

# The Conjunctive Disjunctive Graph Node Kernel

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## Abstract

Gene-disease associations are inferred on the basis of similarities between the proteins encoded by genes. Biological relationships used to define similarities range from interacting proteins, proteins that participate in pathways and protein expression profiles. Though graph kernel methods have become a prominent approach for association prediction, most solutions are based on a notion of information diffusion that does not capture the specificity of different network parts. Here we propose a graph kernel method that explicitly models the configuration of each gene's context. An empirical evaluation on several biological databases shows that our proposal achieves state-of-the-art results.

*Keywords:* Graph node kernels, graph decomposition, disease gene prioritization

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## 1. Introduction

Predictive systems for gene-disease associations are often based on a notion of similarity between genes. A common strategy is to encode relations between genes as a network and use graph based techniques to make useful inferences.

5 In the last decades, a number of graph kernel methods have been proposed that directly exploit transitive properties in biological networks. The prototypical method is the Diffusion kernel (DK) [1] inspired by the heat diffusion phenomenon. The key idea is to allow a given amount of *heat* placed on nodes

to *diffuse* through the edges. The similarity between two nodes  $v_i, v_j$  is then  
10 defined as the amount of heat starting from  $v_i$  and reaching  $v_j$  within a given  
time interval. In DK the heat flow is proportional to the number of paths  
connecting two nodes, which introduces an undesired bias that penalize periph-  
eral nodes w.r.t. central ones. This problem is tackled by a modified version  
of DK called Markov exponential diffusion kernel (MED) [2] where a Markov  
15 matrix replaces the Laplacian matrix. Another kernel called Markov diffusion  
kernel (MD) [3], exploits instead the notion of *diffusion distances*, a measure of  
similarity between patterns of heat diffusion. The Regularized Laplacian ker-  
nel (RL) [4] represents instead a normalized version of the random walk with  
restart model and defines the node similarity as the number of paths connecting  
20 two nodes with different lengths. All these approaches can be applied to dense  
networks with high degree nodes. A drawback of these approaches is however  
their relatively low discriminative capacity. This is in part due to the fact that  
information is processed in an additive and independent fashion which prevents  
them from accurately modeling the configuration of each gene’s context. To  
25 address this issue here we propose to employ a *decompositional* graph kernel  
(DGK) [5] technique in which the similarity function between graphs can be  
formed by decomposing each graph into subgraphs and by devising a valid local  
kernel between the subgraphs. To exploit its higher discriminative capacity we  
first decompose the network in a collection of connected sparse graphs and then  
30 we develop a suitable kernel, that we call Conjunctive Disjunctive Node Kernel  
(CDNK).

## 2. Material and methods

We start from the type of similarity notion computed by decomposition  
kernels between graph instances and adapt it to express the similarity between  
35 nodes in a single network. In this work we use three key ideas: 1) genes are  
labeled using their functional profile, 2) we transform the network to distinguish  
highly connected components from sparsely connected ones, and 3) we transform

the neighborhood of each gene in a sparse high dimensional vector that can be easily processed by standard machine learning techniques such as SVMs.

## 40 2.1. Gene Labeling

Gene-disease associations networks typically represent genes as nodes labeled with a gene identifier. Here we take a different approach: we encode the network as a labeled undirected graph where the node labels are built as a discretized functional annotation based on the *gene ontology* [6]. More precisely, we use the  
 45 gene ontology to construct binary vectors representing the bag-of-words encoding for each gene (i.e. if a GO-term is associated with the gene). The resulting representations are then clustered so that genes with similar description profiles receive the same class identifier as label. All subsequent graph processing (including graphs isomorphism detection) takes this discretized labeling into  
 50 account.

## 2.2. Network Decomposition

In gene-disease associations networks it is not uncommon to find nodes with high degrees. Unfortunately these cases cannot be effectively processed by a neighborhood based decomposition kernel since these are based on the notion of  
 55 exact matches and the probability of finding identical neighborhoods decreases exponentially as the degree increases. This means that in a finite network it quickly becomes impossible to find any match and hence learn or generalize at all. As an alternative, we propose to decompose the network in a linked collection of sparse sub-networks where each node has a reduced connectivity. More  
 60 precisely we distinguish two types of edges: *conjunctive* and *disjunctive* edges. Nodes linked by conjunctive edges are going to be used jointly to define the notion of context. Nodes linked by disjunctive edges are instead used to define features based only on the pairwise co-occurrence of the genes at the endpoints. The aim of the following decompositions is to link sparse sub-networks (which  
 65 comprise only conjunctive edges) via disjunctive edges.

*Definitions.* A graph  $G = (V, E)$  is a structure that consists of a node set  $V(G)$  and an edge set  $E(G)$ . The *distance* between two nodes  $u$  and  $v$ , notated as  $\mathcal{D}(u, v)$ , is the length of the shortest path between them. The *neighborhood* with radius  $r$  of a node  $v$  is the set of nodes at a distance no greater than  $r$  from  $v$  and denoted by  $N_r(v)$ . The *neighborhood subgraph* with radius  $r$  of node  $v$ , denoted by  $\mathcal{N}_r^v$ , is the subgraph formed by the nodes in the neighborhood with radius  $r$  of  $v$  and the relative edges with endpoints in  $N_r(v)$ .

*Iterative k-core decomposition* [7]: The node set is partitioned in two groups on the basis of the degree of each node w.r.t. a threshold degree  $D$ . The node partition is used to induce the conjunctive vs disjunctive edge partition: edges that have endpoints in the same part are marked as conjunctive, while edges with endpoints in different parts are marked as disjunctive. We apply the k-core decomposition iteratively considering only the graph induced by the conjunctive edges until no node has a degree <sup>1</sup> greater than  $D$ .

*Clique decomposition* [8]: To model the notion that nodes in a clique are tightly related, we summarize the whole clique with a new 'representative' node. All the cliques (completely connected subgraphs) with a number of nodes greater than a threshold size  $C$  are identified. The endpoints of all edges incident on the clique's nodes are transferred to the representative node. Disjunctive edges are introduced to connect each node in the clique to the representative. Finally all edges with both endpoints in the clique are removed.

In our work a network is transformed by applying first the iterative k-core decomposition and then the clique decomposition.

### 2.3. Node Graph Kernels

We start from the Neighborhood Subgraph Pairwise Distance Kernel (NSPDK) [9] and adapt it to express the similarity between nodes in a single network. The key idea in NSPDK is to decompose graphs in small fragments and count how many pairs of fragments are shared between two instances. We introduce

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<sup>1</sup>The degree is defined by only considering incident conjunctive edges.

two improvements: 1) we partition the features according to the individual  
 95 node's neighborhood, and 2) we introduce a distinction between "disjunctive"  
 and "conjunctive" edges.

### 2.3.1. The Neighborhood Subgraph Pairwise Distance Kernel

The NSPDK is an instance of convolution kernel [5] where given a graph  
 $G \in \mathcal{G}$  and two rooted graphs  $A_u, B_v$ , the relation  $R_{r,d}(A_u, B_v, G)$  is true iff  
 100  $A_u \cong \mathcal{N}_r^u$  is (up to isomorphism  $\cong$ ) a neighborhood subgraph of radius  $r$  of  $G$   
 and so is  $B_v \cong \mathcal{N}_r^v$ , with roots at distance  $\mathcal{D}(u, v) = d$ . We denote  $R^{-1}$  as the  
 inverse relation that returns all pairs of neighborhoods of radius  $r$  at distance  $d$   
 in  $G$ ,  $R_{r,d}^{-1}(G) = \{A_u, B_v | R_{r,d}(A_u, B_v, G) = \text{true}\}$ . The kernel  $\kappa_{r,d}$  over  $\mathcal{G} \times \mathcal{G}$ ,  
 counts the number of such fragments in common in two input graphs:

$$105 \quad \kappa_{r,d}(G, G') = \sum_{\substack{A_u, B_v \in R_{r,d}^{-1}(G) \\ A'_{u'}, B'_{v'} \in R_{r,d}^{-1}(G')}} \mathbf{1}_{A_u \cong A'_{u'}} \cdot \mathbf{1}_{B_v \cong B'_{v'}},$$

where  $\mathbf{1}_{A \cong B}$  is the *exact matching function* that returns 1 if  $A$  is isomorphic to  $B$   
 and 0 otherwise. Finally, the NSPDK is defined as  $K(G, G') = \sum_r \sum_d \kappa_{r,d}(G, G')$ ,  
 where for efficiency reasons, the values of  $r$  and  $d$  are upper bounded to a given  
 maximal  $r^*$  and  $d^*$ , respectively.

### 110 2.3.2. The Conjunctive Disjunctive Node Kernel

We extend NSPDK and define a node kernel  $K(G_u, G_{u'})$  between two copies  
 of the same network  $G$  where we distinguish the nodes  $u$  and  $u'$  respectively.  
 The idea is to define the features of a node  $u$  as the subset of NSPDK features  
 that always have the node  $u$  as one of the roots. In addition we distinguish  
 115 between two types of edges, called *conjunctive* and *disjunctive* edges. When  
 computing distances to induce neighborhood subgraphs, only conjunctive edges  
 are considered. When choosing the pair of neighborhoods to form a single  
 feature, we additionally consider roots  $u$  and  $v$  that are not at distance  $d$  but  
 such that  $u$  is connected to  $w$  via a disjunctive edge and such that  $w$  is at  
 120 distance  $d$  from  $v$ . In this way disjunctive edges can still allow an *information*

flow even if their endpoints are only considered in a pairwise fashion and not jointly.

Formally, we define two relations: the *conjunctive relation*  $R_{r,d}^\wedge(A_u, B_v, G_u)$  identical to the NSPDK relation  $R_{r,d}(A_u, B_v, G)$ , and (ii)  $\mathcal{D}(u, v) = d$ ; the  
125 *disjunctive relation*  $R_{r,d}^\vee(A_u, B_v, G_u)$  is true iff (i)  $A_u \cong \mathcal{N}_r^u$  and  $B_v \cong \mathcal{N}_r^u$  are true, (ii)  $\exists w$  s.t.  $\mathcal{D}(w, v) = d$ , and (iii)  $(u, w)$  is a disjunctive edge. We define  $\kappa_{r,d}$  on the inverse relations  $R_{r,d}^{\wedge^{-1}}$  and  $R_{r,d}^{\vee^{-1}}$

$$\kappa_{r,d}(G_u, G_{u'}) = \sum_{\substack{A_u, B_v \in R_{r,d}^{\wedge^{-1}}(G_u) \\ A'_{u'}, B'_{v'} \in R_{r,d}^{\wedge^{-1}}(G_{u'})}} \mathbf{1}_{A_u \cong A'_{u'}} \cdot \mathbf{1}_{B_v \cong B'_{v'}} + \sum_{\substack{A_u, B_v \in R_{r,d}^{\vee^{-1}}(G_u) \\ A'_{u'}, B'_{v'} \in R_{r,d}^{\vee^{-1}}(G_{u'})}} \mathbf{1}_{A_u \cong A'_{u'}} \cdot \mathbf{1}_{B_v \cong B'_{v'}}.$$

The CDNK is finally defined as  $K(G_u, G_v) = \sum_r \sum_d \kappa_{r,d}(G_u, G_v)$ , where once  
130 again for efficiency reasons, the values of  $r$  and  $d$  are upper bounded to a given maximal  $r^*$  and  $d^*$ .

### 3. Experimental

We perform an empirical evaluation of the predictive performance of several kernel based methods on two of the databases used in [2].

135 **BioGPS:** A gene co-expression network is constructed from BioGPS dataset, which contains 79 tissues, measured with the Affymetrix U133A array. Edges are inserted when the pairwise Pearson correlation coefficient (PCC) between genes is larger than 0.5.

**Pathways:** Pathway information is retrieved from KEGG, Reactome, Phar-  
140 mGKB and the Pathway Interaction Database. If a couple of proteins co-participate in any pathway, the two corresponding genes are linked.

To evaluate the performance of graph node kernels we analyze the *gene prioritization*, i.e. given a set of genes known to be associated to a given disease, gene prioritization is the task to rank the candidate genes based on their prob-  
145 abilities to be related to that disease. Similar to the evaluation process used in [2], we choose 12 diseases [10] with at least 30 confirmed genes. For each disease, we construct a positive set  $\mathcal{P}$  with all confirmed disease genes, and a negative set  $\mathcal{N}$  which contains random genes associated at least to one disease

class which is not related to the class that is defining the positive set. In [2]  
150 the ratio between the dataset sizes is chosen as  $|\mathcal{N}| = \frac{1}{2}|\mathcal{P}|$ . The predictive  
performance of each method is evaluated via a leave-one-out cross validation:  
one gene is kept out in turn and the rest are used to train an SVM model. We  
compute a decision score  $q_i$  for the test gene  $g_i$  as the top percentage value of  
score  $s_i$  among all candidate gene scores. We collect all decision scores for every  
155 gene in the training set to form a global decision score list on which we compute  
the AUC ROC.

**Model Selection:** The hyper parameters of the various methods are set  
using a k-fold on a dataset set that is then never used in the predictive perfor-  
mance estimate. We try the values for diffusion parameter in DK and MED in  
160  $\{10^{-3}, 10^{-2}, 10^{-1}\}$ , time steps in MD in  $\{1, 10, 100\}$  and RL parameter in  
 $\{1, 4, 7\}$ . For CDNK, we try for the degree threshold values in  $\{10, 15, 20\}$ ,  
clique size threshold in  $\{4, 5\}$ , maximum radius in  $\{1, 2\}$ , maximum distance  
in  $\{2, 3, 4\}$ . Finally, the regularization trade off parameter  $C$  for the SVM is  
searched in  $\{10^{-5}, 10^{-4}, 10^{-3}, 10^{-2}, 10^{-1}, 1, 10, 10^2\}$ .

## 165 4. Results and discussion

Table 1 and 2 show the AUC performance of the models trained by using  
different graph node kernels on 11 gene-disease association problems using the  
BioGPS and Pathways datasets to materialize the gene relation network. We  
note that CDNK ranks first in 7 out of 11 cases using both networks. CDNK  
170 is the top performant kernel also when considering the average AUC ROC and  
the average rank with 73.3/2.0, 76.5/1.8, with a difference w.r.t. the second  
best of 5.5% and 1% on BioGPS and Pathways, respectively. MED and RL  
show similar and moderate results with small gap between them. DK and MD  
exhibit modest performance on average and are ranked last in many cases: 7  
175 times out of 11 for MD in BioGPS and 10 out of 11 for DK in Pathways. Low  
performance cases include networks that have high *average* node degree which  
is likely to yield very sparse and fragmented network decompositions.

	<b>BioGPS</b>							
Disease	DK	MD	MED	RL	CDNK1	CDNK2	CDNK3	CDNK4
1	51.9/8	57.4/7	59.0/6	59.2/5	65.1/4	69.5/2	69.3/3	<b>70.3/1</b>
2	81.7/5	78.5/6	75.2/7	75.0/8	88.3/2	<b>88.8/1</b>	85.1/4	86.8/3
3	64.3/7	59.6/8	71.6/3	71.8/2	65.5/5	<b>72.5/1</b>	64.7/6	66.4/4
4	65.3/7	58.2/8	67.8/6	67.8/5	71.9/4	<b>78.7/1</b>	73.9/3	77.0/2
5	64.0/8	64.1/7	66.5/5	66.2/6	75.9/4	76.2/3	76.9/2	<b>77.4/1</b>
6	74.6/5	70.2/8	71.0/7	71.2/6	79.3/2	<b>83.7/1</b>	76.7/4	79.0/3
7	73.0/5	66.7/8	75.4/3	75.6/2	68.8/6	73.9/4	67.3/7	<b>76.9/1</b>
8	74.4/8	76.8/3	76.2/5	76.4/4	74.7/7	<b>77.7/1</b>	76.0/6	76.8/2
9	71.5/2	65.6/8	67.7/5	69.9/3	66.8/7	<b>71.7/1</b>	67.1/6	68.1/4
10	54.0/6	50.3/8	56.1/5	51.1/7	77.6/4	<b>82.7/1</b>	80.5/2	80.0/3
11	58.2/7	51.3/8	59.3/6	59.3/5	71.8/4	<b>80.2/1</b>	75.3/3	77.1/2
$\overline{AUC}$	66.6	63.5	67.8	67.6	73.2	<b>77.8</b>	73.9	76.0
$\overline{Rank}$	6.18	7.18	5.27	4.82	4.45	<b>1.55</b>	4.18	2.36

Table 1: *Predictive performance on 11 gene-disease associations in percentage using network induced by the BioGPS. Best results are in bold. We report the AUC ROC and the rank for each kernel method in which CDNK1 uses ontology for discrete labels, CDNK2 uses ontology for both discrete and continuous labels, CDNK3 uses node degree for discrete labels and CDNK4 uses degree and ontology for both discrete and continuous labels, respectively.*



	Pathways							
Disease	DK	MD	MED	RL	CDNK1	CDNK2	CDNK3	CDNK4
1	74.7/8	76.4/7	78.7/6	78.8/5	80.2/3	<b>82.4/1</b>	80.6/2	79.4/4
2	55.1/8	64.9/7	76.6/6	76.6/5	81.1/2	80.3/3	79.8/4	<b>82.2/1</b>
3	55.0/8	62.7/7	64.1/5	65.6/4	67.1/3	63.6/6	68.5/2	<b>71.5/1</b>
4	54.3/8	65.2/7	<b>73.7/1</b>	73.7/2	66.1/5	68.1/3	67.5/4	65.6/6
5	52.9/8	55.7/7	62.7/5	62.7/6	68.3/2	<b>69.6/1</b>	66.3/4	66.8/3
6	83.4/8	92.7/7	96.5/2	<b>96.5/1</b>	93.0/6	94.1/5	94.4/4	95.5/3
7	84.5/8	88.3/7	89.4/3	89.5/2	88.5/6	88.5/5	88.7/4	<b>90.5/1</b>
8	53.7/8	65.6/7	72.0/6	72.3/5	72.5/3	72.5/2	72.3/4	<b>76.5/1</b>
9	52.5/8	64.9/5	64.2/7	64.2/6	<b>81.3/1</b>	81.0/2	79.6/3	78.8/4
10	68.8/6	65.4/8	74.4/5	74.4/4	66.9/7	76.8/2	76.1/3	<b>79.5/1</b>
11	53.7/8	69.2/7	74.6/5	74.1/6	77.0/2	<b>78.7/1</b>	75.4/4	77.0/3
$\overline{AUC}$	62.6	70.1	75.2	75.3	76.5	77.8	77.2	<b>78.5</b>
$\overline{Rank}$	7.82	6.91	4.64	4.18	3.64	2.82	3.45	<b>2.55</b>

Table 2: *Predictive performance on 11 gene-disease associations in percentage using network induced by the Pathways. Best results are in bold. We report the AUC ROC and the rank for each kernel method in which CDNK1 uses ontology for discrete labels, CDNK2 uses ontology for both discrete and continuous labels, CDNK3 uses node degree for discrete labels and CDNK4 uses degree and ontology for discrete and continuous labels, respectively.*

## 5. Conclusions

We have shown how decomposing a network in a set of connected sparse  
180 graphs allows us to take advantage of the discriminative power of CDNK, a  
novel decomposition kernel, to achieve state-of-the-art results. In future work  
we will investigate how to 1) decompose networks in a data driven way and  
2) extend the CDNK approach to gene-disease association problems exploiting  
multiple heterogeneous information sources.

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