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

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**

- 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**

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

**Impact on genome architecture**

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 by-products of another?

How many additional reactions are needed to grow on a new carbon source?

**Percolation in random networks**

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

**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

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**Funding:** National Institute of General Medical Sciences GM079799 to DV