

Variations of Care Coordination Metrics for Sharing Patients among Physicians: A Social Network Analytic Approach

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ABSTRACT

Social network based analytic approaches have been previously proposed to identify key metrics of care coordination amongst physicians attending to patients in hospitals. Optimizing care coordination is a primary national concern that can yield significant cuts in medical care costs. A recent study identified the metric 'care density', which designates whether patients, whose providers frequently share patients with one another, tend to have lower costs of care and likelihood of hospitalization. However, their proposed formulation of the metric 'care density' for estimating care coordination of patients amongst physicians is not completely accurate.

In this paper, our objective is to compare the accuracy of the previously proposed 'care density', with three novel variations, namely, 'weighted care density', 'time varying care density', and 'time varying weighted care density', in terms of predicting the cost of care. Our proposed metrics are conceptually based on the former care density metric, however, they also takes other variables into consideration, such as patient hospitalization time frame and number of physician visitations for more accurate estimates.

Transcriptional Network growing Models using Motif-based Preferential Attachment

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ABSTRACT

Understanding the underlying architecture of gene regulatory networks (GRNs) has been one of the major goals in systems biology and bioinformatics as it can provide insights in disease dynamics and drug development, among others. Such GRNs are characterized by their scale-free degree distributions and the existence of network motifs, which are small subnetworks that appear more abundantly in GRNs than in

their randomized versions. Such motifs may serve as "building blocks" of complex networks, so there is a great need for null models that preserve characteristics (e.g., distributions, frequencies etc) of these motifs. Here we address this problem by proposing a network growing algorithm, wherein the central idea is to build a model transcriptional network, motif-by-motif, by preferentially attaching a full downlink motif to the substrate with each growth step. The accuracy of this algorithm was evaluated extensively using computer simulation, and shows improved performance over existing network-growth models in terms of degree and motif distributions.