

Making Expected Plot Outcomes

Samantha L. Davis

August 28, 2015

1 Goals

The goal of this vignette is to generate "expected plot outcomes" for analysis and comparison with SORTIE-ND. I need to develop parameters for "density" (number of trees) and basal area in each size class: seedling, sapling, and adult.

Seedlings are anything with no DBH, so we can only get density from them. We can also rely on the seedling subset data to increase those data's reliability.

Saplings are individualized. They're anything with a DBH between the minimum adult DBH and 0. So we'll need to classify those individually by species; maybe tag them all in the dataset then do a big aggregate.

Adults are easy.

2 Setup

First, I need to load the libraries and import that appropriate files.

```
> library(MakeMyForests)
> library(disperseR)
> library(SortieIO)
> head(ssdSeedlings)
```

	plot	subplot	sppcode	maxht	year	nSeedlings
1	bellow	8	PICO	10	1999	0
2	bellow	8	PICO	10	2000	0
3	bellow	8	PICO	10	2001	2
4	bellow	8	PICO	10	2002	0
5	bellow	8	PICO	10	2003	0
6	bellow	8	PICO	10	2004	0

```
> head(expandedTrees)
```

	species	plot	subplot	treeid	ingrowth	firstrec	deathyear	x	y	measyear	dbh
1	ABCO crackers		1	1	NA	1992	NA	89902.54	48132.50	1992	4.4
2	ABCO crackers		1	1	NA	1992	NA	89902.54	48132.50	1997	5.0
3	ABCO crackers		1	1	NA	1992	NA	89902.54	48132.50	2002	5.6

```

4      ABCO crackers      1      1      NA      1992      NA 89902.54 48132.50      2007 6.0
5      ABCO crackers      1      1      NA      1992      NA 89902.54 48132.50      2012 6.2
6      ABCO crackers      1      2      NA      1992      NA 89908.76 48133.72      1992 8.7
  nSdl
1      1
2      1
3      1
4      1
5      1
6      1

>
>
>
>

```

Okay, I need to transform `ssdSeedlings` into something useable.

```

> ## clean up
> seedlings <- ssdSeedlings[which(ssdSeedlings$nSeedlings >0) ,]
> seedlings <- aggregate(seedlings$nSeedlings, by=list(seedlings$plot,
+                                                       seedlings$subplot,
+                                                       seedlings$sppcode,
+                                                       seedlings$year),
+                         FUN=sum)
> colnames(seedlings) <- c("plot", "subplot", "species", "measyear", "nSdl")
> expandedSeedlings <- data.frame(species=seedlings$species,
+                                  plot=seedlings$plot, subplot=seedlings$subplot,
+                                  treeid=0, ingrowth=NA, firstrec=seedlings$measyear,
+                                  deathyear=NA, x=NA, y=NA,
+                                  measyear=seedlings$measyear, dbh=NA, stage="seedling",
+                                  basalarea=NA, mindbh=NA,
+                                  nSdl=seedlings$nSdl, stringsAsFactors=F)
> ## set up nSdl in expandedTrees so we can merge
> expandedTrees$nSdl <- 1
> head(expandedTrees)

  species      plot subplot treeid ingrowth firstrec deathyear      x      y measyear dbh
1  ABCO crackers      1      1      NA      1992      NA 89902.54 48132.50      1992 4.4
2  ABCO crackers      1      1      NA      1992      NA 89902.54 48132.50      1997 5.0
3  ABCO crackers      1      1      NA      1992      NA 89902.54 48132.50      2002 5.6
4  ABCO crackers      1      1      NA      1992      NA 89902.54 48132.50      2007 6.0
5  ABCO crackers      1      1      NA      1992      NA 89902.54 48132.50      2012 6.2
6  ABCO crackers      1      2      NA      1992      NA 89908.76 48133.72      1992 8.7
  nSdl
1      1
2      1

```

```

3     1
4     1
5     1
6     1

> expandedSeedlings <- rbind(expandedTrees, expandedSeedlings)

Aggregate:

> plotChars <- aggregate(expandedTrees$basalarea,
+                         by=list(expandedTrees$plot,
+                               expandedTrees$species,
+                               expandedTrees$measyear,
+                               expandedTrees$stage),
+                         FUN=length)
> colnames(plotChars) <- c("plot", "species", "year", "stage", "AbsDen")
> ## do the seedlings separately
> plotSdls <- aggregate(expandedSeedlings$nSdl,
+                      by=list(expandedSeedlings$plot,
+                              expandedSeedlings$species,
+                              expandedSeedlings$measyear),
+                      FUN=sum)
> colnames(plotSdls) <- c("plot", "species", "year", "nSdl")
> test <- merge(plotSdls,
+               plotChars[plotChars$stage=="seedling",c(1,2,3,5)],
+               by=c("plot", "species", "year"),
+               all=T)
> test[is.na(test$nSdl), "nSdl"] <- 0
> test[is.na(test$AbsDen), "AbsDen"] <- 0
> test$sum <- test$nSdl + test$AbsDen
> test$AbsDen <- test$sum
> test <- test[,c(1:3,5)]
> test$stage <- "seedling"
> rawr <- merge(test, plotChars,
+               by=c("plot", "species", "year", "stage"),
+               all=T)
> rawr[rawr$stage=="seedling", "AbsDen.y"] <- rawr[rawr$stage=="seedling", "AbsDen.x"]
> plotChars <- rawr[, c(1:4,6)]
> colnames(plotChars) <- c("plot", "species", "year", "stage", "AbsDen")
> absBA <- aggregate(expandedTrees$basalarea,
+                   by=list(expandedTrees$plot,
+                           expandedTrees$species,
+                           expandedTrees$measyear,
+                           expandedTrees$stage),
+                   FUN=sum)
> colnames(absBA) <- c("plot", "species", "year", "stage", "AbsBA")
> plotChars <- merge(plotChars, absBA,

```

```

+           by=c("plot", "species", "year", "stage"), all=T)
> ## put in plot normalizer
> plotChars <- merge(plotChars, ssdPlotDesc[,c(1,3)])
> plotChars$AbsDenByHa <- plotChars$AbsDen/plotChars$size_ha
> plotChars$AbsBAByHa <- plotChars$AbsBA/plotChars$size_ha
> plotChars$year <- as.numeric(plotChars$year)
> ## prepping for input into big table
> ## making years into steps
> uniqueplots <- unique(plotChars$plot)
> for(i in 1:length(uniqueplots)){
+   plotChars[
+     plotChars$plot==uniqueplots[i], "year"] <- plotChars[
+       plotChars$plot==uniqueplots[i], "year"] -
+       ssdPlotDesc[ssdPlotDesc$plot==uniqueplots[i], "minYear"]
+     + 1
+   }
> ## make fake plot names into real plot names
> ##
>
> plotChars <- convertPlotNames(plotChars, "plot", F)
> plotChars <- plotChars[!is.na(plotChars$plot),]

```

Ok, so we developed our plotchars table, now we need to format it correctly and get it to overwrite "realPlots".

```

> plotCharUniques <- unique(plotChars[, c("plot", "species", "year")])
> ## set up end table
>
> ## get ready to fill with the variables that we have
>
> ## change colnames to match some
> colnames(plotChars)[c(1:3,9)] <- c("Species", "Step", "Stage", "Plot")
> AdultAbsBA <- subset(plotChars, Stage=="tree",
+   select=c("Plot", "Step", "Species", "AbsBA"))
> SaplAbsBA <- subset(plotChars, Stage=="sapling",
+   select=c("Plot", "Step", "Species", "AbsBA"))
> AdultAbsDen <- subset(plotChars, Stage=="tree",
+   select=c("Plot", "Step", "Species", "AbsDen"))
> SdlAbsDen <- subset(plotChars, Stage=="seedling",
+   select=c("Plot", "Step", "Species", "AbsDen"))
> SaplAbsDen <- subset(plotChars, Stage=="sapling",
+   select=c("Plot", "Step", "Species", "AbsDen"))
> newRealPlots <- data.frame(Plot=plotCharUniques[,1],
+   Step=plotCharUniques[,3],
+   Species=plotCharUniques[,2],
+   stringsAsFactors=F)
> newRealPlots <- merge(newRealPlots, AdultAbsBA, all=T)

```

```

> newRealPlots <- merge(newRealPlots, AdultAbsDen, all=T)
> colnames(newRealPlots)[4:5] <- c("AdultAbsBA", "AdultAbsDen")
> newRealPlots <- merge(newRealPlots, Sap1AbsBA, all=T)
> newRealPlots <- merge(newRealPlots, Sap1AbsDen, all=T)
> colnames(newRealPlots)[6:7] <- c("Sap1AbsBA", "Sap1AbsDen")
> newRealPlots <- merge(newRealPlots, Sd1AbsDen, all=T)
> colnames(newRealPlots)[8] <- c("Sd1AbsDen")
> head(newRealPlots)

```

	Plot	Step	Species	AdultAbsBA	AdultAbsDen	Sap1AbsBA	Sap1AbsDen	Sd1AbsDen
1	BBBPIPO	0	ABCO	6.97691162	44	1.248244859	113	167
2	BBBPIPO	0	CADE	23.18374115	310	3.123211430	385	713
3	BBBPIPO	0	PILA	0.62500404	5	0.940746622	58	83
4	BBBPIPO	0	PIPO	17.21646202	34	0.203435093	12	48
5	BBBPIPO	0	QUCH	0.08263193	4	0.000447678	3	77
6	BBBPIPO	0	QUKE	14.90317784	282	0.275058861	23	315

```

> tail(newRealPlots)

```

	Plot	Step	Species	AdultAbsBA	AdultAbsDen	Sap1AbsBA	Sap1AbsDen	Sd1AbsDen
678	WTABMA	7	PIXX	NA	NA	NA	NA	1
679	WTABMA	8	ABMA	NA	NA	NA	NA	400
680	WTABMA	9	ABMA	NA	NA	NA	NA	927
681	WTABMA	9	ABXX	NA	NA	NA	NA	28
682	WTABMA	9	PIMO	NA	NA	NA	NA	1
683	WTABMA	9	PIXX	NA	NA	NA	NA	2

3 Mortality

We should also get some death rates / mortality in there while we're at it. That might take a bit more hunting around for where the data and previous calculations are located.

4 Mortality