LOGIC-BASED INTEGRATIVE CAUSAL DISCOVERY

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HETEROGENEOUS DATA SETS MEASURING THE SAME SYSTEM UNDER STUDY

Variables	Thrombosis	Contraceptives	Protein C	Breast Cancer	Protein Y	Protein Z
Study				the state of the s		
	Yes	No	10.5	Yes	-	-
1	No	Yes	5.3	No	-	-
observational data					-	-
	No	Yes	0.01	No	-	-
2	-	-	-	Yes	0.03	9.3
	-	-	-			
observational data	-	-	-	No	3.4	22.2
	No	No	0 (Control)	No	3.4	-
3	Yes	No	0 (Control)	Yes	2.2	-
					-	-
experimental data	Yes	Yes	5.0 (Treat.)	Yes	7.1	-
	No	Yes	5.0 (Treat.)	No	8.9	-
	No	No (Ctrl)	-	-	-	-
4	No	No (Ctrl)	-	-	-	-
experimental data			-	-	-	-
	Yes	Yes(Treat)	-	-	-	-

ISOLATED ANALYSIS



INTEGRATIVE CAUSAL ANALYSIS



Data can not be pooled together:

Missing variables cannot be treated as missing values.

They come from different experimental/sampling conditions (different distributions).

INTEGRATIVE CAUSAL ANALYSIS



Data can not be pooled together:

Missing variables cannot be treated as missing values.

They come from different experimental/sampling conditions (different distributions).



Data come from the same causal mechanism.

INTEGRATIVE CAUSAL ANALYSIS



SEMI MARKOV CAUSAL GRAPHS



Semi Markov Causal Graph $\,G\,$

- Directed edges represent direct causal relationships.
- Bi-directed edges represent confounding (latent confounders).
- Both types of edges allowed for a single pair of variables.
- No directed cycles (no causal feedback).

SEMI MARKOV CAUSAL GRAPHS



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Joint Probability Distribution ${\mathcal P}$

		Z		
Х	Y	Yes	No	
Yes	Yes	0,01	0,04	
Yes	No	0,01	0,04	
No	Yes	0,000045	0,044955	
No	No	0,000855	0,854145	

- Joint probability distribution entails conditional (in) dependencies.
- $Ind(X, Y|\mathbf{Z}): P(X|Y, \mathbf{Z}) = P(X|\mathbf{Z})$

• $Dep(X, Y|\mathbf{Z}): P(X|Y, \mathbf{Z}) \neq P(X|\mathbf{Z})$

SEMI MARKOV CAUSAL GRAPHS

Semi Markov Causal Graph G



Joint Probability Distribution ${\mathcal P}$

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Causal Markov Assumption:

Every variable is independent of its **non-effects** given its **direct causes**.



Ind(Y, Z | X)

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Causal Faithfulness Assumption:

Independences stem **only** from the causal structure, **not the parameterization** of the distribution.

 $Ind(Y, Z \mid X)$



Causal Markov Assumption:

Every variable is independent of its **non-effects** given its **direct causes.**

Causal Faithfulness Assumption:

Independences stem **only** from the causal structure, **not the parameterization** of the distribution.

Ind(Y, Z | X)

 $Dep(Y, Z | \emptyset)$ $Dep(X, Z | \emptyset)$ Dep(X, Z | Y) $Dep(Y, X | \emptyset)$ Dep(Y, X | Z)



Causal Markov Assumption:

Every variable is independent of its **non-effects** given its **direct causes.**

Causal Faithfulness Assumption: Independences stem **only** from the causal structure, **not the parameterization** of the distribution.

All independencies in the joint probability distribution can be identified in G using the graphical criterion of **m**-separation.

Ind(Y, Z | X)

$Dep(Y,Z \mid$	Ø)
$Dep(X,Z \mid$	Ø)
$Dep(X,Z \mid$	Y)
Dep(Y, X	Ø)
Dep(Y, X	Z)

*m***-SEPARATION**

A path $X_1, ..., X_n$ between X_1 and X_n is *m*-connecting given *V* if for every triple (X_{i-1}, X_i, X_{i+1}) on the path:

- If $X_{i-1} * \rightarrow X_i \leftarrow * X_{i+1}$ (colliding triplet), X_i or one of its descendants $\in V$
- Otherwise, $X_i \notin V$

m-connecting path => information flow => dependence

No *m*-connecting path => no information flow => independence (*m*-separation)

Colliders $X_{i-1} * \rightarrow X_i \leftarrow X_{i+1}$ are **special** and create an asymmetry that will allow us to orient causal direction.

CAUSAL MODELLING







Conditional (in)dependencies (expected) in the joint probability distribution





Paths (mseparations/connections) in the causal graph

REVERSE ENGINEERING



Data set *D* measuring a set of variables

causal graph?

REVERSE ENGINEERING





??

Data set D measuring a set of variables Find the (in)dependencies using statistical tests.

causal graph?

Ε

2

?

C

?

?

[D]

G:

Α

?

?

2

В

?

REVERSE ENGINEERING









Data set *D* measuring a set of variables Find the (in)dependencies using statistical tests.

Find a graph that satisfies the implied mconnections/separations.

MARKOV EQUIVALENCE



A, B E, C	Ind
A , B Ø	Dep
E, C A, B, C	Dep

- More than one graphs entail the same set of conditional independencies.
- The graphs have some common features (edges/orientations).
- For some types of causal graphs, Markov equivalence classes share the same skeleton.
 - not semi-Markov causal graphs

CAUSAL DISCOVERY



Sound and complete algorithms (e.g., FCI) take as input a data set and output a summary of all the graphs that satisfy all identified conditional independencies.

INTEGRATIVE CAUSAL DISCOVERY





Causal graph(s) that simultaneously fit all data.

Data sets measuring overlapping variable sets under intervention/selection.

INTEGRATIVE CAUSAL DISCOVERY







Causal graph(s) that simultaneously fit all data.

Data sets measuring overlapping variable sets under intervention/selection.

- Every data set imposes some constraints.
- Observational data impose m-separation/m-connection constraints on the candidate graph.
- Different variables?
- Experimental data?
- Data sampled under selection?

INTERVENTIONS (MANIPULATIONS)



Values of the manipulated variable are **set** solely **by the intervention procedure**

e.g. a randomized variable in a randomized control trial.

INTERVENTIONS





- If you know the causal model, you can model interventions.
- Values of B are set solely by the intervention procedure: If you know direct causal relations, remove all edges into the manipulated variable.
- This procedure is called graph surgery.
 - The resulting graph is called the manipulated graph (symb. *G^B*)

CAUSAL DISCOVERY WITH INTERVENTIONS



A, B E, C	Ind
<i>A, B</i> Ø	Dep
<i>E</i> , <i>C</i> <i>A</i> , <i>B</i> , <i>C</i>	Dep





A m-connecting path from A to D given Ø in G^B
 A m-connecting path from A to D given B in G^B
 G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G

Dataset D_i measuring a subset of variables, some of which are manipulated

Conditional independencies in D_i

Path constraints on the causal graph after manipulation

SELECTION BIAS



- Samples are selected based on the value of one of your variables.
- e.g. you perform your study in a specific region/on the internet; casecontrol study for a rare disease.



SELECTION BIAS IN CAUSAL MODELS





- If you know the causal model, you can model selection bias.
- Samples are selected based on the value of D; The value of D directly affects the probability of being selected.
- S is a child of D, S=1 for all your samples.
- Selected graph, symb. G_D

CAUSAL DISCOVERY WITH SELECTION BIAS



<i>A</i> , <i>B</i> <i>E</i> , <i>C</i> , <i>S</i> =1	Ind
<i>A</i> , <i>B</i> S=1	Dep
<i>E</i> , <i>C</i> <i>A</i> , <i>B</i> , <i>D</i> , <i>S</i> =1	Dep





Dataset D_i measuring a subset of variables, some of which are selected upon

Conditional independencies in D_i

Path constraints on the underlying causal graph after selection

INTEGRATIVE CAUSAL DISCOVERY



- Every data set imposes some constraints.
- Observational data impose path constraints on the candidate graph.
- Experimental data impose path constraints on the candidate graph after manipulation.
- Data sampled under selection impose path constraints on the candidate graph after selection.
- Easily handles overlapping variable sets
 - Each study imposes constraints on the observed variables.

LOGIC-BASED INTEGRATIVE CAUSAL DISCOVERY



- Suppose you know nothing about the causal structure G of A, B, C.
- In a data set where B is manipulated, $Ind(A, C|\emptyset)$
- In path terms: \nexists m-connecting path between A and C given \emptyset in G^B .



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A-C does not exist $\neg E_{A \rightarrow C} \land \neg E_{A \leftarrow C} \land \neg E_{A \leftrightarrow C}$

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A-C does not exist $\neg E_{A \rightarrow C} \land \neg E_{A \leftarrow C} \land \neg E_{A \leftrightarrow C}$

A-B-C is not m-connecting $\neg(E_{B\rightarrow A} \land E_{B\rightarrow C})$

- Suppose you know nothing about the causal structure G of A, B, C.
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A-C does not exist $\neg E_{A \rightarrow C} \land \neg E_{A \leftarrow C} \land \neg E_{A \leftrightarrow C}$

A-B-C is not m-connecting $\neg (E_{B \to A} \land E_{B \to C})$

Logic formula: $(\neg E_{A \to C} \land \neg E_{A \leftarrow C} \land \neg E_{A \leftrightarrow C}) \land \neg (E_{A \leftarrow B} \land E_{B \to C})$

CONVERSION TO LOGIC FORMULA: EXAMPLE






CONVERSION TO FIRST-ORDER LOGIC: INPUT CONSTRAINTS

1) As many (conditional) **dependencies** and **independencies** from multiple datasets as desired, even datasets over different variables

2) Meta-Information about the datasets

- for each variable and dataset, whether it was used for selection, or not, or unknown
- for each variable and dataset, whether it was manipulated (soft or hard), not, or unknown
- 3) Structural prior knowledge
- presence/absence of direct edges, paths or dependencies
- root/leaf nodes
- any structural constraint that can be expressed in first-order logic

CONVERSION TO FIRST-ORDER LOGIC: LOGIC VARIABLES AND SEMANTICS

Logic variables represent **features of the graph** and datasets:

edges, directed paths, m-connecting paths, selection targets, intervention targets

 $X \to Y$ X has an arrow into Y Set to **true** if $Dep(X, Y | \mathbf{Z})$ is determined in dataset D and **false** otherwise $X \leftrightarrow Y$ X and Y are confounded $X \dashrightarrow Y$ X is an ancestor of Y $X \cdots Y$ $mconn(X, Y, \mathbf{Z})$ in dataset D Z,D $X \cdots > Y$ $mconn(X, Y, \mathbf{Z})$ in dataset D (path into Y) Set to **true** if X is known to be used Z,Dfor selection in dataset D $X \cdot \cdot -Y$ $mconn(X, Y, \mathbf{Z})$ in dataset D (path out of Y) X is used for selection in dataset D Set to **true** if *X* is a known target of a X_{D}^{I} X is manipulated (hard) in dataset D manipulation in dataset D

CONVERSION TO FIRST-ORDER LOGIC : INFERENCE RULES ETIO ALGORITHM (KDD 2016)





















STATISTICAL ERRORS RESULT IN CONFLICTING INPUTS



Convert p-values to probabilities

Solve a subset of constraints optimizing a function of the probabilities

EXISTING ALGORITHMS

Vary in:

- Type of constraints:
 - different types of paths (m-connecting, inducing, ancestral).
 - translation to logic formula.
- Types of heterogeneity:
 - Soft/hard interventions, selection.
- Preprocessing:
 - Heuristics to limit number of constraints / paths.
- Conflict Resolution
 - Method for calculating probabilities.
 - Conflict resolution strategy (greedy/ max SAT / weighted max SAT).
- CS solver
 - Initially SAT solvers, more recently ASP.
- Scalability
 - Depends on choices above. Be exact/ focus on scalability.
 - Difficult to determine
 - huge variance depending on the problem.

CSAT+ [Triantafillou, et al., AISTATS 2010] LOCI [Claassen and Heskes, UAI 2011] SAT-Based Causal Discovery [Hyttinen, et al., UAI 2013] Constraint-Based CD [Hyttinen, et al., UAI 2014] COmbINE [Triantafillou and Tsamardinos, JMLR 2015] ETIO [Borboudakis and Tsamardinos, KDD 2016] ACI [S. Magliacane, T. Claassen, J.M. Mooij, *arXiv*]

MORE

- Using conversion to logic for causal discovery from time-course data
 - Causal Discovery from Subsampled Time Series Data by Constraint
 Optimization, [Hyttinen, Plis, Järvisalo, Eberhardt and Danks, arXiv, 2016]
- Using conversion to logic for identifying chain graphs.
 - Learning Optimal Chain Graphs with Answer Set Programming
 - [Sonntag, Järvisalo, Penã, Hyttinen, UAI 2015]
- Using conversion to logic to identify semi-Markov causal graphs.
 - [Penã, UAI 2016]
- Using conversion to logic to estimate causal effects for an unknown graph
 - [Hyttinen, Eberhardt and Järvisalo, UAI 2015]
- Massive proof-of-concept proof the techniques work for real data and can become quantitative
 - [Tsamardinos, et al. JMLR 2012]
- More details, examples, references in recent UAI 2016 Tutorial Triantafillou & <u>Tsamardinos</u>

USE CASE: THE INSURANCE DATASET REAL CAUSAL GRAPH



APPLICATION ON REAL PROBLEMS

Insurance Data Datasets	Age	SeniorTrain	MakeModel	VehicleYear	DrivQuality	Airbag	Antilock	Ruggedness	Mileage	CarValue	Cushioning	Accident	MedicalCost	LiabilityCost	PropertyCost
Observational							X			X					
Selected based on Antilock								X			X	X	X		
Soft Intervention on Cushioning							X			X					
Prior Knowledge						An	ything Costs Age	-X- -X-	 A AI C 	nge Nythin Costs	g				

USE CASE: THE INSURANCE DATASET PROVED ANCESTRY RELATIONS



USE CASE: THE INSURANCE DATASET PROVED ANCESTRY RELATIONS (TRANSITIVE REDUCTION)



USE CASE: THE INSURANCE DATASET PROVED ANCESTRIES AND DIRECT CAUSAL RELATIONS



USE CASE: THE INSURANCE DATASET NON-TRIVIAL INFERENCES



KEY-POINTS

Integrative logic-based causal discovery.

Different data distributions, same causal mechanism: use causal modeling to connect.

Can handle datasets of different variable sets, different experimental conditions, prior causal knowledge.

Identify the set of causal graphs that simultaneously fit all datasets and reason with this set.

Convert problem to SAT or ASP; exploit 40 years of SAT-solving technology.

Query-based approach to avoid explosion of possible solutions!

Vision of automatically analyzing a large portion of available datasets in a domain.

ACKNOWLEDGEMENTS

Mens x machina group, University of Crete. Jan Lemeire, Frederick Eberhardt, Antti Hyttinen, Joris Mooij

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SNEAK PREVIEWS TO MXM RESEARCH

LOGIC-BASED CAUSAL DISCOVERY

- Scalability, robustness
- Relax assumptions such as Faithfulness
- Making quantitative predictions
- Extend for temporal data
- Add Verma constraints
- Application to a real-life insurance problem

FEATURE SELECTION – FASTER, BETTER, MULTIPLE SOLUTIONS, BIG DATA

Forward-Backward Selection (FBS)

- very slow, especially for data with many variables
- returns single solution

We extended FBS

- Improving computational performance by 1-3 orders of magnitude
- Reducing number of selected variables, selecting up to 5 times fewer variables
- With comparable or better predictive performance
- With the ability to return multiple, statistically equivalent solutions

Extended single solution FBS also for Big Data

- Further improving computational performance, able to run on millions of samples and variables
- Vastly outperforming state-of-the-art feature selection methods on Big Data
- Almost linear speedup with available cores
- Super-linear scalability with sample size

LEARNING ORDINARY DIFFERENTIAL EQUATION MODELS



Trajectories of Lorenz96 climate model. It is a chaotic system of Ordinary Differential Equations given by:

$$\dot{x}_n = x_{n-1}x_{n+1} - x_{n-1}x_{n-2} - x_n + F,$$

 $n = 1, ..., N$

Algorithms for learning the *structure* and the parameters of a Dynamical System from *time-course* measurements

(1) *Eliminate* the time dimension by transforming the original problem to an *atemporal* one.

(2) *Solve* the transformed problem using the *Sparse Signal Identification* theory.

R PACKAGE MXM: DESCRIPTION

Main focus of the package:

- Variable Selection
- (Causal) Bayesian Networks

Available variable selection methods span prototypical algorithms (forward, backward regression) and advanced ones (SES, MMPC)

• A plethora of different data types can be addressed: continuous, ordinal, categorical, survival, proportions, longitudinal, clustered.

Algorithmic and implementation optimization (e.g., several function are implemented directly in C++)

AYTOMATED MACHINE LEARNING



- Commercial CLC-Bio (a QIAGEN company) plugin for high-throughput data analysis.
- Automatically identifies multiple signatures.
- Can handle various data types.
 - Including binary, multi-class, continuous, and time-to-event outcomes.
- Computationally efficient, fine-tuned implementation.
 - Easily handles even tens of thousands of molecular quantities.
- High quality results, using state-of-the art techniques.
- Interpretable output, helping the user understand the results.
- Soon available as a cloud service

CASE-STUDY: CLASSIFICATION ANALYSIS IN BREAST **TUMORS**



RESEARCH ARTICLE

LaBreche et al. BMC Medical Genomics 2011, 4:61 http://www.biomedcentral.com/1755-8794/4/61

Open Access

Integrating Factor Analysis and a Transgenic Mouse Model to Reveal a Peripheral Blood Predictor of Breast Tumors

Heather G LaBreche^{1,2*}, Joseph R Nevins^{1,2} and Erich Huang^{1,3,4}

125 gene expression profiles of patients

31 normal, 94 breast tumor (37 benign, 57 malignant)

54,675 gene expression probesets

Introduced in LaBreche et al., BMC medical genomics (2011)

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1 Selecting the data

2 Choose the type of analysis

3 Tuning-effort level

ANALYSIS RESULTS 4 Performance Metrics

Metric	Average	95% Confidence Interval
Accuracy	0,977	[0,946, 1,000]
Area Under the ROC Curve	0,985	[0,951, 1,000]
Precision for class 1.0	0,983	[0,900, 1,000]
Precision for class 2.0	0,970	[0,930, 1,000]
Recall for class 1.0	0,917	[0,817, 1,000]
Recall for class 2.0	1,000	[0,940, 1,000]
Sensitivity for class 1.0	0,917	[0,817, 1,000]
Sensitivity for class 2.0	1,000	[0,940, 1,000]
Specificity for class 1.0	1,000	[0,940, 1,000]
Specificity for class 2.0	0,917	[0,817, 1,000]

¹LaBreche et al. achieve 0.97 Area Under the ROC Curve

²Analysis took less than 3 minutes on a laptop

5 Individual feature contribution







SINGLE-CELL NETWORK RECONSTRUCTION SYSTEM (SCENERY)

Architecture

Web-based, open architecture

Wizard design pattern: Step-based User Interface

Modularity: Easy to incorporate new analysis methods

Functionalities

Visualization: Histograms, Scatter/Density/Violin plots, Network graphs

Univariate Analysis : Population Comparison, Regression

Network Reconstruction Analysis

- (Conditional) Association Networks (COR, MMPC)
- Probabilistic Causal Networks (PC, FCI, IDA)
- Bayesian Networks (HC)
- Currently available methods: MMPC, PC, HC, FCI, IDA, COR



USE CASE

Data: Bendall et al., *Science*, 2011

- (a) Overlapping density plots for the marker p38 on 2 donors.
- (b) Reconstructed network (MMPC) on selected protein markers: SYK, BLNK, PLC2, p38 and MAPKAPK2.



 SCENERY

 Data Loading
 Experiment Setup
 Perform Analysis
 Share
 Select another Analysis Method

 Calibrate your Analysis
 Select Marking:
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 Select Another Analysis Method

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G. Athineou, G. Papoutsoglou, S. Triantafullou, I. Basdekis, V. Lagani, I. Tsamardinos (2016): SCENERY: a Web-Based Application for Network Reconstruction and Visualization of Cytometry Data, PACBB 2016.

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