

## Introduction

"Going beyond Given Information", there are two basic ways in which this can be achieved viz. Deductively or Inductively. In Deductive inferences we draw out inferences that were previously unstated but were implicit. However, in Inductive inferences we arrive at conclusions in a more fundamental way, which are likely but not certain as per the given set of information.

## Property Induction

$P_1, \dots, P_n \rightarrow C$  (property) : n-premise argument  
where,  $P_i$  is the  $i$ th premise and  $C$  is the conclusion.

For example, Hippos have skin that is more resistant to penetration than most synthetic fibers. Therefore housecats have skin that is more resistant to penetration than most synthetic fibers. Can be represented as hippos  $\rightarrow$  housecats (thick skin).

### *Inductive Phenomena*

The most systematic studies of property induction have generally used blank properties. For arguments involving animal species, blank properties are properties that are recognized as biological but about which little else is known. For example, "X has enzyme X132". For reasons described below, we usually classify arguments according to inductive context instead of the blankness of the property involved. Arguments like horses  $\rightarrow$  cows (enzyme) belong to the **default biological context**. We call it the default context since it remains active even when a recognizably biological property ("X has enzyme X132") is replaced with a completely blank property ("X has property P").

Premise-conclusion similarity is the effect that argument strength increases as the premises become more similar to the conclusion: for example, horses  $\rightarrow$  dolphins (enzyme) is weaker than seals  $\rightarrow$  dolphins (enzyme).

Typicality is the effect that argument strength increases as the premises become more typical of the conclusion category. For example, seals  $\rightarrow$  mammals (enzyme) is weaker than horses  $\rightarrow$  mammals (enzyme), since seals are less typical mammals than horses.

Diversity is the effect that argument strength increases as the diversity of the premises increases. For example, horses, rhinos  $\rightarrow$  mammals (enzyme) is weaker than seals, squirrels  $\rightarrow$  mammals (enzyme).

*Problem* The problem is especially difficult because arguments that are strong according to one criterion may be weak according to another: for example, seals, squirrels  $\rightarrow$  mammals (enzyme) has premises that are quite diverse, but are not very typical of the conclusion. For reasons of this sort, our primary measure of model performance will consider quantitative predictions across collections of many arguments.

The strength of an argument often depends critically on the property involved. For example, brontosaurus  $\rightarrow$  triceratops (cold blood) is relatively strong, but brontosaurus  $\rightarrow$  triceratops (weighs one ton) is relatively weak

Consider the arguments flies  $\rightarrow$  bees (P) and flowers  $\rightarrow$  bees (P) where P is a completely blank predicate ( $\diamond$ has property P $\diamond$ ). The first argument triggers the default biological context, but the second argument invokes knowledge about feeding relations. For this reason we will classify arguments according to the inductive context they trigger instead of the property they use. This brief survey of the literature suggests that property induction depends on the inductive context in subtle and intricate ways.

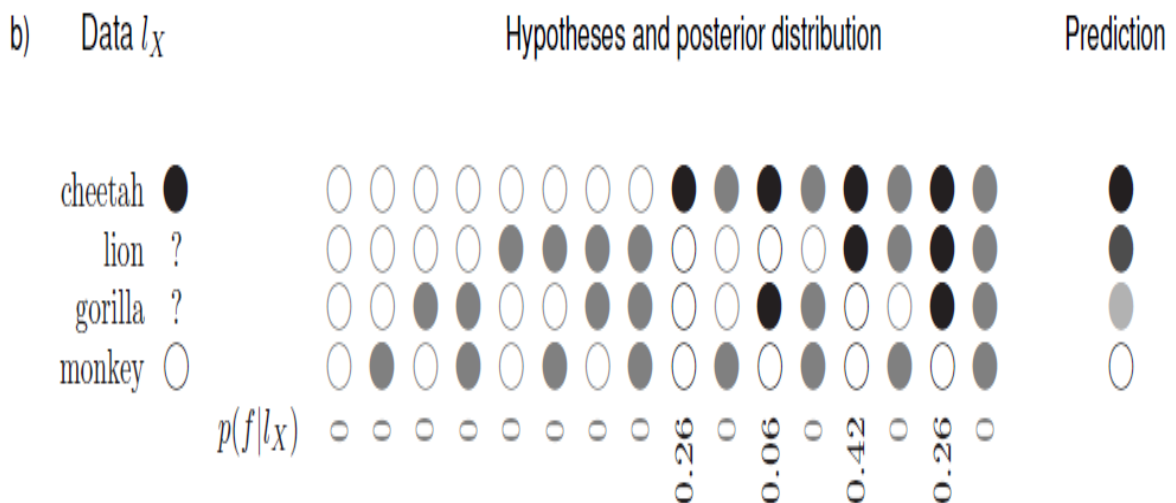
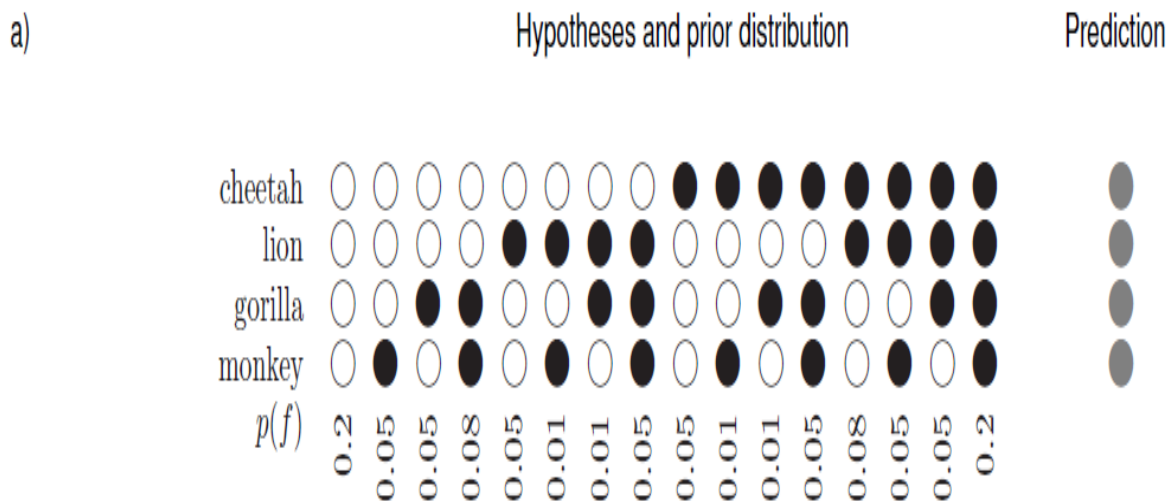
### *Formal Models*

The SCM proposes that the strength of an inductive argument is a linear combination of two factors: the similarity of the conclusion to the premises and the extent to which the premises  $\diamond$ cover $\diamond$  the smallest superordinate taxonomic category including both premises and conclusion.

Instead of founding a model on similarity, an appealing alternative is to start with a collection of features. In some settings it will be necessary to assume that the features are extracted from another kind of input (linguistic input, say), but in general the move from similarity to features is a move towards models that can be directly grounded in experience.

### **Bayesian Property Induction**

We formalize this Bayesian approach by specifying a framework with two components: a recipe for specifying prior distributions, and an engine for inductive inference. *The Bayesian Inference Engine*



### Generating a Prior

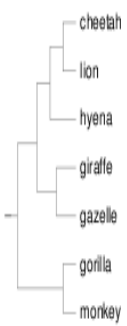


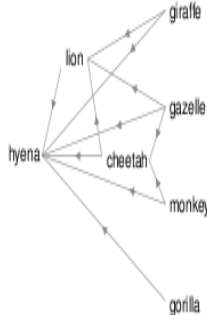
The prior distribution  $p(f)$  should capture expectations about the property or feature of interest. Formalizing the relevant prior knowledge may initially seem like a difficult problem if there are  $n$  species, somehow we need to generate  $2n$  numbers, one for each possible feature vector.

Instead, we develop an approach where the prior  $p(f)$  is generated by two kinds of background knowledge: knowledge about relationships between the categories in a domain, and knowledge about how the property of interest depends on these relationships.

These two aspects of background knowledge can be formalized as a structure  $S$  and a stochastic process  $T$  defined over this structure.

A central theme of our work is that that different kinds of structures can capture different kinds of relationships between categories. Tree structures can capture taxonomic relationships between

categories, multidimensional spaces can capture proximity relationships between categories, graphs can capture directed relationships between categories, and formulae in predicate logic can capture all of these relationships and many others besides.

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We will occasionally use the term **theory** to refer to a structured statistical model that generates a prior  $p(f)$  for Bayesian inference. Each of the theories we consider is a combination of a structure and a stochastic process defined over that structure.

## Taxonomic Reasoning

Generating a prior for any inductive context involves a two-step procedure.

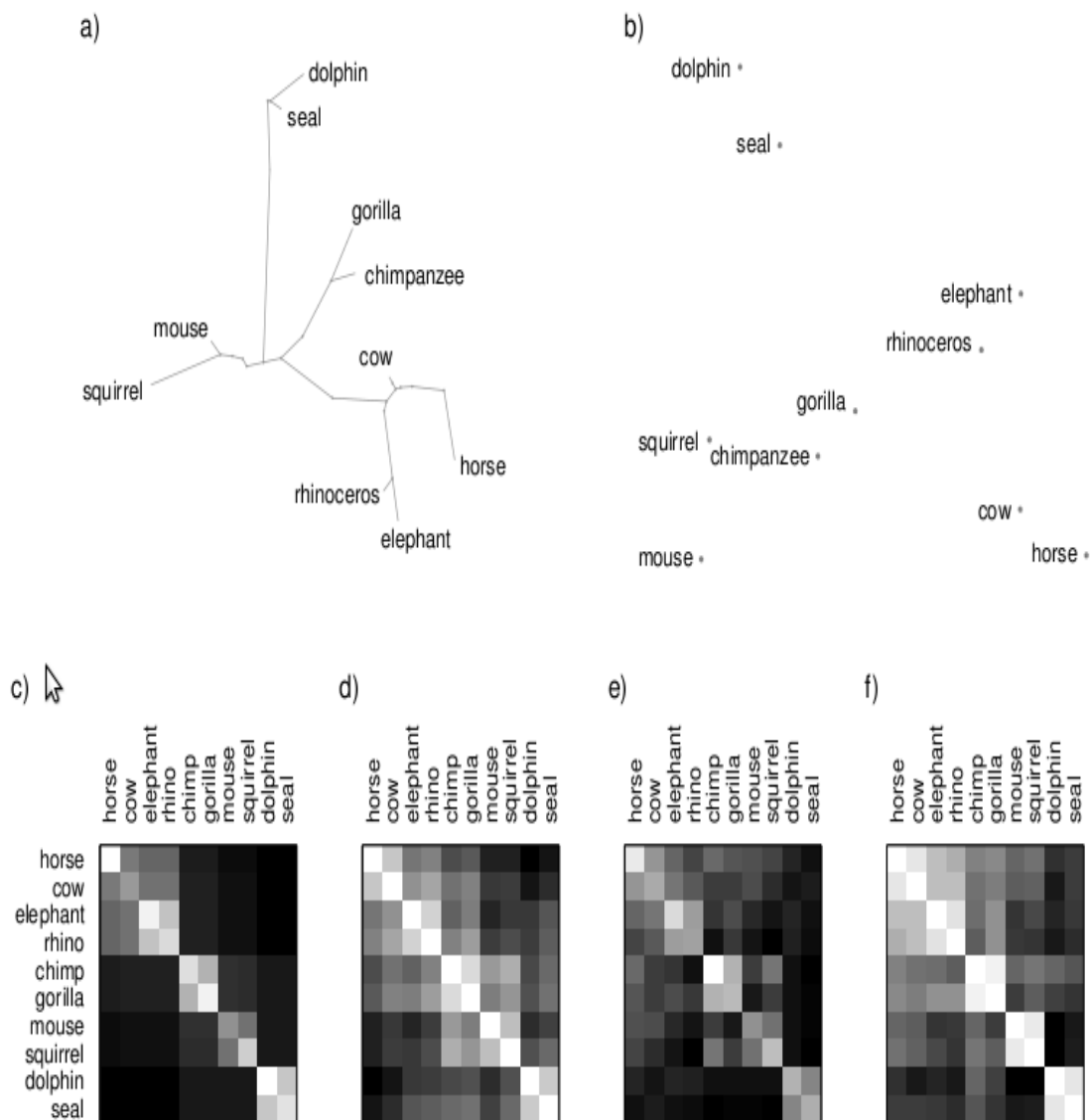
First we must identify the structure that best captures the relevant relationships between the categories in the domain.

Next we must identify a stochastic process that captures knowledge about how properties tend to be distributed over this representation.

A natural representation for the default biological context is a tree structure where the animals are located at the leaves of the tree.

The tree structure ensures that species nearby in the tree will tend to have similar properties. The process, however, should allow species to share a property even if they are very distant in the tree: as a biologist might say, we need to allow for the possibility of convergent evolution. We also need to allow for exceptions—for example, even though penguins may be located near all the other birds in the tree, we know that they lack some important avian features. All of these requirements can be captured by a process we will call the diffusion process.

We describe the diffusion process as a recipe for generating a single feature vector. If we create a large sample of feature vectors by following the recipe many times, the prior probability of any feature vector is proportional to the number of times it appears in the sample.



More formally, suppose that we are working with a set of  $n$  species, and we have a tree structure  $S$  where the species are located at the leaves of the tree. To generate a binary feature  $f$ , we first generate a continuous feature  $y$  that includes a real-valued label for every node in graph  $S$ . The feature  $y$  is drawn from a prior which ensures that it tends to vary smoothly over structure  $S$ . Formally,  $y$  is drawn from a multivariate Gaussian distribution with zero mean and a covariance matrix that encourages nearby nodes in the tree to have similar labels.

If we sample continuous features  $y$  using this covariance matrix, pairs with high covariance (e.g. chimps and gorillas) will tend to have similar feature values.

After generating a continuous feature  $y$ , we convert it to a binary vector  $f$  by thresholding at zero. The complete generative model can be written as:

$$y \sim N(0, K)$$

$$f_i = F(y_i)$$

where,  $F(y_i) = 1$  if  $y_i > 0$

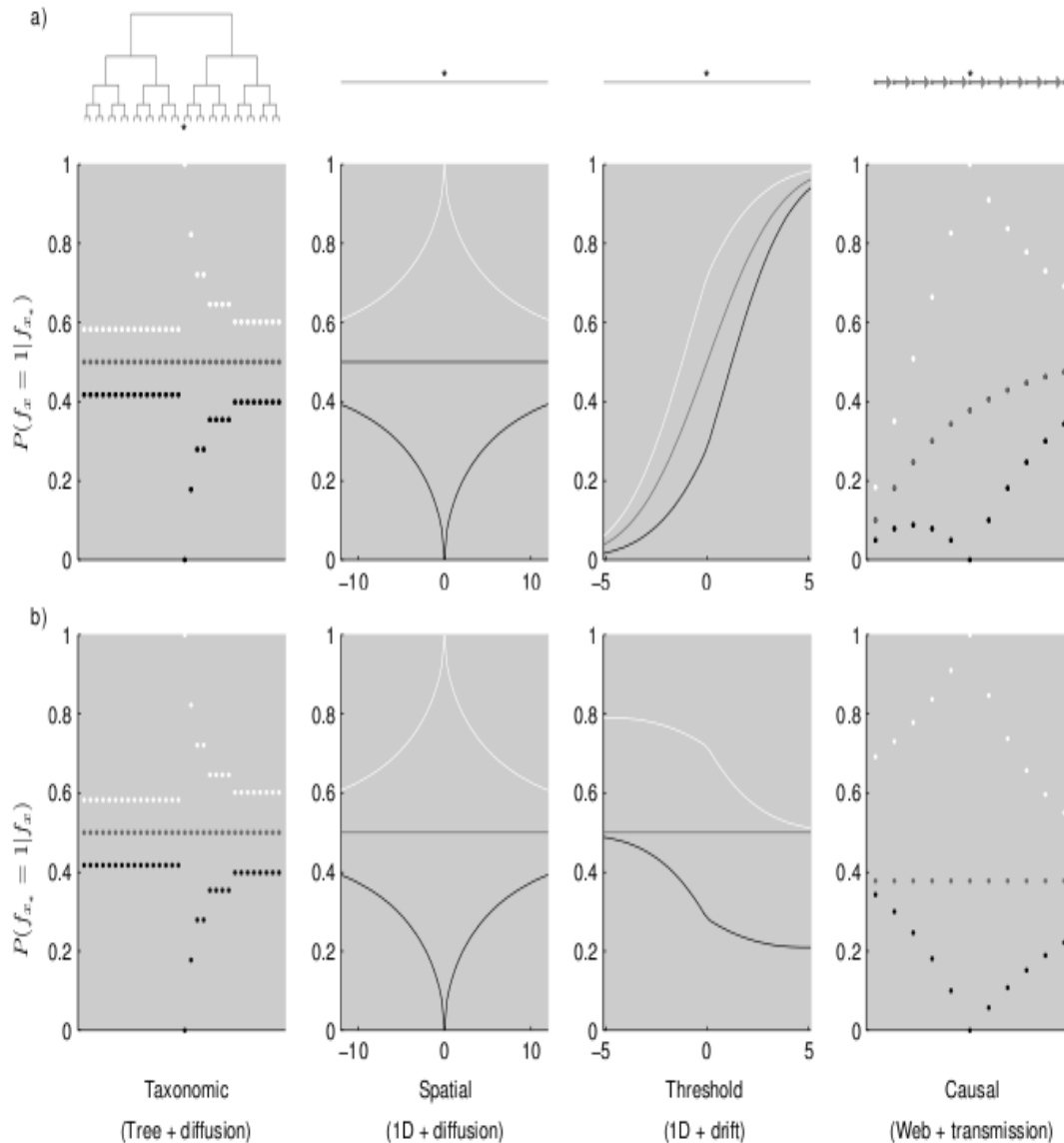
else 0

The diffusion property leads to:

Symmetry is the first of these phenomena: for all pairs of categories  $(a, b)$ , the diffusion process predicts that  $a \rightarrow b$  and  $b \rightarrow a$  are equally strong.

Distance effect: the strength of a one-premise argument decreases as the distance between premise and conclusion increases.

## **Spatial Reasoning**



## Threshold Reasoning

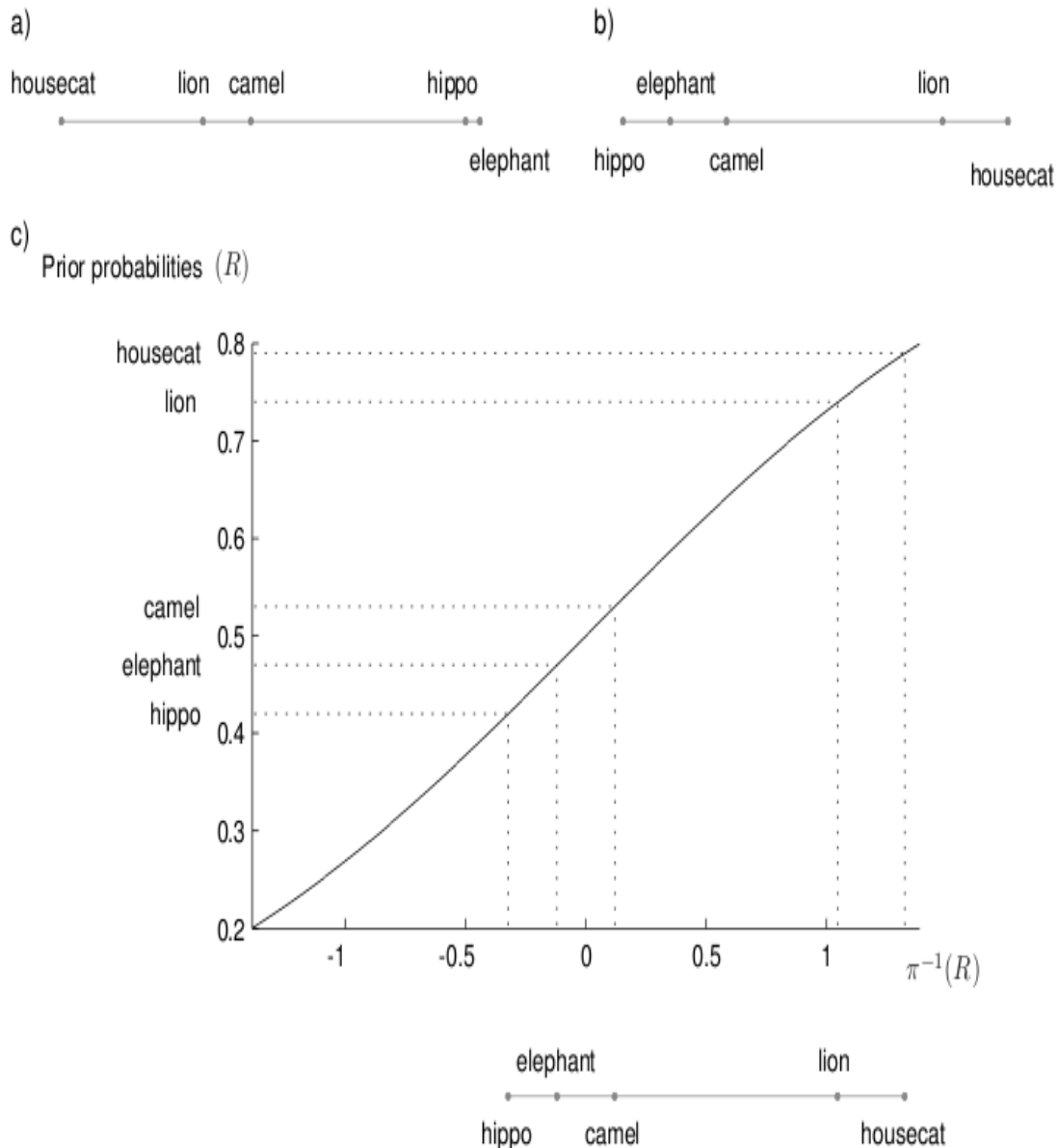
Like the taxonomic and spatial models, our threshold model uses a prior  $p(f)$  induced by a stochastic process defined over a structure. The structure is a one-dimensional space that corresponds to a familiar dimension. For the sake of example, suppose that the underlying dimension is skin toughness (Figure 10a), and that skin toughness can be measured on a scale from 0 to 100. The property of interest should correspond roughly to a threshold along this dimension: all species with skin toughness greater than some value should have  $\blacklozenge$  skin that is more resistant to penetration than most synthetic fibers.  $\blacklozenge$  To capture this intuition, we introduce a stochastic process called the drift process that tends to generate features shared by all categories beyond some point in the underlying dimension.

## Causal Reasoning

Our threshold model captures one kind of reasoning that cannot be explained by similarity alone,

but many other examples can be found in the literature (S. A. Gelman & Markman, 1986; Heit & Rubinstein, 1994; Shafto & Coley, 2003; Medin et al., 2005). One class of examples focuses on causal relations: for example, gazelles  $\rightarrow$  lions (babesiosis) is stronger than lions  $\rightarrow$  gazelles (babesiosis), where babesiosis is an infectious disease.

Like all of our models, the causal model relies on a structure and a stochastic process. The structure captures knowledge about predator-prey relationships among a group of species. This knowledge can be represented as a food web, or a directed graph with an edge from B to A if B is eaten by A. The stochastic process captures knowledge about how diseases are transmitted over a food web.



The curve also suggests that the causal model leads to asymmetry: inferences up the food chain are stronger than inferences in the opposite direction.

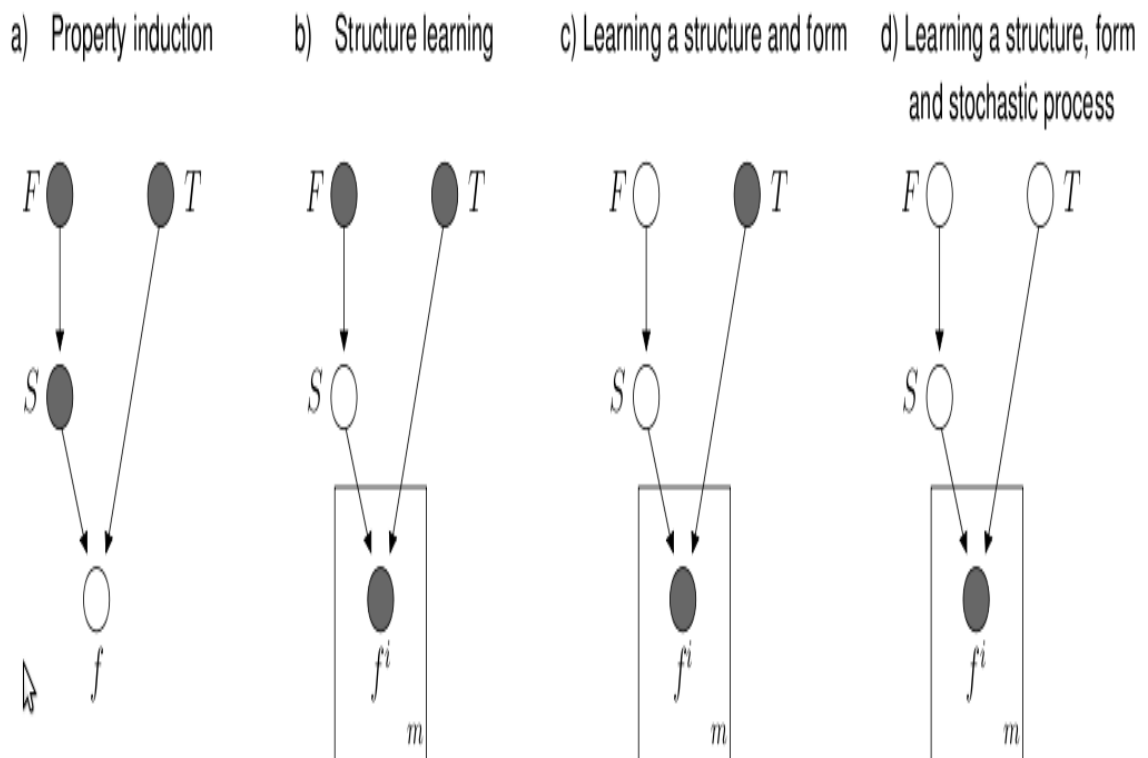
The causal model provides a good account of inferences about the disease property, but not the genetic property, and the taxonomic model shows the opposite pattern of results. This double dissociation provides further evidence that different prior distributions are needed in different



inductive contexts, and that a Bayesian approach to property induction can capture very different patterns of inference when provided with an appropriately structured prior.

### Acquiring Background Knowledge

Each of our models relies on a structure and a stochastic process, and this section discusses how these components of background knowledge can be acquired by a learner.



### REFERENCES

[1]Structured statistical models of inductive reasoning, Charles Kemp & Joshua B. Tenenbaum