How to Test DAG Models

Johannes Textor



Why Test DAG Models?

Categorical Data Continuous Data

Mixed Data

How to Test DAG Models

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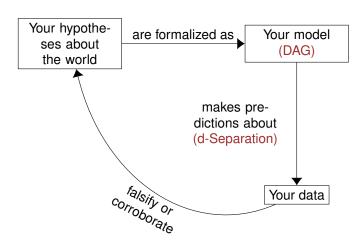
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1 Why Test DAG Models?

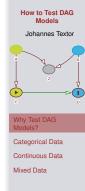
2 Categorical Data

3 Continuous Data

The Model Building Cycle



This doesn't only apply to DAGs, but many other kinds of models as well.



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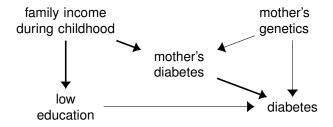
- DAGs are models of variable relationships in a certain domain.
- DAGs encode certain assumptions about these relationships.
- Any inference drawn from the DAG (such as an adjustment) set) hinges on the assumptions that are made.
- Incorrect assumptions may lead to incorrect inferences.

To guard against wrong inference, we can test our model before we use it.

Caveats

- Model testing never guarantees a correct model! It can only refute, but never prove it.
- Bad actors can use model testing to iteratively tweak a model until it perfectly fits a given dataset.

How Can We Tell If This DAG Is Correct?



Rothman, Greenland & Lash, Modern Epidemiology, 2008

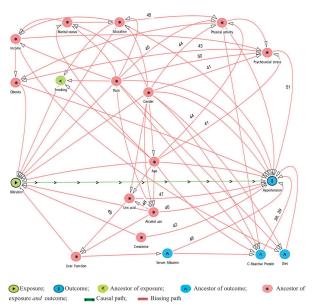


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How Can We Tell If This DAG Is Correct?



Wang and Bautista, IJE 2015, https://doi.org/10.1093/ije/dyu242

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Testing Graphical Causal Models Using the R Package "dagitty"

Ankur Ankan, Inge M. N. Wortel, Johannes Textor X

First published: 16 February 2021 | https://doi.org/10.1002/cpz1.45

Paper is available at: https://doi.org/10.1002/cpz1.45

Code is available at: https://github.com/ankurankan/2020-dagitty-manual/

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d-Separation in DAGs

Definition

A path in a DAG is a sequence of variables (possibly with repetitions) that are connected by edges.

Note that this differs from the "intuitive" concept of a path because we allow to move against arrow directions: $x \to m \leftarrow y$ is a path too!

d-Separation

A path is d-separated if

- It contains a collider x → m ← y where m and all descendants of m are not conditioned on;
- It contains a non-collider x → m → y, x ← m → y or x ← m ← y where m is conditioned on.

This means that:

- A one-arrow path x → y is never d-separated.
- Conditioning may close but also open paths.

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How d-Separation Links DAGs to Data

Theorem (Verma & Pearl, 1984)

If conditioning on \mathbf{Z} d-separates X and Y in a DAG G, then $X \perp \!\!\! \perp Y \mid \mathbf{Z}$ in every probability density P that factorizes according to G.

DAG structure	What it claims about the data
$X \to Y$	Nothing
$X \to Y \to Z$	$X \perp\!\!\!\perp Y \mid Z$
$I \to X \to Y \to Z$	
	I
	I
	$X \perp \!\!\! \perp Z \mid Y$

- Larger DAGs can make more claims about the data.
- Each claim depends on at least one missing arrow.



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It depends!

- The general theory of d-separation is non-parametric, but
- depending on the type of data involved, different statistical tests are needed.

We will cover a few example tests for the following cases:

- Categorical data only
- Continous data only
- Mix of ordinal and continous data

Main Types of Conditional Independence Tests

There are three main approaches to test a statement $X \perp \!\!\!\perp Y \mid Z$:

- Stratification-based tests split the dataset according to the values of Z, perform a simple independence test X ⊥ Y in each part, and combine the results.
- Variable importance-based tests compare the fit of a model \(\hat{p}(X \cong Y, Z)\) to a simpler model \(\hat{p}(X \cong Z)\). If X \(\preceq Y \cong Z\), the simpler model should fit just as well.
- Residualization-based tests fit two (regression) models
 \(\mathbb{E}[X|Z] \) and \(\mathbb{E}[Y|Z] \), and test for independence between
 the residuals.

Each approach has distinct advantages and disadvantages.



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The Chi-Square Test for Conditional Independence

To test conditional independence $X \perp\!\!\!\perp Y \mid Z$, we

- split the dataset according to Z;
- 2 perform a simple chi-square test of $X \perp Y$ in each part;
- 3 combine the results.

Combining results of chi-square tests

If $T_0 \sim \chi^2(a)$ and $T_1 \sim \chi^2(b)$ are two chi-square distributed variables with a and b degrees of freedom, then

$$T_1 + T_2 \sim \chi^2(a+b)$$

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The Root Mean Square Error of Approximation (RMSEA)

Instead of a p-value, which conflates information about dependence strength and sample size, an effect size is often more useful. For chi-square tests, various effect sizes can be defined. An important one is the RMSEA:

$$RMSEA = \sqrt{\frac{\chi^2/df - 1}{N - 1}}$$

Properties of the RMSEA

- Under independence, the expected RMSEA is 0.
- Under dependence, the RMSEA converges to a constant positive value as N → ∞ (the p-value converges to 0).
- Higher RMSEA means stronger dependence.

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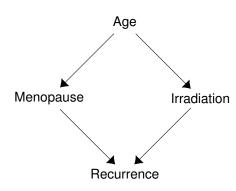


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Simulated Example: Breast Cancer Recurrence



Implications:

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```
Sq")
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```

```
Let's start with the first implied independence: Irradiation \bot Menopause | Age
```

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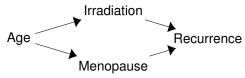
There's no strong evidence against independence here.

Now let's test the second implied independence: Age \bot Recurrence | Irradiation, Menopause

The data strongly contradict this.

Summary of Test Results

We assumed the following DAG:



- We refuted the second claim:
 Age

 Recurrence | Irradiation, Menopause.

```
r <- dagitty::localTests("Age->{Irradiation Menopause}->Recurrence",
d, type="cis.chisq")
dagitty::plotLocalTestResults( r, pch=19, ylim=c(0.8,2.2) )

Irrd_||_Mnps|Age
Age_||_Rcrr|Irrd,Mnps

0.0 0.1 0.2 0.3 0.4 0.5

test statistic (95% CI)
```

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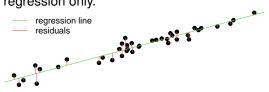
Continuous Data

Residual Correlation Tests for Continuous Data

For continuous data, stratification-based tests are not generally used. Instead, the residualization-based approach is more common:

- Regress X on \mathbf{Z} and get residuals $r_X = X E[X \mid \mathbf{Z}]$.
- Regress Y on **Z** and get residuals $r_Y = Y E[Y \mid \mathbf{Z}]$.
- If r_X and r_Y correlate, then $X \perp \!\!\! \perp Y \mid \mathbf{Z}$ does not hold.

This approach can be used with many types of regression (Gaussian process, Kernel ridge, ...). However, we will focus on linear regression only.



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Example: Protein Signalling Network

RESEARCH ARTICLE

Causal Protein-Signaling Networks Derived from Multiparameter Single-Cell Data

Karen Sachs^{1,*}, Omar Perez^{2,*}, Dana Pe'er^{3,*}, Douglas A. Lauffenburger^{1,†}, Garry P. Nolan^{2,†}

- + Author Affiliations
- ←¹† To whom correspondence should be addressed. E-mail: lauffen@mit.edu (D.A.L.); gnolan@stanford.edu (G.P.N.)
- ← These authors contributed equally to this work.

Science 22 Apr 2005: Vol. 308, Issue 5721, pp. 523-529 DOI: 10.1126/science.1105809

Sachs *et al.* were interested in the interactions between a set of 11 proteins. They had measured the expression of these proteins on single cells using flow cytometry.

Their data is continuous, but flow cytometry data needs to be transformed for linearity to be reasonable.

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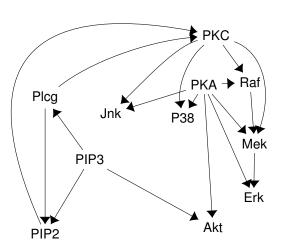


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The "Consensus" Protein Signalling Network



According to Sachs *et al.*, this network represents the expert consensus at their time of writing. Let's test this!



Testing the Consensus Network

```
# Download preprocessed protein signaling data
data <- read.csv( "https://git.io/JX4jh" )</pre>
# Residual correlation with bootstrapped CIs
r <- localTests( x=model, data=data, type="cis", R=50 )
r <- r[order( abs( r$estimate ) ),] # Worst tests last
tail(r)
##
                                    estimate std.error 2.5% 97.5%
## Akt || P38 | PKA. PKC
                                        0.21
                                                0.0095 0.20 0.23
## Erk || P38 |
                                                0.0076 0.22
                                                              0.25
                  PKA. PKC
                                        0.24
## Akt _||_ Erk | PIP2, PKA, Plcg
                                     0.90
                                                0.0025 0.89
                                                              0.90
## Akt || Erk | Mek. PKA
                                       0.90
                                                0.0025 0.89 0.90
## Akt _||_ Erk | PKA, PKC
                                       0.90
                                                0.0021 0.89 0.90
## Akt _||_ Erk |
                  PIP3. PKA
                                        0.90
                                                0.0026 0.89
                                                              0.90
plotLocalTestResults( tail( r ), xlim=c(-1,1) )
   Akt _||_ P38 | PKA, PKC
                                                   0
   Erk | P38 | PKA, PKC
Akt _||_ Erk | PIP2, PKA, Plcg
    Akt || Erk | Mek, PKA -
   Akt || Erk | PKA, PKC
                                                                   Θ
   Akt | | Erk | PIP3, PKA
                      -1.0
                                 -0.5
                                             0.0
                                                         0.5
                                                                    1.0
```

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A Latent Variable Approach for Heterogeneous Datasets

We'll now discuss a "mixed" approach for datasets containing both discrete and continuous data, which is applicable if all of your variables are:

- continuous; or
- binary; or
- 3 ordinal (=categorical with an ordering).

Non-ordinal categorical can be incorporated via "dummy coding", but this works well only if they have no parents in the DAG.

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```
hsb2 <- read.table(header=T, sep=",",
"https://stats.idre.ucla.edu/wp-content/uploads/2016/02/hsb2-2.csv")
head(hsb2)
```

Let's consider this example dataset on schooling performance:

```
id female race ses schtyp prog read write math science socst
     70
                                        57
                                              52
                                                   41
                                                            47
                                                                  57
                                                   53
  2 121
                                        68
                                              59
                                                            63
                                                                  61
     86
                                              33
                                                   54
                                                           5.8
                                                                  31
                                        44
                                                   47
                                                           53
                                                                  56
  4 141
                                        63
                                              44
  5 172
                                        47
                                              52
                                                   57
                                                           53
                                                                  61
                                              52
                                                            63
## 6 113
                                        44
                                                   51
                                                                  61
```

```
##
## 1 2 3
## 47 95 58
```

table(hsb2\$ses)

The "socioeconomic status" (SES) is an ordinal composite measure based on multiple indicators. We can think of this as an underlying continuous measure that has been "binned". Is there a way to "un-bin" it?

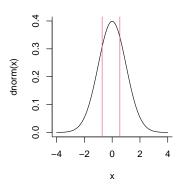
Threshold Functions

Let's assume that SES is standard normally distributed, and the binned values are obtained by applying cutoffs.



The most likely cutoffs are those where the Gaussian probability density mass is split into the same fractions as those we observe in the data.

```
y <- table(hsb2$ses)/nrow(hsb2)</pre>
##
##
## 0.23 0.47 0.29
y \leftarrow cumsum(y)
##
## 0.23 0.71 1.00
y <- qnorm( y )
   -0.72 0.55
```



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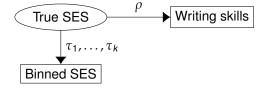


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Polyserial Correlations

A polyserial correlation is an estimated correlation between one continuous variable with another that's given as binned measurements.



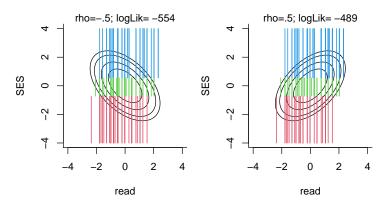
The polyserial correlation ρ can be estimated in two steps:

- Infer thresholds for the discrete latent variable.
- Optimize the value for the latent correlation to maximize the likelihood of the data conditional on the thresholds.

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Polyserial Correlations

In the optimization, we determine the latent correlation that maximizes the sum of the shown line integrals of the resulting 2D Gaussian distribution.



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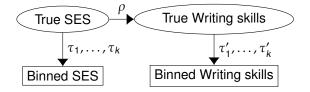


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A polychoric correlation is an estimated correlation between two latent variables that are both given as binned measurements.

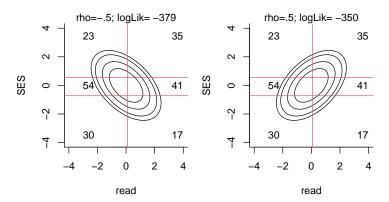


The polychoric correlation ρ can be estimated in two steps:

- 1 Infer thresholds for the discrete latent variables.
- 2 Choose the value for the latent correlation that maximizes the likelihood of the data given the correlation and the thresholds.

Polychoric Correlations

In the optimization, we determine the latent correlation that maximizes the likelihood to obtain the shown number of observations in each rectangle.



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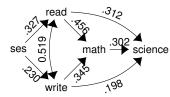
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By appropriate pre-processing of our data, we can generate a correlation matrix in which the ordinal variables are represented by polychoric correlations.

We can then apply standard SEM methodology to this matrix, since all SEM testing and fitting can be performed based on only the correlation matrix.



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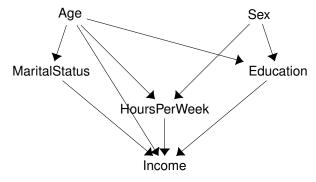


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A More Complex Example

Let's consider a hypothetical (incorrect) causal diagram for a part of the widely known 1994 "adult census income" dataset:



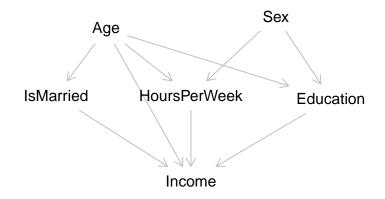
Note the conspicuous absence of the gender pay gap in this model.



Putting Everything Together

Step 1: We build our DAG.

```
g <- dagitty('Age [pos="-2.5,-2"] Education [pos="2,0.2"]
HoursPerWeek [pos="-0.8,0.1"] Income [pos="-0.8,2.8"]
IsMarried [pos="-3.5,0.1"] Sex [pos="0.9,-2.4"]
Age -> { Education HoursPerWeek Income IsMarried }
{ Education HoursPerWeek IsMarried } -> Income
Sex -> { Education HoursPerWeek }')
plot(g)
```



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Step 2: We load and preprocess our data.

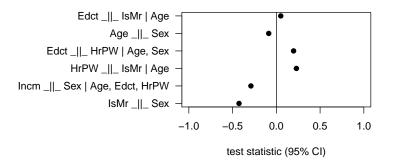
We need to make sure that our analysis is aware of the ordering between the categories (where meaningful).

Putting Everything Together

Step 3: We test our DAG.

```
plotLocalTestResults(localTests(
```

g, sample.cov=M, sample.nobs=nrow(d)), xlim=c(-1,1), pch=19



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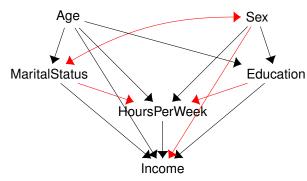


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Updated Model

From the test results, we decide to add 4 edges that could be missing here.



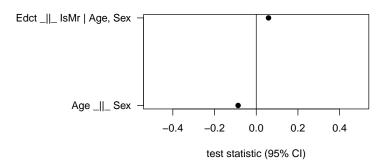
Note that the bi-directed edge does not represent a causal link, but is just meant to "absorb" the sample correlation between Sex and Marital Status that should really not be there.



```
Step 2: We test our DAG (again).
```

```
plotLocalTestResults(localTests(
```

g, sample.cov=M, sample.nobs=nrow(d)), xlim=c(-.5,.5), pch=19

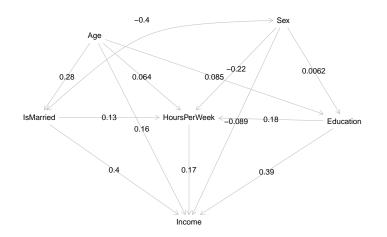


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Using lavaan to Estimate Path Coefficients



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Summary

- DAGs imply conditional independence constraints on compatible probability distributions.
- 2 The d-separation criterion allows to read off these constraints from the graphical model structure.
- The dagitty package implements methodology for (human-focused) DAG model testing.



Current Protocols 1(2), 2021. doi: 10.1002/cpz1.45

Felix Thoemmes, Yves Rosseel, Johannes Textor: Local Fit Evaluation of Structural Equation Models Using Graphical Criteria.

Psychological Methods 23(1):27-41, 2018. https://psyarxiv.com/2kgxr/



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