

## CHAPTER 1

# Results and Discussion

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An introduction to what is going to be included in this section. What results etc.

In this section, we will investigate how the algorithms ?? and ?? works in junction and individually. We shall observe how the algorithms can fail and what may be done to correct such cases.

Overordnet pointe er at genere forskellige mulige graphiske modeller, som senere ville kunne bruges til at lave PGM el.l. Er nok bedst som et ekspolartivt værktøj, og vi undersøger her forskellige situationer, og hvornår der kan ske fejl ud fra om det er lange kæder af kausalitet eller mere komplekse strukturer

## 1.1 Gaussian chains

In this section we discuss the errors made from the assumption that indirect effects can be computed as a sum of powers of the direct effects, i.e.  $G_{indir} = \sum_{k \geq 1} G_{dir}^k$ . In particular, on a theoretical level, we shall observe the error in  $G_{obs}$  based on the above assumption of how similarities are *convolved* which we equate with the noise  $N$  from ??, although it is a systematic error. To do this, we shall in this section use a multivariate Gaussian to be able to control the correlation and as an extension of this, the mutual information between pairs of random variables. As we already know, correlation and mutual information is independent of the mean and variance of each of the variables however for a bivariate Gaussian the mutual information is given by the correlation as stated in the following proposition.

**Proposition 1.1.** *Given a bivariate normal distribution  $\mathbf{X} \sim \mathcal{N}(\boldsymbol{\mu}, \Sigma)$  where*

$$\Sigma = \begin{bmatrix} \sigma_1^2 & \rho\sigma_1\sigma_2 \\ \rho\sigma_1\sigma_2 & \sigma_2^2 \end{bmatrix}$$

*Then the mutual information  $I(X_1, X_2) = -\frac{1}{2} \ln(1 - \rho^2)$ .*

*Proof.* This follows by direct computation Using e.g. that  $I(X_1, X_2) = h(X_1) + h(X_2) - h(X_1, X_2)$   $\square$

Thus, if we know a correlation structure of a Gaussian random vector, we also know the mutual information between every pair of variables which we shall now use in the following made up example. Namely, what we shall denote as a Gaussian chain defined as a Gaussian random vector in the following way. Let  $\mathbf{X}$  be a  $d$ -dimensional Gaussian random vector, the  $\mathbf{X}$  is a standard Gaussian chain if it can be written in the following way in terms of  $d$  independent standard normal variables  $Z_i$  up to a permutation i.e. there exists a permutation of the variables of the random vector  $\mathbf{X}$  that permits the following structure.

$$\begin{aligned} X_1 &= Z_1 \\ X_2 &= \vec{\rho}_{1,2} X_1 + \sqrt{1 - \vec{\rho}_{1,2}^2} Z_2 \\ X_3 &= \vec{\rho}_{2,3} X_2 + \sqrt{1 - \vec{\rho}_{2,3}^2} Z_3 \\ &\vdots \\ X_d &= \vec{\rho}_{d-1,d} X_{d-1} + \sqrt{1 - \vec{\rho}_{d-1,d}^2} Z_d \end{aligned} \tag{1.1}$$

It follows that the marginals have variance 1 as clearly  $\text{Var}[X_1] = \text{Var}[Z_1] = 1$  and for  $i > 1$ ,  $\text{Var}[X_i] = \vec{\rho}_{i-1,i}^2 \text{Var}[X_{i-1}] + (1 - \vec{\rho}_{i-1,i}^2) \text{Var}[Z_i] = 1$  by independence of  $X_{i-1}$  and  $Z_i$ . Thus, the above structure also implies the Cholesky factorization of the correlation matrix for  $\mathbf{X}$ , namely

$$L = \begin{bmatrix} 1 & & & & & \\ \vec{\rho}_{1,2} & \sqrt{1 - \vec{\rho}_{1,2}^2} & & & & \\ \vec{\rho}_{2,3}\vec{\rho}_{1,2} & \vec{\rho}_{2,3}\sqrt{1 - \vec{\rho}_{1,2}^2} & \sqrt{1 - \vec{\rho}_{2,3}^2} & & & \\ \vdots & & & \ddots & & \\ \prod_{i=2}^d \vec{\rho}_{i-1,i} & \dots & \sqrt{1 - \vec{\rho}_{j-1,j}^2} \prod_{i=j+1}^d \vec{\rho}_{i-1,i} & \dots & \sqrt{1 - \vec{\rho}_{d-1,d}^2} & \end{bmatrix}$$

Which will allow us to both sample from such a chain and calculate  $G_{dir}$  and  $G_{obs}$  theoretically. However, in this example, it is easier to calculate the correlation between the variable  $X_i$  and  $X_j$  directly. As the variance of each variable is 1 we simply calculate the covariance. We assume without loss of generality that  $i < j$  whence

$$\text{Cov}[X_i, X_j] = \text{Cov}\left[X_i, \vec{\rho}_{j-1,j} X_{j-1} + \sqrt{1 - \vec{\rho}_{j-1,j}^2} Z_j\right] = \vec{\rho}_{j-1,j} \text{Cov}[X_i, X_{j-1}]$$

which by induction implies  $\rho_{i,j} = \prod_{k=i+1}^j \vec{\rho}_{k-1,k} = \rho_{j,i}$ . At this point, we are almost ready to use the algorithms from the previous chapter. First, we will only use ?? to deconvolve the network based on theoretical correlations and later mutual information. However, before doing so, we note that from the definition in Equation 1.1 the random variable  $\mathbf{X}$  exhibits a Markovian property. Namely, the  $X_i$  above can be understood discrete stochastic process as they are successively drawn based only on the previous variable  $X_{i-1}$  i.e.  $f(x_i | X_{i-1}, X_{i-2}, \dots, X_1) = f(x_i | X_{i-1})$ . Thus, if the algorithm works as intended, we should observe that the deconvolved network is a *chain* of variables as shown in the Figure 1.1. Thus, we now have the expected result, and we



**Figure 1.1:** The graphical representation of a Gaussian chain. Arrows signify a possible causal structure. If furthermore, one assumes that  $X_1$  is generated first, then  $X_2$  and so on, this is the only causal structure that would make sense.

proceed with using correlation and mutual information to try and rediscover this structure in the following two sections

### 1.1.1 Gaussian chain deconvolution using correlation

In this section, we will use the observed correlations as elements of  $G_{obs}$ . In particular, the  $(i,j)$  entry of  $G_{obs}$  is  $\rho_{i,j} = \prod_{k=i+1}^j \vec{\rho}_{k-1,k}$  when  $i < j$  and 0 otherwise. This makes  $G_{obs}$  strictly upper triangular. Note that although it makes sense to consider the correlation between a variable and itself, we shall as discussed before set the diagonal to 0. The reason for this becomes clear when we try to convolve  $G_{dir}$  based on the initial definition of a general Gaussian chain in Equation 1.1. We note that in ?? we usually (without an assumption of the topology of the random variables) use a symmetrical  $G_{obs}$ . We shall however postpone this discussion a bit and first use an upper triangular  $G_{obs}$ . In particular, we shall observe that we perfectly recover the *directional* correlations  $\vec{\rho}_{k-1,k}$  from Equation 1.1 through ??.

As  $G_{obs}$  is in this case strictly upper triangular, the spectral radius is 0 and hence we have no problems with convergence of the infinite sum of powers of (the uniquely defined)  $G_{dir}$ . From the above, it is clear that  $G_{obs}$  is given as follows

$$G_{obs} = \begin{bmatrix} 0 & \vec{\rho}_{1,2} & \vec{\rho}_{1,2} \vec{\rho}_{2,3} & \cdots & \prod_{k=2}^d \vec{\rho}_{k-1,k} \\ 0 & \vec{\rho}_{2,3} & \cdots & \prod_{k=3}^d \vec{\rho}_{k-1,k} \\ \ddots & & & \vdots \\ 0 & & \vec{\rho}_{d-1,d} & 0 \\ & & & 0 \end{bmatrix} \quad (1.2)$$

Now, let  $G_{dir}$  be given as follows

$$G_{dir} = \begin{bmatrix} 0 & \vec{\rho}_{1,2} \\ 0 & \vec{\rho}_{2,3} \\ \ddots & \ddots \\ 0 & \vec{\rho}_{d-1,d} \\ & 0 \end{bmatrix}$$

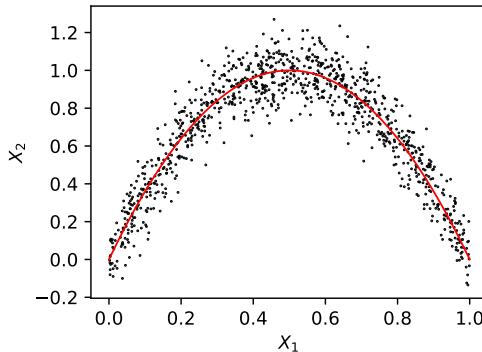
then  $G_{dir}^2$  is given by

$$G_{dir}^2 = \begin{bmatrix} 0 & 0 & \vec{\rho}_{1,2} \vec{\rho}_{2,3} \\ 0 & 0 & \vec{\rho}_{2,3} \vec{\rho}_{3,4} \\ \ddots & \ddots & \ddots \\ 0 & 0 & \vec{\rho}_{d-2,d-1} \vec{\rho}_{d-1,d} \\ 0 & 0 & 0 \end{bmatrix}$$

It is not hard to show that in fact  $\sum_{k \geq 1} G_{dir}^k = \sum_{k=1}^d G_{dir}^k = G_{obs}$ . Thus, if we know a graph topological ordering of the random variables corresponding to the structural causal model, we completely recover (without any error) the direct

dependencies/correlation from to the initial definition in Equation 1.1. This result holds for a general *chain* where  $Z_i$  can follow any distribution as long as they are uncorrelated. This follows from the above computation of  $\text{Cov}[X_i, X_j]$ , where no assumption of  $Z_j$  was needed except for correlation 0.

From the above, we might think that if we have a topological ordering of the random variables this is the preferred method, and it is as long as correlation is a good enough measure of similarity/codependency. Albeit this is only shown for the special case of a chain, in Section 1.2 we consider the more general case and conclude that this indeed holds. Regarding the comment on correlation being a good enough measure of similarity, a prototypical case is when joint probability density function of two variables resemble a parabola. Namely, let  $X_1 \sim \mathcal{U}(0, 1)$  and  $X_2 | X_1 \sim \mathcal{N}\left(1 - 4(x_1 - 1/2)^2, \sigma^2\right)$  i.e.  $X_2 = 1 - 4(X_1 - 1/2)^2 + \epsilon$  where  $\epsilon \sim \mathcal{N}(0, \sigma^2)$ . In Figure 1.2, 1000 samples from this distribution is shown for  $\sigma = 1/10$  along with the expectation  $\mathbb{E}[X_2|X_1]$ . It is not hard to show that the covariance between  $X_1$  and  $X_2$  is 0 however we clearly see a relationship between the two variables. In fact, computing the mutual information results in  $I(X_1, X_2) \approx 1.030$  implying  $X_1 \not\perp X_2$  i.e. there exists a higher order (non-linear) dependency. Thus, if the algorithm permits, we would prefer mutual information to correlation as we can then use observed higher order relationships to infer a causal structure. On a more technical point of view, we note that



**Figure 1.2:** 1000 samples generated from  $X_1 \sim \mathcal{U}(0, 1)$  and  $X_2 | X_1 \sim \mathcal{N}\left(1 - 4(x_1 - 1/2)^2, \sigma^2\right)$  with  $\sigma = 1/10$ . The mutual information is calculated theoretically to be  $I(X_1, X_2) \approx 1.030$  and repeated simulations show that the empirical correlation is symmetric around 0 supporting the claim that the underlying correlation is in fact 0

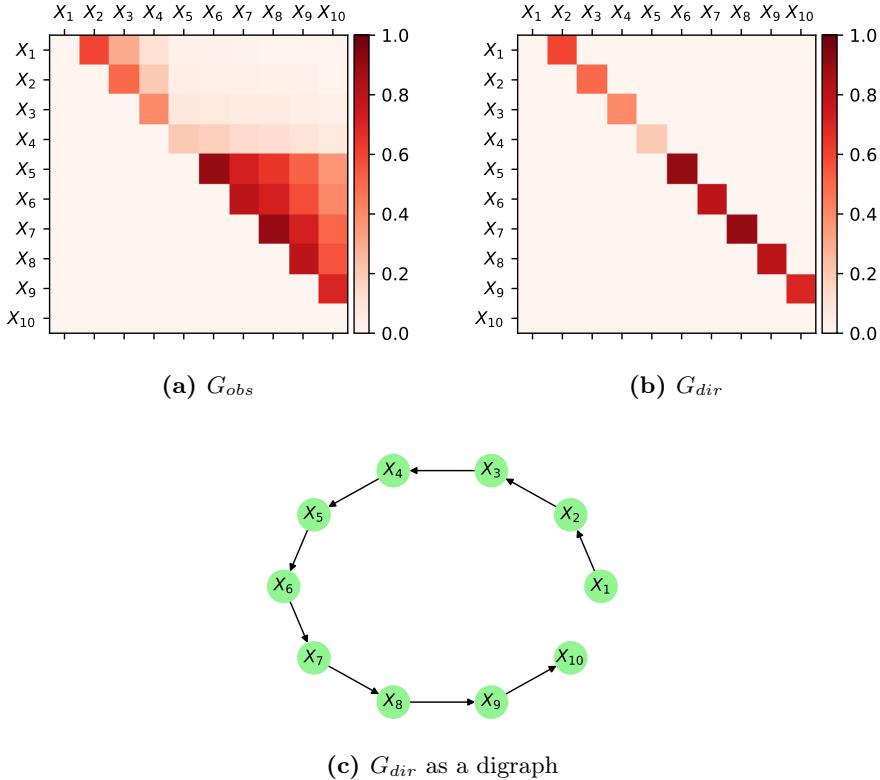
mutual information is a measure of how dense the joint distribution is, invariant to scale. In a way, it is a measure of how close the joint distribution is to a lower

dimensional manifold.

We proceed with a 10-Gaussian chain defined by the following correlations:

$$\begin{aligned} \rho_{1,2} &= 0.6, & \rho_{2,3} &= 0.5, & \rho_{3,4} &= 0.4 \\ \rho_{4,5} &= 0.2, & \rho_{5,6} &= 0.9, & \rho_{6,7} &= 0.8 \\ \rho_{7,8} &= 0.9, & \rho_{8,9} &= 0.8, & \rho_{9,10} &= 0.7 \end{aligned} \quad (1.3)$$

We have chosen correlations of different sizes to check if the deconvolution is robust in presence of both strong and weak links. In particular,  $X_5$  is only  $\rho_{4,5}^2 = 4\%$  of  $X_4$  and the remaining 96% is noise/inde describable variance i.e. a very weak link between the first part of the chain up to and including  $X_4$  and the rest. However, as discussed above, if let  $G_{obs}$  be upper triangular, we should completely rediscover these direct relations which is indeed also the case. In particular, from Figure 1.3 we observe that the inferred network, represented by  $G_{dir}$ , is indeed a chain of variables and is exactly equal to the theoretical  $G_{dir}$  as we would expect (up to very small rounding errors of the size  $10^{-16}$ ). The estimated  $G_{dir}$  is also shown as a directed graph which the initial topological assumption implies, with edges wherever  $G_{dir}$  is non-zero.



**Figure 1.3:** Results from using an upper triangular  $G_{obs}$  and correlation to infer the causal network structure. (a) shows the upper triangular  $G_{obs}$  with the correlation between every pair of variables. (b) shows the deconvolved  $G_{obs}$  and as we expect, the superdiagonal contains the original correlations given in Equation 1.3. (c) shows  $G_{dir}$  represented as a digraph and matches the expected result.

We now proceed to investigate what happens when we remove the prior information of the topological ordering. Namely, if  $G_{obs}$  is no longer triangular but symmetric. In particular, let  $T_{dir}$  be given as  $G_{dir}$  above. We then have that  $G_{dir}$  in the symmetric case is  $T_{dir} + T_{dir}^T$  and similarly for  $G_{obs}$ ,  $G_{obs} = T_{obs} + T_{obs}^T$ . Clearly,  $I + G_{obs}$  is positive definite as it is a proper correlation matrix. However, that also implies that we might have eigenvalues of  $G_{obs}$  less than or equal to  $-1/2$  which we know from ?? is not the result of a  $G_{dir}$  such that ?? holds as then the infinite sum diverges. However, as  $-1$  is not an eigenvalue of  $G_{obs}$ , we will investigate what happens if one tries to use ?? anyway.

But first, we shall discuss the errors being made using the symmetric  $G_{obs}$  and  $G_{dir}$  instead of triangular. Namely, we investigate the powers of  $G_{dir}$ :

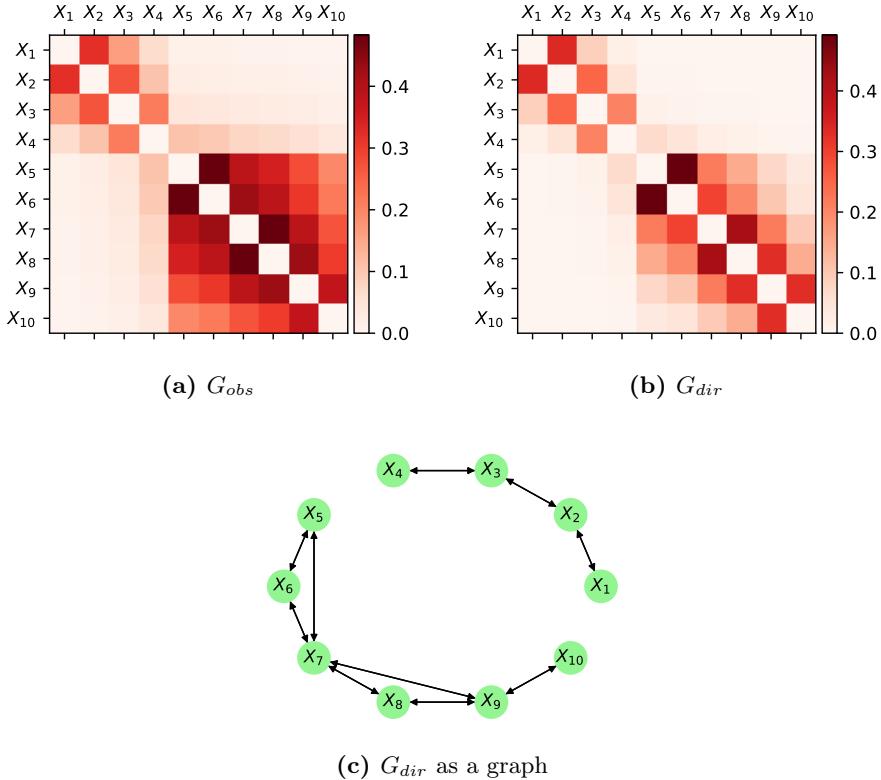
$$G_{dir}^2 = (T_{dir} + T_{dir}^T)^2 = T_{dir}^2 + (T_{dir}^T)^2 + T_{dir}T_{dir}^T + T_{dir}^TT_{dir}$$

Higher power can be calculated similarly, but for the second power we already observe an error. The first two terms corresponds to a reflection of the second order effects that we saw above and know to be true, whence the final two terms, that add to a diagonal matrix, is an error and will propagate with higher order powers of  $G_{dir}$ . Through simple calculation the resulting error is

$$T_{dir}T_{dir}^T + T_{dir}^TT_{dir} = \begin{bmatrix} \rho_{1,2}^2 + \rho_{2,3}^2 & & & \\ & \rho_{2,3}^2 + \rho_{3,4}^2 & & \\ & & \ddots & \\ & & & \rho_{d-2,d-1}^2 + \rho_{d-1,d}^2 \end{bmatrix}$$

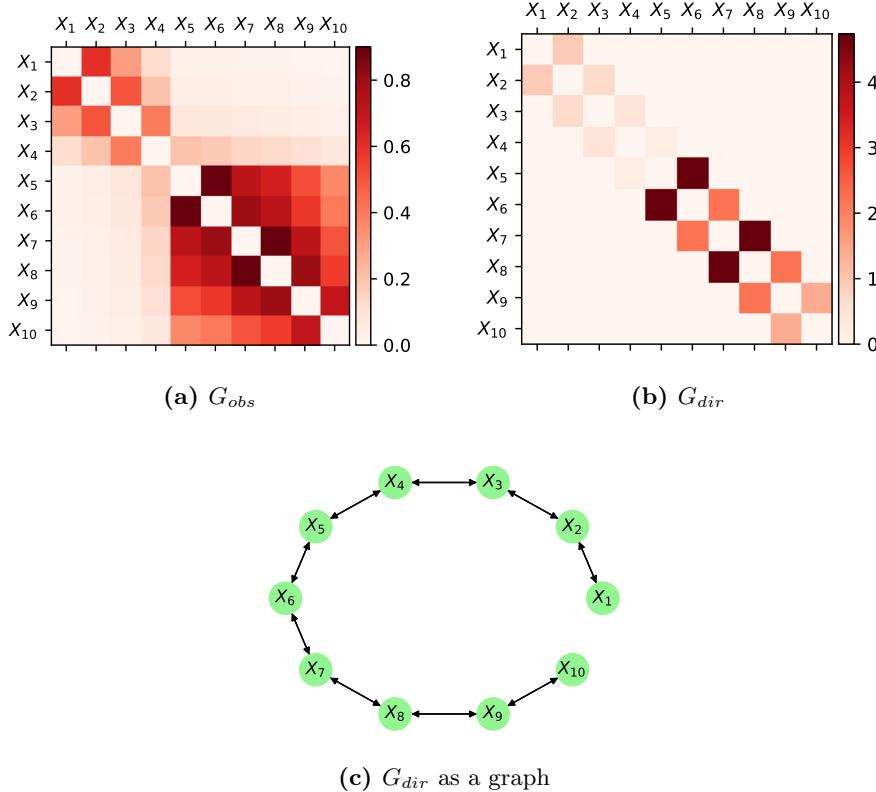
Thus, for chains, we expect larger errors for sub-chains with strong links i.e. a subgraph of a chain that is also a chain where the correlation from one variable to the next is large. Using  $G_{obs} = T_{obs} + T_{obs}^T$  we have that the smallest eigenvalue is approximately  $\lambda_{\min} \approx -0.92263$  thus, multiplying  $G_{obs}$  with a constant  $c_s < 0.54192$  will make  $G_{dir}$  have spectral radius at most 1. The results vary with one or two edges for the choice of  $c_s$  and in the following we have chosen  $c_s = 0.53651$  resulting in  $\rho(G_{dir}) \approx 0.98020$  and  $\tilde{G}_{obs}$  and  $\tilde{G}_{dir}$  as seen in Figure 1.4. From Figure 1.4b we see that some correlation/association seem to bleed to variables 2 or 3 edges away which we of course know is not true given the Markov property discussed above. However, it is also clear that the error here is that the original assumption does not hold since using a symmetric  $G_{obs}$  imply that the measure of similarity flows both ways where in this case it is very much unidirectional.

From Figure 1.4 conclude that we are somewhat able to rediscover the causal structure. Not surprisingly, we observe that the weak link between  $X_4$  and  $X_5$  is one of the first to break and that we observe some extra edges between the later more strongly linked sub-chain as by the above discussion. Finally, before presenting the results for the unscaled  $G_{obs}$  (where the smallest eigenvalue is smaller than  $-1/2$ ) we note that changing the parameter  $\alpha$  in ?? did not have much of an effect indicating that the network is quite sparse (as we also know it to be) as even removing 65% of the smallest correlations from  $G_{obs}$  did not have any effect. The chosen threshold of  $t = 0.2$  on  $G_{dir}$  seemed to be the best compromise of a connected graph and the density of the edges (although this is somewhat biased from prior knowledge of the true graphical structure).



**Figure 1.4:** Using a symmetric  $G_{obs}$  as shown in (a), we observe that higher order effects start to emerge as can be seen in (b). The main response is still in the superdiagonal and subdiagonal as we expect, where some similarity seems to bleed to nearby nodes/variables thus making the threshold used important for the resulting graph. For (c), a threshold  $t = 0.2$  was used to obtain a decent compromise between connectedness and denseness of the direct association.

Finally, we try using the unscaled  $G_{obs}$  in ???. Interestingly, we find that the true structure emerges as can be seen from Figure 1.5. Although the *correlations* in Figure 1.5b are not really correlations they do resemble those discovered in Figure 1.3b. On closer inspection, it is not apparent how they are related except that it is a non-linear relationship. Although in this case it seemed to work not rescaling  $G_{obs}$  in order to discover the causal structure we will in general not apply this to real world scenarios as the method is not well-defined in terms of assumptions and what the resulting  $G_{dir}$  should be interpreted as. Thus, at this point we have a rather good understanding of how the method works on Gaussian chains if one uses correlation as a measure of association. Furthermore,



**Figure 1.5:** Using an unscaled (symmetric)  $G_{obs}$  results in a good recovery of the causal structure as seen in (b) and (c). However, at this point it is not clear whether it holds only for chains and using correlation or if it is a more general phenomenon.

if one knows (a plausible) topological ordering of the variables, we are able to perfectly rediscover the network of direct dependencies. However, as noted above, correlation is not always a good measure of similarity. Thus, we proceed experimenting with mutual information on the same Gaussian chain.

### 1.1.2 Gaussian chain deconvolution using mutual information

In this section, we continue the example from the previous section but instead of using correlation as a measure of similarity, we will use mutual information. Immediately, we note that mutual information or Copula entropy does not propagate as assumed in ???. As an example, from Proposition 1.1, we know that the mutual information in the case of a Gaussian chain between a variable  $X_i$  and the next variable  $X_{i+1}$  is  $-1/2 \log(1 - \rho_{i,i+1}^2)$  and similarly, using Equation 1.2, we have that

$$I(X_i, X_{i+2}) = -\frac{1}{2} \log(1 - \rho_{i,i+1}^2 \rho_{i+1,i+2}^2)$$

Thus, if  $G_{dir}$  is triangular, using ?? we should observe the following at the  $(i, i+2)$  entry of  $G_{obs}$  instead

$$\frac{1}{4} \log(1 - \rho_{i,i+1}^2) \log(1 - \rho_{i+1,i+2}^2)$$

I.e. we make an error (which we could take to be the noise  $N$  from ??) for second order effects equal to

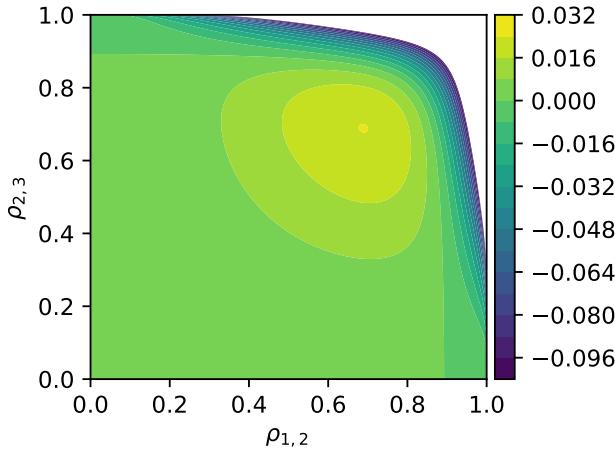
$$-\frac{1}{2} \log(1 - \rho_{i,i+1}^2 \rho_{i+1,i+2}^2) - \frac{1}{4} \log(1 - \rho_{i,i+1}^2) \log(1 - \rho_{i+1,i+2}^2)$$

In general, for a Gaussian chain, we have that

$$N_{i,j} = -\frac{1}{2} \log \left( 1 - \prod_{k=i+1}^j \rho_{k-1,k}^2 \right) - \left( -\frac{1}{2} \right)^{j-i} \prod_{k=i+1}^j \log(1 - \rho_{k-1,k}^2)$$

As we will see in Figure 1.6 and Figure 1.7, for Gaussian chains we can expect some of the same bleeding behavior as observed in Figure 1.4 where we did not use the topological ordering but based the deconvolution on correlation. In particular, from the figures below, we see that for 3-chains, the error is in many cases close to 0 and for most combinations of  $\rho_{1,2}$  and  $\rho_{2,3}$  less than 0.1. Furthermore, we note that the errors are the largest when it is a strongly connected 3-chain i.e. if both  $\rho_{1,2}$  and  $\rho_{2,3}$  are close to 1 which again resemble the behavior seen in the case of a symmetrical  $G_{obs}$  using correlation as the measure of association although in this case, the error does not propagate to the same extent which we shall also see shortly, when applying the deconvolution algorithm. Notice that as only the absolute value of the correlation matters, we only show the error for  $\rho_{1,2}, \rho_{2,3} \geq 0$ .

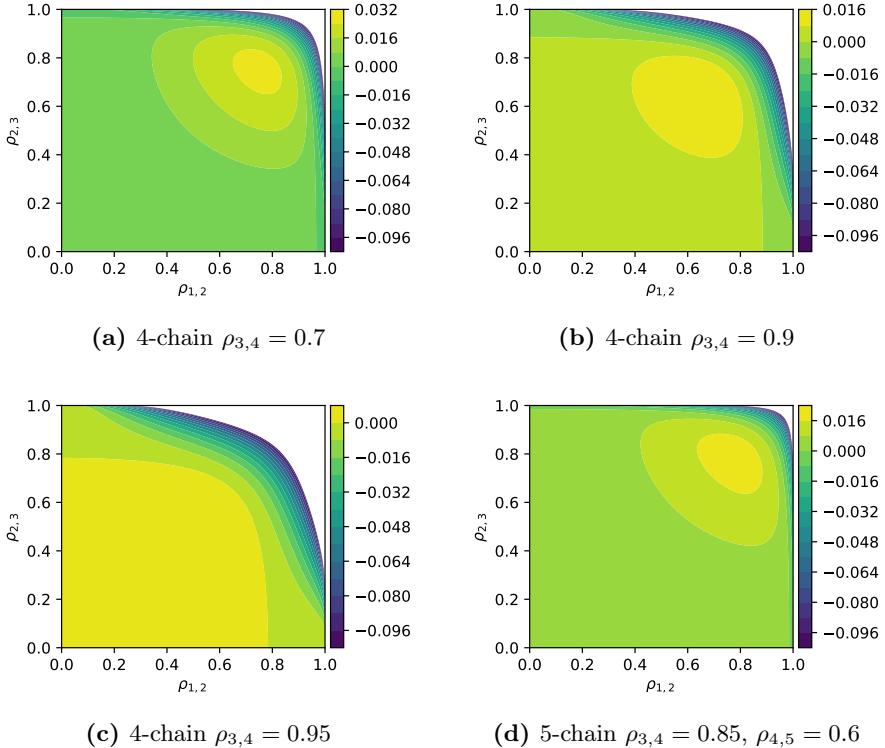
We extend the above discussion to 4- and 5-chains (i.e.  $j = i + 3$  and  $j = i + 4$  in the above expression for  $N_{i,j}$ ) to see how the error propagates in more detail. This is shown in Figure 1.7 for three different scenarios of a 4-chain and a



**Figure 1.6:** The error made by the assumption of  $G_{obs}$  and  $G_{dir}$  for second order observed effect. Although mutual information does not comply with the underlying assumptions, we observe that in the case of a Gaussian 2-chain, we can expect the error to be relatively small.

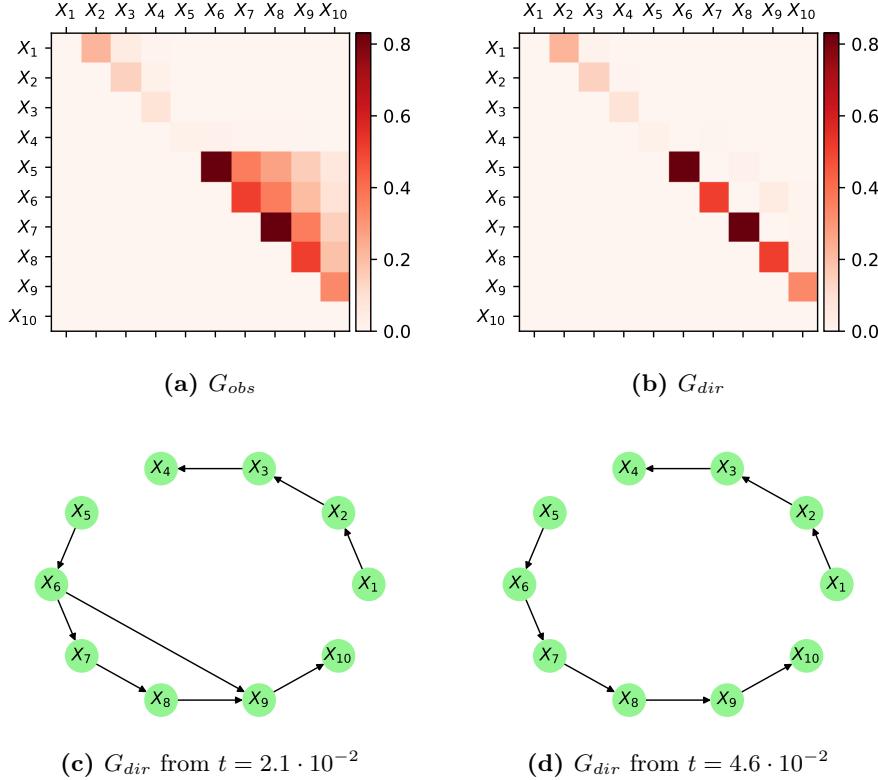
single 5-chain. In particular, as the error  $N_{i,j}$  is symmetric in  $\rho_{1,2}$ ,  $\rho_{2,3}$  and  $\rho_{3,4}$  (and  $\rho_{4,5}$  in the case of a 5-chain) and because it is hard to accurately show four or five dimensional surfaces, we keep to a fixed set of  $\rho_{3,4}$  and  $\rho_{4,5}$  when investigating. For the 4-chain, choosing  $\rho_{2,3} = 0.9$  (corresponding to mutual information about 0.8304) approximately results in the same error as in Figure 1.6 and if  $\rho_{2,3}$  is above e.g. 0.95, we get a worse propagation of errors compared to the 3-chain. Finally, from Figure 1.7d, we see the same picture i.e. that keeping the correlations and hence information between subsequent variable low results in smaller errors in  $G_{obs}$  and hence the inferred  $G_{dir}$ . Note that under the assumption of a topological ordering such that  $G_{obs}$  is strictly upper triangular results in  $\rho(G_{obs}) = 0$  such that no rescaling is necessary (although different choices of the base of the logarithm would have an effect on how much higher order associations influence  $G_{dir}$ ).

Having obtained a good understanding of how shifting to mutual information instead of correlation in the case of Gaussian chains, we continue with the above example now using mutual information as the elements of  $G_{obs}$  based on the correlation matrix from the previous section. Using a triangular  $G_{obs}$  we observe similar behavior to that of original example using a triangular  $G_{obs}$  but with correlation as can be seen from Figure 1.8. In particular, we do not observe the same magnitude of bleeding effects as in Figure 1.4. However, we observe



**Figure 1.7:** Errors of convolving mutual information along a 4-chain (a), (b), (c) and a 5-chain (d). Due to symmetry in the expression of the error, only the first 2 links i.e.  $\rho_{1,2}$  and  $\rho_{2,3}$  are varied on  $[0, 1]$  respectively. Only positive correlations are shown as the sign of the correlation cancels in the expression for the error. We note that large correlations and hence large mutual information on each edge results in larger error. In particular, when not too many of the links are strong, we have almost 0 error.

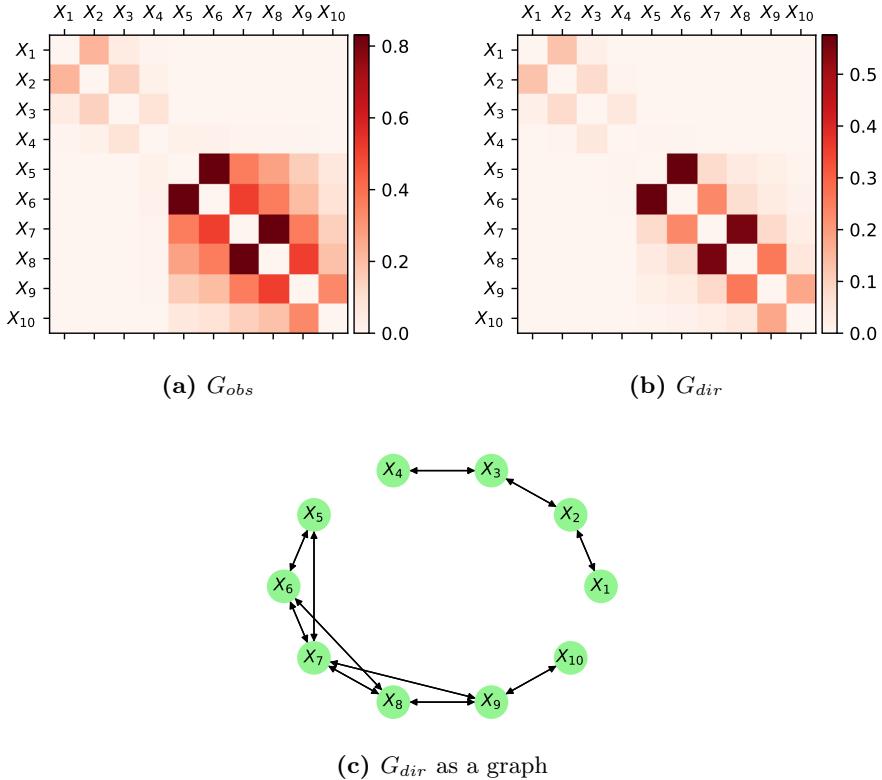
the same tendency to miss weak connections as was also observed in Figure 1.4. All in all, we get very good results using a triangular  $G_{obs}$  even though mutual information does not have the same properties as correlation. In particular, this is what we expected as we have only used  $\rho_{i,i+1} \leq 0.9$ , from the above investigation of the error.



**Figure 1.8:** Using mutual information as the measure of similarity as well as assuming a topological order i.e. making  $G_{obs}$  strictly triangular as seen in (a) we almost perfectly infer  $G_{dir}$  as seen in (b) except for  $[G_{dir}]_{6,9}$ . Choosing cutoffs  $t = 2.1 \cdot 10^{-2}$  (c) and  $t = 4.6 \cdot 10^{-2}$  (d) it is clear that adjusting the threshold we can get a better result than using a symmetric  $G_{obs}$  with correlation.

Finally, we use the corresponding symmetric  $G_{obs}$  (rescaled such that the largest absolute eigenvalue of  $G_{dir}$  is 0.99) which results in  $G_{dir}$  and the graph using a threshold  $t = 4.68 \cdot 10^{-2}$  shown in Figure 1.9. Again, we observe some bleeding on the more strongly connected sub-chain as with the symmetric  $G_{obs}$  using correlation in Figure 1.4. Again, we observe comparable results and note that increasing the threshold would disconnect  $X_3$  and  $X_4$  before removing the higher order effects.

In conclusion, we have seen what errors can arise in the discovered network using both correlation and mutual information as the measure of association. Namely, long strongly connected chains seem to be a problem if one does not know a

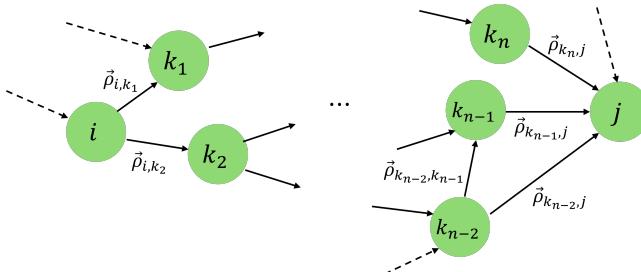


**Figure 1.9:** Using a symmetric  $G_{obs}$  containing the observed mutual information (a) we infer a  $G_{dir}$  (b) comparable to that if we had used correlation instead. Choosing the threshold  $t = 4.88 \cdot 10^{-2}$  seem a good compromise between connectedness and density resulting in an almost identical discovered network structure to that of using a symmetric correlation  $G_{obs}$ .

topological ordering of the variables, in which case these are heavily reduced as seen in Figure 1.3 and Figure 1.8. Thus, we proceed in the next section by considering a more complicated underlying (Gaussian) network to observe if other unwanted effects can occur and if a topological ordering is necessary if the network is not simply a path.

## 1.2 Directed acyclic Gaussian graphs

In this section, we will expand on the results from the previous section by considering a more general structure. In particular, let  $\mathcal{G}$  be a directed acyclic graph with nodes corresponding to variables from a random vector  $\mathbf{X}$  with directed edges indicating direct dependencies. Clearly, such a DAG has a topological ordering and as such we shall index the variables 1 through  $d$  such that if the index of a variable is  $i$ , and  $j$  is the index of another element of the random vector  $\mathbf{X}$ , then  $i < j$  implies there is no (directed) path from  $j$  to  $i$ . Note that since a topological ordering is not necessarily unique, we can not infer that there is a (directed) path from  $i$  to  $j$  or even if  $k$  is reachable from  $j$  (i.e. there exists a path from  $j$  to  $k$ ) it does not follow that  $k$  is reachable from  $i$ . In Figure 1.10 a subset of such a DAG is shown with a possible labelling where  $i < j$  and  $k_m < k_n$  when  $m < n$ . It is then the weights along these directed edges which we will once again call  $G_{dir}$  that we wish to infer based on the transitive closure. As an example, from Figure 1.10, the transitive closure would result in an observed similarity between  $i$  and  $j$  although no single direct edge connects the two variables. From the definition of the labels, it is clear



**Figure 1.10:** A general (linear) network represented as a DAG. The directed edge weights  $\vec{\rho}_{k,l}$  specify how much the variable index  $k$  make up of variable  $l$ . Although  $i$  and  $j$  are not directly connected, multiple paths may exist between the two nodes, making the propagation of similarity more complex from that of a chain.

that  $G_{dir}$  is once again strictly upper triangular as entries below the diagonal corresponds to edges going from a random variable with an index  $i$  to another random variable with index  $j$  such that  $i > j$  which is clearly a contradiction. Also, the diagonal elements are 0 as there can not be any loops in DAGs.

Similarly to the definition of (Gaussian) chains, based on  $d$  independent (or even just pairwise uncorrelated) random variables  $Z_i$  we can define a general network

of random variables  $X_i$  based on  $\mathbf{Z}$  in the following way

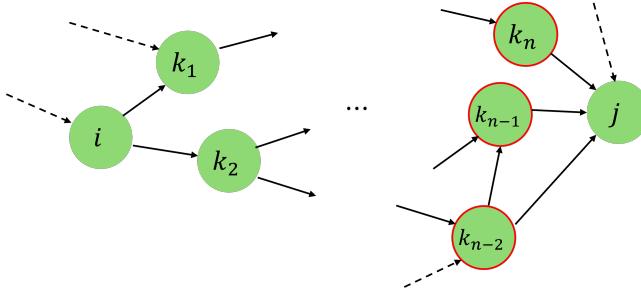
$$\begin{aligned} X_1 &= Z_1 \\ X_2 &= \vec{\rho}_{1,2}X_1 + \sqrt{1 - \vec{\rho}_{1,2}^2}Z_2 \\ X_3 &= \vec{\rho}_{1,3}X_1 + \vec{\rho}_{2,3}X_2 + c_3Z_3 \\ &\vdots \\ X_d &= \sum_{k < d} \vec{\rho}_{k,d}X_k + c_dZ_d \end{aligned} \tag{1.4}$$

where  $c_i$  is chosen such that  $\text{Var}(X_i) = 1$ . This is done to make the analysis later on simpler as then covariance and correlation are equal and  $\vec{\rho}_{i,j}$  becomes the *direct* correlation between the variables indexed  $i$  and  $j$  as shown in Figure 1.10. Of course, for the variance of each random variable to be 1 there must be some constraints on the chosen  $\vec{\rho}_{i,j}$  such as neither one of them can exceed 1 in absolute value. Furthermore, consider the following bound on the variance of  $X_i$  assuming  $c_k$  for  $k < i$  have been chosen such that  $\text{Var}(X_k) = 1$ .

$$\begin{aligned} \text{Var}[X_i] &= \sum_{k < i} \vec{\rho}_{k,i}^2 + 2 \sum_{k < l < i} \vec{\rho}_{k,i}\vec{\rho}_{l,i} \text{Cov}[X_k, X_l] + c_i^2 \\ &\leq \sum_{k < i} \vec{\rho}_{k,i}^2 + 2 \sum_{k < l < i} \vec{\rho}_{k,i}\vec{\rho}_{l,i} + c_i^2 \\ &= \left( \sum_{k < i} \rho_{k,i} \right)^2 + c_i^2 \end{aligned} \tag{1.5}$$

where we have used that  $Z_i$  is uncorrelated with  $X_k$  for  $k < i$  and that the covariance between variables with variance 1 is at most 1 to obtain the inequality. Hence, choosing the sum of the ingoing edges to be at most 1 for every node ensures that the constants  $c_i$  for  $i \in \{2, \dots, d\}$  exist in order to make the variance of each  $X_i$  1. This, we will use in the following example to easily build a network such that  $\vec{\rho}_{i,j}$  is the pure correlation.

However, before constructing an example and using bot correlation and mutual information we must determine the theoretical  $G_{obs}$  for both cases. To do this, we shall consider the  $(i, j)$  element of  $G_{obs}$  when using correlation as a measure of similarity and later use mutual information based on these correlations and Proposition 1.1 in the case of  $\mathbf{Z}$  being a Gaussian random vector. To calculate  $[G_{obs}]_{i,j}$  we shall consider the immediate predecessors to node  $j$  in the graph  $\mathcal{G}$  corresponding to Equation 1.4. The immediate predecessors or *in-neighbors* of a node  $j$  is denoted  $N^-(X_j)$  or in shorthand notation  $N_j^-$ . An example of this is shown in Figure 1.11 where the in-neighbors of  $j$  has been marked in red. With this notation, we proceed with the computation of the  $(i, j)$  entry of  $G_{obs}$  which is the covariance between  $X_i$  and  $X_j$  when  $i < j$  and 0 elsewhere.



**Figure 1.11:** For node  $j$ , the set  $N_j^-$  is illustrated with red borders. It is exactly the set of nodes going directly into  $j$ . We note that an in-neighbor  $l$  of in-neighbor  $k$  of node  $j$  can also be an in-neighbor of  $j$  i.e.  $l$  can influence both  $k$  and  $j$  whilst  $k$  also directly influenced  $j$ . It is in particular these direct dependencies we want to be sure of as their existence makes the network more complex but failing to discover these can lead to a significant reduction in prediction accuracy.

$$\begin{aligned}
 [G_{obs}]_{i,j} &= \text{Cov} \left[ X_i, \sum_{k \in N_j^-} \vec{\rho}_{k,j} X_k + c_j Z_j \right] \\
 &= \text{Cov} \left[ X_i, \sum_{k \in N_j^-} \vec{\rho}_{k,j} X_k \right] \\
 &= \sum_{k \in N_j^-} \vec{\rho}_{k,j} \text{Cov}[X_i, X_k] \\
 &= \sum_{k=1}^{j-1} \vec{\rho}_{k,j} \text{Cov}[X_i, X_k] \\
 &= \vec{\rho}_{i,j} + \sum_{k=1}^d \vec{\rho}_{k,j} [G_{obs}]_{i,k}
 \end{aligned} \tag{1.6}$$

For the fourth equality, we have used that  $\vec{\rho}_{k,j} = 0$  whenever  $k \notin N_j^-$  which again for the fifth equality holds for any  $k \geq j$ . Furthermore, since  $[G_{obs}]_{i,i} = 0$  we need to add  $\vec{\rho}_{i,j}$  to make the final equality hold. It is clear that the above can also be expressed as a matrix equation, namely

$$G_{obs} = G_{obs} G_{dir} + G_{dir}$$

Hence, as  $G_{dir}$  is strictly upper triangular thus making  $I - G_{dir}$  invertible, we can directly express  $G_{obs}$  in terms of  $G_{dir}$ . We find that

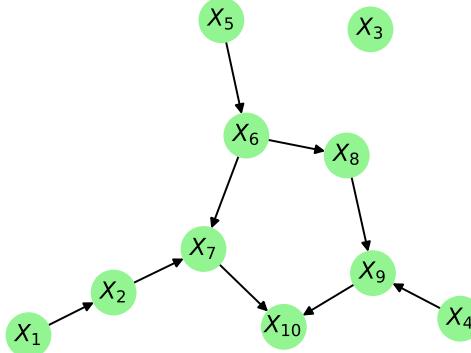
$$G_{obs} = G_{dir} (I - G_{dir})^{-1}$$

which we recognize as ?? hence also for a general network (and not just a chain), using correlation and knowing/assuming a topological order of the random variables we are able to perfectly rediscover  $G_{dir}$  from  $G_{obs}$ .

With the above, we then define an example Gaussian network with the following weights and shown in Figure 1.12 to get a better understanding of this example hopefully should reappear after deconvolution using both correlation and mutual information respectively.

$$\begin{aligned} \vec{\rho}_{1,2} &= 0.7, & \vec{\rho}_{5,6} &= 0.5, & \vec{\rho}_{2,7} &= 0.3 \\ \vec{\rho}_{6,7} &= 0.3, & \vec{\rho}_{6,8} &= 0.7, & \vec{\rho}_{4,9} &= 0.3 \\ \vec{\rho}_{8,9} &= 0.3, & \vec{\rho}_{7,10} &= 0.4, & \vec{\rho}_{9,10} &= 0.2 \end{aligned} \quad (1.7)$$

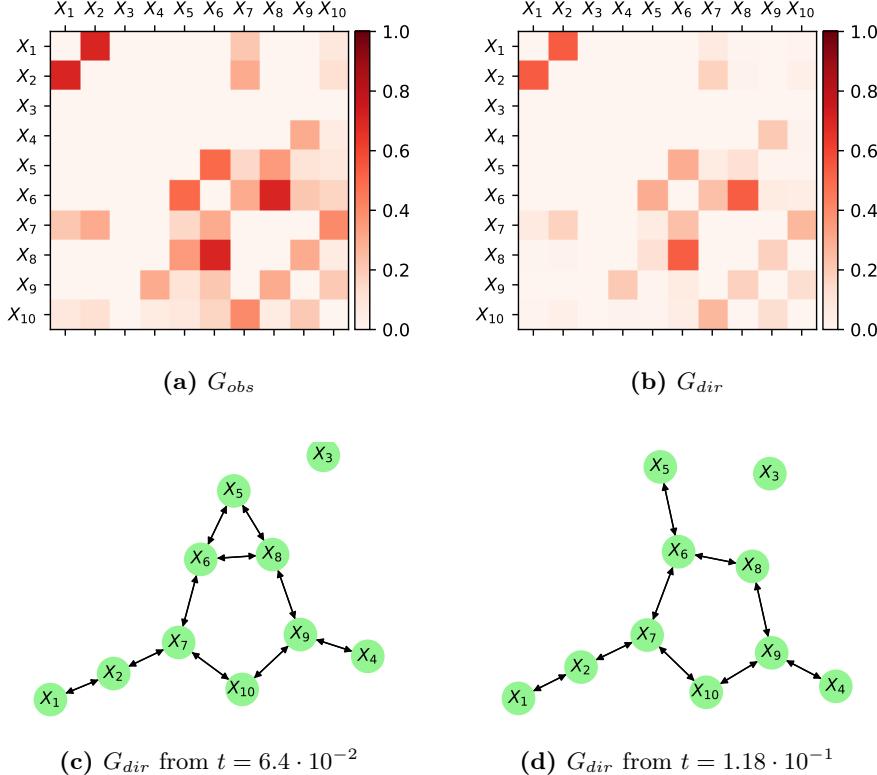
In particular, from Equation 1.5 and Figure 1.6 and Figure 1.7, we suspect that the bleeding effects observed for the Gaussian chain won't appear to the same extent in this case.



**Figure 1.12:** The graph defined in Equation 1.7. Note that  $X_3$  is neither influenced nor influences any other variable. It is of course in our interest to accurately tell if  $X_3$  should be considered if we try to infer a probability distribution on e.g.  $X_{10}$  given observations of the other variables.

Applying the deconvolution algorithm, we obtain the results in ?? which trivially, from the above analysis on  $G_{obs}$ , results in a perfect reconstruction of the network. If instead, we do not assume a topological structure, we can also recover the structure, although we need to tune the threshold as can be seen from Figure 1.13. Tuning the  $\alpha$  and  $\beta$  did not have much of an effect. Actually, decreasing  $\beta$  seemed to worsen the results which is also in line with our expectations as choosing smaller  $\beta$  skews the effects of higher order interactions. Thus,

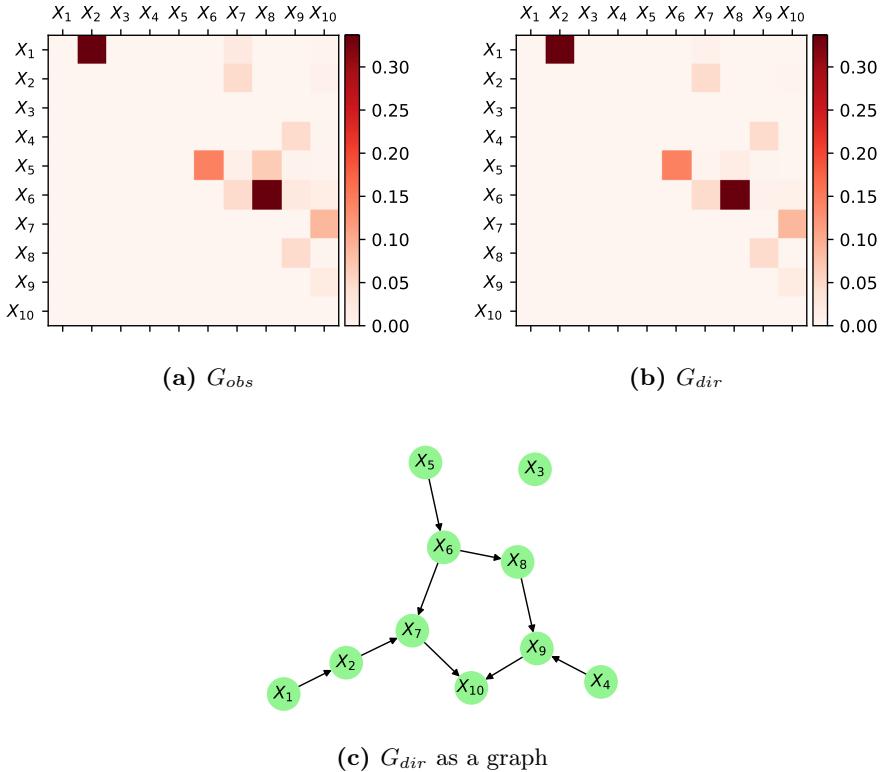
it is primarily the threshold that we want to tune in this case and choosing  $t = 1.18 \cdot 10^{-1}$  we accurately infer the network structure contrary to the results from the Gaussian chain. However, we still observe second order effects i.e. the edge between  $X_5$  and  $X_8$  which was also the case in Figure 1.4 Finally, before



**Figure 1.13:** Not knowing the topological structure and thus using a symmetric  $G_{obs}$  (a) we obtain the  $G_{dir}$  in (b). Clearly, there is some bleeding, but choosing the threshold  $t = 1.18 \cdot 10^{-1}$  we can accurately rediscover the network structure up to a direction on the edges. As with the previous example of Gaussian chains, we observe some tendency to inaccurately filter out second order effects as can be seen in (c) where  $X_5$  and  $X_8$  is connected.

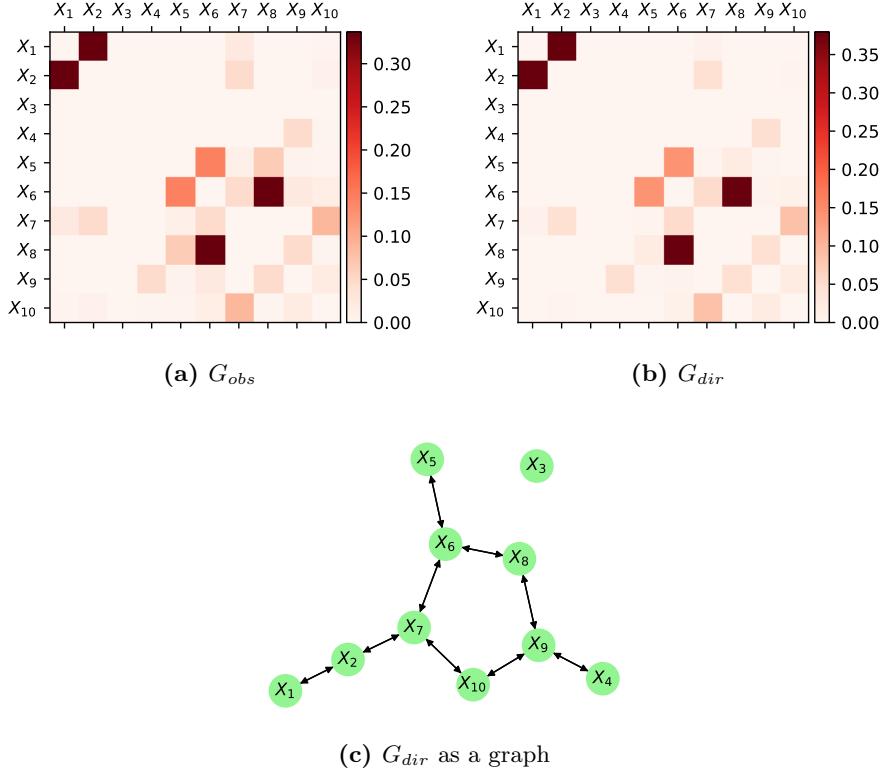
continuing with results regarding the different methods for estimating mutual information, we present the results from above using mutual information instead of correlation as the measure of similarity. Namely, once again assuming the topological order such that  $G_{obs}$  is strictly upper triangular and hence no need for rescaling we get the results shown in Figure 1.14. As expected, we observe on par performance to using correlation. Only the edge from 5 to 8

being almost as strong as 9 to 10 could be a problem i.e. choosing a threshold a little larger than  $t = 1.7 \cdot 10^{-2}$  (which is quite small and has been used for Figure 1.14c) would have resulted in an edge from  $X_5$  to  $X_8$ . Hence, in a real world example we might have chosen to either leave out both edges which depending on the scenario may or may not be an acceptable error or include the both of them.



**Figure 1.14:** Using mutual information instead of correlation results in  $G_{obs}$  shown in (a). The non-linear map from correlation to mutual information only effects the resulting  $G_{dir}$  a little as shown in (b) when comparing to the  $\rho_{i,j}$  from Equation 1.7. Choosing the relatively small threshold  $t = 1.7 \cdot 10^{-2}$  results in a perfect reconstruction of the graph structure.

Furthermore, using a symmetric  $G_{obs}$  instead i.e. no assumption on topology, does not seem to have much of an effect as seen from Figure 1.15. Although there still is a small weight on the edge from  $X_5$  to  $X_8$ , by choosing the threshold  $t = 1.96 \cdot 10^{-2}$  we can accurately construct the true network structure.



**Figure 1.15:** Using a symmetric  $G_{obs}$  instead of an upper triangular  $G_{obs}$  result in near identical  $G_{dir}$  in terms of relative weights on the edges. Namely, the  $G_{dir}$  shown in (b) seem to be almost a scaled version of the (reflected)  $G_{dir}$  derived from a triangular  $G_{obs}$ . Thus, as (c) also shows, we can accurately infer the structure of the network using a threshold  $t = 1.96 \cdot 10^{-2}$ .

In conclusion, we observe a useful property of more general networks that for both mutual information and correlation, the additional assumption of the topological order does not have much of an effect in these cases contrary to what we observed for Gaussian chains and linear chain models in general, when using correlation.

## 1.3 CE computation

Having discussed the strengths and weaknesses of ??, we now turn our attention to ???. Namely, in this section we shall discuss the different methods from ?? and how they perform on two examples. Once again, we shall base our results on two examples. The first is a simple case, where we shall see what to be aware of when initially the observations are transformed through estimated distribution functions as well as how accurate the different methods for estimating the Copula entropy i.e. mutual are. Continuing from the first example, we shall once again consider the network from Section 1.2 specified by Equation 1.7. In particular, we will see how well the combined framework performs on an example we have already seen to be quite solvable if one uses accurate estimates of the mutual information which we previously calculated theoretically.

### 1.3.1 Spline and KDE based CE estimation

Before discussing the first example, we shall however discuss the problem with the spline based method and using histograms in general. Namely, we shall first see that if one were to just simply use a raw binning approach, the number of bins  $N$  influences the estimate a lot and no number of bins seems to perform well on all cases. Namely, let  $\mathbf{X}$  be a bivariate Gaussian with correlation  $\rho$ , then the Copula density looks as in Figure 1.30. In particular, we notice the peaks at  $(0, 0)$  and  $(1, 1)$  which result in a lot of mutual information. Now, simulating  $n = 400$  observations from the joint distribution and transforming to the unit square through the marginal distribution function for varying correlations  $\rho$ , we can compare the estimated mutual information  $I_{estim}$  using the results from ?? to the true mutual information given by  $I_{exact} = -\frac{1}{2} \log(1 - \rho^2)$ . The results are shown in Figure 1.16 where we report the relative size of the estimate and the exact mutual information and in Figure 1.17 where the difference is reported. From Figure 1.16, we might choose  $N \approx 10$  as in [?] however for large correlations, we drastically underestimate mutual information. Increasing the number of bins to e.g.  $N = 50$  corrects this error for large correlations, but then small correlations have a relatively large error of around 0.5 which is a relatively large error when comparing to the error the deconvolution step makes as illustrated in Figure 1.7.

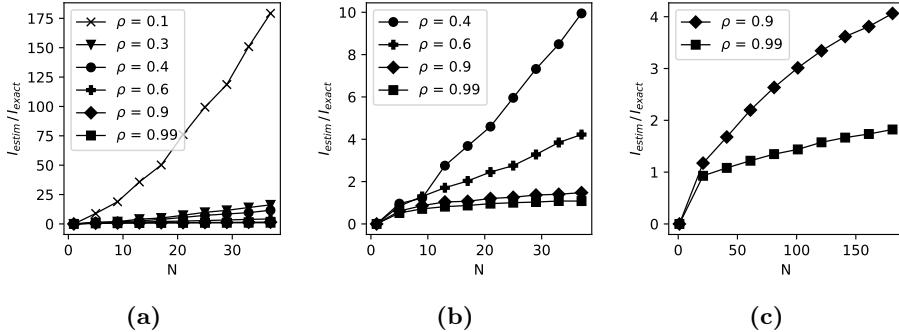


Figure 1.16

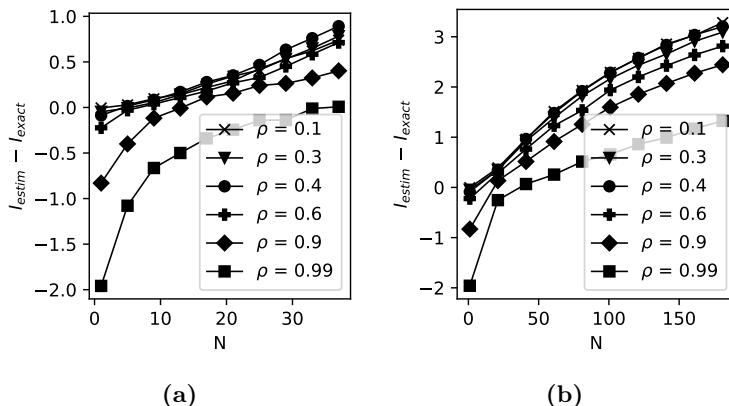
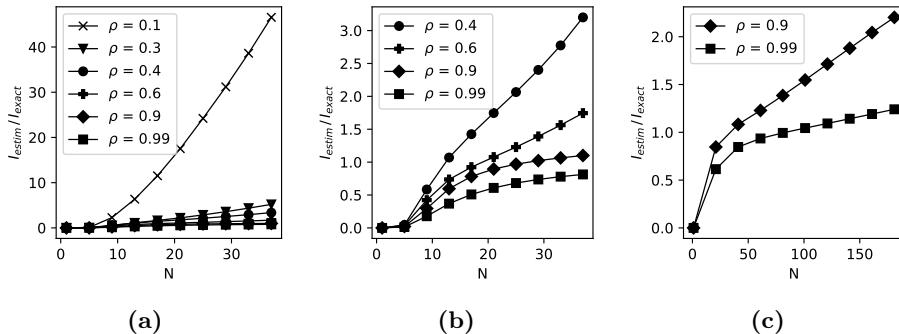
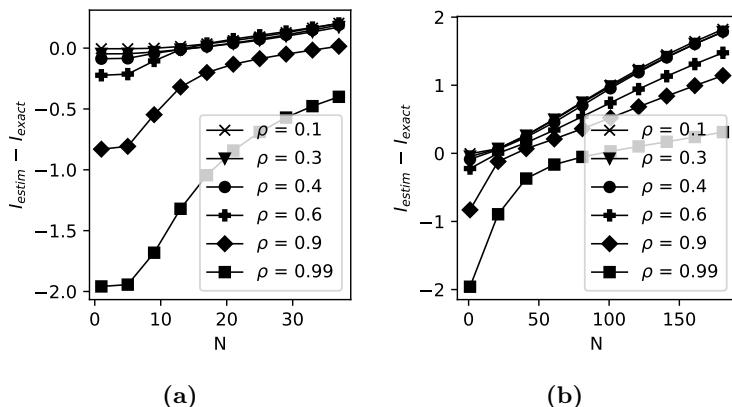


Figure 1.17

We thus proceed with using the B-spline approach. Similar to the above results, in Figure 1.18 and Figure 1.19, we observe that B-spline approach is prone to the same errors as the raw binning approach. However, from Figure 1.19 we see that the error are smaller for the B-spline based approach but also that a better choice for the number of bins is around  $N = 60$  contrary to the results of [?].



**Figure 1.18:** Evaluation of MI for old method for different  $N$ . Ligner der er knæk ved fporhold lig 1. Men ved næremere undersøgelse blev det fundet ud af at det ikke helt er tilfældet, og derudover vil der skulle laves en algoritmisk måde at finde dette knæk på. Savitzky–Golay filter kunne være en mulighed, eller gruppere e.g. 5 forskellige bins og tag gennemsnit. Efter smoothing kan anden afledte tæt på 0 bruges, til at finde hvornår stykket bliver fladt (tilnærmelses vist)

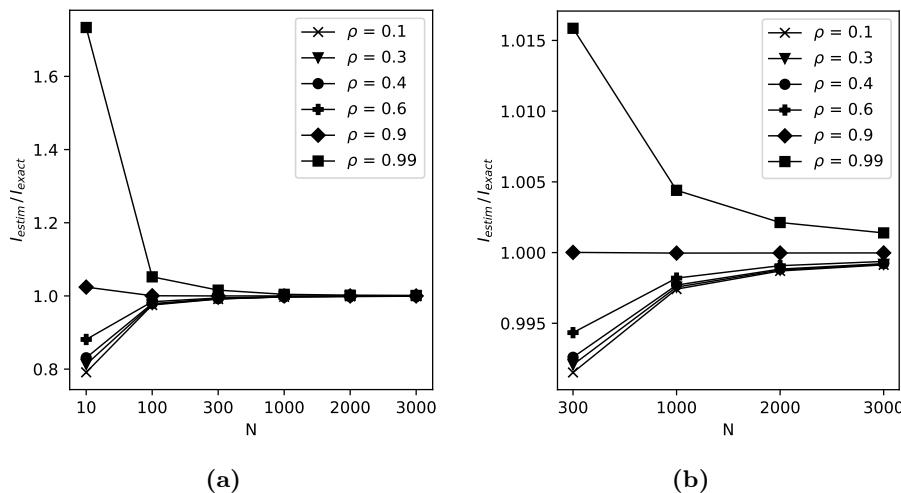


**Figure 1.19:** through repeated trials, we see that this method is actually quite robust when varying the number of observations  $n$

The results for M-splines are shown in ?? and ?? and we observe comparable performance except perhaps for a better estimation of mutual information for large correlations which is what we would expect from our discussion in ??.

The problem we observe with the above methods is that when mutual informa-

tion is large, the Copula density is close to a one-dimensional manifold. Hence, to calculate the mutual information well, need many bins. However, with many bins the estimate becomes more noisy as the support of each spline shrinks with  $\frac{1}{N}$ . However, as seen from Figure 1.20, if we can accurately estimate the Copula density function from observations, we can compute the mutual information perfectly by increasing the fineness of the integral approximation. In particular, the results below where obtained through the theoretical Copula density function evaluated at the bin centers  $(\frac{2i-1}{2N}, \frac{2j-1}{2N})$  for  $i, j \in \{1, \dots, N\}$ . We see that this simple approximation with  $N = 1000$  is good for correlations up to  $\rho = 0.99$ . However, due to numerical limitations, we shall use  $N = 500$  and only 400 observations to evaluate the performance of the KDE from the previous chapter. We note that a more efficient implementation is possible splitting up the computation in multiple parts as the problem with many observations and bins is to compute the joint density function which is of  $\mathcal{O}(N^2n)$



**Figure 1.20:** Evaluation of MI for new method for different N. **Bør sammenligne med artiekln fundet (har sat i bibtex) og original papers (ikke Kina)**

the chosen  $h$  is around 0.085 every time using Scott's rule. As we see from Table 1.1, we have relatively low variance and in general, we compute the mutual information to a higher accuracy than either B-splines and M-splines. Thus, in the following example, we will only consider this method for estimating the mutual information between pairs of variables. In Figure 1.21 we have shown the estimated density and the theoretical copula. We observe that indeed the method accurately estimates the Copula density, although we note that the concept of a local bandwidth as discussed in ?? is likely to improve on the results

$\rho$	$h$	mean error	variance
0.1	$h^{Scott}$	0.01583	$5.3446 \cdot 10^{-5}$
0.3	$h^{Scott}$	0.02302	$3.7957 \cdot 10^{-4}$
0.4	$h^{Scott}$	0.006898	$3.2655 \cdot 10^{-4}$
0.6	$h^{Scott}$	0.007803	$1.0027 \cdot 10^{-3}$
0.9	$h^{Scott}$	-0.1844	$4.4478 \cdot 10^{-4}$
0.99	$h^{Scott}$	-1.007	$1.6328 \cdot 10^{-4}$
0.99	$0.3 h^{Scott}$	-0.3468	$1.0616 \cdot 10^{-3}$

**Table 1.1:** based on 10 trials

as peaks at  $(0, 0)$  and  $(1, 1)$  does not quite resemble those of the theoretical Copula density. In particular, we observe that reducing the bandwidth improves on the estimate and is clearly observe by the improved resemblance with the theoretical Copula density. Although this is at the cost of undersmoothing on the interior. Indeed, a K-means based estimator of the bandwidth  $h$  could work well as the mean distance near  $(0, 0)$  and  $(1, 1)$  is very small compared to the interior. However, we note that as long as observations are not almost on a line, the KDE performs quite well. This, we shall also see in the next section where we couple the above discussions on mutual information estimation with the deconvolution algorithm.

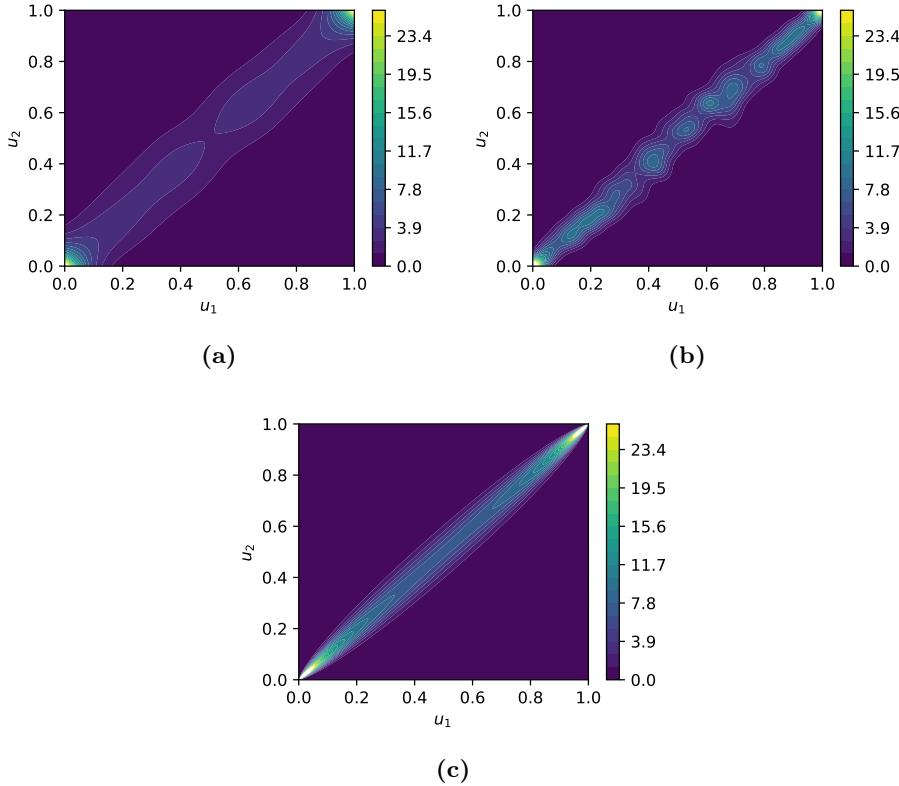


Figure 1.21

### 1.3.2 Exponentiated multivariate Gaussian

Let us consider a simple case with  $\mathbf{Y} = e^{\mathbf{X}}$  (element wise exponentiation) where  $X \sim \mathcal{N}(\mathbf{0}, \Sigma)$  where

$$\Sigma = \begin{bmatrix} \sigma_1^2 & 0.9\sigma_1\sigma_2 & 0 \\ 0.9\sigma_1\sigma_2 & \sigma_2^2 & 0 \\ 0 & 0 & \sigma_3^2 \end{bmatrix} = \text{diag}(\boldsymbol{\sigma}) \begin{bmatrix} 1 & 0.9 & 0 \\ 0.9 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} \text{diag}(\boldsymbol{\sigma})$$

In particular, in terms of Equation 1.4, we have that for  $\mathbf{X}$ ,  $\vec{\rho}_{1,2} = 0.9$ . It is clear that to ??, the mean of  $\mathbf{X}$  is of no importance as it simply corresponds to a scaling of the  $Y_i$  variables. Furthermore, because of ??, theoretically, due to the uniqueness of the Copula  $C$  (as  $\mathbf{Y}$  is continuous) we should expect near equal or very similar results for  $\mathbf{Y}$  and  $\mathbf{X}$  from ???. Additionally, different  $\boldsymbol{\sigma}$  corresponds to different scaling of  $\mathbf{X}$ , and thus we should observe equal or near equal  $G_{dir}$  for all  $\mathbf{Y}$  independently of  $\boldsymbol{\sigma}$ . Initially, we shall see how this hypothesis holds

up when considering the following three examples

$$\boldsymbol{\sigma} = (0.07, 0.3, 0.9), \quad \boldsymbol{\sigma} = (1, 1, 1), \quad \boldsymbol{\sigma} = (1, 2, 3)$$

To draw from this distribution, one can either use built-in functions or use the Cholesky factorization of the correlation matrix to generate proper correlated variables from 3 independent standard normal distributions and then scale with the chosen standard deviation to generate samples from all three cases based on the same seed. We shall do the latter and also generate a generous number of samples (10,000) such that the KDE based methods have the best possible prerequisites whilst also being numerically tractable later on.

In order for the sample size to not influence the results, we simulate a generous number of samples, namely, for the following results we have used  $n = 10,000$  samples. For  $\boldsymbol{\sigma} = (1, 1, 1)$ , ?? and ?? returns the following (using  $\alpha = 1$  and  $\beta = 0.99$ )

$$G_{dir} = \begin{bmatrix} -0.3363 & 0.6552 & 0.08813 \\ 0.6552 & -0.3328 & 0.06480 \\ 0.08813 & 0.06480 & -0.01734 \end{bmatrix} \quad (1.8)$$

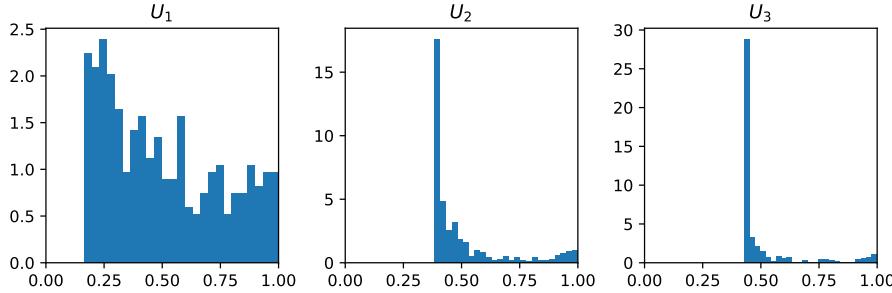
Similarly, for  $\boldsymbol{\sigma} = (0.07, 0.3, 0.9)$ :

$$G_{dir} = \begin{bmatrix} -0.3289 & 0.6610 & 0.004827 \\ 0.6610 & -0.29889 & 0.004977 \\ 0.004827 & 0.004977 & -0.00007197 \end{bmatrix} \quad (1.9)$$

Finally, for  $\boldsymbol{\sigma} = (1, 2, 3)$ :

$$G_{dir} = \begin{bmatrix} -0.1836 & 0.3117 & 0.2252 \\ 0.3117 & -0.4065 & 0.5962 \\ 0.2252 & 0.5962 & -0.3673 \end{bmatrix}$$

For  $\boldsymbol{\sigma} = (1, 1, 1)$  and  $\boldsymbol{\sigma} = (0.07, 0.3, 0.9)$  we observe the most resemblance to the  $\Sigma$ , although the resulting  $G_{dir}$  deviate in the final column. The difference is likely produced by ?? as if the resulting  $G_{obs}$  was the same, then so would  $G_{dir}$  and from the above argument, we know that theoretically this should be the case. For the final example,  $\boldsymbol{\sigma} = (1, 2, 3)$ , we see a completely different result and immediately suspect that there must be some numerical errors. Investigating the partial results of ?? we immediately see a flaw in the supposedly uniform variables  $U_i$  as shown in figure Figure 1.22

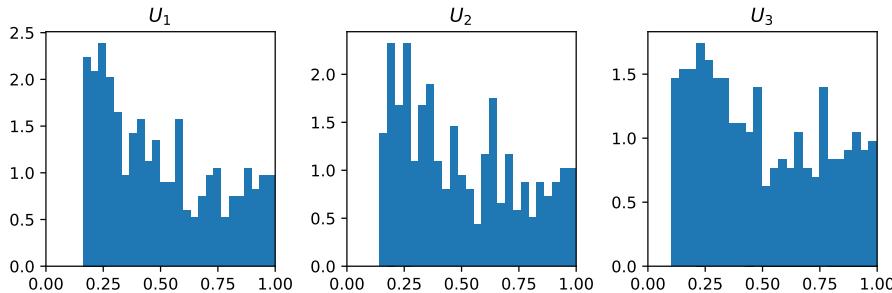


**Figure 1.22:** The samples transformed using  $U_i = F_i(X_i)$  for  $\sigma = (1, 2, 3)$ . These should be uniformly distributed, but clearly this is not the case for  $U_2$  and  $U_3$ . Even  $U_1$  does not quite resemble 10,000 samples from a uniform distribution.

	$U_1$	$U_2$	$U_3$
$D_n$	0.16512	0.38354	0.42764
p-value	0	0	0

**Table 1.2:** based on 10,000 samples for  $\sigma = (1, 2, 3)$ .

Before handling this, the non-uniformity of  $U_1$  in Figure 1.22 is likely also present in the case when  $\sigma = (1, 1, 1)$ . Indeed, Figure 1.23 shows that this is indeed the case.

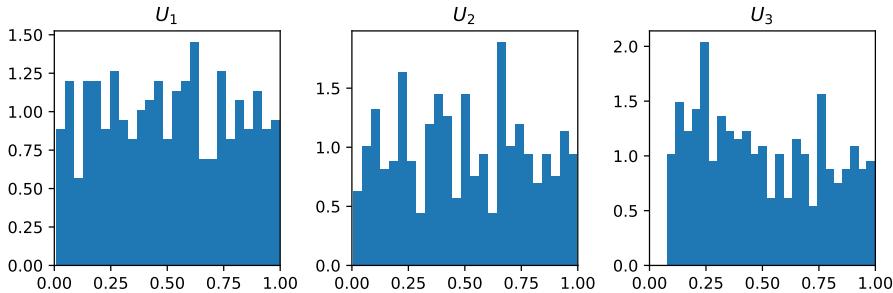


**Figure 1.23:** The samples transformed using  $U_i = F_i(X_i)$  for  $\sigma = (1, 1, 1)$ .

	$U_1$	$U_2$	$U_3$
$D_n$	0.16511	0.14672	0.10561
p-value	0	0	$2.381997515751874 \cdot 10^{-4}$

**Table 1.3:** based on 400 samples for  $\sigma = (1, 1, 1)$ .

Finally, just to be sure,  $\sigma = (0.07, 0.3, 0.9)$  is also shown in Figure 1.24 and seems very reasonable, except for  $U_3$ .



**Figure 1.24:** The samples transformed using  $U_i = F_i(X_i)$  for  $\sigma = (0.07, 0.3, 0.9)$ .

	$U_1$	$U_2$	$U_3$
$D_n$	0.029036	0.029026	0.085611
p-value	0.88427	0.88454	0.0052791

**Table 1.4:** based on 10,000 samples for  $\sigma = (0.07, 0.3, 0.9)$ .

From the above examples, it seems that the larger the variance, the worse the uniforms turn out. Reasons for this could include numerical issues when trying to calculate  $u_i^{(j)}$  from  $y_i^{(j)}$  by  $u_i^{(j)} = \int_{-\infty}^{y_i^{(j)}} f_i(y) dy$  and bad fitting of the kernel density estimate from observations. In particular, for values similar, which happens in the case for large  $\sigma$  such that we observe large negative realizations of  $X_i$ ,  $y_i^{(j)}$  are almost 0, and when computing the integral could result in identical values. Furthermore, from Figure 1.25 we see that indeed the fit is quite poor. Note that we have zoomed in on the interval  $[-200, 200]$  which contains 96.2% of observations. The poor fit is primarily due to the use of Scott's Rule [as discussed above](#) which in this case overshoots the optimal bandwidth by a lot.

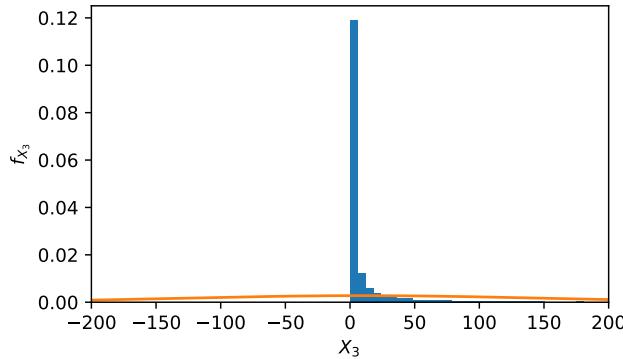


Figure 1.25

The poor fit also explains the high concentration of  $U_3$  around 0.5 in Figure 1.22 as only 54.5% of the probability mass lies above 0.

However, also here ?? proves to be useful. Namely, we can get rid of the numerical issues by transforming  $Y_i$  using e.g.  $\log(\cdot)$  or  $(\cdot)^p$  for  $p > 0$  to get even out the observations more. As the first simply inverts the initial transformation of  $X_i$ , we choose the latter as a more interesting case. In particular, choosing  $p < 1$  will result in a more even distribution. In the following,  $p = 1/10$  has been used to transform  $\mathbf{Y}$  prior to running ?? and the resulting  $u_i^{(j)}$  is shown in Figure 1.26.

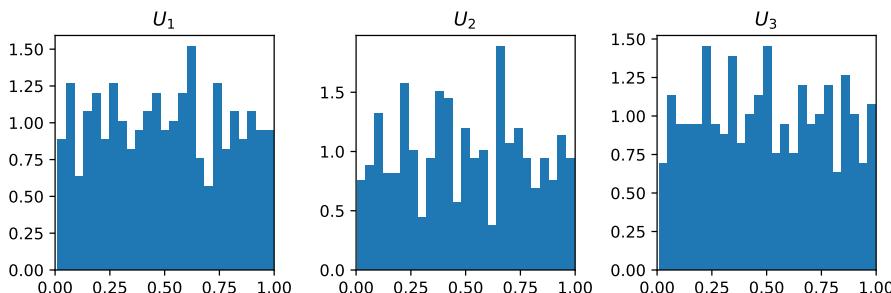
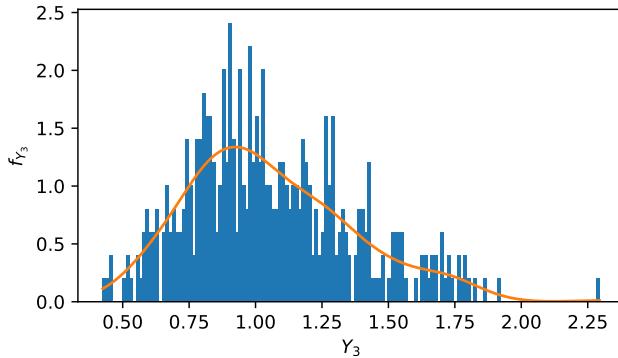


Figure 1.26

The resulting  $u_i^{(j)}$  now seem to follow a uniform distribution and indeed the KDE fits much better as seen in Figure 1.27.

	$U_1$	$U_2$	$U_3$
$D_n$	0.0061099	0.0061435	0.0073148
p-value	0.84838	0.84368	0.65690

**Table 1.5:** based on 10,000 samples for  $\sigma = (1, 2, 3)$  with power transform.

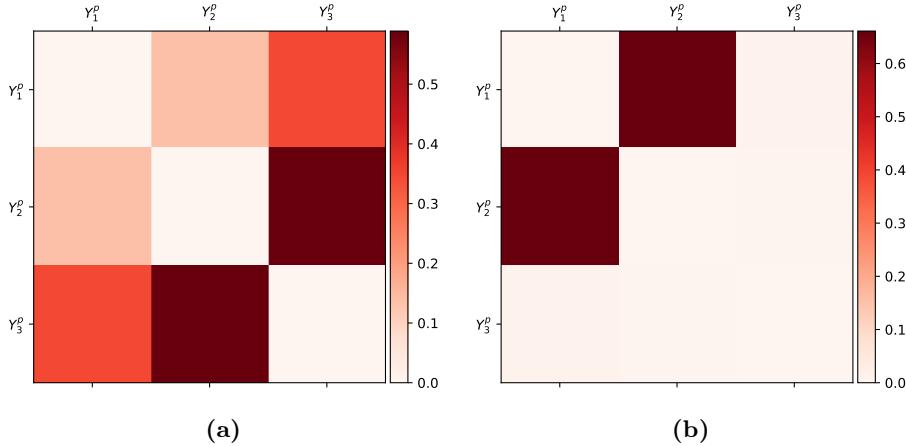


**Figure 1.27**

Turning to ?? and ?? we now find that  $G_{dir}$  is given by

$$G_{dir} = \begin{bmatrix} -0.3290 & 0.6610 & 0.01188 \\ 0.6610 & -0.3289 & 0.004603 \\ 0.01188 & 0.004603 & -0.0002167 \end{bmatrix}$$

Which is indeed much more comparable with the result from before in Equation 1.8 and Equation 1.9. The difference between  $G_{dir}$  from  $\mathbf{Y}$  and  $\mathbf{Y}^p$  is clearly visible in Figure 1.28 and also Figure 1.28b resembles the original correlation structure.



**Figure 1.28:**  $G_{dir}$  resulting from 400 samples from multi variate Gaussian with  $\sigma = (1, 2, 3)$  in (a) with raw samples from  $\mathbf{Y}$  and in (b) the transformed data corresponding to  $\mathbf{Y}^p$ .

Finally, to end this example we shall compare with some theoretical results. Namely, the output  $G_{obs}$  of ?? can also be calculated theoretically. For this, we shall use Proposition 1.1 which permits a theoretical result, namely

$$\begin{aligned} G_{obs} &= \begin{bmatrix} 0 & -\frac{1}{2} \ln(1 - \rho_{12}^2) & -\frac{1}{2} \ln(1 - \rho_{13}^2) \\ -\frac{1}{2} \ln(1 - \rho_{21}^2) & 0 & -\frac{1}{2} \ln(1 - \rho_{23}^2) \\ -\frac{1}{2} \ln(1 - \rho_{31}^2) & -\frac{1}{2} \ln(1 - \rho_{32}^2) & 0 \end{bmatrix} \\ &\cong \begin{bmatrix} 0 & 0.83037 & 0 \\ 0.83037 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \end{aligned}$$

Similarly, prior to deconvolution, using just the sampled  $\mathbf{X}$  (i.e. no exponential transform), ?? returns

$$G_{obs} = \begin{bmatrix} 0. & 0.64069542 & 0.01824538 \\ 0.64069542 & 0. & 0.0135368 \\ 0.01824538 & 0.0135368 & 0. \end{bmatrix}$$

Test om denne G er lige den teoretiske. Eller nærmere, argumenter for hvorfor vi ikke laver en test, eller hvad man kunne gøre. Har samplet fra en simultan normalfordeling, så kan lave en til en mellem MI og korrelation.

From the confidence density for the correlation  $\rho$  given the emperical correlation

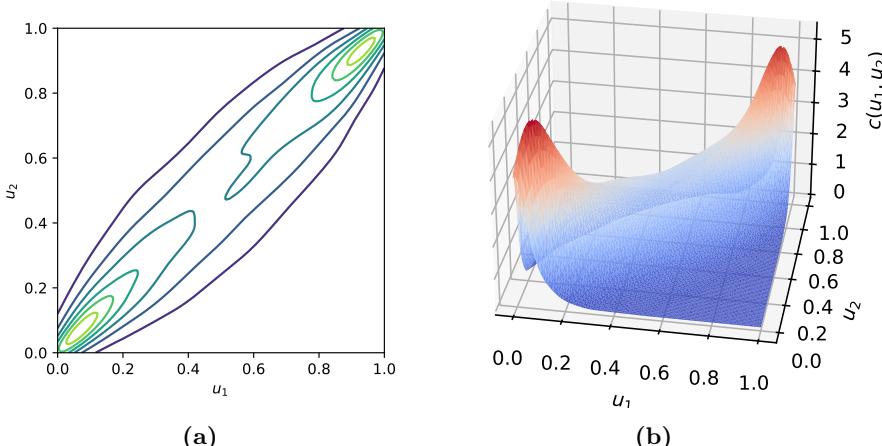
$r$  is given by

$$f(\rho | r, \nu) = \frac{\nu(\nu - 1)\Gamma(\nu - 1)}{\sqrt{2\pi}\Gamma(\nu + \frac{1}{2})} \frac{(1 - r^2)^{\frac{\nu-1}{2}} (1 - \rho^2)^{\frac{\nu-2}{2}}}{(1 - r\rho)^{\frac{2\nu-1}{2}}} F\left(\frac{3}{2}, -\frac{1}{2}, \nu + \frac{1}{2}, \frac{1 + r\rho}{2}\right)$$

from the mutual information, we can calculate the absolute correlation. Notice that the density does not change when reversing both  $r$  and  $\rho$  simultaneously, thus, without loss of generality, assume  $r \geq 0$ , then we can calculate a CI for  $\rho$  (which will be negated if we had used  $-r$  instead and thus would be identical when taking the absolute value). If the original CI  $[a, b]$  contains 0 i.e.  $a < 0$ , we shall write the CI for the absolute correlation as  $[0, b]$  instead. This way, we can compare the absolute correlations and see if they are the same (by checking if the CI contains the theoretical correlation) by [?]. Using numerical integration (fast enough with high numerical accuracy from many bins, 1 mil bins, yielding probability mass 1.0000000000008133), can compute CI for absolute correlation

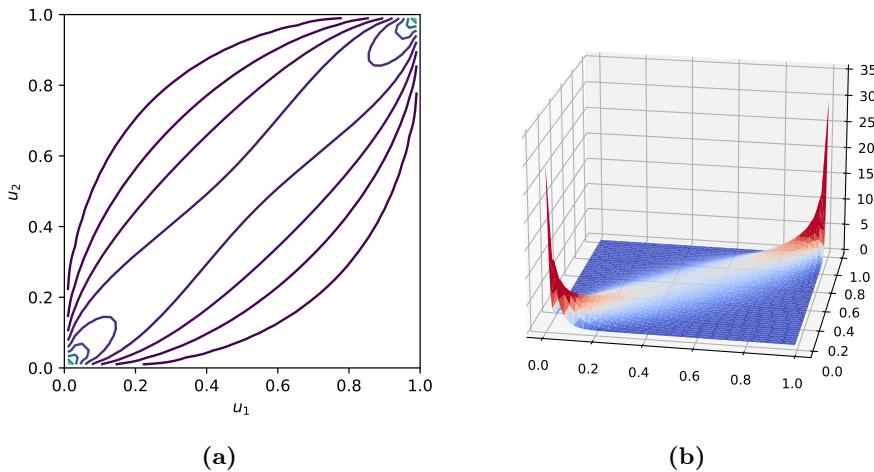
??

Clearly these are not equal, but in this case, the error is suspected to originate from the estimated joint density. For example, considering  $X_1$  and  $X_2$ , we compare the estimated joint copula density and compare to the theoretical reference til et sted hvor gausisk copula står shown in Figure 1.29 and Figure 1.30 respectively.



**Figure 1.29:** Estimated copula density  $c$  with  $\rho = 0.9$  corresponding to  $X_1$  and  $X_2$ .

The noticeable difference is in the corners  $(0, 0)$  and  $(1, 1)$  where the theoretical copula density tends to infinity whereas the estimated density has modes at  $(0.1, 0.1)$  and  $(0.9, 0.9)$ . In particular, simply rescaling the copula density in ?? does not resemble the theoretical boundary which is a known issue [reference til artikel om undershoot peaks og boundary conditions for KDE](#). A better approach may be to use jackknifing [link til afsnit of jackknifing, som også indeholder reference til artikel hvor dette gøres](#).



**Figure 1.30:** Theoretical copula density  $c$  with  $\rho = 0.9$  corresponding to  $X_1$  and  $X_2$ .

We note however, that the underlying structure is still captured i.e. that  $Y_1$  and  $Y_2$  covary while  $Y_3$  does not inform  $Y_1$  or  $Y_2$  and vice versa.

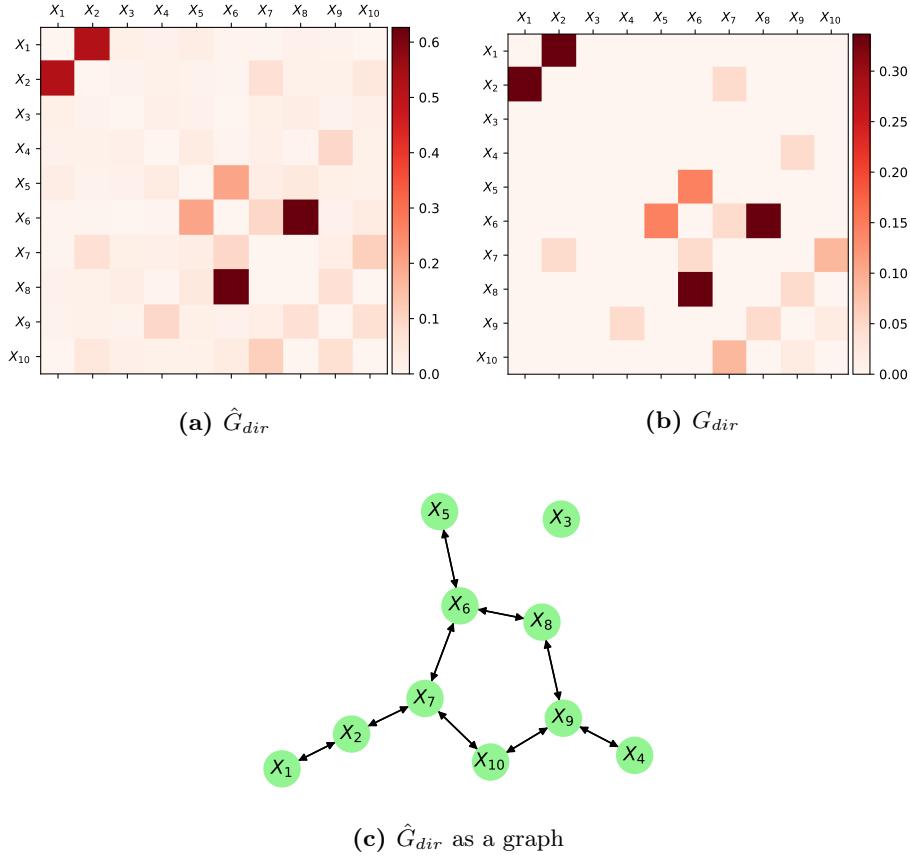
We continue with a similar example to the previous one. The key difference is the number of variables and a more complicated correlation structure to test the algorithms further.

### 1.3.3 Gaussian network revisited - Application of complete framework

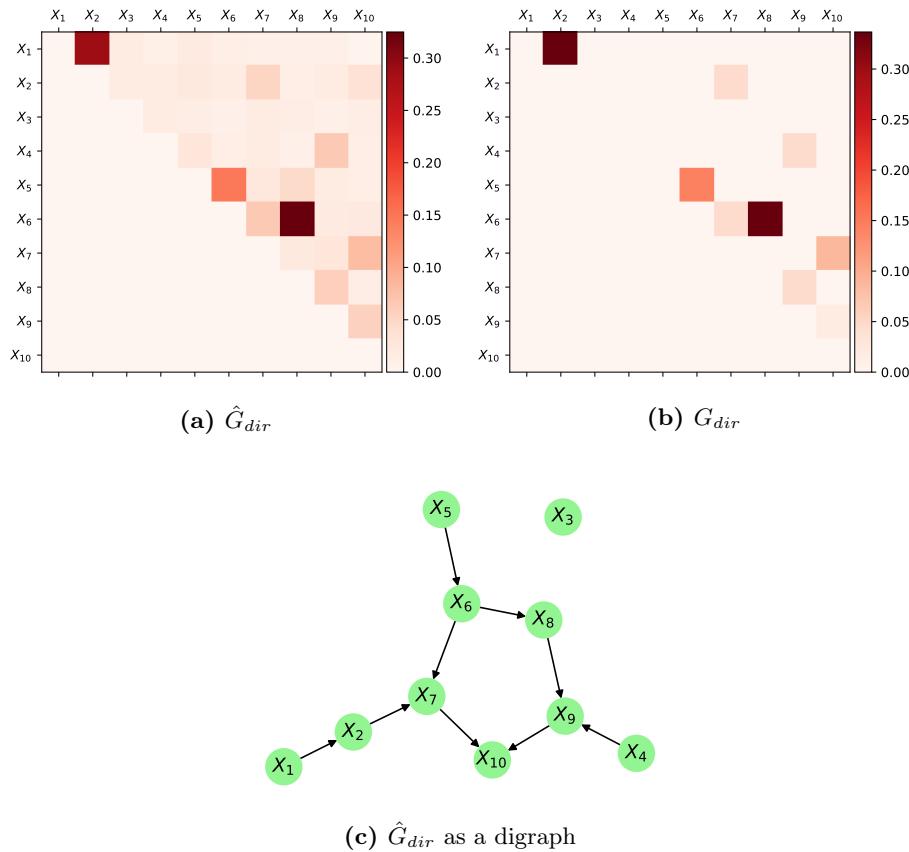
None are significant (marginal distribution).

Also, we expect this to do well, since there are no correlations above 0.7. Thus, from Table 1.1 the errors in the mutual information estimates should be quite small.

the setup is like before that we simulate 400 observations from the network, defined by Equation 1.7



**Figure 1.31:** Using a symmetric  $G_{obs}$



**Figure 1.32:** Using a triangular  $G_{obs}$

casuality svarer til at lave nedre/øvre trekant. Er der forskel i at gør edet før og efter for en symmetrisk matrix? - Ja, men begge metoder på 10 eksempel giver gode resultater. Kommenter at det er matematisk meget forskelligt at filtrere først og så ND efter og omvendt

## 1.4 Pharmaceutical data deconvolution

Finally, we turn our attention to the pharmaceutical production data introduced in ???. Namely, we have at this point used the methodology discussed in chapter 1 both to estimate mutual information, to deconvolve Gaussian networks and chains based on analytical expressions for the correlation between variables and finally in Subsection 1.3.3 where we have combined ?? and ?? to infer the causal structure of a 10-dimensional Gaussian network.

In particular, we saw that the methodology combined produced very accurate results when the mutual information between pairs of random variables were not too large as these proved difficult to estimate to high accuracy without turning to a manual tuning of the bandwidths. We especially want to avoid the manual tuning of the bandwidth in this section, as we shall compute mutual information between 1653 pairs of random variables.

The random variables are the duration and delays of each process as well as the change in level of the tank during these operations. Recall that e.g.  $T_{4.1}^P$  is the duration of process 4.1 while  $T_4^D$  is the delay after all subprocesses of process 4 are completed. Also, for each *temporal* variable  $T_i^P$  and  $T_i^D$ , we have a corresponding change of level  $M_i^P$  and  $M_i^D$ . Initially, we also add the accumulated random variables. Namely, for process 1, we add the random variable  $T_1 = T_1^P + T_1^D$  and likewise for the level changes for all processes. Also, the total duration  $T = \sum_{i=1}^{10} T_i$  and change in level  $M = \sum_{i=1}^{10} M_i$  are added as random variables. The accumulated random variables are initially added to see if our method can *rediscover* these simple causal relations. We will later remove these from our discussion as we try to gain a deeper understanding of the production system.

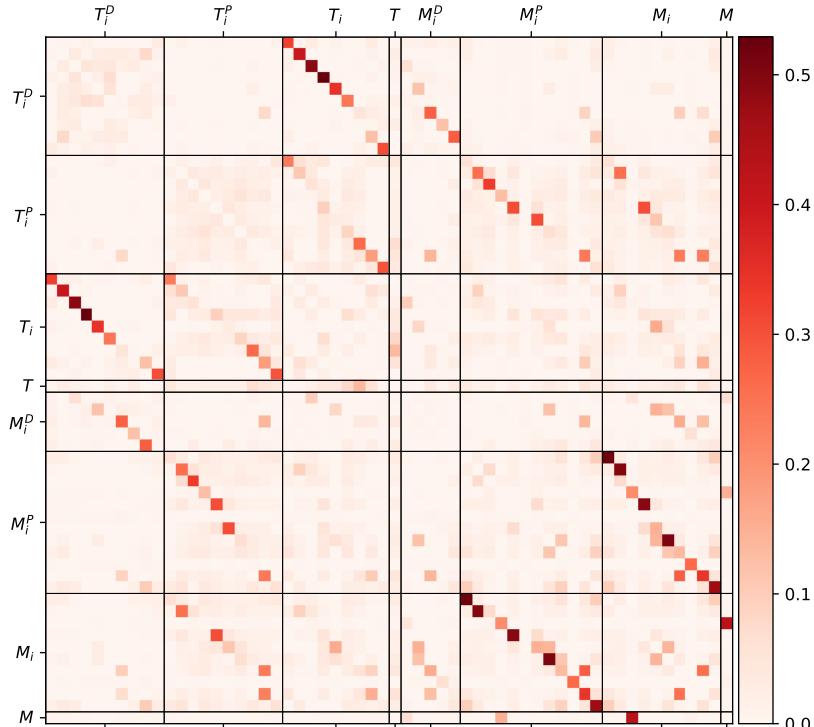
Hence, from the above, we initially have 68 variables. However, some of them are constant and thus out of interest. The constant *random* variables are

$$M_1^D, \quad M_2^D, \quad T_{4.1}^P, \quad M_{4.1}^P, \quad T_{4.3}^P, \quad M_4^P, \quad M_6^D, \quad T_8^P, \quad M_{10}^D$$

However, as  $T_8 = T_8^P + T_8^D$  we shall also exclude either  $T_8$  or  $T_8^D$  due to  $T_8^P$  being constant. In particular,  $T_8$  and  $T_8^D$  can be interchanged at will when computing mutual information according to ???. Here, we have chosen to keep  $T_8^D$  as it is easier to relate to the other processes. Thus, we are only considering 58 random variables and hence  $58 \cdot 57/2 = 1653$  pairs of variables as stated above.

We note that as the resolution in time is 0.001 we add uniform distributed noise from  $[0, 0.001]$  to the durations and delays. In particular, we observe that in some cases equal durations are observed. These would result in non-uniform

marginals like in Subsection 1.3.2 hence making the algorithm fail at computing the mutual information accurately. We note that the experiments to follow have been carried out multiple times to assess the influence of this perturbation to the durations and delays. However, as this did not influence our results in the slightest we will not discuss this further. Furthermore, instead of using a KDE as in Subsection 1.3.2 to transform the (continuous) observations to lie on the unit interval through the distribution function, we have used the empirical distribution function. This was done to ensure that all 58 random variables were transformed appropriately without having to consider transformations (like in Subsection 1.3.2).



**Figure 1.33:**  $G_{dir}$  from a symmetric  $G_{obs}$ . Other than the accumulated variables, we observe strong dependencies between the duration of a process and the change in level during the process by comparing the columns and rows labeled  $T_i^P$  and  $M_i^P$ .

The resulting  $G_{obs}$  is shown in the appendix, ???. We observe that there indeed is a strong dependence between the accumulated variables and their summands such as  $T_1$  and  $T_1^D$  as well as  $T_1^P$ . We immediately use the deconvolution

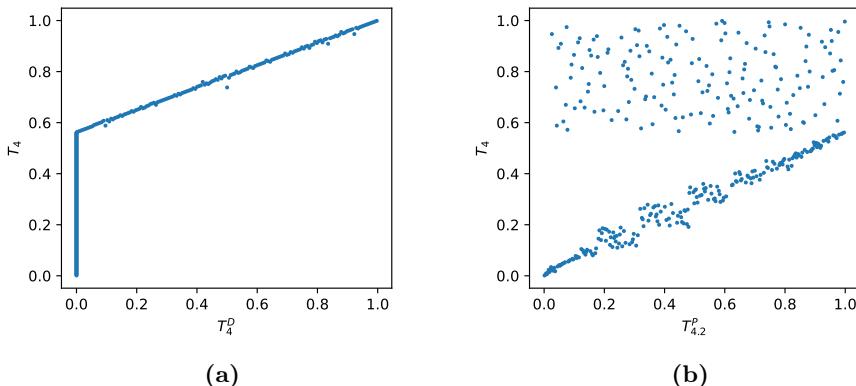
algorithm resulting in the  $G_{dir}$  seen in Figure 1.33

We have labeled sections of  $G_{dir}$  such that each sections corresponds to an ordered list of variables. The variables in each section are

$$\begin{aligned}
 T_i^D &= \{T_1^D, T_2^D, T_3^D, T_4^D, T_5^D, T_6^D, T_7^D, T_8^D, T_9^D, T_{10}^D\} \\
 T_i^P &= \{T_1^P, T_2^P, T_{3,1}^P, T_{3,2}^P, T_{4,2}^P, T_5^P, T_6^P, T_7^P, T_9^P, T_{10}^P\} \\
 T_i &= \{T_1, T_2, T_3, T_4, T_5, T_6, T_7, T_9, T_{10}\} \\
 T &= \{T\} \\
 M_i^D &= \{M_3^D, M_5^D, M_7^D, M_8^D, M_9^D\} \\
 M_i^P &= \{M_1^P, M_2^P, M_{3,1}^P, M_{3,2}^P, M_{4,2}^P, M_{4,3}^P, M_5^P, M_6^P, M_7^P, M_8^P, M_9^P, M_{10}^P\} \\
 M_i &= \{M_1, M_2, M_3, M_4, M_5, M_6, M_7, M_8, M_9, M_{10}\} \\
 M &= \{M\}
 \end{aligned} \tag{1.10}$$

I.e. the section labeled  $T_i^D$  consists of all the delays after each process and so on for the remaining section labels.

From Figure 1.33, we observe that the accumulated durations of each process  $T_i$  is indeed very dependent on both the delay and durations of the process. This is a sign that the algorithm performs well as by definition  $T_i = T_i^D + \sum_{k \in \mathcal{P}_i} T_i^P$  (where  $\mathcal{P}_i$  is defined as the set of subprocesses that constitute the process  $i$ ).



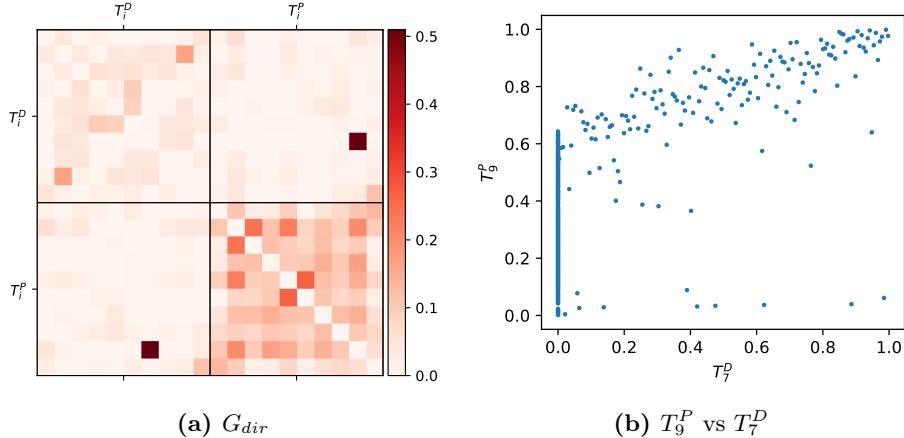
**Figure 1.34:**  $T_4$  vs  $T_4^D$  and  $T_{4,2}^P$  in (a) and (b) respectively. Notice that the continuous part of the variables has been transformed using the empirical distribution function such that the domain is  $[0, 1]$  for all the variables. The transformation allows for an easier assessment of the mutual information between the pairs of variables.

For example, we observe that  $T_4^D$  is strongly associated with  $T_4$  while  $T_{4,2}^P$  is not as strongly associated with  $T_4$ . However, there is still a connection. If we plot  $T_4$  vs.  $T_4^D$  and  $T_{4,2}^P$  respectively (Figure 1.34) we indeed observe that the information between  $T_4^D$  and  $T_4$  is much greater than  $T_{4,2}^P$  and  $T_4$ . As we saw in [Section with data](#), this is because the delays after process 4 are much larger than the duration to begin with. Thus, even though  $T_4^D$  is 0, 56.25% of times, most of  $T_4$  can be explained from this alone, when comparing to the scores between  $T_4$  and the other random variables.

Furthermore, we observe that the total duration  $T$  is mostly explained by  $T_7$  which in turn is explained mostly by  $T_7^P$ . Although there are many other interesting observations such as the most change in levels and masses occurs during process 3, addition of a material and stirring. The level after process 3 is in turn mostly influenced by the stirring but also seem to have some unexplained variation. We observe the unexplained variation from the row corresponding to  $M_3$  which has relatively small associations with the other delays, durations and levels.

At this point, we have observed that the algorithm rediscovers what we already know to be true. Namely, that the total masses and process durations are well explained by the individual processes. However, a more interesting question is how each of the processes affect each other. More precisely, if we only consider each process without the accumulated random variables  $T_i$ ,  $T$ ,  $M_i$  and  $M$ , we hope to discover more interesting dependencies between the processes. Also,  $T_i$  etc. can always be computed from the processes, so we do not really care for these random variables if we want to understand the dynamics of the system.

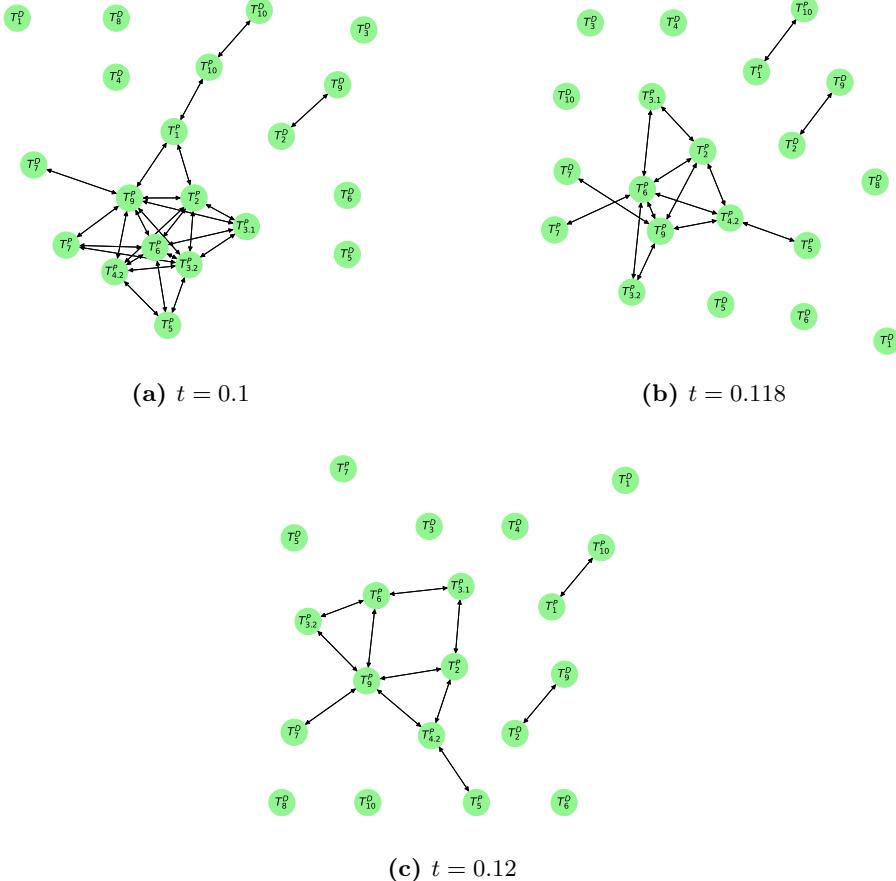
Initially, we consider the durations and delays only. Namely, we choose the submatrix of  $G_{obs}$  corresponding to the sets  $T_i^D$  and  $T_i^P$  from Equation 1.10. Still using a symmetric  $G_{obs}$ ,  $G_{dir}$  is computed as shown in Figure 1.35a. Now, when removing the *trivial* random variables, as they are known to be the sum of others, a clearer image of how the durations and delay of each process depend on each other emerges. A strong association between  $T_9^P$  and  $T_7^D$  is observed. When plotting the observations of the random variables (again with the continuous part transformed through the empirical density function) in Figure 1.35b, we indeed observe that for many batches, if the delay for process 7 is non-zero, then the duration of process 9 is greater than if the delay after process 7 was 0. Furthermore, as we have removed transitive effects, it seems as if this association is direct. I.e. something happens during the delay after process 7, the reaction process, which heavily *influences* to the duration of the cooling process 9. Interestingly, from Figure 1.35a it does not seem like  $T_7^P$  is associated with  $T_9^P$ . In ?? we have shown these two variables plotted against each other and indeed observe that neither is particularly descriptive of the other.



**Figure 1.35:** When only using the durations and delays, we observe  $G_{dir}$  as in (a). A very strong similarity is calculated between  $T_9^P$  and  $T_7^D$ , which when plotted in (b) is not an unreasonable finding. Namely, if the delay after process 7 is 0,  $T_9^P$  is primarily below the 0.6-quantile and otherwise appear to be linearly related to  $T_7^D$ .

In figure Figure 1.36, we have shown  $G_{dir}$  (from Figure 1.35a) as a graph with varying thresholds. It is clear that the durations of each process are dependent on each other and depending on the threshold we conclude anything from a simple network structure (Figure 1.36b and Figure 1.36c) to a much more complicated dependency structure (Figure 1.36a) between the durations of the processes. As is also clear from Figure 1.35a, the delays of the processes are the first random variables we conclude to be independent of both each other and all other process durations except for  $T_2^D$  and  $T_9^D$  corresponding to the delays when adding material and cooling respectively and the link between  $T_7^D$  and  $T_9^P$  discussed above.

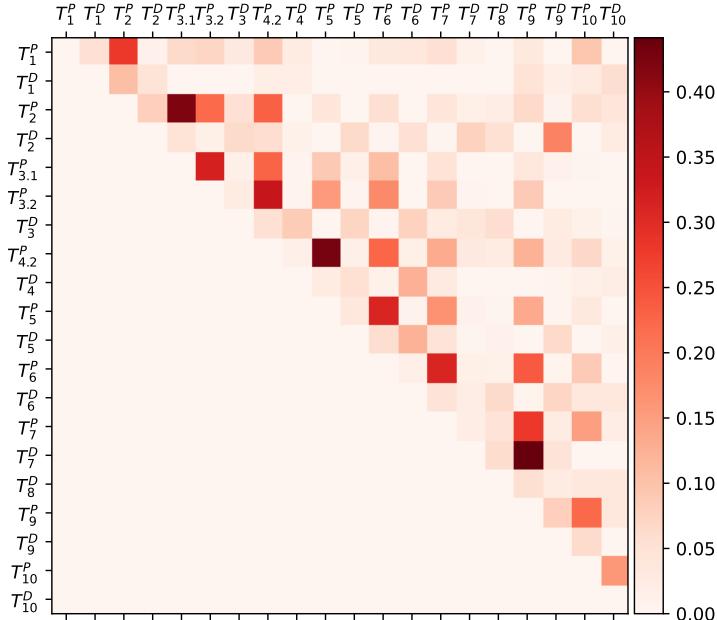
Like in Subsection 1.3.3, we have good understanding of the topological structure of the processes. Namely, as the delay of processes are always *after* the process we have that in terms of a topological structure of the random variables,  $T_i^D$  is always after  $T_i^P$ . For example,  $T_3^D$  is always realized *after*  $T_{3,1}^P$  and  $T_{3,2}^P$  (in that order). Likewise, as shown in [ref to figure about simulation process structure](#), as the processes are executed one by one, the topological structure is a simple chain. This should not be confused with the actual causal structure being a chain as in Section 1.1. As the topological structure is a chain, it is also unique i.e. there is exactly one ordering of the random variables. The topological structure is summarized in Equation 1.4



**Figure 1.36:**  $G_{dir}$  from Figure 1.35 represented as a graph for different thresholds  $t$ . In general, we observe that the delays appear to be indescribable from the other variables and vice versa. As for the actual durations of the processes, depending on the threshold  $t$  outside the considered range [0.1, 0.12] does not change the graph noticeably.

$$\begin{aligned}
 & T_1^P \longrightarrow T_1^D \longrightarrow T_2^P \longrightarrow T_2^D \longrightarrow T_{3.1}^P \longrightarrow T_{3.2}^P \longrightarrow T_3^D \\
 & \longrightarrow T_{4.2}^P \longrightarrow T_4^D \longrightarrow T_5^P \longrightarrow T_5^D \longrightarrow T_6^P \longrightarrow T_6^D \longrightarrow T_7^P \\
 & \longrightarrow T_7^D \longrightarrow T_8^P \longrightarrow T_9^P \longrightarrow T_9^D \longrightarrow T_{10}^P \longrightarrow T_{10}^D
 \end{aligned} \tag{1.11}$$

Using this to order the rows and columns of  $G_{obs}$  and finally only keeping the upper triangular part, we can deconvolve the network once again, but this time using the topological structure. The resulting  $G_{dir}$  is shown in Figure 1.37.

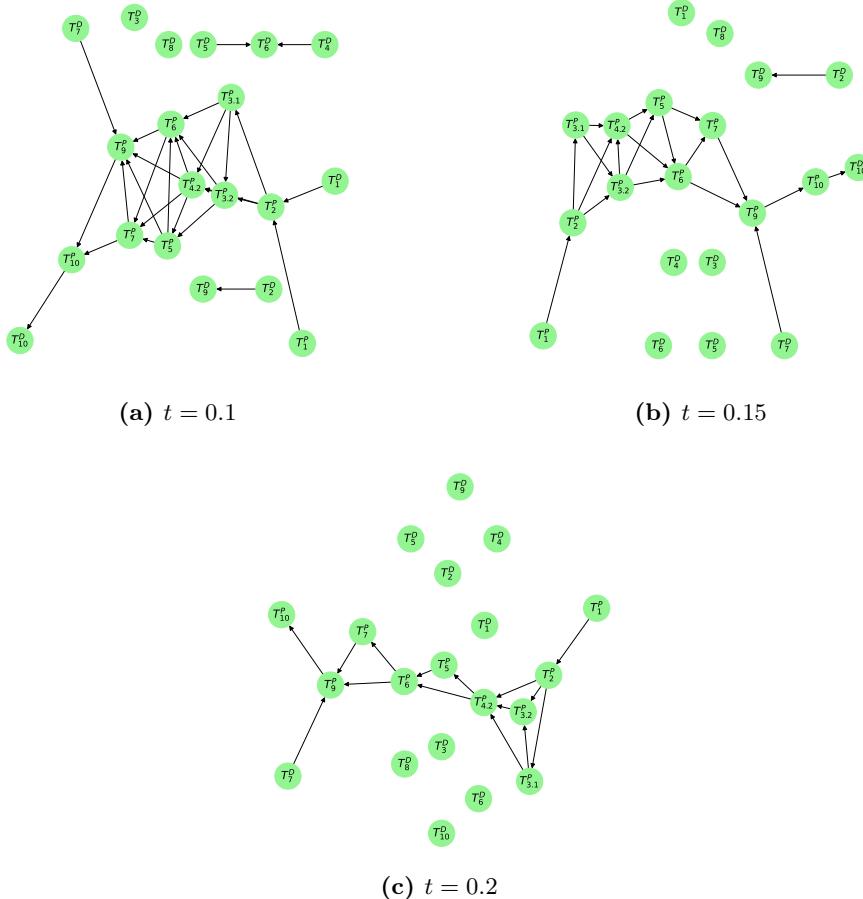


**Figure 1.37:**  $G_{dir}$  based on durations and delays but now with the added assumption of the topological order of the variables. Notice that the order of the variables is different from that of Figure 1.35a and hence not easily comparable. We refer to the graphical representations in Figure 1.36 and Figure 1.38 for comparison of dependence and causal structure.

Although it is hard to compare this  $G_{dir}$  with the one obtained without the assumption of topological structure in Figure 1.35a, we see some differences.  $T_1^P$  and  $T_{10}^P$  are not as directly dependent as originally inferred from the symmetric  $G_{obs}$ . The differences are however more noticeable, when comparing the graphs from before with those in Figure 1.38 where the directed  $G_{obs}$  has been used instead.

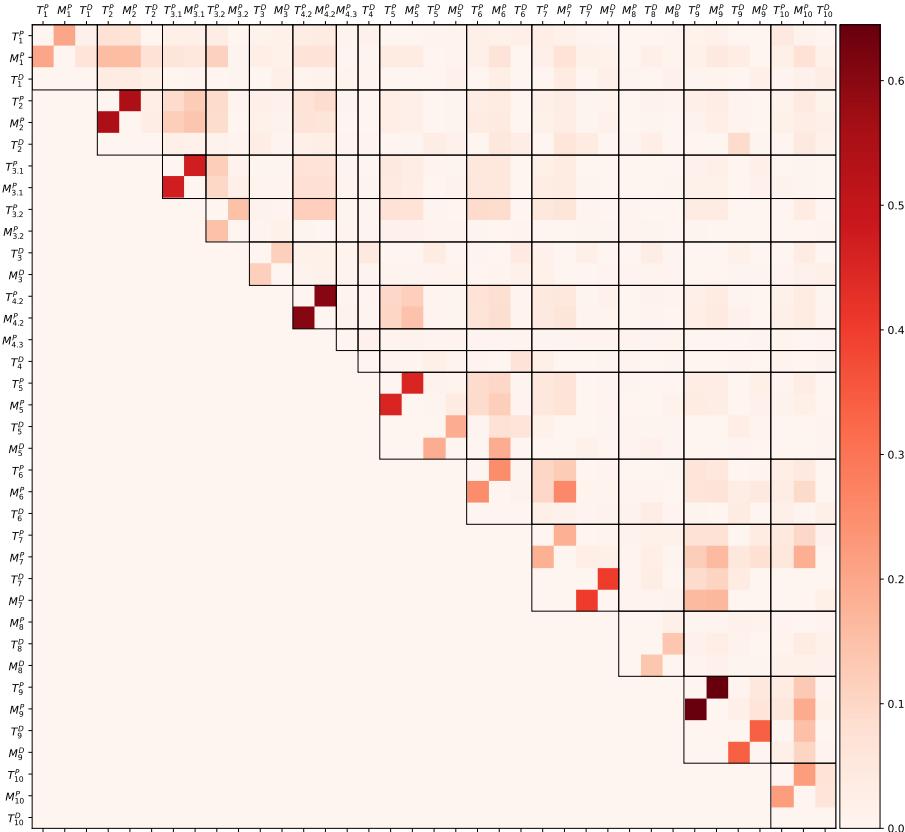
Depending on the chosen threshold  $t$ , we observe that still the delays are the least predictable from other observations as they are not connected to other random variables. This was also the conclusion from Figure 1.36. The major difference is that now  $T_1^P$  influence  $T_{10}^P$  indirectly whereas in Figure 1.36 they were always directly connected. Also, as threshold in  $[0.1, 0.2]$  seem to result in good balance between connectedness complexity of the graph. In our opinion

Figure 1.38b obtains a good balance while also making sense in terms of how processes of a production flow, structured as in [ref til data pharmaceutical flow figure](#), could influence later processes.



**Figure 1.38:** Using a triangular  $G_{obs}$  resulting in a directed graph, we observe once again that the delays are largely unrelated. This hints to most delays should be treated separately when we only concern ourselves with durations of processes. An important difference from these graphs to the previous where no topological order was assumed, is that now  $T_1^P$  only influences  $T_{10}^P$  indirectly where it was a direct link before. In general, we observe that durations only have a direct influence on the next process or the ones after that again. I.e. a more chain-like structure emerges compared to the previous results.

Finally, we shall try once again to use the levels of the tank after each process along with a topological assumption. However, as it is unclear whether it is the duration of a process that influences the change in levels or the other way around, we shall only make  $G_{obs}$  almost triangular. In particular, the entries in  $G_{obs}$  related to durations and levels of the same process such as  $T_1^P$  and  $M_1^P$  are symmetric along the diagonal whilst everything else is removed. This makes  $G_{obs}$  *almost* triangular in the sense that it is triangular but with entries in the subdiagonal (in case of an upper triangular  $G_{obs}$ ). The resulting  $G_{obs}$  can be seen



**Figure 1.39:**  $G_{dir}$  from an *almost* upper triangular  $G_{obs}$ . Like before, we observe a chain like structure. However, with the added random variables of changes in levels during a process, the most significant dependencies are between these and the corresponding duration.

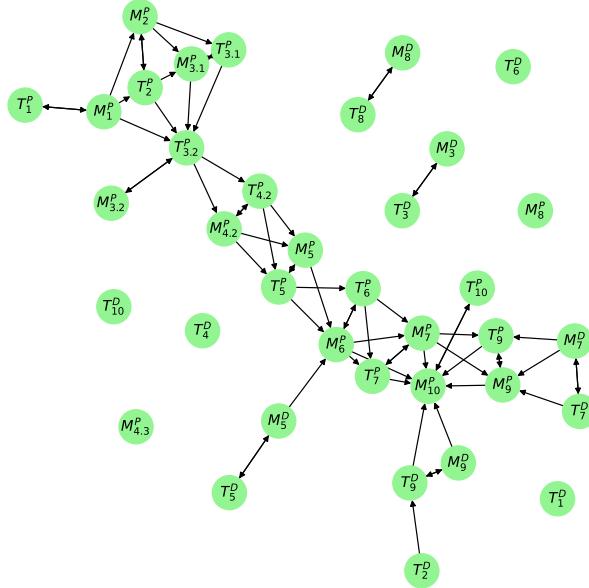
in the appendix, ???. As we would expect, level changes and durations for the same process are often very related and share much information. Unsurprisingly,  $M_{4,3}^P$  does not seem to be related to any other process. This is likely because

the process consists of waiting for a control operator. This also holds when deconvolving the network as seen in Figure 1.39 and from the original result in Figure 1.33 where all the random variables were used (although it is harder to see).

When comparing  $G_{dir}$  in Figure 1.39 to  $G_{obs}$  in ??, we observe that much of the association between processes originate from indirect effects (as expected) either 1, 2 or 3 processes ago. In particular, the delays, durations and level changes of process 9 (cooling) appear to be caused or at least explained well by what takes place during process 7 (reaction) which is not unlikely from a chemical point of view. Process 7, in turn, appears to be influenced mostly by process 6 (product transfer).

In Figure 1.40, we have shown  $G_{dir}$  represented as a graph with a threshold  $t = 0.09$  as this filtered out most small values in  $G_{dir}$  while keeping a reasonable structure with only the edges with the most information carried along. As mentioned above  $M_{4,3}^P$  is alone. Furthermore, we observe that the delays related to process 3 (after adding the final solids) and 8 (post reaction process) are by themselves. The duration of the delay and the change in level are however connected although weakly as per Figure 1.39. This also agrees with Figure 1.38b and Figure 1.38c where when we only used the durations and delays of the processes, we observed that  $T_3^D$  and  $T_8^D$  were unconnected nodes. As another example,  $M_8^P$  is not connected to any of the other variables invariant to the choice of threshold  $t$ . This also makes sense when comparing to REF TIL FIGURE MED DURATIONS VS MASSES OG MASSES VS MASSES where the change in level during the post reaction (process 8) does not seem to be related to any of the other random variables.

Other interesting observations can be made from the graph depending on the interests of the reader. However, we round off our discussion of the pharmaceutical data by noting that we have obtained a causal structure for the random variables that in many ways reflect both our understanding of the production layout from ?? and our observations of data. In particular, we observe a relatively simple structure, where many of the processes are only affected by the previous process. Notable deviations of this are the initial processes 1, 2 and 3.1 where raw materials are added. Each of these processes seem to have an influence on the duration of process 3.2 (the stirring). This also makes sense as the more material is added to the tank, the longer it probably needs to be agitated to ensure a consistent mixture of materials to allow for chemical reactions. Finally, the change in level for process 10 (the transfer of material), appears to be influenced primarily by processes 7 (the chemical reaction) and 9 (cooling) while the duration of process 10 only seems to be related to change in level and no other process directly. This would make sense practically, as we would think that it is the amount of material that is really influenced by the other processes



**Figure 1.40:**  $G_{dir}$  represented as a graph using a threshold  $t = 0.09$ . Once again, we observe a chain like structure, but the added random variables corresponding to changes in levels,  $T^P_{3.2}$  becomes a bottleneck, in the sense most of the behavior of the production system after process 3.2 is irrelevant when knowing the duration of process 3.2. This could also make sense from a practical point of view as the duration of the stirring contains much combined information of the initial processes and hence is a good descriptor of the behavior of the processes later on.

and the duration of transferring the material is only as need to be in order to remove all the material produced.