# Quantifying homophily through skewed link functions in Baysian network models: estimating peer influence

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Research has increasingly focused on examining the role of social networks in shaping human behavior, recognizing their significant influence on contemporary interactions. Several studies have highlighted homophily as a major challenge when attempting to accurately estimate peer effects. Traditional methods typically address homophily in social networks using binary link structures. In this work, we aim to enhance existing methodologies by employing a skewed link function, which allows for more effective management of homophily in the measurement of social influence. This study, situated within the framework of latent space modeling, seeks to integrate two distinct processes—social influence and social selection—into a unified Bayesian model. The model incorporates network structure to assess the relationship between latent homophily among network participants and their behaviors, while quantifying social influence effects. These effects are differentiated based on the strength of node connections. We conducted extensive simulations to evaluate the properties of this approach, followed by its application to real-world data to explore how individual networks influence participation in various life behaviors.