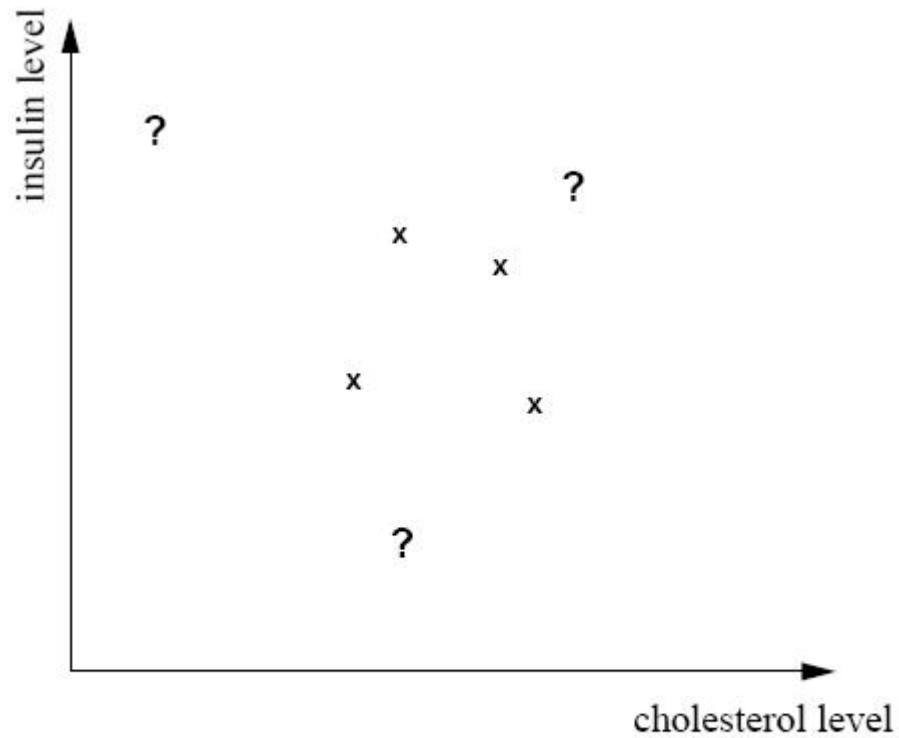


CS340

Bayesian concept learning cont'd

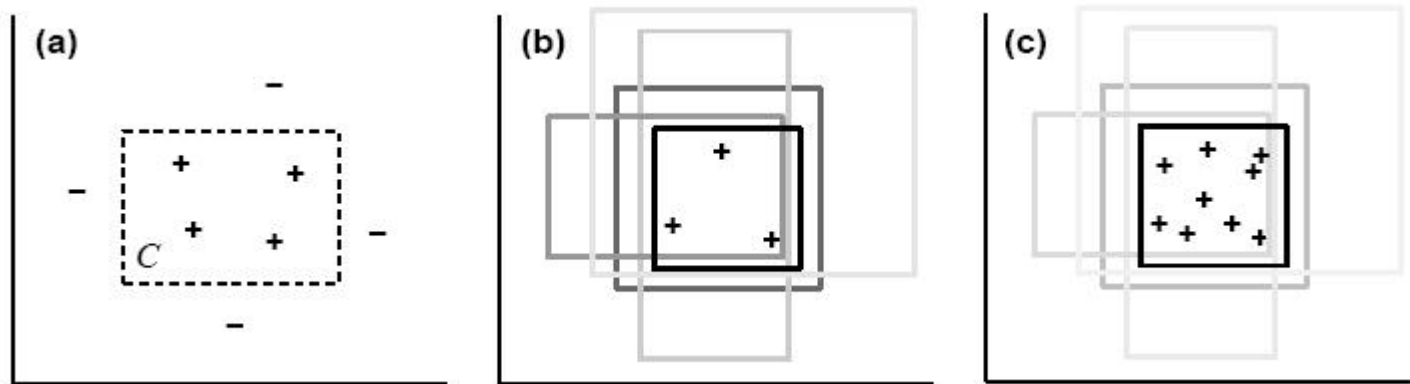
Kevin Murphy

Healthy levels game



"healthy levels"

Hypothesis space



$$h = (\ell_1, \ell_2, s_1, s_2)$$

Healthy levels of insulin/ cholesterol must lie between a minimum and maximum. Healthy levels of a chemical presumably lie between zero and a maximum.

Likelihood (strong sampling)

- $p(X|h) = 1/|h|^n$ if all $x_i \in h$,
where $|h| = s_1 \times s_2$
- $p(X|h) = 0$ if any x_i outside h

Prior $p(h)$

- Use uninformative, but location and scale-invariant, prior (Jeffrey's principle)

$$p(h) \propto \frac{1}{s_1 s_2}$$

This also happens to be conjugate to $p(X|h)$.

- We will explain this later...

Posterior predictive

$$p(y \in C|X) = \int_{h \in H} p(y \in C|h)p(h|X)dh$$

Since the hypothesis space is continuous, we must use an integral instead of a sum...

Insert hairy math

$l - s \leq -r$, where s is size of the rectangle. Hence

$$p(X) = \int_{h \in \mathcal{H}_X} \frac{p(h)}{|h|^n} dh \quad (1.34)$$

$$= \int_{s=r}^{\infty} \int_{l=0}^{l-r} \frac{p(s)}{s^n} dl ds \quad (1.35)$$

$$= \int_{s=r}^{\infty} \left[\int_{l=0}^{l-r} \frac{1}{s^{n+1}} dl \right] ds \quad (1.36)$$

$$= \int_{s=r}^{\infty} \frac{1}{s^{n+1}} [l]_0^{l-r} ds \quad (1.37)$$

$$= \int_{s=r}^{\infty} \frac{s-r}{s^{n+1}} ds \quad (1.38)$$

Now, using integration by parts

$$I = \int_a^b f(x)g'(x)dx = [f(x)g(x)]_a^b - \int_a^b f'(x)g(x)dx \quad (1.39)$$

with the substitutions

$$f(s) = s - r \quad (1.40)$$

$$f'(s) = 1 \quad (1.41)$$

$$f'(s) = s^{-n-1} \quad (1.42)$$

$$g(s) = \frac{s^{-n}}{-n} \quad (1.43)$$

we have

$$p(X) = \left[\frac{(s-r)s^{-n}}{-n} \right]_r^{\infty} - \int_r^{\infty} \frac{s^{-n}}{-n} ds \quad (1.44)$$

$$= \left[\frac{s^{-n+1}}{-n} + \frac{rs^{-n}}{n} - \frac{-1}{n} \frac{s^{-n+1}}{-n+1} \right]_r^{\infty} \quad (1.45)$$

$$= \frac{r^{-n+1}}{n} - \frac{rs^{-n}}{n} + \frac{r^{-n+1}}{n(n-1)} \quad (1.46)$$

$$= \frac{1}{nr^{n-1}} - \frac{r}{nr^{n-1}r} + \frac{1}{n(n-1)r^{n-1}} \quad (1.47)$$

$$= \frac{1}{n(n-1)r^{n-1}} \quad (1.48)$$

To compute the generalization function, let us suppose y is outside the range spanned by the examples (otherwise the probability of generalization is 1). Without loss of generality assume $y > 0$. Let d be the distance from y to the closest observed example. Then we can compute the numerator in Equation 1.33 by replacing r with $r+d$ in the limits of integration (since we have expanded the range of the data by adding y), yielding

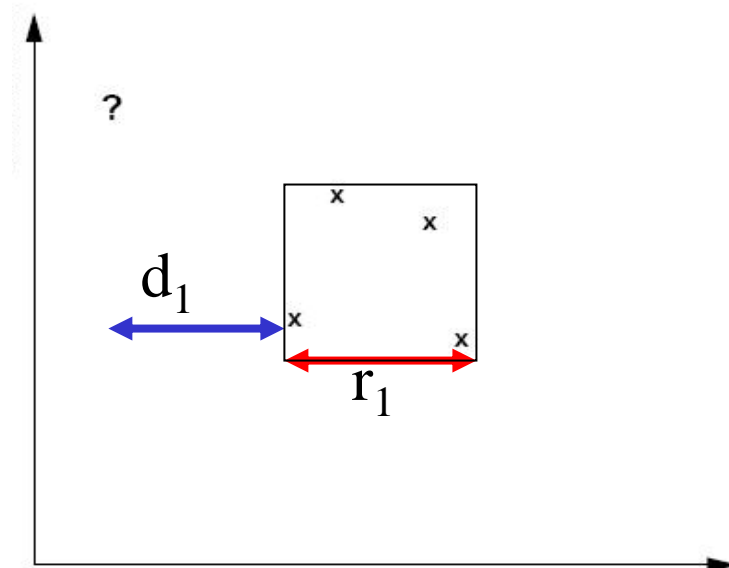
$$p(y \in C, X) = \int_{h \in \mathcal{H}_{X,y}} \frac{p(h)}{|h|^n} dh \quad (1.49)$$

$$= \int_{r+d}^{\infty} \int_0^{l-(r+d)} \frac{p(s)}{s^n} dl ds \quad (1.50)$$

$$= \frac{1}{n(n-1)(r+d)^{n-1}} \quad (1.51)$$

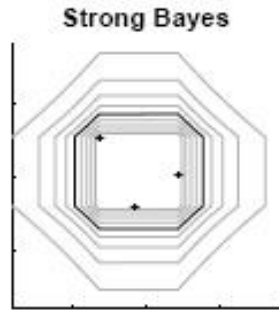
And the answer is...

$$p(y \in C|X) = \left[\frac{1}{(1 + \tilde{d}_1/r_1)(1 + \tilde{d}_2/r_2)} \right]^{n-1}$$

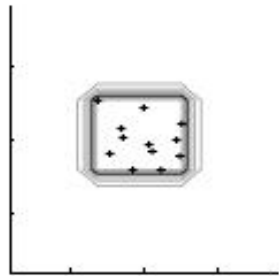
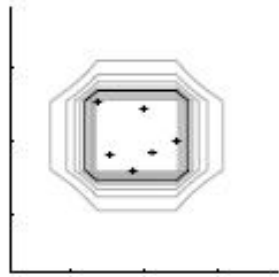


\tilde{d}_i = 0 if $y \in$ range of X_i
= distance of y from closest X_i

Behavior for $n=3, 6, 12$



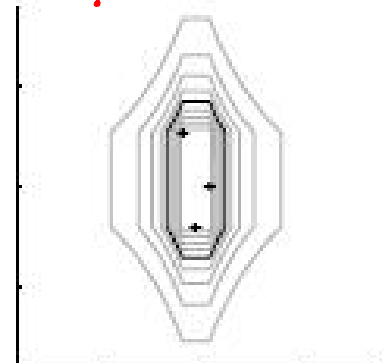
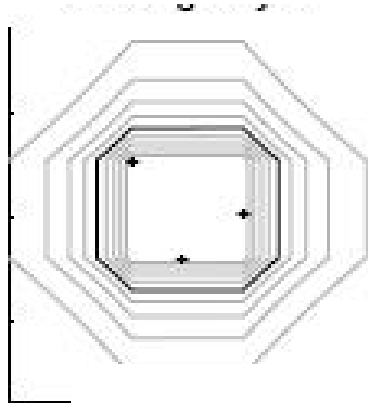
The size principle implies the smallest rectangle has highest likelihood, but there are many other consistent rectangles which are only slightly less likely. These get averaged to give a smooth generalization gradient.



As $N \rightarrow \infty$, the larger hypotheses become exponentially less likely, so we converge on the ML solution (the most specific/ MIN hypothesis)

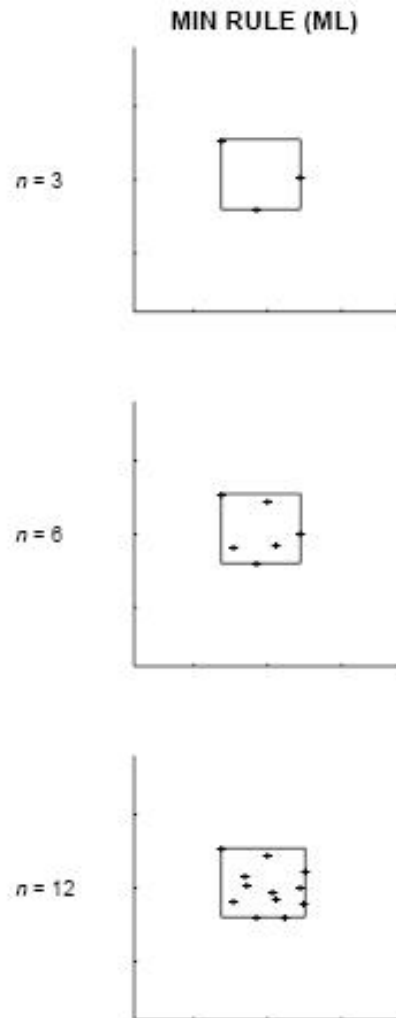
Behavior for different shapes

- $n=3$ in both cases, but on right, $r_1 \ll r_2$, so we generalize more along dimension 2
- Algebraically, d_1/r_1 is big, so $p(y \in C | X)$ is small unless y is inside X
- Intuitively, it would be a suspicious coincidence if the rectangle was wide but r_1



$$p(y \in C | X) = \left[\frac{1}{(1 + \tilde{d}_1/r_1)(1 + \tilde{d}_2/r_2)} \right]^{n-1}$$

Behavior of max likelihood/ MAP



There is no generalization gradient
(a point is either in or out of h).

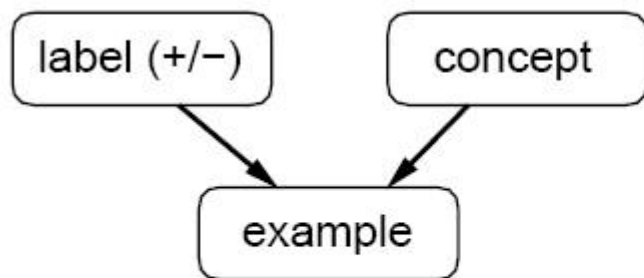
The ML/MAP hyp. is the smallest
enclosing rectangle.

This is a good approximation to
Bayes when N is large.

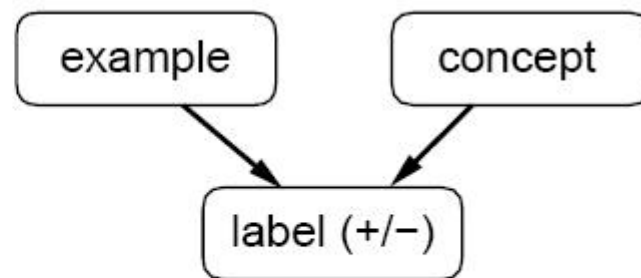
Weak sampling

- Examples are not sampled from the concept, they are just labeled as consistent or not.

$$p(X|h) = \begin{cases} 1 & \text{if } x_1, \dots, x_n \in h \\ 0 & \text{if any } x_i \notin h \end{cases}$$



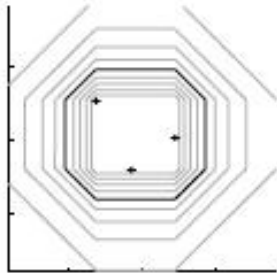
Strong sampling



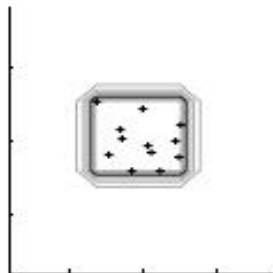
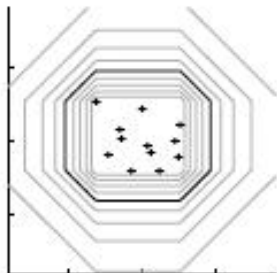
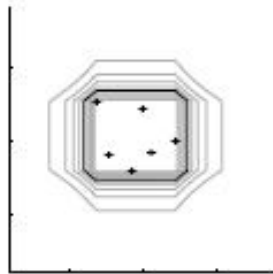
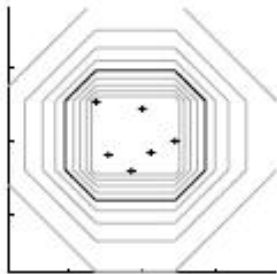
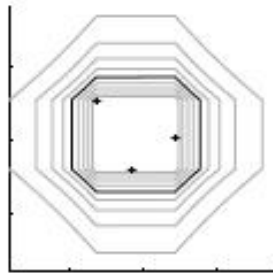
Weak sampling

Behavior of weak Bayes

MAX SIM* (Weak Bayes)



Strong Bayes



We do not get convergence to the ML hypothesis.
If truth is a rectangle, we do not converge to it
(not a consistent estimator).

A more realistic example

- A discrete hypothesis space (the number game)
- A continuous hypothesis space (the healthy levels concept)
- **Word learning**

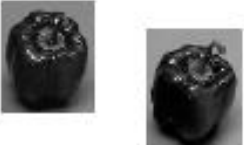









Here is a pog:



Can you give Mr. Frog all the other pogs?

Hierarchical categories

	Vegetables	Vehicles	Animals
subordinate			
basic			
superordinate			

Human data

Example sets:

1 subordinate



3 subordinate



3 basic



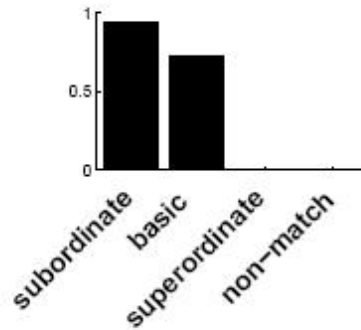
3 superordinate



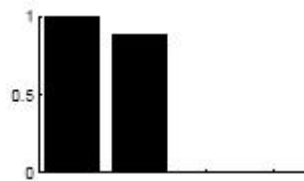
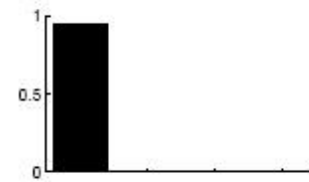
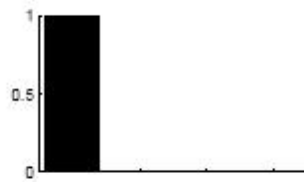
Vegetables

Vehicles

Animals

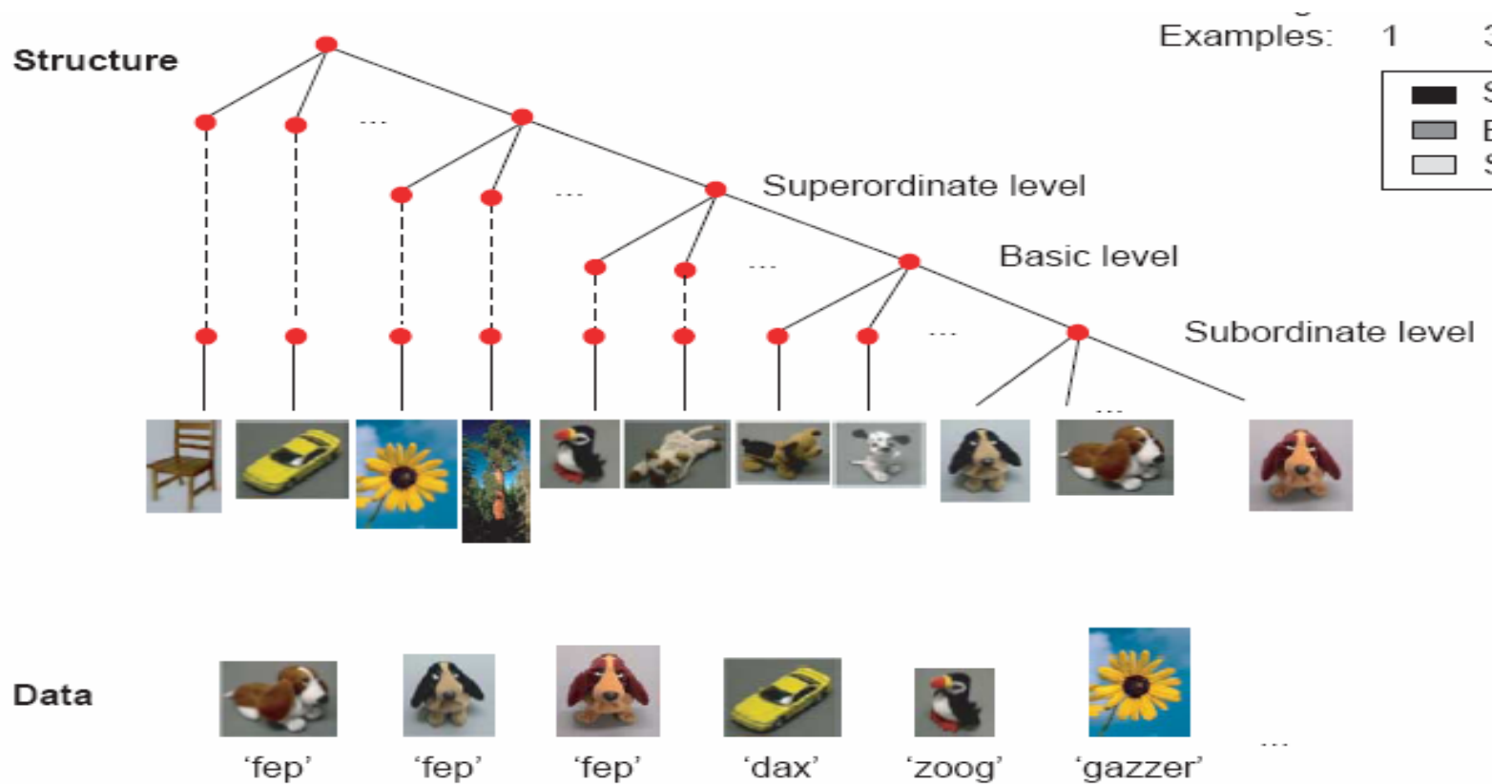


Green peppers? All peppers? All veg?



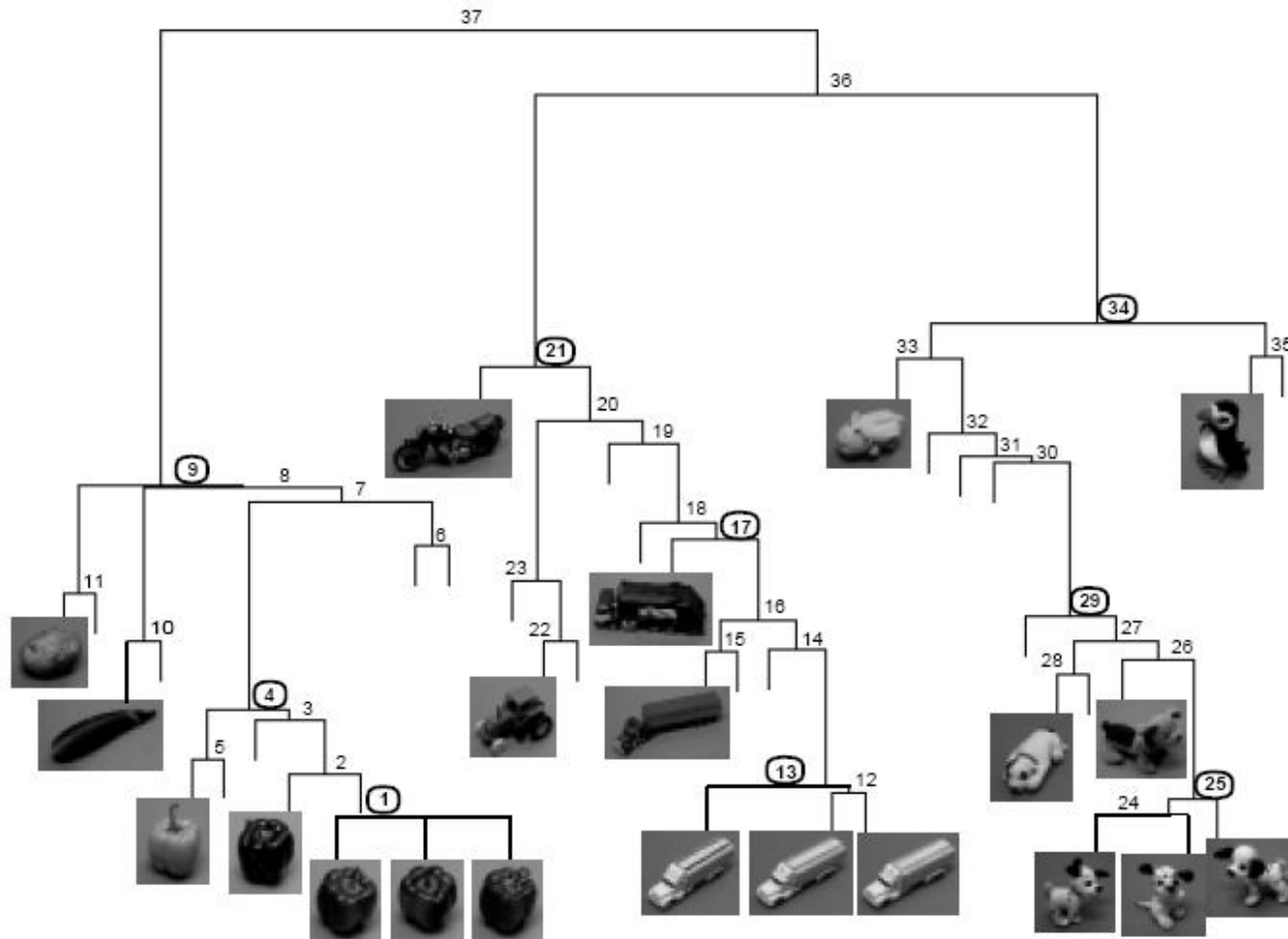
Generalize up to least common ancestor

Hypothesis space



Hypothesis space

Derived by applying agglomerative clustering to human similarity matrix



Hierarchical Clustering

- Cluster based on similarities/distances
- Distance measure between instances \mathbf{x}^r and \mathbf{x}^s

Minkowski (L_p) (Euclidean for $p = 2$)

$$d_m(\mathbf{x}^r, \mathbf{x}^s) = \left[\sum_{j=1}^d (x_j^r - x_j^s)^p \right]^{1/p}$$

City-block distance $d_{cb}(\mathbf{x}^r, \mathbf{x}^s) = \sum_{j=1}^d |x_j^r - x_j^s|$

Agglomerative Clustering

- Start with N groups each with one instance and merge two closest groups at each iteration

- Distance between two groups G_i and G_j :

- Single-link:

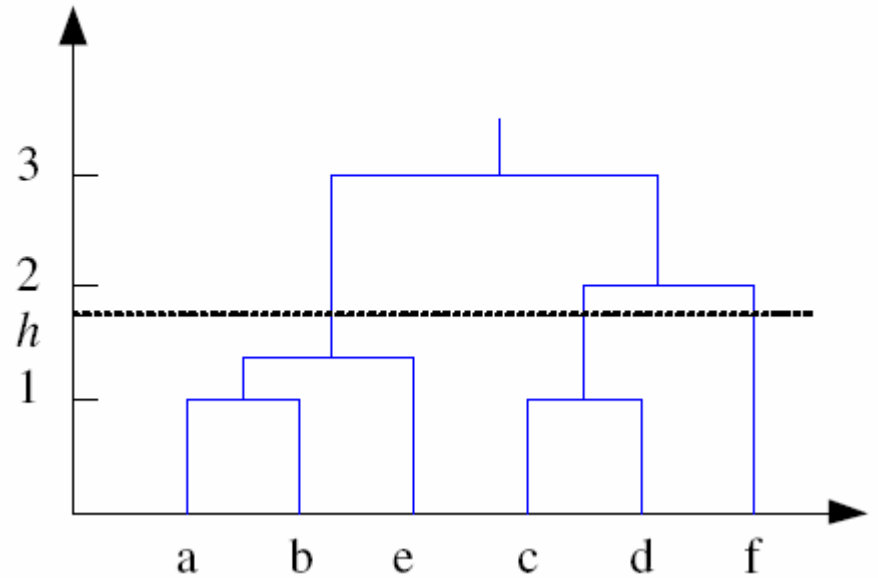
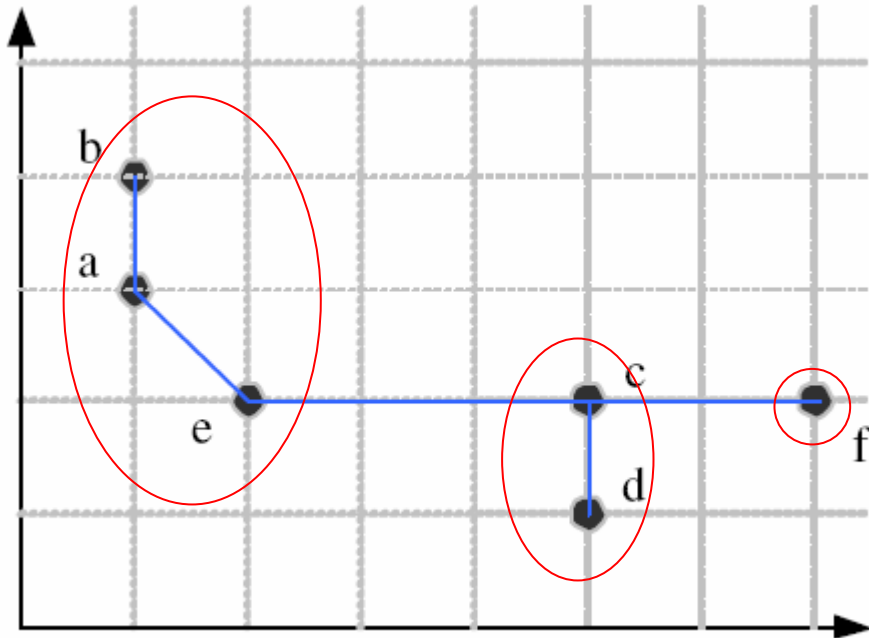
$$d(G_i, G_j) = \min_{x^r \in G_i, x^s \in G_j} d(x^r, x^s)$$

- Complete-link:

$$d(G_i, G_j) = \max_{x^r \in G_i, x^s \in G_j} d(x^r, x^s)$$

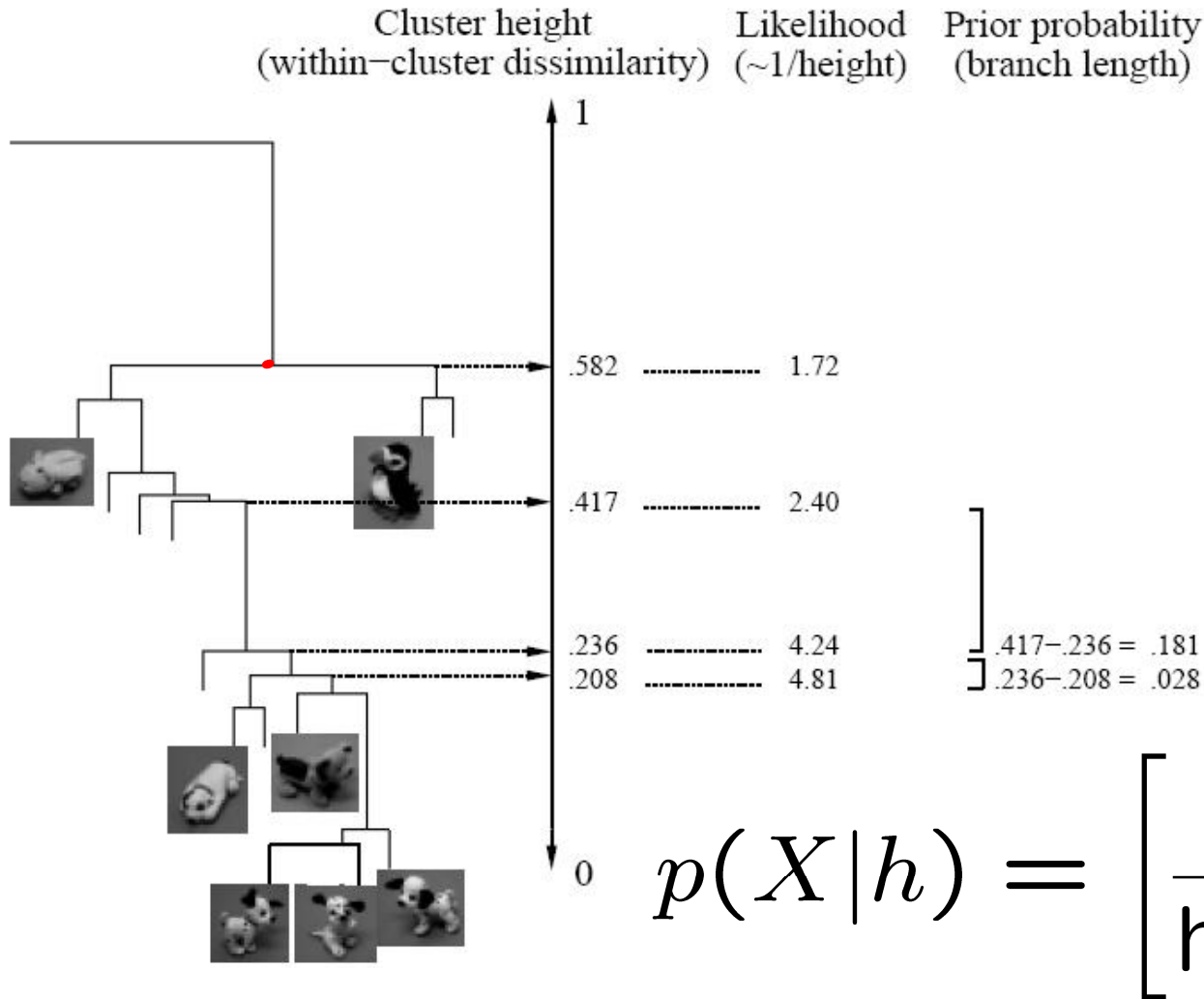
- Average-link, centroid

Example: Single-Link Clustering



Dendrogram

Prior/ likelihood

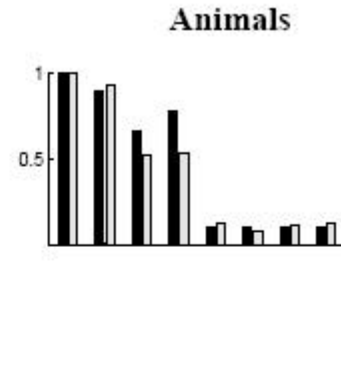
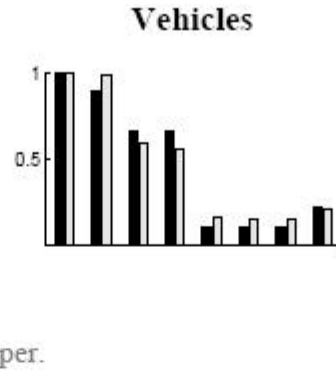
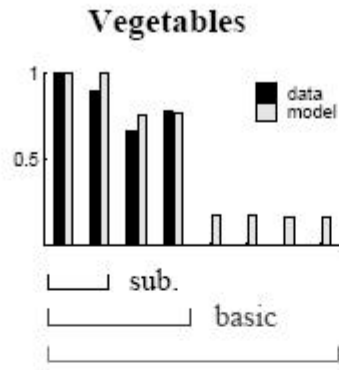


$$p(h) = \text{height}(\text{parent}(h)) - \text{height}(h)$$

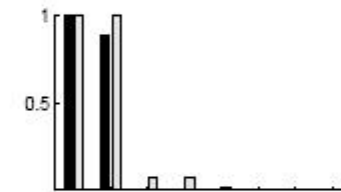
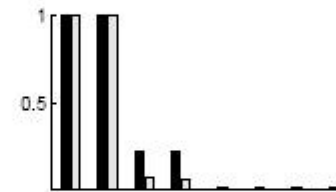
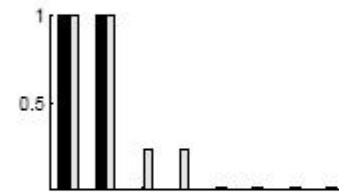
Strong Bayes (w/ basic-level bias)

Example sets:

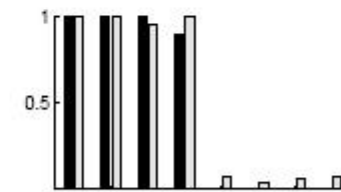
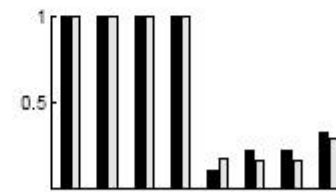
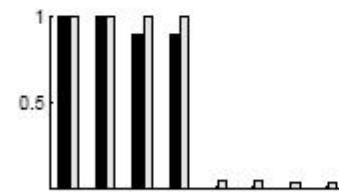
1 subordinate



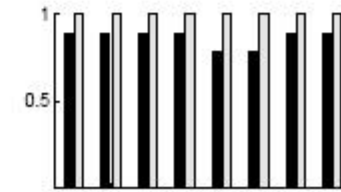
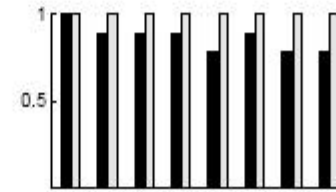
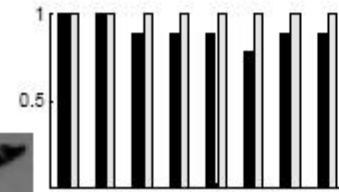
3 subordinate



3 basic



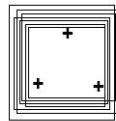
3 superordinate



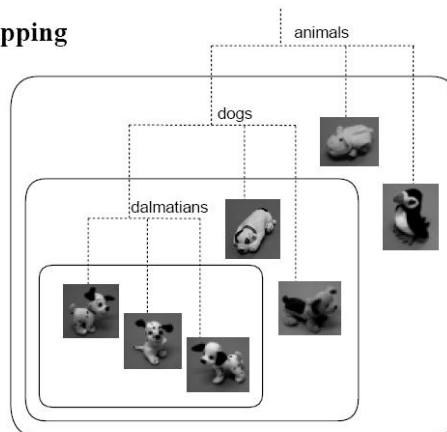
Word learning vs healthy levels

- In the word domain, after about $N=3$ we have an "aha" moment (rule-like learning), but for healthy levels, we need a large sample size, because in the former, hypotheses differ dramatically in size, so we rapidly prefer the smallest consistent, whereas latter averages many.

Healthy levels:
densely overlapping
hypotheses



Word learning:
sparsely overlapping
hypotheses



Rules and exemplars in the number game

- Hyp. space is a mixture of sparse (mathematical concepts) and dense (intervals) hypotheses.
- If data supports mathematical rule (eg $X=\{16,8,2,64\}$), we rapidly learn a rule, otherwise (eg $X=\{6,23,19,20\}$) we learn by similarity, and need many examples to get sharp boundary.