Lecture 1: Basic Statistical Tools

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Discrete Random Variables

A random variable (RV) = outcome (realization) not a set value, but rather drawn from some probability distribution.

A discrete RV $x$ --- takes on values $X_1, X_2, \ldots X_k$

Probability distribution: $P_i = \Pr(x = X_i)$

Probabilities are non-negative and sum to one

$P_i \geq 0, \quad \sum P_i = 1$

Example: Binomial random variable. Let $p = \text{prob of a success}$.

$\text{Prob (k successes in n trials)} = \frac{n!}{(n-k)! \cdot k!} \cdot p^k \cdot (1-p)^{n-k}$

Example: Poisson random variable. Let $\lambda = \text{expected number of successes}$.

$\text{Prob (k successes)} = \frac{\lambda^k \exp(-\lambda)}{k!}$
Continuous Random Variables

A continuous RV $x$ can take on any possible value in some interval (or set of intervals). The probability distribution is defined by the probability density function, $p(x)$

$$p(x) \geq 0 \quad \text{and} \quad \int_{-\infty}^{\infty} p(x) \, dx = 1$$

Prob is area under the curve

$$P(x_1 \leq x \leq x_2) = \int_{x_1}^{x_2} p(x) \, dx$$

Finally, the cdf, or cumulative probability function, is defined as $\text{cdf}(z) = \Pr(x \leq z)$

$$\text{cdf}(x) = \int_{-\infty}^{x} p(x) \, dx$$
Example: The normal (or Gaussian) distribution

\[ \phi(x \mid \mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp \left( -\frac{(x - \mu)^2}{2\sigma^2} \right) \]

Mean \( \mu \), variance \( \sigma^2 \)

Unit normal (mean 0, variance 1)
The variance is a measure of spread about the mean. The smaller $\sigma^2$, the narrower the distribution about the mean.

If $x \sim N(0, 1)$, $y \sim N(\mu, \sigma^2)$, then

$$\sigma \cdot (x + \mu) \sim N(\mu, \sigma^2)$$

$$\frac{y - \mu}{\sigma} \sim N(0, 1)$$
Joint and Conditional Probabilities

The probability for a pair \((x,y)\) of random variables is specified by the joint probability density function, \(p(x,y)\)

\[
P(y_1 \leq y \leq y_2, x_1 \leq x \leq x_2) = \int_{y_1}^{y_2} \int_{x_1}^{x_2} p(x,y) \, dx \, dy
\]

The marginal density of \(x\), \(p(x)\)

\[
p(x) = \int_{-\infty}^{\infty} p(x,y) \, dy
\]
Joint and Conditional Probabilities

\[ p(y|x), \text{ the conditional density } y \text{ given } x \]

\[
P( y_1 \leq y \leq y_2 \mid x ) = \int_{y_1}^{y_2} p(y \mid x) \, dy
\]

Relationships among \( p(x), p(x,y), p(y|x) \)

\( x \) and \( y \) are said to be independent if \( p(x,y) = p(x)p(y) \)

\[
p(x, y) = p(y \mid x) p(x), \quad \text{hence} \quad p(y \mid x) = \frac{p(x, y)}{p(x)}
\]

Note that \( p(y|x) = p(y) \) if \( x \) and \( y \) are independent
Bayes’ Theorem

Suppose an unobservable RV takes on values $b_1 \ldots b_n$

Suppose that we observe the outcome $A$ of an RV correlated with $b$. What can we say about $b$ given $A$?

Bayes’ theorem:

$$\Pr(b_j \mid A) = \frac{\Pr(b_j) \Pr(A \mid b_j)}{\Pr(A)} = \frac{\Pr(b_j) \Pr(A \mid b_j)}{\sum_{i=1}^{n} \Pr(b_i) \Pr(A \mid b_i)}$$

A typical application in genetics is that $A$ is some phenotype and $b$ indexes some underlying (but unknown) genotype
Example: BRCA1/2 & Breast cancer

- NCI statistics:
  - 12% is lifetime risk of breast cancer in females
  - 60% is lifetime risk if carry BRCA 1 or 2 mutation
  - One estimate of BRCA 1 or 2 allele frequency is around 2.3%.
  - Question: Given a patent has breast cancer, what is the chance that she has a BRCA 1 or BRCA 2 mutation?
• Here
  - Event B = has a BRCA mutation
  - Event A = has breast cancer
• Bayes: \( \Pr(B|A) = \Pr(A|B) \times \frac{\Pr(B)}{\Pr(A)} \)
  - \( \Pr(A) = 0.12 \)
  - \( \Pr(B) = 0.023 \)
  - \( \Pr(A|B) = 0.60 \)
  - Hence, \( \Pr(BRCA|Breast\ cancer) = \frac{0.60 \times 0.023}{0.12} = 0.115 \)
• Hence, for the assumed BRCA frequency (2.3%), 11.5% of all patients with breast cancer have a BRCA mutation
Second example: Suppose height > 70. What is the probability individual is QQ? Qq? qq?

<table>
<thead>
<tr>
<th>Genotype</th>
<th>qq</th>
<th>Qq</th>
<th>QQ</th>
</tr>
</thead>
<tbody>
<tr>
<td>Freq(genotype)</td>
<td>0.5</td>
<td>0.3</td>
<td>0.2</td>
</tr>
<tr>
<td>Pr(height &gt;70</td>
<td>genotype)</td>
<td>0.3</td>
<td>0.6</td>
</tr>
</tbody>
</table>

\[
\text{Pr}(\text{height} > 70) = 0.3 \times 0.5 + 0.6 \times 0.3 + 0.9 \times 0.2 = 0.51
\]

\[
\text{Pr}(\text{qq} \mid \text{height} > 70) = \frac{\text{Pr}(\text{qq}) \times \text{Pr}(\text{height} > 70 \mid \text{qq})}{\text{Pr}(\text{height} > 70)}
\]

\[
= \frac{0.5 \times 0.3}{0.51} = 0.294
\]
Expectations of Random Variables

The expected value, $E[f(x)]$, of some function $x$ of the random variable $x$ is just the average value of that function

$$E[f(x)] = \sum_i \Pr(x = X_i) f(X_i) \quad \text{x discrete}$$

$$E[f(x)] = \int_{-\infty}^{+\infty} f(x) p(x) \, dx \quad \text{x continuous}$$

$E[x] = \text{the (arithmetic) mean, } \mu, \text{ of a random variable } x$

$$E(x) = \mu = \int_{-\infty}^{+\infty} x \, p(x) \, dx$$


Expectations of Random Variables

$$E[ (x - \mu)^2 ] = \sigma^2, \text{ the variance of } x$$

$$E \left[ (x - \mu)^2 \right] = \sigma^2 = \int_{-\infty}^{+\infty} (x - \mu)^2 p(x) \, dx$$

More generally, the $r$th moment about the mean is given by $E[ (x - \mu)^r ]$

- $r = 2$: variance.
- $r = 3$: skew
- $r = 4$: (scaled) kurtosis

Useful properties of expectations

$$E[g(x) + f(y)] = E[g(x)] + E[f(y)]$$

$$E(cx) = c \, E(x)$$
The truncated normal

Only consider values of $T$ or above in a normal distribution.

Let $T = \Pr(z > T)$

$$E[z | z > T] = \int_{T}^{\infty} \frac{z p(z)}{\pi T} dz = \mu + \frac{\sigma \cdot p_T}{\pi T}$$

Here $p_T$ is the height of the normal at the truncation point.

Let $\pi_T = \Pr(z > T)$

$$p_T = (2\pi)^{-1/2} \exp \left[ -\frac{(T - \mu)^2}{2 \sigma^2} \right]$$
Let $U \sim N(0,1)$, the unit normal (mean 0, variance 1)

Probit transformation $z_p$ satisfies $P(U < z_p) = p$

Let $\pi = \text{fraction saved}$, so that $T = z_{[1-\pi]}$

Here, $\frac{p_T}{\pi} = \frac{\phi(z_{[1-\pi]})}{\pi}$ In R, $\text{dnorm(qnorm(1-pi))/pi}$

Value for truncated mean

$= \mu + \sigma \times \text{curve value}$

For example, save upper 25%

$\text{dnorm(qnorm(1-0.25))/0.25}$ returns 1.27. Hence, truncated mean is $\mu + \sigma 1.27$

\[
\text{curve(dnorm(qnorm(1-x))/x,0.001,0.5)} \quad \text{Plot this for} \quad 0 < \pi < 0.5
\]
The variance of the truncated distribution (where the uppermost fraction $\pi$ is saved) is

$$\sigma^2 \left[ 1 + \frac{\phi(z_{1-\pi})}{\pi} z_{1-\pi} - \left( \frac{\phi(z_{1-\pi})}{\pi} \right)^2 \right]$$

For example, $p = 0.5$ truncated variance = 36.5% of normal variance

\[
\text{curve}(1 + \text{dnorm(qnorm(1-x))}*\text{qnorm(1-x)}/x - \text{(dnorm(qnorm(1-x))/x)}^2, 0.001, 0.5)
\]
Covariances

- $\text{Cov}(x, y) = E [(x-\mu_x)(y-\mu_y)]$
- $\text{Cov}(x, y) = E [x*y] - E[x]E[y]$

$\text{Cov}(x, y) > 0$, positive (linear) association between $x$ & $y$
Cov(x,y) < 0, negative (linear) association between x & y

\[ \text{cov}(X,Y) < 0 \]

Cov(x,y) = 0, no linear association between x & y

\[ \text{cov}(X,Y) = 0 \]
If $x$ and $y$ are independent, then
\[ E[(y-E[y])(x-E[x])] = E[(y-E[y])] \ast E[(x-E[x])] = 0 \]

However,

$\text{Cov}(x,y) = 0$ DOES NOT imply no association.
Correlation

\[ \text{Cov} = 10 \text{ tells us nothing about the strength of an association} \]

What is needed is an absolute measure of association

This is provided by the correlation, \( r(x,y) \)

\[ r(x, y) = \frac{\text{Cov}(x, y)}{\sqrt{\text{Var}(x) \text{Var}(y)}} \]

\( r = 1 \) implies a perfect (positive) linear association

\( r = -1 \) implies a perfect (negative) linear association
Useful Properties of Variances and Covariances

• Symmetry, \( \text{Cov}(x,y) = \text{Cov}(y,x) \)
• The covariance of a variable with itself is the variance, \( \text{Cov}(x,x) = \text{Var}(x) \)
• If \( a \) is a constant, then
  \( \text{Cov}(ax,y) = a \text{Cov}(x,y) \)
  \( \text{Var}(ax) = a^2 \text{Var}(x) \)
• \( \text{Var}(ax) = \text{Cov}(ax,ax) = a^2 \text{Cov}(x,x) = a^2 \text{Var}(x) \)
• \( \text{Cov}(x+y,z) = \text{Cov}(x,z) + \text{Cov}(y,z) \)
More generally

\[
Cov \left( \sum_{i=1}^{n} x_i, \sum_{j=1}^{m} y_j \right) = \sum_{i=1}^{n} \sum_{j=1}^{m} Cov(x_i, y_j)
\]

Var(x + y) = Var(x) + Var(y) + 2Cov(x, y)

Hence, the variance of a sum equals the sum of the Variances ONLY when the elements are uncorrelated

Question: What is Var(x-y)?
Example: Variance of the sample mean

\[
\sigma^2(\bar{x}) = \sigma^2 \left( \frac{1}{n} \sum_{i=1}^{n} x_i \right) = \sigma \left( \frac{1}{n} \sum_{i=1}^{n} x_i, \frac{1}{n} \sum_{i=1}^{n} x_i \right)
\]

\[
= \frac{1}{n^2} \sum_{i=1}^{n} \sum_{j=1}^{n} \sigma(x_i, x_j)
\]

\[
= \frac{n}{n^2} \sigma(x_i, x_i) + \frac{1}{n^2} \sum_{i \neq j}^{n} \sigma(x_i, x_j)
\]

\[
= \frac{\sigma^2(x)}{n} + \frac{n(n-1)}{n^2} \sigma(x_i, x_j)
\]

\[
= \frac{\sigma^2(x)}{n} + \left(1 - \frac{1}{n}\right) \sigma(x_i, x_j)
\]

Expressing \(\text{Var}(x)\) as \(\text{Cov}(x,x)\)

\(\text{Cov}(\text{sum}) = \text{sum}(\text{Cov})\)

Assumes each \(x_i\) has same \(\text{Var}\), and \(\text{Cov}\) between observations (if present) are the same over all pairs. Example: sibs

Variance for a sib mean inflated by cov btw sibs
Regressions

Consider the best (linear) predictor of $y$ given we know $x$

$$\hat{y} = \bar{y} + b_y \mid x (x - \bar{x})$$

The slope of this linear regression is a function of $\text{Cov}$,

$$b_y \mid x = \frac{\text{Cov}(x, y)}{\text{Var}(x)}$$

The fraction of the variation in $y$ accounted for by knowing $x$, i.e., $\text{Var}(\hat{y} - y)$, is $r^2$
Example:
Predicting breeding value $A$ from phenotypic value $z$

Best linear regression can be written as
$y - \mu_y = B_{x,y} (x - \mu_x) + e$, where $B_{x,y} = \text{Cov}(x,y)/\text{Var}(x)$

For breeding value & phenotypic value
$\text{Cov}(A,z) = \text{Cov}(A,A+D+E) = \text{Cov}(A,A) = \text{Var}(A)$
$\mu_A = 0$ (average breeding value is zero), giving

$A = \text{Var}(A)/\text{Var}(z) \times (z - \mu_z) + e = h^2(z - \mu_z) + e$

Best linear predictor (BLUP) of $A$ given $z$ is $h^2(z - \mu_z)$
Relationship between the correlation and the regression slope:

\[
   r(x, y) = \frac{Cov(x, y)}{\sqrt{Var(x)Var(y)}} = b_{y|x} \sqrt{\frac{Var(x)}{Var(y)}}
\]

If Var(x) = Var(y), then \( b_{y|x} = b_{x|y} = r(x, y) \)

In this case, the fraction of variation accounted for by the regression is \( b^2 \)
\[ r^2 = 0.8 \]
Properties of Least-squares Regressions

The slope and intercept obtained by least-squares: minimize the sum of squared residuals:

\[ \sum e_i^2 = \sum (y_i - \hat{y}_i)^2 = \sum (y_i - a - bx_i)^2 \]

- The average value of the residual is zero
- The LS solution maximizes the amount of variation in y that can be explained by a linear regression on x
- Fraction of variance in y accounted by the regression is \( r^2 \)
- The residual errors around the least-squares regression are uncorrelated with the predictor variable x
- Homoscedastic vs. heteroscedastic residual variances
Different methods of analysis

• Parameters of these various models can be estimated in a number of frameworks

• **Method of moments**
  - Very little assumptions about the underlying distribution. Typically, the mean of some statistic has an expected value of the parameter
  - Example: Estimate of the mean $\mu$ given by the sample mean, $\bar{x}$, as $E(\bar{x}) = \mu$.
  - While estimation does not require distribution assumptions, confidence intervals and hypothesis testing do

• **Distribution-based estimation**
  - The explicit form of the distribution used
Example: Binominal data

- 150 individuals are sampled, with 30 having genotype QQ. What is the population frequency and its confidence interval?

- Assume binominal sampling, with \( p \) = success prob (pop freq) and \( n \) = sample size. Under the binomial

  - \( E(\text{successes}) = n \cdot p \). Using MM, \( 30 = 150 \cdot p \) or \( p = 30/150 = 0.2 \)
  - Sample variance = \( p(1-p)/n \) or here \( 0.2 \cdot 0.8/150 = (0.033)^2 \)
  - Both these expressions simply used expected values

- Confidence intervals: Have to assume something about the distribution of the test statistic, here \( n_1/n \). For large \( n_1 \), normally distributed, giving \( n_1 +/- 1.96 \cdot \text{Sqrt(sample var)} \) at normal approximation of 95% CI for \( p \), or

  - \( 0.2 +/- 1.96 \cdot 0.033 = 0.2 +/- 0.064 \)
  - Hence 13.7% to 26.3% is 95% CI
Distribution-based estimation

• Maximum likelihood estimation
  - MLE
  - REML
  - More in Lynch & Walsh (book) Appendix 3

• Bayesian
  - Marginal posteriors
  - Conjugating priors
  - MCMC/Gibbs sampling
  - More in Walsh & Lynch (online chapters = Vol 2) Appendices 2,3
Maximum Likelihood

\[ p(x_1, \ldots, x_n \mid \theta) = \text{density of the observed data } (x_1, \ldots, x_n) \]

given the (unknown) distribution parameter(s) \( \theta \)

Fisher suggested the method of maximum likelihood ---
given the data \( (x_1, \ldots, x_n) \) find the value(s) of \( \theta \) that
maximize \[ p(x_1, \ldots, x_n \mid \theta) \]

We usually express \[ p(x_1, \ldots, x_n \mid \theta) \] as a likelihood
function \( l(\theta \mid x_1, \ldots, x_n) \) to remind us that it is dependent
on the observed data

The Maximum Likelihood Estimator (MLE) of \( \theta \) are the
value(s) that maximize the likelihood function \( l \) given
the observed data \( x_1, \ldots, x_n \).
This is formalized by looking at the log-likelihood surface, $L = \ln [l(\theta \mid x)]$. Since $\ln$ is a monotonic function, the value of $\theta$ that maximizes $l$ also maximizes $L$ (the MLE).

The curvature of the likelihood surface in the neighborhood of the MLE informs us as to the precision of the estimator $\theta$.

A narrow peak = high precision. A broad peak = lower precision $\theta$.

\[
\text{Var}(\text{MLE}) = -1 \left/ \frac{\partial^2 L(\theta \mid z)}{\partial \theta^2} \right. \quad \text{The larger the curvature, the smaller the variance}
\]
Example: Binominal

\[ l(p \mid n_1, n) = C p^{n_1} (1 - p)^{n - n_1}, \quad C = \frac{n!}{n_1! (n - n_1)!} \]

For our previous example with \( n_1 = 30, n = 150, \) a plot of \( L \) as a function of \( p \) becomes

R code:

```r
curve(dbinom(30,150,x),0,1)
```

Note max (MLE) at \( p = 0.2 \)
Example (cont)

\[ L = \log [l(p \mid n_1, n)] \]
\[ = \log(C') + n_1 \log(p) + (n - n_1) \log(1 - p) \]
\[ \frac{\partial L}{\partial p} = \frac{n_1}{p} - \frac{n - n_1}{1 - p} \]
\[ \frac{\partial L}{\partial p} = 0 \quad \text{when} \quad p = \frac{n_1}{n} \]

Hence, MLE and MM estimators the same
Example (cont)

\[- \frac{\partial L^2}{\partial p^2} = -\partial \left( \frac{n_1}{p} - \frac{n - n_1}{1 - p} \right) / \partial p\]

\[= \frac{n_1}{p^2} + \frac{n - n_1}{(1 - p)^2}\]

\[- \frac{\partial L^2}{\partial p^2} = \frac{30}{0.2^2} + \frac{120}{0.8^2} = 937.\]

\[-1 \left/ \frac{\partial L^2}{\partial p^2} \right. = (0.033)^2\]

95% CI becomes 0.2 +/- 1.96*0.033 or 13.5% to 26.4% (essentially the same as for MM)
Likelihood Ratio tests

Hypothesis testing in the ML frameworks occurs through likelihood-ratio (LR) tests

\[ LR = -2 \ln \left( \frac{\ell(\hat{\Theta}_r | z)}{\ell(\hat{\Theta} | z)} \right) = -2 \left[ L(\hat{\Theta}_r | z) - L(\hat{\Theta} | z) \right] \]

\( \hat{\Theta}_r \) is the MLE under the restricted conditions (some parameters specified, e.g., var = 1)

\( \hat{\Theta} \) is the MLE under the unrestricted conditions (no parameters specified)

For large sample sizes (generally) LR approaches a Chi-square distribution with \( r \) df (\( r \) = number of parameters assigned fixed values under null)
Example

What is the LR for a test of $p = 0.4$ with our binominal example ($n_1 = 30$, $n = 150$)?

\[
\frac{\ell(p)}{\ell(0.2)} = \frac{p^{30}(1 - p)^{120}}{0.2^{30} 0.8^{120}}
\]

\[
-\log \left( \frac{\ell(0.4)}{\ell(0.2)} \right) = -\log \left( \frac{0.4^{30} 0.6^{120}}{0.2^{30} 0.8^{120}} \right) = 13.73
\]

$\Pr(\chi^2_1 > 13.73)$ is found in R using `1-pchisq(13.73,1)` which returns 0.0002110562
Bayesian Statistics

An extension of likelihood is Bayesian statistics

Instead of simply estimating a point estimate (e.g., the MLE), the goal is the estimate the entire distribution for the unknown parameter $\theta$ given the data $x$

$$p(\theta \mid x) = C \ast \text{l}(x \mid \theta) \ast p(\theta)$$

$p(\theta \mid x)$ is the posterior distribution for $\theta$ given the data $x$

$l(x \mid \theta)$ is just the likelihood function

$p(\theta)$ is the prior distribution on $\theta$. 
Bayesian Statistics

Why Bayesian?

• Exact for any sample size
• Marginal posteriors
• Efficient use of any prior information
• MCMC (such as Gibbs sampling) methods

Priors quantify the strength of any prior information. Often these are taken to be diffuse (with a high variance), so prior weights on $\theta$ spread over a wide range of possible values.
Marginal posteriors

• Often we are just interested in a particular set of parameters (say some subset of the fixed effects). However, we also have to estimate all of the other parameters.

• How do uncertainties in these nuisance parameters factor into the uncertainty in the parameters of interest?

• A Bayesian marginal posterior takes this into account by integrating the full posterior over the nuisance parameters.

• While this sound complicated, easy to do with MCMC (Markov Chain Monte Carlo)
Conjugating priors

For any particular likelihood, we can often find a conjugating prior, such that the product of the likelihood and the prior returns a known distribution.

Example: For the mean $\mu$ in a normal, taking the prior on the mean to also be normal returns a posterior for $\mu$ that is normal.

Example: For the variance $\sigma^2$ in a normal, taking the prior on the variance to an inverse chi-square distribution returns a posterior for $\sigma^2$ that is also an inverse chi-square (details in WL Appendix 2).
A normal prior on the mean with mean $\mu_0$ and variance $\sigma_0^2$ (larger $\sigma_0^2$, more diffuse the prior)

$$p(\mu) = \frac{1}{\sqrt{2\pi\sigma_0^2}} \exp \left( -\frac{(\mu - \mu_0)^2}{2\sigma_0^2} \right)$$

If the likelihood for the mean is a normal distribution, the resulting posterior is also normal, with

$$\sigma_\ast^2 = \left( \frac{1}{\sigma_0^2} + \frac{n}{\sigma^2} \right)^{-1} \quad \text{and} \quad \mu_\ast = \sigma_\ast^2 \left( \frac{\mu_0}{\sigma_0^2} + \frac{n\bar{x}}{\sigma^2} \right)$$

Note that if $\sigma_0^2$ is large, the mean of the posterior is very close to the sample mean.
If $x$ follows a Chi-square distribution, then $1/x$ follows an inverse chi-square distribution.

The scaled inverse chi-square distribution is more typically used, where

$$p(x \mid n) \propto x^{-(n/2+1)} e^{-\sigma^2_0/(2x)}$$

The scaled inverse chi-square has two parameters, allowing more control over the mean and variance of the prior

<table>
<thead>
<tr>
<th>Likelihood</th>
<th>Conjugate prior</th>
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<tbody>
<tr>
<td>Normal</td>
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<tr>
<td>$\mu$ unknown, $\sigma^2$ known</td>
<td>Normal</td>
</tr>
<tr>
<td>$\mu$ known, $\sigma^2$ unknown</td>
<td>Inverse Chi-Square</td>
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<td>Multivariate Normal</td>
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<tr>
<td>$\mu$ unknown, $\mathbf{V}$ known</td>
<td>Multivariate Normal</td>
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<tr>
<td>$\mu$ known, $\mathbf{V}$ unknown</td>
<td>Inverse Wishart</td>
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</tbody>
</table>
Example

Let’s return to our binomial example $n_1 = 30, n = 150$

If we use a beta distribution as a prior, then the posterior for a beta*binominal is also a beta

The beta is a two parameter distribution (alpha, beta) the resulting posterior has parameters

$n_1 + \alpha, n - n_1 + \beta$

Taking $\alpha = \beta = 1$ assumes a uniform prior over $(0,1)$
\begin{align*}
\alpha & \leftarrow -1; \quad \beta \leftarrow -1; \quad n_1 \leftarrow 30; \quad n \leftarrow 150; \\
\text{curve}(\text{dbeta}(x, \alpha, \beta), 0, 1) \\
\text{Prior on } x = p \\
\text{Posterior} \\
\text{curve}(\text{dbeta}(x, n_1 + \alpha, n_n1 + \beta), 0, 1)
\end{align*}
95% Bayesian credible interval

Need to solve for the lower 2.5% and upper 97.5% values in the posterior

Using R, \texttt{qbeta(0.025,n1+alpha,n-n1+beta)} returns 14.4% for lower value, while \texttt{qbeta(0.975,n1+alpha,n-n1+beta)} returns 27.1%

MM: 13.7 to 26.3
MLE: 13.5 to 26.4
Bayes (uniform prior) 14.4 to 27.1
Effect of the prior: use alpha = 10, beta = 3

95% CI is 18.3% to 31.4%

Homework: try differ priors to see their effects
MCMC

Analytic expressions for posteriors can be complicated, but the method of MCMC (Markov Chain Monte Carlo) is a general approach to simulating draws for just about any distribution (details in WL Appendix 3).

Generating several thousand such draws from the posterior returns an empirical distribution that we can use.

For example, we can compute a 95% credible interval, the region of the distribution that containing 95% of the probability.
Gibbs Sampling

• A very powerful version of MCMC is the Gibbs Sampler
• Assume we are sampling from a vector of parameters, but that the marginal distribution of each parameter is known
• For example, given a current value for all the fixed effects (but one, say $\beta_1$) and the variances, conditioning on these values the distribution of $\beta_1$ is a normal, whose parameters are now functions of the current values of the other parameters. A random draw is then generated from this distribution.
• Likewise, conditioning on all the fixed effects and all variances but one, the distribution of this variance is an inverse chi-square
When more than two variables are involved, the sampler is extended in the obvious fashion. In particular, the value of the $k$th variable is drawn from the distribution $p(\theta^{(k)} | \Theta^{(-k)})$ where $\Theta^{(-k)}$ denotes a vector containing all of the variables but $k$. Thus, during the $i$th iteration of the sample, to obtain the value of $\theta^{(k)}_i$ we draw from the distribution

$$\theta^{(k)}_i \sim p(\theta^{(k)} | \theta^{(1)} = \theta^{(1)}_i, \ldots, \theta^{(k-1)} = \theta^{(k-1)}_i, \theta^{(k+1)} = \theta^{(k+1)}_{i-1}, \ldots, \theta^{(n)} = \theta^{(n)}_{i-1})$$

For example, if there are four variables, $(w, x, y, z)$, the sampler becomes

$$w_i \sim p(w | x = x_{i-1}, y = y_{i-1}, z = z_{i-1})$$
$$x_i \sim p(x | w = w_i, y = y_{i-1}, z = z_{i-1})$$
$$y_i \sim p(y | w = w_i, x = x_i, z = z_{i-1})$$
$$z_i \sim p(z | w = w_i, x = x_i, y = y_i)$$

This generates one cycle of the sampler. Using these new values, a second cycle is generated.

Full details in WL Appendix 3.