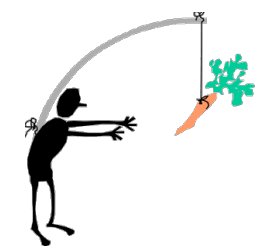


# Multivariate Conditional Anomaly Detection and Its Clinical Application

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## Introduction

### Motivation from the clinical domain [James '13]

- Preventable Medical errors are estimated to be approx. 210k-440k patients/year
- This is the third leading causes of death in America

### Motivation from existing computer-based decision supporting systems

#### (1) Knowledge-driven approach

- A number of solutions exist; primarily built by **medical/clinical experts**
- These solutions are usually very **expensive** and their **coverage is rather incomplete**
- e.g. A Bayesian network for liver disorder diagnosis [Onisko et al. '99]

#### (2) Data-driven approach\*

- Medical errors can be thought as **statistical anomalies** based on past clinical data stored in electronic medical record (EMR) systems
- Cases requiring medical attention for reconsideration could be identified by detecting anomalies in patient care patterns



## Approach

### Phase 1: Multi-dimensional Data Modeling of Clinical Records

#### Objective:

- Model a **conditional joint distribution**  $P(y|x)$  of clinical actions  $y = \{y_1, \dots, y_d\}$  (output) given patient condition  $x = \{x_1, \dots, x_m\}$  (input)
- Learn a function that assigns to each patient condition  $x$ , the **most probable (MAP; maximum a posteriori)** assignment of the clinical actions  $y$

#### Challenge: The number of all possible class assignments is exponential in $d = |Y|$

#### Solutions (\* indicates our contributions)

Model	Binary Relevance (BR) [Boutell et al. '04]	Conditional Tree-structured Bayesian Networks (CTBN) [Batal et al. '13] *	Classifier Chains (CC) [Read et al. '09]
Graphical Representation (e.g., $d = 4$ )			
Mathematical Representation	$\pi(Y_i) = \{\}$	$P(\mathbf{Y} \mathbf{X}) = \prod_{i=1}^d P(Y_i \mathbf{X}, \pi(Y_i))$ $\pi(Y_i) = \text{at most one parent label (tree)}$	$\pi(Y_i) = \text{all preceding labels (chain)}$
Strength	Structure learning is not required (fast)	Optimal tree structures are learned efficiently Exact MAP inference can be performed in a linear time (Max-sum)	Theoretically, CC does not lose any class dependency ( $\therefore$ chain rule)
Weakness	BR disregards all the class dependencies It is a simple collection of marginal models	The dependency can be learned to a tree structure	Learning the optimal structure is NP-hard Exact MAP inference is NP-hard A greedy approx. is used

Mixture	Mixtures-of-CTBNs (MC) [Hong et al. '14] *	Multi-label Mixtures-of-Experts (MLME) [Hong et al. '15] *
Graphical Representation (e.g., $d = 4$ )		
Mathematical Representation	$P(y x) = \sum_{k=1}^K \lambda_k \prod_{i=1}^d P(y_i x, \pi(y_i, T_k))$ $\lambda_k$ : (fixed) weight of the $k$ -th model	$P(y x) = \sum_{k=1}^K g_k(x) \prod_{i=1}^d P(y_i x, \pi(y_i, M_k))$ $g_k(x)$ : weight of the $k$ -th model given $x$
Strength	Can have multiple dependency structures	Can take any of BR, CTBN, CC as the base structures
Weakness	Only permits CTBNs as the base structures	Computationally more demanding Requires to learn the gating function along with the $k$ models

### Why are the marginal models not enough?

Given the joint probability table below, find the most probable assignment (MAP; maximum a posteriori) of  $\mathbf{Y} = (Y_1, Y_2)$

$P(Y_1, Y_2   \mathbf{X} = \mathbf{x})$	$Y_1 = 0$	$Y_1 = 1$	$P(Y_2   \mathbf{X} = \mathbf{x})$
$Y_2 = 0$	0.2	<b>0.45</b>	<b>0.65</b>
$Y_2 = 1$	0.35	0	0.35
$P(Y_1   \mathbf{X} = \mathbf{x})$	<b>0.55</b>	0.45	

→ Prediction on the joint (MAP):  $Y_1 = 1, Y_2 = 0$

→ Prediction on the marginals:  $Y_1 = 0, Y_2 = 0$

### Phase 2: Estimating Anomaly Scores

#### Objective

- Given a trained model and unseen test data, precisely measure the degree of anomaly based on the **conformity between the model and test data**
- MDC models transform the data into probabilistic estimations
- Proper **estimation of anomaly score** on these probabilities will let us correctly identify the anomalous clinical actions
- Caveat:** Blindly picking the minimum probability will not satisfy our needs; E.g., prescriptions with alternative drugs

#### Solutions

	Quantities Involved in Scoring	Scoring Scheme
Univariate Approach	$P(y x)$	The complementary probability $Score_1 = 1 - P(y x)$ Rank percentile of the probability $Score_2 = \text{Rank}[P(y x)] / N_{\text{test}}$
Multivariate Approach	$P(y_i x)$ ** We denote $\phi = \{P(y_i x) : i=1, \dots, d\}$	Robust Mahalanobis Distance [Rousseeuw and Zomeren '90] $Score_3 = rd(P(y_i x) : i=1, \dots, d) = (\phi - \mu)' M^{-1} (\phi - \mu)$ $M$ : minimum covariance determinant (MCD) $\mu$ : mean of $\phi = \{P(y_i x) : i=1, \dots, d\}$ over test data $L_x$ norms ( $L_1, L_2, L_{\text{max}}$ ) $Score_4 = \ 1 - \phi\ _1$ $Score_5 = \ 1 - \phi\ _2$ $Score_6 = \ 1 - \phi\ _{\text{max}}$
Multivariate Conditional Approach	$P(y_i x), x$	One-class SVM [Schölkopf et al. '99] Support Vector Data Description [Tax and Duin '04]

- Using these schemes as basic building blocks, we are working on new anomaly scoring techniques



## Experimental results

### Data: Progress notes obtained from Cincinnati Children's Hospital Medical Center [Pestian et al. '07]

- 978 Instances (patients)
- X: 1,449 features; Freehand notes in the bag-of-words representation
- Y: 45 binary classes; Indicating the diseases diagnosed

### Compared methods:

- Modified Classifier Chain + Robust Mahalanobis (CC.mod+RDist)
  - Conditional Tree BN + Robust Mahalanobis (CTBN+RDist)
  - Binary relevance + complementary probability (BR+comP)
- 10-fold cross validation; On each round, **15%** of randomly selected test data are **perturbed** (anomalies) by **flipping 1-5 class labels**
  - Anomalies represent mistaken diagnoses
  - Metric:** Area under an ROC curve (AUC)

