

principle can lead to inaccurate predictions, as demonstrated by the SARS outbreak in China [69, 92]. A fundamental problem of these compartmental models is the assumption of random mixing; infected individuals can spread disease to anyone else in the population. In reality we know that individuals have distinct contact patterns of whom they come into contact with.

*Contact network epidemiology* is a more powerful approach to studying disease diffusion that uses social contact networks to model close-proximity interactions which can lead to disease spread. For an outbreak of Severe Acute Respiratory Syndrome (SARS) in China, Meyers et al. [71] showed that contact network epidemiology could explain the inaccurate predictions by compartmental models which suggested a large scale epidemic. Eubank et al. [37] used census, land-use, and population-mobility data, to generate contact networks for the city of Portland, OR. Their experiments on these networks suggest that early detection is key for employing targeted vaccination. To study the spread of mycoplasma pneumoniae, Meyers et al. [70] modeled the contact network of a hospital based on the assumption that patients are confined to wards and disease is spread between wards by HCWs. They conclude that, given a uniform distribution of HCWs to wards, limiting the number of wards visited by a HCW and proper protection from airborne droplets are the best approaches to reducing spread of mycoplasma pneumoniae. Ueno and Masuda [105] simulated stochastic SIR simulations on social contact networks, based on patient records for a 129 bed Tokyo hospital with 500-600 employees, to study disease containment strategies. Under a number of assumptions about the contact patterns of HCWs and patients, they