KDD CUP 2001
Task 3 Localization

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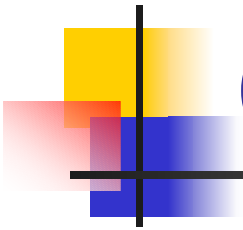


Overview

Task

- Predict the localization of a given gene in a cell among 15 distinct positions

Data

- Relation table with six categorical attributes
  Essential, Class, Complex, Phenotype, Motif, Chromosome Number
- Interaction matrix listing all the interactions between genes

Challenges

- How to use interactions ?
- How to deal with missing values ?

Characteristic of Dataset

•*Class, Complex, Motif*, and *Interaction* are highly correlated with localization (evaluated by entropy).

• Each attribute however has many missing values.
70% of Class, 50% of Complex, 50% of Motif

• Four attributes together complement each other to fill missing values.
Only 14 among 381 test records are isolated.

The Winning Approach

Examined three approaches:

- Decision tree with correlated association rules
- Boosting correlated association rules
- Nearest neighbor strategy

Nearest neighbor worked best
against the training dataset.

The crux was the definition of “neighborhood.”

Definition of Neighborhood

Two records *agree on* an attribute *A* iff

A's values of both records are defined and equal.

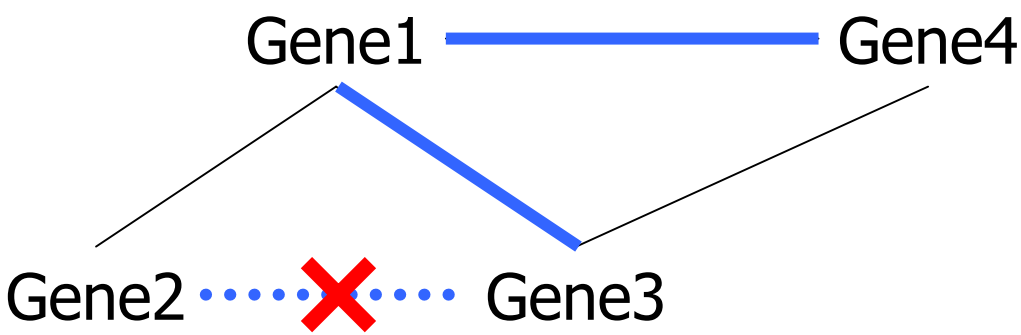
Example of the Relational Table

	Complex	Class	Motif
Gene 1	Translocon	actins	?
Gene 2	?	actins	?
Gene 3	Translocon	?	PS00012
Gene 4	Translocon	?	?

Definition of Neighborhood – Cont'd

Two records *agree on* the interaction matrix iff these records are interacted.

Example of the Interaction Matrix



Definition of Neighborhood – Cont'd

X : a test gene *Y* : a training gene

If *X* and *Y* agree on attribute *A* ,
associate the positive weight of the agreement w_A to *A*.
Otherwise, $w_A = 0$.

Y is a nearest neighbor of X if Y maximizes the sum of weights;

$$w_{\text{Class}} + w_{\text{Complex}} + w_{\text{Motif}} + w_{\text{Interaction}}$$

When X and Y agree on all the attributes,

$$w_{\text{Complex}} >> w_{\text{Class}} >> w_{\text{Motif}} >> w_{\text{Interaction}}$$

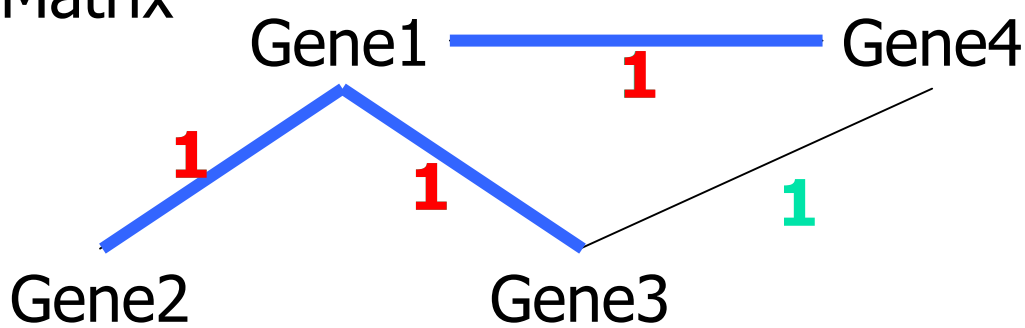
(ex. 1000 >> 100 >> 10 >> 1)

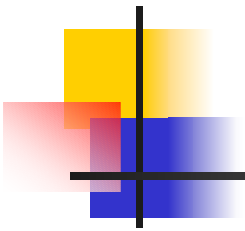
Nearest Neighbors - Example

The Relational Table

W_A		Complex **1000**	Class **100**	Motif **10**	Sum of Weight
Test	Gene 1	Translocon	actins	?	
Training	Gene 2	?	actins	?	**101**
Training	Gene 3	Translocon	?	PS00012	**1001**
Training	Gene 4	Translocon	?	?	**1001**

The Interaction Matrix





Prediction

1. Given a test gene *X*.

2. Predict the localization of *X*
   by a majority vote
   among the nearest neighbors of *X*.

Conclusion

- Data mining machinery automatically selects biologically meaningful four attributes.

- The step of handling missing values was most elaborated and time-consuming.