

# Playing with the Ant Picnic dataset

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## Ant Picnic

- Project leader: Dr. Magdalena Sorger, <https://theantlife.com/> and Kristin Bedell
- Project URL: <http://studentsdiscover.org/lesson/ant-picnic/>
- Data analysis page: <http://studentsdiscover.org/lesson/ant-picnic-data-analysis/>
- Source data: <https://codap.concord.org/releases/latest/static/dg/en/cert/index.html#shared=35710>

## Packages and scripts

### Packages

```
library(dplyr) #Organize data
library(ez) #ezCor function, compute an plot correlation matrix
library(devtools) #For R packages, R scripts
library(gclus) #For order.single function
library(ggplot2) #For plots
library(tidyr) #For data organizing
```

### Scripts

```
scripts.others <- "panelutils.R" #Correlation coefficients upper panel
ghsource.others <- "https://raw.githubusercontent.com/JoeyBernhardt/NumericalEcology/master/"
invisible(source_url(paste0(ghsource.others, scripts.others)))
```

## Reading the data

```
#Reading source data. CSV file downloaded from
#https://codap.concord.org/releases/latest/static/dg/en/cert/index.html#shared=35710
tdir <- tempdir()
setwd(tdir)
ghsource <- 'https://raw.githubusercontent.com/geofis/antpicnic/master/'
fname <- 'antpicnic.csv'
download.file(paste0(ghsource, 'sampledata/'), fname, fname)
d <- read.csv(fname)
str(d)
```

```
## 'data.frame':    1008 obs. of  18 variables:
## $ Country      : Factor w/ 23 levels "Argentina","Australia",...: 10 10 10 10 10 10 10 10 ...
## $ Biome        : Factor w/ 6 levels "Desert","Grassland/Cold desert",...: 6 6 6 6 6 6 6 6 ...
## $ Bait_Type    : Factor w/ 6 levels "Amino Acids",...: 1 1 1 1 1 1 1 1 2 ...
## $ TotalAntBaitType : int  2 2 2 2 2 2 2 2 139 ...
## $ newAttr      : logi  NA NA NA NA NA NA ...
## $ Site_ID      : int  278 282 279 283 281 286 280 284 285 278 ...
```

```
## $ Latitude : num 63.1 65.4 63.1 59.8 65.4 ...
## $ Longitude : num 25.8 29.6 25.8 23.2 29.6 ...
## $ Date : logi NA NA NA NA NA NA ...
## $ Habitat_type : Factor w/ 119 levels "", "3-4 m in the forest (near edge) along a side
## $ Elevation : num 155 260 115 10 222 16 140 50 50 155 ...
## $ Distance_from_shore : int 152 202 153 4 204 1 150 25 2 152 ...
## $ Precipitation : int 589 588 590 604 585 665 573 672 676 589 ...
## $ Temperature : num 2.5 -0.1 2.4 5.3 0 5.2 1.7 5.2 4.8 2.5 ...
## $ Contributor : Factor w/ 35 levels "", "A.E. Mart?nez Bauer; G.C. Mart?nez",...: 31 31
## $ Site_Details : Factor w/ 91 levels "", "1/1/2001",...: 2 3 3 40 42 66 78 89 91 2 ...
## $ Number_of_Ants : int 0 0 0 0 1 0 0 1 0 4 ...
## $ Percent_of_Baits_with_Ants: int 0 0 0 0 20 0 0 20 0 40 ...
```

```
N <- nrow(d)
set.seed(131)
d[sample(1:N,10),1:4]
```

```
## Country Biome Bait_Type
## 209 USA Temperate seasonal forest Amino Acids
## 126 Australia Desert Sugar
## 296 USA Temperate seasonal forest Salt
## 378 USA Woodland/Shrubland Water
## 850 Tanzania Tropical seasonal forest/Savanna Salt
## 531 Ecuador Temperate seasonal forest Olive Oil
## 520 Ecuador Temperate seasonal forest Sugar
## 239 USA Woodland/Shrubland Amino Acids
## 327 USA Woodland/Shrubland Cookie
## 915 Cambodia Tropical seasonal forest/Savanna Water
## TotalAntBaitType
## 209 21
## 126 646
## 296 275
## 378 78
## 850 486
## 531 278
## 520 101
## 239 73
## 327 944
## 915 104
```

## Selected variables

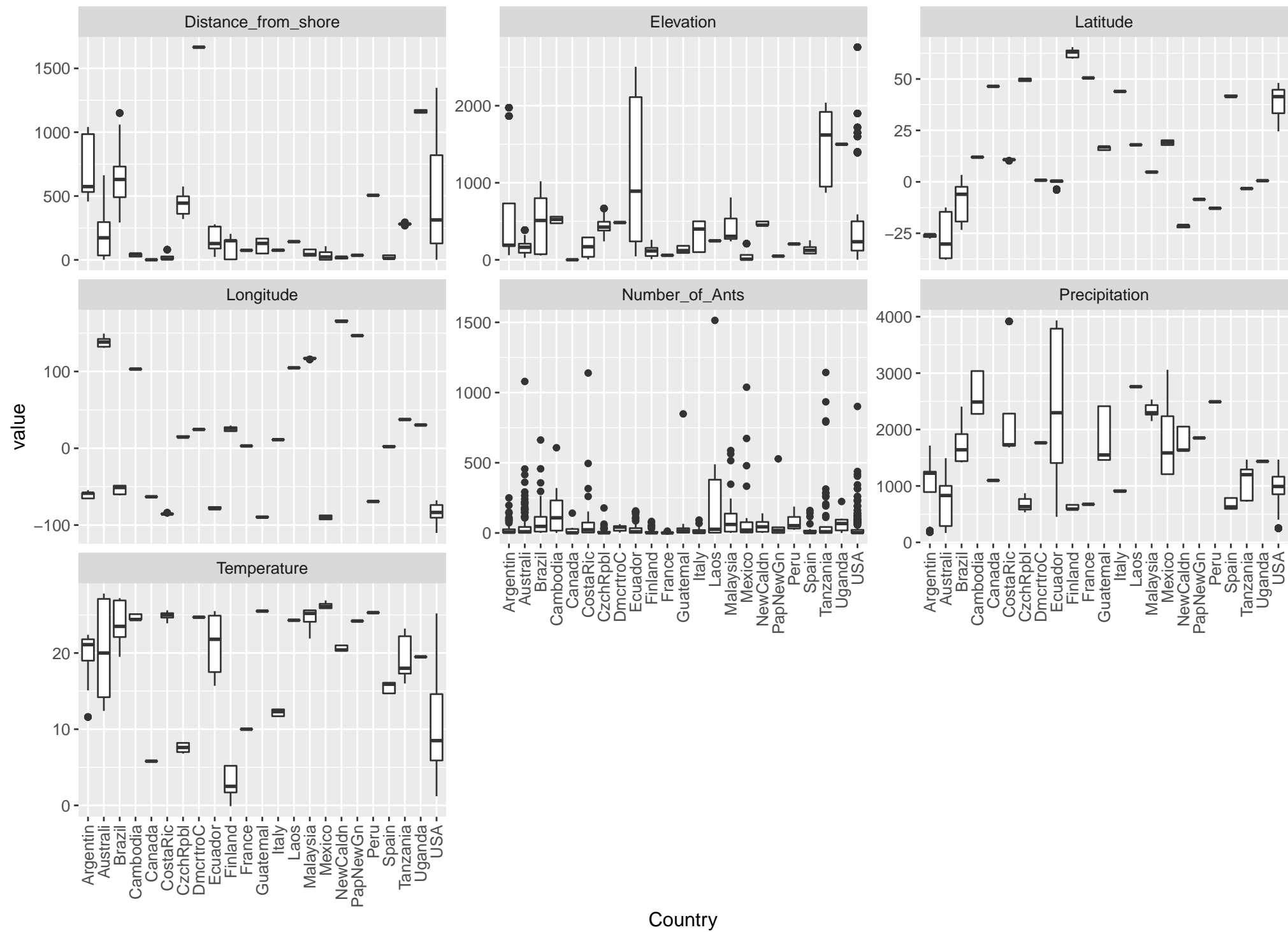
```
d.sel <- d %>% select(
  Country:Bait_Type,
  Latitude:Temperature,
  -Habitat_type,
  -Date,
  Number_of_Ants)
set.seed(131)
d.sel[sample(1:N,10),1:4]
```

```
## Country Biome Bait_Type Latitude
## 209 USA Temperate seasonal forest Amino Acids 33.340000
## 126 Australia Desert Sugar -16.250000
## 296 USA Temperate seasonal forest Salt 33.340000
## 378 USA Woodland/Shrubland Water 48.090100
```

```
## 850 Tanzania Tropical seasonal forest/Savanna      Salt -3.330329
## 531 Ecuador      Temperate seasonal forest      Olive Oil  0.326000
## 520 Ecuador      Temperate seasonal forest      Sugar    0.319000
## 239 USA          Woodland/Shrubland      Amino Acids 40.128694
## 327 USA          Woodland/Shrubland      Cookie   45.959389
## 915 Cambodia Tropical seasonal forest/Savanna      Water   12.004710
```

```
## Environmental variables and number of ants, by country
```

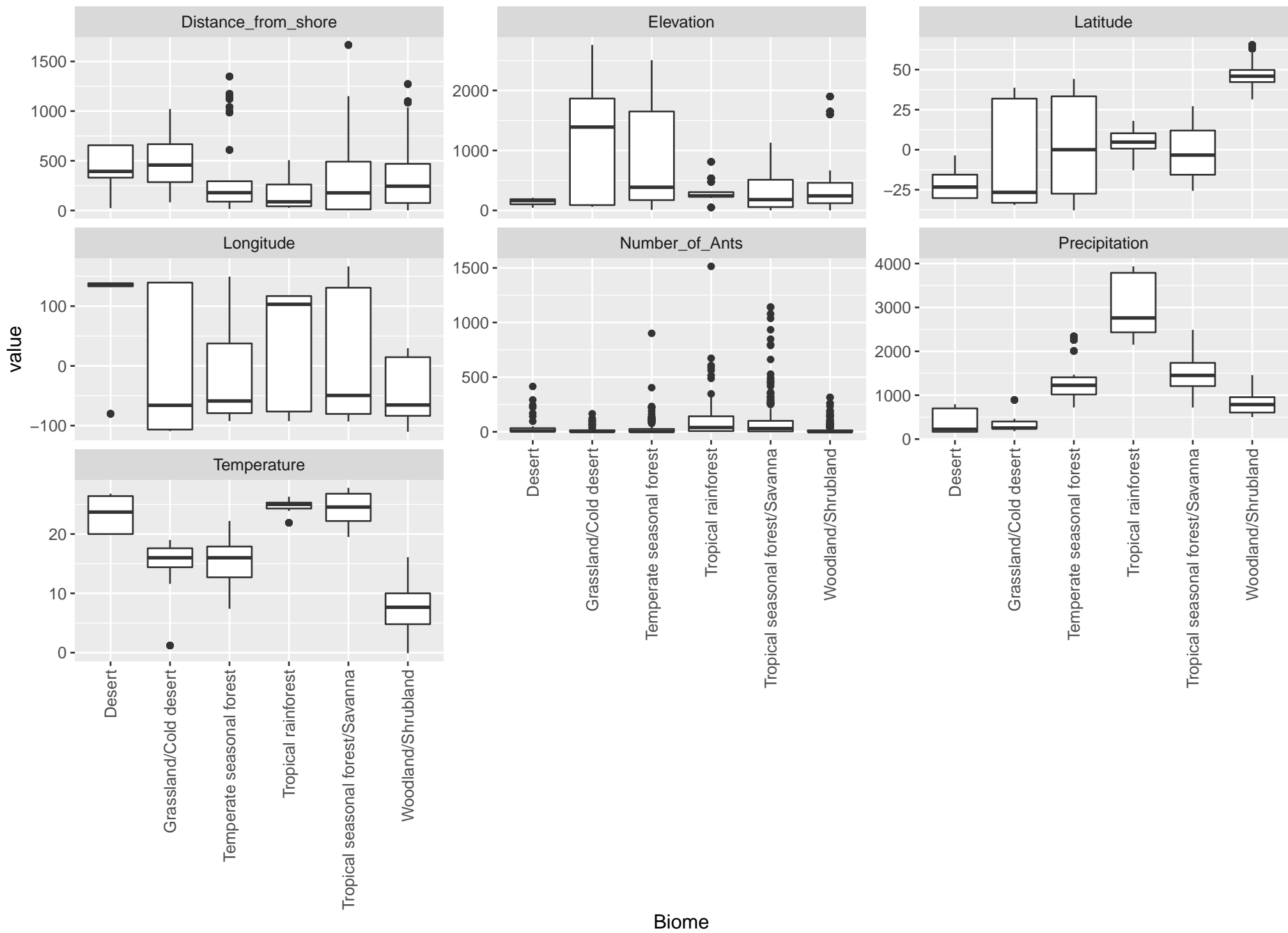
```
basics.country.bp <- d.sel %>% gather(variable,value,-Country,-Biome,-Bait_Type) %>%
  mutate(Country=abbreviate(Country,8)) %>%
  ggplot(aes(x=Country, y=value)) +
  geom_boxplot() +
  theme(
    text = element_text(size = 12),
    axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0.5)
  ) +
  facet_wrap(variable~., scales = 'free_y', nrow=3)
```



```

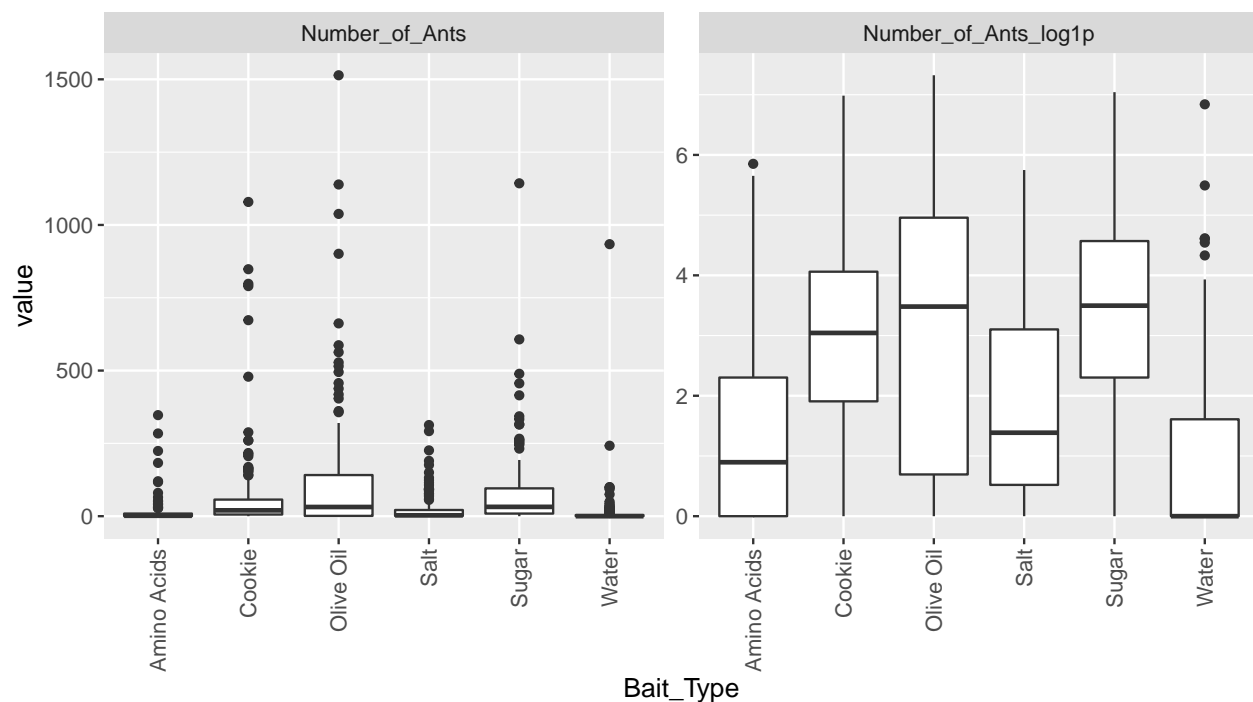
## Environmental variables and number of ants, by biome
basics.biome.bp <- d.sel %>% gather(variable,value,-Country,-Biome,-Bait_Type) %>%
  ggplot(aes(x=Biome, y=value)) +
  geom_boxplot() +
  theme(
    text = element_text(size = 12),
    axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0.5)
  ) +
  facet_wrap(variable~., scales = 'free_y', nrow=3)

```



## Number of ants, by bait type

```
basics.bait.bp <- d.sel %>%
  select(Bait_Type, Number_of_Ants) %>%
  mutate(Number_of_Ants_log1p = log1p(Number_of_Ants)) %>%
  gather(variable, value, -Bait_Type) %>%
  ggplot(aes(x=Bait_Type, y=value)) +
  geom_boxplot() +
  theme(
    text = element_text(size = 12),
    axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0.5)
  ) +
  facet_wrap(variable~., scales = 'free_y', ncol = 2)
basics.bait.bp
```



## Data frame for correlation analysis

```
d.fcor <- d.sel %>% select_if(is.numeric)
set.seed(131)
d.fcor[sample(1:N,10),1:5]
```

##	Latitude	Longitude	Elevation	Distance_from_shore	Precipitation
## 209	33.340000	-81.54000	100	177	1205
## 126	-16.250000	133.36670	211	420	700
## 296	33.340000	-81.54000	100	177	1205
## 378	48.090100	-90.82438	500	816	721
## 850	-3.330329	37.64310	1130	281	948
## 531	0.326000	-78.94900	839	119	2338
## 520	0.319000	-78.95300	943	120	2338
## 239	40.128694	-88.12194	210	1037	951
## 327	45.959389	-68.36153	157	135	999
## 915	12.004710	103.20240	560	46	2488

```
d.fcor.o <- order.single(cor(d.fcor)) #Ordered according to r value
```

```
### Data frame for correlation analysis with transformed variables
```

```
d.fcor.l <- d.fcor %>%  
  mutate(  
    Latitude=abs(Latitude),  
    Longitude=abs(Longitude)) %>%  
  mutate_all(., funs(log1p))  
set.seed(131)  
d.fcor.l[sample(1:N,10),1:5]
```

```
##      Latitude Longitude Elevation Distance_from_shore Precipitation  
## 209 3.5363109  4.413283  4.615121          5.181784      7.095064  
## 126 2.8478121  4.900573  5.356586          6.042633      6.552508  
## 296 3.5363109  4.413283  4.615121          5.181784      7.095064  
## 378 3.8936574  4.519878  6.216606          6.705639      6.582025  
## 850 1.4656435  3.654368  7.030857          5.641907      6.855409  
## 531 0.2821669  4.381389  6.733402          4.787492      7.757479  
## 520 0.2768739  4.381439  6.850126          4.795791      7.757479  
## 239 3.7167060  4.490006  5.351858          6.945051      6.858565  
## 327 3.8492832  4.239332  5.062595          4.912655      6.907755  
## 915 2.5653116  4.646335  6.329721          3.850148      7.819636
```

```
d.fcor.l.o <- order.single(cor(d.fcor.l))
```

```
### Correlation panel using ez package
```

```
ezCor(  
  d.fcor,  
  r_size_lims = c(4,9),  
  label_size = 3) +  
  labs(title="Environmental variables correlation panel")
```



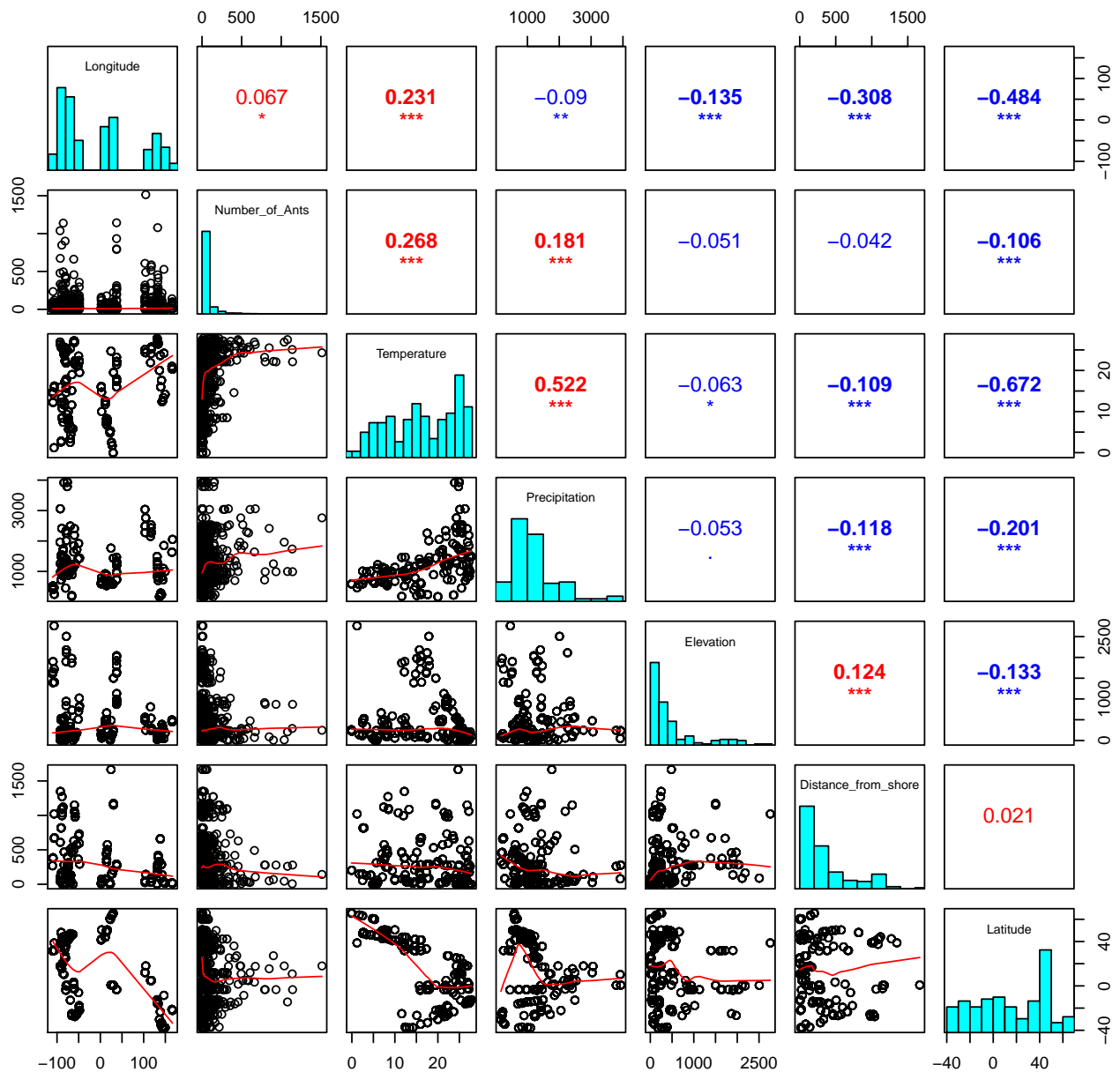
## Environmental variables correlation panel



## Correlation panel of raw variables using pairs function and panelutils.R script

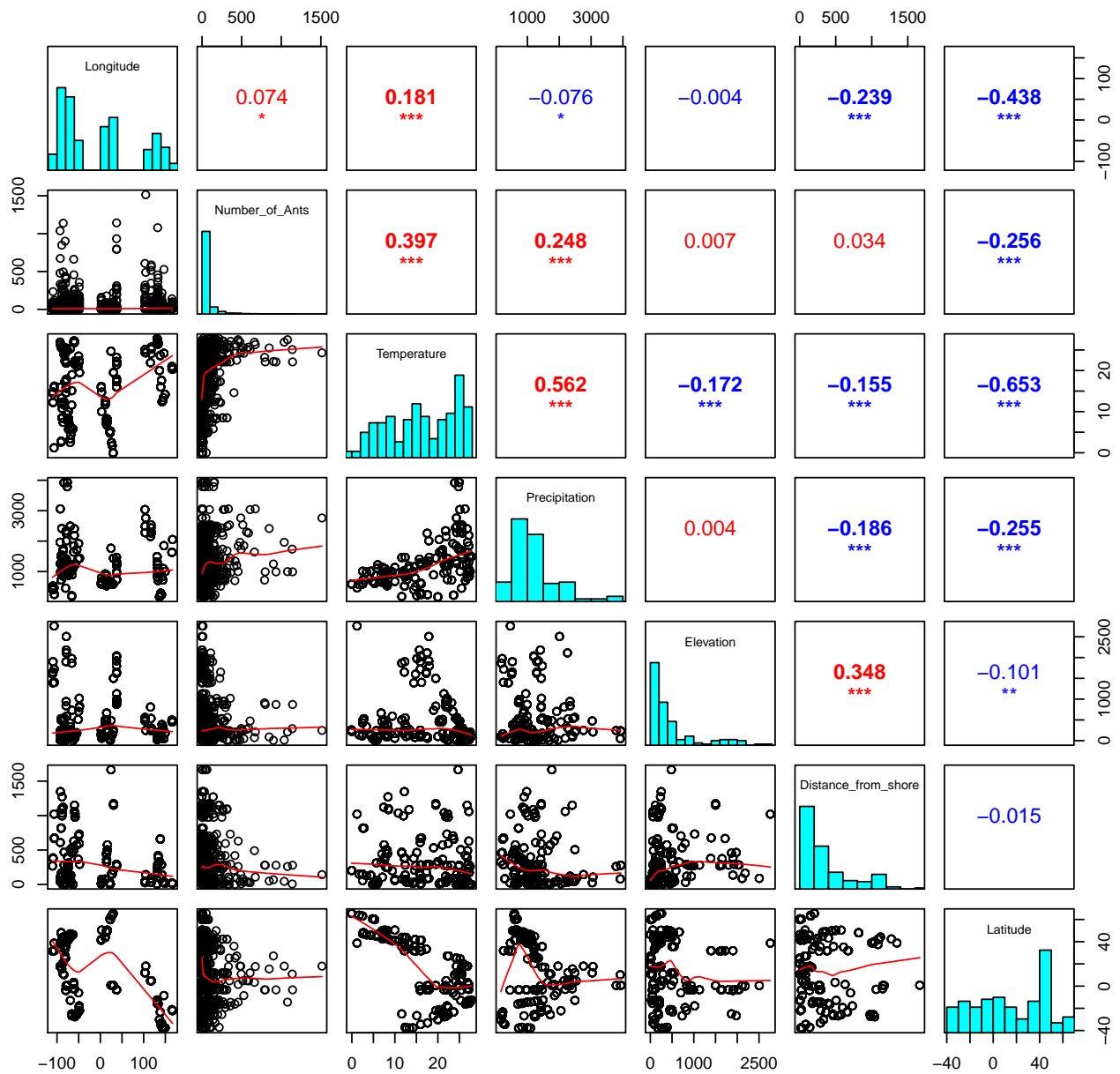
```
#Pearson
pairs(d.fcor[,d.fcor.o],
      lower.panel = panel.smooth,
      upper.panel = panel.cor,
      diag.panel = panel.hist,
      main = "Pearson Correlation Panel")
```

## Pearson Correlation Panel



```
#Spearman
pairs(d.fcor[,d.fcor.o],
      lower.panel = panel.smooth,
      upper.panel = panel.cor,
      diag.panel = panel.hist,
      method = 'spearman',
      main = "Spearman Correlation Panel")
```

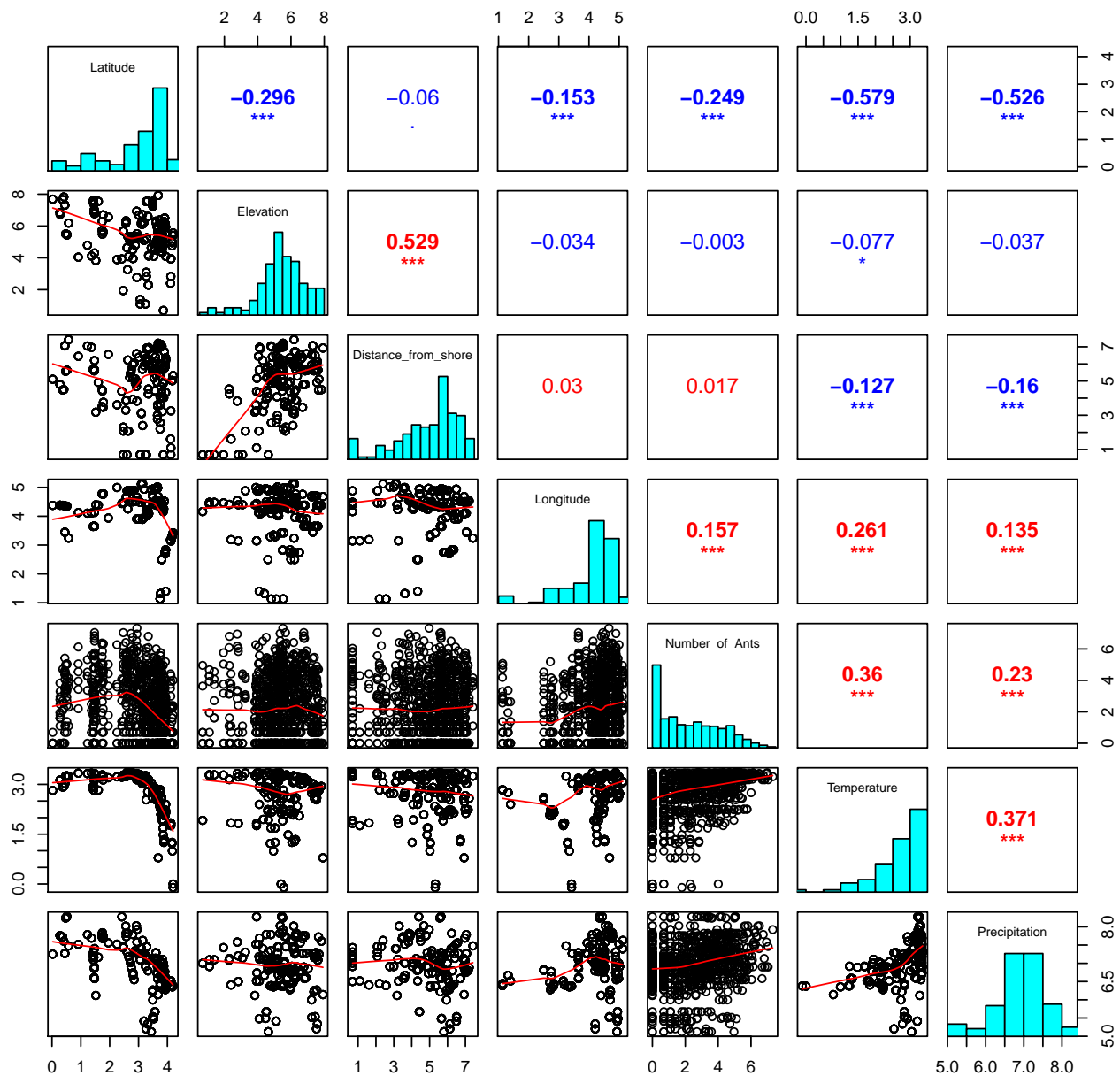
## Spearman Correlation Panel



## Correlation panel of log-transformed variables using pairs function and panelutils.R script

```
#Pearson
pairs(d.fcor.l[,d.fcor.l.o],
      lower.panel = panel.smooth,
      upper.panel = panel.cor,
      diag.panel = panel.hist,
      main = "Pearson Correlation Panel (log1p)")
```

## Pearson Correlation Panel (log1p)



```
#Spearman
pairs(d.fcor.l[,d.fcor.l.o],
      lower.panel = panel.smooth,
      upper.panel = panel.cor,
      diag.panel = panel.hist,
      method = 'spearman',
      main = "Spearman Correlation Panel (log1p)")
```

## Spearman Correlation Panel (log1p)

