

Predicting Disease Complications Using a Stepwise Hidden Variable Approach For Learning Dynamic Bayesian Networks



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Type 2 Diabetes

high blood sugar

what people don't see

blindness blurred vision boils cataracts depression erectile dysfunction foot ulcers frequent urination glaucoma intense fatigue intense hunger intense thirst itchiness kidney disease numbness pain sexual dysfunction skin infections

what people see

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- Motivation
- Data
- Problem
- □ Solution
- Dynamic Bayesian Networks (DBNs)
- Hidden variable discovery approach
 - Pair sampling and Stepwise approach procedure
- Conclusions and future works

Type 2 Diabetes Mellitus (T2DM)



Mortality due to diabetes age 20-79 in 2017 (in millions)





The Data at Maugeri, Pavia:

- Type 2 Diabetes Mellitus (T2DM)
- Patients aged 25 to 65 years.
- 2009 and 2013.
- IRCCS Istituti Clinici Scientifici Maugeri of Pavia, Italy.
- MOSAIC project funded by the European Commission.
- T2DM risk factors:
- Physical examination
- Laboratory data
- MATLAB and Bayes Net toolbox (murphy,2001) Visualization we used Graphviz.

Diabetes is a lifelong condition associated with serious complications



T2DM Data

Visit NO	Patient ID	HbA1c	Retinopathy	Neuropathy	Nephropathy	Liver disease	Hypertension	BMI	Creatinine	Cholestrol	HDL	DBP	SBP	SMK
1	885	0.769	0	0	С) 0	1	0.286	-0.391	2.082	0.020	1.705	0.286	1.335
2	885	0.769	0	0	C) 1	1	0.286	-0.391	2.082	0.020	1.705	0.286	1.335
3	885	0.769	1	0	C) 1	1	0.286	-0.391	2.082	0.020	1.705	0.286	1.335
4	885	0.769	1	0	1	. 1	1	0.286	-0.391	2.082	0.020	1.705	0.286	1.335
1	894	0.151	0	0	1	. 1	1	2.782	-0.511	-0.149	-0.053	0.297	0.286	1.335
2	894	0.151	0	0	1	1	1	2.782	-0.511	-0.149	-0.053	0.297	0.286	1.335
3	894	0.151	0	0	1	1	1	2.782	-0.511	-0.149	-0.053	0.297	0.286	1.335
4	894	-0.056	0	0	1	. 1	1	2.937	-0.511	-0.017	-0.343	0.297	0.794	1.335
5	894	-0.056	0	0	1	. 1	1	2.937	-0.511	-0.017	-0.343	0.297	0.794	1.335
6	894	-0.056	0	0	1	1	1	2.937	-0.511	-0.017	-0.343	0.297	0.794	1.335
7	894	-0.262	0	0	1	. 1	1	2.782	-0.511	0.534	-0.488	0.297	0.540	1.335
8	894	-0.262	0	0	1	. 1	1	2.782	-0.511	0.534	-0.488	0.297	0.540	1.335
9	894	-0.262	0	0	1	. 1	1	2.782	-0.511	0.534	-0.488	0.297	0.540	1.335
10	894	0.151	0	0	1	. 1	1	2.906	-0.511	0.744	-0.488	-0.642	-0.223	1.335
11	894	0.151	0	0	1	. 1	1	2.906	-0.511	0.744	-0.488	-0.642	-0.223	1.335
12	894	0.151	0	0	1	. 1	1	2.906	-0.511	0.744	-0.488	-0.642	-0.223	1.335
13	894	0.151	0	0	1	. 1	1	3.557	-0.391	0.376	0.455	-0.642	-0.223	1.335
14	894	0.151	0	0	1	. 1	1	3.557	-0.391	0.376	0.455	-0.642	-0.223	1.335
15	894	0.151	0	0	1	1	1	3.557	-0.391	0.376	0.455	-0.642	-0.223	1.335
16	894	0.013	0	0	1	1	1	3.324	-0.235	0.744	-0.125	-0.642	-0.223	1.335
1	1010	1.388	0	0	1	0	0	0.162	-0.630	2.450	-0.779	2.175	2.827	1.335
2	1010	1.388	0	0	1	0	1	0.162	-0.630	2.450	-0.779	2.175	2.827	1.335
3	1010	1.388	0	0	1	0	1	0.162	-0.630	2.450	-0.779	2.175	2.827	1.335
4	1010	1.388	0	0	1	0	1	0.162	-0.630	2.450	-0.779	2.175	2.827	1.335
5	1010	2.350	0	0	1	0	1	0.206	-0.511	0.875	0.818	0.297	-0.223	1.335
6	1010	2.350	0	0	1	0	1	0.206	-0.511	0.875	0.818	0.297	-0.223	1.335
7	1010	2.350	0	0	1	0	1	0.206	-0.511	0.875	0.818	0.297	-0.223	1.335
8	1010	2.350	0	0	1	0	1	0.206	-0.511	0.875	0.818	0.297	-0.223	1.335
9	1010	2.350	0	0	1	0	1	0.078	-0.750	1.636	-0.053	-0.642	0.286	1.335

The Problem.

- Predicting comorbidities at the earliest from time-series data is challenging.
- Each patient has a dynamic and unique profile.
- Comorbidities interact.
- Many unmeasured effects.



The solution, Personalising Medicine

Hidden Variable discovery approach

- Finding methods to assess the influences of these latent variables,
- Discover the dependencies between the latent variable and the observed variables.
- Discover Diabetic trigger and eliminate diabetes forever!
- Determining the precise position of the latent variable
- Our key contribution is the combination of the IC* algorithm to identify latent variables within Dynamic Bayesian Networks.

Know what to look for

An example



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http://www.diabeticretinopathy.org.uk/prevention/hba1c_and_retinopathy.htm

Dynamic Bayesian Networks

- Ideal for clinical data:
 - Flexibility in continuous and discrete variable;
 - Handling uncertainty through the modelling of probability distributions;
 - Enables prediction through inference;
 - No limit for minimum sample size;
 - Transparent (querying the model, graphical structure)
 - It can naturally facilitate latent variables ...



IC (Inductive Causation) algorithm

- It Applies conditional independence analyses to infer causal structures;
- IC* algorithm (an extension of IC) learns a partially oriented Directed

Acyclic graph (pattern) with latent variables.





Dynamic links

- Learning the temporal links of our DBNs,
 Using REVerse Engineering ALgorithm (REVEAL) (Liang1998)
- We assumed hidden variable status at time t depends on the corresponding hidden variable at a previous time (t-1).



Pair sampling and Stepwise approach procedure

- Apply IC* algorithm on the balanced data.
- Provide probabilities of states by applying inference rules on all discovered hidden variables.
- Treat the discovered hidden variables as an observed variables.
- Re-apply the IC* and repeat all Steps until no new hidden variables are discovered.
- Having discovered the hidden variables, we build a predictive DBN model.
- Parameter estimation using the expectation-maximization (EM) algorithm.



Static structure with no hidden variable







Static structure with the second hidden variable



Static structure with the third hidden variable

Step 3



Confusion Matrix Results

The step-wise approach with a generally improving classification accuracy of diagnosing targeted complications as a number of hidden variables are added (the blue line represent retinopathy and the red line represents liver disease).





b

а

Inference: Query Rules

QR =

Complication='being at risk of retinopathy' | Evidence)

Evidence =

{risk of having retinopathy is reduced =

'high level of hidden variable 3,

lower level of hidden variable 2,

and very low level of hidden variable 1}



The variations in the latent variable are affected by various comorbidities.

Conclusion and Future Works



- Effectively integrates Bayesian methods with latent variables by adapting the prior probability of the event occurrence for future time points;
- The proposed method is more accurate than using one of hidden variable step or no hidden variables at all;
- Avoiding overfitting in the structure learning, using a stronger stopping rule in the step-wise approach;
- Exploiting mutual information metrics (Ebert, 2007) to filter some of the hidden variable relationships;
- Discovering interesting dependencies between the latent variable and the observed variables;
- Interpreting the impact of hidden (latent) variables in finding temporal phenotypes in the presence of unmeasured diabetic disorders;
 - Concentrating on the continuous investigation of features;
- Exploring Deep Learning methods;



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Thank you for listening!

Any Question?



"Type 2 diabetes

is not going to kill me. I just have to eat right, exercise, lose weight, watch what I eat, and I will be fine for the rest of my life."