

2016 SISG Module 17: Bayesian Statistics for Genetics

Lecture 3: Binomial Sampling

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Outline

Introduction and Motivating Example

Bayesian Analysis of Binomial Data

The Beta Prior

Bayes Factors

Analysis of ASE Data

Conclusions

Introduction

- In this lecture we will continue to consider the Bayesian modeling of binomial data.
- The analysis of **allele specific expression** data will be used to motivate the binomial model.
- **Conjugate priors** will be introduced.
- **Sampling from the posterior** will be emphasized as a method for flexible inference.

Bayes Theorem Recap

- We derive the posterior distribution via **Bayes theorem**:

$$p(\theta|y) = \frac{\Pr(y|\theta) \times p(\theta)}{\Pr(y)}$$

- The denominator:

$$\Pr(y) = \int \Pr(y|\theta) \times p(\theta)d\theta$$

is a **normalizing constant** to ensure the RHS integrates to 1.

- More colloquially:

$$\begin{aligned}\text{Posterior} & \propto \text{Likelihood} \times \text{Prior} \\ & = \Pr(y|\theta) \times p(\theta)\end{aligned}$$

since in considering the posterior we only need to worry about terms that depend on the parameter θ .

Elements of Bayes Theorem for a Binomial Model

- We assume independent responses with a common “success” probability θ .
- In this case, the contribution of the data is through the binomial probability distribution:

$$\Pr(Y = y|\theta) = \binom{N}{y} \theta^y (1 - \theta)^{N-y} \quad (1)$$

and tells us the probability of seeing $Y = y$, $y = 0, 1, \dots, N$ given the probability θ .

- For fixed y , we may view (1) as a function of θ – this is the **likelihood function**.
- The **maximum likelihood estimate** (MLE) is that value

$$\hat{\theta} = y/n$$

that gives the highest probability to the observed data, i.e. maximizes the likelihood function.

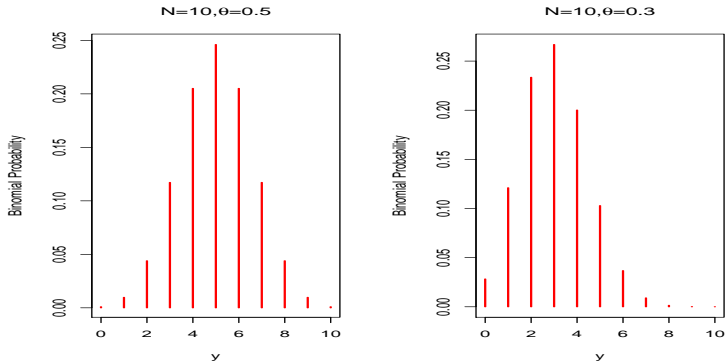


Figure 1 : Binomial distributions for two values of θ with $N = 10$.

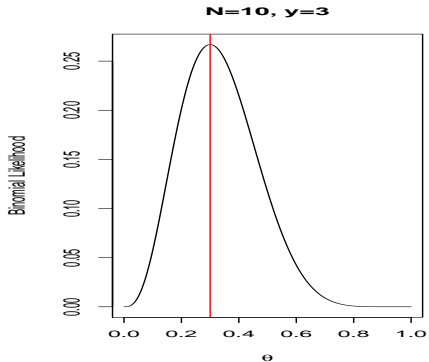
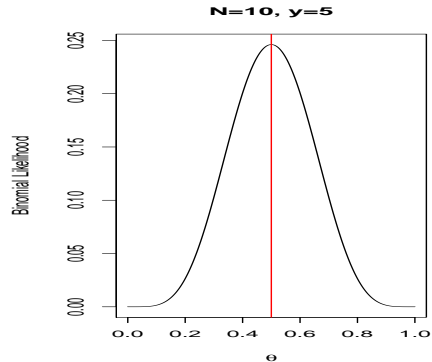


Figure 2 : Binomial likelihoods for values of $y = 5$ (left) and $y = 10$ (right), with $N = 10$. The MLEs are indicated in red.

The Beta Distribution as a Prior Choice for a Binomial θ

- Bayes theorem requires the likelihood, which we have already specified as binomial, and the prior.
- For a probability $0 < \theta < 1$ an obvious candidate prior is the uniform distribution on $(0,1)$: but this is too restrictive in general.
- The **beta distribution**, $\text{beta}(a, b)$, is more flexible and so may be used for θ , with a and b specified in advance. The uniform distribution is a special case with $a = b = 1$.
- The form of the beta distribution is

$$p(\theta) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \theta^{a-1} (1-\theta)^{b-1}$$

for $0 < \theta < 1$, where $\Gamma(\cdot)$ is the gamma function¹.

- The distribution is valid² for $a > 0, b > 0$.

¹ $\Gamma(z) = \int_0^\infty t^{z-1} e^{-t} dt$

²A distribution is valid if it is non-negative and integrates to 1

The Beta Distribution as a Prior Choice for a Binomial θ

- How can we think about specifying a and b ?
- For the normal distribution the parameters μ and σ^2 are just the mean and variance, but for the beta distribution a and b have no such simple interpretation.
- The mean and variance are:

$$E[\theta] = \frac{a}{a+b}$$

$$\text{var}(\theta) = \frac{E[\theta](1 - E[\theta])}{a+b+1}.$$

Hence, increasing a and/or b **concentrates** the distribution about the mean.

- The quantiles, e.g. the median or the 10% and 90% points, are not available as a simple formula, but are easily obtained within software such as R using the function `qbeta(p, a, b)`.

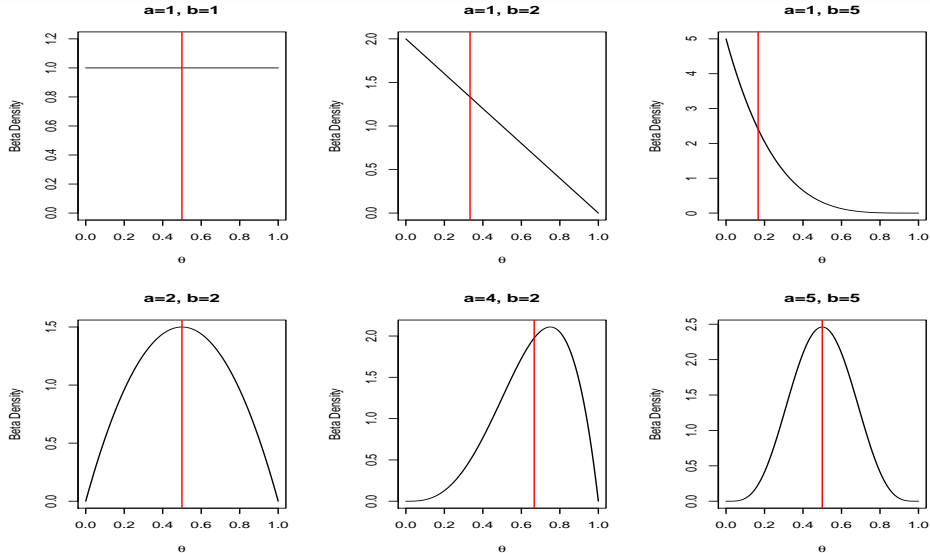


Figure 3 : Beta distributions, $\text{beta}(a, b)$, the red lines indicate the means.

Samples to Summarize Beta Distributions

- Probability distributions can be investigated by generating samples and then examining histograms, moments and quantiles.
- In Figure 4 we show histograms of beta distributions for different choices of a and b .

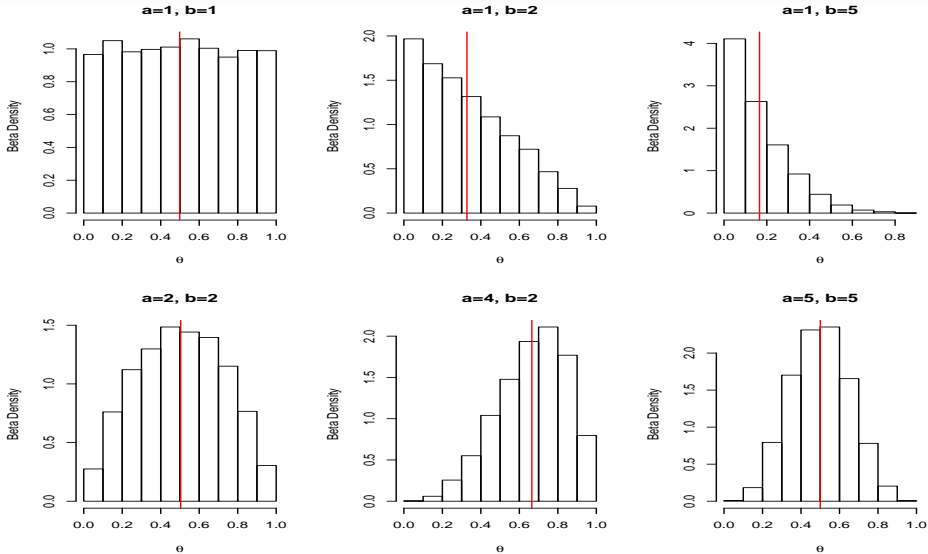


Figure 4 : Random samples from beta distributions; sample means as red lines.

Samples for Describing Weird Parameters

- So far the samples we have generated have produced summaries we can easily obtain anyway.
- But what about **functions** of the probability θ , such as the odds $\theta/(1 - \theta)$?
- Once we have samples for θ we can simply **transform** the samples to the functions of interest.
- We may have clearer prior opinions about the odds, than the probability.
- The histogram representation of the prior on the odds $\theta/(1 - \theta)$ when θ is `beta(10,10)`.

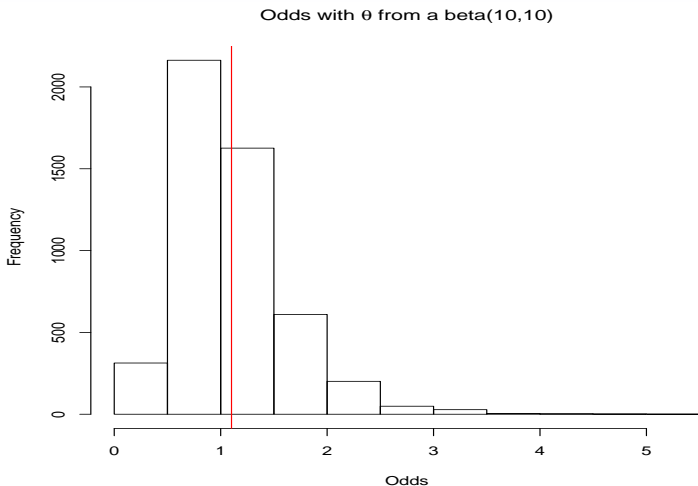


Figure 5 : Samples from the prior on the odds $\theta/(1 - \theta)$ with $\theta \sim \text{beta}(10, 10)$, the red line indicates the sample mean.

Issues with Uniformity

We might think that if we have little prior opinion about a parameter then we can simply assign a **uniform prior**, i.e. a prior

$$p(\theta) \propto \text{const.}$$

There are two problems with this strategy:

- We can't be uniform on all scales since, if $\phi = g(\theta)$:

$$\underbrace{p_{\phi}(\phi)}_{\text{Prior for } \phi} = \underbrace{p_{\theta}(g^{-1}(\phi))}_{\text{Prior for } \theta} \times \underbrace{\left| \frac{d\theta}{d\phi} \right|}_{\text{Jacobian}}$$

and so if $g(\cdot)$ is a nonlinear function, the Jacobian will be a function of ϕ and hence not uniform.

- If the parameter is not on a finite range, an **improper** distribution will result (that is, the form will not integrate to 1). This can lead to an improper posterior distribution, and without a proper posterior we can't do inference.

Are Priors Really Uniform?

- We illustrate the first (non-uniform on all scales) point.
- In the binomial example a uniform prior for θ seems a natural choice.
- But suppose we are going to model on the logistic scale so that

$$\phi = \log \left(\frac{\theta}{1 - \theta} \right)$$

is a quantity of interest.

- A uniform prior on θ produces the very non-uniform distribution on ϕ in Figure 6.
- Not being uniform on all scales is not necessarily a problem, and is correct probabilistically, but one should be aware of this characteristic.

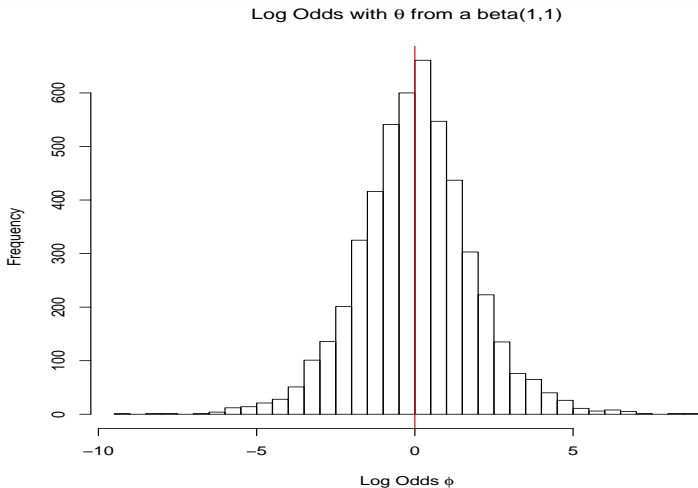


Figure 6 : Samples from the prior on the odds $\phi = \log[\theta/(1 - \theta)]$ with $\theta \sim \text{beta}(1,1)$, the red line indicates the sample mean.

Posterior Derivation: The Quick Way

- When we want to identify a particular probability distribution we only need to concentrate on terms that involve the random variable.
- For example, if the random variable is x and we see a density of the form

$$p(x) \propto \exp\left(c_1 x^2 + c_2 x\right),$$

for constants c_1 and c_2 , then we know x must have a normal distribution.

Posterior Derivation: The Quick Way

- For the binomial-beta model we concentrate on terms that only involve θ .
- The **posterior** is

$$\begin{aligned}
 p(\theta|y) &\propto \Pr(y|\theta) \times p(\theta) \\
 &= \theta^y (1 - \theta)^{N-y} \times \theta^{a-1} (1 - \theta)^{b-1} \\
 &= \theta^{y+a-1} (1 - \theta)^{N-y+b-1}
 \end{aligned}$$

- We recognize this as the important part of a **beta**($y + a, N - y + b$) distribution.
- We know what the **normalizing constant** must be, because we have a distribution which must integrate to 1.

Posterior Derivation: The Long (and Unnecessary) Way

- The posterior can also be calculated by keeping in all the normalizing constants:

$$\begin{aligned}
 p(\theta|y) &= \frac{\Pr(y|\theta) \times p(\theta)}{\Pr(y)} \\
 &= \frac{1}{\Pr(y)} \binom{N}{y} \theta^y (1-\theta)^{N-y} \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \theta^{a-1} (1-\theta)^{b-1}. \quad (2)
 \end{aligned}$$

- The normalizing constant is

$$\begin{aligned}
 \Pr(y) &= \int_0^1 \Pr(y|\theta) \times p(\theta) d\theta \\
 &= \binom{N}{y} \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \int_0^1 \theta^{y+a-1} (1-\theta)^{N-y+b-1} d\theta \\
 &= \binom{N}{y} \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \frac{\Gamma(y+a)\Gamma(N-y+b)}{\Gamma(N+a+b)}
 \end{aligned}$$

- The integrand on line 2 is a beta($y+a$, $N-y+b$) distribution, up to a normalizing constant, and so we know what this constant has to be.

Posterior Derivation: The Long (and Unnecessary) Way

- The normalizing constant is therefore:

$$\Pr(y) = \binom{N}{y} \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \frac{\Gamma(y+a)\Gamma(N-y+b)}{\Gamma(N+a+b)}$$

- This is a probability distribution, i.e. $\sum_{y=0}^N \Pr(y) = 1$ with $\Pr(y) > 0$.
- For a particular y value, this expression tells us the probability of that value **given** the model, i.e. the likelihood and prior we have selected: this will reappear later in the context of **hypothesis testing**.
- Substitution of $\Pr(y)$ into (2) and canceling the terms that appear in the numerator and denominator gives the posterior:

$$p(\theta|y) = \frac{\Gamma(N+a+b)}{\Gamma(y+a)\Gamma(N-y+b)} \theta^{y+a-1} (1-\theta)^{N-y+b-1}$$

which is a **beta**($y+a, N-y+b$).

The Posterior Mean: A Summary of the Posterior

- Recall the mean of a beta(a, b) is $a/(a + b)$.
- The posterior mean of a beta($y + a, N - y + b$) is therefore

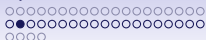
$$\begin{aligned} E[\theta|y] &= \frac{y + a}{N + a + b} \\ &= \frac{y}{N + a + b} + \frac{a}{N + a + b} \\ &= \frac{y}{N} \times \frac{N}{N + a + b} + \frac{a}{a + b} \times \frac{a + b}{N + a + b} \\ &= \text{MLE} \times W + \text{Prior Mean} \times (1-W). \end{aligned}$$

- The **weight** W is

$$W = \frac{N}{N + a + b}.$$

- As N increases, the weight tends to 1, so that the posterior mean gets closer and closer to the MLE.
- Notice that the **uniform** prior $a = b = 1$ gives a posterior mean of

$$E[\theta|y] = \frac{y + 1}{N + 2}.$$



The Posterior Mode

- First, note that the mode of a beta(a, b) is

$$\text{mode}(\theta) = \frac{a - 1}{a + b - 2}.$$

- As with the posterior mean, the posterior mode takes a weighted form:

$$\begin{aligned}\text{mode}(\theta|y) &= \frac{y + a - 1}{N + a + b - 2} \\ &= \frac{y}{N} \times \frac{N}{N + a + b - 2} + \frac{a - 1}{a + b - 2} \times \frac{a + b - 2}{N + a + b - 2} \\ &= \text{MLE} \times W^* + \text{Prior Mode} \times (1 - W^*).\end{aligned}$$

- The **weight** W^* is

$$W^* = \frac{N}{N + a + b - 2}.$$

- Notice that the **uniform** prior $a = b = 1$ gives a posterior mode of

$$\text{mode}(\theta|y) = \frac{y}{N},$$

the MLE. Which makes sense, right?

Other Posterior Summaries

- We will rarely want to report a point estimate alone, whether it be a posterior mean or posterior median.
- Interval estimates are obtained in the obvious way.
- A simple way of performing testing of particular parameter values of interest is via examination of interval estimates.
- For example, does a 95% interval contain the value $\theta_0 = 0$?

Other Posterior Summaries

- In our beta-binomial running example, a 90% posterior **credible interval** (θ_L, θ_U) results from the points

$$0.05 = \int_0^{\theta_L} p(\theta|y) d\theta$$

$$0.95 = \int_0^{\theta_U} p(\theta|y) d\theta$$

- The quantiles of a beta are not available in closed form, but easy to evaluate in R:

```
y <- 7; N <- 10; a <- b <- 1
qbeta(c(0.05, 0.5, 0.95), y+a, N-y+b)
[1] 0.4356258 0.6761955 0.8649245
```

- The 90% credible interval is $(0.44, 0.86)$ and the posterior median is 0.68.

Prior Sensitivity

- For small datasets in particular it is a good idea to examine the sensitivity of inference to the prior choice, particularly for those parameters for which there is little information in the data.
- An obvious way to determine the latter is to compare the prior with the posterior, but experience often aids the process.
- Sometimes one may specify a prior that reduces the impact of the prior.
- In some situations, priors can be found that produce point and interval estimates that mimic a standard non-Bayesian analysis, i.e. have good **frequentist** properties.
- Such priors provide a **baseline** to compare analyses with more substantive priors.
- Other names for such priors are **objective**, **reference** and **non-subjective**.
- We now describe another approach to specification, via **subjective** priors.

Choosing a Prior, Approach One

- To select a beta, we need to specify two quantities, a and b .
- The posterior mean is

$$E[\theta|y] = \frac{y + a}{N + a + b}.$$

- Viewing the denominator as a **sample size** suggests a method for choosing a and b within the prior.
- We need to specify two numbers, but rather than a and b , which are difficult to interpret, we may specify the mean $m_{\text{prior}} = a/(a + b)$ and the prior sample size $N_{\text{prior}} = a + b$
- We then solve for a and b via

$$\begin{aligned} a &= N_{\text{prior}} \times m_{\text{prior}} \\ b &= N_{\text{prior}} \times (1 - m_{\text{prior}}). \end{aligned}$$

- **Intuition:** a is like a prior number of successes and b like the prior number of failures.

Choosing a Prior, Approach One

An Example:

- Suppose we set $N_{\text{prior}} = 5$ and $m_{\text{prior}} = \frac{2}{5}$. It is **as if** we saw 2 successes out of 5.
- Suppose we obtain data with $N = 10$ and $\frac{y}{N} = \frac{7}{10}$.
- Hence $W = 10/(10 + 5)$ and

$$\begin{aligned} E[\theta|y] &= \frac{7}{10} \times \frac{10}{10+5} + \frac{2}{5} \times \frac{5}{10+5} \\ &= \frac{9}{15} = \frac{3}{5}. \end{aligned}$$

- Solving:

$$\begin{aligned} a &= N_{\text{prior}} \times m_{\text{prior}} = 5 \times \frac{2}{5} = 2 \\ b &= N_{\text{prior}} \times (1 - m_{\text{prior}}) = 5 \times \frac{3}{5} = 3 \end{aligned}$$

- This gives a $\text{beta}(y + a, N - y + b) = \text{beta}(7 + 2, 3 + 3)$ posterior.

Beta Prior, Likelihood and Posterior

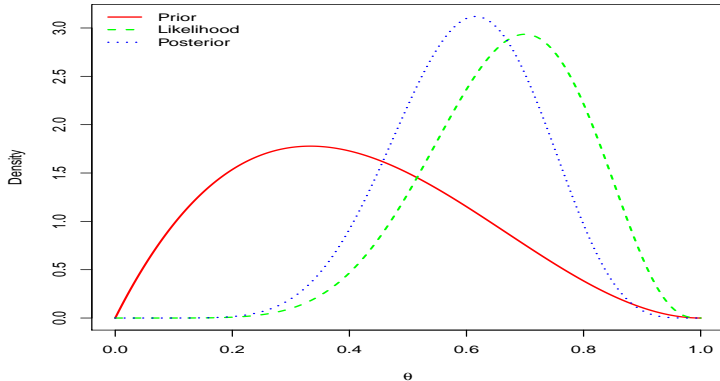


Figure 7 : The prior is $\text{beta}(2,3)$ the likelihood is proportional to a $\text{binomial}(7,3)$ and the posterior is $\text{beta}(7+2,3+3)$.

Choosing a Prior, Approach Two

- An alternative convenient way of choosing a and b is by specifying **two quantiles** for θ with associated (prior) probabilities.
- For example, we may wish $\Pr(\theta < 0.1) = 0.05$ and $\Pr(\theta > 0.6) = 0.05$.
- The values of a and b may be found numerically.
- For example, we may solve

$$[p_1 - \Pr(\theta < q_1|a, b)]^2 + [p_2 - \Pr(\theta < q_2|a, b)]^2 = 0 \quad (3)$$

for a, b .

Beta Prior Choice via Quantile Specification

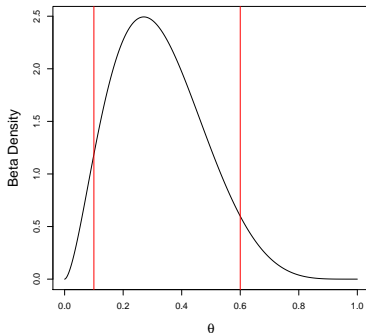


Figure 8 : $\text{beta}(2.73, 5.67)$ prior with 5% and 95% quantiles highlighted.



Bayesian Sequential Updating

- We show how probabilistic beliefs are updated as we receive more data.
- Suppose the data arrives sequentially via two experiments:
 1. Experiment 1: (y_1, N_1) .
 2. Experiment 2: (y_2, N_2) .
- **Prior 1:** $\theta \sim \text{beta}(a, b)$.
- **Likelihood 1:** $y_1|\theta \sim \text{binomial}(N_1, \theta)$.
- **Posterior 1:** $\theta|y_1 \sim \text{beta}(a + y_1, b + N_1 - y_1)$.
- This posterior forms the prior for experiment 2.
- **Prior 2:** $\theta \sim \text{beta}(a^*, b^*)$ where $a^* = a + y_1$, $b^* = b + N_1 - y_1$.
- **Likelihood 2:** $y_2|\theta \sim \text{binomial}(N_2, \theta)$.
- **Posterior 2:** $\theta|y_1, y_2 \sim \text{beta}(a^* + y_2, b^* + N_2 - y_2)$.
- Substituting for a^*, b^* :

$$\theta|y_1, y_2 \sim \text{beta}(a + y_1 + y_2, b + N_1 - y_1 + N_2 - y_2).$$

Bayesian Sequential Updating

- Schematically:

$$(a, b) \rightarrow (a + y_1, b + N_1 - y_1) \rightarrow (a + y_1 + y_2, b + N_1 - y_1 + N_2 - y_2)$$

- Suppose we obtain the data in one go as $y^* = y_1 + y_2$ successes from $N^* = N_1 + N_2$ trials.
- The posterior is

$$\theta|y^* \sim \text{beta}(a + y^*, b + N^* - y^*),$$

which is the same as when we receive in two separate instances.

Predictive Distribution

- Suppose we see y successes out of N trials, and now wish to obtain a **predictive distribution** for a future experiment with M trials.
- Let $Z = 0, 1, \dots, M$ be the number of successes.
- Predictive distribution:

$$\begin{aligned}\Pr(z|y) &= \int_0^1 p(z, \theta|y) d\theta \\ &= \int_0^1 \Pr(z|\theta, y) p(\theta|y) d\theta \\ &= \int_0^1 \Pr(z|\theta) p(\theta|y) d\theta\end{aligned}$$

because of **conditional independence**.

Predictive Distribution

- Continuing with the calculation:

$$\begin{aligned}
 \Pr(z|y) &= \int_0^1 \Pr(z|\theta) \times p(\theta|y) d\theta \\
 &= \int_0^1 \binom{M}{z} \theta^z (1-\theta)^{M-z} \\
 &\quad \times \frac{\Gamma(N+a+b)}{\Gamma(y+a)\Gamma(N-y+b)} \theta^{y+a-1} (1-\theta)^{N-y+b-1} d\theta \\
 &= \binom{M}{z} \frac{\Gamma(N+a+b)}{\Gamma(y+a)\Gamma(N-y+b)} \int_0^1 \theta^{y+a+z-1} (1-\theta)^{N-y+b+M-z-1} d\theta \\
 &= \binom{M}{z} \frac{\Gamma(N+a+b)}{\Gamma(y+a)\Gamma(N-y+b)} \frac{\Gamma(a+y+z)\Gamma(b+N-y+M-z)}{\Gamma(a+b+N+M)}
 \end{aligned}$$

for $z = 0, 1, \dots, M$.

- A likelihood approach would take the predictive distribution as binomial($M, \hat{\theta}$) with $\hat{\theta} = y/N$.

Predictive Distribution

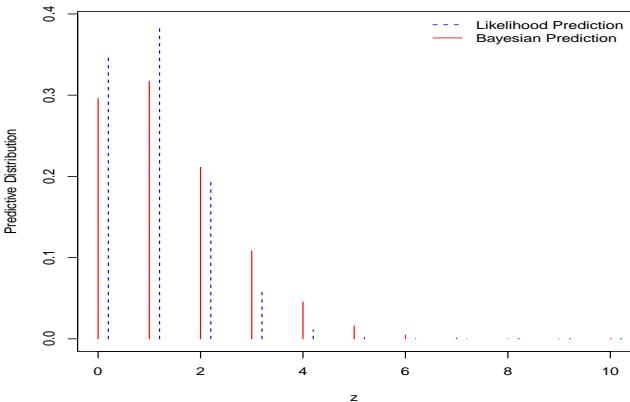


Figure 9 : Likelihood and Bayesian predictive distribution of seeing $z = 0, 1, \dots, M = 10$ successes, after observing $y = 2$ out of $N = 20$ successes (with $a = b = 1$).

Predictive Distribution

- The posterior and sampling distributions won't usually combine so conveniently.
- In general, we may form a **Monte Carlo** estimate of the predictive distribution:

$$\begin{aligned} p(z|y) &= \int p(z|\theta)p(\theta|y)d\theta \\ &= E_{\theta|y}[p(z|\theta)] \\ &\approx \frac{1}{S} \sum_{s=1}^S p(z|\theta^{(s)}) \end{aligned}$$

where $\theta^{(s)} \sim p(\theta|y)$, $s = 1, \dots, S$, is a sample from the posterior.

- This provides an estimate of the distribution at the point z .
- Alternatively, we may sample from $p(z|\theta^{(s)})$ a large number of times to reconstruct the predictive distribution.

Difference in Binomial Proportions

- It is straightforward to extend the methods presented for a single binomial sample to a pair of samples.
- Suppose we carry out two binomial experiments:

$$Y_1|\theta_1 \sim \text{binomial}(N_1, \theta_1) \quad \text{for sample 1}$$

$$Y_2|\theta_2 \sim \text{binomial}(N_2, \theta_2) \quad \text{for sample 2}$$

- Interest focuses on $\theta_1 - \theta_2$, and often in examining the possibility that $\theta_1 = \theta_2$.
- With a sampling-based methodology, and independent beta priors on θ_1 and θ_2 , it is straightforward to examine the posterior $p(\theta_1 - \theta_2|y_1, y_2)$.

Difference in Binomial Proportions

- Savage *et al.* (2008) give data on allele frequencies within a gene that has been linked with skin cancer.
- It is interest to examine differences in allele frequencies between populations.
- We examine one SNP and extract data on Northern European (NE) and United States (US) populations.
- Let θ_1 and θ_2 be the allele frequencies in the NE and US population from which the samples were drawn, respectively.
- The allele frequencies were 10.69% and 13.21% with sample sizes of 650 and 265, in the NE and US samples, respectively.
- We assume independent **beta(1,1)** priors on each of θ_1 and θ_2 .
- The posterior probability that $\theta_1 - \theta_2$ is greater than 0, is **0.12**, so there is little evidence of a difference in allele frequencies between the NE and US samples.

Binomial Two Sample Example

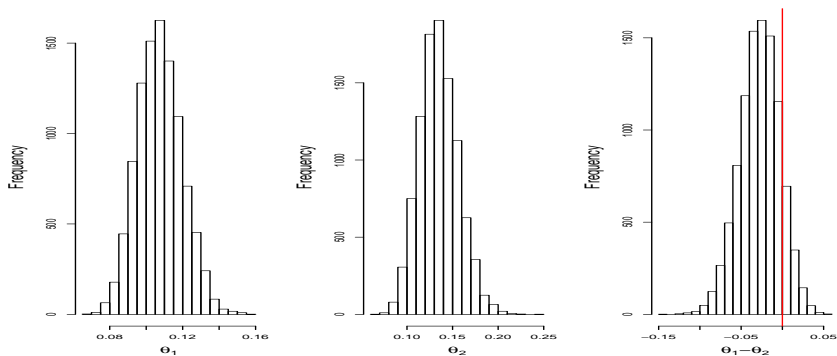


Figure 10 : Histogram representations of $p(\theta_1|y_1)$, $p(\theta_2|y_2)$ and $p(\theta_1 - \theta_2|y_1, y_2)$. The red line in the right plot is at the reference point of zero.

Bayes Factors for Hypothesis Testing

- The **Bayes factor** provides a summary of the evidence for a particular hypothesis (model) as compared to another.
- The Bayes factor is

$$\text{BF} = \frac{\Pr(y|H_0)}{\Pr(y|H_1)}$$

and so is simply the probability of the data under H_0 divided by the probability of the data under H_1 .

- Values of $\text{BF} > 1$ favor H_0 while values of $\text{BF} < 1$ favor H_1 .
- Note the similarity to the **likelihood ratio**

$$\text{LR} = \frac{\Pr(y|H_0)}{\Pr(y|\hat{\theta})}$$

where $\hat{\theta}$ is the MLE under H_1 .

- If there are no unknown parameters in H_0 and H_1 (for example, $H_0 : \theta = 0.5$ versus $H_1 : \theta = 0.3$), then the Bayes factor is identical to the likelihood ratio.

Calibration of Bayes Factors

- Kass and Raftery (1995) suggest **intervals** of Bayes factors for reporting:

| 1/Bayes Factor | Evidence Against H_0 |
|----------------|------------------------------------|
| 1 to 3.2 | Not worth more than a bare mention |
| 3.2 to 20 | Positive |
| 20 to 150 | Strong |
| >150 | Very strong |

- These provide a guideline, but should not be followed without question.

Values Taken by the Negative Log Bayes Factor, as a Function of y

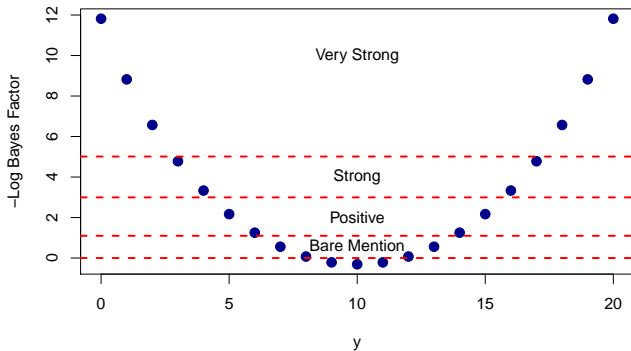


Figure 11 : Negative Log Bayes factor as a function of $y|\theta \sim \text{Binomial}(20, \theta)$ for $y = 0, 1, \dots, 20$ and $a = b = 1$. High values indicate evidence against the null.

Bayesian Analysis of the ASE Data

Three approaches to inference:

1. Posterior Probabilities:

- A simple approach to testing is to calculate the posterior probability that $\theta < 0.5$.
- We can then pick a threshold for indicating worthy of further study, e.g. if $\Pr(\theta < 0.5|y) < 0.01$ or $\Pr(\theta < 0.5|y) < 0.99$

2. Bayes Factors:

- Calculating the Bayes factor.
- Pick a threshold for indicating worthy of further study, e.g. if the Bayes factor is greater than 150.

3. Decision theory:

- Place priors on the null and alternative hypotheses.
- Calculate the posterior odds:

$$\frac{\Pr(H_0|y)}{\Pr(H_1|y)} = \frac{\Pr(y|H_0)}{\Pr(y|H_1)} \times \frac{\Pr(H_0)}{\Pr(H_1)}$$

$$\text{Posterior Odds} = \text{Bayes Factor} \times \text{Prior Odds}$$

- Pick a threshold R , so that if the Posterior Odds $< R$ we choose H_1 .

Bayesian Analysis of the ASE Data

- In Figure 12 we give a histogram of the posterior probabilities $\Pr(\theta < 0.5|y)$ and we see large numbers of genes have probabilities close to 0 and 1, indicating allele specific expression (ASE).
- In Figure 13 we plot $\Pr(\theta < 0.5|y)$ versus the p-values and the general pattern is what we would expect — small p-values have posterior probabilities close to 0 and 1.
- The strange lines in this plot are due to the discreteness of the outcome y .
- In Figure 14 we plot the $-\text{Log}$ Bayes Factor against $\Pr(\theta < 0.5|y)$. Large values of the former correspond to strong evidence of ASE; again we see an agreement in inference, with large values of the negative log Bayes factor corresponding with $\Pr(\theta < 0.5|y)$ close to 0 and 1.

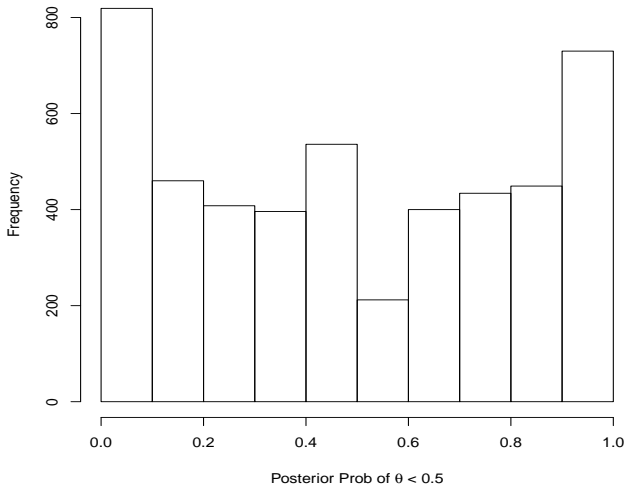


Figure 12 : Histogram of 4,844 posterior probabilities of $\theta < 0.5$.

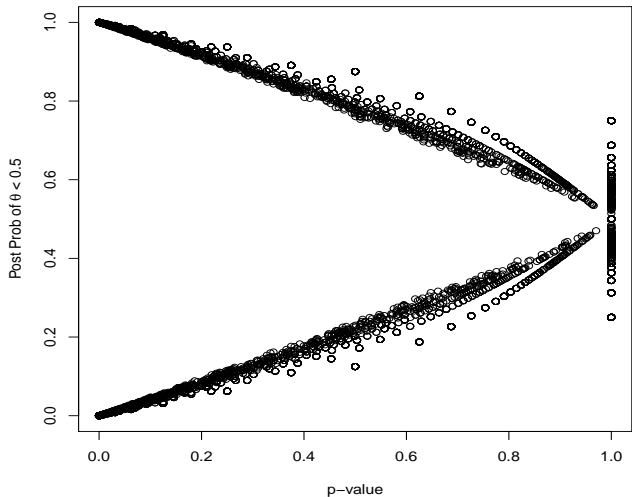


Figure 13 : Posterior probabilities of $\theta < 0.5$ and p -values from exact tests.

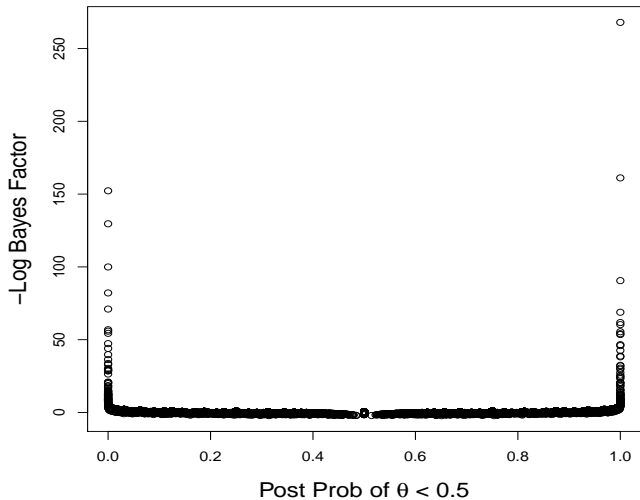


Figure 14 : Negative Log Bayes factor versus posterior probabilities of $\theta < 0.5$.

ASE Example

- Applying a **Bonferroni correction** to control the family wise error rate at 0.05, gives a p -value threshold of $0.05/4844 = 10^{-5}$ and 111 rejections. More on this later!
- There were 278 genes with $\Pr(\theta < 0.5|y) < 0.01$ and 242 genes with $\Pr(\theta < 0.5|y) > 0.99$.
- Following the guideline of requiring **very strong** evidence, there were 197 genes with the Bayes factor greater than 150.
- Requiring less stringent evidence, i.e. **strong** only, there were 359 genes.
- We consider a formal decision theory approach to testing in **Lecture 7**.

ASE Output Data

- Below are some summaries from the ASE analysis – we order with respect to the variable $\log\text{BF}_r$, which is the reciprocal Bayes factor (so that high numbers correspond to strong evidence against the null).
- The `postprob` variable is the posterior probability of $\theta < 0.5$.

```
allvals <- data.frame(Nsum, ysum, pvals, postprob, logBFr)
oBF <- order(-logBFr)
orderallvals <- allvals[oBF,]
head(orderallvals)
  Nsum  ysum      pvals      postprob      logBFr
4751  437     6 5.340324e-119 1.000000e+00 267.9572
4041  625    97 1.112231e-72 1.000000e+00 161.1355
2370  546   468 8.994944e-69 2.621622e-69 152.2517
2770  256   245 1.127211e-58 2.943484e-59 129.6198
2291  150   150 1.401298e-45 3.503246e-46  99.9548
1328  228    19 1.224323e-41 1.000000e+00  90.5573
tail(orderallvals)
  Nsum  ysum      pvals      postprob      logBFr
824   761   382 0.9422103 0.4567334 -2.086604
2163  776   390 0.9142477 0.4429539 -2.091955
3153  769   384 1.0000000 0.5143722 -2.097079
2860 1076   546 0.6474878 0.3129473 -2.146555
2028 1440   707 0.5100331 0.7532969 -2.176356
395   1123  555 0.7202938 0.6508932 -2.211576
```

Conclusions

- **Monte Carlo sampling** provides flexibility of inference.
- All this lecture considered Binomial sampling, for which there is only a single parameter. For more parameters, prior specification and computing becomes more interesting...as we shall see.
- **Multiple testing** is considered in Lecture 7.
- For **estimation** and with middle to large sample sizes, conclusions from Bayesian and non-Bayesian approaches often **coincide**.
- For **testing** it is a different story, as discussed in **Lecture 7**.

Conclusions

Benefits of a Bayesian approach:

- Inference is based on **probability** and output is very intuitive.
- Framework is **flexible**, and so complex models can be built.
- Can incorporate **prior knowledge**!
- If the sample size is large, prior choice is less crucial.

Challenges of a Bayesian analysis:

- Require a **likelihood** and a **prior**, and inference is only as good as the appropriateness of these choices.
- **Computation** can be daunting, though software is becoming more user friendly and flexible (later we will use INLA).
- One should be wary of model becoming **too complex** – we have the technology to contemplate complicated models, but do the data support complexity?

References

- Kass, R. and Raftery, A. (1995). Bayes factors. *Journal of the American Statistical Association*, **90**, 773–795.
- Savage, S. A., Gerstenblith, M. R., Goldstein, A., Mirabello, L., Fargnoli, M. C., Peris, K., and Landi, M. T. (2008). Nucleotide diversity and population differentiation of the melanocortin 1 receptor gene, MC1R. *BMC Genetics*, **9**, 31.
- Skelly, D., Johansson, M., Madeoy, J., Wakefield, J., and Akey, J. (2011). A powerful and flexible statistical framework for testing hypothesis of allele-specific gene expression from RNA-Seq data. *Genome Research*, **21**, 1728–1737.