A Characterization of n-way Fitness Graphs that Imply n-way Epistasis

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Pathogen populations are not static, but instead sporadically mutate, posing a difficult threat to combat as they evolve to resist antibiotics. Fortunately, we can look to genetics to help predict their evolutionary trajectories. In this project I develop a mathematical test to detect gene interactions that may lead to unexpected evolutionary turns. In particular I focus on fitness graphs, graph theory models of population genetics. Epistasis, gene interactions, plays a role in directing evolutionary trajectories, leading to potentially unexpected evolutionary pathways. The goal of my project was to develop a new characterization of fitness graphs that imply n-way epistasis. By approaching the graphs from a bipartite perspective, I prove the characterization to be not only necessary, but also sufficient via Hall's Marriage Theorem. Afterwards, I apply the characterization to various 4-locus fitness graphs. Results suggest a positive correlation between the presence of higher order epistasis and the number of peaks. These findings hold biological significance because populations with multiple peaks are more likely to end up stuck at a suboptimal peak. A peak is suboptimal if its genotype does not have the greatest fitness of all peaks in the graph.

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