

# Specifying prey fat content distributions for Squid diet analysis

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May 6, 2014

```
library(knitr)
options(replace.assign = TRUE, width = 50)

Silverside <- 2.27
Silverside.sd <- 1.02

Sailfin.Molly <- 3.97
Sailfin.Molly.sd <- 1.25

Sheepshead.Minnow <- 3.59
Sheepshead.Minnow.sd <- 1.45

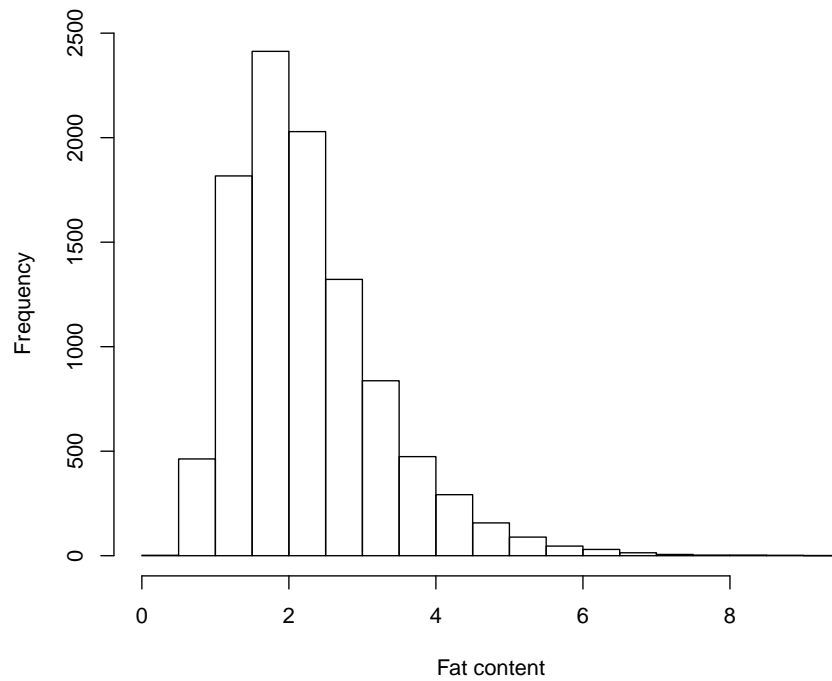
fish.means <- c(Silverside, Sailfin.Molly, Sheepshead.Minnow)

fish.vars <- c(Silverside.sd, Sailfin.Molly.sd, Sheepshead.Minnow.sd)^2
```

Assuming a log normal model for fat content - this is done internally in fastin-R, so the next bit is for illustrative purposes only..

```
fish.ln.vars <- log(fish.vars + fish.means^2) - 2 *
  log(fish.means)
fish.ln.means <- log(fish.means) - fish.ln.vars/2
```

```
hist(rlnorm(10000, meanlog = fish.ln.means[1], sdlog = sqrt(fish.ln.vars[1])),
     30, xlab = "Fat content", main = "")
```

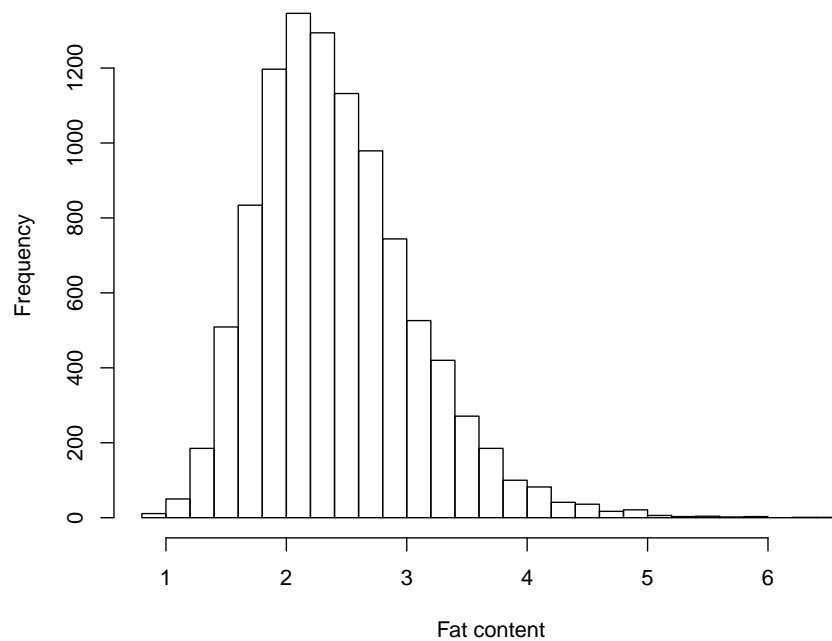


Doing the same for shrimp

```
shrimp.mean <- 2.43
shrimp.var <- 0.66^2

shrimp.ln.var <- log(shrimp.var + shrimp.mean^2) -
  2 * log(shrimp.mean)
shrimp.ln.mean <- log(shrimp.mean) - shrimp.ln.var/2

hist(rlnorm(10000, meanlog = shrimp.ln.mean, sdlog = sqrt(shrimp.ln.var)),
     30, xlab = "Fat content", main = "")
```



Write results to file:

```
fat.cont <- rbind(cbind(fish.ln.means, fish.ln.vars),
  c(shrimp.ln.mean, shrimp.ln.var))
colnames(fat.cont) <- NULL

# add prey names
prey.ix <- t(read.csv("Prey_FA.csv", header = F, stringsAsFactors = F,
  row.names = 1))[, 1]
mulletts <- which(prey.ix == "Striped Mullet")
prey.ix <- prey.ix[-mulletts]

rownames(fat.cont) <- unique(prey.ix)

write.table(fat.cont, file = "fat.cont.csv", col.names = F,
  sep = ",")
```