

# **From Topological Gene Regulatory Networks to Functional Ones Through Interaction-Weight Analysis**

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For complicated model systems of gene regulatory networks (GRNs) consisting of large numbers of genes and interactions, we propose a method to quantitatively compute the importance of different interactions, namely, the weights of interactions which range from zero (dynamically ineffective) to one (dominant driving). And we are able to draw weight maps for evolutionary GRNs. A surprising as well as very useful property of these weight maps is that the weight distributions are often strongly heterogeneous with most of interactions having weak weights while much less ones having dominantly strong weights. These strongly weighted interactions form simple functional networks, showing clearly network cores and skeletons, which are subnetworks embedded in complicated topological GRNs. Though the numbers of nodes in cores and interactions in skeletons are incomparably smaller than those in the corresponding topological networks, the cores and skeletons determine the dynamics and pattern formations (even the detailed trajectories of nodes) of the original GRNs surprisingly well. From these functional networks the mechanisms underlying the evolutionary dynamics of GRNs can be well understood.