ETH
Eidgenössische Technische Hochschule Zürich
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D-BSSE
Department of Biosystems
Science and Engineering

Statistical Models in Computational Biology

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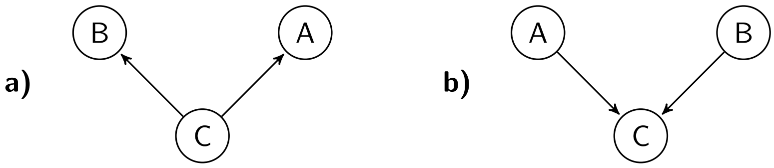
Due date: 29th Feb 2024 before 13:00
Form groups by due date and announce them to smcb@bsse.ethz.ch
Submit on Moodle, not by email

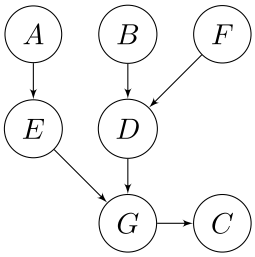
Problem 1: Conditional independence and BNs **(3 points)**

Consider the following graphical structures, corresponding to (different) Bayesian networks. For which network does the statement $A \perp B \mid C$ hold? For which does the statement $A \perp B$ hold? Prove your answers by the laws of probability.



Problem 2: Markov blanket **(2 points)**

Consider the following graphical structure of a Bayesian network:



Determine the Markov blanket $\mathrm{MB}(D)$ of node D and show that the conditional probability $P(D \mid A, B, C, E, F, G)$ is the same as $P(D \mid \mathrm{MB}(D))$.

Problem 3: Learning Bayesian networks from protein data **(5 points)**

In this exercise, we will use the R package `BiDAG`[1] to learn Bayesian networks from protein data. Download the data here The data provided consists of the measurements of 11 phosphorylated proteins and phospholipids derived from primary immune system cells, subjected to both general and specific molecular interventions [2].

(a) First, run `set.seed(42)` for reproducibility. Read in the data in R. Report the number of variables n and the number of observations N. Visualize the transformed data using the `ggpairs` function in the R package `GGally`. Randomly split the data into 80% training data

[1] Run `install.packages("BiDAG")` in the R console. Then load the package by running `library(BiDAG)`.

and 20% test data. Initialize the parameters using the function `BiDAG::scoreparameters` with the training data and the Bayesian Gaussian equivalent (BGe) score [3, 4]. (1 point)

[Note: The BGe score is a fully-decomposable marginal likelihood function $P(\mathcal{D} \mid \mathcal{G})$ for scoring Bayesian networks. The main underlying assumption is that the data is normally distributed with $\mathcal{N}(\mu, W^{-1})$. The precision matrix W follows a Wishart prior $\mathcal{W}_n(T^{-1}, \alpha_w)$, where $\alpha_w > n - 1$ is the degrees of freedom and T is the positive definite parametric matrix. The mean vector μ follows a normal prior $\mathcal{N}(\nu, \alpha_\mu W)$ with $\alpha_\mu > 0$.]

(b) Learn a Bayesian network using the `BiDAG::iterativeMCMC` function. Plot the directed acyclic graph (DAG). Evaluate the log BGe score of the test data against the estimated DAG using the function `BiDAG::scoreagainstDAG`. (1 point)

(c) One of the arguments in the `scoreparameters` function is `bgepar = list(am = 1, aw = NULL)`, which corresponds to the hyper-parameters α_μ and α_w for the BGe score. By default, $\alpha_\mu = 1$ and $\alpha_w = n + \alpha_\mu + 1$.

Now, consider the set of values $\{10^{-5}, 10^{-3}, 10^{-1}, 10, 10^2\}$ for `am` and keep `aw = NULL` fixed. For each value, repeat the process of splitting the data, initializing the parameters, and learning the DAG for 10 times. Then, report the average number of edges in the DAGs and the average log BGe score of the test data in a table as the one shown below. Remember to run `set.seed(42)` for reproducibility. (*Hint: running the code parallelly with the package* `parallel` *can help reduce the runtime. In this case, run RNGkind("L'Ecuyer-CMRG") for reproducibility.*)

Parameter am	10^{-5}	10^{-3}	10^{-1}	10	10^2
Average number of edges					
Average BGe score of the test data					

What do you observe? Choose the value of `am` corresponding to the highest test BGe score and plot the DAG re-learned from the whole dataset. (3 point)

References

[1] Suter, P., Kuipers, J., Moffa, G., & Beerenwinkel, N. (2023). Bayesian structure learning and sampling of bayesian networks with the r package BiDAG. *Journal of Statistical Software, 105, 1–31.*

[2] Sachs, K., Perez, O., Pe'er, D., Lauffenburger, D. A., & Nolan, G. P. (2005). Causal protein-signaling networks derived from multiparameter single-cell data. *Science, 308(5721), 523-529.*

[3] Geiger, D., & Heckerman, D. (2002). Parameter priors for directed acyclic graphical models and the characterization of several probability distributions. *The Annals of Statistics, 30(5), 1412-1440.*

[4] Kuipers, J., Moffa, G., & Heckerman, D. (2014). Addendum on the scoring of Gaussian directed acyclic graphical models. *The Annals of Statistics, 42(4), 1689-1691.*