Genetic network complexity: weights matter more than topology

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1. Appropriate level of description?

Can we understand genetic networks like we understand electronic circuits?  
Not every detail matters, but knowing only topology is insufficient.  
Goal: build a toy model where the appropriate level of description can be constructed explicitly. How much do microscopic quantitative details matter?

2. Model: weighted graphs and complexity

Genes: binary variables; interactions have variable strength.  
A gene is activated if its inputs exceed a threshold:  
\[ s_i = \text{sgn}\left( \sum_j J_{ij}s_j + h_i \right) \]  

\textit{Capacity} of a network: number of solutions (= number of cell types it can encode)  
Each node implements a Boolean function from a \textit{finite} set with a \textit{non-arbitrary measure}.  
For a given topology, we can enumerate all of its \textit{non-equivalent and equiprobable} (!) realizations as a weighted graph.

Define \textit{complexity} as the diversity of possible causal relations in the graph.  
Links are satisfied or frustrated. Define an \textit{active} link as a link whose satisfied state is essential for equation (1) to hold. Each solution defines a binary sequence: the pattern of active links. Define diversity of a set of sequences as the length of the shortest path connecting all of them on a hypercube (traveling salesman).

How is complexity affected by the choice of topology vs. the choice of weights?

3. Conclusions: weights matter more

1. Relative importance of weights vs. topology is of order 1.
2. Optimal weights outperform optimal topology (for 85% of topologies with \( N \leq 10 \))
3. Larger networks are not automatically more complex

For an information-processing network:

1. Topology and weights have effects of the same order.
2. High-complexity graphs operate in a non-generic parameter regime.
3. Evolving weights is a better strategy than changing topology / adding nodes

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