

Key4

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2024-06-03

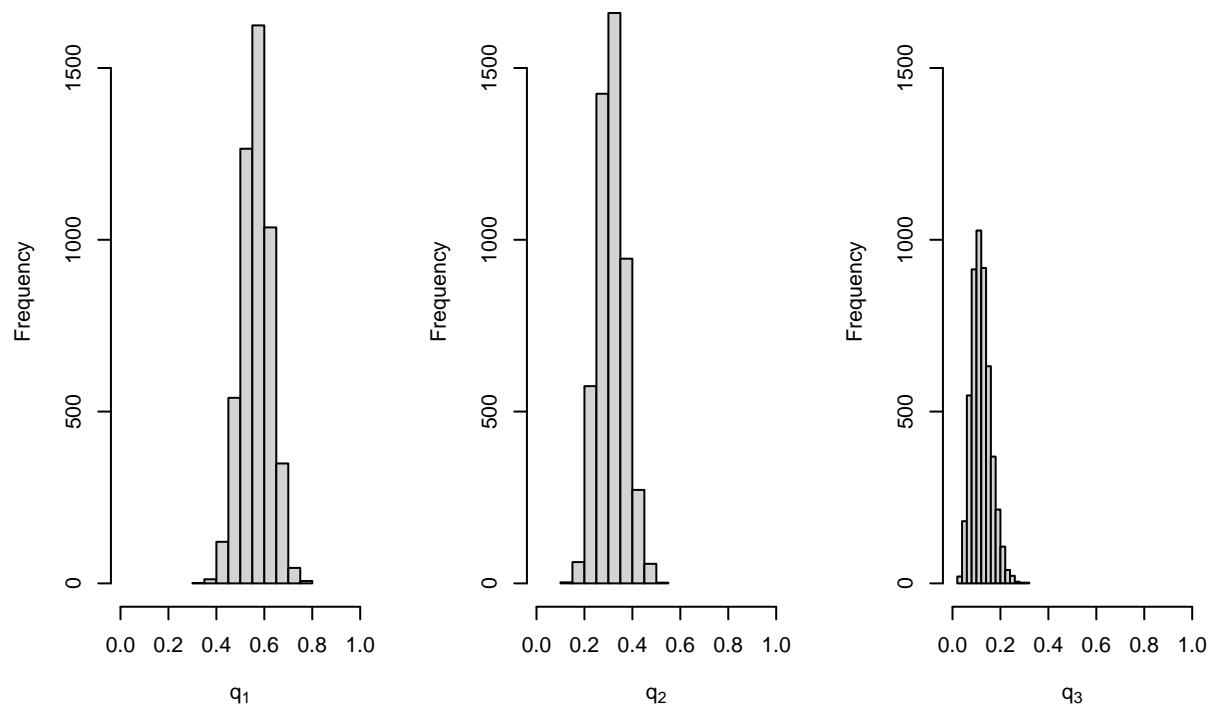
Exercise 4 – Key

- Repeat the analyses in these notes for the Lidicker et al data discussed in class, ie with $n_1 = 37$, $n_2 = 20$, $n_3 = 7$. In particular,
- With a $Dirichlet(1,1,1)$ prior on the 3 probabilities, generate samples, and examine the various summaries, including marginal allele frequencies and the inbreeding coefficient f

Most of the work is done with code supplied in the example, changing the data to that specified here:

```
library("DirichletReg")
set.seed(4)
post.sample <- as.data.frame( rdirichlet(5000,c(37+1,20+1,7+1)) )
names(post.sample) <- c("q1","q2","q3")

par(mfrow=c(1,3))
with(post.sample, hist(q1,xlab=expression(q[1]),main="",xlim=c(0,1), ylim=c(0,1700)))
with(post.sample, hist(q2,xlab=expression(q[2]),main="",xlim=c(0,1), ylim=c(0,1700)))
with(post.sample, hist(q3,xlab=expression(q[3]),main="",xlim=c(0,1), ylim=c(0,1700)))
```



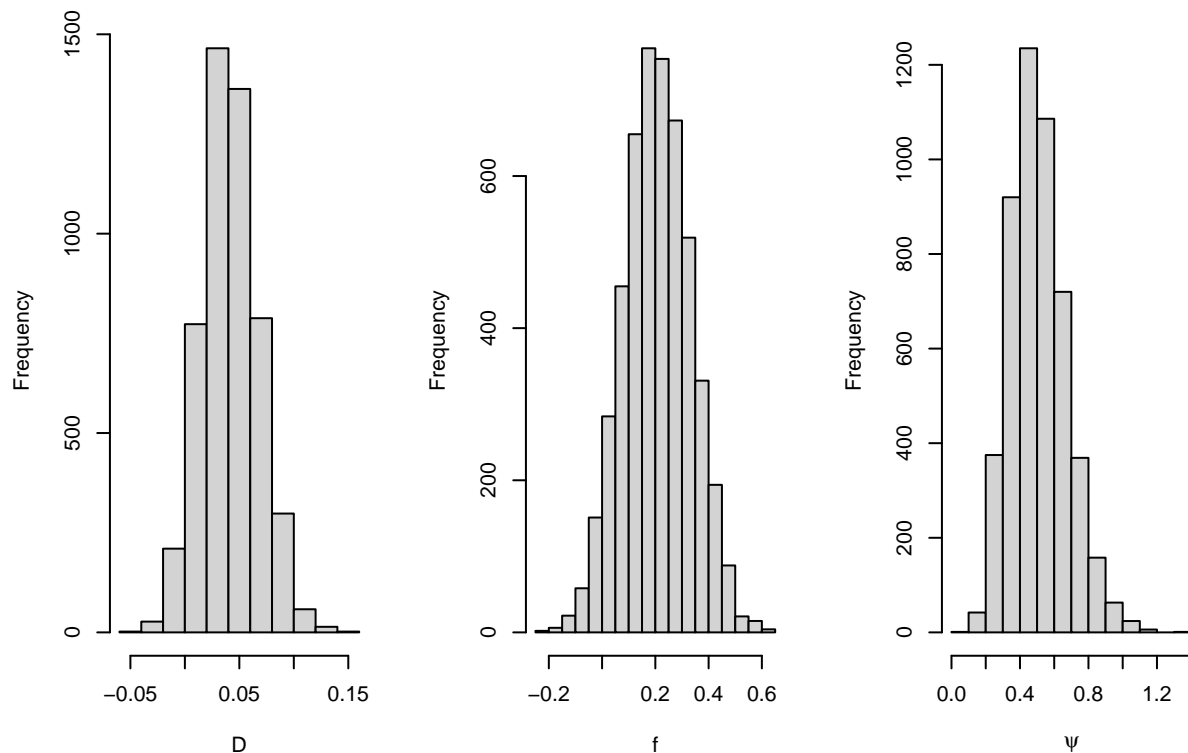
For the assessment of the posterior on functions of parameters:

```

post.sample$p1 <- with(post.sample, q1 + 0.5*q2)
post.sample$p2 <- with(post.sample, 0.5*q2 + q3)
post.sample$D <- with(post.sample, q1 - p1^2)
post.sample$f <- with(post.sample, (q1 - p1^2)/p1/p2)
post.sample$psi <- with(post.sample, q2^2/(p1 * p2))

par(mfrow=c(1,3))
with(post.sample, hist(D,xlab=expression(D),main=""))
with(post.sample, hist(f,xlab=expression(f),main=""))
with(post.sample, hist(psi,xlab=expression(psi),main=""))

```



- Download and install the INLA package from the website in the course notes. Run the LHON example using the commands from the slides. If you get this to work, repeat the Session 3 exercise switching the informative prior from β_1 to β_0 .

See course sites for special instructions getting INLA to work.

```
library("INLA")
# setup data
cc.dat <- data.frame(x=c(0,1,2), success=c(6,8,75), fail=c(10,66,163))

# Informative prior on beta1
Upper975 <- 1.5
sigma <- log(Upper975)/qnorm(0.975)
cc.inla1 <- inla(success~x,family="binomial",data=cc.dat,Ntrials=success+fail,
  control.fixed=list(mean.intercept=c(0),prec.intercept=c(1/10),
    mean=c(0),prec=c(1/sigma^2)),
  control.compute = list(config = TRUE))

#Switch around to informative on beta0
cc.inla2 <- inla(success~x,family="binomial",data=cc.dat,Ntrials=success+fail,
  control.fixed=list(mean.intercept=c(0),prec.intercept=c(1/sigma^2),
    mean=c(0),prec=c(1/10)),
  control.compute = list(config = TRUE))
```

A quick way to visualize the difference: sample from the posteriors

```
set.seed(4)
post1 <- inla.posterior.sample(5000, cc.inla1)
post1a <- inla.posterior.sample.eval(c("Intercept", "x"), post1)
post2 <- inla.posterior.sample(5000, cc.inla2)
post2a <- inla.posterior.sample.eval(c("Intercept", "x"), post2)

par(mfrow=c(1,2))
plot(post1a[1,], post1a[2,], xlab=expression(beta[0]), ylab=expression(beta[0]), col="#0000FF20", pch=1)
plot(post2a[1,], post2a[2,], xlab=expression(beta[0]), ylab=expression(beta[0]), col="#0000FF20", pch=1)
```

