Causal learning in signaling networks

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Signaling networks are crucial control circuits that determine cellular behavior. Probabilistic graphical models can be used to elucidate signaling regulatory interactions, as was initially demonstrated using single cell proteomics data, a data-rich domain. Despite the large number of available data points in this domain, a number of challenges remain for causal inference pertaining to the representation of distributions, the underlying dynamics of the system, variable noise, and other issues. I will discuss these challenges and some methods to overcome them. I’ll also discuss applications for characterizing networks in health and disease.

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