

— GUIDE —

Assignment 1: Compute Blood Types

AI-2 Systems Project (Winter Semester 2024/2025)

Jan Frederik Schaefer

Friedrich-Alexander-Universität Erlangen-Nürnberg, Department Informatik

This document is intended to help you solve the assignment “Assignment 1: Compute Blood Types” [AS]. You do not have to read it, but we do recommend to at least take a look at the tips and common issues.

1 A few tips

1. Make sure you understand Bayesian Networks. In the past, students tried to solve the assignment with diagnostic edges because it “feels right” (the arrows point from the things you know to the things you want to know). However, you should really use causal edges. The Basian Network allows you to compute arbitrary conditional probabilities, even if the arrows point from the unknown things to the known things.
2. The problems vary in difficulty. It might be a good idea to start with variations that work well for you. In particular, `problem-a-*.json` problems have a minimal family (father, mother, child). If you have difficulties getting started, you could try to solve such a problem on paper first and then try to use a library for Bayesian networks to do the computations for you.
3. Do not be stingy with nodes. If a conditional probability table seems to get overly complicated, it might help to add more intermediate nodes.
4. Part of the problem is to find a suitable library for Bayesian inference (inference through variable elimination should be efficient enough). It might make sense to try out the library with a minimal example before integrating it with the rest of the code to make sure it actually works as expected.
5. Getting the encoding as a Bayesian network right is somewhat tricky. Make sure that you correctly distinguish between the ABO allele pairs of a person and their observed blood type (state vs evidence variables).

6. For some problems, it might help to add people to the family tree that were not explicitly mentioned in the problem file.
7. Getting the family tree right is tricky too. Visualizing the inferred family tree can help with debugging.

References

- [AS] *Assignment 1: Compute Blood Types*. URL: <https://kwarc.info/teaching/AISysProj/WS2425/assignment-2.1.pdf>.