Extinction risk from climate change: factor interactions

June 4th, 2024

Load libraries and data

```r
rm(list = ls())
 root.dir = "C:/Users/mcu08001/Documents/1New Research/CC MetaRisk2/Analysis"

 # load libraries
library(coda); library(ggplot2); library(dplyr); library(ggpubr);
library(tidytext);

 # load data
data<-read.table("MetaRisk2 aggthres 5.txt",header=T);

# Combine CCVA and Expert because expert has very few studies and is similar
to CCVA
data$Model.Type[data$Model.Type == "Expert"] = "Expert.CCVA"
data$Model.Type[data$Model.Type == "CCVA"] = "Expert.CCVA"

 # List of all study names
study.names <- unique(data$Study)
```

Functions

```r
# create function to sample full dataset n times without replacement
factor.n <- function(data) {

  # Calculate factors of interest - removed those that are not different from
median
  factor.p <- data.frame("Asia" = length(unique(data$Study[data$Region ==
"Asia"])))
  factor.p$AustraliaNewZealand <- length(unique(data$Study[data$Region ==
"AustraliaNewZealand"]))
  factor.p$SouthAmerica <- length(unique(data$Study[data$Region ==
"Samerica"]))
  factor.p$Amphibians <- length(unique(data$Study[data$Taxa ==
"Amphibians"]))
  factor.p$Birds <- length(unique(data$Study[data$Taxa == "Birds"]))
  factor.p$NorthTemperate <- length(unique(data$Study[data$N.Middle == "Y"]))
  factor.p$Arctic <- length(unique(data$Study[data$Arctic == "Y"]))
  factor.p$Mountain <- length(unique(data$Study[data$Mtn == "Y"]))
  factor.p$Freshwater <- length(unique(data$Study[data$Fresh == "Y"]))
```

```r
  factor.p$Island <- length(unique(data$Study[data$Island == "Y"]))
  factor.p$Threatened <- length(unique(data$Study[data$Threatened == "Y"]))
  factor.p$Endemic <- length(unique(data$Study[data$Endemic == "Y"]))
  factor.p$Expert.CCVA <- length(unique(data$Study[data$Model.Type ==
"Expert.CCVA"]))
  factor.p$Mechanistic <- length(unique(data$Study[data$Model.Type ==
"Mechanistic"]))
  factor.p$SAR <- length(unique(data$Study[data$Model.Type == "SAR"]))
  factor.p$SpeciesInteractions <- length(unique(data$Study[data$Sp.int ==
"Y"]))
  factor.p$Demography <- length(unique(data$Study[data$Demography.LH ==
"Y"]))
  factor.p$None <- length(unique(data$Study[data$Disp.Mod == "None"]))
  factor.p$Universal <- length(unique(data$Study[data$Disp.Mod ==
"Universal"]))
  factor.p$TemperatureRise <- mean(data$Pre.Ind.Rise, na.rm = T)


 return(factor.p)
 #return(data.sub)
}
```

Test interactions

```r
# create function to sample full dataset n times without replacement
sample.studies <- function(data, n.s, t) {

  # Initialize a list to store the sampled data frames
  sampled_data_list <- data.frame(matrix(NA, nrow = t, ncol = 20))

    for (i in 1:t) {
    # Sample n unique values without replacement    sampled.values <-
sample(study.names, 5)
    sampled.values <- sample(study.names,n.s)
    # Filter the original data frame to include only rows with the sampled
unique values
    sampled.data <- data[data[["Study"]] %in% sampled.values, ]
    # Sample using factor.n function for all factors of interest
    factor.sample <- factor.n(sampled.data)
    #Add to list
    sampled_data_list[i,] <- factor.sample
  }

 return(sampled_data_list)
}
```

Test Amphibians

```r
# Subset data
data.sub <- data[data$Taxa == "Amphibians",]
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 2 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
```

```r
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Amphibians" &
res_transposed$Factors != "Birds",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on amphibian risk") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()

## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

fig
```
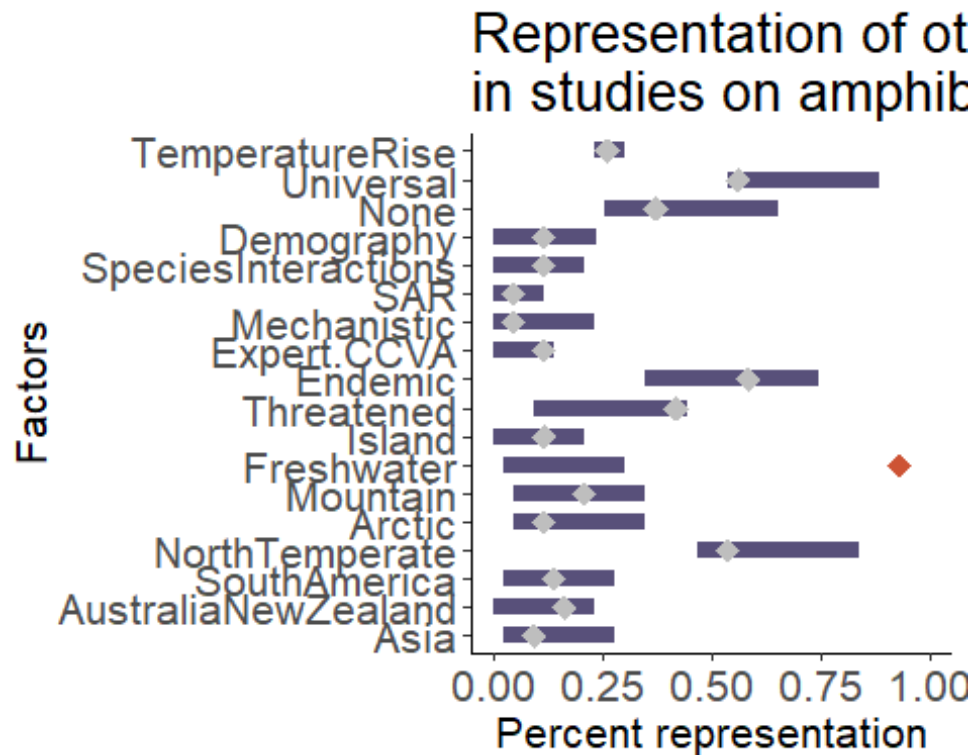
Representation of ot
in studies on amphib

```
ggsave("Amphibian factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Birds

```
# Subset data
data.sub <- data[data$Taxa == "Birds",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10
```

```r
#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 2 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Amphibians" &
res_transposed$Factors != "Birds",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on bird risk") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```
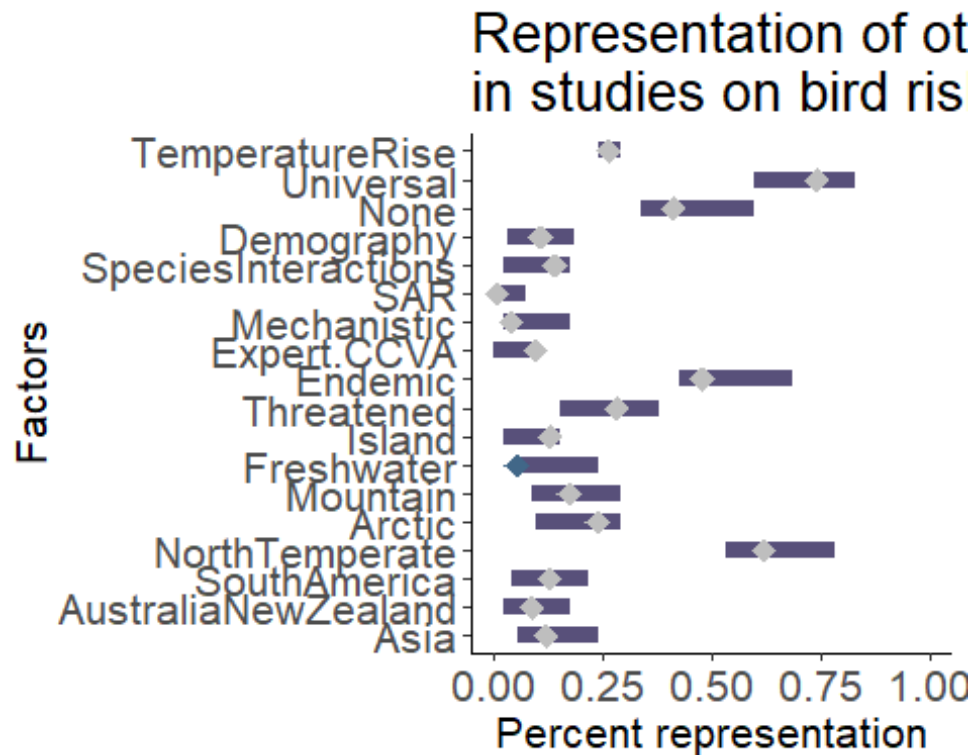
Representation of ot
in studies on bird ris

```
ggsave("Bird factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Asia

```
#subset data
data.sub <- data[data$Region == "Asia",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10
```

```r
#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 3 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Asia" &
res_transposed$Factors != "AustraliaNewZealand" & res_transposed$Factors !=
"SouthAmerica",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on Asian risk") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```
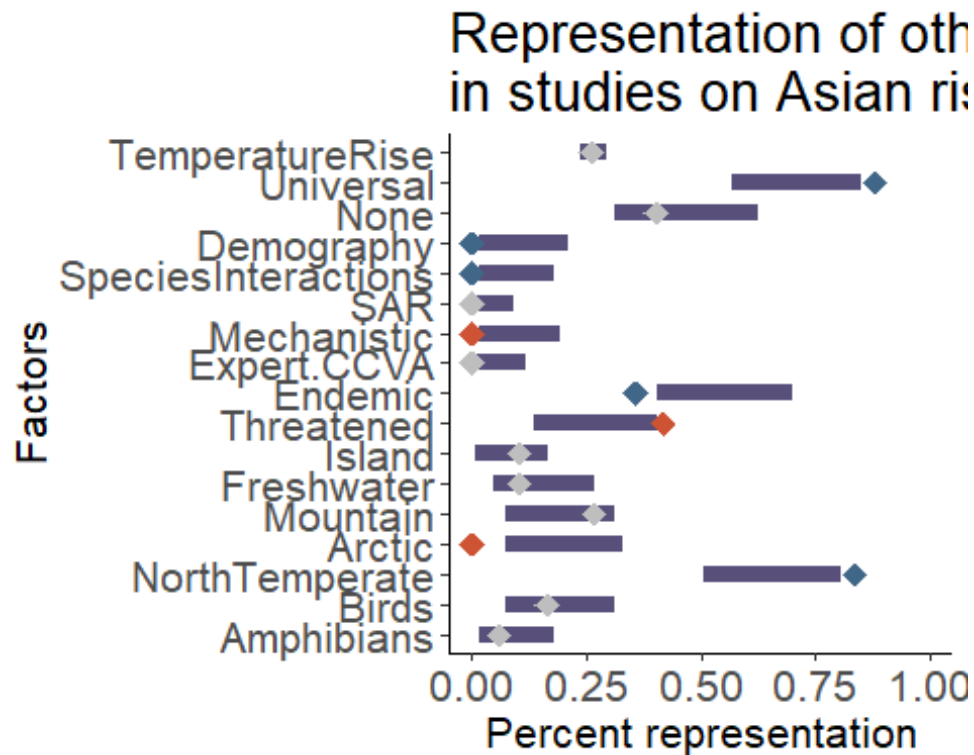
Representation of oth
in studies on Asian ri:

```
ggsave("Asia factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Australia New Zealand

```
#subset data
data.sub <- data[data$Region == "AustraliaNewZealand",] #change

# Considered Auatralia and New Zealand as islands for main analysis
data.sub$Island[data.sub$Region == "AustraliaNewZealand"] = "Y"

n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)
```

```r
#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 6 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Asia" &
res_transposed$Factors != "AustraliaNewZealand" & res_transposed$Factors !=
"SouthAmerica" & res_transposed$Factors != "Arctic" &
                                  res_transposed$Factors !=
"NorthTemperate"&
                                  res_transposed$Factors != "Island",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
```
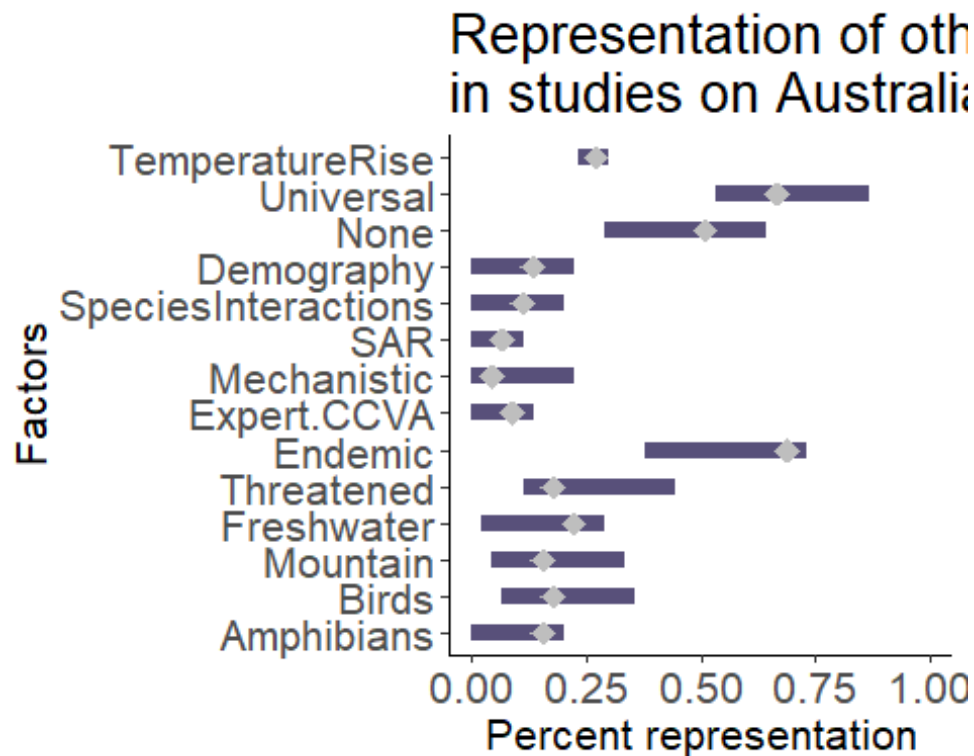
```
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on Australia/NZ risk") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```



```
ggsave("AusNZ factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test South America

```
#subset data
data.sub <- data[data$Region == "Samerica",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact
```

```r
# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 5 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Asia" &
res_transposed$Factors != "AustraliaNewZealand" & res_transposed$Factors !=
"SouthAmerica" & res_transposed$Factors != "Arctic" &
                                  res_transposed$Factors !=
"NorthTemperate",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
```
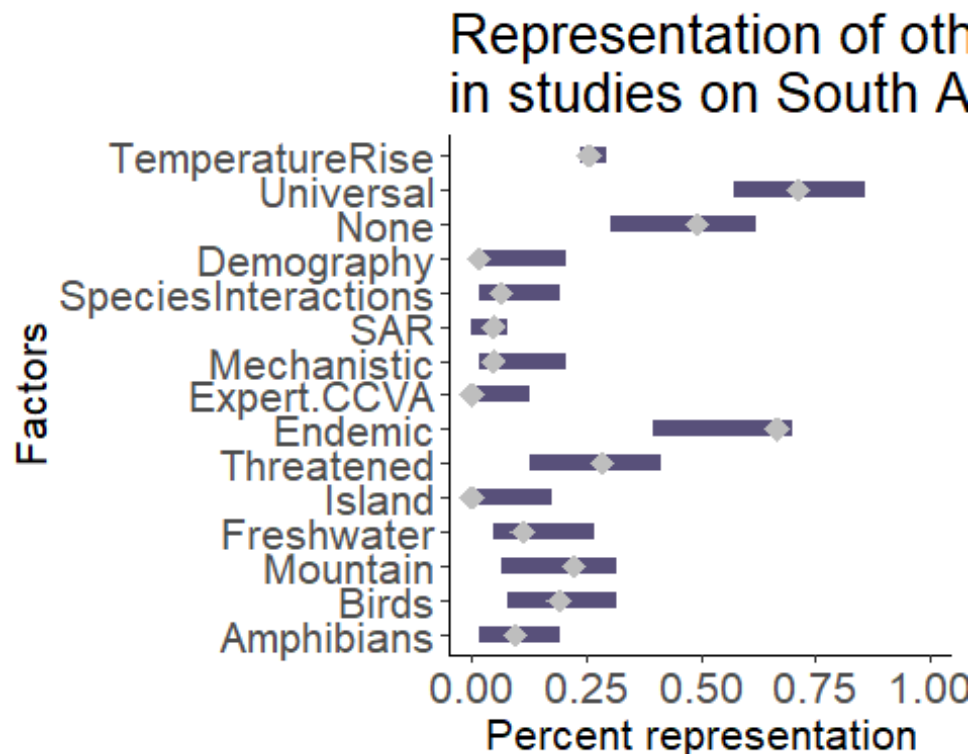
```
   geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
   theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on South American risk") +
   labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```



```
ggsave("Samerica factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test North temperate

```
#subset data
data.sub <- data[data$N.Middle == "Y",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
```

```r
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 5 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "NorthTemperate" &
res_transposed$Factors != "Arctic" & res_transposed$Factors != "SouthAmerica"
& res_transposed$Factors != "AustraliaNewZealand" & res_transposed$Factors !=
"Asia",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
```

```
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on North Temperate risk") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```


Representation of oth in studies on North Te
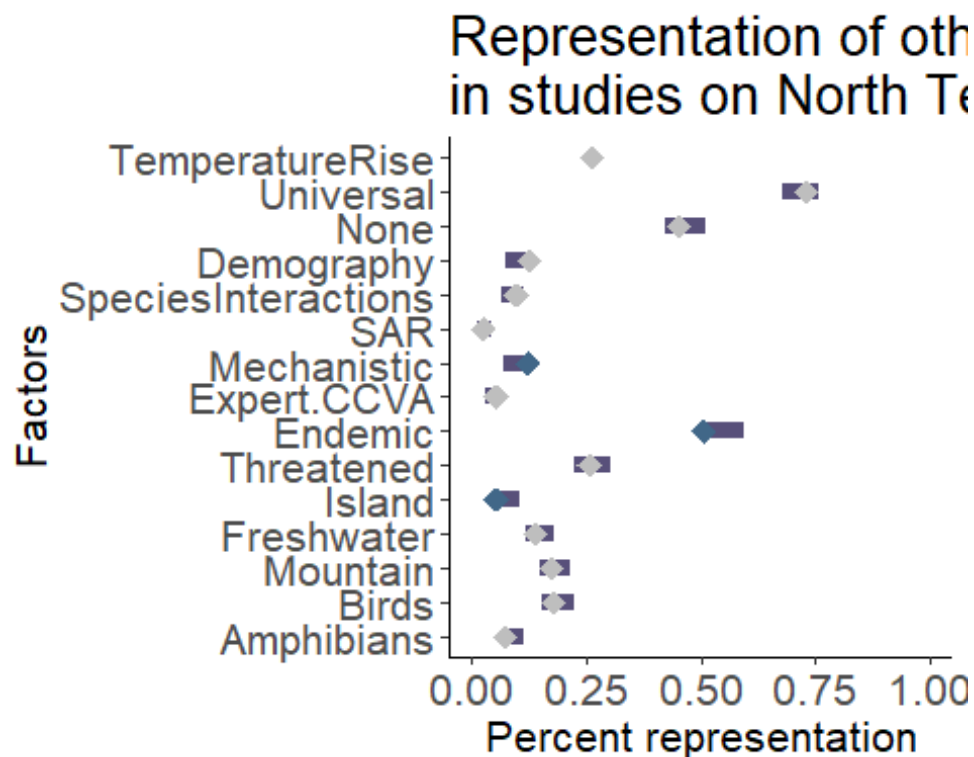
```
ggsave("N Temp factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Arctic

```
#subset data
data.sub <- data[data$Arctic == "Y",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n
```

```r
# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 5 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "NorthTemperate" &
res_transposed$Factors != "Arctic" & res_transposed$Factors != "SouthAmerica"
& res_transposed$Factors != "AustraliaNewZealand" & res_transposed$Factors !=
"Asia",]

fig <- ggplot(res_transposed) +
```

```r
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on Arctic risk") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```
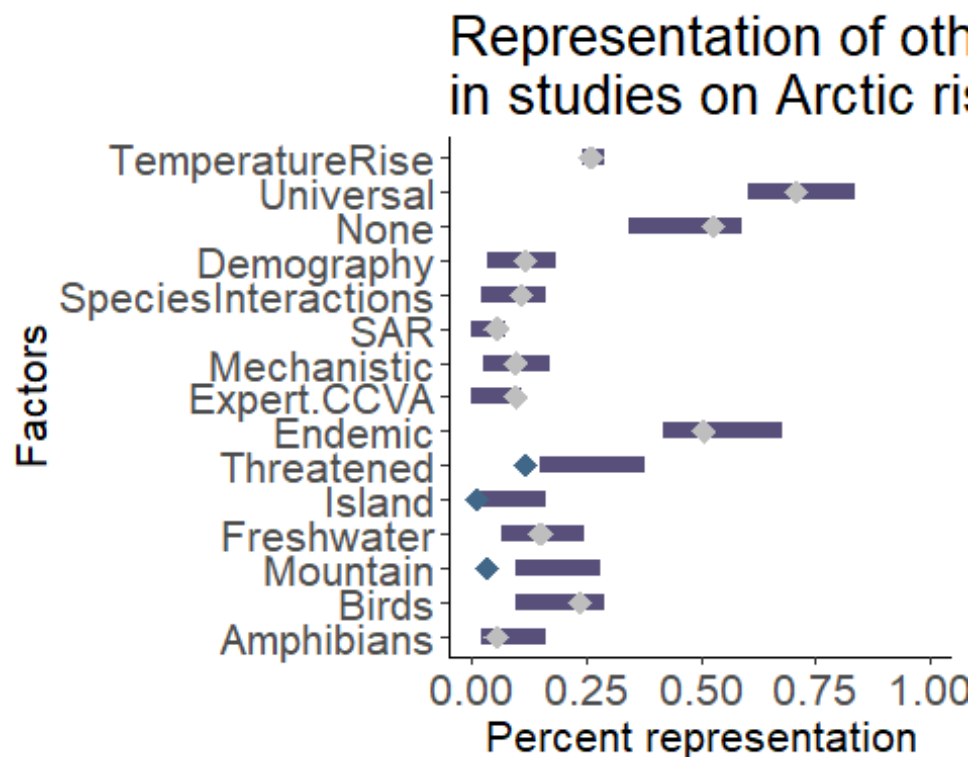


```r
ggsave("Arctic factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Mtn

```r
#subset data
data.sub <- data[data$Mtn == "Y",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n
```

```r
# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 1 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Mountain",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
```
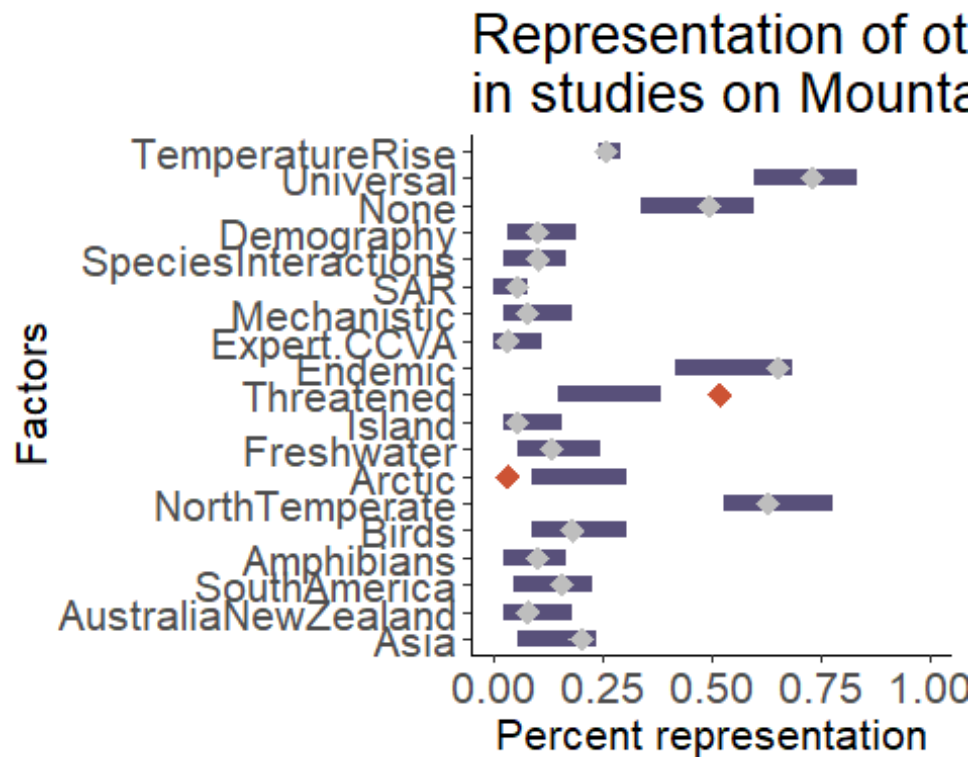
```
   geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
   theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on Mountain risk") +
   labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```



```
ggsave("Mountain factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Freshwater

```
#subset data
data.sub <- data[data$Fresh == "Y",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
```

```r
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 1 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Freshwater",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
```
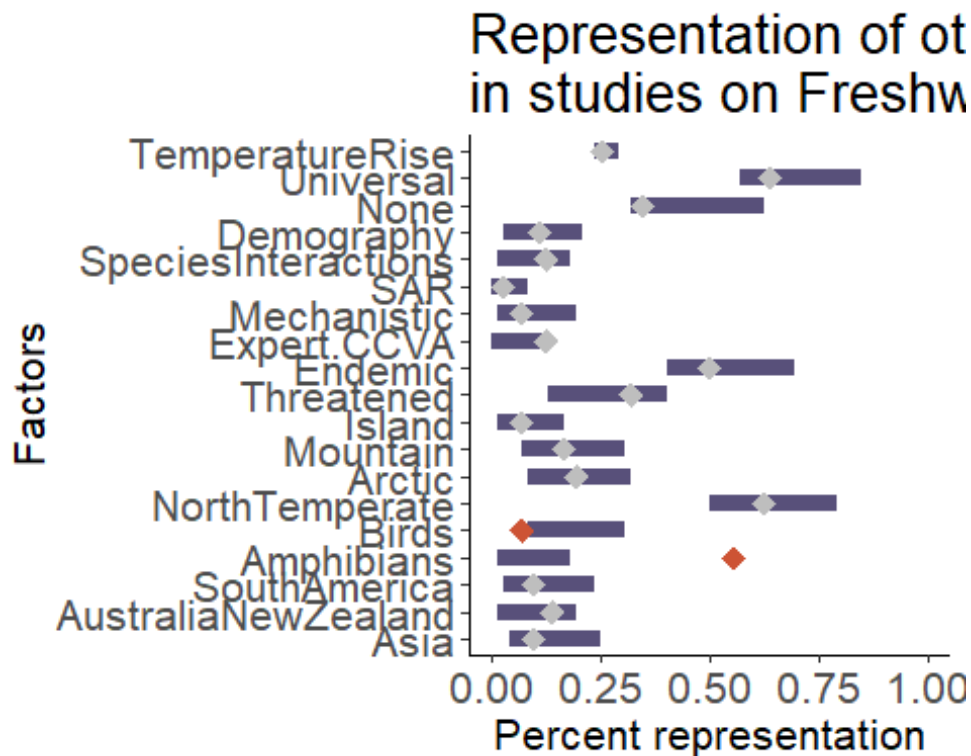
```r
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on Freshwater risk") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```



```r
ggsave("Freshwater factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Island

```r
#subset data
data.sub <- data[data$Island == "Y" | data$Region == "AustraliaNewZealand",]
#change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact
```

```r
# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 2 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Island" &
res_transposed$Factors != "AustraliaNewZealand",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
```
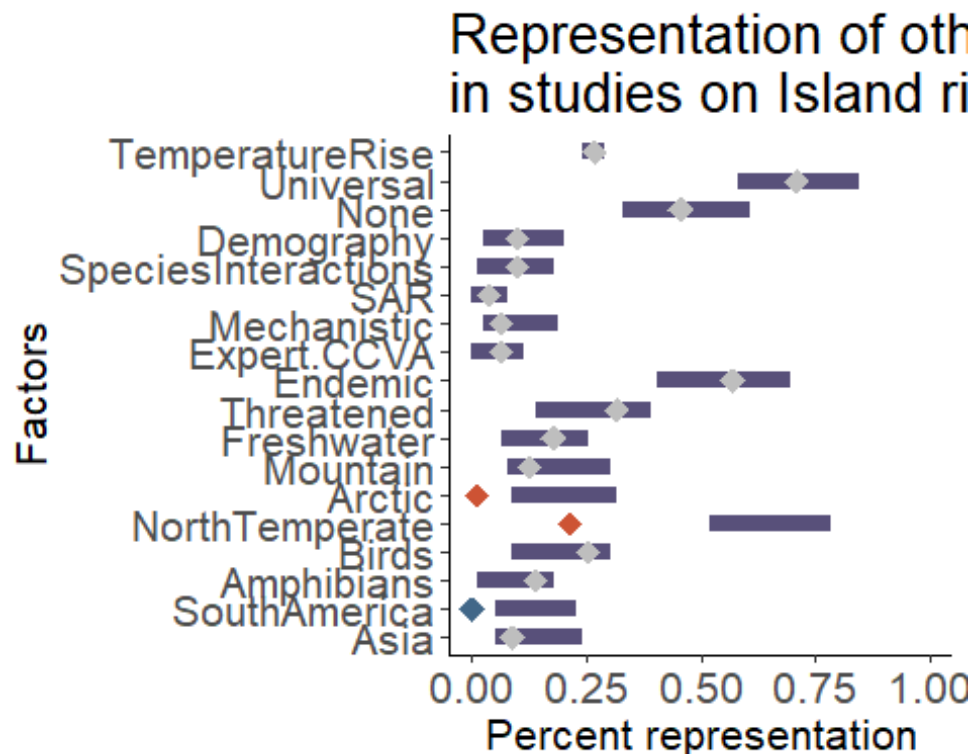
```r
   theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies on Island risk") +
   labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```



```r
ggsave("Island factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Threatened

```r
#subset data
data.sub <- data[data$Threatened == "Y",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact
```

```r
# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 1 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Threatened",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies with pre-existing threats") +
```
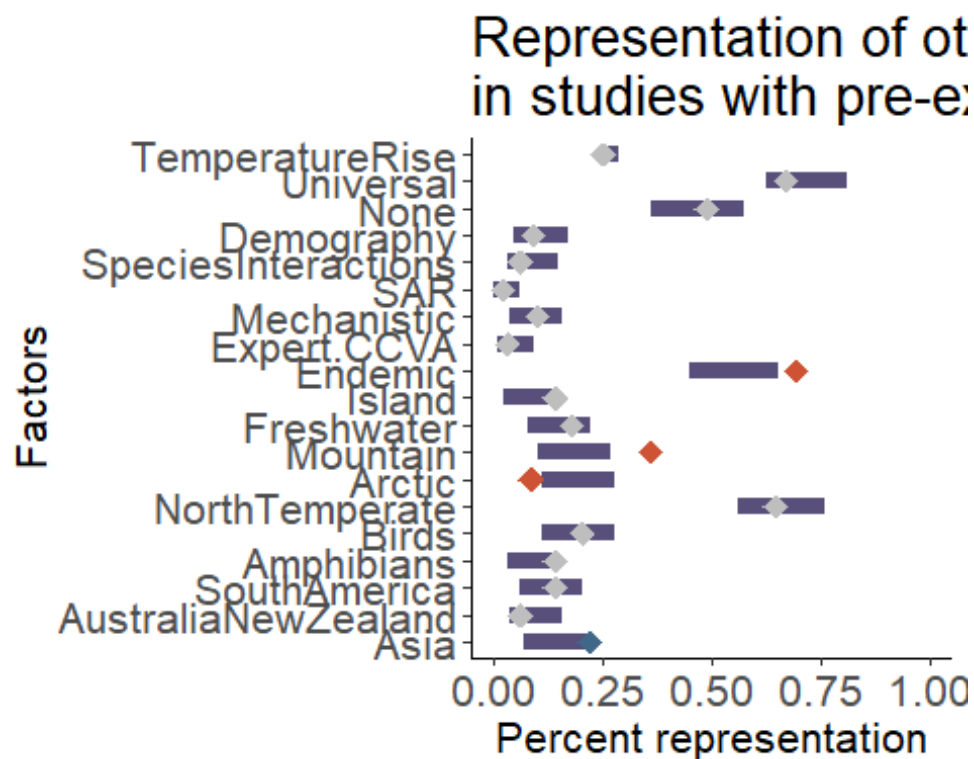
```
   labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```


Representation of ot
in studies with pre-e:

```
ggsave("Threat factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Endemic

```
#subset data
data.sub <- data[data$Endemic == "Y",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)
```

```r
#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 1 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Endemic",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies for Endemic species risk") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
```
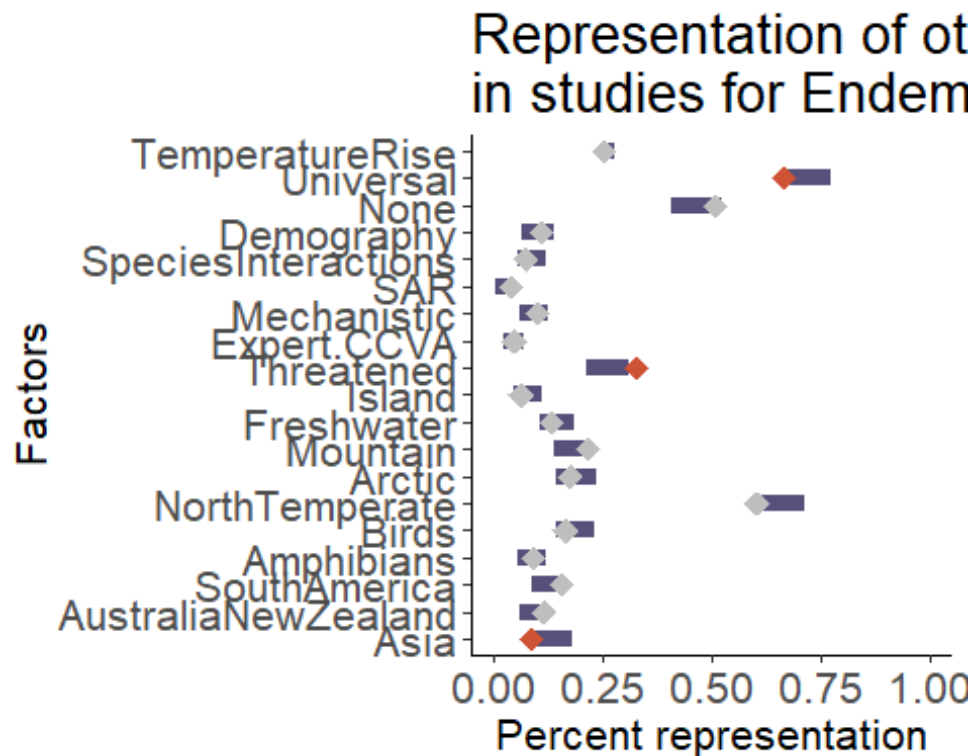
```
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```


Representation of ot
in studies for Endem

ggsave("Endemic factors.png",width=7,height=9,unit="in",dpi=1200)

Test CCVA

```
#subset data
data.sub <- data[data$Model.Type == "Expert.CCVA",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
```

```r
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 4 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Expert.CCVA" &
res_transposed$Factors != "Expert" & res_transposed$Factors != "Mechanistic"
&
                                  res_transposed$Factors != "SAR",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies for Expert/CCVA models") +
  labs(x="Percent representation",y="Factors") +
```
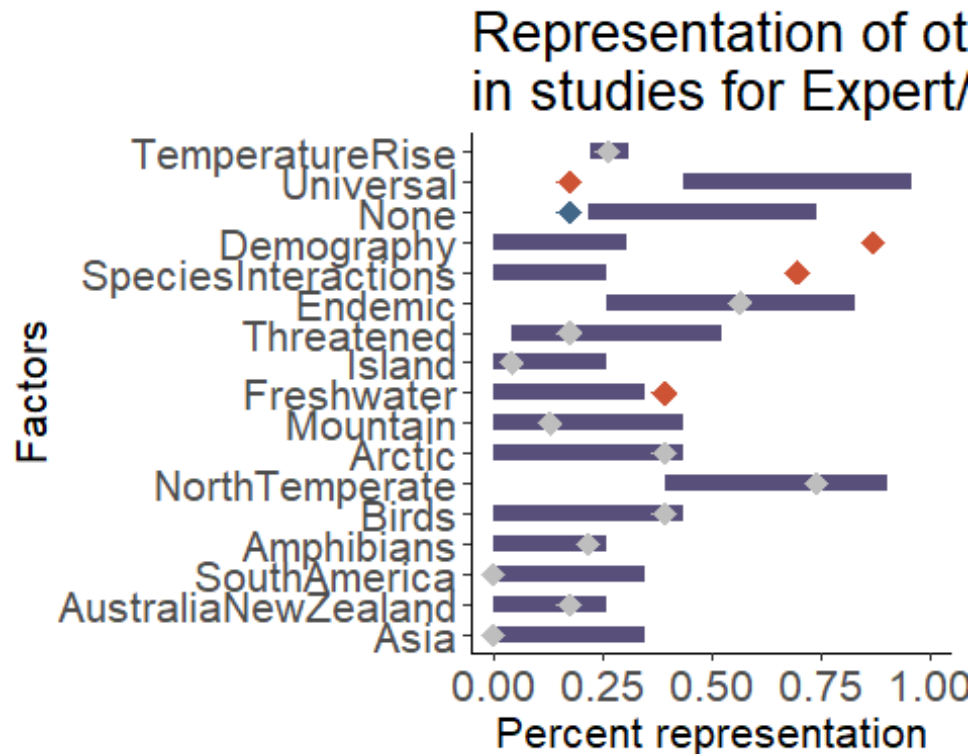
```r
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```



```r
ggsave("Expert CCVA factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test Mechanistic models

```r
#subset data
data.sub <- data[data$Model.Type == "Mechanistic",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)
```

```r
#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 4 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Expert.CCVA" &
res_transposed$Factors != "Expert" & res_transposed$Factors != "Mechanistic"
&
                                 res_transposed$Factors != "SAR",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies for Mechanistic model risk") +
```
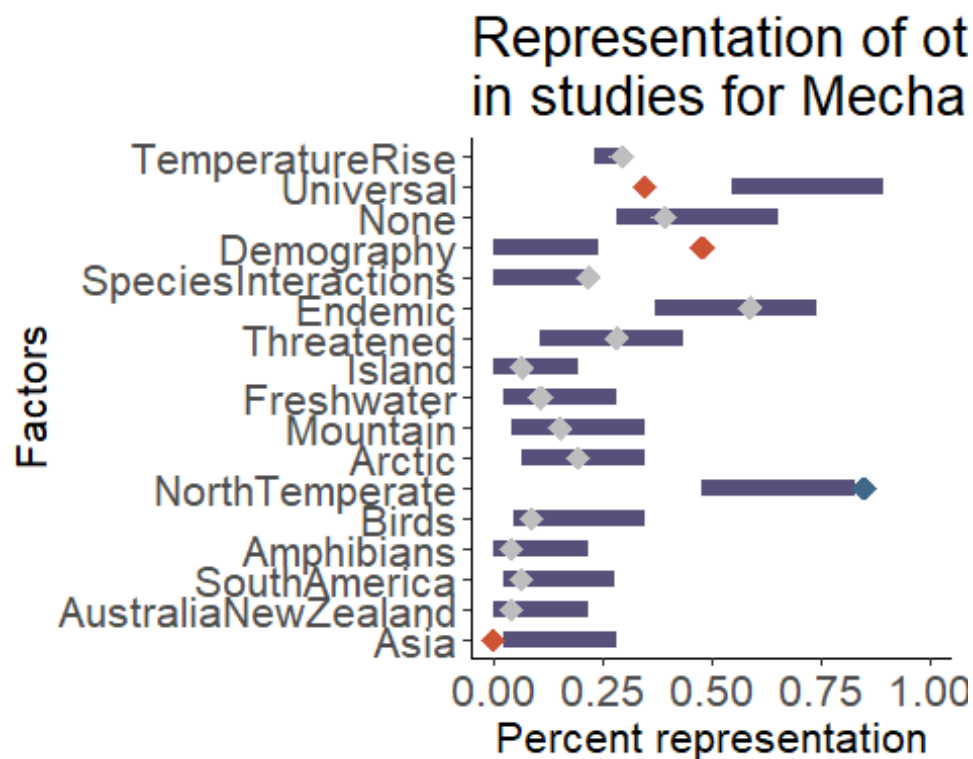
```
    labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```



```
ggsave("Mechanistic factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test SAR models

```
#subset data
data.sub <- data[data$Model.Type == "SAR",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)
```

```r
#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 4 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Expert.CCVA" &
res_transposed$Factors != "Expert" & res_transposed$Factors != "Mechanistic"
&
                                  res_transposed$Factors != "SAR",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
```
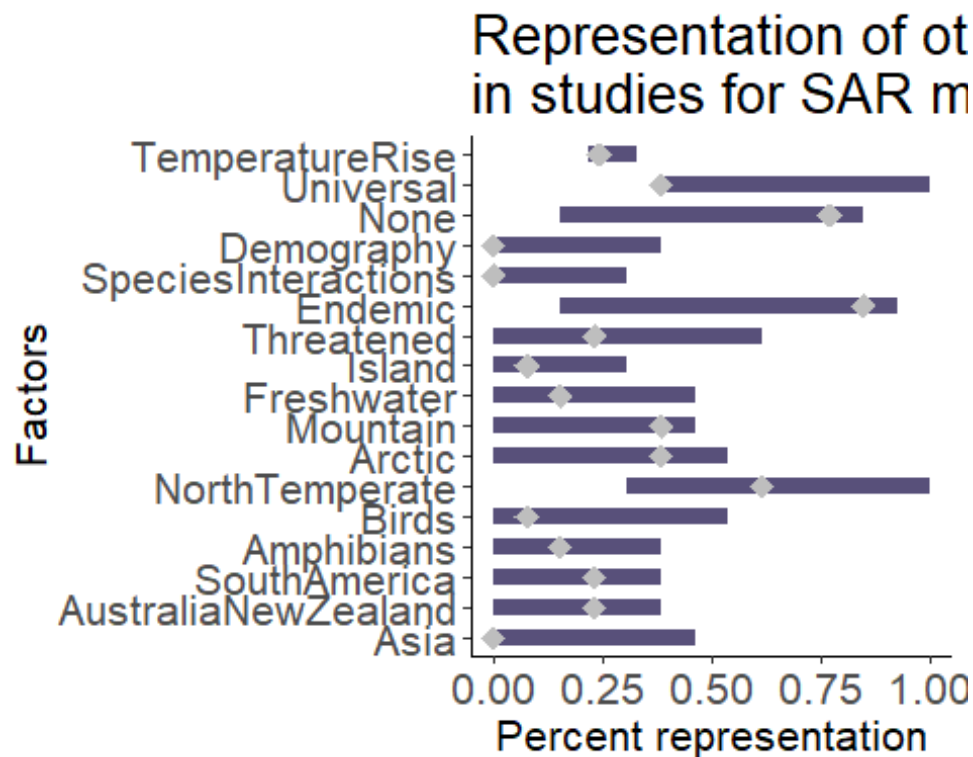
```
studies for SAR model risk") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```


Representation of ot
in studies for SAR m

```
ggsave("SAR factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test models with species interactions

```
#subset data
data.sub <- data[data$Sp.int == "Y",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
```

```r
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 1 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors !=
"SpeciesInteractions",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
linewidth = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies with species interactions") +
```
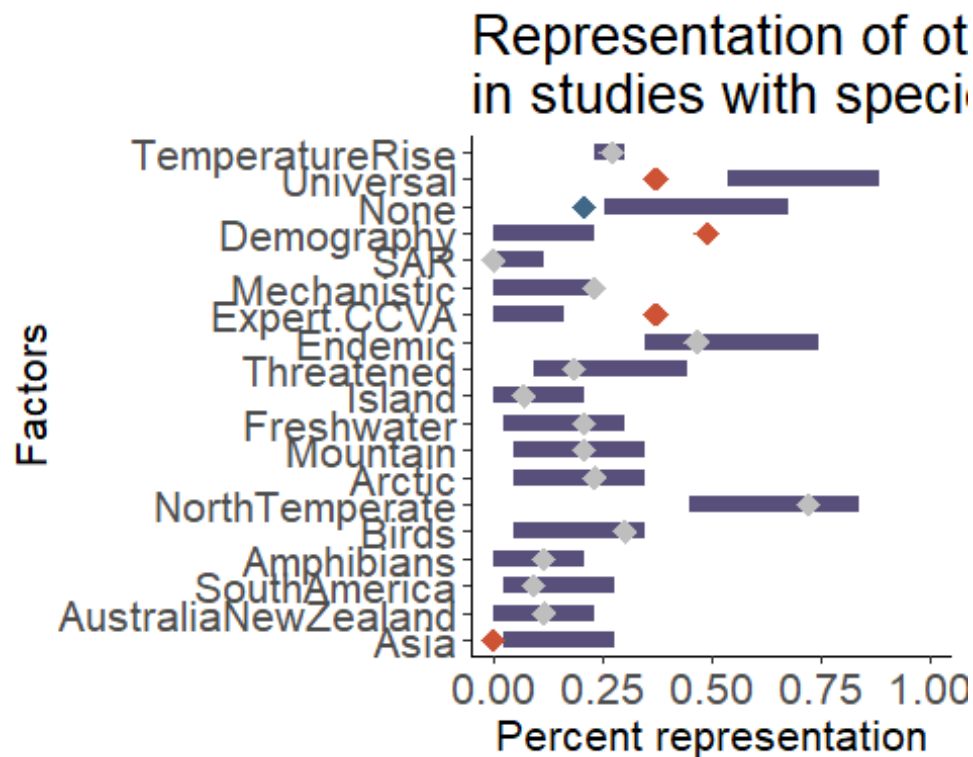
```
    labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```



```
ggsave("Sp int factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test models with demography

```
#subset data
data.sub <- data[data$Demography.LH == "Y",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)
```

```r
#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 1 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Demography",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies with demography") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
```
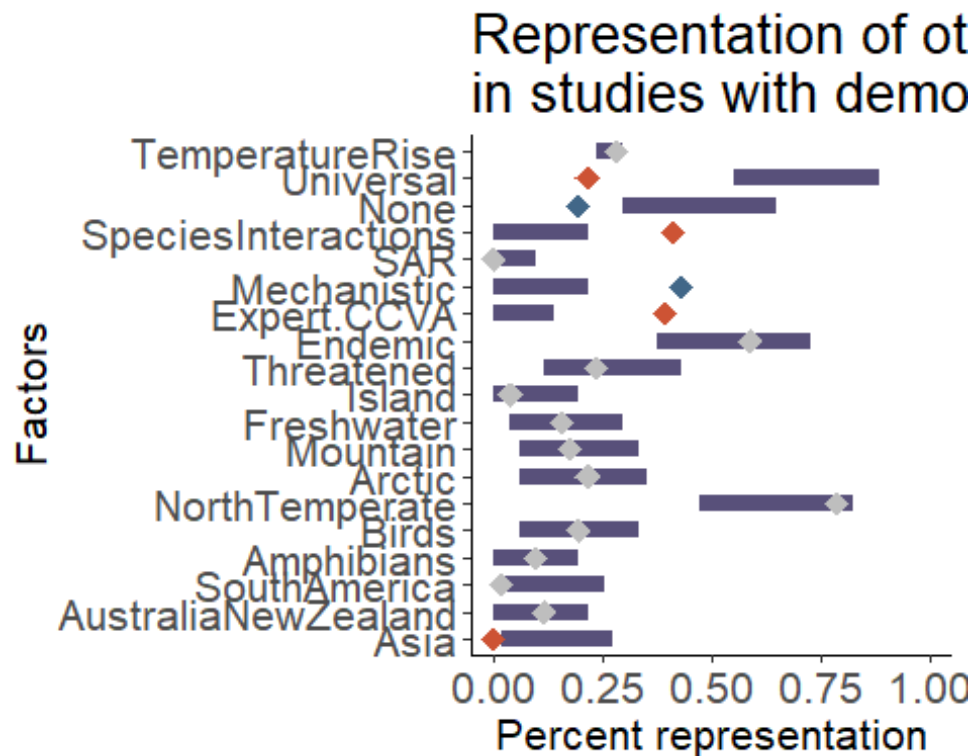
```
20),axis.text = element_text(size=16),legend.position = "none") +
scale_y_reordered()
fig
```


Representation of ot
in studies with demo

Factors (y-axis): TemperatureRise, Universal, None, SpeciesInteractions, SAR, Mechanistic, Expert.CCVA, Endemic, Threatened, Island, Freshwater, Mountain, Arctic, NorthTemperate, Birds, Amphibians, SouthAmerica, AustraliaNewZealand, Asia

Percent representation (x-axis): 0.00 0.25 0.50 0.75 1.00

```
ggsave("Demog factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test models with no dispersal

```
#subset data
data.sub <- data[data$Disp.Mod == "None",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
```

```r
see on graph
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10

#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 2 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI

Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))

# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)

res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"

# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "None" &
res_transposed$Factors != "Universal",]

fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies with no dispersal") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
```
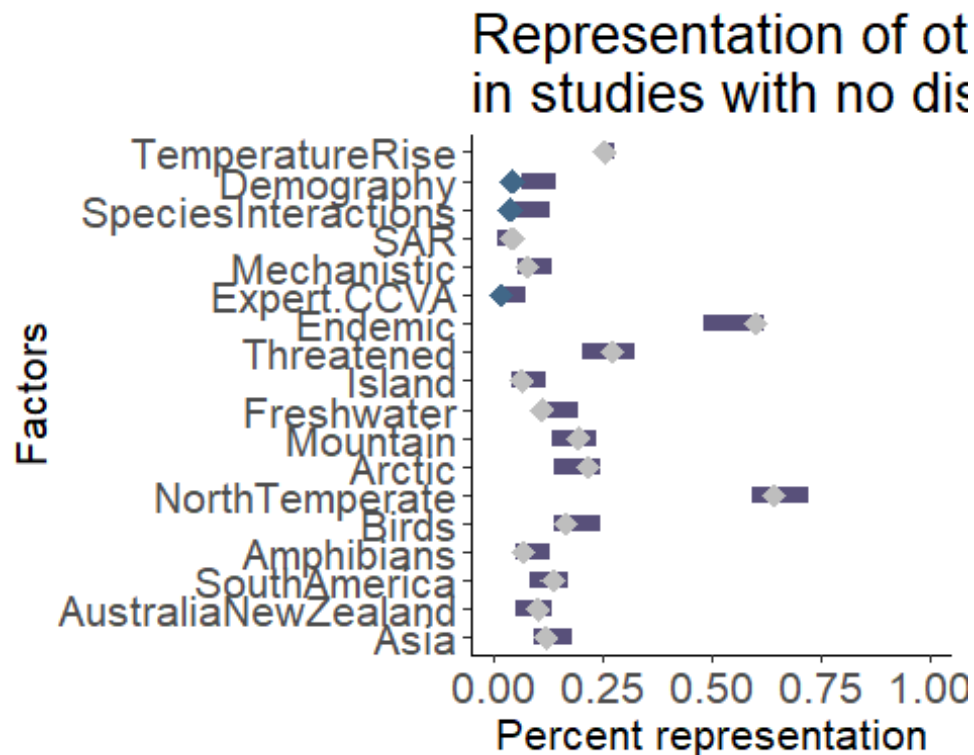
```
scale_y_reordered()
fig
```


Representation of ot
in studies with no dis

```
ggsave("No disp factors.png",width=7,height=9,unit="in",dpi=1200)
```

Test models with universal dispersal

```
#subset data
data.sub <- data[data$Disp.Mod == "Universal",] #change
n.fact <- length(unique(data.sub$Study))

#Calculate factors for observed data
Obs.factor <- factor.n(data.sub)/n.fact
Obs.factor$TemperatureRise <- Obs.factor$TemperatureRise * n.fact/10 #correct
this - pre ind rise should not be divided by n

# Obtain samples for comparison
Rand.factor <- sample.studies(data,n.fact,10000)/n.fact

# Add colnames
colnames(Rand.factor) <- colnames(Obs.factor)

#correct this - pre ind rise should not be divided by n, divide by 10 so can
see on graph
```

```r
Rand.factor$TemperatureRise <- Rand.factor$TemperatureRise * n.fact/10


#Need to apply correction for multiple tests, Bonferroni = alpha/s tests =
0.05/21 = .0024, so CIs are
N.tests = 20 - 2 #number of multiple comparisons
L.CI = .05/N.tests
U.CI = 1 - L.CI


Obs.factor[2:6,] <- apply(Rand.factor, 2, function(col) quantile(col, c(L.CI,
.1, 0.5, 0.9, U.CI), na.rm = TRUE))


# Transpose the data frame
res_transposed <- as.data.frame(t(Obs.factor))
res_transposed <- cbind(Factors = rownames(res_transposed), res_transposed)
rownames(res_transposed) <- NULL
colnames(res_transposed) <- c("Factors", "obs", "LCI",
"x.1","x.5","x.9","UCI")
res_transposed$Factors = factor(res_transposed$Factors, levels =
colnames(Obs.factor))
res_transposed$Direction <-
c("lo","hi","hi","hi","lo","lo","lo","hi","hi","hi","hi","hi","hi","lo","hi",
"hi","hi","hi","lo",NA)


res_transposed$col <- rep("grey",nrow(res_transposed))
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "lo"] = "#CD5334"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "lo"] = "#416788"
res_transposed$col[res_transposed$obs < res_transposed$LCI &
res_transposed$Direction == "hi"] = "#416788"
res_transposed$col[res_transposed$obs > res_transposed$UCI &
res_transposed$Direction == "hi"] = "#CD5334"


# Eliminate the subject and those that cannot be true (e.g., amphibian
studies cannot be also bird studies)
res_transposed <- res_transposed[res_transposed$Factors != "Universal" &
res_transposed$Factors != "None",]


fig <- ggplot(res_transposed) +
  geom_errorbar(aes(x = x.5, y = Factors, xmin = LCI, xmax = UCI), width = 0,
size = 3, color = "#58507A") +
  geom_point(aes(x = obs, y = Factors),size = 4, shape = 18, color =
res_transposed$col) + xlab("") +
  theme_classic()+ xlim(0,1) + ggtitle("Representation of other factors \nin
studies with universal dispersal") +
  labs(x="Percent representation",y="Factors") +
theme(axis.title=element_text(size=16),plot.title = element_text(size =
20),axis.text = element_text(size=16),legend.position = "none") +
```
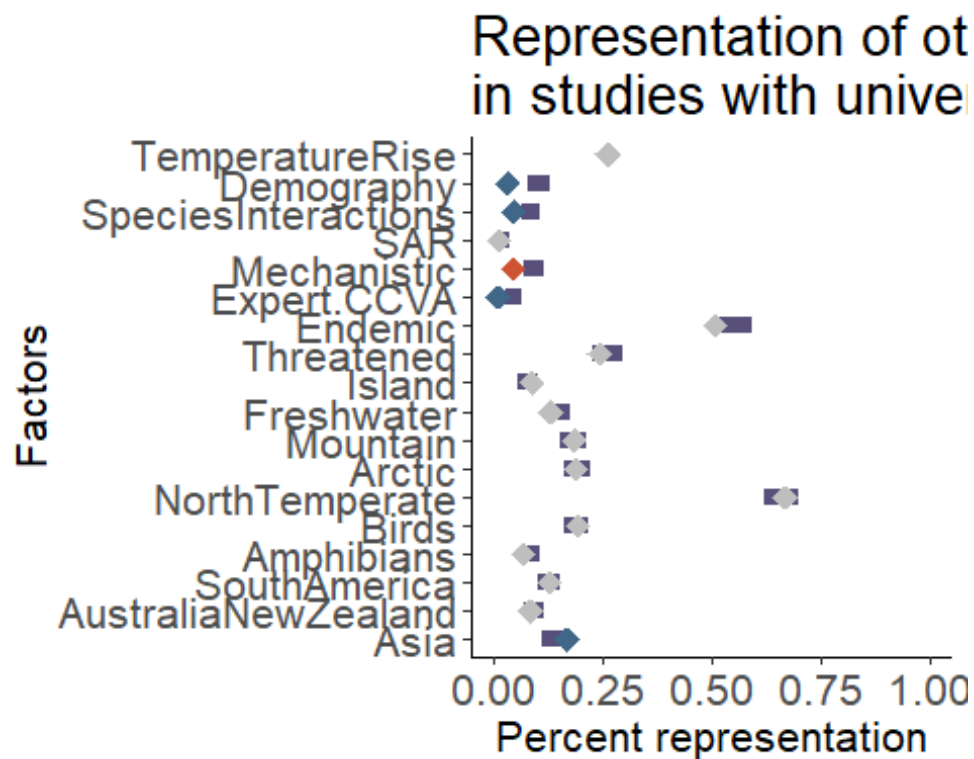
```
scale_y_reordered()
fig
```


Representation of ot
in studies with unive

```
ggsave("UNI disp factors.png",width=7,height=9,unit="in",dpi=1200)
```