Case Study 1

This case study was developed primarily by E.Wolkovich, D.Loughnan and X.Wang with the input of the full manuscript author team.

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).

Simulate population data

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

```
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)
```

```r
  estimated_slope <- coef(model)["time"]
  pval <- coef(summary(lm(y ~ time)))[["time", "Pr(>|t|)"]]
  return(c(estimated_slope, pval))
}
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

Search for populations:

We want to 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

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
```

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.

```
# Decided to run with 1546
set.seed(1546)
# Dropping -1600, 1600 with p-value smaller than 0.05.
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

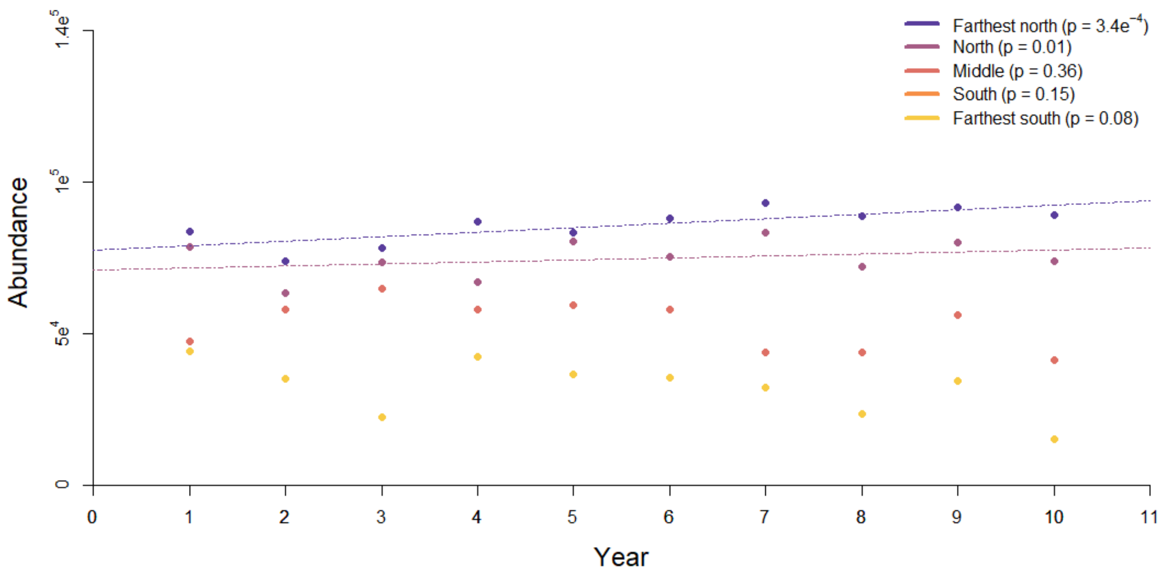
With traditional Fisherian approach, we use lm model to plot

```
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