Data Break 1: Myrtle Trees

August 28, 2019

What do we have?

- Event locations for a strand of 327 myrtle trees in a rectangular plot 170.5×213.0 meters.
- 221 healthy trees.
- 106 diseased trees.
- Research question: Is the spatial pattern of diseased trees the same as the spatial pattern of health trees?
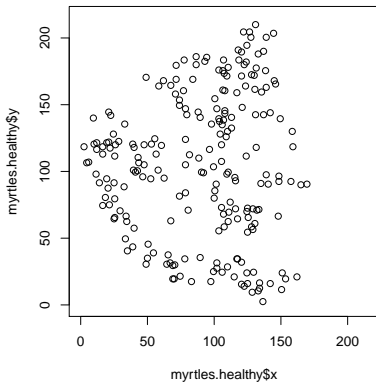
Reading in data

```
path <- "c:/classes/spatial.class/"

myrtles.healthy <-
scan(paste(path,"myrtles.healthy.d",sep=""),
    list(x=0,y=0))
```
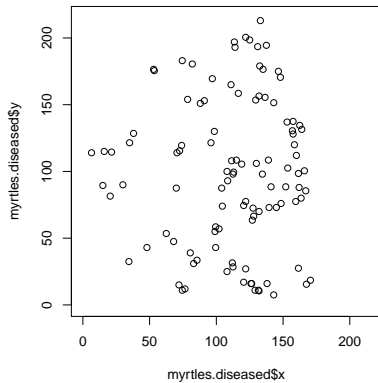
Plotting the data

```
par(pty="s", mfrow=c(1,2))
plot(myrtles.healthy$x, myrtles.healthy$y,
     xlim=c(0,215), ylim=c(0,215))
title("Healthy")
plot(myrtles.diseased$x, myrtles.diseased$y,
     xlim=c(0,215), ylim=c(0,215))
title("Diseased")
```

Plot

Testing CSR

- Consider test statistic by Pielou (1959)
- Test statistic $P = \pi\lambda \sum X_i^2 / n$
- X_i = distance from event i to its nearest neighbor
- Pielou (1959) suggests $P \overset{a}{\sim} N(1, 1/n)$.
  methodsblog.com/2017/03/10/ec-pielou/
- Let's try a Monte Carlo test.

Finding the nearest neighbor distances

For first event location:

```
dist1 <- sqrt(
  (myrtles.all$x[1] - myrtles.all$x)^2 +
  (myrtles.all$y[1] - myrtles.all$y)^2
  )
```

Now find minimum distance (that is not zero!)

```
min(dist1[dist1!=0])
```

Looping to find all NN distances

```
mindist.all <- 0*(1:length(myrtles.all$x))

for (i in 1:length(myrtles.all$x)) {
  dist <- sqrt(
    (myrtles.all$x[i] - myrtles.all$x)^2 +
    (myrtles.all$y[i] - myrtles.all$y)^2 )

    mindist.all[i] <- min(dist[dist!=0])
}
```

Calculating P

```
n.all <- length(myrtles.all$x)

area.all <-
  (max(myrtles.all$x)-min(myrtles.all$x))*
  (max(myrtles.all$y)-min(myrtles.all$y))

lambda.all <- n.all/area.all

pielou.all <- pi*lambda.all*
              sum(mindist.all^2)/n.all
```

We observe $P = 0.6568$ for all myrtles.

Is P significant?

- p-value based on $N(1, 1/n) = 0.9999$
- How would we do a Monte Carlo test?
- Same calculations, use CSR values *inside the same study area*.

Coding a Monte Carlo test

```
num.sim <- 99
pielou.all.sim <- 0*(1:num.sim)

for (sim in 1:num.sim) {
  # define CSR data

  #define vector of min NN distances

  # find min distances
  # (a loop within the simulation loop)

  # calculate pielou.all.sim[sim]
  #(Pielou's statistic for the
  # "sim-th" CSR data set).
}
```
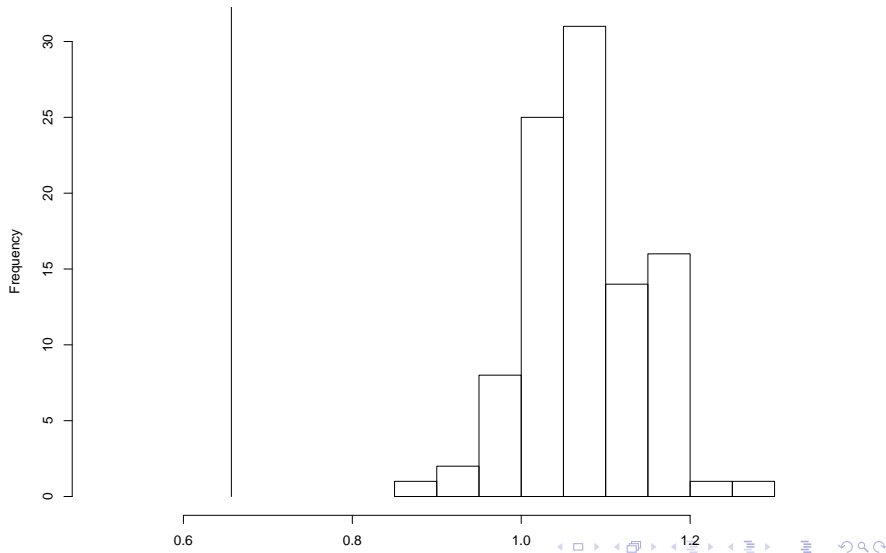
Results

Make histogram of Monte Carlo values and indicate observed value
from data.

```
par(pty="m")
hist(pielou.all.sim,
     xlim=c(0.5,max(pielou.all.sim)),
     freq=F)

test <- (0:200)/100
lines(test,dnorm(test,mean=1,
        sd=sqrt(1/n.all)))

segments(pielou.all,0,pielou.all,100)
```

Plot

Histogram of pielou.all.sim

```
p.val <-
length(pielou.all.sim[pielou.all.sim>pielou.all])/
  (num.sim+1)
```