

# Stochastic Simulation and Power Analysis

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March 21, 2021

Biol 520C: Statistical modelling for biological data

1. Housekeeping
2. Stochastic Simulation and the Monte Carlo Method
3. Power Analysis
4. Power Analysis in Action
5. Pseudocode

# Housekeeping

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- I will also be spending some time on an overview of all the material we covered. If you want me to clarify anything in particular, let me know so I can schedule some time for it.
- We have an extra lecture at our disposal so I'm going to split the last round of talks up over three lectures so we can have more time for discussion (schedule is on canvas).



# Stochastic Simulation and the Monte Carlo Method

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In the past any of these types of projects would require sophisticated analyses but simulations make these accessible to a broader range of biologists (learning sim. methods is easier than learning high level math).





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Monte Carlo = Stochastic Simulation

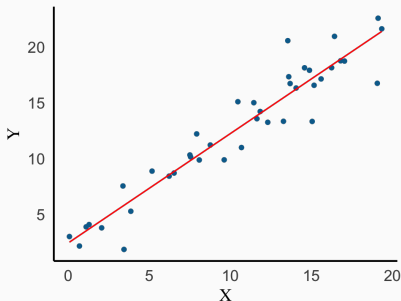


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Linear <- function(x) {  
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  B_1 <- 1  
  mu = B_0 + B_1*x  
  rnorm(n = length(x), mean = mu, sd = 2)}
```

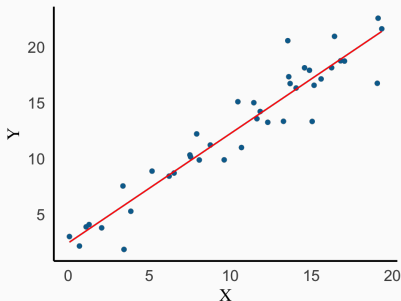
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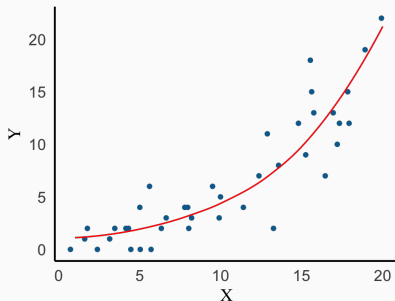
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X <- runif(40, 0, 20)  
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```
Counts <- function(x) {  
  B_0 <- 0.01  
  B_1 <- 0.15  
  eta = exp(B_0 + B_1*x)  
  rpois(n = length(x), lambda = eta)}
```

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X <- runif(40, 0, 20)  
Y <- Counts(X)
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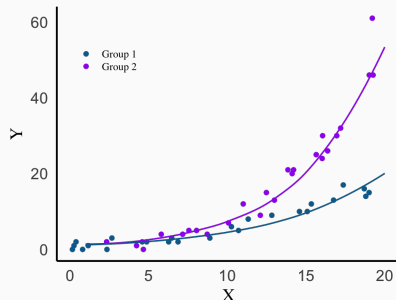
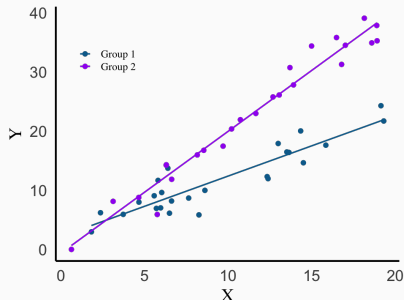
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Linear <- function(x) {  
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  mu = B_0[group] + B_1[group]*x  
  rnorm(n = length(x), mean = mu, sd = 2)}  
X <- runif(50, 0, 20)  
Y <- Linear(X)
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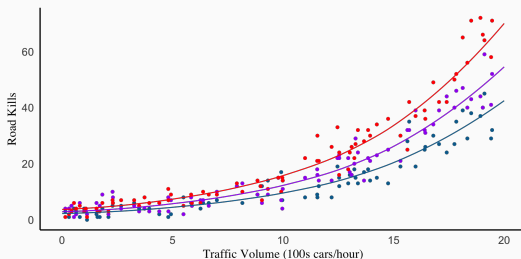
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```
Road_Kills <- function(x, x_2) {  
  B_0 <- 0.01  
  B_1 <- 0.15  
  B_2 <- 0.05  
  eta = exp(B_0 + B_1*x + B_2*x_2)  
  rpois(n = length(x), lambda = eta)}  
  
X <- runif(80, 0, 20)  
  
Deaths_15C <- Road_Kills(X, 15)  
Deaths_20C <- Road_Kills(X, 20)  
Deaths_25C <- Road_Kills(X, 25)
```







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POP <- as.vector(200)
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POP2 <- as.vector(200)
for(i in 1:200){
  Births <- rpois(1, 40)
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  RK_Deaths <- Road_Kills(2, 15)
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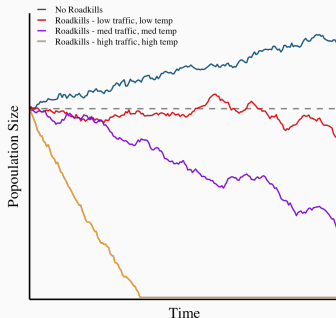
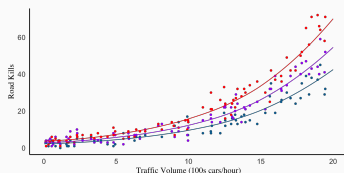
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Always approach simulation studies with care and make sure the computational system you put together matches the biological reality of the system you are trying to study.

# Power Analysis

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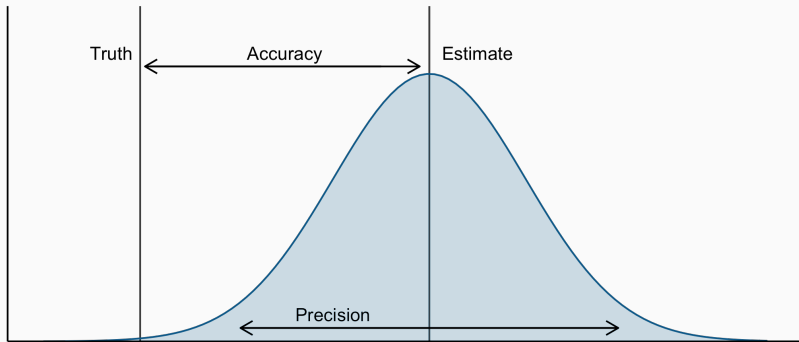
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Power analysis in our context involves a special kind of simulation study aimed at exploring how much data you would need in order to get reasonably accurate estimates of your parameters, detect significance of parameters with true effects, and/or detect differences between groups.

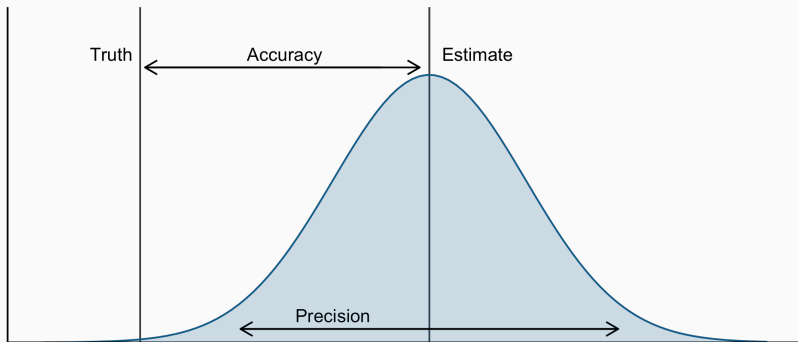


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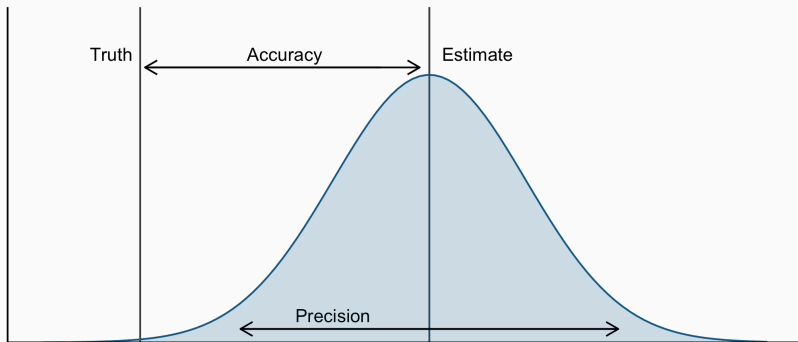
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Accuracy specifies how likely your answer is to be correct

Precision describes variability in the estimates.







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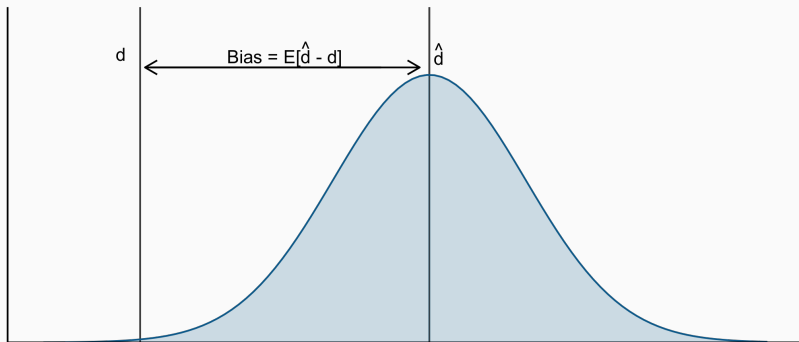
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5. Coverage (accuracy)
6. Power (precision)



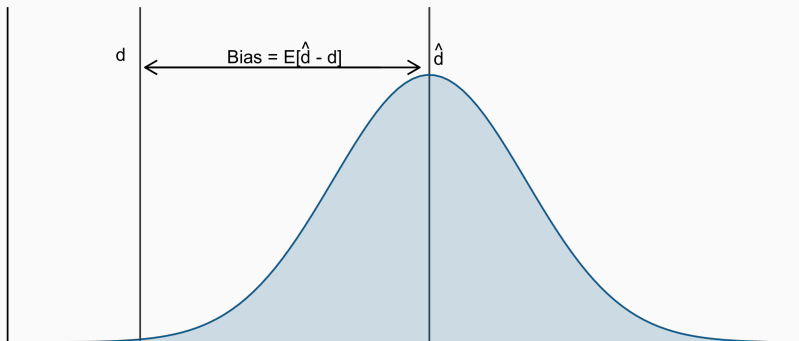


Bias is the expected difference between an estimate ( $\hat{d}$ ) of a parameter and its true value ( $d$ ).



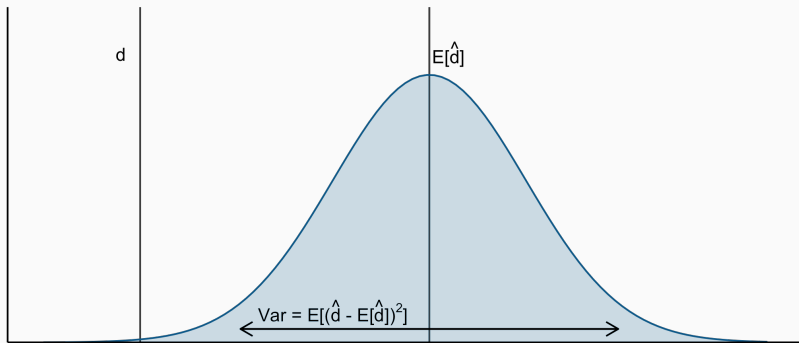
Bias is the expected difference between an estimate ( $\hat{d}$ ) of a parameter and its true value ( $d$ ).

Ideally estimators should be asymptotically unbiased (as  $n \rightarrow \infty$   $E[\hat{d} - d] \rightarrow 0$  )



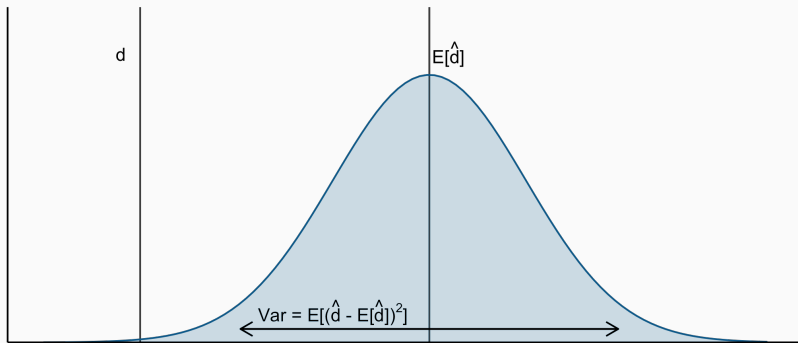


Variance measures the variability of individual estimates ( $\hat{d}$ ) around the mean estimate ( $E[\hat{d}]$ ).



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Low variance will give narrow CIs, large variance will give wide CIs

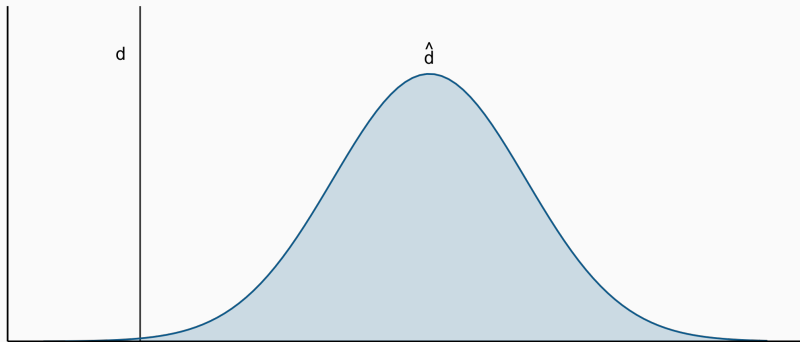


# MSE (accuracy & precision)



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Okanagan Campus

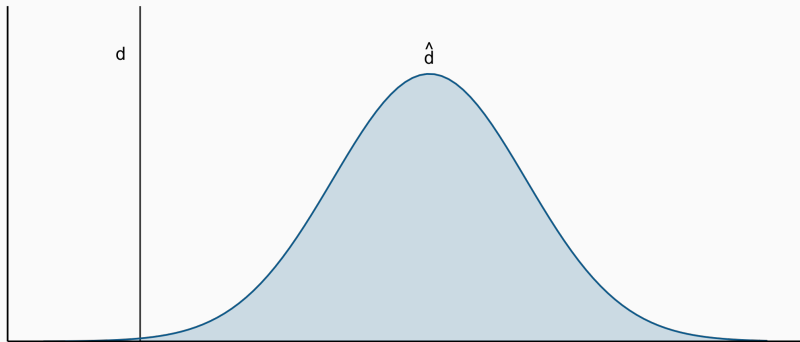
Mean squared error (MSE) is a measure that combines both accuracy and precision and is calculated as  $E[(\hat{d} - d)^2]$ .





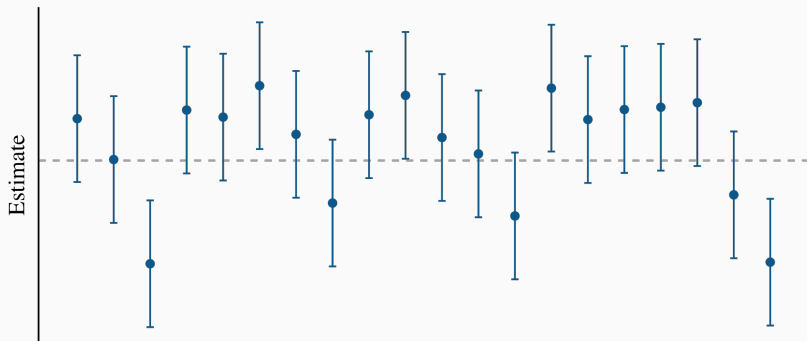
Mean squared error (MSE) is a measure that combines both accuracy and precision and is calculated as  $E[(\hat{d} - d)^2]$ .

It provides a measure of total variation around the truth.



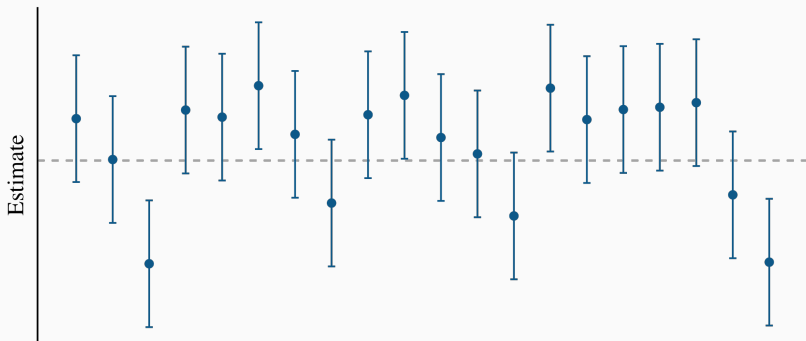


CI coverage described the accuracy of a set of confidence intervals.



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If 95% CIs are behaving like they should, they will include (cover) the truth 95% of the time.

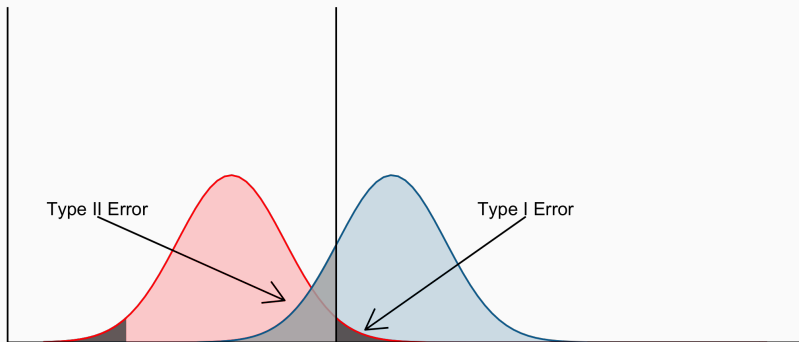




Type I ( $\alpha$ ) – False positive (i.e., observe an effect that isn't present).

Type II ( $\beta$ ) – False Negative (don't detect an effect that is present).

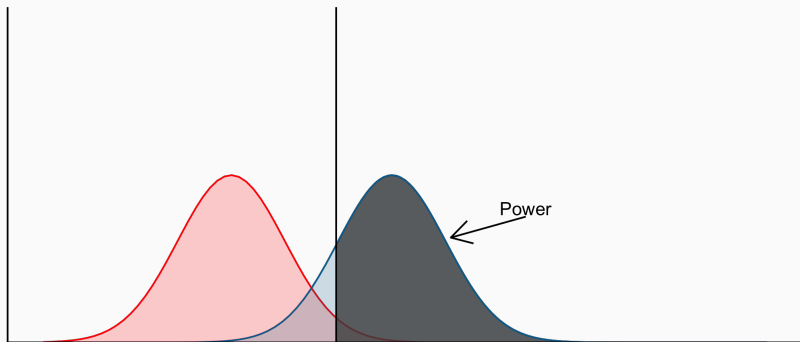
Statistical power ( $1-\beta$ ) – a measure of our ability to detect a real effect.



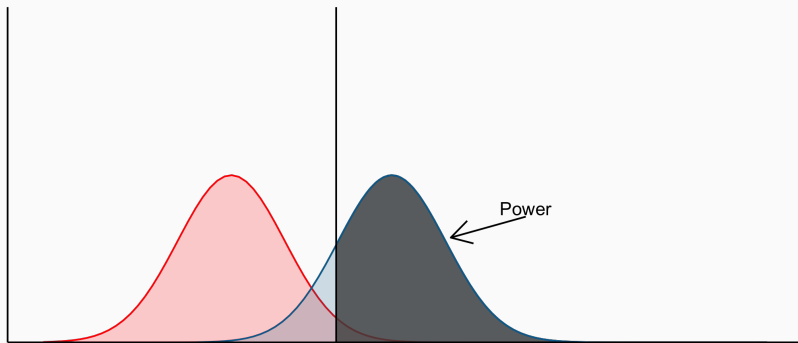
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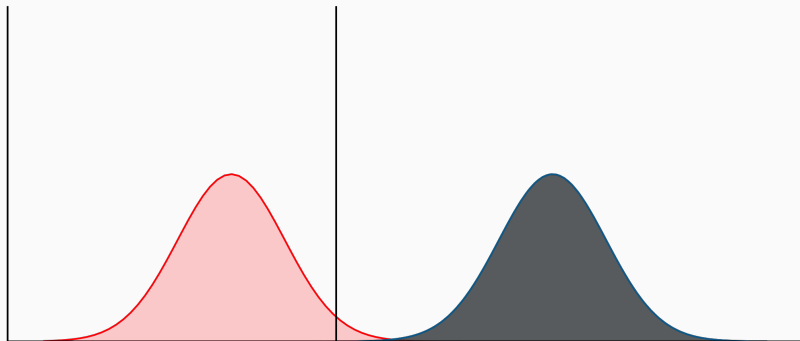
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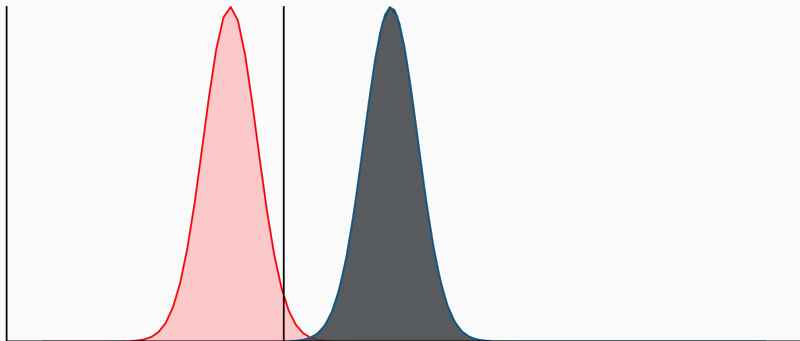


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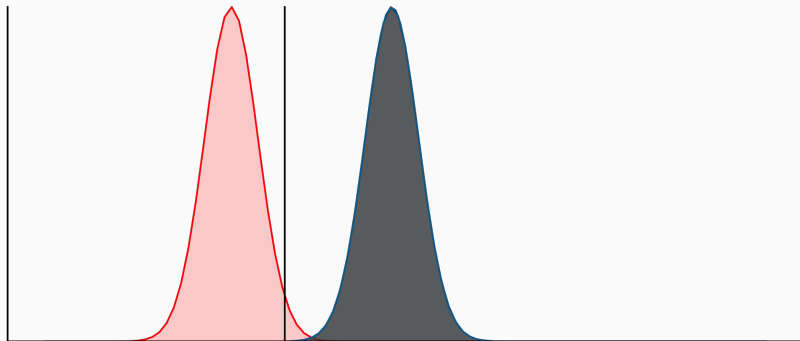
1) increase effect size



If we want to increase the power of a test there are two options:  
1) increase effect size; or 2) make the distributions narrower ( $\uparrow N$ )



Some experimental designs can change effects sizes but we usually don't have control over this, so we typically  $\uparrow$  sample sizes to  $\uparrow$  power.



# Power Analysis in Action

---



Let's estimate the statistical power of detecting a linear trend with a sample size of 20.

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Linear <- function(x) {  
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nSims <- 500
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nSims <- 500  
  
pval <- numeric(nSims)  
  
for(i in 1:nSims){  
  X <- runif(20, 0, 20)  
  Y <- Linear(X)  
  fit <- lm(Y ~ X)  
  pval[i] <- coef(summary(fit))["X", "Pr(>|t|)"]}
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sum(pval < 0.05)/nSims  
0.326
```

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We can code this using nested for loops.

```
nSims <- 500  
n <- seq(5,150,5)
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n <- seq(5,150,5)

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for(j in 1:length(n)){

  pval <- numeric(nSims)
  for(i in 1:nSims){
    X <- runif(n[j], 0, 20)
    Y <- Linear(X)
    fit <- lm(Y ~ X)
    pval[i] <-coef(summary(fit))["X", "Pr(>|t|)"]
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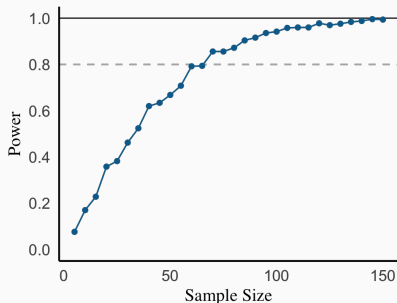
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```





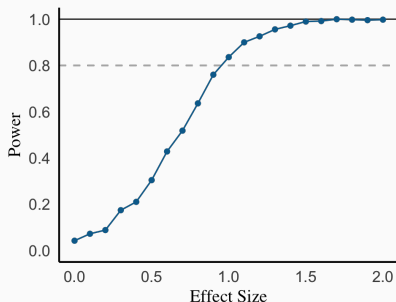
Let's say we knew our maximum sample size was 20, we could also estimate the smallest effect size (slope) we could reasonably detect.

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Linear <- function(x, B_1) {  
  B_0 <- 2  
  B_1 <- B_1  
  mu = B_0 + B_1*x  
  rnorm(n = length(x), mean = mu, sd = 8)}  
  
nSims <- 500  
B_1 <- seq(0,2,0.1)  
POWER <- numeric(length(B_1))  
  
for(j in 1:length(B_1)){  
  pval <- numeric(nSims)  
  for(i in 1:nSims){  
    X <- runif(20, 0, 20)  
    Y <- Linear(X, B_1[j])  
    fit <- lm(Y ~ X)  
    pval[i]<-coef(summary(fit))["X", "Pr(>|t|)"]  
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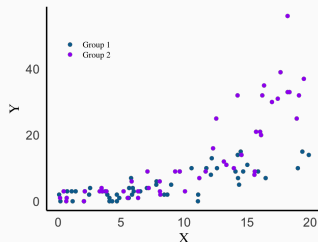
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  mu = B_0 + B_1*x  
  rnorm(n = length(x), mean = mu, sd = 8)}  
  
nSims <- 500  
B_1 <- seq(0,2,0.1)  
POWER <- numeric(length(B_1))  
  
for(j in 1:length(B_1)){  
  pval <- numeric(nSims)  
  for(i in 1:nSims){  
    X <- runif(20, 0, 20)  
    Y <- Linear(X, B_1[j])  
    fit <- lm(Y ~ X)  
    pval[i]<-coef(summary(fit))["X", "Pr(>|t|)"]  
  }  
  POWER[j] <- sum(pval < 0.05)/nSims  
}
```



We might also be interested in estimating our ability to detect differences between groups.

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```
Counts <- function(x,group) {  
  B_0 <- c(0.01, 0)  
  B_1 <- c(0.15, 0.2)  
  eta = exp(B_0[group] + B_1[group]*x)  
  rnbinom(n = length(x), mu = eta, size = 10)  
}  
  
nSims <- 500  
n <- seq(10,100,10)  
POWER <- numeric(length(n))  
  
for(j in 1:length(n)){  
  pval <- numeric(nSims)  
  for(i in 1:nSims){  
    X <- runif(n[j], 0, 20)  
    group <- factor(rep(1:2, each = n[j]/2))  
    Y <- Counts(X,group)  
    fit <- glm.nb(Y ~ X + group,link = "log")  
    pval[i] <- coef(summary(fit))["group2", "Pr  
      (>|z|)"]  
  }  
  POWER[j] <- sum(pval < 0.05)/nSims  
}
```

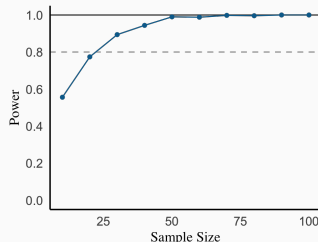
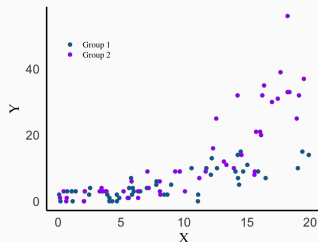


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Counts <- function(x,group) {
  B_0 <- c(0.01, 0)
  B_1 <- c(0.15, 0.2)
  eta = exp(B_0[group] + B_1[group]*x)
  rnbinom(n = length(x), mu = eta, size = 10)
}

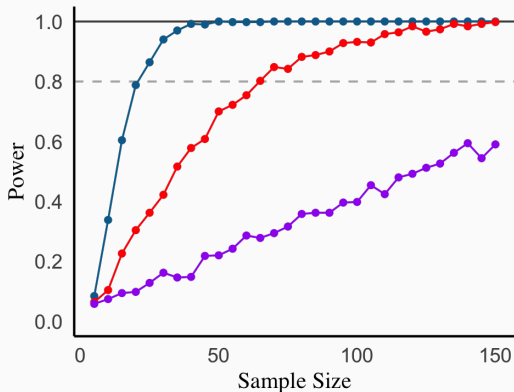
nSims <- 500
n <- seq(10,100,10)
POWER <- numeric(length(n))

for(j in 1:length(n)){
  pval <- numeric(nSims)
  for(i in 1:nSims){
    X <- runif(n[j], 0, 20)
    group <- factor(rep(1:2, each = n[j]/2))
    Y <- Counts(X,group)
    fit <- glm.nb(Y ~ X + group,link = "log")
    pval[i] <- coef(summary(fit))["group2", "Pr
      (>|z|)"]
  }
  POWER[j] <- sum(pval < 0.05)/nSims
}
```





Regression models often contain multiple parameters with different effect sizes and we might be interested in knowing the power for different effects.



Blue:  $\beta_1 = 1$ ; Red:  $\beta_2 = 0.5$ ; Purple:  $\beta_3 = .01$



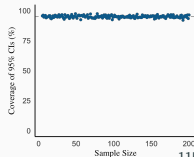
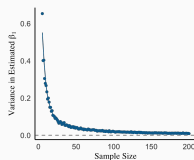
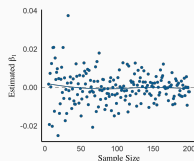
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```
Linear <- function(x) {
  B_0 <- 2
  B_1 <- 0.5
  mu = B_0 + B_1*x
  rnorm(n = length(x), mean = mu, sd = 8)}

nSims <- 500
n <- seq(5,200,1)
BIAS <- numeric(length(n))
VARIANCE <- numeric(length(n))
COVERAGE <- numeric(length(n))
for(j in 1:length(n)){
  bias <- numeric(nSims)
  coverage <- numeric(nSims)
  for(i in 1:nSims){
    X <- runif(n[j], 0, 20)
    Y <- Linear(X)
    fit <- lm(Y ~ X)
    bias[i] <- coef(fit)[2] - 0.5
    coverage[i] <- (0.5 <= confint(fit)[2,2] & 0.5 >= confint(fit)[2,1])
  }
  BIAS[j] <- mean(bias)
  VARIANCE[j] <- var(bias)
  COVERAGE[j] <- sum(coverage)/nSims
}
```



# Pseudocode

---



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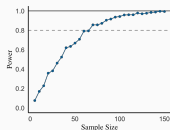
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A pseudocode can also be translated to another coding language more easily.



The pseudocode for estimating the statistical power of detecting a linear trend would look like this:



- 
1. Define  $\sigma$ ,  $\beta_0$ ,  $\beta_1$ , the # of sims, and the sample sizes to test.
  2. Build a function for simulating from simple linear model.
  3. Build a for loop that simulates data and fits models nSims times.
  4. Extract and store the p values from each iteration.
  5. Nest this in a for loop that iterates over the different sample sizes.
  6. Calculate the power for each sample size and store the results.
  7. Plot the results for interpretation.
-



Hilborn & Mangel (1997) is full of examples of pseudocode if you're interested in seeing what that looks like.



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Always remember that the more moving pieces a simulation setup has, the harder the outcomes can be to understand. Carefully tailored simulations are often more informative than complex simulations that we can't keep track of.

Simulations can also help us understand the statistical power of our data/model ... but good experimental design is more important than simulation based power analysis (don't overthink it).

## References

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Hilborn, R. & Mangel, M. (1997). *The ecological detective: confronting models with data*. vol. 28. Princeton University Press.

Bolker, B. M. (2008). *Ecological models and data in R*. Princeton University Press.