

# Parameter restrictions for the sake of identification: Example 2

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## Hyperparameters and supposed values

```
### user-specified "known" prevalence of C
lam.tld <- .15

### or use a prior, mode at supposed value

tmp <- 22    ### ess
a <- 1+ lam.tld*(tmp-2)
b <- tmp-a

lam.bar <- a/(a+b)    ### prior mean
```

## Theoretical RAMSE values

Note: hard-wired for *Dirichlet*(1,1,1,1) distribution on cell probs, prior model weights (1/3,1/3,1/3).

```
sg2 <- lam.bar*(1-lam.bar)/(a+b+1)

rmse <- matrix(NA,2,2)

rmse[1,1] <- sqrt(sg2)

rmse[1,2] <- sqrt(sg2 + .25*(lam.bar-lam.tld)^2)

rmse[2,1] <- sqrt((1/3)*sg2 + (1/3)*(lam.bar-lam.tld)^2)

rmse[2,2] <- sqrt((1/3)*sg2 + (.5/3)*(lam.bar-lam.tld)^2)

rmse <-rmse*sqrt(1/3)    ### var( v(phi)) term

round(rmse,4)
```

```
##      [,1] [,2]
## [1,] 0.0464 0.0473
## [2,] 0.0288 0.0278
```

Not strictly necessary, but check that we can get the same answer by simulation

```
### nature generates from M0

phi0.tr <- rdirichlet(10000, rep(1,4))
phi1.tr <- rdirichlet(10000, rep(1,4))
```

```

lam.tr <- rbeta(10000, a, b)

dfun <- function(pr) {
  pr[4]/(pr[2]+pr[4]) - pr[3]/(pr[1]+pr[3])
}

d0.tr <- apply(phi0.tr, 1, dfun)
d1.tr <- apply(phi1.tr, 1, dfun)

mse.0.0 <- mean((lam.bar-lam.tr)^2*(d1.tr-d0.tr)^2)

### nature generates from M1
mse.1.0 <- (lam.bar-lam.tld)^2*mean((d1.tr-d0.tr)^2)

### nature generates from M2
mse.2.0 <- 0 ### check

### nature generates from M0
mse.0.mix <- mean((.5*lam.bar+.5*lam.tld-lam.tr)^2*(d1.tr-d0.tr)^2)

### nature generates from M1
mse.1.mix <- (.5*lam.bar-.5*lam.tld)^2*mean((d1.tr-d0.tr)^2)

### nature generates from M2
mse.2.mix <- 0

## RMSE table of interest
rmse <- matrix(NA,2,2)

rmse[1,] <- sqrt(c(mse.0.0, mse.0.mix))

rmse[2,1] <- sqrt((mse.0.0+mse.1.0+mse.2.0)/3)

rmse[2,2] <- sqrt((mse.0.mix+mse.1.mix+mse.2.mix)/3)

round(rmse, 4)

##      [,1]    [,2]
## [1,] 0.0458 0.0465
## [2,] 0.0284 0.0274

```

““