# Functional alignment of Regulatory Netowrks: A study of temperate phages

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THE relationship between the design and functionality of molecular networks is now a key issue in biology. Comparison of regulatory networks performing similar tasks can provide insights into how network architecture is constrained by the functions it directs. Here, we discuss methods of network comparison based on network architecture and signaling logic. Introducing local and global signaling scores for the difference between two networks, we quantify similarities between evolutionarily closely and distantly related bacteriophages. Despite the large evolutionary separation between phage λ and 186, their networks are found to be similar when difference is measured in terms of global signaling. We finally discuss how network alignment can be used to pinpoint protein similarities viewed from the network perspective.