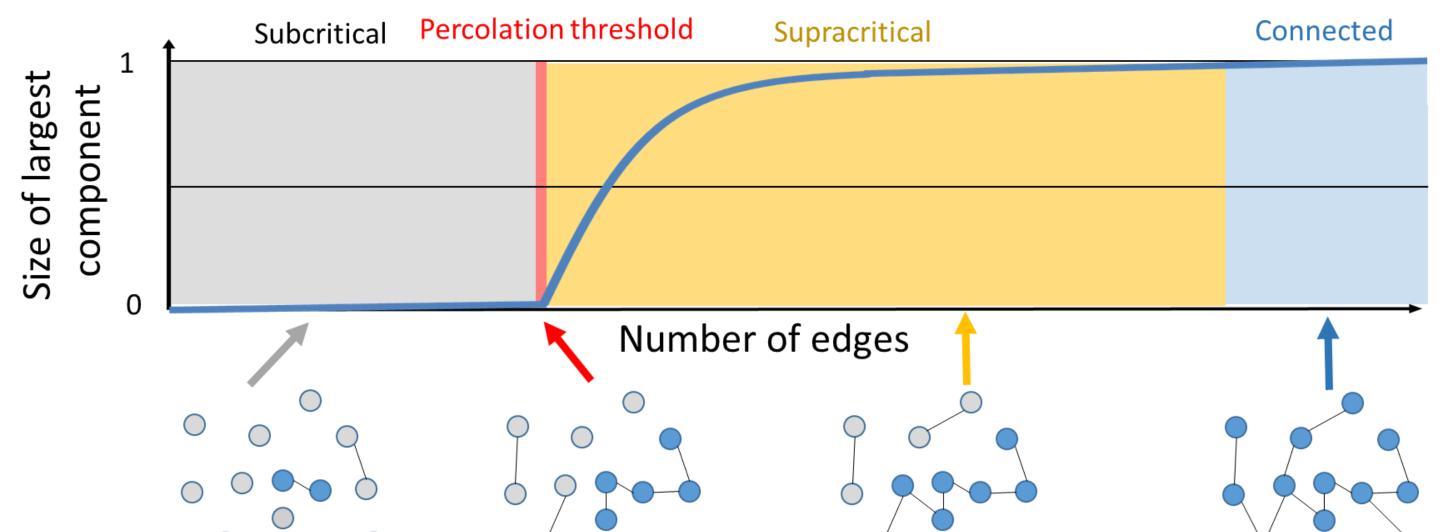
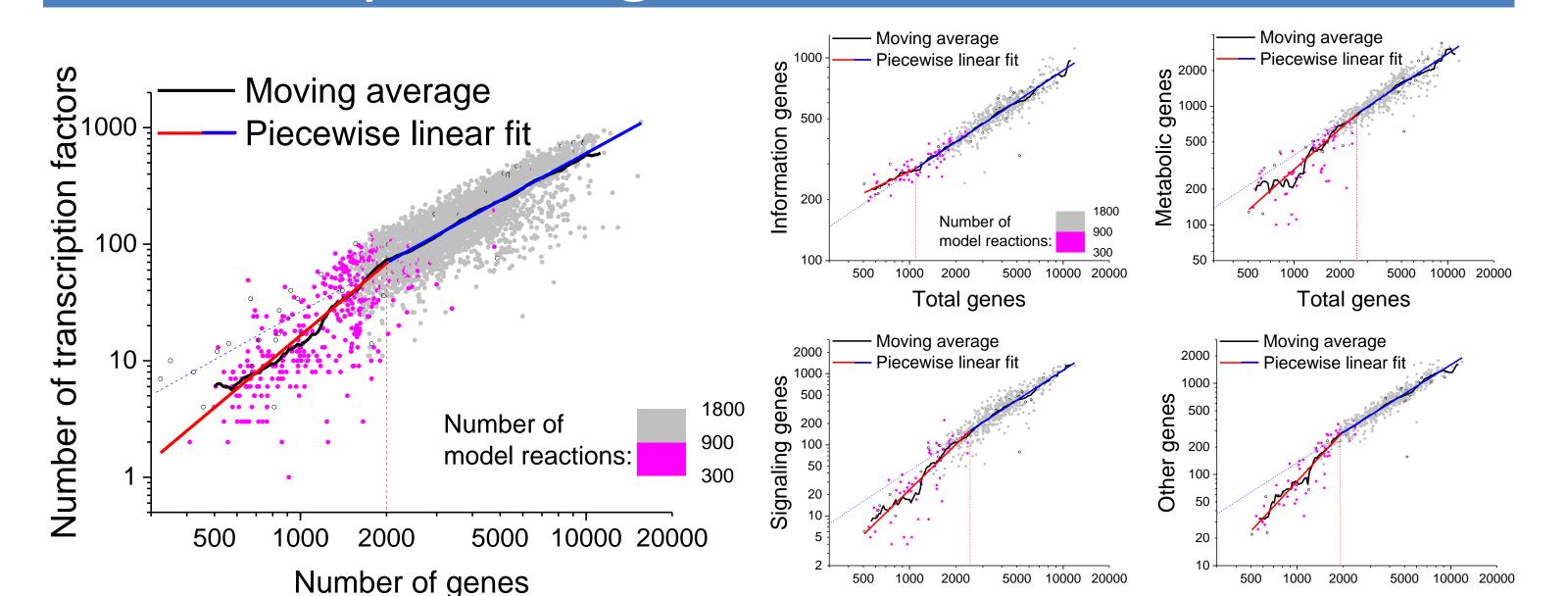


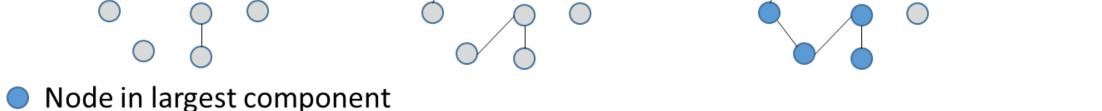
Department of Systems Biology, Columbia University Medical Center, New York, NY 10032, gap2118@cumc.columbia.edu

A percolation process describes the changes in the connectivity of a network as nodes or edges are removed



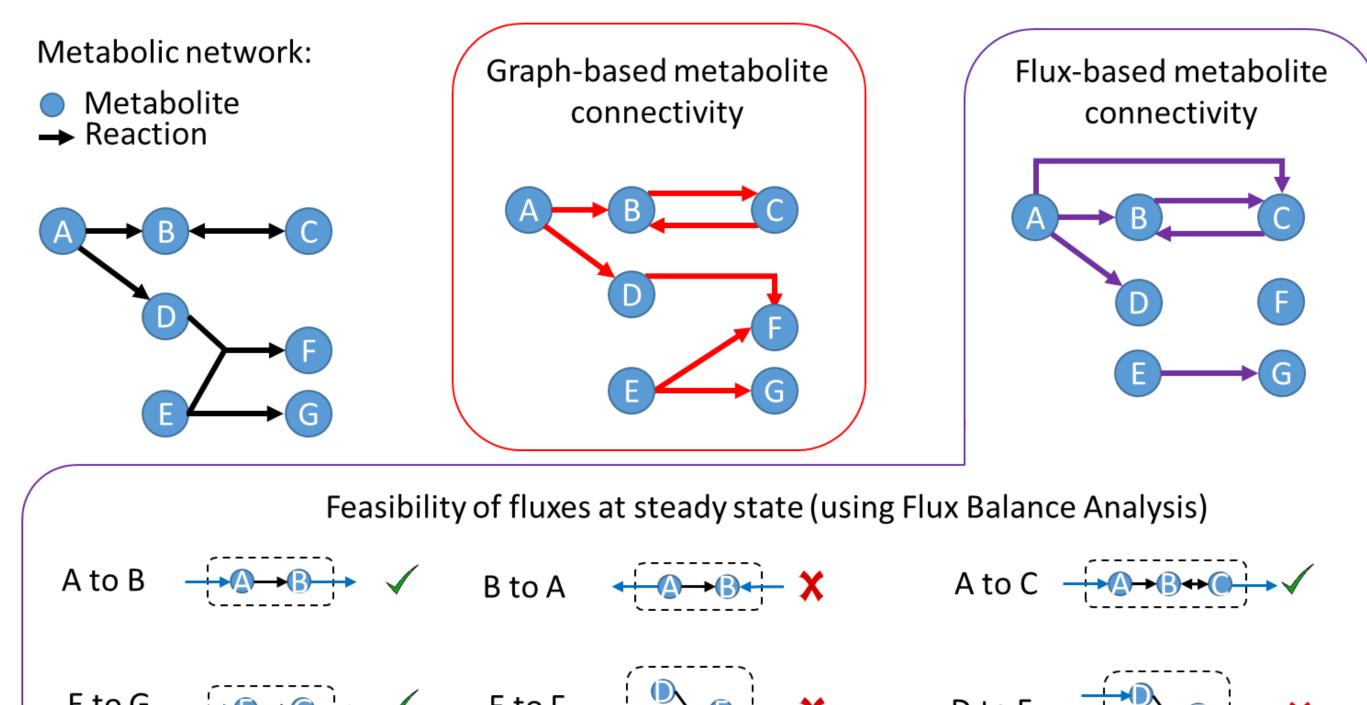
Impact on genome architecture





Can metabolic network diversity across bacteria be seen as a percolation process? If so, what are its consequences for microbial physiology, ecology and evolution?

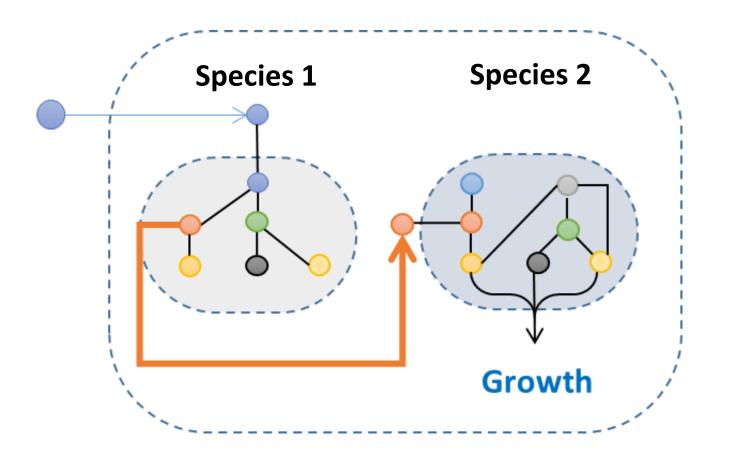
Defining metabolic network connectivity

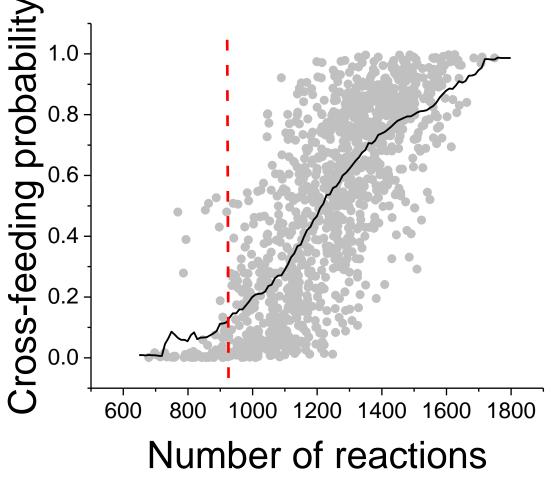


Condition-specific genes are lost more rapidly with decreasing genome size below percolation threshold

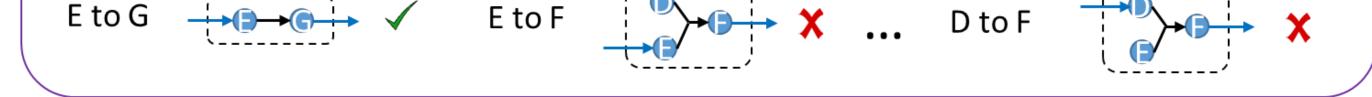
Species interactions and evolvability

How likely is one species to benefit from metabolic byproducts of another?





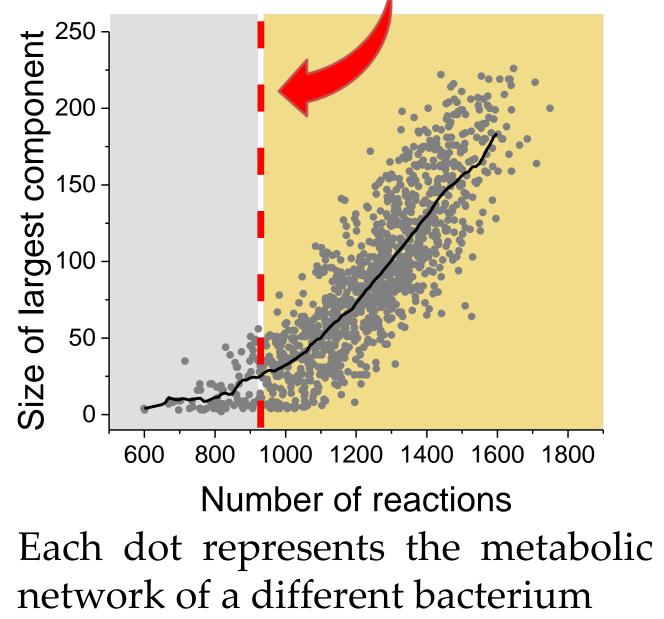
How many additional reactions are needed to grow on a new carbon source? $\begin{bmatrix} 25 \\ 25 \end{bmatrix}$ More evolvable



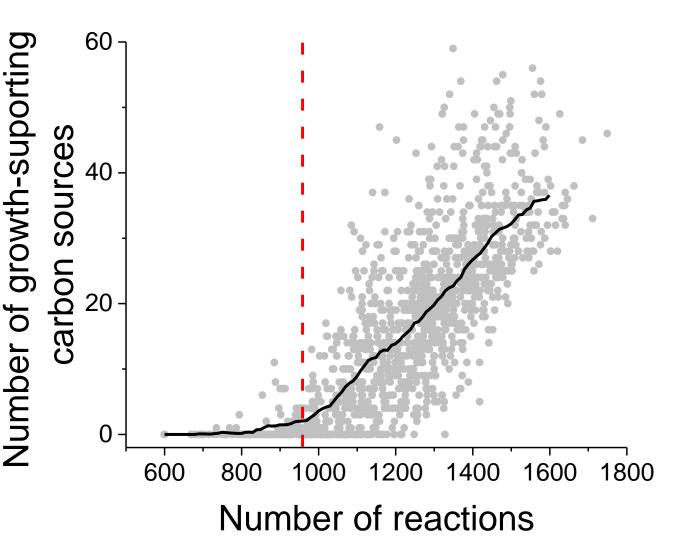
- Metabolic networks were defined based on the ability of mass (carbon) to flow between metabolites (right)
- 1,181 networks were obtained from Kbase, each from a different bacterial genus

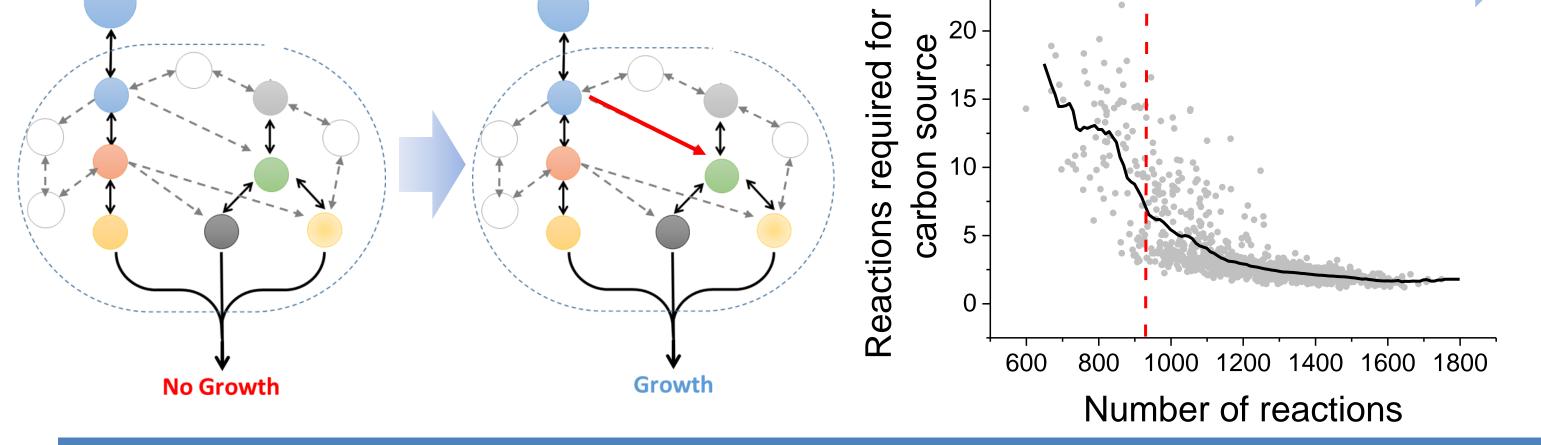
A percolation transition in metabolism

Percolation threshold

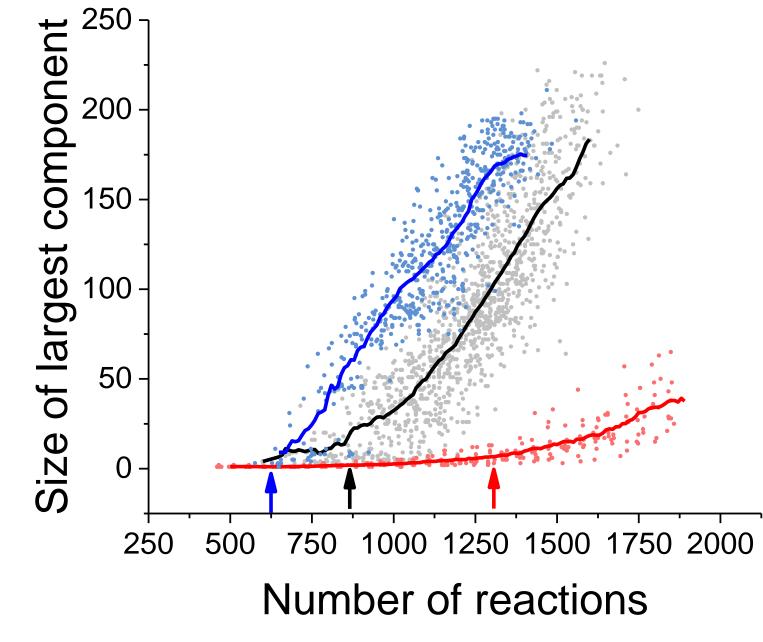


How many carbon sources support growth?





Percolation in random networks



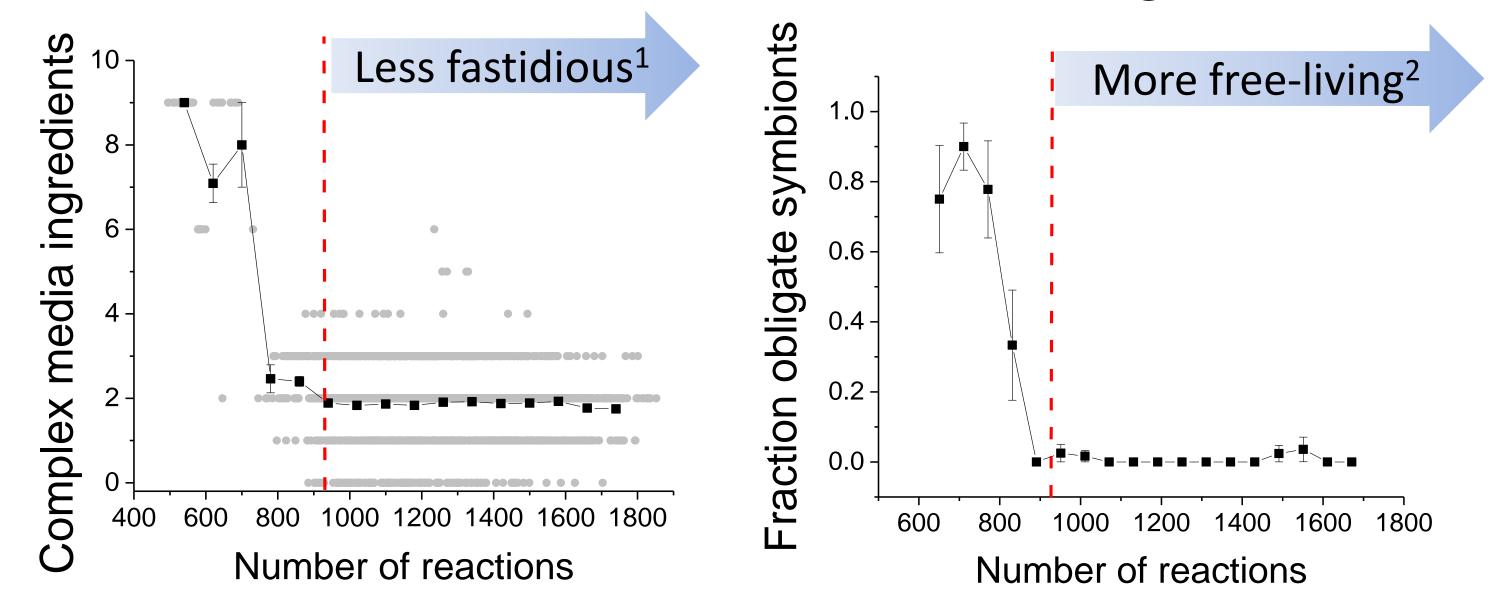
— Random networks, same probability per reaction.

---- Optimal networks, least number of reactions per carbon source supporting growth.

Arrows indicate percolation thresholds

Bacterial evolution avoids metabolic networks that are large and disconnected or small and connected.

Critical threshold at ~900 reactions or ~2,000 genes



Obligate parasitic or symbiotic lifestyles are common below the percolation threshold

^{1.} Known growth media: komodo.modelseed.org^{2.} Lifestyle classification: Burstein et al. 2015. Nat Commun. **6**, 8493

Conclusions

- Differences in the connectivity of bacterial metabolic networks can be described as a percolation process
- Species with less than ~2,000 genes tend to be more fastidious, less easily evolvable, and less likely to cross-feed with a randomly chosen bacterium
- Differences are explained by metabolite interconversions supported by the giant component present in larger metabolic networks

Funding: National Institute of General Medical Sciences GM079759 to DV