

Causal inference in sparse and partially observed large-scale social networks

Keywords: causal inference, social networks, privacy-preserving data, information diffusion, statistical network modelling

Extended Abstract

Introduction The study of social networks holds a central place in the social sciences. Ties between individuals are conduits of social influence that underpin many real-world behaviours: at the level of individuals—like health outcomes [1]—and societies—like political mobilisation [2]. The advent of social media platforms has rendered the role of *online* social networks even more significant in determining *offline* outcomes. It has generated opportunities to collect observational and experimental data on individuals to understand how social contagion spreads across their ties and which causal interventions can enhance their diffusion rates [3]. However, such data is highly sensitive and privacy-invading [4]. Recent availability of aggregated social network data—like Facebook’s Social Connectedness Index (SCI) [5] that provides an aggregate number of Facebook friendships between regions at multiple spatial resolutions—allows us to design a privacy-preserving approach to study interventions on large-scale social networks that are partially observed. Our work provides analytical progress and a statistical framework couched in the language of causal inference to address the challenge of estimating causal effects when social connections *and* outcomes are observed only as aggregated data.

Causal inference with network interference Causal inference typically assumes “no interference” between treated units such that the treatment of one could not affect the outcome of another [6]. However, as described, individuals are embedded in a social network that facilitates treatments to spill over connected individuals and renders this assumption untenable. In this setting, one aims to identify two kinds of average treatment effects: the average direct effect of treatment on an individual, and the average indirect “spillover” effect of a friend’s treatment on the individual. Current approaches to estimate both treatment effects suffer from assuming either that the network is fully observed [7]—which does not hold here—or that the effects are either marginally additive [8, 9] or dependent only on the fraction of treated friends [10]—which neglects the non-linearity of actual diffusion processes on social networks [11].

Empirically motivated exposure model We assume that a randomised treatment of the networked individuals seeds a parameterised diffusion of the treatment over the (partially observed) network grounded in a realistic information spreading process [12]. This process yields probabilities of individuals being “exposed” to the treatment, that we show can be analytically determined using a self-consistent equation when the network is sparse—the number of connections of an individual does not scale with the size of the entire network—which holds well for large-scale social networks. This yields a hierarchical Bayesian model for the outcome of an individual or an *aggregated* set of individuals, conditioned on the partially observed network structure and diffusion parameters. In other words, performing inference using aggregated data on outcomes yields a posterior distribution over the diffusion parameters.

Direct and indirect treatment effects We can conveniently describe both direct and indirect treatment effects in terms of the diffusion parameters, allowing us to further infer a posterior distribution over the treatment effects. We demonstrate our approach using the SCI data [5] and a single simulated intervention on the Facebook network of the entire United Kingdom (UK) where the treatments are assigned, and the outcomes and social connections are observed, only at the aggregate level of sub-national regions; see Figure 1. Our statistical framework is able to infer treatment effects in a completely privacy-preserving manner, at varying levels of treatment saturation, using a single experiment design and the consequently generated data on regionally aggregated outcomes. Our methodology can be especially useful to design public health messaging campaigns for large-scale deployment on online social media platforms, and to estimate their causal impact using only regionally aggregated health outcomes [13].

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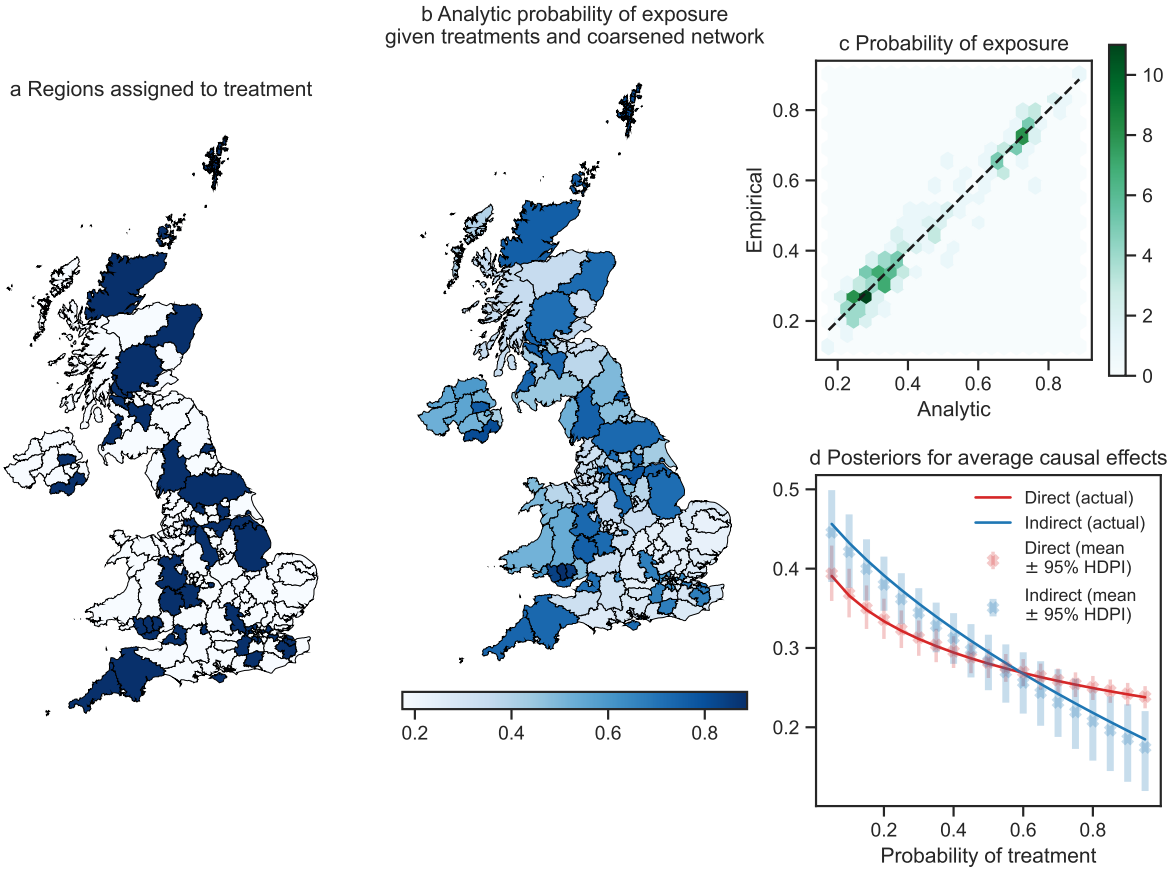


Figure 1: A realistic causal network exposure model permits inference of direct and indirect treatment effects in randomised experiments on large-scale networks using only aggregate data. Regions of the United Kingdom are randomly assigned to a “treatment” (a; see regions in blue) that seeds a diffusion process allowing treatments to spread over the social network yielding (non-zero) probabilities to be exposed to the treatment (b). Given a parameterised diffusion process, the probabilities of being exposed to treatment are analytically solved using a self-consistent equation that agrees well with empirical estimates (c). Bayesian inference of diffusion parameters using only regionally aggregated outcomes after a single experiment permits inference of both direct and indirect “spillover” effects of the treatment on the outcome at varying levels of treatment saturation (d).