

# Solutions

## Coverage file upload and inspection

```
# d<-read.table('C:/Users/daniel/Documents/science/teaching/cesky
# krumlov
# 2016/course.materials/R.files/coverage.chrI.txt', h=T)
dim(d)

## [1] 415215      4

d[c(1:3, 415213:415215), ]

##      habitat individual position      sequence
## 1      stream      ind_A      1655 TGCATTTTATCTGAGTACTA
## 2      stream      ind_A      1655 TGCATTTTATCTGAGTACTA
## 3      stream      ind_A      1655 TGCATTTTATCTGAGTACTA
## 415213 lake      ind_D 28160288 TGCATGTTGAAATCCCCACC
## 415214 lake      ind_D 28160288 TGCATGTTGAAATCCCCACC
## 415215 lake      ind_D 28160288 TGCATGTTGAAATCCCCACC
```

Identify the unique RAD loci, and calculate the proportion of stream reads at each locus by using a loop

```
uloci <- unique(d$position) # the unique RAD locus positions
uloci[1:6]

## [1] 1655 27508 50938 79760 97931 110275

cov <- NULL # empty data container
for (i in 1:length(uloci)) {
  loc <- d[which(d$position == uloci[i]), 1]
  Nstr <- length(which(loc == "stream"))
  cov <- c(cov, Nstr/length(loc))
}
cov[1:6]

## [1] 0.526 0.407 0.349 0.360 0.425 0.451
```

Draw a dot plot of coverage, and add the LOESS profile

```
plot(uloci, cov, cex = 0.5)  
smo <- predict(loess(cov ~ uloci, span = 0.02, degree = 0))  
lines(uloci, smo, col = "blue", lwd = 2)
```

