

Multilabel Structured Output Learning with Random Spanning Trees of Max-Margin Markov Networks (supplementary material) by: Mario Marchand, Hongyu Su, Emilie Morvant, Juho Rousou, and John Shawe-Taylor

Lemma 1

Let $\hat{\mathbf{w}}_T \stackrel{\text{def}}{=} \mathbf{w}_T / \|\mathbf{w}_T\|$, $\hat{\phi}_T \stackrel{\text{def}}{=} \phi_T / \|\phi_T\|$. Let $\mathcal{U}(G)$ denote the uniform distribution over the set of all spanning trees of G . Then we have

$$F(\mathbf{w}, x, y) = \mathbb{E}_{T \sim \mathcal{U}(G)} a_T \langle \hat{\mathbf{w}}_T, \hat{\phi}_T(x, y) \rangle, \text{ where } a_T$$

$$\mathbb{E}_{T \sim \mathcal{U}(G)} a_T \leq 1$$

$$\frac{1}{\ell^{1/2}} \frac{\ell}{2} \sum_{T \in \mathcal{S}(G)} \mathbb{E}_{T \sim \mathcal{U}(G)} \|\mathbf{w}_T\|$$

Structured Prediction of Network Response

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Abstract

information propagation, opinion formation, adoption of technological innovations, viral marketing, and disease spreading (De Choudhury et al., 2010; Watts & Dodds, 2007).

Influence models typically consider actions of the network nodes. Examples of such actions include a product or (re)posting a news story in a network. Often, network nodes perform actions as a result of influence from neighbouring nodes. A number of different models have been proposed to capture influence in a network, most notably the independent cascade model and the linear-threshold models (Kempe et al., 2003). On the other hand, performing an action may also result in an external (out of the network) effect, a situation that has also been subject to modeling (Anagnostopoulos et al., 2008). A natural question is: can we infer the hidden network structure, and the influence of nodes, from the actions of nodes? In this paper, we study the problem of inferring the hidden network structure, and the influence of nodes, from the actions of nodes. We propose a method for inferring the hidden network structure, and the influence of nodes, from the actions of nodes. Our method is based on the idea of using the actions of nodes to infer the hidden network structure, and the influence of nodes. We show that our method is able to infer the hidden network structure, and the influence of nodes, from the actions of nodes. Our method is based on the idea of using the actions of nodes to infer the hidden network structure, and the influence of nodes. We show that our method is able to infer the hidden network structure, and the influence of nodes, from the actions of nodes.

A central question in the study of network influence is: can we infer the hidden network structure, and the influence of nodes, from the actions of nodes? In this paper, we study the problem of inferring the hidden network structure, and the influence of nodes, from the actions of nodes. We propose a method for inferring the hidden network structure, and the influence of nodes, from the actions of nodes. Our method is based on the idea of using the actions of nodes to infer the hidden network structure, and the influence of nodes. We show that our method is able to infer the hidden network structure, and the influence of nodes, from the actions of nodes. Our method is based on the idea of using the actions of nodes to infer the hidden network structure, and the influence of nodes. We show that our method is able to infer the hidden network structure, and the influence of nodes, from the actions of nodes.

The present paper is motivated by the fact that the influence between two nodes is not only dependent on the nodes themselves, but also depends on the action under consideration. For example, if u and v represent users in a social network, then the influence of u on v may be different depending on the topic of the interaction. In this paper, we study the problem of inferring the hidden network structure, and the influence of nodes, from the actions of nodes. We propose a method for inferring the hidden network structure, and the influence of nodes, from the actions of nodes. Our method is based on the idea of using the actions of nodes to infer the hidden network structure, and the influence of nodes. We show that our method is able to infer the hidden network structure, and the influence of nodes, from the actions of nodes.

Abstract

We show that the usual score function for conditional Markov networks can be written as the expectation over the scores of their spanning trees. We also show that a small random sample of these output trees can attain a significant fraction of the margin obtained by the complete graph and we provide conditions under which we can perform tractable inference. The experimental results confirm that practical learning is scalable to realistic datasets using this approach.

1 Introduction

Finding a hyperplane that minimizes the number of misclassifications is \mathcal{NP} -hard. But the support vector machine (SVM) substitutes the hinge for the discrete loss and, modulo a margin assumption, can nonetheless efficiently find a hyperplane with a guarantee of good generalization. This paper investigates whether the problem of inference over a complete graph in structured output prediction can be avoided in an analogous way based on a margin assumption.

We first show that the score function for the complete output graph can be expressed as the expectation over the scores of random spanning trees. A sampling result then shows that a small random sample of these output trees can attain a significant fraction of the margin obtained by the complete graph. Together with a generalization bound for the sample of trees, this shows that we can obtain good generalization using the average scores of a sample of trees in place of the complete graph. We have thus reduced the intractable inference problem to a convex optimization not dissimilar to a SVM. The key inference problem to enable learning with this ensemble now becomes finding the maximum violator for the (finite sample) average tree score. We then provide the conditions under which the inference problem is tractable. Experimental results confirm this prediction and show that

*Most of this work was carried out while E. Morvant was affiliated with IST Austria, Klosterneuburg.

Multi-task Drug Bioactivity Classification with Graph Labeling Ensembles

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Multilabel Classification through Random Graph Ensembles

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Structured Prediction of Network Response Supplementary Material

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As searching for an optimal configuration of node labels $\{y_e \in \{\text{nn, pn, pp}\}\}_{e \in E}$. For each edge e and its endpoints u, v , we find a set of node labels that maximizes the sum

MAX-CUT problem (Garey & Johnson, 1979), where the graph is partitioned into two parts so that the number of edges between the parts is maximized.

MAX-CUT problem. Given an instance of MAX-CUT, i.e., a graph $G = (V, E)$ and a set of node labels $\{y_e \in \{\text{nn, pn, pp}\}\}_{e \in E}$, the problem is to find a set of node labels $\{y_e \in \{\text{nn, pn, pp}\}\}_{e \in E}$ that maximizes the sum $\sum_{e \in E} s_{\text{nn}}(e) + s_{\text{pn}}(e) + s_{\text{pp}}(e)$. It is not difficult to see that the reduction only shows that the MAX-CUT problem is also optimal to this special case.

Inference algorithm

Algorithm 1. The algorithm starts with an activated set of nodes A and labels $\{y_e \in \{\text{nn, pn, pp}\}\}_{e \in E}$. We show in Eq. 1 that the inference problem enables us to design an efficient algorithm.

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(v_i).

Let $F_m(v)$ and positions in the list (line 6). The

Structured Output Prediction of Anti-cancer Drug Activity

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Abstract. We present a structured output prediction method for anti-cancer drug activity. Our method is based on a Markov network that encodes the similarity between molecules and the similarity between molecules and cancer cell lines in one shot. Statistical dependencies are encoded by a Markov network that represents similarity according to an auxiliary kernel based on molecular fingerprints. We apply the method to separate correct multilabel classification from the multilabel classification of molecules with NCI-Cancer data containing drug-like molecules against 59 cancer cell lines. Our method outperforms the state-of-the-art methods.

1 Introduction

Machine learning has become increasingly important in the search of viable molecular structures for drug discovery. In particular, Quantitative Structure-Activity Relationship (QSAR) models (relating the molecular structures to bioactivity, toxicity, etc.) are routinely built using statistical methods. In particular, the costly pre-clinical experiments can be focused to the most promising candidates that are available [16].

Molecular classification—the task of predicting the bioactivity of interest—has been tackled with inductive logic programming [9] and artificial neural networks [11, 16, 4]. These methods have emerged as a way to handle the non-linear properties of chemical data. However, these methods have obtained promising results only when focusing on a single target variable. In drug screening applications where large numbers of targets are of interest, the task is more challenging.

In this paper we propose, to our knowledge, a new approach for molecular classification. Our method is based on a Markov network that encodes the similarity between molecules and the similarity between molecules and cancer cell lines in one shot. Statistical dependencies are encoded by a Markov network that represents similarity according to an auxiliary kernel based on molecular fingerprints. We apply the method to separate correct multilabel classification from the multilabel classification of molecules with NCI-Cancer data containing drug-like molecules against 59 cancer cell lines. Our method outperforms the state-of-the-art methods.