

# Principles of Bayesian Inference

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1

- Classical statistics: model parameters are *fixed* and *unknown*.
- A Bayesian thinks of parameters as random, and thus having distributions (just like the data). We can thus think about unknowns for which no reliable frequentist experiment exists, e.g.  $\theta$  = proportion of US men with untreated prostate cancer.
- A Bayesian writes down a *prior* guess for parameter(s)  $\theta$ , say  $p(\theta)$ . He then combines this with the information provided by the observed data  $\mathbf{y}$  to obtain the *posterior* distribution of  $\theta$ , which we denote by  $p(\theta | \mathbf{y})$ .
- All statistical inferences (point and interval estimates, hypothesis tests) then follow from posterior summaries. For example, the posterior means/medians/modes offer point estimates of  $\theta$ , while the quantiles yield credible intervals.

2

- The key to Bayesian inference is “learning” or “updating” of prior beliefs. Thus, posterior information  $\geq$  prior information.
- Is the classical approach wrong? That may be a controversial statement, but it certainly is fair to say that the classical approach is limited in scope.
- The Bayesian approach expands the class of models and easily handles:
  - repeated measures
  - unbalanced or missing data
  - nonhomogenous variances
  - multivariate data
 – and many other settings that are precluded (or much more complicated) in classical settings.

3

- We start with a model (likelihood)  $f(\mathbf{y} | \theta)$  for the observed data  $\mathbf{y} = (y_1, \dots, y_n)'$  given unknown parameters  $\theta$  (perhaps a collection of several parameters).
- Add a prior distribution  $p(\theta | \lambda)$ , where  $\lambda$  is a vector of hyper-parameters.
- The posterior distribution of  $\theta$  is given by:

$$p(\theta | \mathbf{y}, \lambda) = \frac{p(\theta | \lambda) \times f(\mathbf{y} | \theta)}{p(\mathbf{y} | \lambda)} = \frac{p(\theta | \lambda) \times f(\mathbf{y} | \theta)}{\int f(\mathbf{y} | \theta) p(\theta | \lambda) d\theta}$$

We refer to this formula as *Bayes Theorem*.

4

- Calculations (numerical and algebraic) are usually required only up to a proportionality constant. We, therefore, write the posterior as:

$$p(\theta | \mathbf{y}, \lambda) \propto p(\theta | \lambda) \times f(\mathbf{y} | \theta).$$

- If  $\lambda$  are known/fixed, then the above represents the desired posterior. If, however,  $\lambda$  are unknown, we assign a prior,  $p(\lambda)$ , and seek:

$$p(\theta, \lambda | \mathbf{y}) \propto p(\lambda) p(\theta | \lambda) f(\mathbf{y} | \theta).$$

The proportionality constant does not depend upon  $\theta$  or  $\lambda$ :

$$\frac{1}{p(\mathbf{y})} = \frac{1}{\int p(\lambda) p(\theta | \lambda) f(\mathbf{y} | \theta) d\lambda d\theta}$$

- The above represents a *joint* posterior from a *hierarchical model*. The *marginal* posterior distribution for  $\theta$  is:

$$p(\theta | \mathbf{y}) = \int p(\lambda) p(\theta | \lambda) f(\mathbf{y} | \theta) d\lambda.$$

5

- Point estimation is easy: simply choose an appropriate distribution summary: posterior mean, median or mode.
- **Mode** sometimes easy to compute (no integration, simply optimization), but often misrepresents the “middle” of the distribution – especially for one-tailed distributions.
- **Mean**: easy to compute. It has the “opposite effect” of the mode – chases tails.
- **Median**: probably the best compromise in being robust to tail behaviour although it may be awkward to compute as it needs to solve:

$$\int_{-\infty}^{\theta_{median}} p(\theta | \mathbf{y}) d\theta = \frac{1}{2}.$$

6

- The most popular method of inference in practical Bayesian modelling is interval estimation using *credible sets*. A  $100(1 - \alpha)\%$  credible set  $C$  for  $\theta$  is a set that satisfies:

$$P(\theta \in C | \mathbf{y}) = \int_C p(\theta | \mathbf{y}) d\theta \geq 1 - \alpha.$$

- The most popular credible set is the simple equal-tail interval estimate  $(q_L, q_U)$  such that:

$$\int_{-\infty}^{q_L} p(\theta | \mathbf{y}) d\theta = \frac{\alpha}{2} = \int_{q_U}^{\infty} p(\theta | \mathbf{y}) d\theta$$

Then clearly  $P(\theta \in (q_L, q_U) | \mathbf{y}) = 1 - \alpha$ .

- This interval is relatively easy to compute and has a direct interpretation: **The probability that  $\theta$  lies between  $(q_L, q_U)$  is  $1 - \alpha$ .** The frequentist interpretation is extremely convoluted.

7

- Example: Consider a single data point  $y$  from a Normal distribution:  $y \sim N(\theta, \sigma^2)$ ; assume  $\sigma$  is *known*.

$$f(y|\theta) = N(y|\theta, \sigma^2) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left(-\frac{1}{2\sigma^2}(y - \theta)^2\right)$$

- $\theta \sim N(\mu, \tau^2)$ , i.e.  $p(\theta) = N(\theta|\mu, \tau^2)$ ;  $\mu, \tau^2$  are known.
- Posterior distribution of  $\theta$

$$\begin{aligned} p(\theta|y) &\propto N(\theta|\mu, \tau^2) \times N(y|\theta, \sigma^2) \\ &= N\left(\theta \mid \frac{\frac{1}{\tau^2}}{\frac{1}{\sigma^2} + \frac{1}{\tau^2}}\mu + \frac{\frac{1}{\sigma^2}}{\frac{1}{\sigma^2} + \frac{1}{\tau^2}}y, \frac{1}{\frac{1}{\sigma^2} + \frac{1}{\tau^2}}\right) \\ &= N\left(\theta \mid \frac{\sigma^2}{\sigma^2 + \tau^2}\mu + \frac{\tau^2}{\sigma^2 + \tau^2}y, \frac{\sigma^2\tau^2}{\sigma^2 + \tau^2}\right). \end{aligned}$$

8

- Interpret: Posterior mean is a weighted mean of prior mean and data point.
- The direct estimate is shrunk towards the prior.
- What if you had  $n$  observations instead of one in the earlier set up? Say  $\mathbf{y} = (y_1, \dots, y_n)'$ , where  $y_i \stackrel{iid}{\sim} N(0, \sigma^2)$ .
- $\bar{y}$  is a *sufficient statistic* for  $\mu$ ;  $\bar{y} \sim N\left(\mu, \frac{\sigma^2}{n}\right)$
- Posterior distribution of  $\theta$

$$\begin{aligned} p(\theta | \mathbf{y}) &\propto N(\theta | \mu, \tau^2) \times N\left(\bar{y} | \theta, \frac{\sigma^2}{n}\right) \\ &= N\left(\theta \mid \frac{\frac{1}{\tau^2}}{\frac{n}{\sigma^2} + \frac{1}{\tau^2}}\mu + \frac{\frac{n}{\sigma^2}}{\frac{n}{\sigma^2} + \frac{1}{\tau^2}}\bar{y}, \frac{1}{\frac{n}{\sigma^2} + \frac{1}{\tau^2}}\right) \\ &= N\left(\theta \mid \frac{\sigma^2}{\sigma^2 + n\tau^2}\mu + \frac{n\tau^2}{\sigma^2 + n\tau^2}\bar{y}, \frac{\sigma^2\tau^2}{\sigma^2 + n\tau^2}\right) \end{aligned}$$

9

- Example: Let  $Y$  be the number of successes in  $n$  independent trials.

$$P(Y = y|\theta) = f(y|\theta) = \binom{n}{y} \theta^y (1 - \theta)^{n-y}$$

- Prior:  $p(\theta) = \text{Beta}(\theta|a, b)$ :

$$p(\theta) \propto \theta^{a-1} (1 - \theta)^{b-1}.$$

- Prior mean:  $\mu = a/(a + b)$ ; Variance  $ab/((a + b)^2(a + b + 1))$
- Posterior distribution of  $\theta$

$$p(\theta|y) = \text{Beta}(\theta|a + y, b + n - y)$$

10

- We will compute the posterior distribution  $p(\theta | \mathbf{y})$  by drawing samples from it. This replaces numerical integration (quadrature) by "Monte Carlo integration".
- One important advantage: we only need to know  $p(\theta | \mathbf{y})$  up to the proportionality constant.
- Suppose  $\theta = (\theta_1, \theta_2)$  and we know how to sample from the *marginal posterior distribution*  $p(\theta_2 | \mathbf{y})$  and the *conditional distribution*  $P(\theta_1 | \theta_2, \mathbf{y})$ .
- How do we draw samples from the joint distribution:  $p(\theta_1, \theta_2 | \mathbf{y})$ ?

11

- We do this in two stages using *composition sampling*:
  - First draw  $\theta_2^{(j)} \sim p(\theta_2 | \mathbf{y})$ ,  $j = 1, \dots, M$ .
  - Next draw  $\theta_1^{(j)} \sim p(\theta_1 | \theta_2^{(j)}, \mathbf{y})$ .
- This sampling scheme produces *exact* samples,  $\{\theta_1^{(j)}, \theta_2^{(j)}\}_{j=1}^M$  from the posterior distribution  $p(\theta_1, \theta_2 | \mathbf{y})$ .
- Gelfand and Smith (*JASA*, 1990) demonstrated *automatic marginalization*:  $\{\theta_1^{(j)}\}_{j=1}^M$  are samples from  $p(\theta_1 | \mathbf{y})$  and (of course!)  $\{\theta_2^{(j)}\}_{j=1}^M$  are samples from  $p(\theta_2 | \mathbf{y})$ .
- In effect, composition sampling has performed the following "integration":

$$p(\theta_1 | \mathbf{y}) = \int p(\theta_1 | \theta_2, \mathbf{y}) p(\theta_2 | \mathbf{y}) d\theta_2.$$

12

- Suppose we want to predict new observations, say  $\tilde{\mathbf{y}}$ , based upon the observed data  $\mathbf{y}$ . We will specify a *joint* probability model  $p(\tilde{\mathbf{y}}, \mathbf{y} | \theta)$ , which defines the *conditional predictive distribution*:

$$p(\tilde{\mathbf{y}} | \mathbf{y}, \theta) = \frac{p(\tilde{\mathbf{y}}, \mathbf{y} | \theta)}{p(\mathbf{y} | \theta)}.$$

- Bayesian predictions follow from the *posterior predictive* distribution that averages out the  $\theta$  from the conditional predictive distribution with respect to the posterior:

$$p(\tilde{\mathbf{y}} | \mathbf{y}) = \int p(\tilde{\mathbf{y}} | \mathbf{y}, \theta) p(\theta | \mathbf{y}) d\theta.$$

- This can be evaluated using composition sampling:
  - First obtain:  $\theta^{(j)} \sim p(\theta | \mathbf{y})$ ,  $j = 1, \dots, M$
  - For  $j = 1, \dots, M$  sample  $\tilde{\mathbf{y}}^{(j)} \sim p(\tilde{\mathbf{y}} | \mathbf{y}, \theta^{(j)})$
- The  $\{\tilde{\mathbf{y}}^{(j)}\}_{j=1}^M$  are samples from the posterior predictive distribution  $p(\tilde{\mathbf{y}} | \mathbf{y})$ .

- Direct Monte Carlo: Some algorithms (e.g. composition sampling) can generate *independent* samples *exactly* from the posterior distribution. In these situations there are **NO** convergence problems or issues. Sampling is called *exact*.
- Markov Chain Monte Carlo (MCMC): In general, exact sampling may not be possible/feasible. MCMC is a far more versatile set of algorithms that can be invoked to fit more general models. Note: anywhere where direct Monte Carlo applies, MCMC will provide excellent results too.
- Convergence issues: There is no free lunch! The power of MCMC comes at a cost. The initial samples do not necessarily come from the desired posterior distribution. Rather, they need to *converge* to the true posterior distribution. Therefore, one needs to assess convergence, discard output before the convergence and retain only post-convergence samples. The time of convergence is called **burn-in**.
- Diagnosing convergence: Usually a few parallel chains are run from rather different starting points. The sample values are plotted (called trace-plots) for each of the chains. The time for the chains to "mix" together is taken as the time for convergence.
- Good news! All this is **automated** in WinBUGS. So, as users, we need to only configure how to specify good Bayesian models and implement them in WinBUGS.