

# Bayesian Model Specification

## 3: Bayesian Qualitative/Quantitative Inference

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# Bayesian Qual/Quant Inference

Recall from our earlier discussion that if I judge **binary**  $(y_1, \dots, y_n)$  to be part of **infinitely exchangeable sequence**, to be **coherent** my joint predictive distribution  $p(y_1, \dots, y_n)$  must have simple **hierarchical** form

$$\begin{aligned}\theta &\sim p(\theta) \\ (y_i|\theta) &\stackrel{\text{IID}}{\sim} \text{Bernoulli}(\theta),\end{aligned}$$

where  $\theta = P(y_i = 1) =$  **limiting value of mean of  $y_i$**  in infinite sequence.

Writing  $s = (s_1, s_2)$  where  $s_1$  and  $s_2$  are the **numbers of 0s and 1s**, respectively in  $(y_1, \dots, y_n)$ , this is **equivalent** to the model

$$\begin{aligned}\theta_2 &\sim p(\theta_2) \\ (s_2|\theta_2) &\sim \text{Binomial}(n, \theta_2),\end{aligned} \tag{1}$$

where (in a slight change of notation)  $\theta_2 = P(y_i = 1)$ ; i.e., in this simplest case the form of the **likelihood function** (Binomial( $n, \theta_2$ )) is determined by **coherence**.

The **likelihood function** for  $\theta_2$  in this model is

$$l(\theta_2|y) = c \theta_2^{s_2} (1 - \theta_2)^{n-s_2} = c \theta_1^{s_1} \theta_2^{s_2}, \tag{2}$$

from which it's evident that the **conjugate prior** for the **Bernoulli/Binomial likelihood** (the choice of prior having the property that the **posterior** for  $\theta_2$  has the same **mathematical form** as the **prior**) is the family of **Beta**( $\alpha_1, \alpha_2$ ) densities

$$p(\theta_2) = c \theta_2^{\alpha_2-1} (1 - \theta_2)^{\alpha_1-1} = c \theta_1^{\alpha_1-1} \theta_2^{\alpha_2-1}. \tag{3}$$

for some  $\alpha_1 > 0, \alpha_2 > 0$ .

# Bayesian Qual/Quant Inference

With this prior the **conjugate updating rule** is evidently

$$\left\{ \begin{array}{l} \theta_2 \sim \text{Beta}(\alpha_1, \alpha_2) \\ (s_2|\theta_2) \sim \text{Binomial}(n, \theta_2) \end{array} \right\} \rightarrow (\theta_2|y) \sim \text{Beta}(\alpha_1 + s_1, \alpha_2 + s_2), \quad (4)$$

where  $s_1$  ( $s_2$ ) is the **number of 0s (1s)** in the data set  $y = (y_1, \dots, y_n)$ .

Moreover, given that the **likelihood** represents a **(sample) data set** with  $s_1$  0s and  $s_2$  1s and a **data sample size** of  $n = (s_1 + s_2)$ , it's clear that

(a) the **Beta**( $\alpha_1, \alpha_2$ ) prior acts like a **(prior) data set** with  $\alpha_1$  0s and  $\alpha_2$  1s and a **prior sample size** of  $(\alpha_1 + \alpha_2)$ , and

(b) to achieve a relatively **diffuse (low-information-content)** prior for  $\theta_2$  (if that's what **context** suggests I should aim for) I should try to specify  $\alpha_1$  and  $\alpha_2$  **not far from 0**.

Easy **generalization** of all of this: suppose the  $y_i$  take on  $l \geq 2$  **distinct values**  $v = (v_1, \dots, v_l)$ , and let  $s = (s_1, \dots, s_l)$  be the **vector of counts** ( $s_1 = \#(y_i = v_1)$  and so on).

If I judge the  $y_i$  to be part of an **infinitely exchangeable sequence**, then to be **coherent** my joint predictive distribution  $p(y_1, \dots, y_n)$  must have the **hierarchical** form

$$\begin{array}{l} \theta \sim p(\theta) \\ (s|\theta) \sim \text{Multinomial}(n, \theta), \end{array} \quad (5)$$

where  $\theta = (\theta_1, \dots, \theta_l)$  and  $\theta_j$  is the **limiting relative frequency** of  $v_j$  values in the infinite sequence.

# Bayesian Qual/Quant Inference

The **likelihood** for (vector)  $\theta$  in this case has the form

$$l(\theta|y) = c \prod_{j=1}^l \theta_j^{s_j}, \quad (6)$$

from which it's evident that the **conjugate prior** for the **Multinomial likelihood** is of the form

$$p(\theta) = c \prod_{j=1}^l \theta_j^{\alpha_j - 1}, \quad (7)$$

for some  $\alpha = (\alpha_1, \dots, \alpha_l)$  with  $\alpha_j > 0$  for  $j = 1, \dots, l$ ; this is the **Dirichlet**( $\alpha$ ) distribution, a **multivariate generalization** of the Beta family.

Here the **conjugate updating rule** is

$$\left\{ \begin{array}{l} \theta \sim \text{Dirichlet}(\alpha) \\ (s|\theta) \sim \text{Multinomial}(n, \theta) \end{array} \right\} \rightarrow (\theta|y) \sim \text{Dirichlet}(\alpha + s), \quad (8)$$

where  $s = (s_1, \dots, s_l)$  and  $s_j$  is the **number of  $v_j$  values** ( $j = 1, \dots, l$ ) in the data set  $y = (y_1, \dots, y_n)$ .

Furthermore, by **direct analogy** with the  $l = 2$  case,

(a) the **Dirichlet**( $\alpha$ ) prior acts like a **(prior) data set** with  $\alpha_j$   $v_j$  values ( $j = 1, \dots, l$ ) and a **prior sample size** of

$$\sum_{j=1}^l \alpha_j, \text{ and}$$

(b) to achieve a relatively **diffuse**

**(low-information-content)** prior for  $\theta$  (if that's what **context** suggests I should aim for) I should try to choose all of the  $\alpha_j$  **not far from 0**.

# Bayesian Qual/Quant Inference

To summarize:

(A) if the **data vector**  $y = (y_1, \dots, y_n)$  takes on  $l$  **distinct** values  $v = (v_1, \dots, v_l)$  (**real numbers or not**) and I judge (my uncertainty about) the infinite sequence  $(y_1, y_2, \dots)$  to be **exchangeable**, then (by a **representation theorem** of de Finetti) **coherence** compels me (i) to **think about** the quantities  $\theta = (\theta_1, \dots, \theta_l)$ , where  $\theta_j$  is the **limiting relative frequency** of the  $v_j$  values in the infinite sequence, and (ii) to **adopt** the Multinomial model

$$\theta \sim p(\theta) \tag{9}$$
$$p(y_i|\theta) = c \prod_{j=1}^l \theta_j^{s_j},$$

where  $s_j$  is the **number** of  $y_i$  values equal to  $v_j$ ;

(B) if context suggests a **diffuse** prior for  $\theta$  a convenient (**conjugate**) choice is **Dirichlet**( $\alpha$ ) with  $\alpha = (\alpha_1, \dots, \alpha_l)$  and all of the  $\alpha_j$  **positive but close to 0**; and

(C) with a **Dirichlet**( $\alpha$ ) prior for  $\theta$  the **posterior** is **Dirichlet**( $\alpha'$ ), where  $s = (s_1, \dots, s_l)$  and  $\alpha' = (\alpha + s)$ .

Note, remarkably, that the  $v_j$  values themselves **make no appearance** in the model; this modeling approach is **natural** with **categorical** outcomes but can also be used when the  $v_j$  are **real numbers**.

For example, for **real-valued**  $y_i$ , if (as in the **IHGA case study** in Part 1) interest focuses on the (**underlying population**) **mean** in the infinite sequence  $(y_1, y_2, \dots)$ , this is  $\mu_y = \sum_{j=1}^l \theta_j v_j$ , which is just a **linear function** of the  $\theta_j$  with **known coefficients**  $v_j$ .

# Bayesian Qual/Quant Inference

This fact makes it possible to draw an **analogy** with the **distribution-free** methods that are at the heart of **frequentist non-parametric** inference: when your **outcome variable** takes on a **finite number** of **real** values  $v_j$ , **exchangeability** compels a **Multinomial likelihood** on the **underlying frequencies** with which the  $v_j$  occur; you are not required to build a **parametric model** (e.g., normal, lognormal, ...) on the  $y_i$  values themselves.

In this sense, therefore, model (14)—particularly with the **conjugate Dirichlet** prior—can serve as a kind of **low-technology Bayesian non-parametric** modeling: this is the basis of the **Bayesian bootstrap** (Rubin 1981).

Moreover, if you're **in a hurry** and you're already familiar with WinBUGS you can readily carry out **inference** about quantities like  $\mu_y$  above in that environment, but there's **no need to do MCMC** here: **ordinary Monte Carlo** (MC) sampling from the **Dirichlet**( $\alpha'$ ) posterior distribution is perfectly **straightforward**, e.g., in R, based on the following **fact**:

To generate a **random draw**  $\theta = (\theta_1, \dots, \theta_l)$  from the **Dirichlet**( $\alpha'$ ) distribution, with  $\alpha' = (\alpha'_1, \dots, \alpha'_l)$ , **independently draw**

$$g_j \stackrel{\text{indep}}{\sim} \Gamma(\alpha'_j, \beta), \quad j = 1, \dots, l \quad (10)$$

(where  $\Gamma(a, b)$  is the **Gamma distribution** with parameters  $a$  and  $b$ ) and compute

$$\theta_j = \frac{g_j}{\sum_{m=1}^l g_m}. \quad (11)$$

**Any**  $\beta > 0$  will do in this calculation;  $\beta = 1$  is a **good choice** that leads to **fast random number generation**.

# Bayesian Qual/Quant Inference

The **downloadable version** of R doesn't have a **built-in function** for making **Dirichlet draws**, but it's easy to write one:

```
rdirichlet = function( n.sim, alpha ) {  
  
  l = length( alpha )  
  
  theta = matrix( 0, n.sim, l )  
  
  for ( j in 1:l ) {  
  
    theta[ , j ] = rgamma( n.sim, alpha[ j ], 1 )  
  
  }  
  
  theta = theta / apply( theta, 1, sum )  
  
  return( theta )  
  
}
```

The **Dirichlet**( $\alpha$ ) distribution has the following **moments**: if  $\theta \sim \text{Dirichlet}(\alpha)$  then

$$E(\theta_j) = \frac{\alpha_j}{\alpha_0}, \quad V(\theta_j) = \frac{\alpha_j(\alpha_0 - \alpha_j)}{\alpha_0^2(\alpha_0 + 1)}, \quad C(\theta_j, \theta_{j'}) = -\frac{\alpha_j\alpha_{j'}}{\alpha_0^2(\alpha_0 + 1)},$$

where  $\alpha_0 = \sum_{j=1}^l \alpha_j$  (note the **negative correlation** between components of  $\theta$ ).

This can be used to **test** the function above:

# Bayesian Qual/Quant Inference

```
> alpha = c( 5.0, 1.0, 2.0 )

> alpha.0 = sum( alpha )

> test = rdirichlet( 100000, alpha )    # 15 seconds at 550 Unix MHz

> apply( test, 2, mean )

[1] 0.6258544 0.1247550 0.2493905

> alpha / alpha.0

[1] 0.625 0.125 0.250

> apply( test, 2, var )

[1] 0.02603293 0.01216358 0.02071587

> alpha * ( alpha.0 - alpha ) / ( alpha.0^2 * ( alpha.0 + 1 ) )

[1] 0.02604167 0.01215278 0.02083333

> cov( test )

           [,1]      [,2]      [,3]
[1,] 0.026032929 -0.008740319 -0.017292610
[2,] -0.008740319 0.012163577 -0.003423259
[3,] -0.017292610 -0.003423259 0.020715869

> - outer( alpha, alpha, "*" ) / ( alpha.0^2 * ( alpha.0 + 1 ) )

           [,1]      [,2]      [,3]
[1,] -0.043402778 -0.008680556 -0.017361111
[2,] -0.008680556 -0.001736111 -0.003472222 # ignore diagonals
[3,] -0.017361111 -0.003472222 -0.006944444
```



# Bayesian Qual/Quant Inference

**Example:** re-analysis of **IHGA data** from Part 1; recall **policy** and **clinical interest** focused on  $\eta = \frac{\mu_E}{\mu_C}$ .

Group	Number of Hospitalizations								<i>n</i>	Mean	SD
	0	1	2	3	4	5	6	7			
Control	138	77	46	12	8	4	0	2	287	0.944	1.24
Experimental	147	83	37	13	3	1	1	0	285	0.768	1.01

In this **two-independent-samples** setting I can apply de Finetti's representation theorem **twice, in parallel**, on the  $C$  and  $E$  data.

I don't know much about the **underlying frequencies** of 0, 1, ..., 7 hospitalizations under  $C$  and  $E$  **external** to the data, so I'll use a **Dirichlet**( $\epsilon, \dots, \epsilon$ ) **prior** for both  $\theta_C$  and  $\theta_E$  with  $\epsilon = 0.001$ , leading to a **Dirichlet**(138.001, ..., 2.001) **posterior** for  $\theta_C$  and a **Dirichlet**(147.001, ..., 0.001) **posterior** for  $\theta_E$  (other small positive choices of  $\epsilon$  yield **similar results**).

```
> alpha.C = c( 138.001, 77.001, 46.001, 12.001, 8.001, 4.001, 0.001,
  2.001 )
> alpha.E = c( 147.001, 83.001, 37.001, 13.001, 3.001, 1.001, 1.001,
  0.001 )
> theta.C = rdirichlet( 100000, alpha.C ) # 17 sec at 550 Unix MHz
> theta.E = rdirichlet( 100000, alpha.E ) # also 17 sec
> print( post.mean.theta.C = apply( theta.C, 2, mean ) )
[1] 4.808015e-01 2.683458e-01 1.603179e-01 4.176976e-02 2.784911e-02
[6] 1.395287e-02 3.180905e-06 6.959859e-03
> print( post.SD.theta.C <- apply( theta.C, 2, sd ) )
[1] 0.0294142963 0.0261001259 0.0216552661 0.0117925465 0.0096747630
[6] 0.0069121507 0.0001017203 0.0048757485
```

# Bayesian Qual/Quant Inference

```
> print( post.mean.theta.E <- apply( theta.E, 2, mean ) )

[1] 5.156872e-01 2.913022e-01 1.298337e-01 4.560130e-02 1.054681e-02
[6] 3.518699e-03 3.506762e-03 3.356346e-06

> print( post.SD.theta.E <- apply( theta.E, 2, sd ) )

[1] 0.029593047 0.026915644 0.019859213 0.012302252 0.006027157
[6] 0.003501568 0.003487824 0.000111565

> mean.effect.C <- theta.C %*% ( 0:7 )

> mean.effect.E <- theta.E %*% ( 0:7 )

> mult.effect <- mean.effect.E / effect.C

> print( post.mean.mult.effect <- mean( mult.effect ) )

[1] 0.8189195

> print( post.SD.mult.effect <- sd( mult.effect ) )

[1] 0.08998323

> quantile( mult.effect, probs = c( 0.0, 0.025, 0.5, 0.975, 1.0 ) )

      0%      2.5%      50%      97.5%     100%
0.5037150 0.6571343 0.8138080 1.0093222 1.3868332

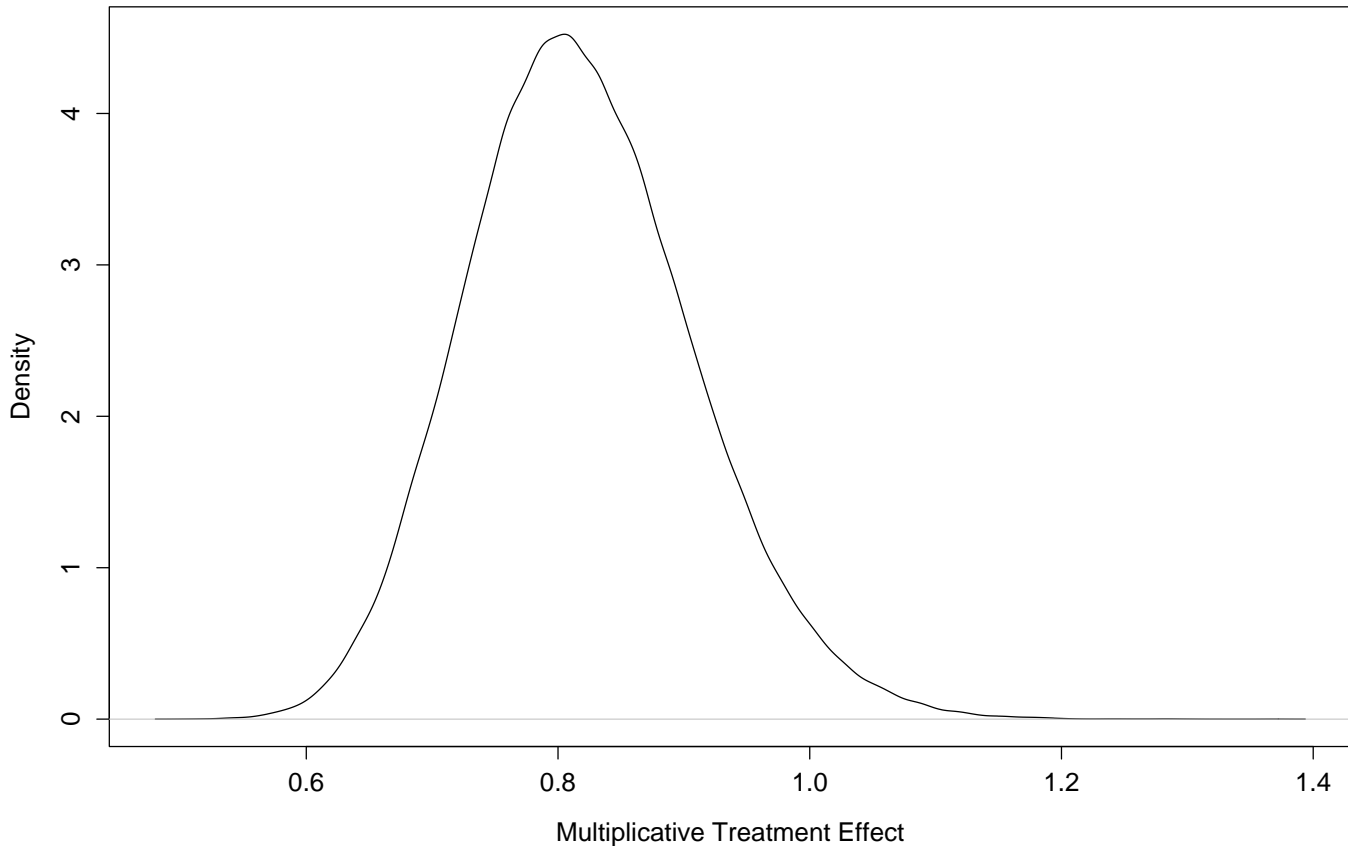
> postscript( "mult.effect.ps" )

> plot( density( mult.effect, n = 2048 ), type = 'l', cex.lab = 1.25,
        xlab = 'Multiplicative Treatment Effect', cex.axis = 1.25,
        main = 'Posterior Distribution for Multiplicative Treatment Effect',
        cex.main = 1.25 )

> dev.off( )
```

# Bayesian Qual/Quant Inference

Posterior Distribution for Multiplicative Treatment Effect



Model	Posterior Mean	Posterior SD	Central 95% Interval
REPR	0.830	0.0921	(0.665, 1.02)
Dir-Mult	0.819	0.0900	(0.657, 1.01)

In this example the **low-tech BNP, Dirichlet-Multinomial, exchangeability-plus-diffuse-prior-information** model has **reproduced the parametric REPR results** almost exactly and without a **complicated search through model space** for a **“good”** model.

**NB** This approach is an application of the **Bayesian bootstrap** (Rubin 1981), which (for complete validity) includes the **assumption** that the **observed  $y_i$  values form a complete set of {all possible values the outcome  $y$  could take on}**.

# Bayesian Qual/Quant Inference

**This is clearly not true in the IHGA case study, and yet in that case the Bayesian qualitative/quantitative inferential approach did a terrific job of reproducing what we will later see is an excellent parametric model for the IHGA data, without any parametric modeling assumptions.**