Lab 3: Bayesian simulations

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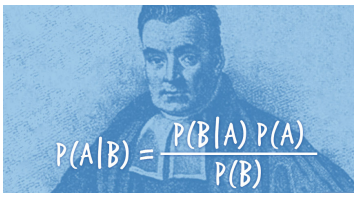
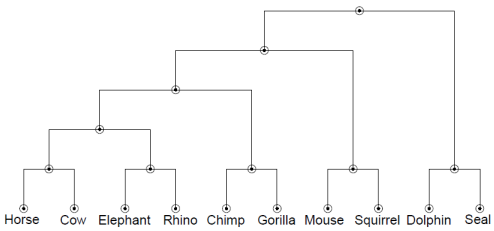


Learning Goals for this lab:

- Understand how probabilities were calculated for the animal similarity task developed by Sanjana and Tenenbaum in R
- Calculate the predictions of the Bayesian model and compare them to the results from Human generalizations.
- Answer questions related to Sanjana and Tenenbaum and Xu and Tenenbaum.
- Discuss the pros and cons of Bayesian learning
- Reflect on the usefulness of Bayesian models for learning about vocabulary development.
- You are encouraged to work together for questions 1-4. Question 5 should be answered individually. Make clear who you worked with in your submission, and all parties should upload a finished single document pdf lab report to Nestor.
- This lab is due on April 8th.

Part 1: Creating a hypothesis space

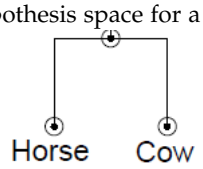
Bayesian Learning is an important topic in computational approaches to cognition. The first step in recreating the Bayesian models from the Sanjana and Tenenbaum paper is the creation of the hypothesis space. This will have to be based on human similarity judgments about how similar different animals are. Recall that the following hierarchy has already been determined:



From this graph, we need to determine the the hypothesis space. "*Elements of the hypothesis space H represent natural subsets of the objects in the domain – subsets likely to be the extension of some novel property or concept. Our goal in building up H is to capture as many hypotheses as possible that people might employ in concept learning*" (page 3).

So first, every node will be a hypothesis. That gives 19 hypothesis spaces. But this is not enough. We also need all possible combinations of two animals (all unions of two clusters from Figure 1). And we also include a third layer, with all unions of three clusters from Figure 1. Of course, we should remove any doubles. This is then the power set of the base clusters.

But let's begin with something more simple. We'll determine the hypothesis space for a much smaller subset.



So the hypothesis space of this tiny graph will be each of the nodes (3, horse, cow, and horse& cow combined together) and then all the possible combinations of nodes into clusters, e.g. horse+cow, horse+(horse& cow) and cow+(horse& cow). This is easy to calculate by hand for such a small graph, but for the bigger graph we will want to use the choose function from R.

The R script contains all the information you need.`Lab_3_Generalizations.R` Create the hypothesis space. Let's first recall what the experiment is were modelling. Here's what the paper said:

Subjects were told that they were training to be veterinarians, by observing examples of particular animals that had been diagnosed with novel diseases. They were required to judge the probability that horses could get the same disease given the examples observed.

So the subjects were told that one, two or three animals of a given type had the novel disease, and then they had predict its probability for horses. So basically subjects are asked to predict the probability of a cluster that contains the animals presented and a horse, given that you were are given 1, 2 or 3 animals as a premise.

Do Part 1, and then answer the following questions.

1. *Simple Generalization*

A. What is the probability of a horse getting the disease when one cow has the disease according to the model?

B. How does this probability change when two cows have the disease? Why is this?

C. In the simulation the value of phi is set to 20. What effect does setting the value to 10 or 30 have on the outcome? What does this tell you about what effect phi has?

D. In the final step where the likelihood matrix is updated by the updated belief, when the premise is simply one horse, how do we get the value 1 for the generalisation results of 1 for horse? Explain your answer by showing the matrix multiplication.

Part 2: Recreating the Sanjana & Tenenbaum paper

Now we'll actually create the model that was in the paper. The same steps as above are involved, but because there are so many more animals and the graph is bigger, it's less transparent.

Begin again by creating the hypothesis space. Then answer the following questions.

2. What does the hypothesis space look like?

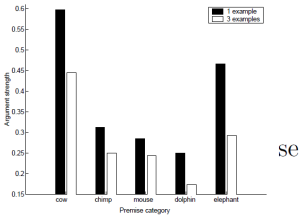
A. How many unique single clusters are there in the tree structure?

B. How many unique pairs of clusters are there?

C. How many unique triples are there?

D. After removing duplicates, how many clusters remain?

Now do Step 2 of Part 2 and calculate the priors and the likelihoods. This will then allow you calculate the generalisations for all the animals given different premises.



3. Comparing the model to Humans

A. Sanjana and Tenenbaum compared their model to human judgments by calculating correlation scores. We'll be more visual. For the animals in the diagram, calculate their generalization probability for cases with one and three examples. Then create a diagram similar to Figure 2. Note that Figure 2 only gives generalizations for the conclusion that a horse can get sick with the disease for each premise.

B. Two what degree does your model resemble human generalizations? In what ways is it different.

4. Evaluating Sanjana and Tenenbaum

A. In this work the graph is based on similarity judgements, and the hypothesis space derived from these judgments is then used to predict generalizations of diseases. Two what degree is it the case that we are simply recreating what we've used as input? Would it be possible to generate the graphical structure backwards from the generalization results (and what would this mean?)

5. *Discussion Questions*

These questions should be answered individually.

A. In the first lecture 5 advantages for computational modelling were presented (1. Explicitness,2. Study complex predictions or interactions,3. Inspiration,4. Practicality and 5. Control and Explanation). In the work of Sanjana and Tenenbaum, which of these advantages can be said to be relevant for this work (i.e. did the computational modeling make some assumptions more explicit?...etc.) Your answers should not be longer than 400 Words.

B. The results from Xu and Tenenbaum's showed that Bayesian models can also model choices about superordinate and subbordinate categories. What was the difference between their straightforward Bayesian model and the one that best fit the adult data?

C. Xu and Tenenbaum's Bayesian models are considered quite a succesful example of modelling. Do you agree with this characterization, that in this study the modelling was particularly illuminating? Explain your answer.