BE/Bi 103: Data Analysis in the Biological Sciences

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8 Hierarchical models

In this lecture, we will investigate **hierarchical models**, in which some model parameters are dependent on others in specific ways. This is best learned by example.

8.1 A hierarchical model example

In Tutorial 3b, we studied reversals under exposure to blue light in *C. elegans* with Channelrhodopsin in two different neurons. Let's consider one of the strains which contains a Channelrhodopsin in the ASH sensory neuron. We found that 9 out of 35 worms reversed under exposure to blue light. We used this measurement to estimate the probability p of reversal. Specifically, we found that the posterior probability of reversal given r our of n trials showed reversals was[10]

$$P(p \mid r, n, I) = \begin{cases} \dfrac{(n+1)!}{(n-r)!r!}\, p^r (1-p)^{n-r} & 0 \leq p \leq 1 \\ 0 & \text{otherwise.} \end{cases} \tag{8.1}$$

This posterior assumed a uniform prior $P(p \mid I)$ on $0 \leq p \leq 1$, and a binomial likelihood, $P(r \mid n, p, I)$.

Next year, we will do the experiment again. Actually, we could image doing the experiment over and over again, each time getting a value of r and n. Conditions may change from experiment to experiment. For example, we may have different microscope set-ups, slight differences in the strain of worms we're using, etc. We are left with some choices on how to model the data.

8.1.1 Pooled data: identical parameters

We could pool all of the data together. In other words, let's say we measure r_1 out of n_1 reversals in the first set of experiments, r_2 out of n_2 reversals in the second set, etc., up to k total experiments. We could pool all of the data together to get

$$r = \sum_{i=1}^{k} r_i \text{ out of } n = \sum_{i=1}^{k} n_i \text{ reversals.} \tag{8.2}$$

[10] In Tutorial 3b, we used n_r for the number of reversals. We use r here because we will have some more subscripts and we want to keep notation clean.

We then compute our posterior as in equation (8.1). Here, the assumption is that the result in each experiment are governed by *identical parameters*. That is to say that we assume $p_1 = p_2 = \cdots = p_k = p$.

This is similar to what we did in section 1.9, in which we looked at how a single hypothesis (or parameter value) is informed by more data.

8.1.2 Independent parameters

As an alternative, we could instead say that the parameters in each experiment are totally independent of each other. In this case, we assume that p_1, p_2, ..., p_k are all independent of each other. Thus, the posterior probability is

$$P(\mathbf{p} \mid \mathbf{r}, \mathbf{n}, I) = \prod_{i=1}^{k} \frac{(n_i + 1)!}{(n_i - r_i)! r_i!} p_i^{r_i} (1 - p_i)^{n_i - r_i}, \tag{8.3}$$

where $\mathbf{p} = \{p_1, p_2, \ldots p_k\}$, with $\mathbf{n}$ and $\mathbf{r}$ similarly defined, and the posterior is understood to be zero if any the p_i's fall our of the interval $[0, 1]$.

When we make this assumption, we often report a value of p that is given by the mean of the p_i's with some error bar.

8.1.3 Best of both worlds: a hierarchical model

Each of these extremes have their advantages. We are often trying to estimate a parameter that is more universal that out experiments, e.g., something that describes worms with Channelrhodopsin in the ASH neuron generally. So, pooling the experiments makes sense. On the other hand, we have reason to assume that there is going to be a different value of p in different experiments, as biological systems are highly variable, not to mention measurement variations. So, how can we capture both of these effects.

We can consider a model in which there is a "master" reversal probability, which we'll call q to avoid too many p's, and the values of p_i may vary from this p according to some probability distribution, $P(p_i \mid q, I)$. So now, we have parameters $p_1, p_2, \ldots, p_k$ and q. So, the posterior can be written using Bayes's theorem,

$$P(q, \mathbf{p} \mid \mathbf{r}, \mathbf{n}, I) = \frac{P(\mathbf{r}, \mathbf{n} \mid q, \mathbf{p}, I)\, P(q, \mathbf{p} \mid I)}{P(\mathbf{n}, \mathbf{r} \mid I)}. \tag{8.4}$$

Note, though, that the observed values of r do not depend directly on q, only on $\mathbf{p}$. In other words, they only depend indirectly on q. So, we can write $P(\mathbf{r}, \mathbf{n} \mid q, \mathbf{p}, I) = P(\mathbf{r}, \mathbf{n} \mid \mathbf{p}, I)$.

Thus, we have

$$P(q, \mathbf{p} \mid \mathbf{r}, \mathbf{n}, I) = \frac{P(\mathbf{r}, \mathbf{n} \mid \mathbf{p}, I)\, P(q, \mathbf{p} \mid I)}{P(\mathbf{n}, \mathbf{r} \mid I)}. \tag{8.5}$$

Next, we can rewrite the prior using the definition of conditional probability.

$$P(q, \mathbf{p} \mid I) = P(\mathbf{p} \mid q, I)\, P(q \mid I). \tag{8.6}$$

Substituting this back into our expression for the posterior, we have

$$P(q, \mathbf{p} \mid \mathbf{r}, \mathbf{n}, I) = \frac{P(\mathbf{r}, \mathbf{n} \mid \mathbf{p}, I)\, P(\mathbf{p} \mid q, I)\, P(q \mid I)}{P(\mathbf{n}, \mathbf{r} \mid I)}. \tag{8.7}$$

Now, if we read off the numerator of this equation, we see a chain of dependencies. The experimental results $\mathbf{r}$ depend on parameters $\mathbf{p}$. Parameters $\mathbf{p}$ depend on *hyperparameter* q. Hyperparameter q then has some prior distribution. Any model that can be written as a chain of dependencies like this is called a **hierarchical model**, and the parameters that do not directly influence the data are called **hyperparameters**.

So, the hierarchical model captures both the experiment-to-experiment variability, as well as the master regulator of outcomes. Note that the product $P(\mathbf{p} \mid q, I)\, P(q \mid I)$ comprises the prior, and it is therefore independent of the data.

8.2 Exchangeability

The conditional probability, $P(\mathbf{p} \mid q, I)$, can take any reasonable form. In the case where we have no reason to believe that we can distinguish any one p_i from another prior to the experiment, then the label "i" applied to the experiment may be exchanged with the label of any other experiment. I.e., $P(p_1, p_2, \ldots, p_k \mid q, I)$ is invariant to permutations of the indices. Parameters behaving this way are said to be **exchangeable**. A common (simple) exchangeable distribution is

$$P(\mathbf{p} \mid q, I) = \prod_{i=1}^{k} P(p_i \mid q, I), \tag{8.8}$$

which means that each of the parameters is an independent sample out of a distribution $P(p_i \mid q)$, which we often take to be the same for all i. This is reasonable to do in the worm reversal example.

8.3 Choice of the conditional distribution/prior

We need to specify out prior, which for this hierarchical model means that we have to specify the conditional distribution, $P(p_i \mid q, I)$, as well as $P(q \mid I)$ For the latter, we will take it to be uniform on $[0, 1]$. For the conditional distribution, we will assume it is beta-distributed, which is defined on the interval $[0, 1]$ and can be peaked. The beta distribution can be written as

$$P(p \mid \alpha, \beta) = \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha)\Gamma(\beta)}\, p^{\alpha-1}(1-p)^{\beta-1}, \tag{8.9}$$

where it is parametrized by positive constants α and β. If α and β are both greater than unity, the distribution is peaked, and the mode is

$$p^* \equiv \omega = \frac{\alpha - 1}{\alpha + \beta - 2}. \tag{8.10}$$

The "concentration," $\kappa = \alpha + \beta$, of the distribution describes its spread. As κ gets larger, the distribution becomes tighter. So, we might want to think of the conditional distribution in terms of ω and κ. We can convert back to α and β using

$$\alpha = \omega(\kappa - 2) + 1 \tag{8.11}$$

$$\beta = (1 - \omega)(\kappa - 2) + 1. \tag{8.12}$$

We have $0 < \omega < 1$ and $2 < \kappa$. A reasonable model would be to take $\omega = q$ with some concentration κ. This gives an additional hyperparameter, κ, which describes experiment-to-experiment variability. We will take $P(\kappa \mid I) \propto 1/\kappa$, as we typically do for scale parameters. Thus, our full posterior is

$$P(q, \kappa, \mathbf{p} \mid \mathbf{r}, \mathbf{n}, I) \propto P(\mathbf{r}, \mathbf{n} \mid \mathbf{p}, I)\, \kappa^{-1} \left(\prod_{i=1}^{k} P(p_i \mid q, \kappa) \right), \tag{8.13}$$

nonzero on $0 \leq q, \mathbf{p} \leq 1$ and $\kappa > 2$, where

$$P(p_i \mid q, \kappa) = \frac{\Gamma(\kappa)}{\Gamma(q(\kappa-2)+1)\Gamma((1-q)(\kappa-2)+1)}\, p^{q(\kappa-2)}(1-p)^{(1-q)(\kappa-2)}. \tag{8.14}$$

As before, we have a binomial likelihood, where we assume the experiments are independent.

$$P(\mathbf{r}, \mathbf{n} \mid \mathbf{p}, I) = \prod_{i=1}^{k} \frac{n_i!}{(n_i - r_i)! r_i!}\, p_i^{r_i}(1 - p_i)^{n_i - r_i}. \tag{8.15}$$

8.4 Implementation

In some cases, we can do some macho integration and work out analytical results for the posterior of a hierarchical model. This usually involves choosing conjugate priors. Most often, though, we need to resort to numerical methods. To see the worm reversal problem solved with a hierarchical model, see the implementation here.

8.5 Generalization

The worm reversal problem is easily generalized. You can imagine having more levels of the hierarchy. This is just more steps in the chain of dependencies that are factored in the prior. For general parameters $\boldsymbol{\theta}$ and hyperparameters $\boldsymbol{\phi}$, we have

$$P(\boldsymbol{\theta}, \boldsymbol{\phi} \mid D, I) = \frac{P(D \mid \boldsymbol{\theta}, I)\, P(\boldsymbol{\theta} \mid \boldsymbol{\phi}, I)\, P(\boldsymbol{\phi} \mid I)}{P(D \mid I)} \tag{8.16}$$

for a two-level hierarchical model. As we have seen in the course, the work is all in coming up with the models for the likelihood $P(D \mid \boldsymbol{\theta}, I)$ and prior, $P(\boldsymbol{\theta} \mid \boldsymbol{\phi}, I)\, P(\boldsymbol{\phi} \mid I)$. For coming up with the conditional portion of the prior, $P(\boldsymbol{\theta} \mid \boldsymbol{\phi}, I)$, we often assume a Gaussian distribution because this often describes experiment-to-experiment variability. Bayes's theorem gives you the posterior, and it is then "just" a matter of computing it of sampling from it.