

hw6R.R

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```
set.seed(121)
N <- 1000
NN <- c(1:N)
ts <- c(1:5000)
x1 <- matrix(0,length(ts),length(NN))
x2 <- matrix(0,length(ts),length(NN))
phi <- matrix(0,length(ts),length(NN))
phizc <- rep(0,length(ts))
z <- rep(0,N)
d <- rep(0,N)
for (i in ts){
  myts <- ts(rnorm(N))
  for (j in NN){
    x1[i,j] <- ifelse(z[j]>=0,1,0)
    z[j] <- 0.8*z[j] + rnorm(1)
    x2[i,j] <- ifelse(z[j]>=0,1,0)
    d[j] <- d[j] + (x2[i,j]-x1[i,j])^2
    phi[i,j] <- cos(3.14159*d[j]/999)
    if (j == N){
      phizc[i] <- phi[i,N]
    }
  }
}
Reg <- lm(formula = phizc ~ phi[,1])
summary(Reg)
```

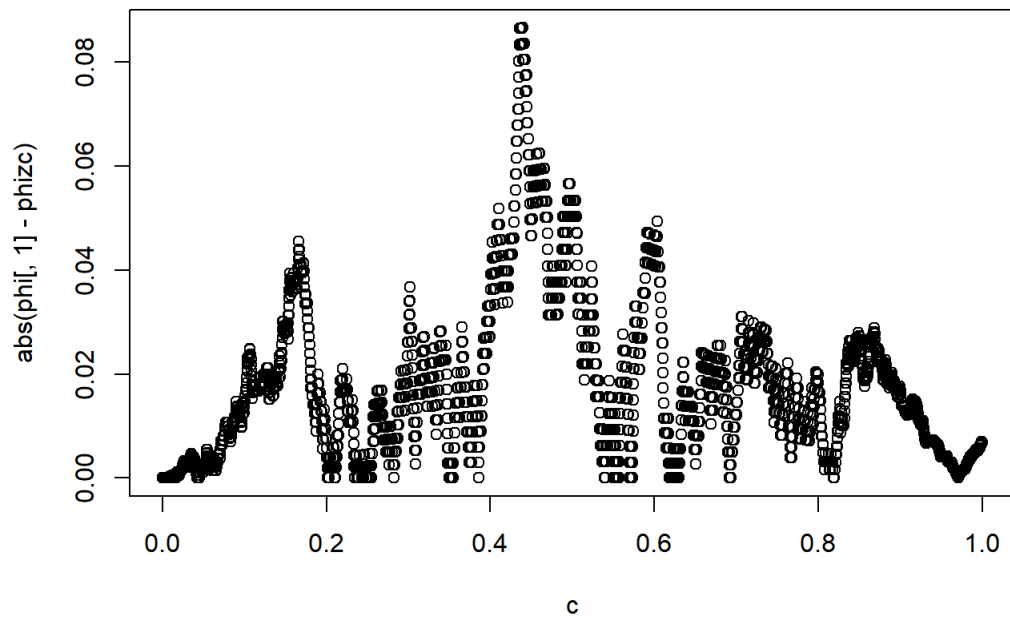
```
##
## Call:
## lm(formula = phizc ~ phi[, 1])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.061180 -0.011878 -0.000299  0.010469  0.075776
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0111330  0.0002994   37.18  <2e-16 ***
## phi[, 1]    0.9979654  0.0004176 2389.63  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02115 on 4998 degrees of freedom
## Multiple R-squared:  0.9991, Adjusted R-squared:  0.9991
## F-statistic: 5.71e+06 on 1 and 4998 DF,  p-value: < 2.2e-16
```

```
c <-seq(0,1,1/(5000-1))
length(c)
```

```
## [1] 5000
```

```
plot(c,abs(phi[,1]-phizc),main = "Absolute difference between the values of phi and phizc")
```

Absolute difference between the values of phi and phizc



```
#We used the 1st column, but we can use any; we observe that as c goes to 1, their difference goes to 0 and this is true
#for every column.
```