Trans-species learning of cellular signaling systems with bimodal deep belief networks

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Abstract

Motivation

Model organisms play critical roles in biomedical research of human diseases and drug development. An imperative task is to translate information/knowledge acquired from model organisms to human. Here, we aim to predict human cell responses to diverse stimuli, based on the responses of rat cells treated with the same stimuli.

Results

We hypothesized that rat and human cells share a common signal-encoding mechanism but employ different proteins to transmit signals, and we developed a bimodal deep belief network (bDBN) and a semi-restricted bimodal deep belief network (sbDBN) to represent the common encoding mechanism and perform transspecies learning. These "deep learning" models include hierarchically organized latent variables capable of capturing the statistical structures in the observed proteomic data in a distributed fashion. The results show that the models significantly outperform two current state-of-the-art classification algorithms. Our study demonstrated great potential in using deep hierarchical models to simulate cellular signaling systems.

Availability

The software is available at the following URL:

http://pubreview.dbmi.pitt.edu/TransSpeciesDeepLearning/g.

The data are available through SBV IMPROVER website,

https://www.sbvimprover.com/challenge-2/overview, upon publication of the report by the organizers.