Case Study 1

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This code for the case study includes two sections. The first section explains how to simulate data that fits our needs. We aim to simulate population data where the population is declining, but the p-value remains greater than 0.05. The second section is on data visualization, comparing how the results differ when using Fisherian approaches and Bayesian approaches.

Data simulation

To simulate data that fits our needs, we use a simple linear function and add noise. We want the population data to exhibit either an increasing or decreasing trend, but some trends are not statistically significant (with a p-value greater than 0.05).

Function

Function to simulate a population with linear growth and noise:

```
simulate_population <- function(a, b, t, noise_sd) {
  y <- numeric(t)
  time <- 1:t
  y <- a*time + b + rnorm(t, 0, noise_sd)
    # y is the population of certain time
    # a is the increasing/decreasing rate
    # b is the starting population size
    # time is the x variable
    # noise_sd
  model <- lm(y ~ time)
  # Extract the estimated slope (coefficient of time)
  estimated_slope <- coef(model)["time"]
  pval <- coef(summary(lm(y ~ time)))[["time", "Pr(>|t|)"]]
  return(c(estimated_slope, pval))
}
```

Simulate population data

Simulate population data with different increasing and decreasing rates as well as different noises

```
t <- 10
a <- seq(from=-2000, to=2000, by=200)
b <- 100000
noise_sd <- seq(from=1000, to=10000, by=400)

dfout <- data.frame(givenslope=numeric(), noise=numeric(), estslope=numeric(),
                    pval=numeric())

for (i in 1:length(a)) {
  for (j in 1:length(noise_sd)){
    simpopout <- simulate_population(a[i], b, t, noise_sd[j])
    dfadd <- data.frame(givenslope=a[i], noise=noise_sd[j],
                        estslope=simpopout[1], pval=simpopout[2])
    dfout <- rbind(dfout, dfadd)
  }
}
```

Select populations

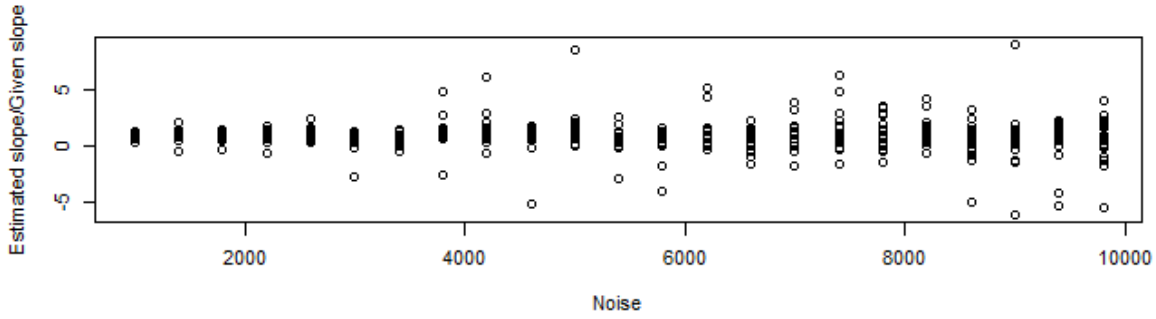
p-values

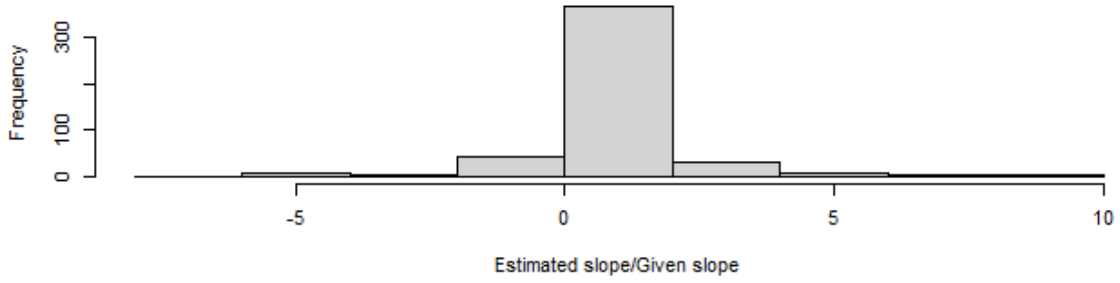
Set p-value thresholds to 0, 1, 2 where 0 is <0.05, 1 is 0.05 to 0.15 and 2 is > 0.15, and we are looking for 1 appears for both positive slope and negative slope, which means not statistically significant.

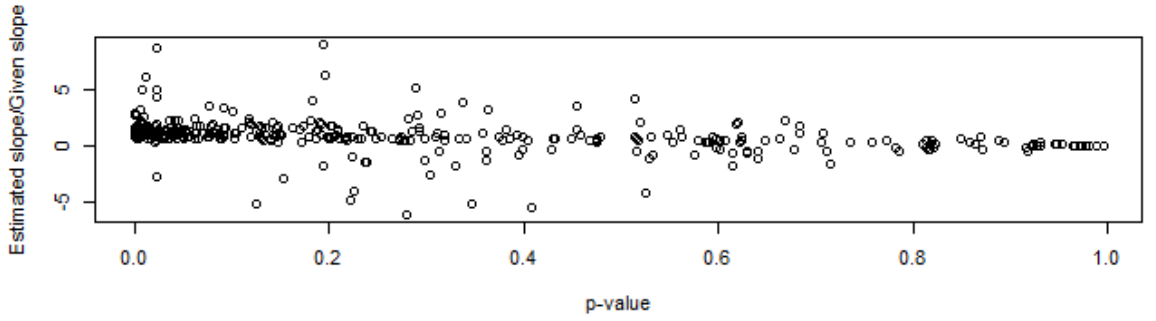
Visualization suggests that MAYBE noise of 7000-9000 could work

Estimated slopes

Which noise range can still give us similar estimated slopes close to given slopes







Visualization suggests that noise of 7000-9000 also fits.

Search for populations:

Semi-brute force search for cases were:

(1) All the estimated slopes are pretty close to given slopes and

(2) The bottom populations has a p-value between 0.05-0.15

```
a <- seq(from=-2000, to=2000, by=200)
a <- a[-c(5:17)]
# remove middle close-to-zero slopes, as though are hard to get pval low
noise_sd <- seq(from=7000, to=9000, by=400)
srhere <- 0.3

for(seedz in c(333:3999)){
  set.seed(seedz)
  for (j in 1:length(noise_sd)){
    dfout <- data.frame(noise=numeric(), sloperatio=numeric(), pval=numeric(),
                        smratio=numeric())
    for (i in 1:length(a)) {
      simpopout <- simulate_population(a[i], b, t, noise_sd[j])
      smratiohere  <- ifelse((abs(simpopout[1]/a[i])<(1+srhere)
                              & abs(simpopout[1]/a[i])>(1-srhere)), 0, 1)
      dfadd <- data.frame(noise=noise_sd[j], sloperatio=simpopout[1]/a[i],
                          pval=simpopout[2], smratio=smratiohere)
      dfout <- rbind(dfout, dfadd)
    }
      if(sum(dfout$smratio)==0 & dfout$pval[1]>0.05 & dfout$pval[1]<0.15){
    print(paste("try seed: ", seedz, "with noise of ", noise_sd[j]))
  }
  }
}
```

```
[1] "try seed:  423 with noise of  7000"
[1] "try seed:  1546 with noise of  7000"
[1] "try seed:  1869 with noise of  7800"
[1] "try seed:  2154 with noise of  7800"
[1] "try seed:  2954 with noise of  7800"
[1] "try seed:  3069 with noise of  7400"
[1] "try seed:  3201 with noise of  7400"
[1] "try seed:  3488 with noise of  8600"
[1] "try seed:  3545 with noise of  8600"
[1] "try seed:  3786 with noise of  8600"
```

We got seeds: 423, 1546, 1869, 2154, 2954, 3069, 3201, 3488, 3545 and 3786.

Try different seeds

After checking different seeds, we finally decided on seed 1546

```
      givenslope noise  estslope        pval
time       -2000  8600 -1708.306 0.146969632
time1      -1800  8200 -2121.081 0.031744531
time2      -1600  7800 -1494.864 0.190847601
time3      -1400  7400 -1330.010 0.164436645
time4       1400  7000  1499.433 0.035391410
time5       1600  6600  1260.549 0.116379852
time6       1800  6200  1600.972 0.005141529
time7       2000  5800  2212.688 0.004420759
```

We dropped the 2nd population with p-value smaller than 0.05.

Data analysis

The following code performs data analysis and visualization using both the traditional Fisherian approach and the Bayesian approach. For the Fisherian approach, we use an `lm` model and plot the p-values for different populations, indicating whether the increase or decrease is statistically significant. For the Bayesian approach, we use Stan code with priors and plot the posterior distribution.

```r
# Decided to run with 1546
set.seed(1546)
# Dropping -1600, 1600
a <- c(-2000, -1600, -1400,  600, 1400 , 1600,  2000)
t <- 10
time <- 1:t
b <- seq(40000, 101000, by=10000)
noise_sd <- c(7000, 6600, 6200, 5800, 5400, 5000,4600)
```

Traditional Fisherian approach

With traditional Fisherian approach, we use lm model to plot

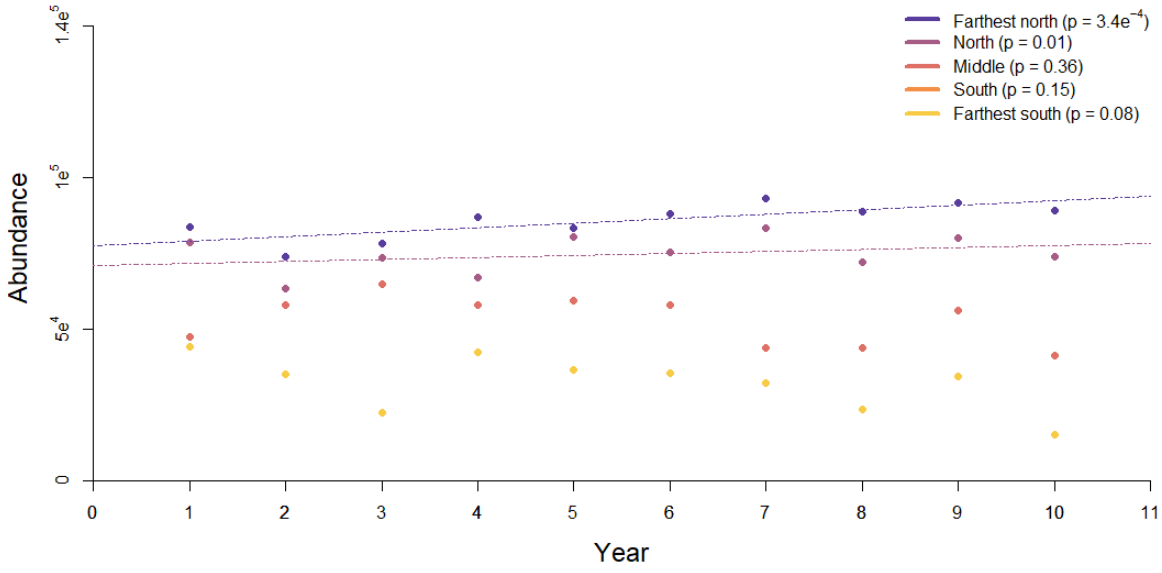
```r
output <- data.frame(iter = seq(1:(length(a)*length(time))),
                     pop = rep(1:length(a), each = length(time)),
                     year = rep(1:t, times = length(a)))
output$pred <- NA

abund <- vector()
for(i in 1:length(a)){
```

```
  y <- numeric(t)
  time <- 1:t
  y <- a[i]*time + b[i] + rnorm(t, 0, noise_sd[i])
  abund <- rbind(abund, y)
}

abund <- data.frame(reshape2::melt(t(abund)))
output$pred <- abund$value
```

Visualization



Bayesian approach

With Bayesian approach, we run the stan code:

```
data {
  int<lower=0> N; //No. obs
  int<lower=0> Ngrp; //No. in group---population or species
  int group[N]; // Group type
```

```
  vector[N] year;
  real ypred[N]; //response
}

parameters {
  real a[Ngrp] ;
  real b[Ngrp];
  real mu_a;
  real<lower=0> sigma_a;
  real mu_b;
  real<lower=0> sigma_b;
  real<lower=0> sigma_y;

}

model {

real mu_y[N];

for(i in 1:N){
     mu_y[i]=a[group[i]]+b[group[i]]*year[i];
  }

a ~ normal(mu_a, sigma_a);
b ~ normal(mu_b, sigma_b);

    //Priors
mu_a ~normal(188, 50);
sigma_a ~normal(0,50);
mu_b ~normal(0,10); //could also be centred at zero, 10
sigma_b ~normal(0,10); //sigma_b 0,10
sigma_y ~normal(0,10);

ypred ~ normal(mu_y, sigma_y);
}
```

```
'data.frame':   50 obs. of  4 variables:
 $ iter: int  1 2 3 4 5 6 7 8 9 10 ...
 $ pop : int  1 1 1 1 1 1 1 1 1 1 ...
 $ year: int  1 2 3 4 5 6 7 8 9 10 ...
 $ pred: num  43951 34961 22390 42250 36469 ...
```

```
mdlPop <- stan("partialPoolSimMdl.stan",
               data = datalistGrp)

sum <- summary(mdlPop)$summary

intercept <- sum[grep("a\\[", rownames(sum)), "mean"]
slopes <- sum[grep("b\\[", rownames(sum)), "mean"]

# Posterior distribution
post <- rstan::extract(mdlPop)
```

Visualization