

BIOS6621-Homework7

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```
library(pwr)
ZincDose <- read.csv("C:/Users/Goodgolden5/Desktop/BIOS6621-Gary
Grunwald/Week11/ZincDose.txt", sep="")
ZincSD2<- sd(ZincDose$X2mg); ZincSD2

## [1] 0.3500204          Fine, 1.5/1.5

findN <- function(diff, sd, alpha, power){
  N <- 2*sd^2*(qnorm(power)+qnorm(1-alpha/2))^2/diff^2
  N
}
ceiling(findN(0.6, ZincSD2, 0.05, 0.90))

## [1] 8          Right, 1.5/1.5

find.n <- pwr.t.test( d=0.6, sig.level=0.05, power=0.9, type= "one.sample", alternative="two.sided");
ceiling(find.n$n)

## [1] 32          A couple errors here: 1) There's a trick with this software, notice you never put the SE

find.N <- power.t.test( power=0.9, sig.level= 0.05, delta=0.6, type="one.sample",
alternative="two.sided")
ceiling(find.N$n)          Another tip-off is usually the N from T is a bit higher than from Z but not much,

## [1] 32
```

Sample Size estimate: The standard deviation for ingested zinc of 2mg treatment was used as an estimate of within group variation, based on an assumption that $\sigma_1 = \sigma_2$ and $n_1 = n_2$. This value, obtained as the residual standard deviation from a regression analysis 0.350mg/D. Assuming an alpha level of 0.05 for a two-sided test comparing two groups, a sample size of 8 per group provides 90% power to detect a difference. 0.5/0.5

Statistical analysis: Primary outcomes are ingested zinc mg/D. Statistical analyses will be carried out using R. Repeated measures analysis of variance with between-subject factors of different level of zinc treatment with t-test. These methods provide valid handling of the occasional missing observations.

Sample size section is fine for yours though why not use 32 instead?