Zambia Individual Bids

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24 July 2018

1. Load the packages

```
library(rmarkdown)
library(tidyr)
library(dplyr)
library(ggplot2)
library(readr)
library(gridExtra)
library(scales)
library(openxlsx)
```

2. Set working directory and load the data

```
setwd ("C:/Users/wwainwright/Documents/R/Zambia_Analysis")
Zambia <-
read.csv("C:/Users/wwainwright/Documents/R/Zambia_Analysis/LPOutput/Individua
l/Data/LPOutput_IndividualNEW4.csv")
attach(Zambia)
```

3. Aggregate the data for summary stats

```
# GMA / non-GMA sites
aggregate(Zambia[, 10:20], list(Zambia$GMA), mean)

# Ecoregion 1 / Ecoregion 2
aggregate(Zambia[, 10:20], list(Zambia$Ecoregion1), mean)

# Male / Female
aggregate(Zambia[, 10:20], list(Zambia$Male), mean)
```

4. Subset data into GMA and non-GMA / Ecoregion 1 and Ecoregion 2

```
GMA <- Zambia[Zambia$GMA == "1" ,]
nonGMA <- Zambia[Zambia$GMA == "0" ,]

Eco1 <- Zambia[Zambia$ECOREGION == "1" ,]
Eco2 <- Zambia[Zambia$ECOREGION == "2" ,]
```

5. Makes all the 0 values in data sheet be N/A

```
Zambia[Zambia==0]<-NA
GMA[GMA==0]<-NA
nonGMA[nonGMA==0]<-NA
```

```
Eco1[Eco1==0]<-NA
Eco2[Eco2==0]<-NA
```

6. Bar Plot of farmer bids (cost per hectare) for GMA sites

```
(wbar1 <- ggplot(GMA, aes(x = reorder(RESPONDENT, USDHA), y = USDHA)) +
geom_bar(position = position_dodge(width = 0.1),
    width = 0.15, stat = "identity", colour = "black", fill = "#00868B") +
geom_smooth(method = "loess",
    se = TRUE, color = "blue", aes(group = 1)) + ylab("Cost per hectare
(USD)") +
    xlab("Farmer bid offer GMA sites") + theme(panel.border =
element_blank(),
    panel.background = element_blank(), axis.text.x = element_blank(),
axis.ticks.x = element_blank(),
    panel.grid.minor = element_line(size = 0.1, linetype = "solid", colour =
"black")))
```

7. Bar Plot of farmer bids (cost per hectare) for non-GMA sites

```
(wbar2 <- ggplot(nonGMA, aes(x = reorder(RESPONDENT, USDHA), y = USDHA)) +
geom_bar(position = position_dodge(width = 0.1),
    width = 0.15, stat = "identity", colour = "black", fill = "#00868B") +
geom_smooth(method = "loess",
    se = TRUE, color = "blue", aes(group = 1)) + ylab("Cost per hectare
(USD)") +
    xlab("Farmer bid offer non-GMA sites") + theme(panel.border =
element_blank(),
    panel.background = element_blank(), axis.text.x = element_blank(),
axis.ticks.x = element_blank(),
    panel.grid.minor = element_line(size = 0.1, linetype = "solid", colour =
"black")))
```

8. Aesthetics for the plots

```
# Arrange the plots into a panel
limits <- c(0, 1500)
breaks <- seq(limits[1], limits[2], by = 100)

# Set a common axis
wbar1.common.y <- wbar1 + scale_y_continuous(limits = limits, breaks =
breaks)
wbar2.common.y <- wbar2 + scale_y_continuous(limits = limits, breaks =
breaks)

# build the plots
wbar1.common.y <- ggplot_gtable(ggplot_build(wbar1.common.y))
wbar2.common.y <- ggplot_gtable(ggplot_build(wbar2.common.y))

# copy the plot height from p1 to p2
wbar1.common.y$heights <- wbar2.common.y$heights
```

```
# Display
grid.arrange(wbar1.common.y, wbar2.common.y, ncol = 2, widths = c(11, 9))
```

9. Boxplot of selected farmer bids (US/ha) for the different selection goals

```
# Turn your 'treatment' column into a character vector
Zambia$Objective <- as.character(Zambia$Objective)
# Then turn it back into an ordered factor
Zambia$Objective <- factor(Zambia$Objective, levels =
unique(Zambia$Objective))

# Order the Budget scenarios Turn your 'treatment' column into a character
# vector
Zambia$Model <- as.character(Zambia$Model)
# Then turn it back into an ordered factor
Zambia$Model <- factor(Zambia$Model, levels = unique(Zambia$Model))

# Order the Ecoregions Turn your 'treatment' column into a character vector
Zambia$Ecoregion <- as.character(Zambia$Ecoregion)
# Then turn it back into an ordered factor
Zambia$Ecoregion <- factor(Zambia$Ecoregion, levels =
unique(Zambia$Ecoregion))

# PLot the box plot
(box2 <- ggplot(Zambia, aes(Objective, PriceHa)) + geom_boxplot(aes(fill =
Ecoregion),
    notch = FALSE) + ylab("Total cost per hectare (USD))") + xlab("Objective
Function") +
    guides(fill = guide_legend(title = "Ecoregion")) + theme(axis.text.x =
element_text(size = 11,
    angle = 90, vjust = 1, hjust = 1), axis.line = element_line(color =
"black",
    size = 0.1), panel.background = element_blank()))

box2 + theme(legend.position = "top", legend.text = element_text(size = 12))
```

10. Creating categorical variables and calculating means of categories

```
# Creating factors with different levels from continuous variables, with
# right-closed=FALSE.  Scale is based on best-worst scoring (i.e. 5=good and
# 1=bad).

# For area
AreaIF <- cut(Zambia$Area, breaks = c(0, 0.5, 1, 1.5, 2, 2.5, 3, 100), labels
= c("1",
    "2", "3", "4", "5", "6", "7"), right = FALSE)
AreaIF[1:50]

# For plots
```

```r
PlotIF <- cut(Zambia$Plots, breaks = c(0, 1, 2, 3, 4, 5, 6, 100), labels =
c("1",
    "2", "3", "4", "5", "6", "7"), right = FALSE)
PlotIF[1:50]

# For PriceHa
PriceHaIF <- cut(Zambia$PriceHa, breaks = c(0, 25, 35, 45, 55, 65, 75, Inf),
    labels = c("7", "6", "5", "4", "3", "2", "1"), right = FALSE)
PriceHaIF[1:50]

# For Age
AgeIF <- cut(Zambia$Age, breaks = c(0, 25, 30, 35, 40, 45, 50, 100), labels =
c("7",
    "6", "5", "4", "3", "2", "1"), right = FALSE)
AgeIF[1:50]

# For Farmsize
FarmsizeIF <- cut(Zambia$FarmSize, breaks = c(0, 2, 3, 4, 5, 6, 7, 100),
labels = c("7",
    "6", "5", "4", "3", "2", "1"), right = FALSE)
FarmsizeIF[1:50]

# For CWR species richness
RichnessIF <- cut(Zambia$Richness, breaks = c(0, 1, 2, 3, 4, 5, 6, 100),
labels = c("1",
    "2", "3", "4", "5", "6", "7"), right = FALSE)
RichnessIF[1:50]


# Convert FACTOR to a NUMERIC factor
AgeIF = as.numeric(AgeIF)
is.numeric(AgeIF)

AreaIF = as.numeric(AreaIF)
is.numeric(AreaIF)

PlotIF = as.numeric(PlotIF)
is.numeric(PlotIF)

PriceHaIF = as.numeric(PriceHaIF)
is.numeric(PriceHaIF)

FarmsizeIF = as.numeric(FarmsizeIF)
is.numeric(FarmsizeIF)

RichnessIF = as.numeric(RichnessIF)
is.numeric(RichnessIF)

# Summary stats on the NUMERIC fator
```

```
summary(AgeIF)
hist(AgeIF)

summary(AreaIF)
hist(AreaIF)

summary(PlotIF)
hist(PlotIF)

summary(PriceHaIF)
hist(PriceHaIF)

hist(FarmsizeIF)

summary(RichnessIF)
hist(RichnessIF)

# Calculate the means of the factors subject to each model and corrisponding
# objective function
G <- aggregate(cbind(AgeIF, AreaIF, PlotIF, PriceHaIF, FarmsizeIF,
RichnessIF) ~
    Zambia$Objective, FUN = mean)
K <- aggregate(cbind(Zambia$YoungFarmer, Zambia$LargePlot, Zambia$Female,
Zambia$GMA,
    Zambia$SmallFarms, Zambia$Ecoregion1) ~ Zambia$Objective, FUN = sum)

# Write the object 'G' and 'K' to a .csv file
setwd("C:/Users/wwainwright/Documents/R/Zambia_Analysis/LPOutput/Individual/D
ata/RadarChart/NEW")
write.xlsx(G, file = "RadarMean.csv")
write.csv(K, file = "RadarSum.csv")
```

11. Create radar Plots for the four different selection goals

```
# Load in the data.  The spreadsheets are different data matrices for the
models.
BASIC<-
read.csv("C:/Users/wwainwright/Documents/R/Zambia_Analysis/LPOutput/Individua
l/Data/RadarChart/NEW/BASIC.csv")
Area <-
read.csv("C:/Users/wwainwright/Documents/R/Zambia_Analysis/LPOutput/Individua
l/Data/RadarChart/NEW/AREA.csv")
Div <-
read.csv("C:/Users/wwainwright/Documents/R/Zambia_Analysis/LPOutput/Individua
l/Data/RadarChart/NEW/DIVERSITY.csv")
Equ <-
read.csv("C:/Users/wwainwright/Documents/R/Zambia_Analysis/LPOutput/Individua
l/Data/RadarChart/NEW/EQUITABILITY.csv")

# To arrange all the plots into a planel with 2 rows and 2 column
```

```
op <- par(
  oma=c(0,0,0,0), # Room for the title and legend
  mar=c(3,3,3,3),
  mfrow=c(1,2)
)

# Plot 1: Basic model plot
colors_border=c( rgb(0.2,0.5,0.5,0.9), rgb(0.8,0.2,0.5,0.9) ,
rgb(0.7,0.5,0.1,0.9) )
colors_in=c( rgb(0.2,0.5,0.5,0.4), rgb(0.8,0.2,0.5,0.4) ,
rgb(0.7,0.5,0.1,0.4) )
radarchart( BASIC  , axistype=1 ,
            #custom polygon
            pcol=colors_border , pfcol=colors_in , plwd=4 , plty=1,
            #custom the grid
            cglcol="black", cglty=1, axislabcol="black",
caxislabels=seq(0,100,25), cglwd=1.0,
            # Title for the chart
            title="A) Untargeted goal", line = 1,
            #custom labels
            vlcex=1,
            vlabels=c("Young\nFarmers", "Larger\nPlots",
                      "Female\nFarmers", "GMA\nSites", "CWR\nVerified",
"Commu-\nnities"))

# Plot 2: Area model plot
colors_border=c( rgb(0.2,0.5,0.5,0.9), rgb(0.8,0.2,0.5,0.9) ,
rgb(0.7,0.5,0.1,0.9) )
colors_in=c( rgb(0.2,0.5,0.5,0.4), rgb(0.8,0.2,0.5,0.4) ,
rgb(0.7,0.5,0.1,0.4) )
radarchart( Area  , axistype=1 ,
            #custom polygon
            pcol=colors_border , pfcol=colors_in , plwd=4 , plty=1,
            #custom the grid
            cglcol="black", cglty=1, axislabcol="black",
caxislabels=seq(0,100,25), cglwd=1.0,
            # Title for the chart
            title="B) Targeted goal", line = 1,
            #custom labels
            vlcex=1,
            vlabels=c("Young\nFarmers", "Larger\nPlots",
                      "Female\nFarmers", "GMA\nSites", "CWR\nVerified",
"Commu-\nnities"))

# Plot 3: Diversity model plot
colors_border=c( rgb(0.2,0.5,0.5,0.9), rgb(0.8,0.2,0.5,0.9) ,
rgb(0.7,0.5,0.1,0.9) )
colors_in1=c( rgb(0.2,0.5,0.5,0.4), rgb(0.8,0.2,0.5,0.4) ,
rgb(0.7,0.5,0.1,0.4) )
radarchart( Div  , axistype=1 ,
```

```
            #custom polygon
            pcol=colors_border , pfcol=colors_in , plwd=4 , plty=1,
            #custom the grid
            cglcol="black", cglty=1, axislabcol="black",
caxislabels=seq(0,100,25), cglwd=0.8,
            # Title for the chart
            title="C) Diversity goal", line = 1,
            #custom labels
            vlcex=1,
            vlabels=c("Young\nFarmers", "Larger\nPlots",
                      "Female\nFarmers", "GMA\nSites", "CWR\nVerified",
"Commu-\nnities"))

# Plot 4: Equitability model plot
colors_border=c( rgb(0.2,0.5,0.5,0.9), rgb(0.8,0.2,0.5,0.9) ,
rgb(0.7,0.5,0.1,0.9) )
colors_in=c( rgb(0.2,0.5,0.5,0.4), rgb(0.8,0.2,0.5,0.4) ,
rgb(0.7,0.5,0.1,0.4) )
radarchart( Equ  , axistype=1 ,
            #custom polygon
            pcol=colors_border , pfcol=colors_in , plwd=4 , plty=1,
            #custom the grid
            cglcol="black", cglty=1, axislabcol="black",
caxislabels=seq(0,100,25), cglwd=0.8,
            # Title for the chart
            title="D) Equity goal",line = 1,
            #custom labels
            vlcex=1,
            vlabels=c("Young\nFarmers", "Larger\nPlots",
                      "Female\nFarmers", "GMA\nSites", "CWR\nVerified",
"Commu-\nnities"))
```

12. Plotting a panel of charts based on different variables and selection goals

```
# Load in the data file
Zambia <-
read.csv("C:/Users/wwainwright/Documents/R/Zambia_Analysis/LPOutput/Individua
l/Data/LPOutput_IndividualNEW2.csv")

# Ordered box plot of selected farmer bids (US/ha) for the different
selection goals

# Order the Objective functions

#Turn your 'treatment' column into a character vector
Zambia$Objective <- as.character(Zambia$Objective)
#Then turn it back into an ordered factor
Zambia$Objective <- factor(Zambia$Objective, levels=unique(Zambia$Objective))

# Order the Ecoregions scenarios
```

```r
#Turn your 'treatment' column into a character vector
Zambia$Ecoregion <- as.character(Zambia$Ecoregion)
#Then turn it back into an ordered factor
Zambia$Ecoregion <- factor(Zambia$Ecoregion, levels=unique(Zambia$Ecoregion))

# PLot the box plot
(box2 <- ggplot (Zambia, aes(Objective, PriceHa)) +
geom_boxplot(aes(fill=Ecoregion), notch=FALSE)+
    ylab("Total cost per hectare (USD))") +
    xlab("Objective Function") +
    ggtitle("A) Cost per hectare from farms selected for conservation
services")+
    guides(fill=guide_legend(title="Ecoregion"))+
    theme(
      axis.text.x=element_text(size=11, angle=0, vjust=0.5, hjust=0.5),
      axis.line = element_line(color="black", size = 0.1),
      panel.background = element_blank(),
      legend.position = c(.02, .98),
      legend.justification = c("left", "top"),
      legend.box.just = "left",
      legend.margin = margin(6, 6, 6, 6)))

# Plot a line chart based on average farm size

# Creating an object called x, based on x variables, and then plotting in a
model, ordered by Farm Size
x = Zambia %>%
  select(ID, Objective, FarmSize)

# Plotting the point graph based on X
p <- x %>%
  mutate(ID=reorder(ID, FarmSize)) %>%
  ggplot(aes(ID, FarmSize, colour=Objective, group=1)) +
  geom_point() +
  labs(x="Farmer", y="Farm size (ha)")+
  ggtitle("B) Size of farms selected for conservation services")+
  scale_y_log10() + # This is to plot using the log of the data
  facet_wrap(~Objective) +
  theme(
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank(),
        axis.line = element_line(colour = "black"),
        panel.background = element_blank(),
        legend.position="none")
p

# Plotting the age of farmers and price per ha (bar plot)

v = Zambia %>%
```

```r
  select(ID, Objective, FarmSize, PriceHa, Age, Bidoffer, Averagesizeplot,
PricePlot, Area, Plots)

# Plotting the point graph based on v
  mutate(v$Age=reorder(v$Age, v$PriceHa)) %>%

  u <- ggplot(v, aes(Age, PriceHa), y=PriceHa) +
    geom_bar(position=position_dodge(width=0.1), width = 0.15,
stat="identity", colour=Zambia$Objective, fill="#00868B") +
    geom_smooth(method = "glm", se=FALSE, color="blue", aes(group=1)) +
    ggtitle("C) Cost per hectare and age of farmers selected for conservation
services")+
    ylab("Price per hectare (USD)") +
    xlab("Age") +
    facet_wrap(~Objective) +
  theme(
      panel.background = element_blank(),
      axis.line = element_line(colour = "black"),
      legend.position="bottom", legend.direction="horizontal",
      legend.title = element_blank())
u

# Plot a line chart based on total area (Y) and total plots (x)

# Creating an object called k, based on k variables, and then plotting in a
model, ordered by Farm Size
k = Zambia %>%
  select(ID, Objective, FarmSize, Area, Plots)

# Plotting the point graph based on X
g <- k %>%
  #filter(Model=="Medium") %>%
  mutate(ID=reorder(Area, Plots)) %>%
  ggplot(aes(Plots, Area, colour=Objective, group=1)) +
  geom_point() +
  geom_smooth(method = "glm", se=FALSE, color="blue", aes(group=1)) +
  labs(x="Area (Ha)", y="Plots")+
  ggtitle("D) Area and plots selected for conservation services")+
  facet_wrap(~Objective) +
  theme(panel.background = element_blank(),
        axis.line = element_line(colour = "black"),
        legend.position="none")
g

# Arrange the plots (box2, p, u and g) into a grid
blank<-rectGrob(gp=gpar(col="white"))   # Create a blank plot to use as a
space
grid.arrange(box2, p, blank, blank, u, g, heights=c(0.475, 0.05, 0.475),
nrow=3) # plot with the blank space
```

13. Line Plot of CWR occurance at selected sites

```
# Read in the data
Zam <-
read.csv("C:/Users/wwainwright/Documents/R/Zambia_Analysis/LPOutput/Individua
l/Data/CWR/CPT2.csv")

# Inspecting the data frame
dim(Zam)
lapply(Zam, class)
str(Zam)

# Check the variables are factors with different levels
Zam$Model

# Plot a line chart with different colours for each Model
P <- ggplot(Zam, aes(x=CWR, y=Count, group=Model)) +
      #facet_wrap(~Zam$Objective)+
      geom_line(linetype="dashed", size=1.3, aes(color=Model))+
      geom_point(aes(color=Model))+
      ylab("Number of sites selected inhabited by CWR species\n") +
      xlab("\nCWR Species") +
      theme(
      axis.text.x=element_text(face= c('italic', 'bold.italic', 'italic',
'italic',
                                       'bold.italic', 'italic', 'italic',
'italic',
                                       'bold.italic', 'bold.italic'), # Makes
some of the labels italic, others bold and italic
                                size=12, angle=50, vjust=0.5, hjust=0.5),
      axis.line = element_line(color="black", size = 0.1),
      axis.title=element_text(size=12),
     panel.border = element_blank(),
     panel.background = element_blank())
P

# Puts the legend on the top and increases the size
P + theme(legend.position="top", legend.text=element_text(size=12)) +
  # Takes the plot and changes the axis lables from original to modification
    scale_x_discrete(labels=c("EchinochloaC" = "(1) Echinochloa.C",
"EleusineC" = "(2) Eleusine.C"
                              , "EleusineI" = "(3) Eleusine.I", "OryzaL" =
"(4) Oryza.L", "PennisetumP" = "(5) Pennisetum.P"
                              , "PennisetumP2" = "(6) Pennisetum.P(2)",
"SolanumI" = "(7) Solanum.I",
                              "SorghumB" = "(8) Sorghum.B", "VignaJ" = "(9)
Vigna.J", "VignaU" = "(10) Vigna.U"))
```