Prior to any of the codes run throughout this report, all packages and CSVs were loaded into R using R version 3.6.2 using the code below. If an area is highlighted, more detail will be provided on it following the code.

```
#packages installed= data.table, dplyr, formattable, tidyr using function install.packages("") for example
install.packages ("tidyr")

library(tidyr)

library(ggplot2)

library(data.table)

library(dplyr)

library(formattable)

library(qwraps2)


#Actual.Eco.Site is a column I added to the Plots TerrADat csv to assign the ecological site

#CSVs have to be saved as CSV with the names as follows: plots = "Allyears_plots" , soil horizon =
"Allyears_soilhorizons"

#query results = "Allyears_query", plant specis = "PSPPALL" , species richness = "Allyears_species_rich"

#LPI detail = "LPI_all"
```

<-your csvs from TerrADat must be saved in Documents with this exact name. Otherwise you need to change your file path and name in the code

```
#Plotdata has the actual.eco.site assigned, the "match" code below is adding a column that will assign
actual.eco.site to every row

##using the Plotdata csv

Plotdata<-read.csv("~/Allyears_plots.csv")

soildata<-read.csv("~/Allyears_soilhorizons.csv")
```

Actual.Eco.Site is a column you create with this exact name in the plots csv. In the column you assign the name of your zone, allotment, eco site, strata etc.

```
soildata$Actual.Eco.Site<-
Plotdata$Actual.Eco.Site[match(soildata$PrimaryKey,Plotdata$PrimaryKey)]

AIMdata<-read.csv("~/Allyears_query.csv")

AIMdata$Actual.Eco.Site<-Plotdata$Actual.Eco.Site[match(AIMdata$Primary.Key,Plotdata$PrimaryKey)]

PSPSdata<-read.csv("~/PSPPALL.csv")

PSPSdata$Actual.Eco.Site<-
Plotdata$Actual.Eco.Site[match(PSPSdata$PrimaryKey,Plotdata$PrimaryKey)]
```

```
SPdata<-read.csv("~/Allyears_species_rich.csv")

SPdata$Actual.Eco.Site<-Plotdata$Actual.Eco.Site[match(SPdata$PrimaryKey,Plotdata$PrimaryKey)]

ST<-read.csv("~/LPI_all.csv")
```

#when downloading LPI detail from TerrADat online you will have to label the ==PrimaryKey column PrimaryKey, you can use the View()==

##command to ensure you're matching with the correct column

```
ST<-ST %>%

  select(HeightWoody,HeightHerbaceous,SpeciesWoody,SpeciesHerbaceous,PrimaryKey)

STN<-na.omit(ST)

STN$Actual.Eco.Site<-Plotdata$Actual.Eco.Site[match(STN$PrimaryKey,Plotdata$PrimaryKey)]
```

Actual.Eco.Site is useful for post stratification and to allow you to input ecological sites, zone or allotment names rather than just using the data provided in TerrADat. This is relied on through the code and must have this exact name in your spreadsheet. The match() function allows us to use primary key to assign the Actual.Eco.Site names to all of the spreadsheets. TerrADat LPI detail has an error of no column name for primary key. You must open the csv and manually give the column the name "PrimaryKey". View() allows you to open your csv in R. Na.omit() removes all NAs in the csv. In that step we are removing the species that do not have cover values assigned.

Stratum descriptions

Stratum descriptions give the general site characteristics. Characteristics include ecological sites (ESs), elevation, slope, annual precipitation, landscape type, soil profile and common species. The stratum description provides understanding for the general basis of stratum grouping and provides reasoning for why similar management is necessary for these plots.

Methods

ESs were determined using Web Soil Survey. The plot's soil profile was compared to the ES typical profile (available in Web Soil Survey) using the TerrADat Plots and Soil Horizons records. Variation between the two were recorded and added to the stratum descriptions. Elevation, slope, annual precipitation and landscape type were determined using TerrADat Plots records. Soil characteristics were determined using the TerrADat Soil Horizons records, and vegetation was determined using the TerrADat Species Richness Detail. Vegetation listed in the stratum description will not be a comprehensive list of all species present. Instead, vegetation will be common species unless otherwise noted. Common species is defined as species being present on at least 20% of plots within the stratum in accordance with dominant species.

Code

```
BH<-subset(Plotdata,Actual.Eco.Site=="BH")

 summary(BH$AvgPrecip)
 summary(BH$Slope)
```

```
summary(BH$Elevation)
summary(BH$EcolSite)
summary(BH$LandscapeType)
#

BH<-subset(soildata,Actual.Eco.Site=="BH")

summary(BH$Texture)
summary(BH$RockFragments)
summary(BH$Effer)
summary(BH$ESD_PctClay)
#
```

Summary () function provides range and mean. Subset () function selects only the data assigned to that Actual.Eco.Site . In this case it is a stratum, Basalt Hills (BH).

Example Results

```
BH<-subset(Plotdata,Actual.Eco.Site== BH )
summary(BH$AvgPrecip)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  7.00    9.00   10.38   11.23   12.69   30.30

> summary(BH$LandscapeType)
              Dunes       Fan Piedmont        Flat Plain
                  0                 10                 0
Floodplain/Flood basin  Hills/Mountains*         Other
                  0                 27                 0
          Terrace**
                  2
> |
```

Number of plots within each category will appear below the category if in the formatting such as that in the landscape type example.

Example Reporting

Annual precipitation ranges from 7-30.3 inches with a mean of 11.23 inches. Slope ranges from 1.19-58% with a mean of 16.27%. Elevation ranges from 2,285-2,769 meters with a mean of 2,501 meters. Landscape type is predominantly Hills/Mountains (27 plots) followed by Fan Piedmont (10 plots) and Terraces (2 plots).

Soil Stability

Soil stability is used to estimate the degree of soil structural development and erosion resistance. The test reflects the soils biotic integrity.

Method

Soil stability samples were calculated using the soil stability results in the Query Results in TerrADat for all strata. Specifically Soil.Stability.All, Soil.Stability.Protected and Soil.Stability.Unprotected columns were used.

Code

```
#soil stability
AIMdata1<-AIMdata %>%
  select(Soil.Stability.All,Soil.Stability.Protected,Soil.Stability.Unprotected,Actual.Eco.Site)

BH<-subset(AIMdata1,Actual.Eco.Site=="BH")

    #BH
    Type<-c("All Samples","Under Plant Cover","No Cover")
    Mean<-
    c(round(mean(BH$Soil.Stability.All),digits=2),round(mean(BH$Soil.Stability.Protected),digit
    s=2),round(mean(BH$Soil.Stability.Unprotected),digits=2))
    Minimum<-
    c(round(min(BH$Soil.Stability.All),digits=2),round(min(BH$Soil.Stability.Protected),digits=
    2),round(min(BH$Soil.Stability.Unprotected),digits=2))
    Maximum<-
    c(round(max(BH$Soil.Stability.All),digits=2),round(max(BH$Soil.Stability.Protected),digits=
    2),round(max(BH$Soil.Stability.Unprotected),digits=2))
    St.Dev.<-
    c(round(sd(BH$Soil.Stability.All),digits=2),round(sd(BH$Soil.Stability.Protected),digits=2)
    ,round(sd(BH$Soil.Stability.Unprotected),digits=2))
    ME<-
    c(round(1.282*(sd(BH$Soil.Stability.All)/BHN2),digits=2),round(1.282*(sd(BH$Soil.Stability.
    Protected)/BHN2),digits=2),round(1.282*(sd(BH$Soil.Stability.Unprotected)/BHN2),digits=2))
    BHdataframe<-data.frame(Type,Mean,Minimum,Maximum,ME)
    blank_bold<-formatter("span",
                            style = x ~ style("font-weight" = ifelse(x == Type, "bold", NA)))
    formattable(BHdataframe, list(
      Type = blank_bold))
```

Select() function allows for choosing the columns we are interested in. <- essentially means equals and allows us to create a vector and assign it a name. We then later combine these vectors into a data frame using data.frame . Round() changes the number of decimals. Obvious functions here are mean(), max() and min(). ME is calculating the margin of error with an 80% CI (z=1.282). Formattable () produces a table and is formatted using the formatter() function.

Example Results

Table . Summary of soil stability test results in the BH stratum. ME is the margin of error calculated using an 80% confidence interval.

Type	Mean	Minimum	Maximum	ME
All Samples	3.36	1.06	5.22	0.03
Under Plant Cover	3.89	1.20	5.88	0.04
No Cover	2.76	1.00	5.18	0.04

Example Reporting

Soil stability has an average of 3.36 for all samples with a difference of more than 1 between samples under and not under cover (Table).

Surface cover

Surface cover assists in understanding wind and water erosion, water infiltration and the sites ability to recover from disturbance. Surface cover is also specific to stratum and provides specific indicator benchmarks.

Method

Vegetation and surface cover data and invasive species were determined using the TerrADat LPI detail records. Percent of cover types were determined using the TerrADat project Query Results. Grass, forb, shrub, succulent and tree included noxious and nonnoxious species percent any hit. Shrub included shrub and subshrub noxious and nonnoxious percent any hit. For litter, TerrADat Total Percent Litter First Hit was used which includes woody and herbaceous litter. Foliar cover analysis was completed using Foliar Cover Percent Any Hit in the TerrADat project Query Results. Foliar Cover Percent Any Hit was determined using the LPI results and was defined as all vegetation cover.

Code

```
#surface cover
AIMdata$shrub.subshrub<-AIMdata$Shrub.Cover.Pct.Any.Hit+AIMdata$Noxious.SubShrub.Cover.Pct.Any.Hit+AIMdata$N
AIMdata$succulent<-AIMdata$Noxious.Succulent.Cover.Pct.Any.Hit+AIMdata$NonNoxious.Succulent.Cover.Pct.Any.Hi
AIMdata$tree<-AIMdata$Noxious.Tree.Cover.Pct.Any.Hit+AIMdata$NonNoxious.Tree.Cover.Pct.Any.Hit
AIMdata$noxiousforb<-AIMdata$Noxious.Annual.Forb.Cover.Pct.Any.Hit+AIMdata$Noxious.Perennial.Forb.Cover.Pct.
AIMdata$nonnoxiousforb<-AIMdata$NonNoxious.Annual.Forb.Cover.Pct.Any.Hit+AIMdata$NonNoxious.Perennial.Forb.C

#calculating Population Size, will be used throughout the entire script
BH<-subset(AIMdata,Actual.Eco.Site=="BH")
BHN<-count(BH,Primary.Key)
BHN2<-sum(BHN$n)
#calculating surface cover

AIMdata1<-AIMdata %>%
    select(Bare.Soil.Pct,Forb.Cover.Pct.Any.Hit,Grass.Cover.Pct.Any.Hit,Total.Litter.Cover.Pct.First.Hit,Rock.

AIMdata2<-gather(AIMdata1,covertype,covervalue,-Actual.Eco.Site)
Covers<-c("Bare Soil", "Forb","Grass", "Litter", "Rock","Shrub","Succulent","Tree","Foliar")
AIMdata2$covertype <- factor(AIMdata2$covertype, levels =
c("Bare.Soil.Pct","Forb.Cover.Pct.Any.Hit","Grass.Cover.Pct.Any.Hit","Total.Litter.Cover.Pct.First.Hit","Roc

BH<-subset(AIMdata2,Actual.Eco.Site=="BH")

BHpop<-paste("BH Surface Cover    n=",BHN2)
    #BH
SC<-ggplot(BH,aes(x=covertype,y=covervalue,col=covertype))+geom_point(alpha=0.4)
```

```
SC2<-SC+geom_boxplot()+ggtitle(paste0(BHpop))+labs(x="Cover Type",y="Average Percent
Cover",colour="Cover Type")
SC2+scale_x_discrete(labels= Covers)+scale_color_hue(labels =
Covers)+theme(axis.text.x=element_text(colour="gray20",angle = 45, hjust=1))
```

$ is used when creating a row in the dataframe. Count() provides the number of unique values. Sum() takes the sum of the requested values. Gather() changes the dataset from a long data set to a wide. Ggplot() is creating a scatterplot of the data requested and is then followed with more commands to convert it to whichever plot style needed (in this example geom_boxplot()). Paste() converts to a vector and concatenates the requested terms.
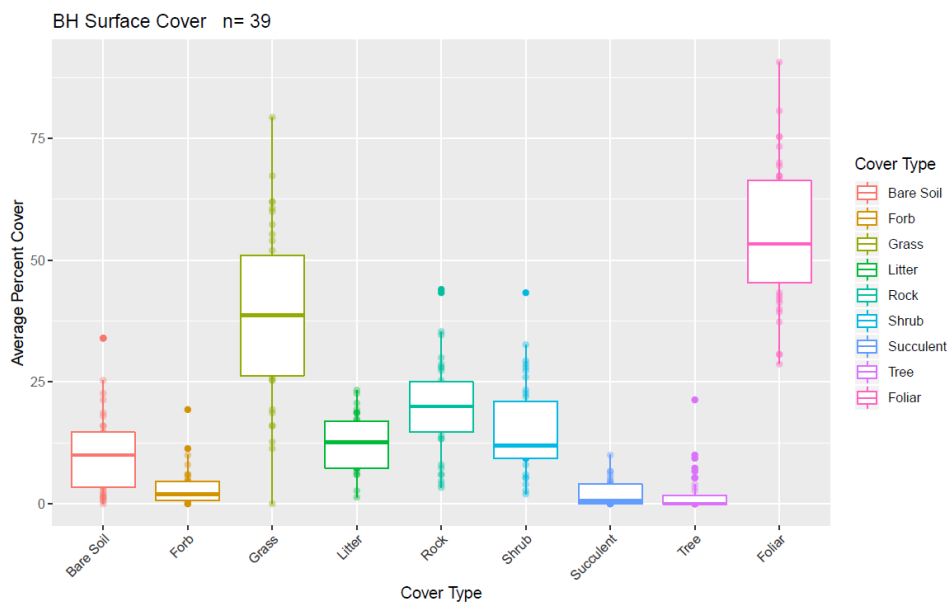
Example Results

Figure 4. Surface and vegetation cover using line-point intercept results for the BH stratum. n=population size.

Example Reporting

Grass and rock are the most dominant cover type in the BH stratum (Figure).

Dominant and Common Species

Dominant and common species are important indicators of land health. Dominant and common species represent biodiversity and are a result of their ecosystem.

Method

 Dominant and common species were determined using the TerrADat LPI detail records. Dominant species calculations were developed based on the commonly used definition of dominant species being the most abundant species. Abundance was determined by occurrence due to the relationship between the two (Gaston et al. 2000). Studies have used the most frequent occurrence (Kompala-Baba et al. 2019) or a set percentage of occurrence such as more than 10% or a mean of 20% (Dzwonko and

Loster 1989, Garcia-Palacios et al 2010) or a combination of both (Frieswyk et al. 2007). Due to the variety of sites within a single stratum, if occurring on 20% of plots for the stratum and if it had the highest percent cover, it was considered abundant. A specific criterion for percent cover was not selected due to high variation in ecosite types. Dominant species were determined by **1.** Calculating percent any hit of each species for each plot. **2.** Selecting species located on 20% or more of the sites for each stratum. **3.** Calculating the average for the species from step 2, the average includes plots that have a value of 0. **4.** Selecting the 2-4 species that had the highest average from step 3 and categorizing by growth habit (forb, graminoid, sedge, shrub, subshrub, succulent or tree). Common species used the same definition. Common species includes all species and dominant species is the four species with the highest percent cover per plot.

Code

```
#Dominant Species
##if a blank table is produced, no species meet the criteria of being present on 20% of the
plots. To adjust criteria change proportion on filter(dom_ss>=.2)
##SS_avg is the average species per plot. The first table produced lists species that are
only on 20% of the plots and ranks the
##species from greatest cover per plot to the least cover per plot

PSPS1<-PSPSdata[!is.na(PSPSdata$AH_SpeciesCover),]


##BH STRATA
##list of dominant species in order of species with highest percent occurence per plot,
note this step is only to determine the species
##present on 20% of the plots in the stratum. Other columns created will be used/modified
later in the code
BHD<- PSPS1 %>%
  select(PrimaryKey,AH_SpeciesCover,Species,Actual.Eco.Site,GrowthHabit) %>%
  group_by(Actual.Eco.Site) %>%
  filter(Actual.Eco.Site=="BH") %>%
  group_by(Species) %>%
  mutate(N_category=n()) %>%
  count(PrimaryKey,AH_SpeciesCover,Species,Actual.Eco.Site, GrowthHabit,N_category) %>%
  ungroup() %>%
  mutate(dom_ss=N_category/length(unique(PrimaryKey))) %>%
  filter(dom_ss >= .2) %>%
  group_by(Species) %>%
  mutate(SS_avg=sum(AH_SpeciesCover)/length(unique(PrimaryKey)))
BH<-BHD %>%
  mutate(zero=(length(unique(BHD$PrimaryKey))-N_category)) %>%
  arrange(desc(SS_avg))
PSPS3<-BH[!duplicated(BH$Species),]
PSPS4<- PSPS3 %>%
  select(Species)
```

```r
formattable(PSPS4)


##the zero output will show how many plots for each species need to have a 0 value added in
order to properly represent the data
BH1<-head(PSPS3,4)
BH2<-BH1 %>%
  select(Species,zero)
formattable(BH2)


##adding plots with 0 value, replace domss and species name and zero # based on results of
last step
#insert your dominant species code below, do not get rid of the quotes!
domss<-c("BOGR2","HECO26","KRLA2","PIED")
BHA<-BH %>%
  filter(Species %in% domss)
BH6<-BHA %>%
  select(Species,AH_SpeciesCover,PrimaryKey,GrowthHabit)
BH7<-as.data.frame(BH6)
#(species name, zero #)
A<-rep("BOGR2",2)
B<-rep("HECO26",22)
C<-rep("KRLA2",22)
D<-rep("PIED",30)
#(growthhabit, zero #)
A2<-rep("NonWoody",2)
B2<-rep("NonWoody",22)
C2<-rep("Woody",22)
D2<-rep("Woody",30)
Species_list<-c(A,B,C,D)
#the first number should be the total of all the zero values you are adding
AH_SpeciesCover_list<-replicate(76,0)
#the second number (after the colon) is also the total of all the zero values being added
PrimaryKey_list<-1:76
GrowthHabit_List<-c(A2,B2,C2,D2)
zeros<-
data.frame(Species=Species_list,AH_SpeciesCover=AH_SpeciesCover_list,PrimaryKey=PrimaryKey_
list,GrowthHabit=GrowthHabit_List)
#the below line of code will generate a warning message due to primarykey for zeros being
NA, continue with the code
BH8<-rbind(as.data.frame(BH7),zeros)
##BOX PLOT TITLES
BHpop<-paste("BH Percent Cover of Dominant Species    n=",BHN2)
```

!is.na() means is not NA and keeps the values in the dataframe and rows that are not NAs. Group() pairs categories with the same value and ungroup() returns to the initial data frame. Filter() chooses the values that meet the specified criteria. Mutate() creates a new column in the data set. Arrange() sorts the data based on the requested criteria. !duplicated() selects the values that are not duplicated. Head() only displays a portion of the dataframe. "Last step" in the code is adding plots with a dominant species value of 0 into the data frame. This is necessary to accurately show the spread of the data and correctly get the average of the species across all plots. Rbind() combines data frames. We created a data frame of dominant species with a value of zero and are adding it to the data frame which has the percent of species per plot.
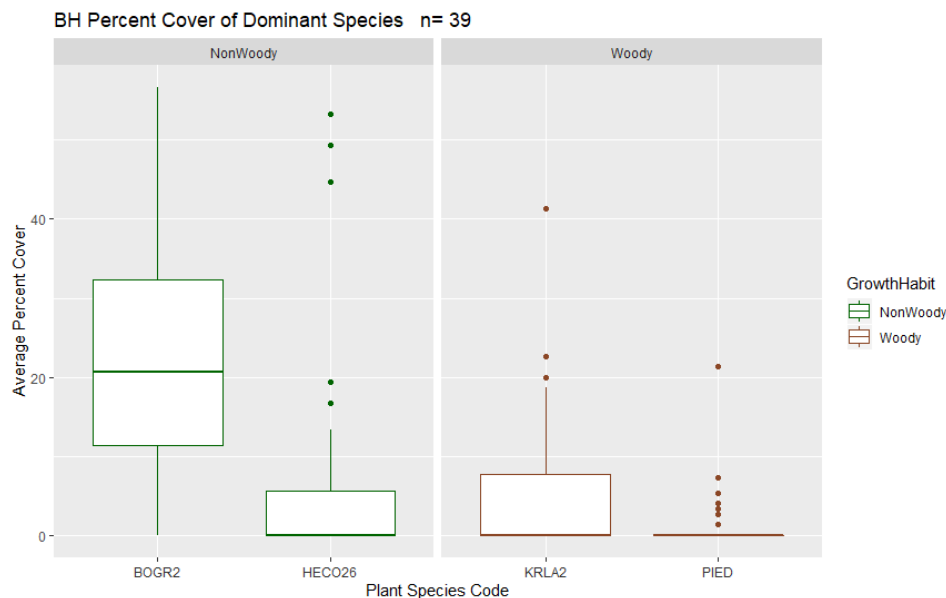
Example Results

Figure . Dominant species categorized by growth habit (woody or nonwoody) in the BH stratum based on LPI results. n=population size.

Example Reporting

Graminoid species BOGR2 and HECO26 and woody species KRLA2 dominated the stratum (Figure).

Gap

Gap is an important indicator of wind and water erosion, potential weed invasion and wildlife habitat (hiding cover and thermal environment).

Method

TerrADat Gap Detail (based on gap intercept results) was used to determine gap values. For all strata canopy gaps were placed into four groups based on size. The groups included gaps sized 25-50 cm, 51-100 cm, 101-200 cm and 200+ cm.

Code

```
Gapdata<-AIMdata %>%
```

```r
        select(Gap.Cover.25.to.50.Pct,Gap.Cover.51.to.100.Pct,Gap.Cover.101.to.200.Pct,Gap.Cover.20
        0.Plus.Pct,Actual.Eco.Site)
        Gapdata$CanopyCover<-100-
        (AIMdata$Gap.Cover.25.to.50.Pct+AIMdata$Gap.Cover.51.to.100.Pct+AIMdata$Gap.Cover.101.to.20
        0.Pct+AIMdata$Gap.Cover.200.Plus.Pct)
        Gapdata$Gaps<-
        Gapdata$Gap.Cover.25.to.50.Pct+Gapdata$Gap.Cover.51.to.100.Pct+Gapdata$Gap.Cover.101.to.200
        .Pct+Gapdata$Gap.Cover.200.Plus.Pct

        BHG<-subset(Gapdata,Actual.Eco.Site=="BH")
        #
        summary(BHG$Gaps)
        summary(BHG$CanopyCover)
        Gapdata<-AIMdata %>%

        select(Gap.Cover.25.to.50.Pct,Gap.Cover.51.to.100.Pct,Gap.Cover.101.to.200.Pct,Gap.Cover.20
        0.Plus.Pct,Actual.Eco.Site)
        Gapdata$CanopyCover<-100-
        (AIMdata$Gap.Cover.25.to.50.Pct+AIMdata$Gap.Cover.51.to.100.Pct+AIMdata$Gap.Cover.101.to.20
        0.Pct+AIMdata$Gap.Cover.200.Plus.Pct)
        Gapdata2<-gather(Gapdata,Gapsize,Percentofplot,-Actual.Eco.Site)
        Gapdata2$Gapsize <- factor(Gapdata2$Gapsize, levels =
        c("CanopyCover","Gap.Cover.25.to.50.Pct", "Gap.Cover.51.to.100.Pct",
        "Gap.Cover.101.to.200.Pct","Gap.Cover.200.Plus.Pct"))

        BHG2<-subset(Gapdata2,Actual.Eco.Site=="BH")
BHpop<-paste("BH Proportion Canopy Gap and Cover   n=",BHN2)
        GC<-ggplot(BHG2,aes(x="",y=Percentofplot,fill=Gapsize))
        GC2<-GC+geom_bar(width=0.5,position="fill", stat =
        "identity")+ggtitle(paste0(BHpop))+coord_flip()
        GC3<-GC2+scale_fill_manual(values=c("cadetblue3",
        "khaki1","sienna1","firebrick3","firebrick4"),labels=c("Canopy Cover (No Gap)","25-50
        (cm)","51-100 (cm)", "101-200 (cm)", "200+ (cm)"))
        GC3+theme(axis.title.y = element_blank())+labs(y="Percent of
        Plot")+scale_y_continuous(labels=scales::percent)
        #
```

Example Results

```
summary(BHG$Gaps)
 Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
13.12   31.93   41.00   41.48   51.66   70.97
summary(BHG$CanopyCover)
 Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
29.03   48.34   59.00   58.52   68.07   86.88
```

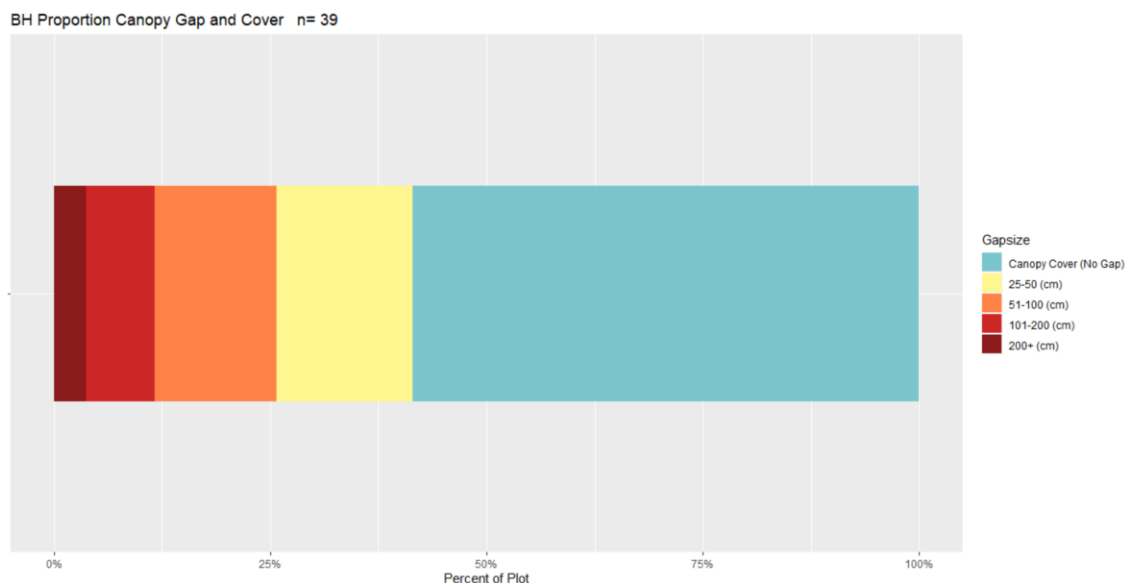BH Proportion Canopy Gap and Cover n= 39

Figure . Bar chart of average canopy cover and canopy gaps per plot for the BH stratum based on Gap Intercept results. Canopy cover was determined by subtracting the percent canopy gaps from 100. n=population size.

Example Reporting

Percent canopy gap ranges from 13.12-31.93% of the plot. Percent canopy cover ranges from 29.03-86.88% of the plot. The average percent of canopy gaps per plot is 41.48% and the average canopy cover is 58.52% (Figure).

Benchmarks

Benchmarks allow for an easy assessment of plot condition and results indicate management plan needs.

Method

Two methods for comparing plots to stratum indicator benchmarks are available. Method one is for areas with set benchmarks based on previous research. TerrADat Query Results were used in the comparison of actual values (calculations for each category outlined in section 6.1.1) to benchmark values. Method two creates benchmarks and is most insightful when there are multiple years of data for the area available. TerrADat Query Results were used to calculate the mean and standard deviation of each indicator. Indicators included bare soil, soil stability, rock, litter, gap, succulent, tree, shrub, grass, forb, forb height, grass height, noxious species, nonnoxious species and preferred forb number. The Empirical Rule states approximately 95% of the population would be within two standard deviations of the mean. Therefore, the benchmark for each indicator was set to the mean +/- two standard deviations. Bins were created for meeting (value of 1) or not meeting the indicator benchmark (value of 0) and meeting (1) or not meeting (0) all benchmarks. For each plot, the average percent of indicator benchmarks met was

calculated using these bins. For the stratum, the number of plots meeting all indicator benchmarks was calculated using the meeting/not meeting all benchmark bins. NAs were not included in the calculation. Plots within allotments with the lowest percent of indicators meeting benchmarks were recorded. If there was more than one plot in the allotment and one of the plots did not reach benchmark, it was noted. Number of plots meeting benchmark within each allotment was calculated using master sample and intensification results.

Code

Due to the size of the code, code and description of code functions are on Github in the file "Benchmark code and description".

Example Results

Method 1.

Table 35. Percent of master sample sites meeting the sampled stratum benchmarks.

Strata	Benchmark Category	% Meeting Benchmark
SD	Percent Bare Ground (10-40%)	72.22%
	Soil Aggregate Stability (>3)	61.11%
	Litter (5-20%)	27.78%
	Native (nonnoxious) Species (≥20%)	77.78%
	Percent Grass Cover (5-15%)	55.56%
	Percent Forb Cover (5-10%)	16.67%
	Percent Shrub Cover (10-35%)	27.78%
	Percent Nonnative (noxious) Species (≤15)	100.00%
	Number of Forbs (>5)	27.78%
	Shrub Density (≥0.25 shrub/m^2)	62.50%
SS	Percent Bare Ground (10-35%)	66.67%
	Soil Aggregate Stability (≥4)	11.11%
	Litter (10-40%)	66.67%
	Percent Grass Cover (>10%)	55.56%
	Percent Forb Cover (5-40%)	11.11%
	Percent Sage Cover (5-25%)	66.67%
	Percent Other Shrub Cover (5-15%)	44.44%
	Percent Tree Cover (<3%)	77.78%
	Grass Height (>10 cm)	100%
	Forb Height (>3 cm)	100%
	Sage Height (25-56 cm)	75%
	Percent Nonnative (noxious) Species (≤10)	100.00%

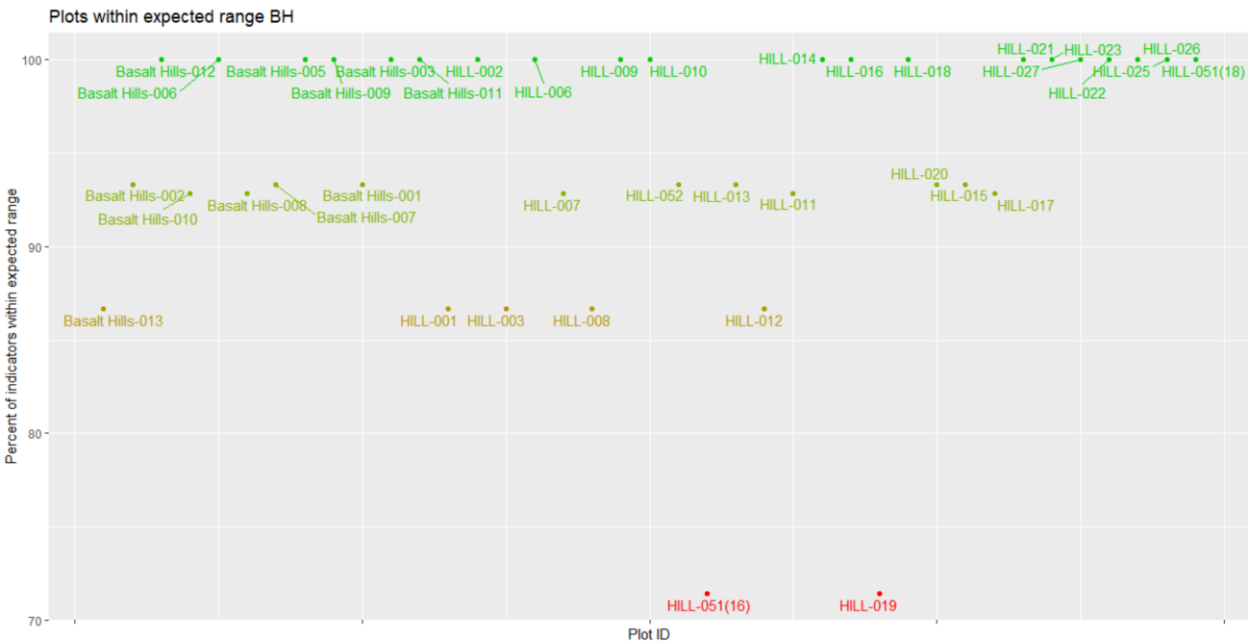Display of Plots within Benchmark by Benchmark Category
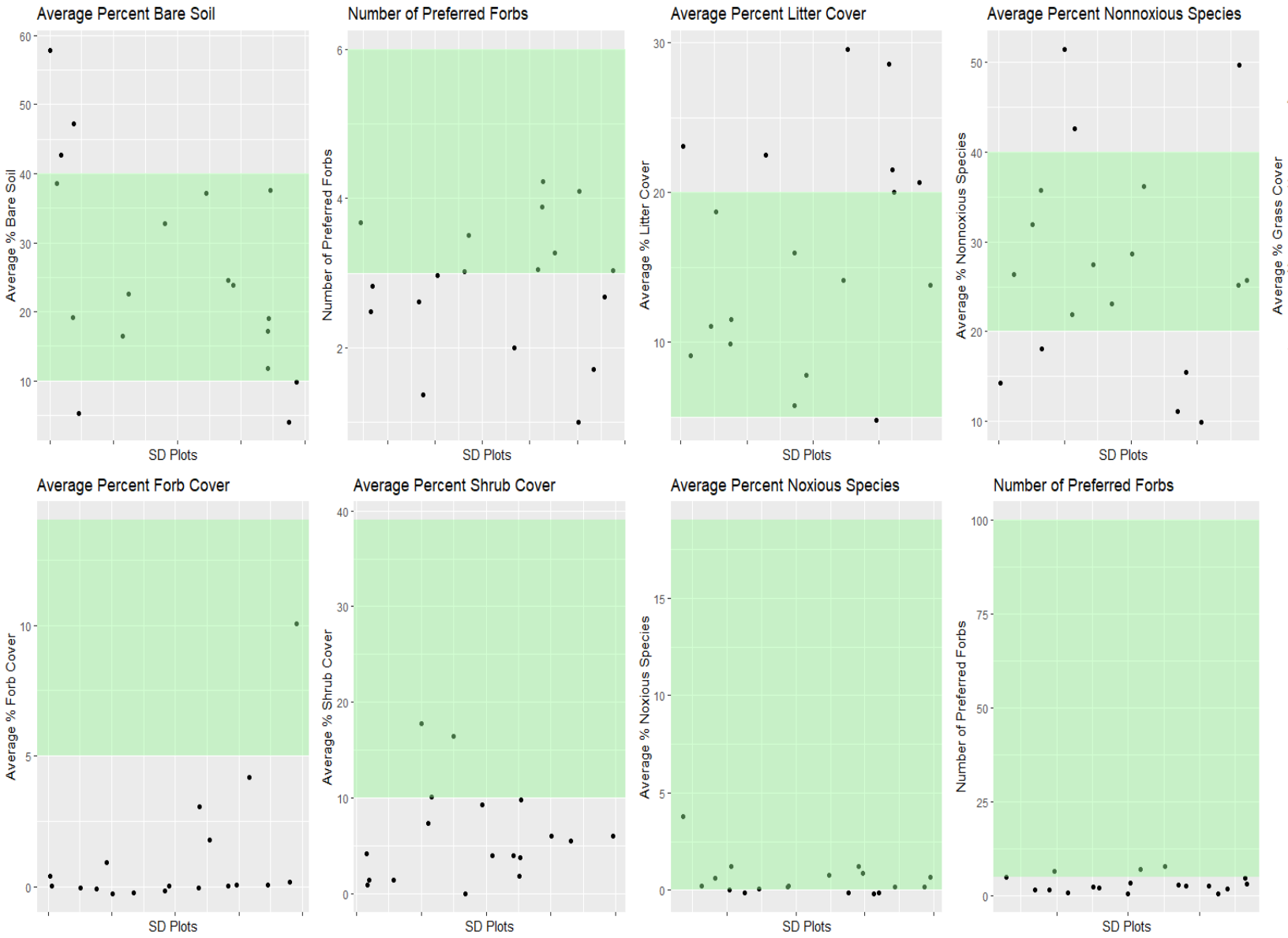
Method 2:

Figure . Percent of indicators meeting their expected benchmark range for each plot in the BH stratum.

Table . Percent of plots in the BH stratum that met each indicator.

Strata	Indicator	Percent.Meeting
BH	Percent Bare Ground	94.87
	Soil Aggregate Stability	94.87
	Litter	97.44
	Nonnoxious Species	97.44
	Percent Grass Cover	94.87
	Percent Forb Cover	94.87
	Percent Shrub Cover	97.44
	Percent Noxious Species	100.00
	Number of Forbs	97.44
	Percent Rock Cover	94.87
	Percent Tree Cover	97.44
	Percent Succulent Cover	97.44
	Percent Gap Cover	97.44
	Forb Height	100.00
	Grass Height	66.67
	Total Percent of Plots Meeting Benchmark	51.28

Table . Number of plots meeting all stratum indicator benchmarks. Displays allotments with at least 3 plots and at least one plot not meeting all benchmarks.

Allotment	Plots Meeting Benchmark (#)	Plots in Allotment (#)	Plots Meeting Benchmark (%)
Flat Top	0	3	0
McIntyre Gulch	0	3	0
Dry Lakes	0	3	0
North Tracy	1	4	25
Llano	1	4	25
East Bend	1	4	25
Foothills	1	4	25
Poncha Pass East	5	15	33.33
Poncha Pass-West	1	3	33.33
Noland Gulch	1	3	33.33
Pinon	2	6	33.33
Pinon Hills	2	6	33.33
None	14	31	45.16
Tracy Common	5	11	45.45
Trickle Mountain	7	15	46.67
McMahon/Greenie	5	10	50
Rajadero Canyon	2	4	50
Bishop Rock	3	6	50
Twin Lakes	2	4	50
Lakes	2	4	50
Poison Gulch	3	5	60
Little Mogotes	3	5	60
Valley View Hot Spng	3	5	60
River	2	3	66.67
Hat Springs	2	3	66.67
Capulin	2	3	66.67
Cross Creek	2	3	66.67
Blanca WHA	2	3	66.67
East Carnero Creek	3	4	75
Pup Peak	4	5	80

Example Reporting

20 plots (51.28%) met all indicator benchmarks in the BH stratum (Figure , Table). Within the allotments, 2/4 McMahon/Greenie, ½ Pup Peak and 3/5 Poncha Pass East plots did not meet all of the indicator benchmarks (Appendix). The plots meeting the least amount of indicator benchmarks included HILL-051(16) within the Pup Peak allotment and HILL-019 within the Llano allotment (Appendix). Grass height and cover, and forb height were the most common indicator benchmarks not met (Table).

Summary:

The summary section provides analysis methods and a comparison of the strata. Also included in this section of the report is the summary table.

Method

Presence of noxious species affects the ecosystem and is important for management purposes. Therefore, foliar cover was further divided into noxious and nonnoxious categories. The nonnoxious category was calculated using all Nonnoxious Plant Species Percent Any Hit in Query Results. The noxious category was calculated using all Noxious Plant Species Percent Any Hit in Query Results.

Annual grasses often occur prior to establishment of perennial grasses. Therefore, annual grass can be indicator of the site recovery or site condition. Annual and perennial grass covers were determined by using TerrADat Query Results, Annual Grass Percent Any Hit and Perennial Grass Percent Any Hit based on LPI results.

Stratum description will include a final summary table including categories surface indicators, dominant species, gap, height and species richness. Herbaceous heights were calculated using Average Herbaceous Height in TerrADat which is based of heights observed during LPI. Shrub/subshrub and tree heights were calculated from LPI detail in TerrADat. The average heights of shrub/subshrub and tree did not include none (0) values. The TerrADat Species Richness Detail records (based on observations during species richness) were used to calculate species richness.

Code

Due to the length of this code a separate report is available on Github in the Summary description and code file.

Example Results

Table . Strata with the highest value of each covertype. Values are all percent except for soil stability and are the average value for all plots within the stratum.

Covertype	Value	Strata
Rock Fragment	19.98	BH
Litter	24.22	FORE
Bare Soil	49.54	SAL
Foliar Cover	60.71	LOA
Shrub/Sub-shrub	18.93	LB
Grass	42.74	LOA
Succulent	4.67	MO
Tree	33.50	FORE
Forb/Herb	10.22	OTH
Soil Stability	4.57	FORE

Figure . Surface and vegetation cover for all master sample stratum based on LPI results.
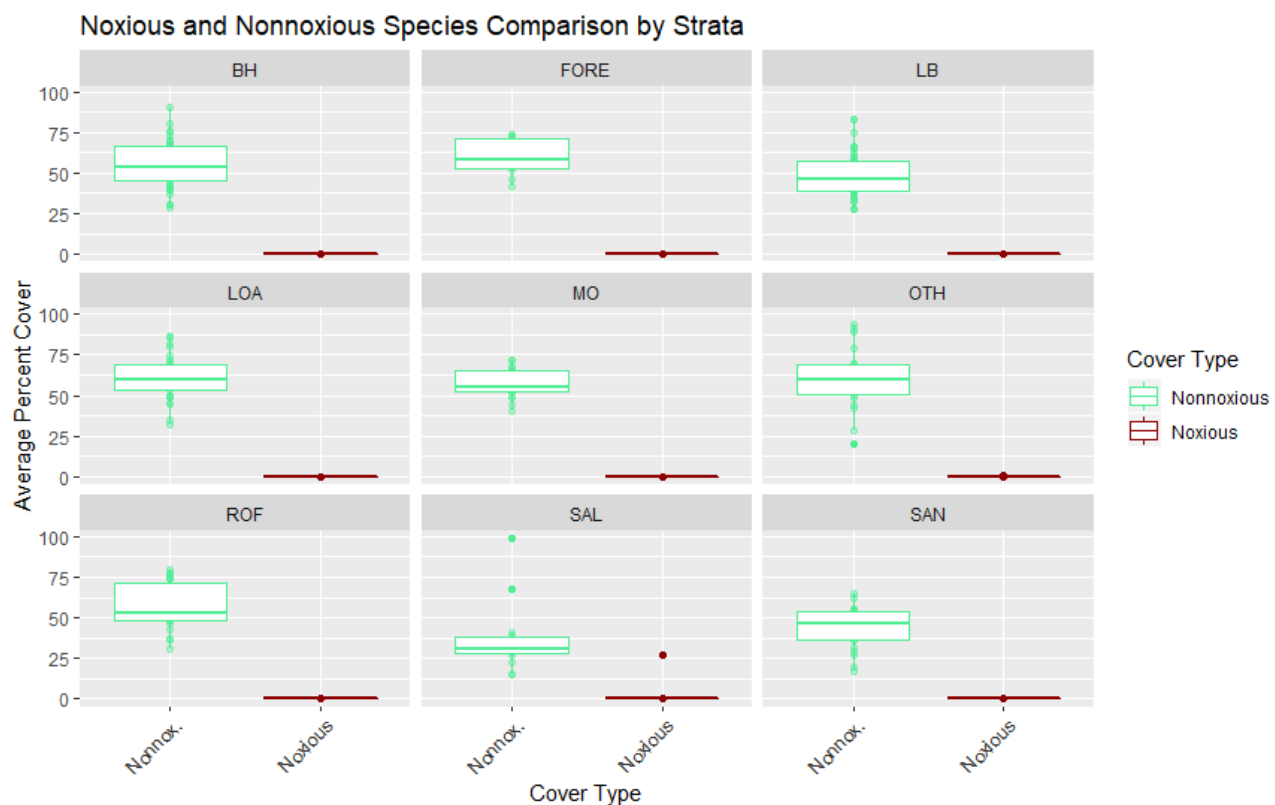
Figure . Percent nonnoxious and noxious species for the master sample categorized by stratum based on LPI results.
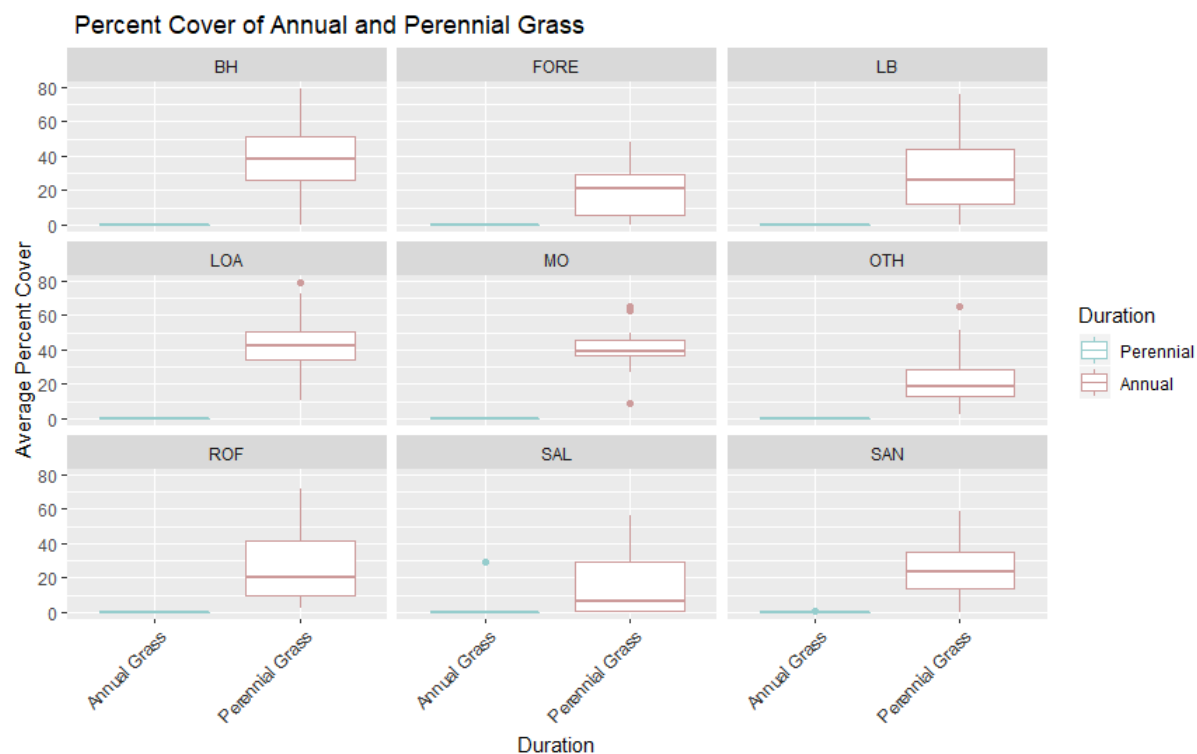

Figure 3. Percent perennial and annual grass hit during LPI for the master sample categorized by stratum.

Example Reporting

For all strata in SLVFO percent nonnoxious species is greater than percent noxious species (Figure). Average noxious species per plot was greatest in the SAL stratum (1.71%) followed by the OTH stratum (0.03%). Average percent nonnoxious species per plot was greatest in the LOA stratum (60.71%) followed by the OTH stratum (60.29%). Average percent nonnoxious species per plot was lowest in the SAL stratum (36.21%).

Annual and perennial grass covers were determined by using TerrADat Query Results, Annual Grass Percent Any Hit and Perennial Grass Percent Any Hit based on LPI results. For strata with grass cover, perennial grass was greater than annual grass for all strata. SAL and SAN have annual grass present on one plot (Figure).