

Online Supplement

Learning Hidden Causal Structure from Temporal Data: Model Identifiability Experiments

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Here we present some simple experiments for model identifiability. This serves the purpose of assessing whether certain structures are more difficult to recover than others. We assess this by generating sequences of observations from causal structures initialized with plausible parameter settings, then running the inference procedure on these data and seeing whether the mode of the posterior distribution over structures matches the true generative model. In order to have a comparable presentation of the results for the order and delay model, we present simulation data in the form of confusion matrices for both models. This is to be read as follows: Each row corresponds to the generated traces from one structure, and each column provides the predictions made by a particular structure. The classification is perfect if the matrix forms an identity matrix.

Order model

Methods

Sequences of observations are simulated by forward-sampling 1000 traces of length 20 from each structure. The predictions corresponds to the mode of the posterior distribution over structures.

Results

First, we look at the proportion of sequences for which the true generative structure could be recovered with the order model, as presented in Figure 1. Here, we find systematic deviations from the ground truth.

While causal chains could be always be identified, independent causes and common hidden causes were recovered less often. Causal cycles were never recovered, with causal chains being inferred instead.

What explains these mis-identifications in an order-only approach? Going through a concrete example: For an example sequence of length two, where X precedes Y , we see that this is consistent with all causal structures, except for a chain, where Y causes X .¹ The probabilities under the model are as follows: For the independent structure we have $(\frac{1}{3})^2 = \frac{1}{9}$, for a chain X causes Y $(\frac{1}{1})^2 = 1$, for a common hidden cause $\frac{1}{3} \cdot \frac{1}{1} = \frac{1}{3}$, and finally for a causal chain $\frac{1}{2} \cdot \frac{1}{1} = \frac{1}{2}$. We can see that the probability is highest for the causal chain (X causes Y), as it is the most specific among these structures (the Bayesian Ockham’s razor “penalises” models for their flexibility). Whenever a more flexible structure (such as independent events or common hidden causes) generates a trace that is also compatible with a more specific structure, the more specific structure will be preferred.

Going through the structures in more detail:

- **Independent:** This structure is the most general and can, by chance, emulate all other structures. It is easy to see that the probability of obtaining a sequence that is only compatible

¹Observing just one event that is not accepted leads the probability of that trace, and thus that structure, to be zero.

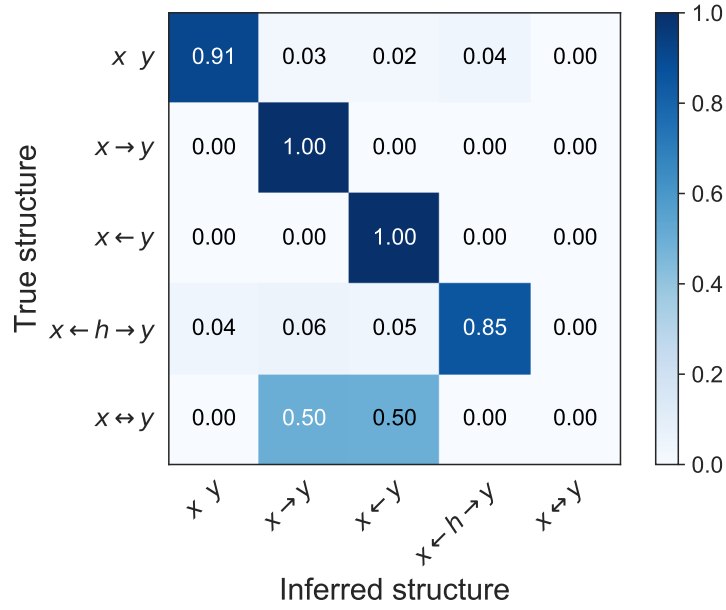


Figure 1: Order model identifiability for 20 events per sequence. Values correspond to relative frequencies.

with an independent structure goes to one as the length of the trace goes to infinity. Hence, we can see that this structure becomes more identifiable as we gather more observations.

- **Causal chain** (X causes Y or Y causes X): Whenever a trace is consistent with a causal chain, the model prefers it as its generative structure, as it is the most specific.
- **Common hidden cause**: This structure is the second most flexible structure and as the independent structure, becomes more identifiable with an increasing number of observations.
- **Cycle**: Depending on the first observation, this structure is either consistent with an X causes Y chain or a Y causes X chain. As both of these are only consistent with one trace (that of alternating observations), this formalisation of a causal cycle can never be identified from order information alone.

We see that order information is useful but not sufficient to distinguish between our causal structures.

Delay model

Methods

As the delay model assumes a mostly uninformative prior on its parameters, we choose a parameterization for simulating sequences that reflects parameters that were deemed plausible for each structure, as determined by an informal sample of volunteer participants. The parameterization as well as visualizations of example sequences are provided in Table 1. For generating the data, we set the variance of the observation model for all structures to $\sigma^2 = 10^{-5}$. We simulated 10 sequences per structure, each of length 20. In order to get comparable results across all experiments, the timings of the generated sequences were down-sampled into frames and then converted back into absolute time².

²Not discretizing the sequences did not yield meaningfully different results.

Structure	μ_a	σ_a^2	μ_b	σ_b^2
Independent	2.0	0.4	2.5	0.4
X causes Y	2.0	0.4	0.5	0.1
Y causes X	0.4	0.1	2.0	0.4
Common hidden cause	2.0	0.4	0.5	0.1
Cycle	1.0	0.1	1.0	0.1

Table 1: Parameterisation for sampled event sequences in identifiability experiments.

Results

As presented in Figure 2, looking at the delay model, we find that the generative model can be successfully recovered in all structures most of the time, while the independent structure is most difficult with the chosen parameters. In the case of independent causes, the particle filter appears to “see structure” early on in a sequence of observations, and commit to that inference by resampling particles that are consistent with the hypothesized structure. The beginning of a sequence of observations can e.g. seem consistent with a causal chain X causes Y , and given a high-variance proposal distribution, stay consistent enough with the data to dominate the inference. Further, while the mean delays in the transition model in our chosen parameterization differ by only $0.5s$, we found that increasing this offset to $1s$ let us identify the independent structure considerably more often. It is clear that certain parameters can always lead to identifiability problems. For instance, if the variance in all delay distributions is close to zero, then the structural information degenerates. However, these identifiability results indicate that under reasonable parameterizations, we can distinguish between the different causal structure most of the time.

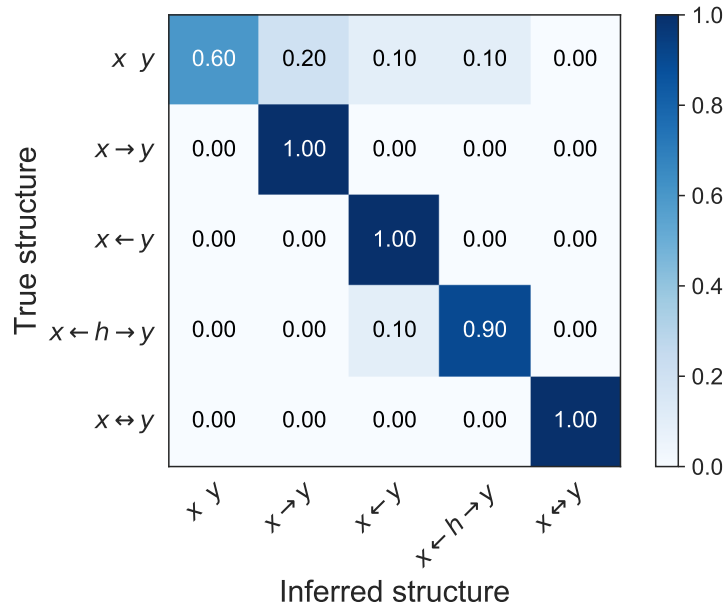


Figure 2: Delay model identifiability for 20 steps. Values correspond to relative frequencies.