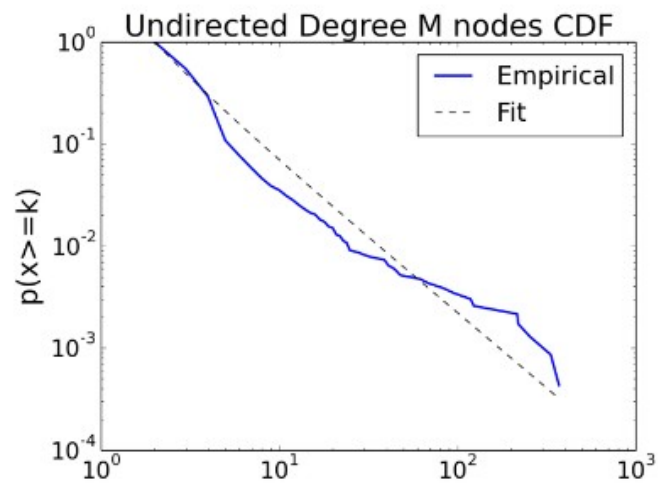


**III.** Resultant whole-cell network which represents a whole organism.

**II.** Feed model with large-scale data regarding a desired organism.



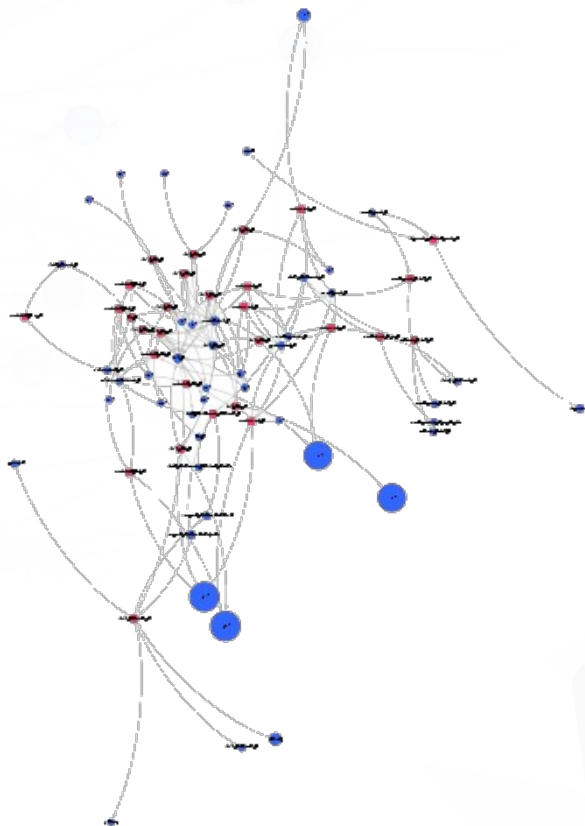
# Topology





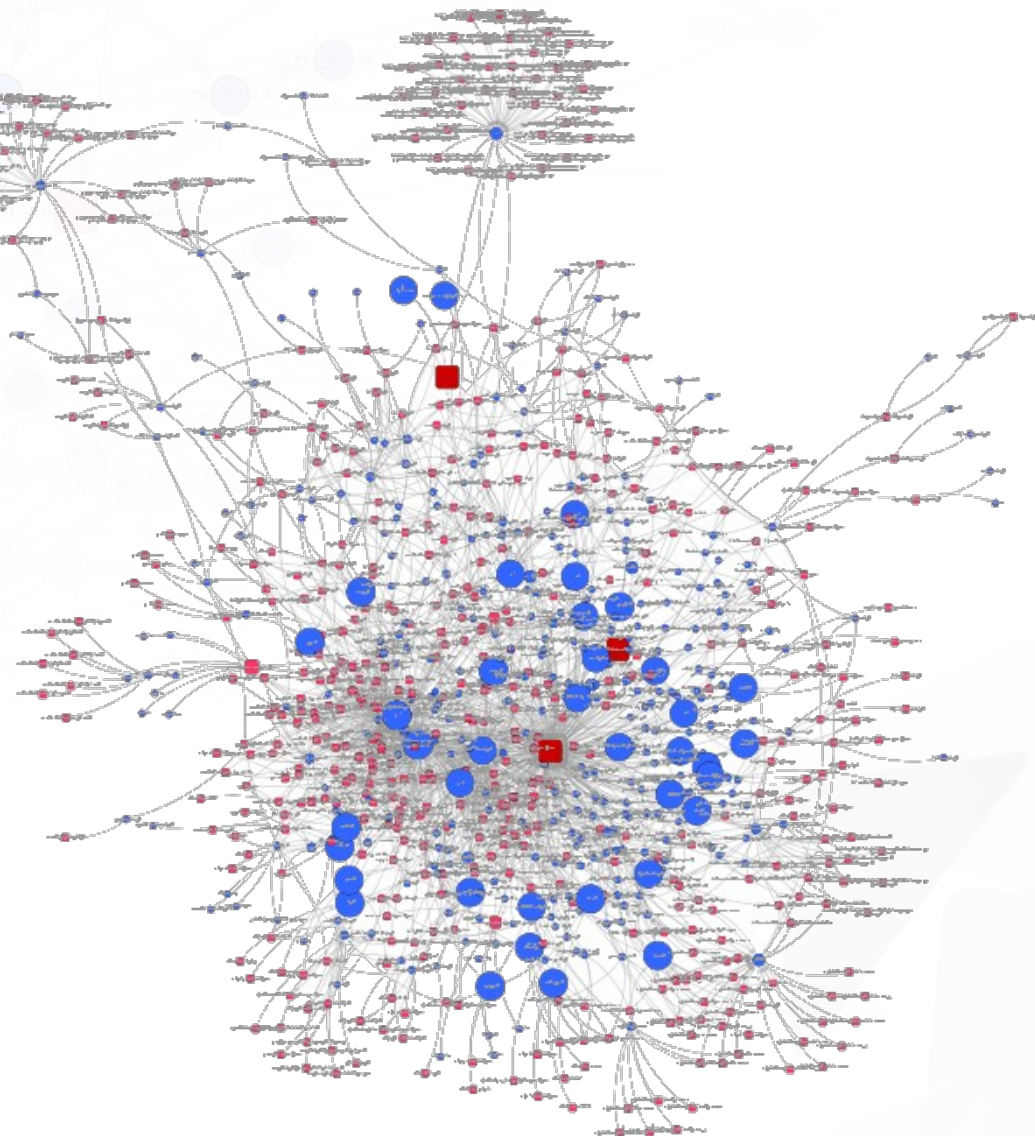
# Pathway Interactions

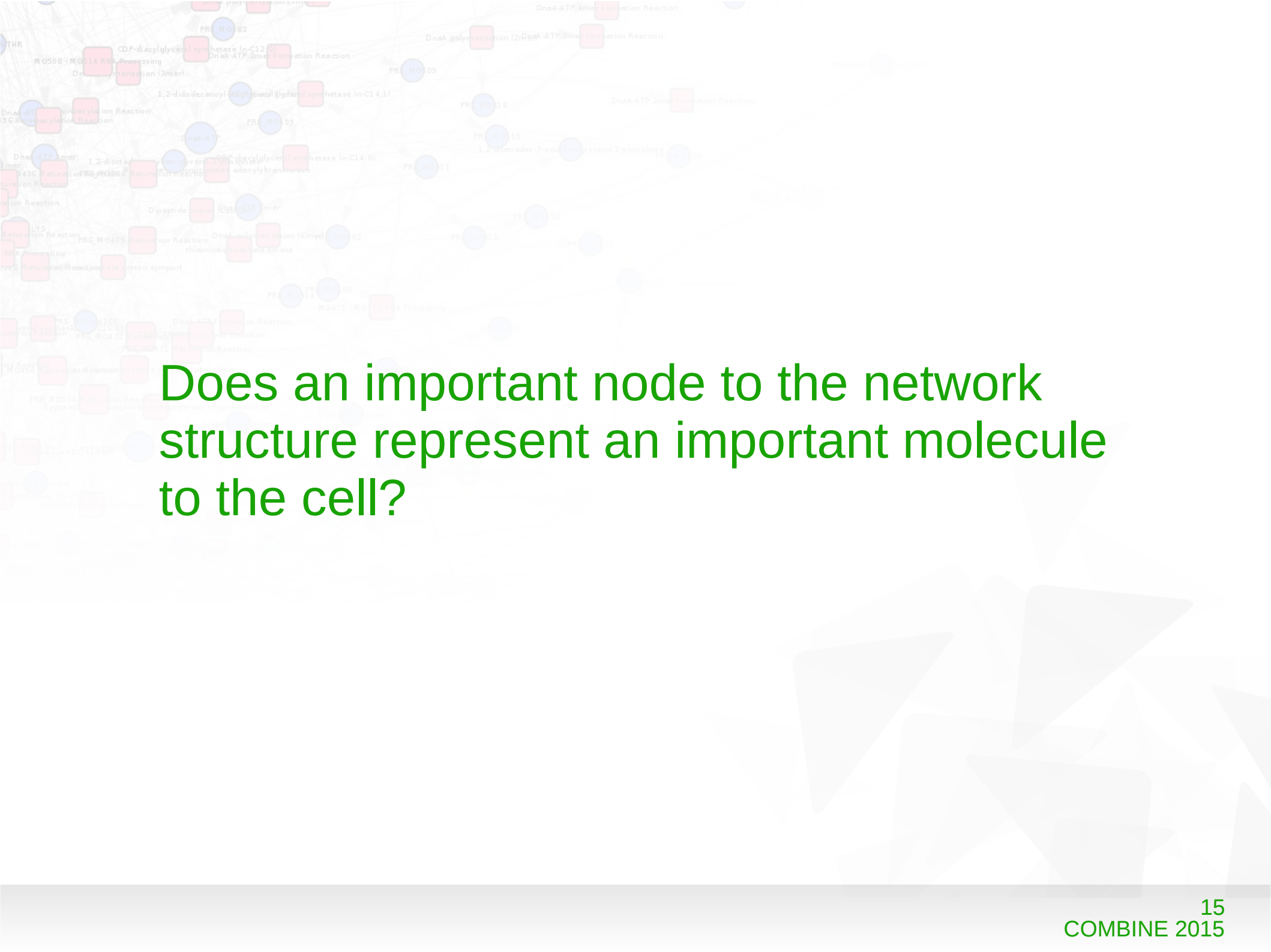
Glycolysis pathway:



# Pathway Interactions

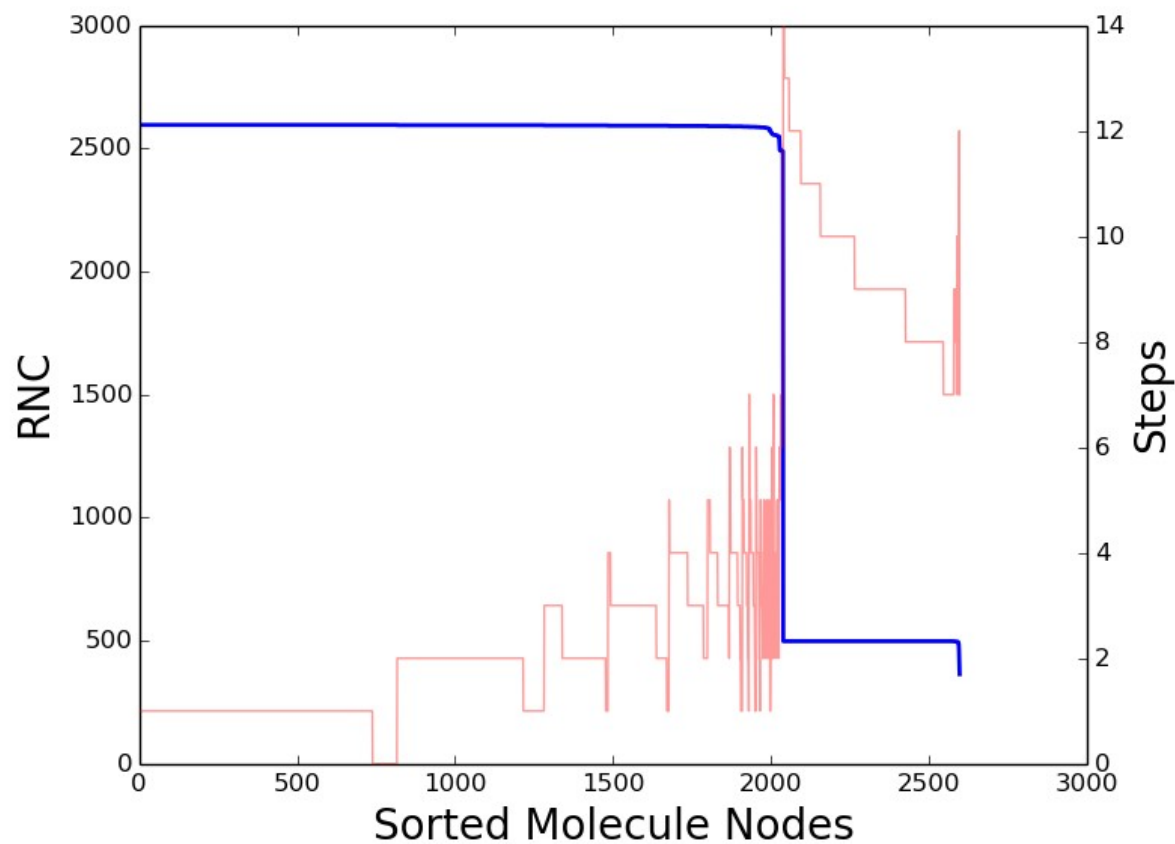
Secondary reactions that involves glycolysis reactants and products:





Does an important node to the network  
structure represent an important molecule  
to the cell?

# Remaining Nodes Count





# Essential Genes Prediction

	Karr's Model	Glass Set	<i>B. subtilis</i> orthologs	Mushegian & Koonin Set	Gil Core Set
<b>Matches</b>	379	261	389	300	375
<b>False Positives</b>	29	20	85	41	71
<b>False Negatives</b>	113	240	51	184	79
<b>Accuracy</b>	85.28%	89.85%	56.85%	79.19%	63.96%

A complex network diagram of the whole-cell network of Mycoplasma genitalium. The network consists of numerous nodes, represented by small colored circles (red, blue, green, and grey), interconnected by a dense web of thin grey lines. The nodes are distributed across the entire slide, with a higher concentration in the upper left and middle sections. Some nodes are labeled with text, such as 'DnaA-ATP 3mer Formation Reaction' and 'DnaA-ATP 2mer Formation Reaction'. The overall structure is highly interconnected, illustrating the scale-free topology of the network.

# Conclusions

- ▶ We found a good way to integrate different cellular processes;
- ▶ The whole-cell network of *Mycoplasma genitalium* have the scale-free topology;
- ▶ We could predict, with only structural information, good accuracy and low computational cost, 197 essential genes to the cell growth and reproduction.

# Acknowledgements

## Advisors:



Dr. Marcos G. Quiles



Dr. Claudia B. L. Camps





Thank you ...

▼ ... for the attention!