# Bayes Rule with Continuous Random Variables

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### **Obligatory Disclosure**

- Ben is an employee of Columbia University, which has received several research grants to develop Stan
- Ben is also a manager of GG Statistics LLC, which uses Stan for business purposes
- According to Columbia University policy, any such employee who has any equity stake in, a title (such as officer or director) with, or is expected to earn at least \$5,000.00 per year from a private company is required to disclose these facts in presentations
- I do not have any connection to Mapp Biopharmaceutical, which we are going to use as an example today

#### **Beta Distribution**

• The Beta distribution for  $\pi\in\Theta=[0,1]$  has two positive shape parameters a and b and its PDF involves the Beta function  $B(a,b)=rac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)}$ :

$$f(\pi|a,b) = \frac{1}{B(a,b)} \pi^{a-1} (1-\pi)^{b-1} \propto \pi^{a-1} (1-\pi)^{b-1}$$

- · Its expectation is  $\mu=rac{a}{a+b}$  & mode is  $M=rac{a-1}{a+b-2}$  but only exists if a,b>1
- . Its median,  $m pprox rac{a-rac{1}{3}}{a+b-rac{2}{3}}$ , always exists but approximation assumes a,b>1
- · Given  $M,m\in(0,1)$ , you can solve for a>1 and b>1
  - $a = rac{m(4M-3)+M}{3(M-m)}$  while  $b = rac{m(1-4M)+5M-2}{3(M-m)}$
  - But m must be between  $\frac{1}{2}$  and M in order for a>1 and b>1

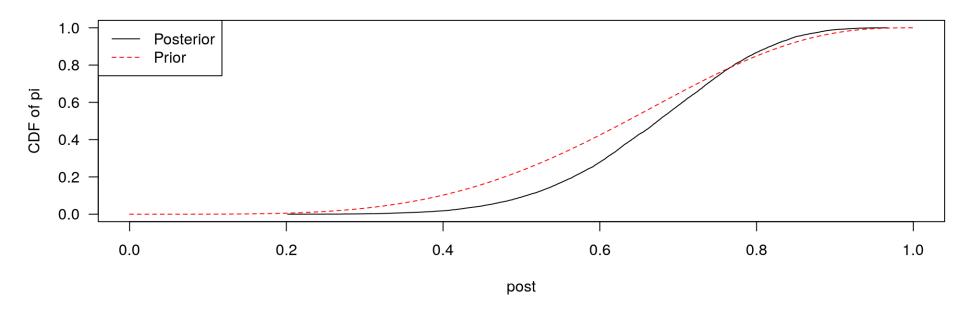
#### Matching the Prior Predictive Distribution in Stan

```
functions { /* saved as ebola rng.stan in R's working directory */
 vector ebola rng(int S, real M, real m, int N, int y) { // must have a rng suffix
    real common = 3 * (M - m);
    real a = (m * (4 * M - 3) + M) / common;
    real b = (m * (1 - 4 * M) + 5 * M - 2) / common;
   vector[S] post; // size equal to number of simulations
   int s = 1:
   if (a < 1 \mid | b < 1) reject("M and m are inconsistent");
   while (s \le S) {
     real pi tilde = beta rng(a, b); // draw from prior distribution
     int y tilde = binomial rng(N, pi tilde); // draw from prior predictive distribution
     if (y tilde == y) {
                                              // keep iff matches observed data
       post[s] = pi tilde;
                                              // indexing (mostly) works like in R
                                              // s += 1; is equivalent to s = s + 1;
       s += 1;
    return sort asc(post);
                                               // easier to plot CDF if sorted ascending
```

### Updating Beliefs about the Success Probability

```
rstan::expose_stan_functions("ebola_rng.stan") # puts Stan functions into R's workspace M <- 2 / 3; m <- 0.635; a <- (m * (4 * M - 3) + M) / (3 * (M - m)) b <- (m * (1 - 4 * M) + 5 * M - 2) / (3 * (M - m)) N <- 7L; y <- 5L; S <- 100000L; post <- ebola_rng(S, M, m, N, y) # call as an R function
```

```
plot(post, y = (1:S) / S, type = "l", xlim = 0:1, ylab = "CDF of pi") curve(pbeta(pi, a, b), from = 0, to = 1, add = TRUE, col = 2, lty = 2, xname = "pi") legend("topleft", legend = xname = xname
```

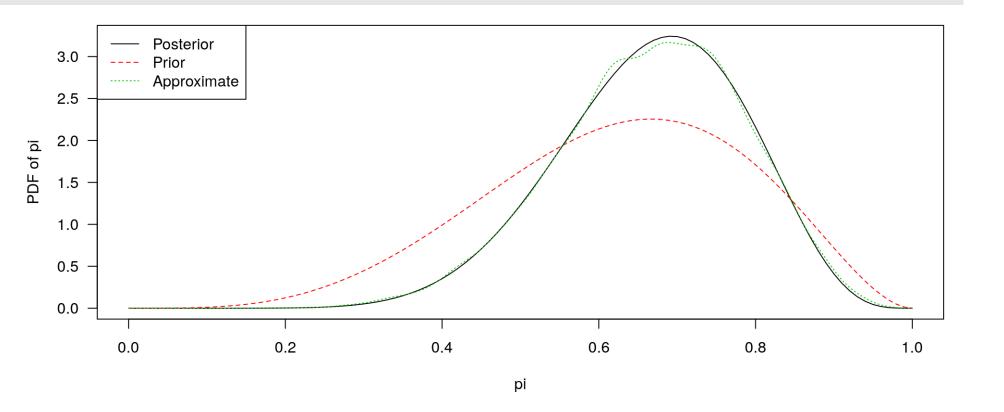


### **Numerator of Bayes Rule**

```
functions { /* saved as numerator.stan in R's working directory */
      vector numerator(vector pi, real M, real m, int N, int y) {
              real common = 3 * (M - m);
              real a = (m * (4 * M - 3) + M) / common;
              real b = (m * (1 - 4 * M) + 5 * M - 2) / common:
              int K = rows(pi); vector[K] log pi = log(pi);
             vector[K] log1m pi = log1m(pi); // log1m(x) == log(1 - x) but numerically accurate
             vector[K] log prior = (a - 1) * log pi + (b - 1) * log1m pi - lbeta(a, b); // l prefix
             vector[K] log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log pi + (N - y) * log likelihood = y * log li
              return exp(log prior + log likelihood); // equals exp(log prior) * exp(log likelihood)
rstan::expose stan functions("numerator.stan")
 (denom < -integrate(numerator, lower = 0, upper = 1, M = M, m = m, N = N, y = y)$value)
## [1] 0.2179323
```

### Same Info from the Probability Density Functions

```
curve(numerator(pi, M, m, N, y) / denom, from = 0, to = 1, xname = "pi", ylab = "PDF of pi") curve(dbeta(pi, a, b), from = 0, to = 1, col = 2, lty = 2, xname = "pi", add = TRUE) lines(density(post, from = 0, to = 1), col = 3, lty = 3) legend("topleft", legend = c("Posterior", "Prior", "Approximate"), col = 1:3, lty = 1:3)
```



### Deriving the Posterior Distribution Analytically

- Survivals are Binomial with probability  $\pi$ . Thus, BEFORE you see the results  $f(y|N,\pi)=\binom{N}{y}\pi^y(1-\pi)^{N-y}$  while the Beta PDF is again  $f(\pi|a,b)=\frac{1}{B(a,b)}\pi^{a-1}(1-\pi)^{b-1}$ , so  $B(a,b)=\int_0^1\pi^{a-1}(1-\pi)^{b-1}d\pi$
- AFTER y=5 out of N=7 people were cured, what are your beliefs about  $\pi$ ?

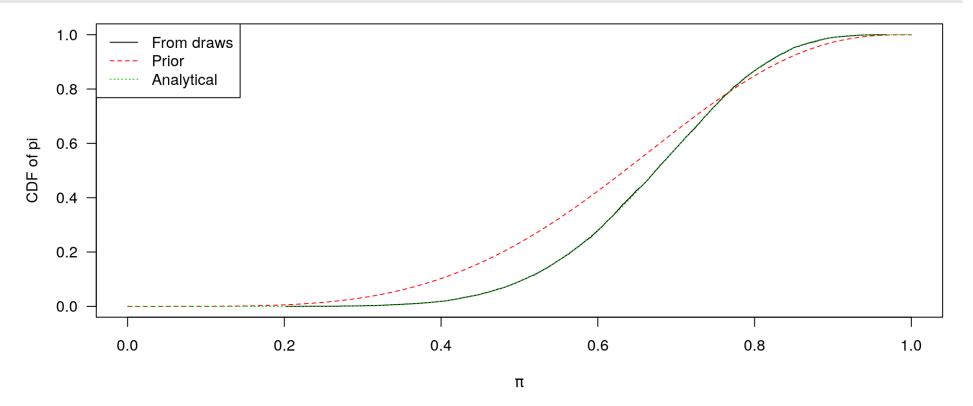
$$f\left(\pi|\,a,b,N,y\right) = \frac{f\left(\pi|\,a,b\right)L\left(\pi;N,y\right)}{\int_{0}^{1}f\left(\pi|\,a,b\right)L\left(\pi;N,y\right)d\pi} \propto \\ \pi^{a-1}\left(1-\pi\right)^{b-1}\pi^{y}\left(1-\pi\right)^{N-y} = \pi^{a+y-1}\left(1-\pi\right)^{b+N-y-1} = \pi^{a^*-1}\left(1-\pi\right)^{b^*-1}$$

where  $a^*=a+y$  and  $b^*=b+N-y$ 

•  $f(\pi|a^*,b^*)$  has the kernel of a Beta PDF and therefore the normalizing constant must be the reciprocal of  $B(a^*,b^*)$ 

# Checking the Posterior CDF

```
plot(post, y = (1:S) / S, type = "l", xlim = 0:1, xlab = expression(pi), ylab = "CDF of pi")
curve(pbeta(pi, a, b), from = 0, to = 1, add = TRUE, col = 2, lty = 2, xname = "pi")
curve(pbeta(pi, a + y, b + N - y), from = 0, to = 1, add = TRUE, col = 3, lty = 3, xname = "pi")
legend("topleft", legend = c("From draws", "Prior", "Analytical"), col = 1:3, lty = 1:3)
```

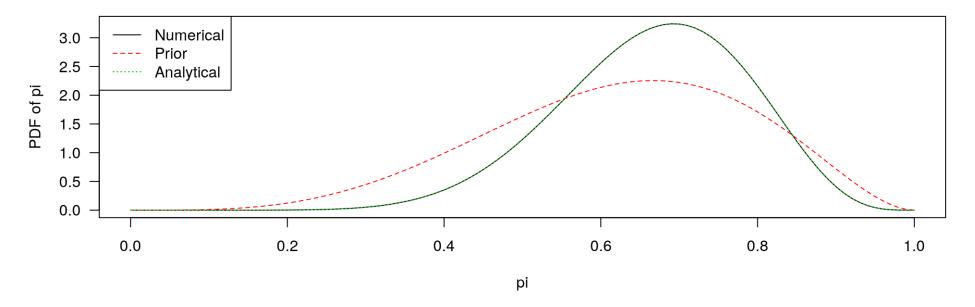


## Checking the Posterior PDF

```
c(exact = (a + y) / (a + y + b + N - y), approximate = mean(post)) # posterior expectation

## exact approximate
## 0.6666667 0.6665921

curve(numerator(pi, M, m, N, y) / denom, from = 0, to = 1, xname = "pi", ylab = "PDF of pi")
curve(dbeta(pi, a, b), from = 0, to = 1, col = 2, lty = 2, xname = "pi", add = TRUE)
curve(dbeta(pi, a + y, b + N - y), from = 0, to = 1, col = 3, lty = 3, xname = "pi", add = TRUE)
legend("topleft", legend = c("Numerical", "Prior", "Analytical"), col = 1:3, lty = 1:3)
```



### **Properties of this Posterior Distribution**

- The first approach illustrates a key point: The posterior PDF is the function closest to the prior PDF that satisfies a constraint given by the observed data
- · Posterior expectation is between the prior expectation and sample mean

```
c(prior = a / (a + b), posterior = (a + y) / (a + y + b + N - y), sample = y / N)
```

```
## prior posterior sample
## 0.6232877 0.6666667 0.7142857
```

- · As  $N\uparrow\infty$  with a and b fixed, the posterior mean approaches  $rac{y}{N}$
- · It does not matter if the data arrives one observation at a time, all at once, or somewhere in between. After N tries and y successes your posterior distribution will be the same, namely Beta with parameters  $a^* = a + y$  and  $b^* = b + N y$ , and contains all the information available from past data
- · Ergo, you can use your posterior PDF as your prior PDF for the next dataset