

# Streptococcus heftans

## A Bayesian Analysis

### The Rfuns Project

## Background

Suppose that *Streptococcus heftans* (fictitious) is an uncommon oral bacteria that has recently been found to cause rare heart infections affecting chambers and valves, especially in the elderly and those with existing chronic heart diseases. The prevalence for *S. heftans* has never been rigorously estimated, but is believed to be less than 0.005 (0.5% of the population), is very likely to be less than 0.01, and is virtually certain to be less than 0.05.

## Statistical Analysis

Maya Cardiya, Ph.D. plans to test  $n = 500$  patients to determine if they carry *S. heftans*. Her protocol's statistical plan calls for the use of a beta-binomial model. The true prevalence  $\pi$  is unknown, so it will be modeled with a beta prior. Tailoring to this particular study, a subjective prior sets the prior median at 0.01 and the 0.99 quantile at 0.05.

- a. Find the beta prior. (Use `beta.select` from `LearnBayes` to find the shape parameters)

```
quantile1 = list(p = 1 - 0.5, x = 0.1)
quantile2 = list(p = 1 - 0.99, x = 0.05)
params <- beta.select(quantile1, quantile2)
```

The beta prior distribution is given  $g(\pi) = \frac{\Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0)\Gamma(\beta_0)} \cdot \pi^{\alpha_0-1} \cdot (1 - \pi)^{\beta_0-1}$ .

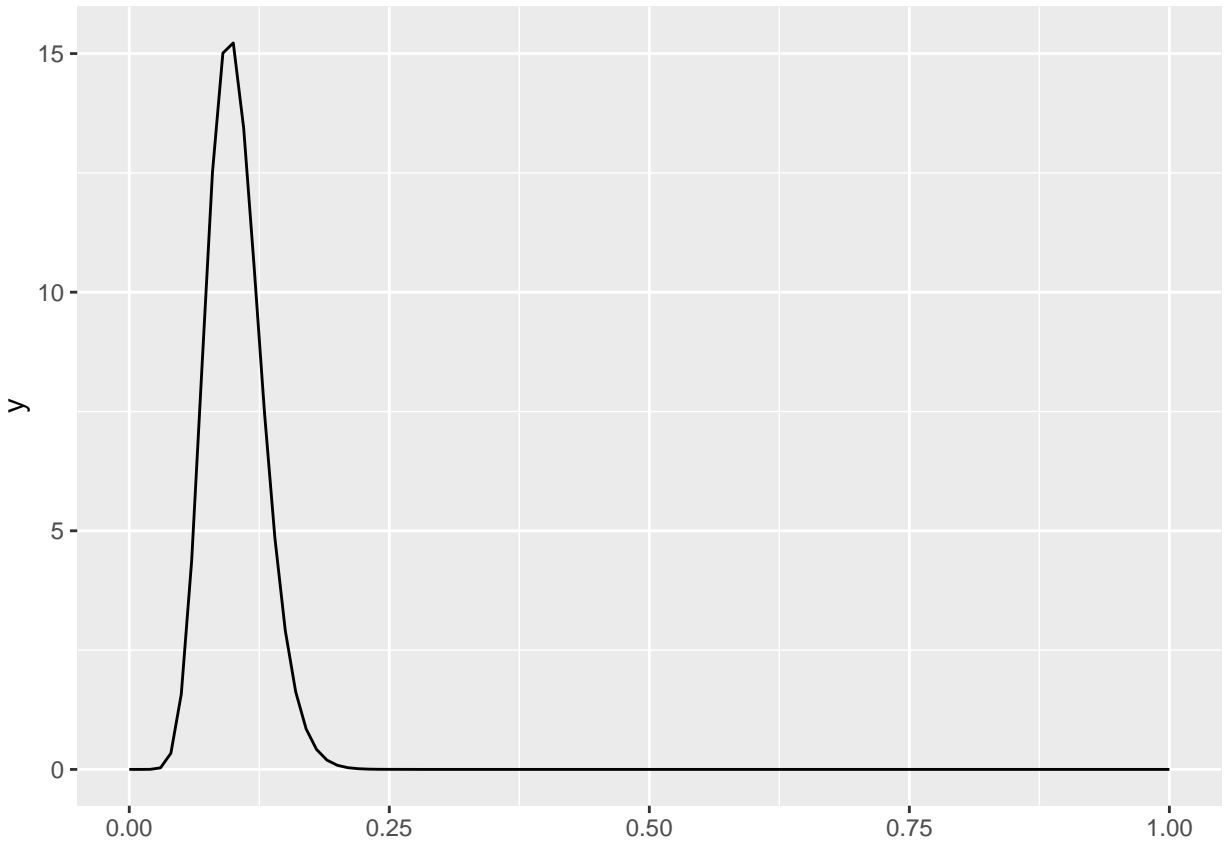
Plug in  $\alpha_0 = 13.38$  and  $\beta_0 = 117.77$ .

$$\begin{aligned} g(\pi) &= \frac{\Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0)\Gamma(\beta_0)} \cdot \pi^{\alpha_0-1} \cdot (1 - \pi)^{\beta_0-1} \\ &= \frac{\Gamma(13.38 + 117.77)}{\Gamma(13.38)\Gamma(117.77)} \cdot \pi^{13.38-1} \cdot (1 - \pi)^{117.77-1} \end{aligned}$$

- b. Dr. Cardiya's protocol calls for one interim analysis near 50% of testing. Of the first 241 subjects, 7 tested positive for *S. heftans*.

- i. Calculate the interim posterior distribution. Make a plot of the prior, likelihood and interim posterior distribution. Use the range  $0 < \pi < 0.1$  since that's where the action is.

```
ggplot()+
  stat_function(fun = dbeta,
               args = list(shape1=params[1],
                           shape2=params[2]))
```



- ii. Contrast the prior median with the posterior median. Also contrast the middle 95% of the beta prior with the middle 95% of the interim posterior distribution.
- iii. Contrast the prior probability that less than 1 percentage of the population have S. heftans with the posterior probability.
- iv. Suppose testing 247 more subjects yields 5 positives. Using the interim posterior distribution as your prior, repeat i,ii,iii for the final posterior distribution. Make a table showing the prior/posterior median, 95% percentile interval and spread of the interval.
- v. Calculate the 95% Highest Posterior Density intervals for the final analysis in part c. Compare your Bayesian analysis with the results from a large sample Wald confidence interval for a binomial proportion.
- e. Let's now quickly cause a merge conflict in this controlled environment.
- f. All group members create a code chunk so that all members of the group have any particular line inside of the chunk. For example, everyone create a code chunk so that line, lets say 43, is inside of that code chunk.
- ii. Now on that shared line, one member of your group write your name. Then, commit the change, pull, and push. None of the other members of the group do anything at this point.
- iii. Now another member of the group, on that same line write your own name. Commit the change and pull. This should result in a merge conflict because there are two different things written on this line of code.
- iv. Resolve the merge conflict by writing all of your names on that line, one person committing, pulling, and pushing, then all other members of the group pulling.

## Acknowledgment

Thanks to Ralph O'Brien for this problem.