

## **Project Summary**

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My work focuses on examining the architecture of gene expression networks. Understanding these networks is fundamental for the understanding of forces that guide evolution. It has been argued that some chaperone proteins like Hsp90 can buffer certain amount of mutations, preventing them to influence the phenotype in stable environments and releasing them when under environmental stress. This way, they release phenotypic variations when they are mostly needed. My task is to model gene expression networks in more detail taking into account the buffering mechanism and see how different types of chaperone proteins in combination with different topologies influence the evolvability of these networks, where evolvability accounts for the ability of an system to produce evolutionary improvement or adaptation. I will use a model that is an extension of models used by Siegal and Bergman to simulate the effects of gene knock-out and canalization.