KU Leuven Summer School Segment 6 Bayesian Calibration

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Need a simple sandbox to play in

A stripped-down misclassification problem.

Interested in the prevalance, r, of a disease in a population.

The diagnostic test for the condition is known to have perfect *specificity*, i.e., no false positives.

But there is ambiguity about the *sensitivity*, i.e., could be some false negatives.

The diagnostic test is applied to a random sample of n individuals from the target population.

Generative model (collapsed version)

- $ightharpoonup r \sim Unif(0,1)$
- ▶ $Sn \sim \text{Beta}(a, b)$
- $ightharpoonup (Y^*|r,Sn) \sim Bin(n,r \times Sn)$

And let's make things quite focussed:

Inputs:

- ▶ Dataset (Y*, n)
- Expert opinion (hyperparameters) (a, b)

Output:

- ightharpoonup (general) posterior distribution of (r, Sn)
- ▶ (specific) 80% equal-tailed credible interval for *r*

Computational implementation

Would be easy to implement in JAGS.

But nice to have something **faster**, and less beholden to **diagnostics**, to support **simulation studies**.

Turns out this is a nearly conjugate situation

- possible to do iid Monte Carlo draws from a decent approximation to the posterior distribution
- possible to correct for the approximation error via importance weights that do not depend on the data

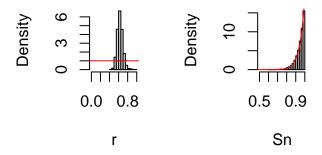
See the appendix for bespoke code, if interested.

Example

Say the data are $(Y^*, n) = (60,100)$.

Say the investigator believes that the diagnostic test could be *slightly* insensitive, chooses hyperparameters (a, b) = (19, 1)

Marginal posterior distributions of r and Sn, compared to prior



And then focus on the credible interval

From bespoke code, 80% credible interval for r:

```
cred.int(60,100, hyp=list(a=19,b=1))
## [1] 0.558 0.713
```

For comparison, the corresponding interval if the investigator assumes $\mathit{Sn}=1$

```
qbeta(c(0.1,0.9), shape1=1+60, shape2=1+(100-60))
## [1] 0.536 0.660
```

Thought (well simulation) experiment #1A

Frequentist coverage of the 80% credible interval? At a particular spot in the parameter space.

```
n <- 100; r.tr <- 0.7; sn.tr <- 0.85; m <- 1600

ystr <- cover <- rep(NA, m)
intrvl <- matrix(NA, m, 2)

for (i in 1:m) {
   ystr[i] <- rbinom(1, size=n, prob=r.tr*sn.tr)
   intrvl[i,] <- cred.int(ystr[i],n, hyp=list(a=19, b=1))
   cover[i] <- (intrvl[i,1]<r.tr) & (r.tr<intrvl[i,2])
}</pre>
```

Experiment #1A, continued

[1] 0.154

```
## r.tr sn.tr ystr
                    cover
## [1,] 0.7 0.85 52 0.477 0.628
## [2,] 0.7 0.85 50 0.455 0.608
## [3.] 0.7 0.85 51 0.466 0.616
## [4,] 0.7 0.85 64 0.598 0.753
## [5,] 0.7 0.85 58 0.534 0.691
## [6,] 0.7 0.85 57 0.526 0.679
## [7,] 0.7 0.85 57 0.527 0.682
## [8.] 0.7 0.85 67 0.630 0.785
### frequentist coverage
mean(cover)
## [1] 0.571
### average width
mean(intrvl[,2]-intrvl[,1])
```

head(cbind(r.tr, sn.tr, ystr,intrvl,cover),8)

Thought experiment #1B

Frequentist coverage of the 80% credible interval? At a different spot in the parameter space.

```
n <- 100; r.tr <- 0.8; sn.tr <- 0.97; m <- 1600

ystr <- cover <- rep(NA, m)
intrvl <- matrix(NA, m, 2)

for (i in 1:m) {
    ystr[i] <- rbinom(1, size=n, prob=r.tr*sn.tr)
    intrvl[i,] <- cred.int(ystr[i],n, hyp=list(a=19, b=1))
    cover[i] <- (intrvl[i,1]<r.tr) & (r.tr<intrvl[i,2])
}</pre>
```

Experiment #1B, continued

[1] NaN

```
head(cbind(r.tr, sn.tr, ystr,intrvl,cover),8)
## r.tr sn.tr ystr
                              cover
## [1,] 0.8 0.97 83 0.801 0.935
## [2,] 0.8 0.97 80 0.767 0.909
## [3.] 0.8 0.97 82 0.789 0.928
## [4,] 0.8 0.97 74 0.703 0.854
## [5,] 0.8 0.97 70 0.660 0.815
## [6,] 0.8 0.97 81 0.778 0.918
## [7,] 0.8 0.97 75 0.716 0.864
## [8.] 0.8 0.97
                 80 0.767 0.912
### frequentist coverage
mean(cover)
## [1] 0.894
### average length
mean(intrvl[.2]-intrvl[,1])
```

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Thought experiment #2A

Repeated sampling of (parameter,data) pairs

```
n <- 100; m <- 6400
r.tr <- sn.tr <- ystr <- cover <- rep(NA, m)
intrvl <- matrix(NA, m, 2)</pre>
for (i in 1:m) {
   r.tr[i] <- runif(1)
   sn.tr[i] <- rbeta(1, shape1=19, shape2=1)</pre>
   ystr[i] <- rbinom(1, size=n, prob=r.tr[i]*sn.tr[i])</pre>
   intrvl[i,] <- cred.int(ystr[i],n, hyp=list(a=19, b=1))</pre>
   cover[i] <- (intrvl[i,1]<r.tr[i]) & (r.tr[i]<intrvl[i,2])</pre>
```

Thought experiment #2A, continued

```
head(cbind(r.tr, sn.tr, ystr,intrvl,cover),10)
```

```
##
    r.tr sn.tr ystr
                      cover
##
   [1.] 0.260 0.877 16 0.127 0.230
##
   [2,] 0.508 0.947 37 0.325 0.466 0
   [3,] 0.142 0.962 13 0.101 0.194 1
##
   [4,] 0.806 0.964 80 0.768 0.911
##
##
   [5,] 0.150 0.984 16 0.127 0.232
## [6,] 0.639 0.964 63 0.590 0.744
## [7,] 0.194 0.916 21 0.172 0.286
## [8,] 0.854 0.994 83 0.800 0.934
## [9,] 0.402 0.956 38 0.336 0.475
## [10,] 0.689 0.978 70 0.662 0.813
```

```
mean(cover)
```

```
## [1] 0.793
```

Is this general?

Let $A(Y^*)$ be the credible interval Under the **generative model:**

$$Pr\{\theta \in A(Y^*)\} = E\{I_{A(Y^*)}(\theta)\}$$
=

Thought experiment #2B

Repeated sampling of (parameter,data) pairs from a different distribution.

```
n <- 100; m <- 1600
r.tr <- sn.tr <- ystr <- cover <- rep(NA, m)
intrvl <- matrix(NA, m, 2)</pre>
for (i in 1:m) {
   r.tr[i] <- runif(1)
   sn.tr[i] \leftarrow rbeta(1, shape1=15, shape2=5)
   ystr[i] <- rbinom(1, size=n, prob=r.tr[i]*sn.tr[i])</pre>
   intrvl[i,] <- cred.int(ystr[i],n, hyp=list(a=19, b=1))</pre>
   cover[i] <- (intrvl[i,1]<r.tr[i]) & (r.tr[i]<intrvl[i,2])</pre>
```

TE #2B, continued

```
head(cbind(r.tr, sn.tr, ystr,intrvl,cover),10)
```

```
##
        r.tr sn.tr ystr
                                  cover
##
   [1.] 0.8037 0.724 53 0.4864 0.637
##
   [2,] 0.3861 0.734 25 0.2103 0.332
   [3,] 0.5380 0.804 47 0.4267 0.574 1
##
   [4,] 0.0894 0.848 13 0.0996 0.193
##
##
   [5,] 0.6420 0.738 55 0.5061 0.661
## [6,] 0.5261 0.824 39 0.3456 0.489
##
   [7,] 0.8525 0.882 79 0.7568 0.902
## [8,] 0.2517 0.675 27 0.2293 0.357
## [9.] 0.6042 0.779 46 0.4162 0.563
## [10,] 0.5692 0.764 47 0.4238 0.573
```

```
mean(cover)
```

```
## [1] 0.397
```

Frequentist coverage of the Bayesian interval revisited

Same as 1A and 1B, just with more data now.

Thought Experiment #1A*

```
n <- 200; r.tr <- 0.7; sn.tr <- 0.85; m <- 1600
ystr <- cover <- rep(NA, m)
intrvl <- matrix(NA, m, 2)</pre>
for (i in 1:m) {
   ystr[i] <- rbinom(1, size=n, prob=r.tr*sn.tr)</pre>
   intrvl[i,] <- cred.int(ystr[i],n, hyp=list(a=19, b=1))
   cover[i] <- (intrvl[i,1]<r.tr) & (r.tr<intrvl[i,2])</pre>
mean(cover)
## [1] 0.429
mean(intrvl[,2]-intrvl[,1])
## [1] 0.123
```

Thought Experiment #1B*

```
n <- 200; r.tr <- 0.8; sn.tr <- 0.97; m <- 1600
ystr <- cover <- rep(NA, m)
intrvl <- matrix(NA, m, 2)</pre>
for (i in 1:m) {
   ystr[i] <- rbinom(1, size=n, prob=r.tr*sn.tr)</pre>
   intrvl[i,] <- cred.int(ystr[i],n, hyp=list(a=19, b=1))
   cover[i] <- (intrvl[i,1]<r.tr) & (r.tr<intrvl[i,2])</pre>
mean(cover)
## [1] 0.922
mean(intrvl[,2]-intrvl[,1])
## [1] 0.125
```

In textbook problems, what do we expect?

textbook = full information = fully identified

► Frequentist coverage of *x*-percent credible interval is approximately *x*, at *every* point in the parameter space.

(Approximately meaning asymptotically.)

(Asymptotically, Bayesian and frequentist match up.)

▶ Width of interval scales as $\frac{1}{\sqrt{n}}$

In problems like the one here, what happens instead (1 of 3)

- ► Frequentist coverage of x-percent credible interval *varies* widely across the parameter space
- ▶ But no matter what, the average (in a certain sense) of the frequentist coverage is *exactly* x.

In problems like the one here, what happens instead (2 of 3)

- ► At some places in the parameter space, the frequentist coverage (of the x-percent credible interval) goes to as n goes to infinity.
- ► And at all the other places, it goes to
- And we can say something very specific about the set of parameter values for which the limiting frequentist coverage is , namely that

In problems like the one here, what happens instead (3 of 3)

- ▶ The width of the x-percent interval will scale like:
- ► This will not win you friends with your subject-area collaborators, but it is what it is.
- ▶ Check this matches up with $\#1A \rightarrow \#1A$, $\#1B \rightarrow \#1B$

Musings about Bayesian coverage (1 of 4)

Clearly having calibration in Bayesian coverage sense is not as strong as having calibration in a frequentist coverage sense In math terms, say a given interval estimation procedure applied at a given sample size has frequentist coverage $fc(\theta)$, when the parameter value is θ .

Frequentist x-percent confidence interval: $fc(\theta) = x$, for every θ .

Bayesian x-percent credible interval using prior $\pi(\theta)$?

Only full/general guarantee is that $\int fc(\theta)\Pi(\theta)d\theta = x$

Musings (2 of 4)

But in many low-info problems, there **do not exist** interval estimation procedures satisfying $fc(\theta) = x$. (Either for fixed n, or in the large n limit)

In such problems, the Bayesian calibration is the only game in town?

Sidebar: Considerable technical literature (mostly in econometrics) on trying to construct procedures with $fc(\theta) \ge x$, for every θ .

Musings (3 of 4)

What's the narrative to practitioners?

I choose prior π as my pre-data "projection" about the state of the world (i.e., the underlying parameter values).

Post-data, I will be reporting an x-percent credible interval for a (scalar) target parameter.

Then with respect to my joint projection (of parameters and data), there is an x-percent chance I will cover the truth.

Musings (4 of 4)

Or phrased a little differently ...

I direct a lab that will, over time, study the relationship between **different** exposure, disease pairs

I aspire to specify my prior distribution to correctly reflect the pair-to-pair variation in these associations.

If I meet my aspiration, then, in the long-run, x percent of the x-percent credible intervals the lab reports will contain the truth.

And now that you are primed to think about operating characteristics under repeated sampling of (parameter, data) pairs . . .

There is a sense of best possible estimation, as well as a sense of correct coverage

Let $\pi_{Nature}(\theta)$ be the distribution giving rise to the repeated sampling (along with the distribution of data D given θ)

Amongst any and all estimators the minimum mean-squared error (across the repeated sampling) is achieved by the posterior mean of ψ when the investigator's choice of prior distribution matches that of nature.

Thoughts?

Appendix

```
show(full.pst)
```

```
## function(ystr, n, hyp, m=10000) {
##
##
     ### draws from approx posterior in (rstr, sn) parameterization
     rstr <- rbeta(m, 1+ystr, 1+(n-ystr))
##
     sn <- rbeta.trnc(m, rstr, hyp$a-1, hyp$b)</pre>
##
##
##
     ### importance weights to correct for approximation
     impwht <- 1-pbeta(rstr, hyp$a-1, hyp$b)</pre>
##
##
     impwht <- m*impwht/sum(impwht)</pre>
##
##
     ### back to (r, sn) parameterization
##
     r <- rstr/sn
##
##
     # resample according to the weights,
##
     # to get MC representation of actual posterior
##
     tmp <- sample(1:m, replace=T, prob=impwht)</pre>
     list(r=r[tmp], sn=sn[tmp])
##
## }
## <bytecode: 0x0000025c95ceb490>
```

Appendix, continued

show(cred.int)

```
## function(ystr, n, hyp, m=10000, cr.lev=0.8) {
##
     rstr <- rbeta(m, 1+ystr, 1+(n-ystr))
##
##
##
     sn <- rbeta.trnc(m, rstr, hyp$a-1, hyp$b)</pre>
##
     r <- rstr/sn
##
##
##
     impwht <- 1-pbeta(rstr, hyp$a-1, hyp$b)</pre>
##
     impwht <- m*impwht/sum(impwht)</pre>
##
##
     c(weighted.quantile(r, impwht, (1-cr.lev)/2),
##
       weighted.quantile(r, impwht, (1+cr.lev)/2))
## }
```

Appendix, continued

```
show(rbeta.trnc)

## function(m, lwr, a, b) {

## qbeta( runif(m, pbeta(lwr,a, b), 1), a,b)
## }
```