

HabplanR Vignette

A complimentary R tool for the harvest scheduling program Habplan, including pre- and post-processing of Habplan files, and the incorporation of spatial configuration for decision-making.



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Introduction to HabplanR

The *HabplanR* package was developed to compliment Habplan software. Habplan is a landscape management and harvest scheduling program that performs multi-objective optimization via a Metropolis-Hastings algorithm. The functionality of Habplan is still sought after in today's landscape management problems; however, the use of Habplan is limited, requiring in-depth knowledge of not only the management issue at hand, but also about tedious file-formatting and input requirements for the program to run efficiently. This is where *HabplanR* comes in!

The main functions of *HabplanR* are to provide important ecological context to the multi-objective optimization performed by Habplan, and to streamline the use of the program. Specifically, the *HabplanR* R package has the following objectives:

- Use forest condition data to create Habplan-appropriate input files
- Use forest condition data to develop context-specific Habitat Suitability Index values
- Set Habplan program parameters and configurations within the R environment prior to program initiation
- Visualize Habplan outputs
- Perform spatial analyses focused at either the forest stand, habitat patch or entire landscape level

The following vignette provides a working example of using the *HabplanR* package.

The *HabplanR* package is currently open-access on a GitHub repository. To download and install the package, we first need the devtools package.

```
#Install devtools:  
install.packages("devtools") #Ignore if previously installed  
#Load devtools into the session:  
library(devtools)
```

We can now use the devtools package to install *HabplanR* from GitHub.

```
install_github("maxdoltonjones/HabplanR", build_vignettes = TRUE, force = TRUE)  
  
#The installation might ask if any package updates are needed. If this is prompted,  
#skip these by running the number three (3):  
3
```

The installation of the package should also prompt the installation of all package dependencies (other packages which are needed for *HabplanR* to work). However, if this is not the case, run the following lines (this may take a few minutes or so):

```
install.packages("readr")
install.packages("dplyr")
install.packages("ggplot2")
install.packages("broom")
install.packages("spdep")
install.packages("terra")
install.packages("tidyterra")
install.packages("landscapemetrics")
```

Again, if these packages are already installed, the dependencies will be loaded at the same time as *HabplanR* is loaded. However, we can also load all of the dependencies separately.

```
#We include the package versions used to create this vignette

library(readr) #v.2.1.2
library(dplyr) #v.1.0.10
library(ggplot2) #v.3.3.6
library(broom) #v.1.0.5
library(spdep) #v.1.2-7
library(terra) #v.1.6-17
library(tidyterra) #v.0.0.3.2
library(landscapemetrics) #v.1.5.5
```

The *HabplanR* package works by saving and loading files from the working directory. It is important to set the working directory to the location where all of the input files are located, and where output files will be saved. This working directory will stay consistent for the entire vignette.

```
setwd("FILEPATH HERE")
```

Within the working directory that we just assigned, we need the following files:

- Stand_info.csv (Stand IDs, acreage, and description)
- fvs_results-new.csv (Stand data from projected growth model)

Now load in the *HabplanR* package.

```
library(HabplanR)
```

We now need to read in the data. First we will import a csv file which contains information about the forest stands we are interested in. The information we are interested in with this file is the stand acreage, which will link to a specific stand id. We will name this std.info

```
#Load in stand information - needed mostly for acreage
std.info <- read_csv("Stand_info.csv")

#Take a look at the data
head(std.info)
#> # A tibble: 6 x 3
#>   std_id    acres description
```

```

#> <chr>     <dbl> <chr>
#> 1 15588_1   57.2 Planted Longleaf Pine Forest
#> 2 15588_10   9.88 Planted Loblolly Pine Forest
#> 3 15588_100  14.3 Planted Longleaf Pine Forest
#> 4 15588_101  13.0 Natural Loblolly Pine Forest
#> 5 15588_102  19.0 Upland Hardwood Forest
#> 6 15588_103  1.45 Mesic Hardwood Forest

```

The next data we need are the results from a simulation software which provides outputs based on a particular management regime to a stand, or set of stands. For this vignette, we are using data output from Forest Vegetation Simulator (FVS; <https://www.fs.usda.gov/fvs/>). We will call these data std.data.

```

#Next, load in the data resulting from the Forest Vegetation Simulator (FVS)
std.data <- read_csv("fvs_results_new.csv")

#Take a look at the data
head(std.data)

```

```

#> # A tibble: 6 x 36
#>   ...1 Regime~1 Regim~2 StandID Year Age   BA    TPA Pine_~3 Pine_~4 Pine_~5
#>   <dbl> <chr>   <chr>   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
#> 1     0 Batch2 Thin 1~ 15588_1  2017   9  5.53  266.   1.35   0      0
#> 2     1 Batch2 Thin 1~ 15588_1  2020  12  8.82  265.   1.83   0      0
#> 3     2 Batch2 Thin 1~ 15588_1  2023  15  8.17  169.   2.10   0      0
#> 4     3 Batch2 Thin 1~ 15588_1  2026  18 10.8   168.   2.79   0      0
#> 5     4 Batch2 Thin 1~ 15588_1  2029  21 14.0   168.   3.43   0.294  0
#> 6     5 Batch2 Thin 1~ 15588_1  2032  24 17.6   167.   3.42   1.27   0
#> # ... with 25 more variables: Hdwd_Pulp_Tons <dbl>, Hdwd_Saw_Tons <dbl>,
#> # Harv_P_Pulp_Tons <dbl>, Harv_P_CNS_Tons <dbl>, Harv_P_Saw_Tons <dbl>,
#> # Harv_H_Pulp_Tons <dbl>, Harv_H_Saw_Tons <dbl>, LL_BA_1to4 <dbl>,
#> # LL_BA_4to8 <dbl>, LL_BA_8to12 <dbl>, LL_BA_12to16 <dbl>,
#> # LL_BA_16to20 <dbl>, LL_BA_20andup <dbl>, Pine_BA_1to4 <dbl>,
#> # Pine_BA_4to8 <dbl>, Pine_BA_8to12 <dbl>, Pine_BA_12to16 <dbl>,
#> # Pine_BA_16to20 <dbl>, Pine_BA_20andup <dbl>, Hdwd_BA_1to4 <dbl>, ...

```

Function: data conversion - *HabConvert*

We are going to create a flow file (Habplan input file) for the HSI values we have just calculated and inserted into our data frame.

Each line of the flow file has to have the standID, regimeID, years, and flow outputs.

We need to provide the custom function with four arguments:

1. std.data: the flow information in csv format (above)
2. std.info: the information file for each forest stand (above)
3. col: the column of data interested in from std.data (below)
4. nyear: the number of years the simulator is run for (35 in this example)

Look at the column headings to decide which column has flow results.

```

colnames(std.data)
#> [1] "RegimeKey"      "Regime Activity"   "StandID"        "Year"
#> [5] "Age"           "BA"                 "TPA"            "Pine_Pulp_Tons"
#> [9] "Pine_CNS_Tons" "Pine_Saw_Tons"    "Hdwd_Pulp_Tons" "Hdwd_Saw_Tons"
#> [13] "Harv_P_Pulp_Tons" "Harv_P_CNS_Tons" "Harv_P_Saw_Tons" "Harv_H_Pulp_Tons"
#> [17] "Harv_H_Saw_Tons" "LL_BA_1to4"       "LL_BA_4to8"     "LL_BA_8to12"
#> [21] "LL_BA_12to16"   "LL_BA_16to20"    "LL_BA_20andup" "Pine_BA_1to4"
#> [25] "Pine_BA_4to8"   "Pine_BA_8to12"   "Pine_BA_12to16" "Pine_BA_16to20"
#> [29] "Pine_BA_20andup" "Hdwd_BA_1to4"   "Hdwd_BA_4to8"   "Hdwd_BA_8to12"
#> [33] "Hdwd_BA_12to16" "Hdwd_BA_16to20" "Hdwd_BA_20andup" "HSI"

```

From the column names, we are interested in “Harv_P_Pulp_Tons” (pulp pinewood harvested [tons/acre]) and “HSI” (stands over a specific habitat suitability index value), which are column number 13 and 36 respectively. We can input a column number into our function. We also need to provide “nyear” which is the number of years (or time periods) that you are interested in (e.g., nyyear = 35 could equal 35 years or 35 3-year periods). Lastly, if the column that you are interested in is HSI, then you also need to provide a threshold amount for the habitat to be available for your species. The HSI is on a scale between 0-1, so a threshold of 0.5 would mean that anything below 0.5 would be deemed as not habitat, whereas any values above 0.5 would be habitat and therefore added to the flow file. Below, we have set the HSI threshold value to 0.7 for creating our HSI flow file.

Later in the vignette, we provide an additional function for creating HSI values using growth model data and user-defined formula.

```

#Create flow file for Harv_P_Pulp_Tons
out.flow.1 <- habConvert(std.data = std.data, std.info = std.info, col = 13,
                        nyyear = 35)

#Create flow file for HSI
out.flow.2 <- habConvert(std.data = std.data, std.info = std.info, col = 36,
                        nyyear = 35, HSI = 0.7)

```

Now we will have two flow files saved in our working directory:

- Harv_P_Pulp_Tons.dat
- HSI.dat

For the HSI flow file, if a stand has an HSI over our threshold for that time period, then the flow will show the acreage of the stand. If the HSI was below our threshold, the flow will equal zero. The Harv_P_Pulp_Tons flow file contains data for each time period extracted directly from the FVS growth model.

Function: create project file - *WriteProj*

Another utility of HabplanR is creating project files that can be loaded into habplan to set parameters and other configurations.

The only arguments needed for the function to work are the object names for each flow component that needs to be included.

Because Habplan inputs allow for customization, we provide code that will allow users the same level of input manipulation. Below, we give examples on how to set up these arguments, which will be wrapped into our project file using our custom function.

First, setup the main information needed by Habplan prior to flow setup. We need to create four objects in the R environment for the function to create a project file:

- npoly: The number of unique forest stands.
- config: The configuration of flow components and subcomponents (see below and page 46 of Habplan Manual)
- wd: The working directory where flow files are stored, and output files are to be stored.
- iter: The number of iterations of Habplan (see page 13 of Habplan Manual)

Config is a string of numbers, where each number represents a flow component or subcomponent to be considered during the Habplan run. The first number represents the number of flows (N), followed by N pairs of numbers that represent clearcut and blocksize subcomponents (0 or 1). The final three numbers are Biol1, Biol2, and Spatial Model subcomponents (0 or 1; see section 10, 11, and 12 of Habplan Manual). Our assigned configuration below states that we are considering two flow components only, with no additional subcomponents.

```
#Overarching information for habplan run:  
#Get the number of stands for later  
npoly <- length(unique(std.data$StandID))  
#We can override config by using the following:  
config <- "2,0,0,0,0,0,0,0"  
#wd is the working directory where data are stored (end with '/' as shown below)  
wd <- "FILEPATH HERE/" #same as original working directory assigned above  
#iter is the number of iterations needed for the habplan run  
iter <- "10000"
```

Next, we will input the specific information needed for each flow component. This is where specific objectives, weights, and targets are assigned to produce the most suitable outcome based on the forest stands and management aims.

For this vignette, we will work with two flow files, our HSI and harvested pine pulpwood flows that we created above. We want to achieve the highest acreage of appropriate HSI, while also being able to harvest as much pine pulpwood as possible.

To maintain a relatively simple workflow for our vignette, we will input all parameters but focus on three main objects that we will edit to achieve our schedule outcomes. The edited objects will be thlo (Lower Threshold), thhi (Upper Threshold), and the model (The modeled targets throughout our study period). The numbers assigned to thlo and thhi determine how much upper and lower flexibility there is in our targets. For example, setting thlo and thhi to 50 and 150 respectively means that our target can not deviate any lower than 50 units, and no higher than 150. If we're wanting to achieve results that maximise output/yield then setting a large thhi may help.

Below we are setting our model for both flows as 1000 in the first year, 2500 in year 20, and 5000 in year 30 (assigned as 1,1000;20,2500;30,5000;). Our thlo and thhi are set to 1000 and 5000 respectively, allowing broad fluctuations from our targets.

```
#Info for f1 component ----  
f1.file <- paste0(wd,"HSI.dat")  
f1.bystone <- ""  
f1.time0 <- "10000"  
f1.goal0 <- "0.1"  
f1.thlo <- "1000"  
f1.thhi <- "5000"  
f1.goalplus <- ".05"
```

```

f1.goalf <- "0.5"
f1.slope <- "0.0"
f1.weightf <- "1.0"
f1.weight0 <- "1.0"
f1.model <- "1,1000;20,2500;30,5000;"
f1.title <- "Breed.dat"
#Combine f1 components for writing
f1.comp <- c('<flow title="F1 Component">',
  paste0('<file value=""', f1.file, '" />'),
  paste0('<bygone value=""', f1.bypgone, '" />'),
  paste0('<time0 value=""', f1.time0, '" />'),
  paste0('<goal0 value=""', f1.goal0, '" />'),
  paste0('<threshLo value=""', f1.thlo, '" />'),
  paste0('<threshHi value=""', f1.thhi, '" />'),
  paste0('<goalPlus value=""', f1.goalplus, '" />'),
  paste0('<goalF value=""', f1.goalf, '" />'),
  paste0('<slope value=""', f1.slope, '" />'),
  paste0('<weightF value=""', f1.weightf, '" />'),
  paste0('<weight0 value=""', f1.weight0, '" />'),
  paste0('<model value=""', f1.model, '" />'),
  paste0('<title value=""', f1.title, '" />'),
  '<bounds height="330" width="366" x="553" y="443" />',
  "</flow>")

#Info for f2 component ----
f2.file <- paste0(wd, "Harv_P_Pulp_Tons.dat")
f2.bypgone <- ""
f2.time0 <- "1000"
f2.goal0 <- "0.1"
f2.thlo <- "1000"
f2.thhi <- "5000"
f2.goalplus <- ".05"
f2.goalf <- "0.5"
f2.slope <- "0.0"
f2.weightf <- "1.0"
f2.weight0 <- "1.0"
f2.model.1 <- "1,1000;20,2500;30,5000;"
f2.title <- "Harv_P_Pulp_Tons.dat"
#Combine f2 components for writing
f2.comp <- c('<flow title="F2 Component">',
  paste0('<file value=""', f2.file, '" />'),
  paste0('<bygone value=""', f2.bypgone, '" />'),
  paste0('<time0 value=""', f2.time0, '" />'),
  paste0('<goal0 value=""', f2.goal0, '" />'),
  paste0('<threshLo value=""', f2.thlo, '" />'),
  paste0('<threshHi value=""', f2.thhi, '" />'),
  paste0('<goalPlus value=""', f2.goalplus, '" />'),
  paste0('<goalF value=""', f2.goalf, '" />'),
  paste0('<slope value=""', f2.slope, '" />'),
  paste0('<weightF value=""', f2.weightf, '" />'),
  paste0('<weight0 value=""', f2.weight0, '" />'),
  #paste0('<model value="1,', f2.target, ';', f2.next.year, ',',

```

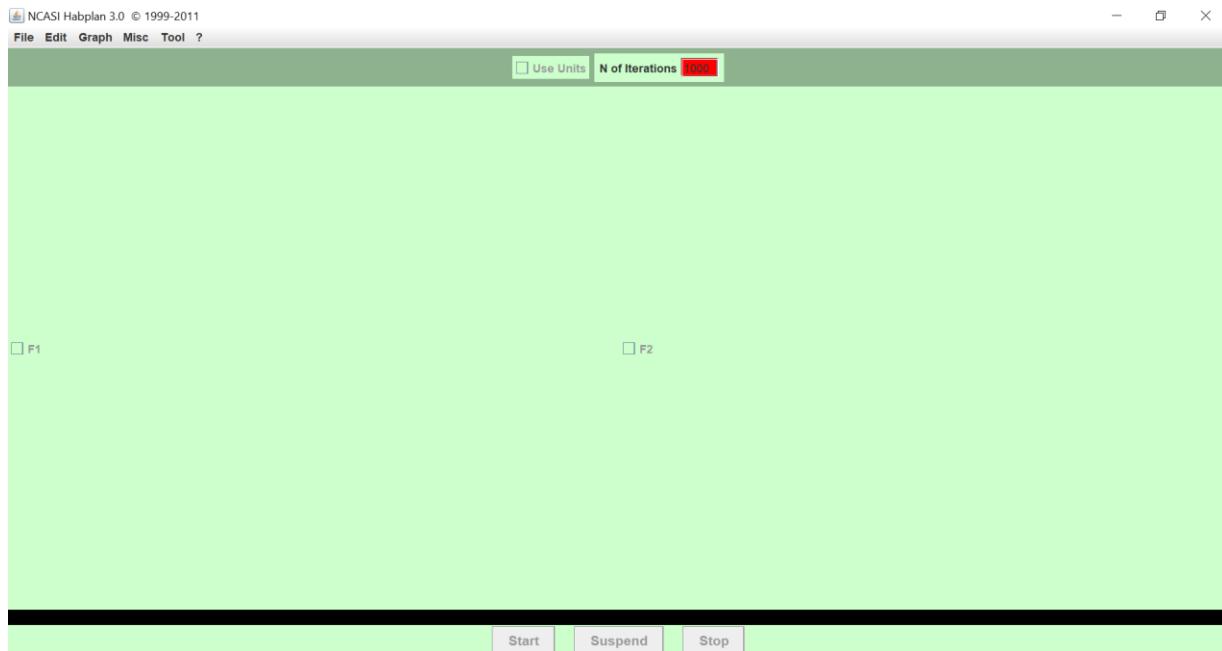
```
#      f2.next.target, '" />'),
paste0('<title value="', f2.title, '" />'),
'<bounds height="331" width="368" x="1260" y="440" />',
"</flow>")
```

```
#Provide each of these flow component objects to the function and run
writeProj(f1.comp = f1.comp, f2.comp= f2.comp)
```

Now we have a project file saved to our working directory. Let's open habplan and see if this has worked. The Habplan program needs to be stored in the working directory that was assigned earlier, so that it can be run from RStudio below.

```
#Open Habplan (if run from here, R functionality will cease until Habplan is closed)
shell("h", wait=TRUE)
```

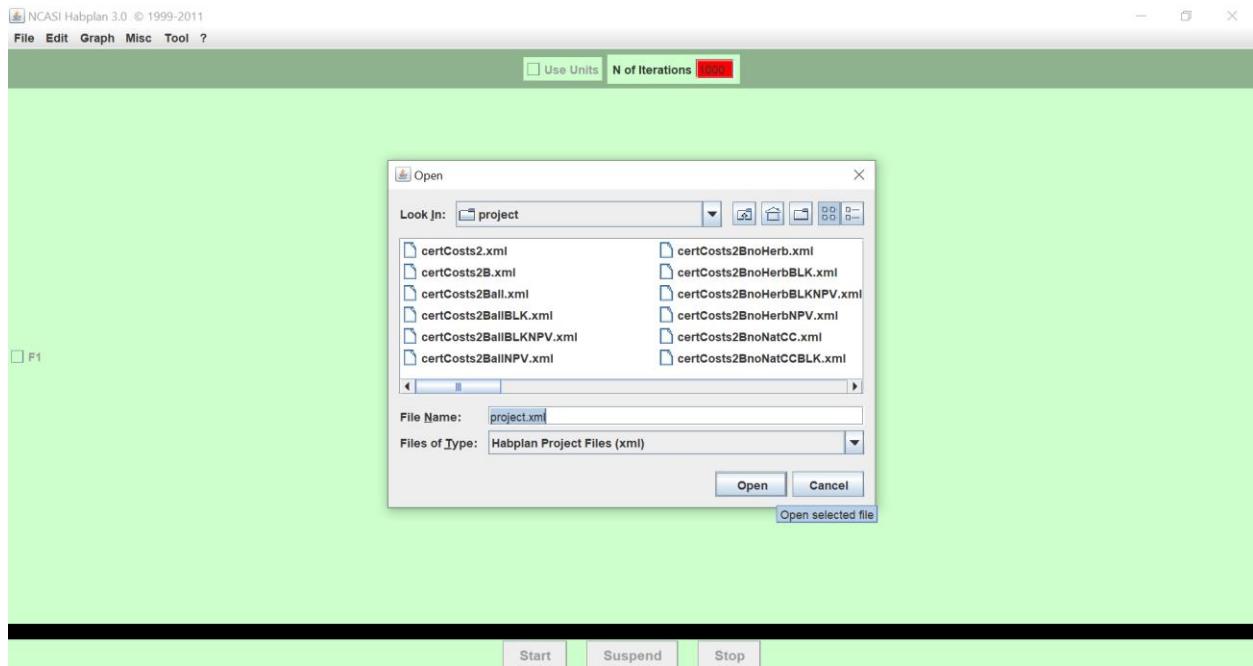
When you first open Habplan from the R script, the following window will open. Note that you will be unable to run anything in your R session when Habplan has been opened via R. Additionally, your start-up screen may look slightly different – this is ok!



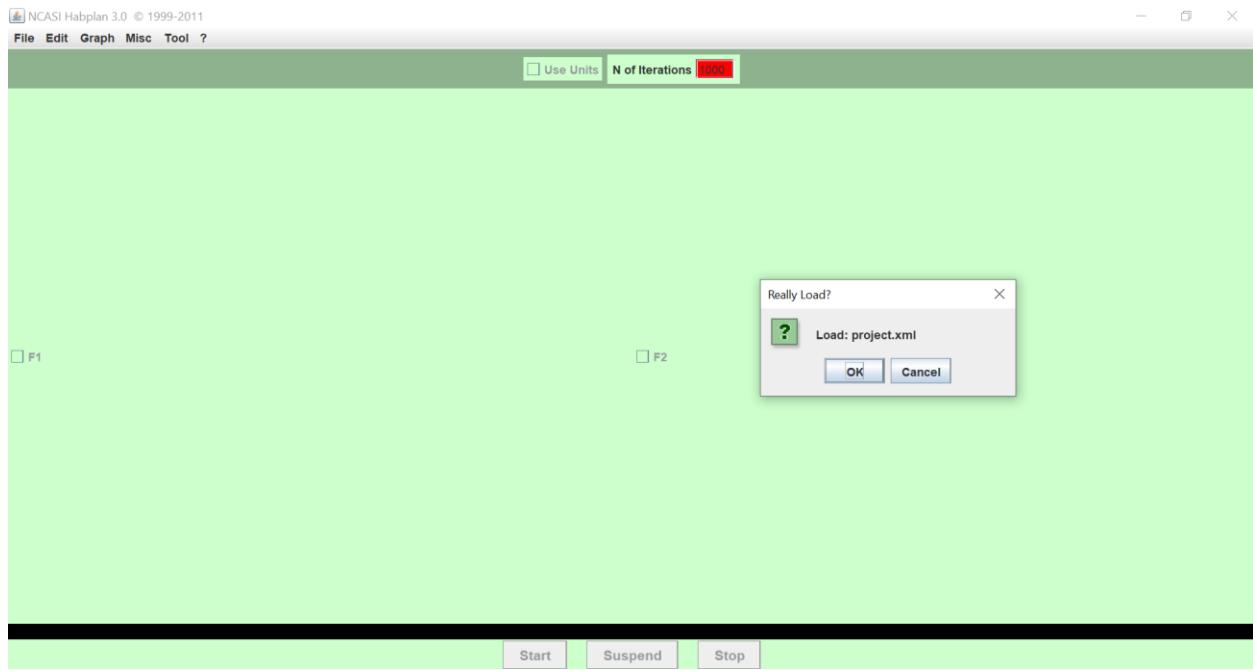
To open the project file we have just created, we can navigate to File > Open... Make sure to navigate to the correct project file (the one created via the R script) if there are multiple saved on your computer.



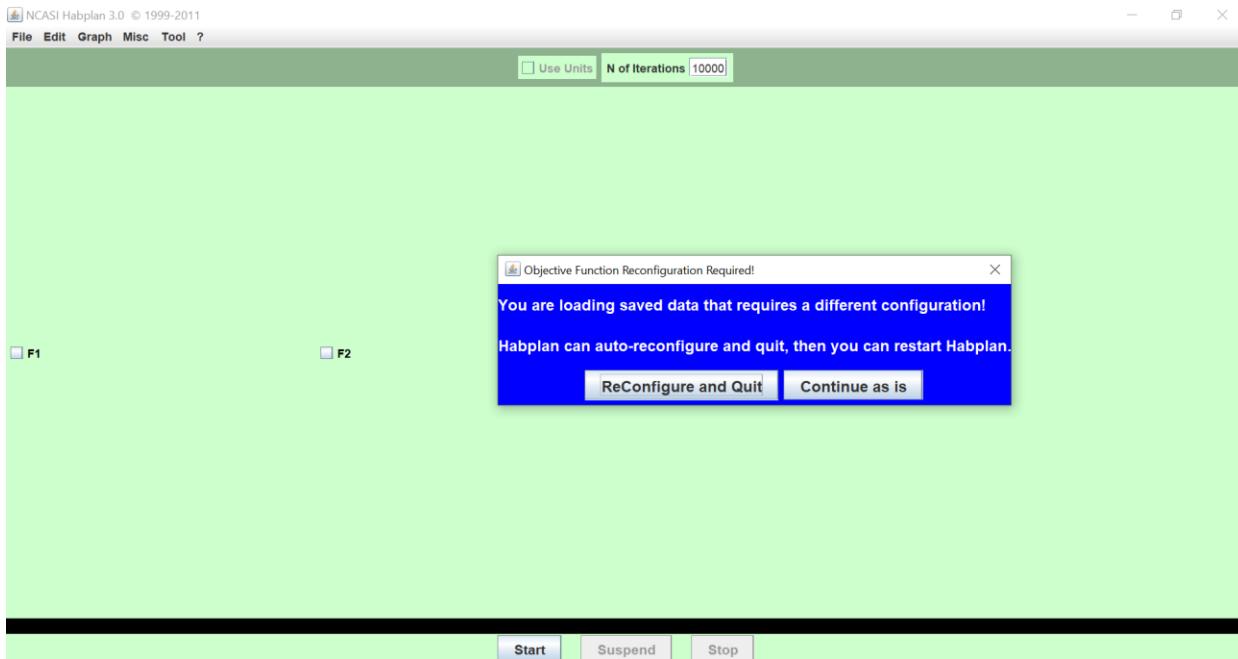
A new window will open to select the appropriate file, which will have saved in the set working directory as project.xml. Habplan will automatically select this file when the window opens, so we can go ahead and click Open.



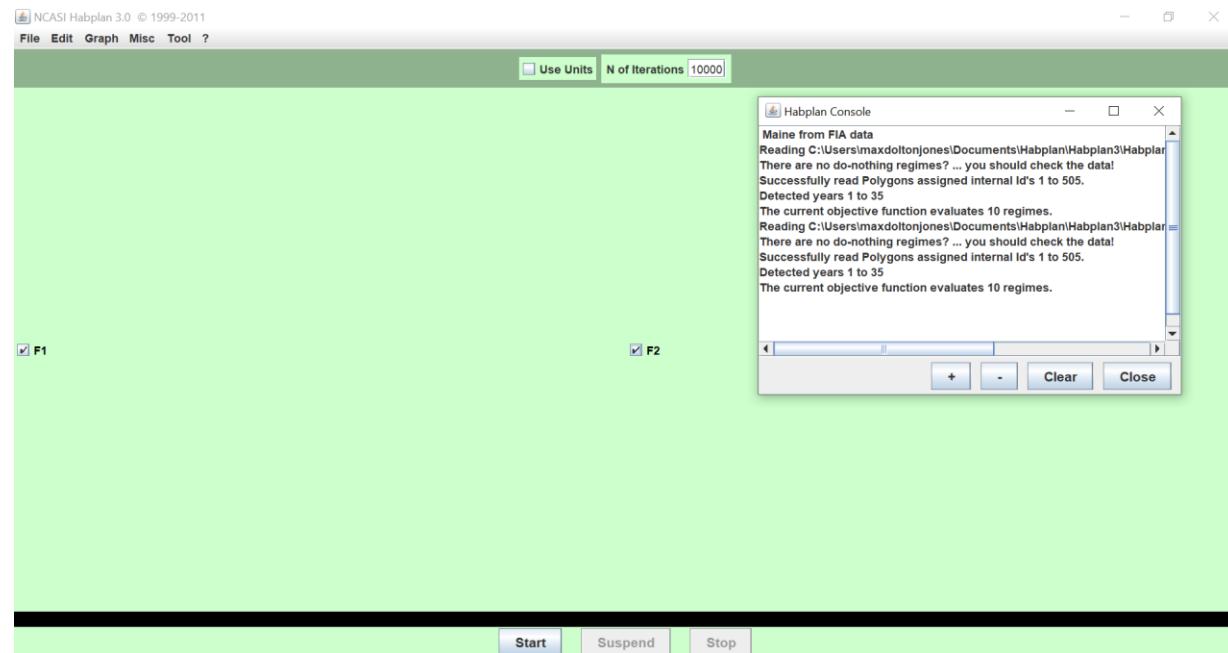
A new window will then open. Click OK to load the project file.



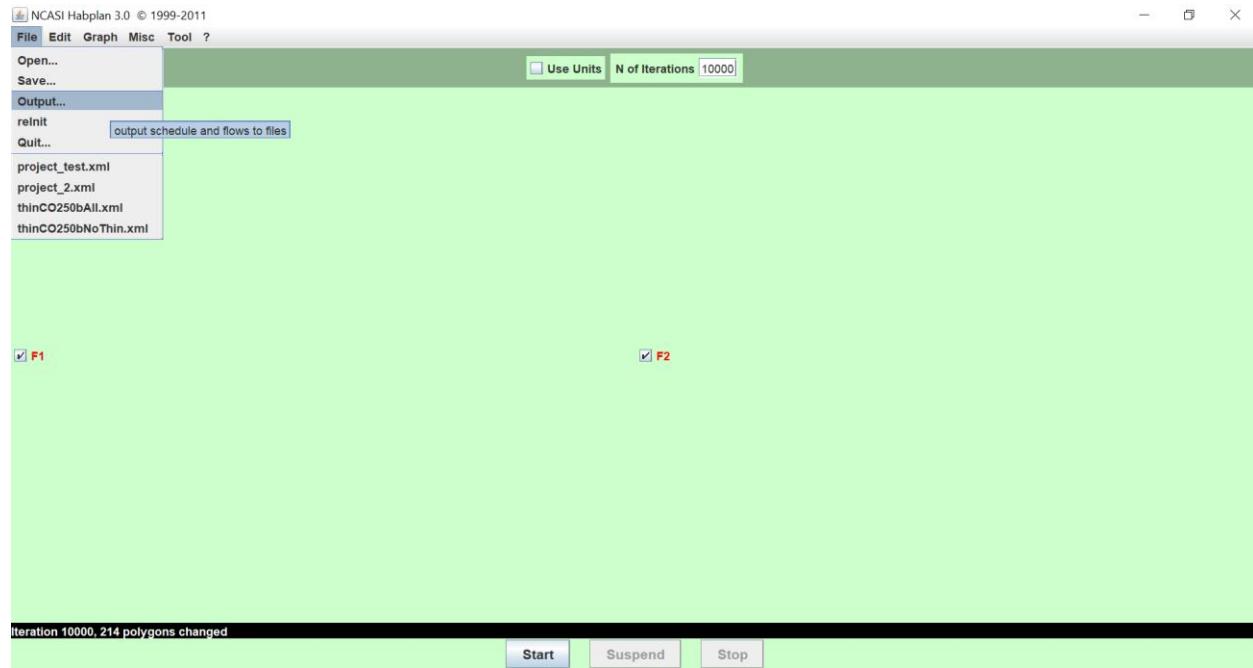
When opening the project file, you may encounter the following pop-up window. This means that the configuration file has a different configuration than the project file. In this circumstance, select ReConfigure and Quit, which will close Habplan. Once that happens, re-run the R code `shell("h", wait=TRUE)` and perform the above steps again once Habplan has reopened.



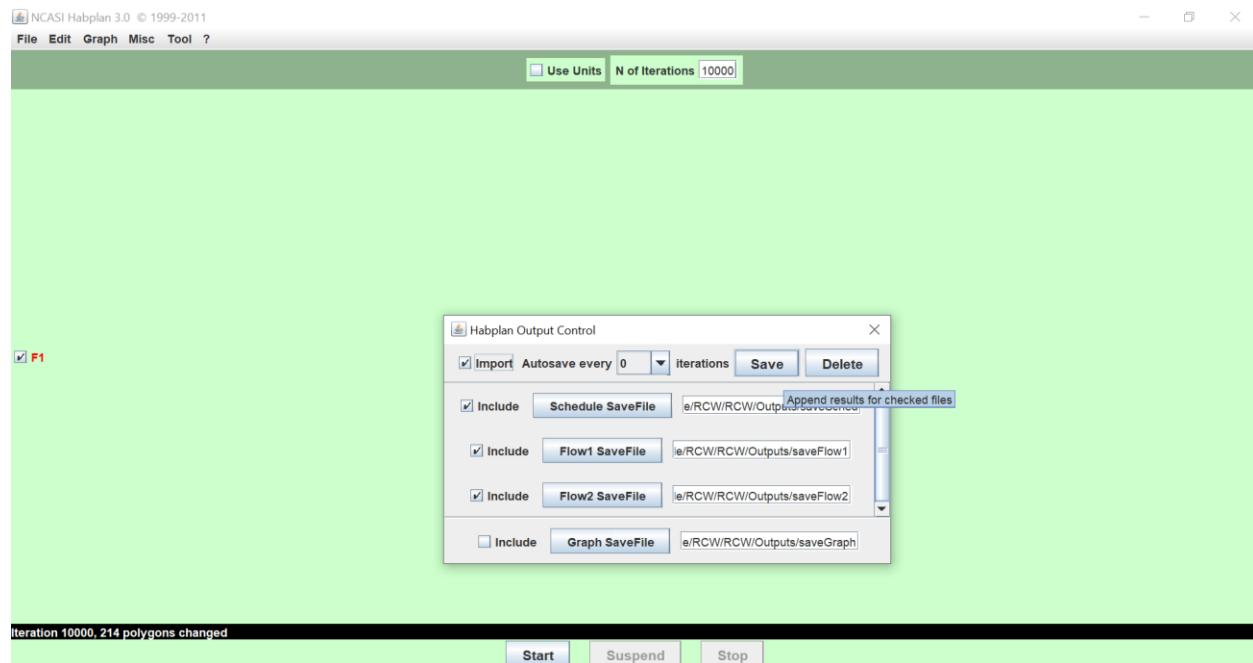
Another new window will now be available titled Habplan Console, where the program will provide updates and any errors discovered. We will also have the opportunity to select the flow components on the main window, named F1 and F2 in our example. Including other flows in the project file will add new component check boxes. Go ahead and select the two check boxes on the main window so that they appear as below. Once they have been selected, click “Start” to begin Habplan.



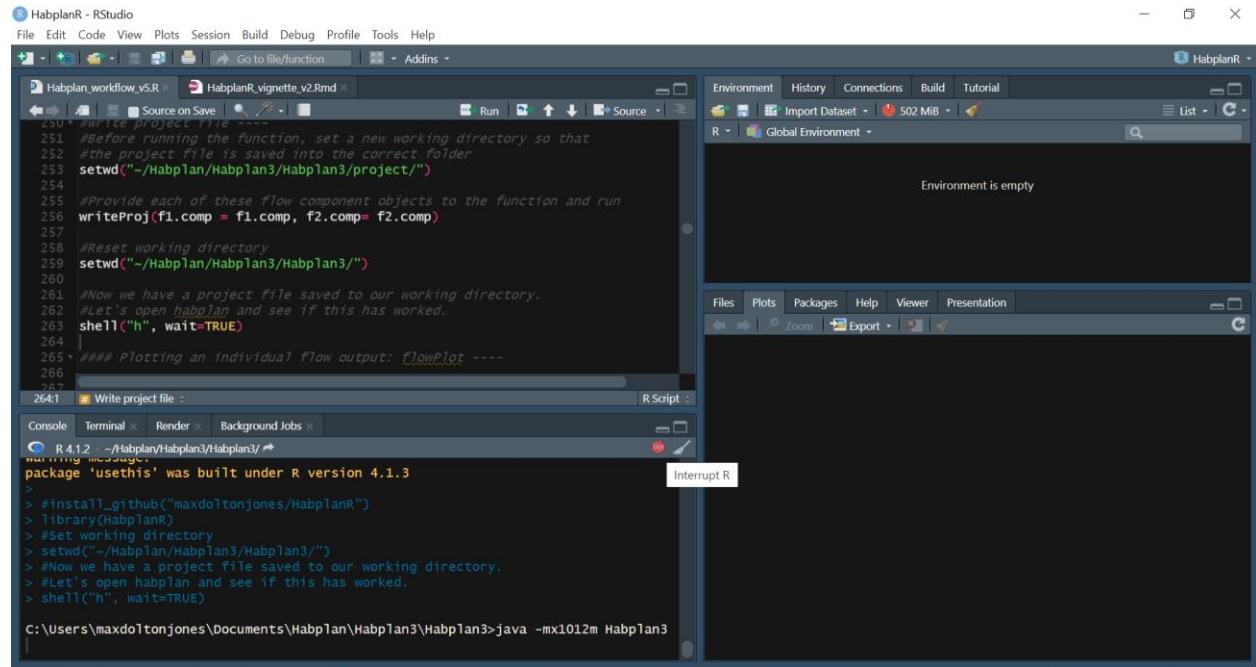
The progress of the Habplan run can be seen in the bottom left corner of the main Habplan window. Once the allocated number of iterations has been completed (which we have set to 10,000 in our script), we can save the output. To do this navigate to File > Output...



A new window will open titled Habplan Output Control. All of the check boxes will be pre-selected, so we can simply click “Save” to save the output flow files and recommended schedule.



We are now finished with Habplan for the time being. We can either close all Habplan windows, or just go back into RStudio and select the red STOP button on the top right of the console to close Habplan.



The screenshot shows the RStudio interface with the following components:

- File Bar:** File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help.
- Source Editor:** Shows the code for `Habplan_workflow_v3.R` and `HabplanR.vignette.v2.Rmd`. The Rmd file contains R code for setting up a project, writing flow component objects, and plotting individual flow outputs.
- Environment Tab:** Shows the Global Environment tab with the message "Environment is empty".
- Console Tab:** Shows the R session output. It includes commands for installing the package from GitHub, loading it, setting the working directory, and running a Java command to start Habplan. The output indicates the package was built under R version 4.1.3.
- Interrupt R:** A button located in the bottom right corner of the Console tab.

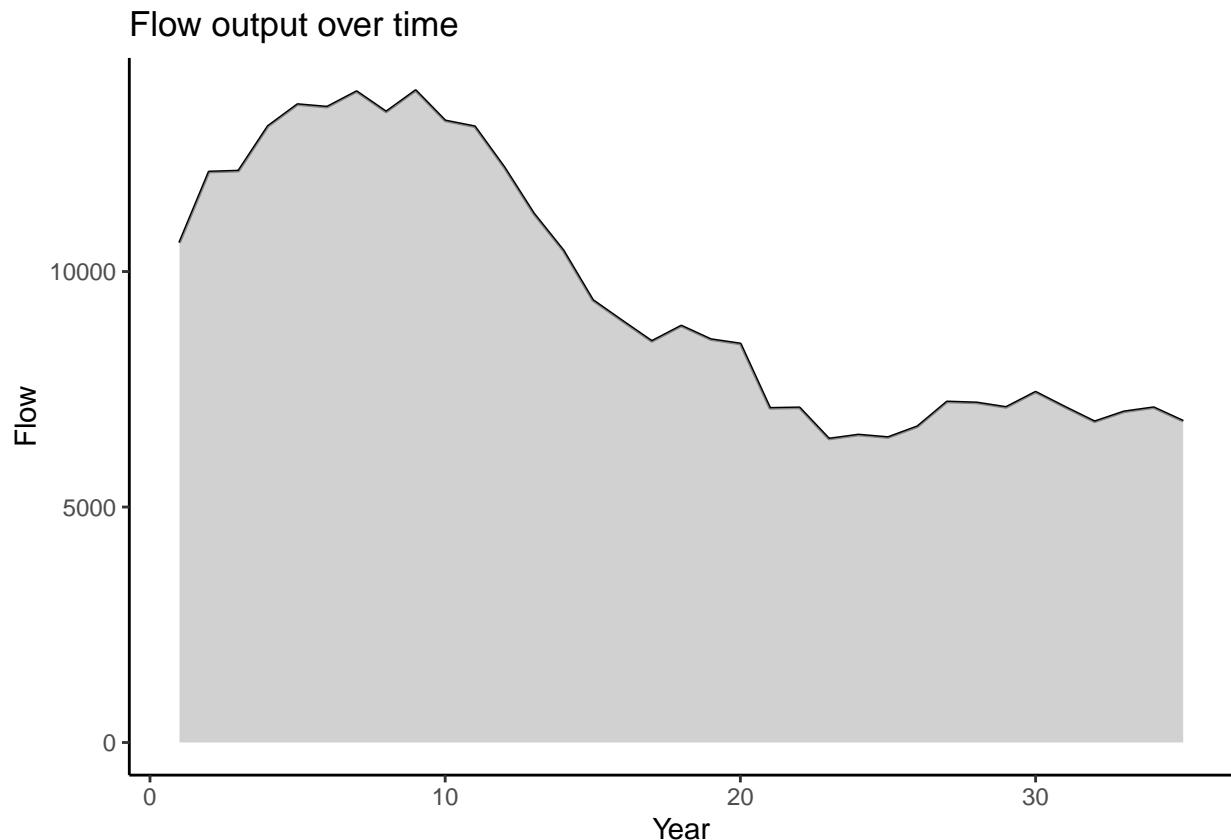
Function: plotting an individual flow output - *FlowPlot*

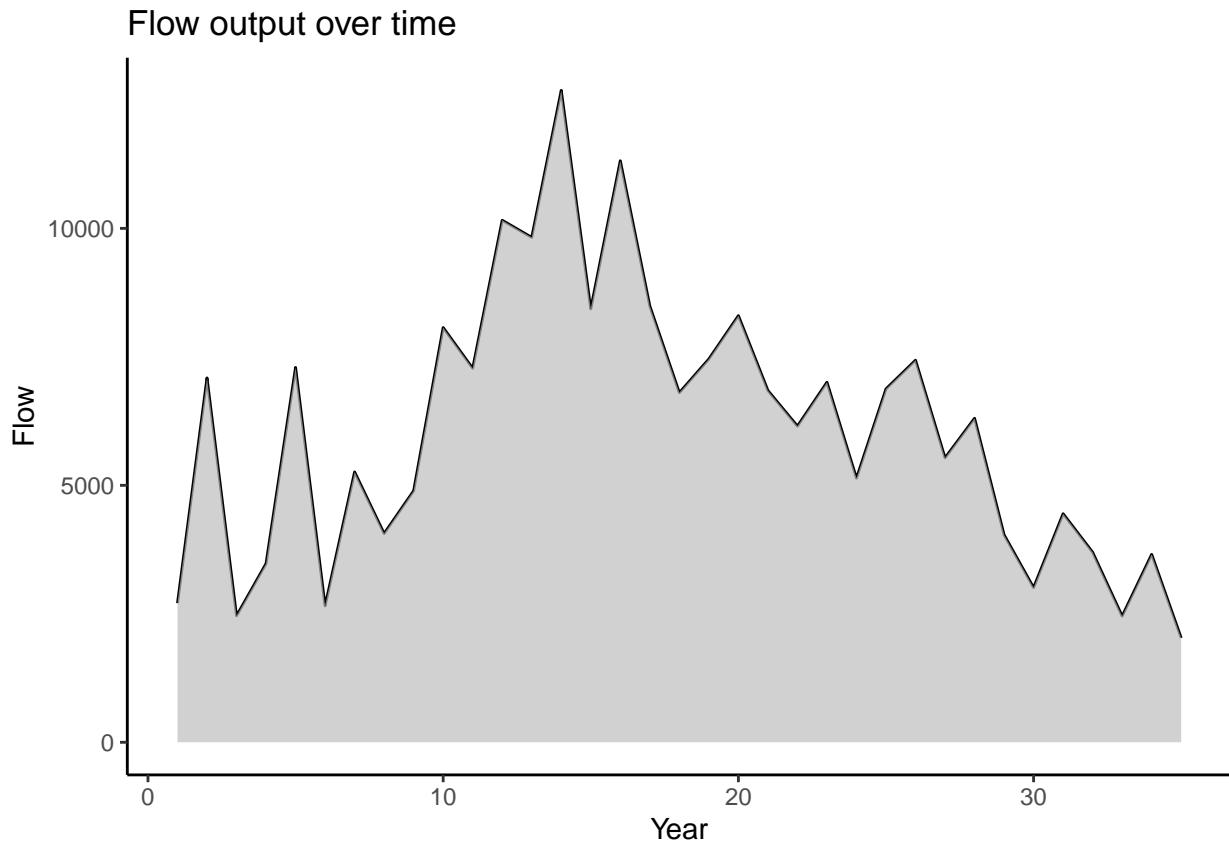
After running habplan, we will have several flows saved to our working directory. The option still exists to interactively watch the charts in a habplan window. However, we provide a function to visualize each flow individually.

First read in the flow output file, and then feed this file into the function.

```
#Read in one of the flow files
flow1 <- read.csv("./saveFlow1", sep="", header = F)
flow2 <- read.csv("./saveFlow2", sep="", header = F)

#Input the flow file into the function, and number of years
flowPlot(flow.data = flow1, nyear = 35)
flowPlot(flow.data = flow2, nyear = 35)
```





The first figure above shows the output flow from our HSI component throughout our study period, and the second shows the hard pulpwood yield. Due to the simulation component of Habplan, the graphs created may not look exactly as shown throughout the vignette.

Because we now have a possible solution based on the above output flows, to help make our decision on whether or not this is a viable solution, we will run an addition function *HabSpace*. This function takes the output flow information from Habplan and visualizes the flow for each year of interest.

Function: spatial contiguity assessment - *HabSpace*

The *HabSpace* function was created to look at the spatial contiguity of the landscape based on the management schedule output from Habplan. Thus, it is designed to look at the spatial aspect of the HSI flows specifically.

First, read in the shapefile containing all forest stands.

```
#Read in stand shapefiles
site.shp <- vect("./Stands_final.shp")
```

IMPORTANT The shapefile needs a data column called “StdID”

We will add the shapefile of stands, and the flow of choice to the function. As before, we will set the nyear. We now have two more options with this function, mode and dist.

There are two modes to choose from, terrestrial or avian - depending on the species the HSI has been built around. If avian is chosen, the dist setting sets the distance in meters (or the unit of the shapefile) that the species of interest can comfortably travel to reach neighboring habitat patches. If the user has a terrestrial

species which may still bridge gaps if the distance is short enough, e.g. crossing a road, then the avian option should be selected, and a smaller dist assigned.

The HabSpace function creates several .csv files and figures, and saved these within the working directory. The function will re-write any files in the working directory if the function is run again, so be careful if any files need to be saved; renaming these files will make sure that they are not overwritten.

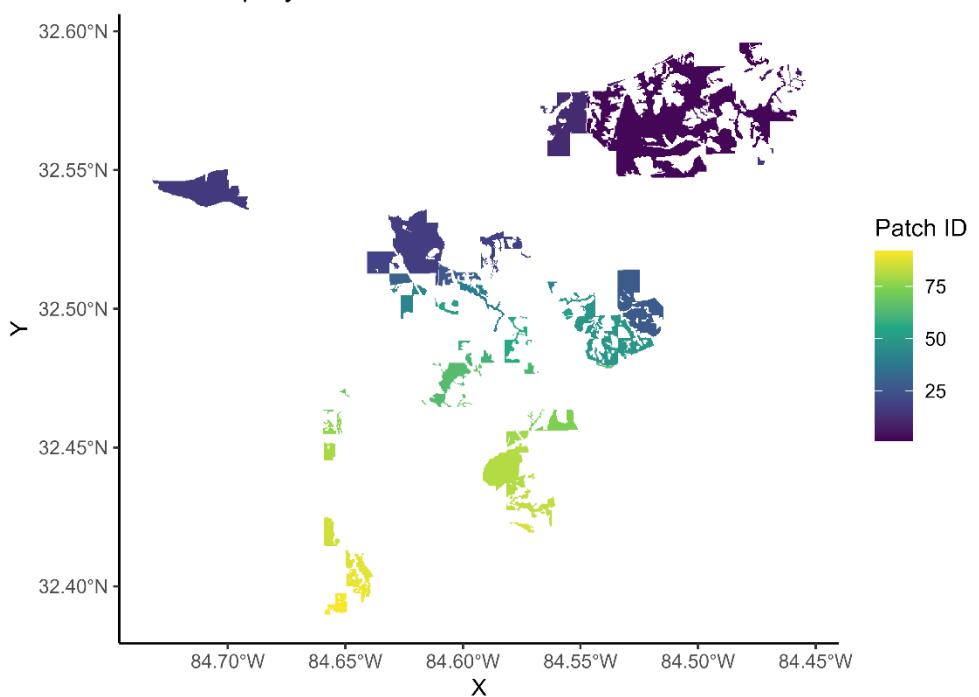
The HabSpace function may take several minutes to complete!

```
#Want to create a shapefile output for each year, to look at change  
#of regime for each stand over time.
```

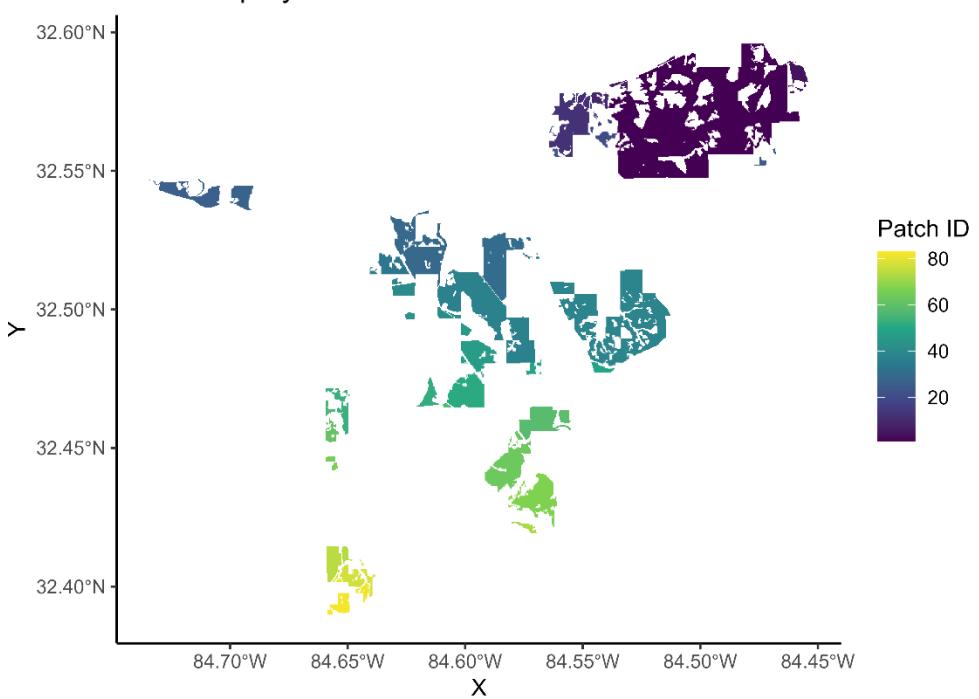
```
space.test <- HabSpace(site.shp = site.shp, flow = flow1, nyear = 35,  
mode = "terrestrial", dist = 500, level = "patch")
```

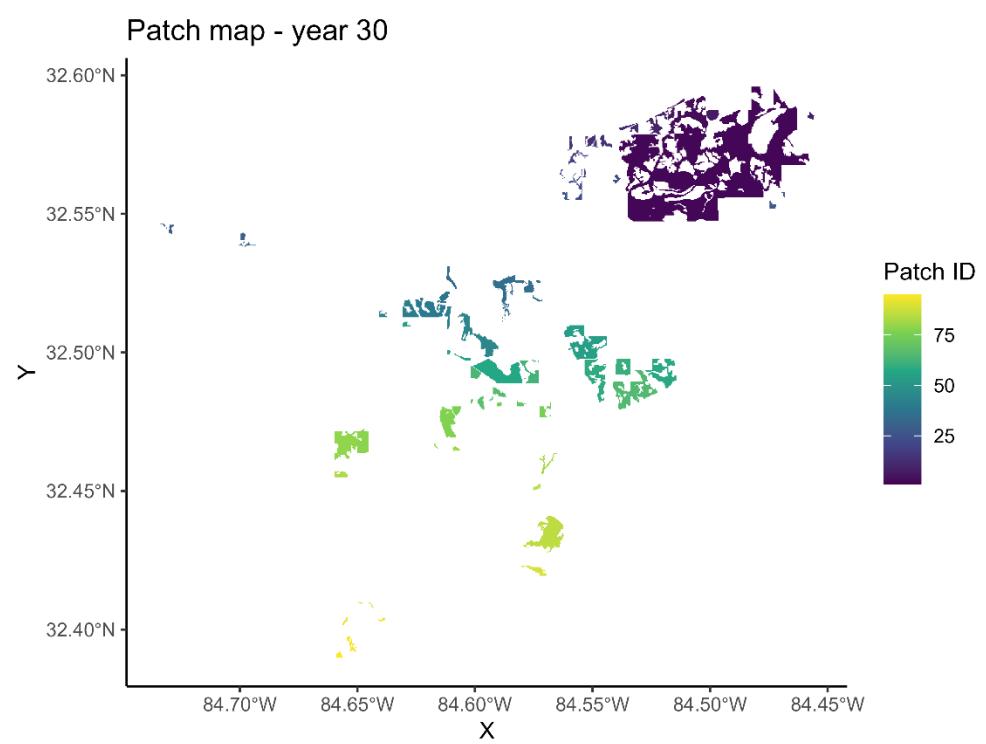
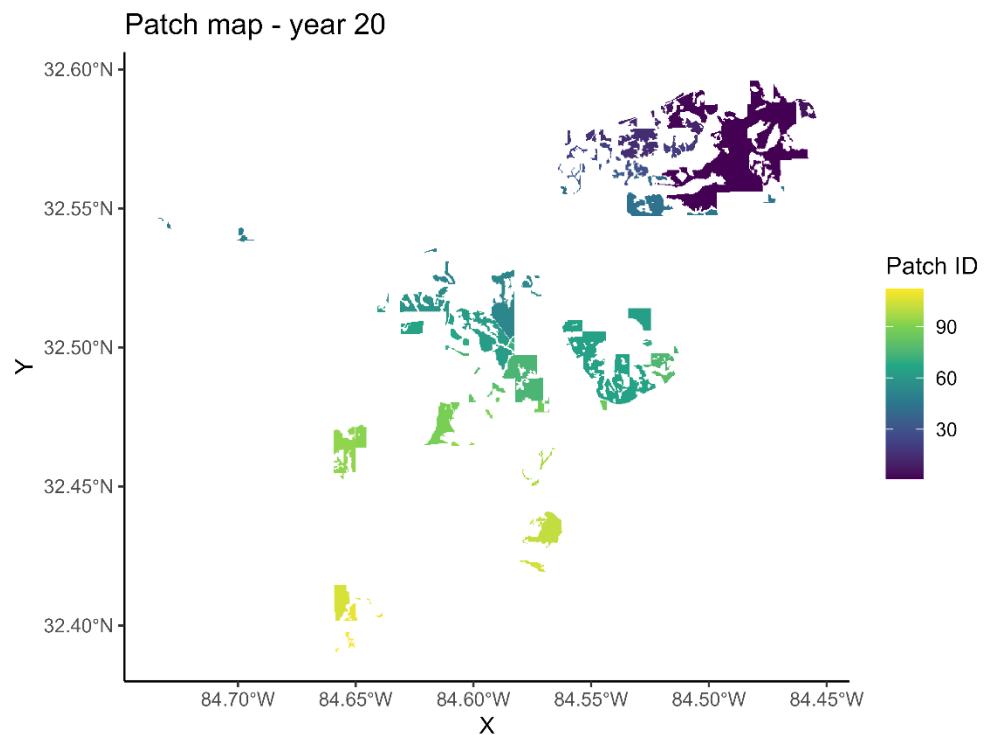
The above function will create maps for each year and save these in the working directory. We have also saved summary graphs, raw data, and summary data for each year.

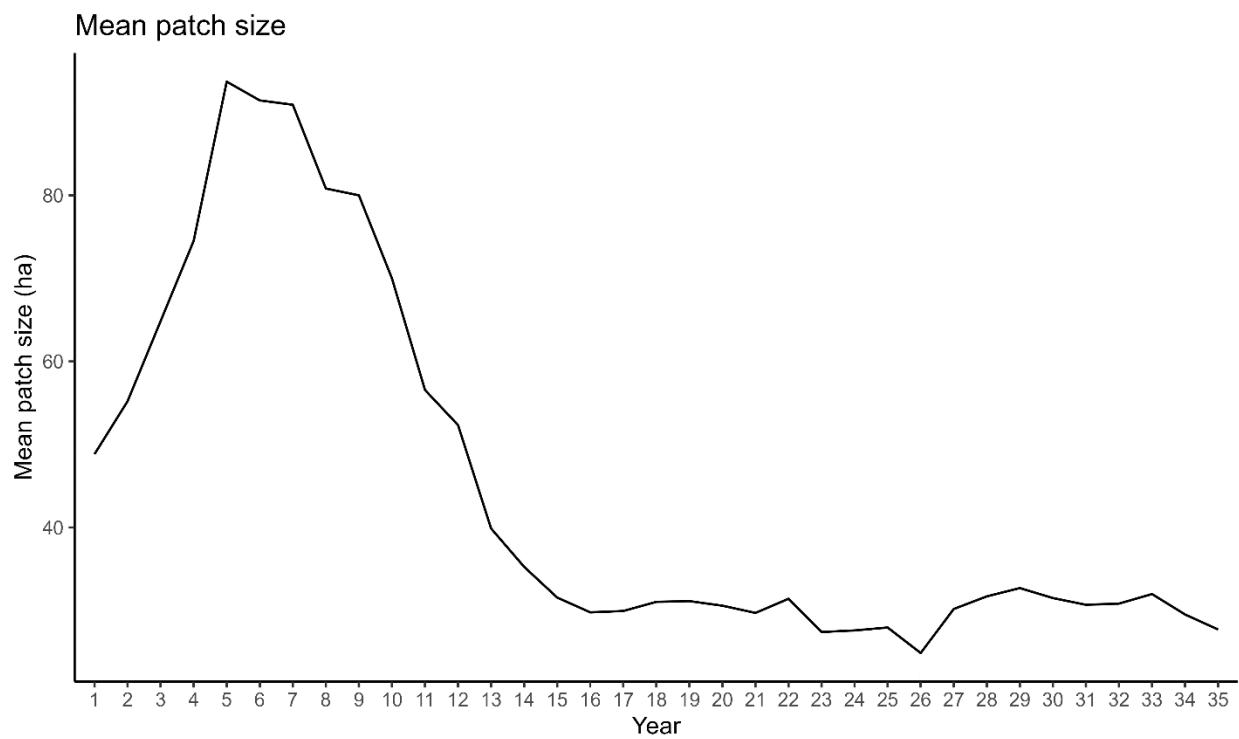
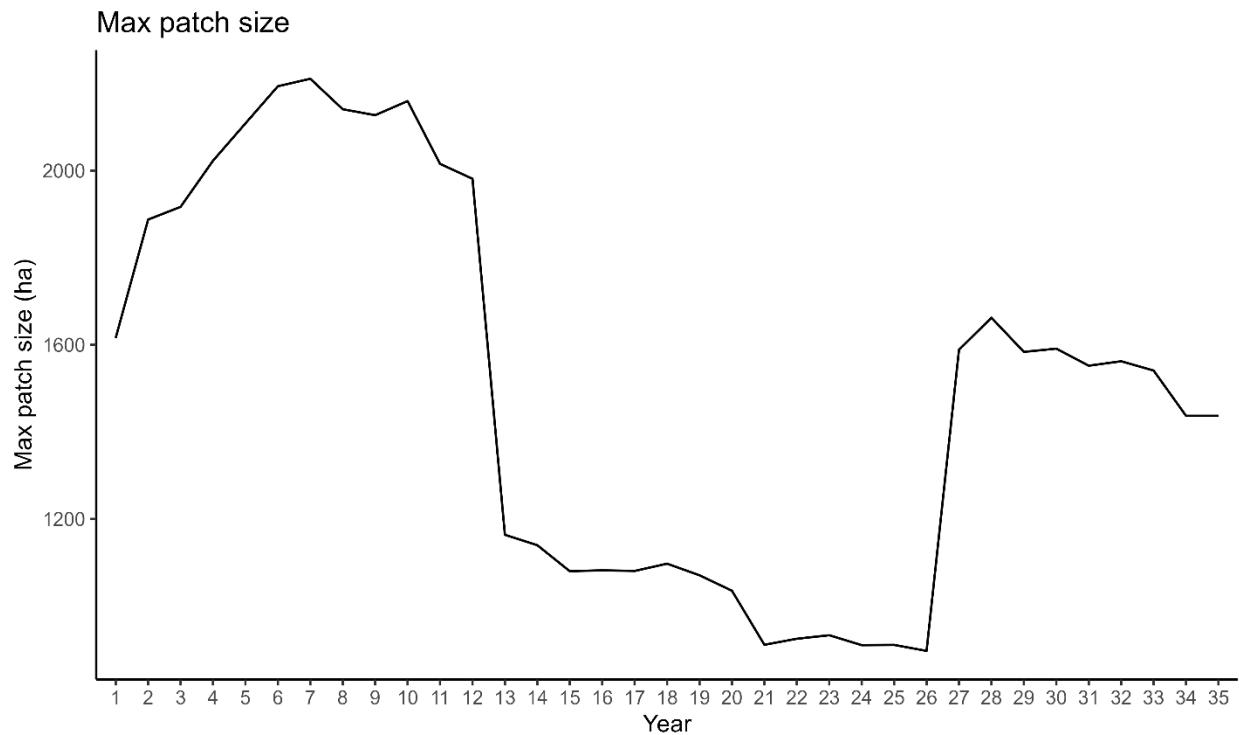
Patch map - year 1



Patch map - year 10







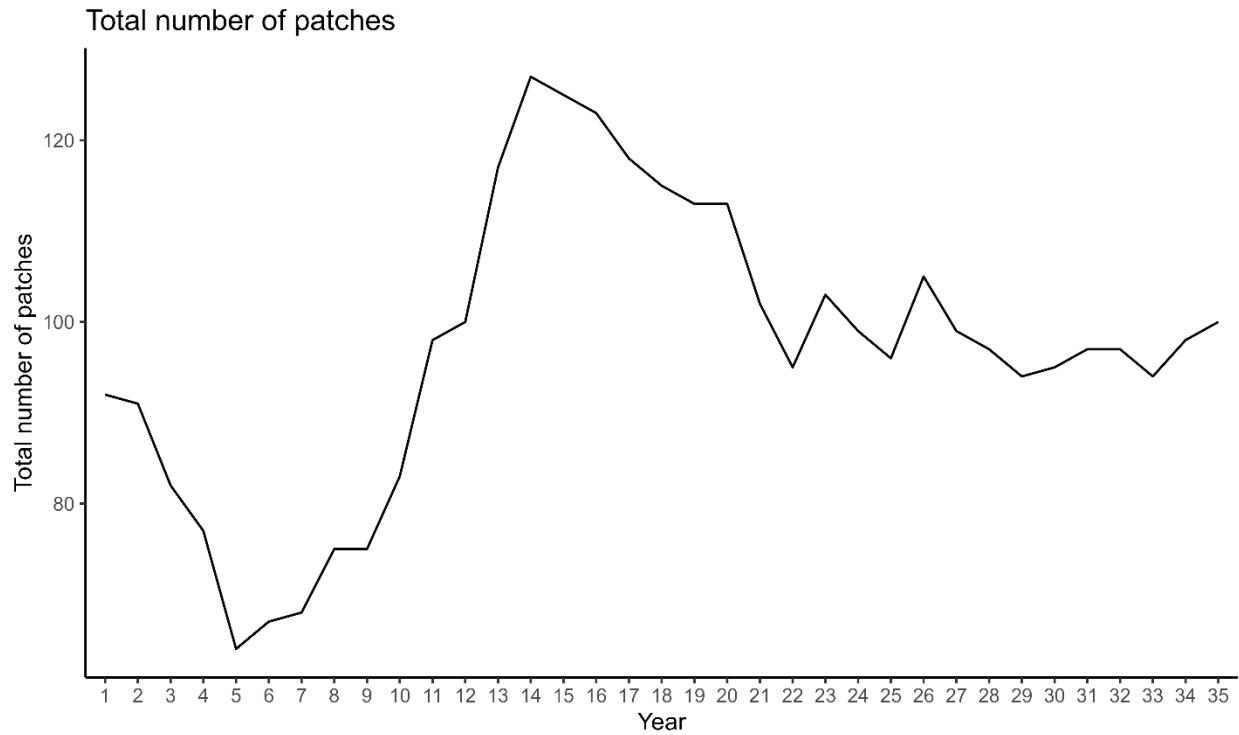


Table 1. Example of landscape-level metrics output from the `habSpace` function (using the *landscapemetrics* package).

| Level | Metric | Value |
|-------|--------|----------|
| patch | area | 305.93 |
| patch | cai | 96.31615 |
| patch | circle | 0.767424 |
| patch | contig | 0.986315 |
| patch | core | 294.66 |
| patch | enn | 5022.848 |
| patch | frac | 1.09194 |
| patch | gyrate | 840.0852 |
| patch | ncore | 1 |
| patch | para | 0.004544 |
| patch | perim | 13900 |
| patch | shape | 1.986282 |

Because we have everything to assess the Habplan run, we are now going to adjust the thlo, thhi, and model objects. For our lower threshold, we are going to decrease this to 500 acres to prevent too much negative deviation from our target, but instead have a much higher thhi to allow more yield from the target if Habplan can find a schedule which permits that. Additionally, we will change the model targets to 500 in year 1, 2500 in year 20, and 7500 in year 30 (1,500;20,2500;30,7500). We will apply the same changes to both flow components.

```
#Info for f1 component ----
f1.file <- paste0(wd, "HSI.dat")
f1.bypgone <- ""
f1.time0 <- "10000"
f1.goal0 <- "0.1"
f1.thlo <- "500"
f1.thhi <- "10000"
f1.goalplus <- ".05"
f1.goalf <- "0.5"
f1.slope <- "0.0"
f1.weightf <- "1.0"
f1.weight0 <- "1.0"
f1.model <- "1,500;20,2500;30,7500;"
f1.title <- "Breed.dat"
#Combine f1 components for writing
f1.comp <- c('<flow title="F1 Component">',
  paste0('<file value=""', f1.file, '" />'),
  paste0('<bypgone value=""', f1.bypgone, '" />'),
  paste0('<time0 value=""', f1.time0, '" />'),
  paste0('<goal0 value=""', f1.goal0, '" />'),
  paste0('<threshLo value=""', f1.thlo, '" />'),
  paste0('<threshHi value=""', f1.thhi, '" />'),
  paste0('<goalPlus value=""', f1.goalplus, '" />'),
  paste0('<goalF value=""', f1.goalf, '" />'),
  paste0('<slope value=""', f1.slope, '" />'),
  paste0('<weightF value=""', f1.weightf, '" />'),
  paste0('<weight0 value=""', f1.weight0, '" />'),
  paste0('<model value=""', f1.model, '" />'),
  paste0('<title value=""', f1.title, '" />'),
  '<bounds height="330" width="366" x="553" y="443" />',
  "</flow>")

#Info for f2 component ----
f2.file <- paste0(wd, "Harv_P_Pulp_Tons.dat")
f2.bypgone <- ""
f2.time0 <- "1000"
f2.goal0 <- "0.1"
f2.thlo <- "500"
f2.thhi <- "10000"
f2.goalplus <- ".05"
f2.goalf <- "0.5"
f2.slope <- "0.0"
f2.weightf <- "1.0"
f2.weight0 <- "1.0"
f2.model.1 <- "1,500;20,2500;30,7500;"
```

```

f2.title <- "Harv_P_Pulp_Tons.dat"
#Combine f2 components for writing
f2.comp <- c('<flow title="F2 Component">',
  paste0('<file value=""', f2.file, '" />'),
  paste0('<bygone value=""', f2.bygone, '" />'),
  paste0('<time0 value=""', f2.time0, '" />'),
  paste0('<goal0 value=""', f2.goal0, '" />'),
  paste0('<threshLo value=""', f2.thlo, '" />'),
  paste0('<threshHi value=""', f2.thhi, '" />'),
  paste0('<goalPlus value=""', f2.goalplus, '" />'),
  paste0('<goalF value=""', f2.goalf, '" />'),
  paste0('<slope value=""', f2.slope, '" />'),
  paste0('<weightF value=""', f2.weightf, '" />'),
  paste0('<weight0 value=""', f2.weight0, '" />'),
  #paste0('<model value="1', f2.target, ';', f2.next.year, ',',
  #      f2.next.target, '" />'),
  paste0('<title value=""', f2.title, '" />'),
  '<bounds height="331" width="368" x="1260" y="440" />',
  "</flow>")
```

We can re-run the writeProj function to create a new project file. The writeProj function will overwrite the project file in the working directory, so make sure to rename the existing project file if it needs to be saved.

```

#Provide each of these flow component objects to the function and run
writeProj(f1.comp = f1.comp, f2.comp= f2.comp)
```

Now we have a project file saved to our working directory. Let's open Habplan and see if this has worked. Follow the same instructions above for running Habplan once it has opened.

```

#Open Habplan (if run from here, R functionality will cease until Habplan is closed)
shell("h", wait=TRUE)
```

Function: plotting an individual flow output - *FlowPlot*

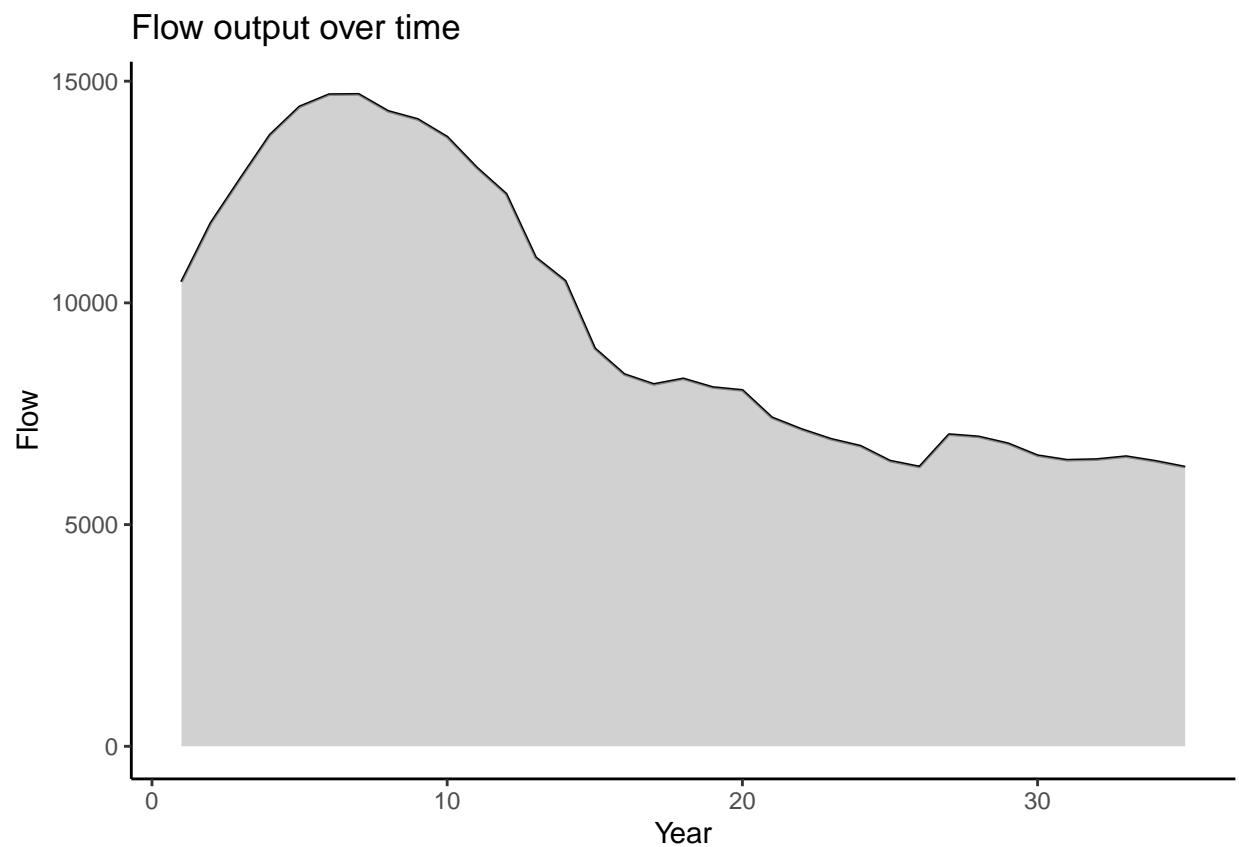
After running habplan, we will have several flows saved to our working directory. The option still exists to interactively watch the charts in a habplan window. However, we provide a function to visualize each flow individually.

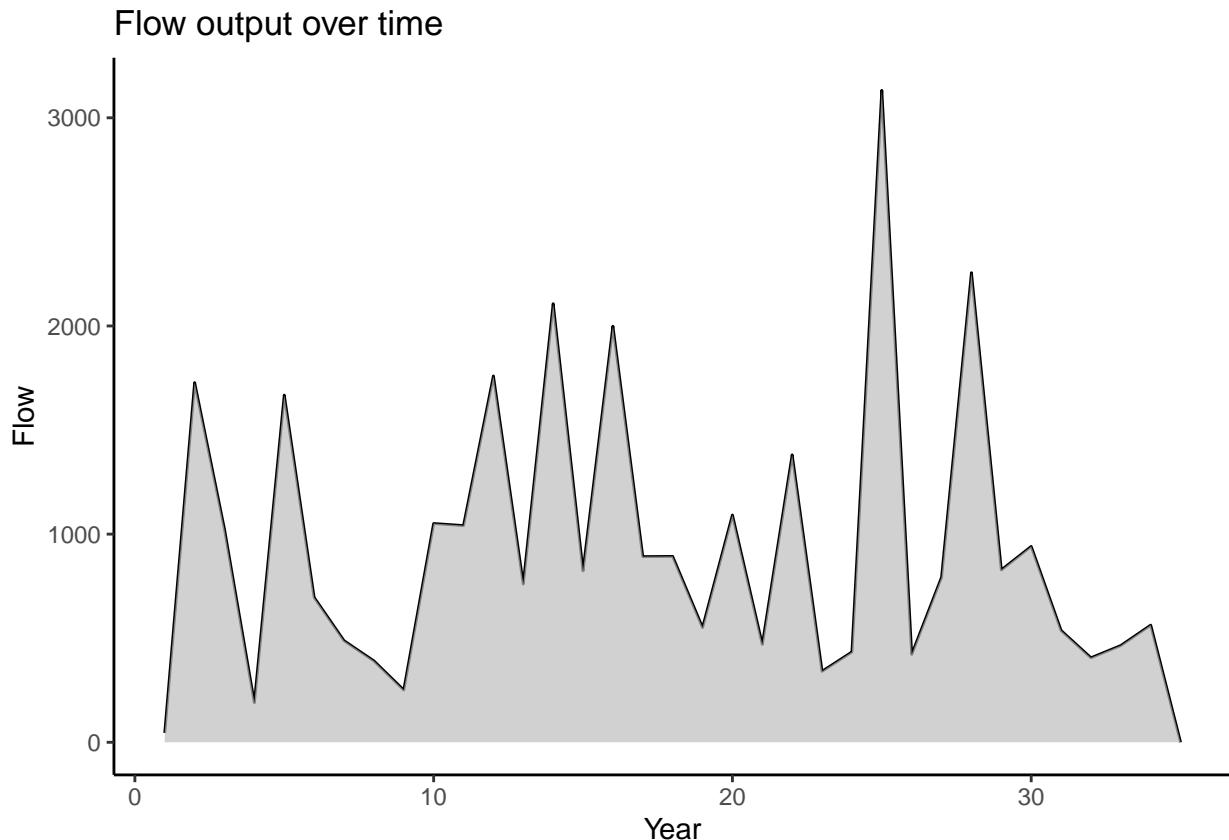
First read in the flow output file, and then feed this file into the function.

```

#Read in one of the flow files
flow1 <- read.csv("./saveFlow1", sep="", header = F)
flow2 <- read.csv("./saveFlow2", sep="", header = F)

#Input the flow file into the function, and number of years
flowPlot(flow.data = flow1, nyear = 35)
flowPlot(flow.data = flow2, nyear = 35)
```





Again, the first figure above shows the output flow from our HSI component throughout our study period, and the second shows the hard pulpwood yield. From a first glance of these figures, it appears that the outputs have not changed substantially. Let's re-run the *HabSpace* function to assess the spatial component of the recommended schedule.

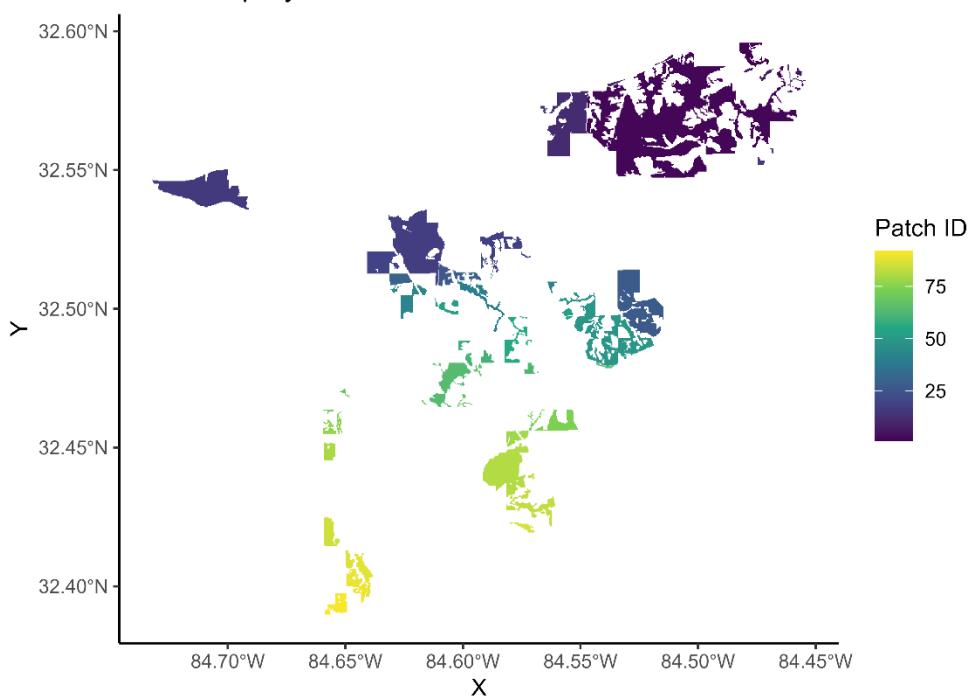
Function: spatial contiguity assessment - *HabSpace*

The HabSpace function may take several minutes to complete!

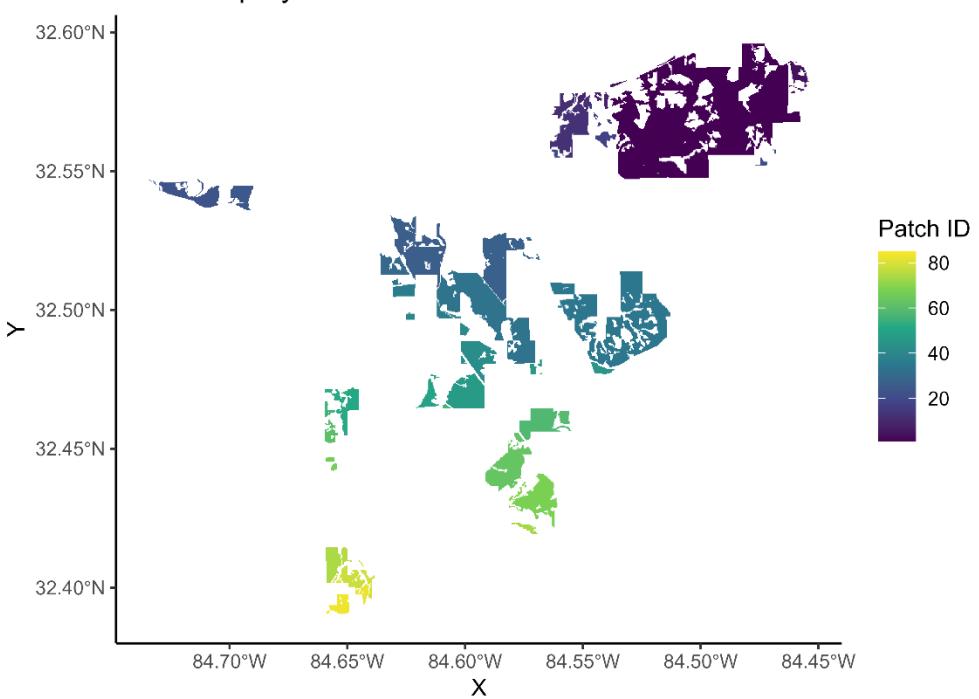
```
#Want to create a shapefile output for each year, to look at change
#of regime for each stand over time.
```

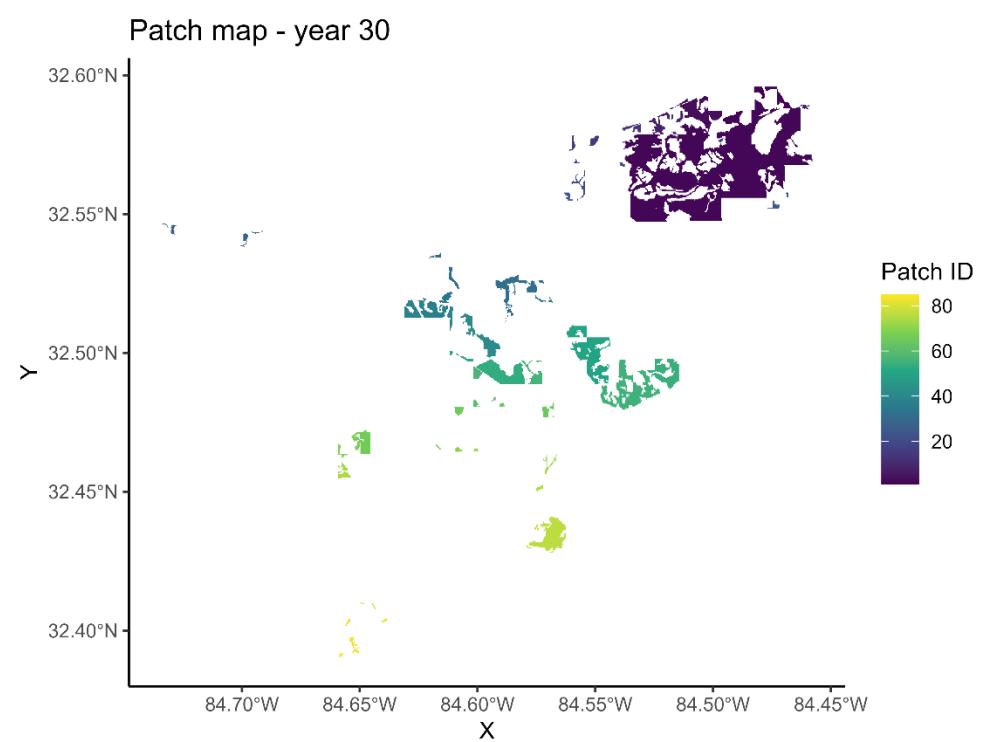
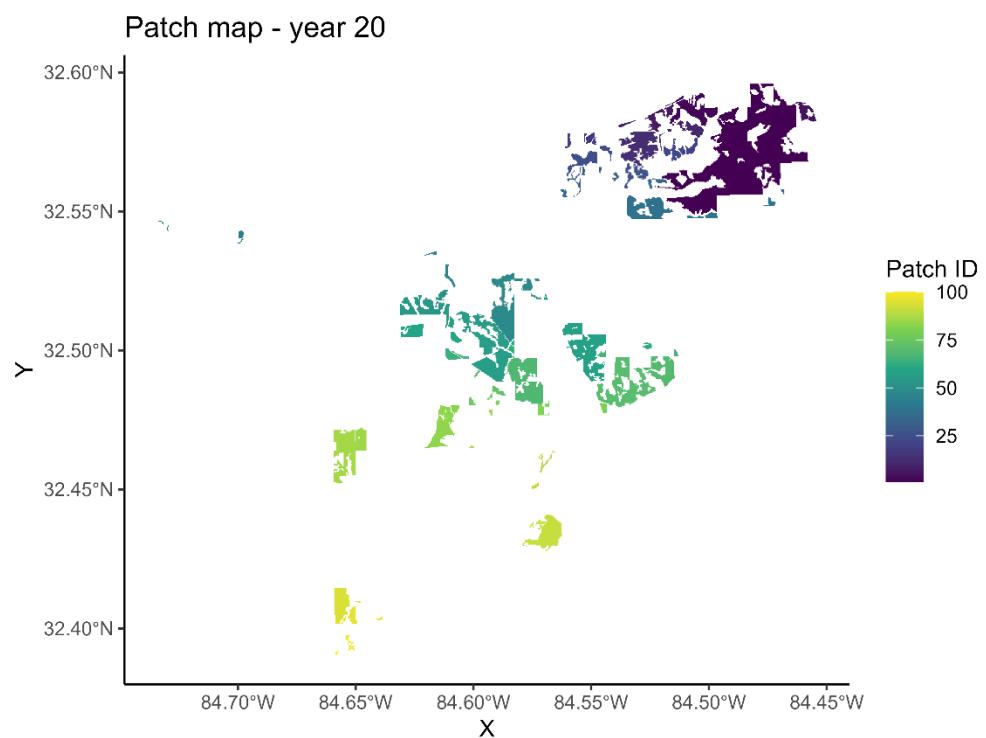
```
space.test <- HabSpace(site.shp = site.shp, flow = flow, nyear = 35,
                        mode = "terrestrial", dist = 500, level = "patch")
```

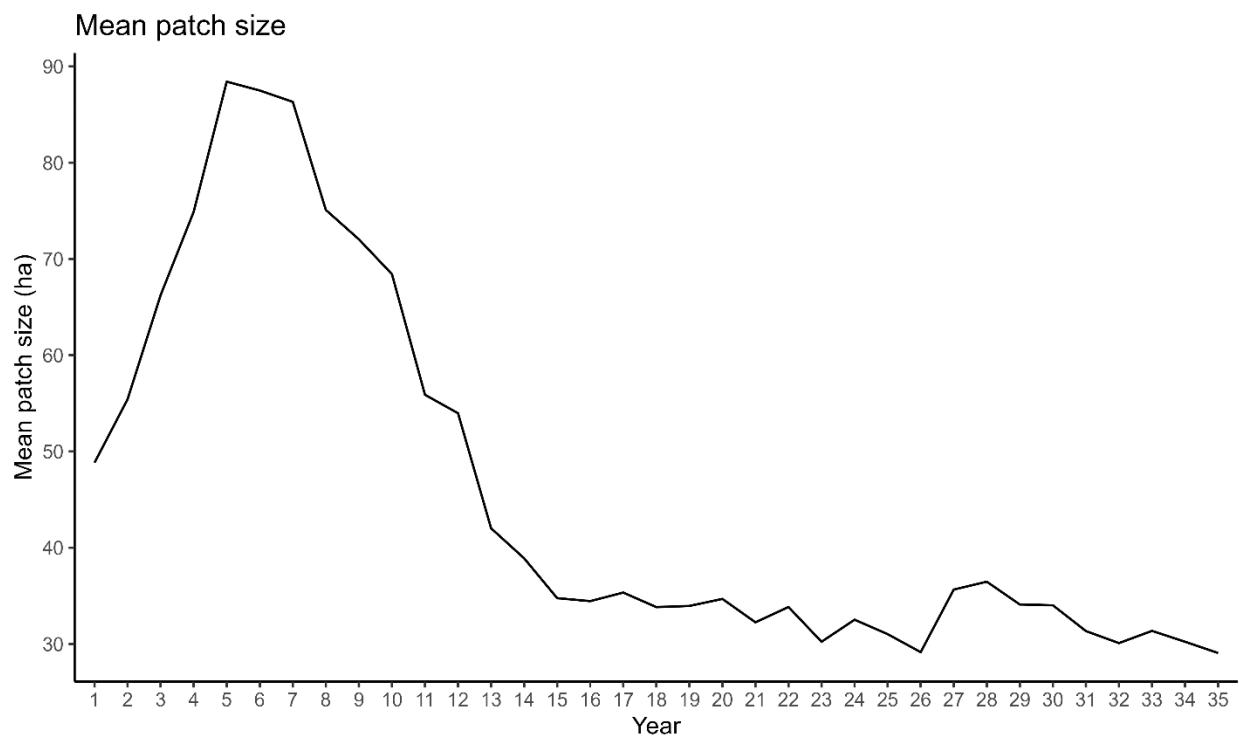
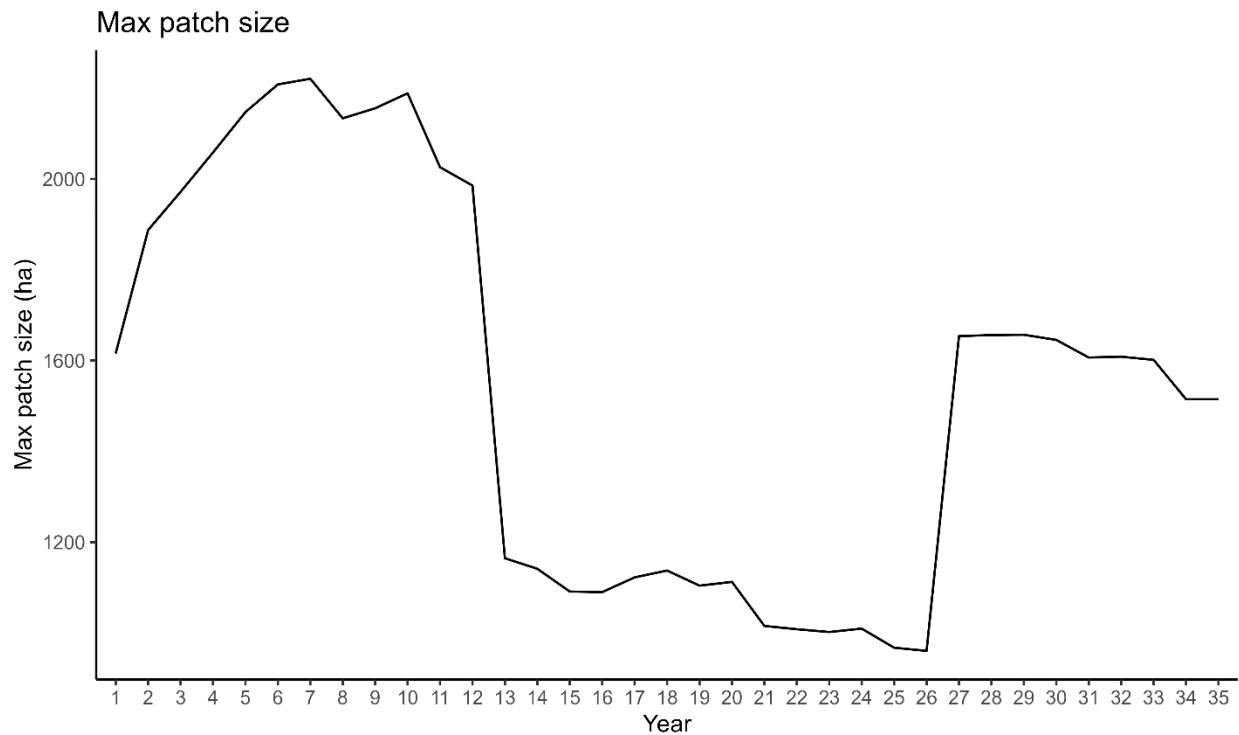
Patch map - year 1

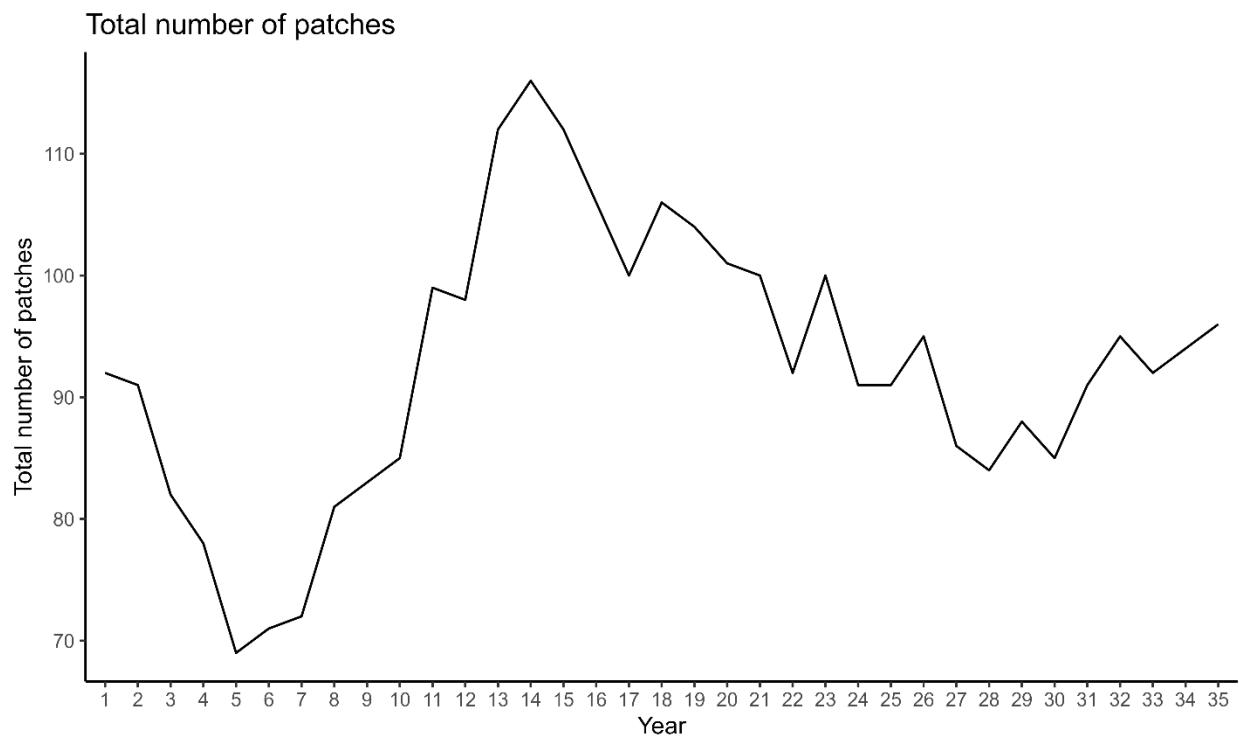


Patch map - year 10









For this final run, we are going to apply more substantial changes to each flow component, with unique values for each one.

For the HSI flow component, we are going to have a much broader thlo set to 5000 acres, but keep the thhi at 10000. However, we are going to set much different targets for the model. We are now aiming for 15000 in year 1, 5000 in year 20, and only 2000 by year 30 (1,15000;20,5000;30,2000).

For the hard pulpwood flow component, we believe we should be able to achieve much higher values. We will therefore set the thlo to 2000, but have the thhi be 100000. With such a large upper threshhold, we can set relatively conservative targets for our model. We will aim for 100 in year 1, 2000 in year 20, and keep this at 2000 for year 30 (1,100;20,2000;30,2000).

```
#Info for f1 component ----
f1.file <- paste0(wd,"HSI.dat")
f1.bypgone <- ""
f1.time0 <- "10000"
f1.goal0 <- "0.1"
f1.thlo <- "5000"
f1.thhi <- "10000"
f1.goalplus <- ".05"
f1.goalf <- "0.5"
f1.slope <- "0.0"
f1.weightf <- "1.0"
f1.weight0 <- "1.0"
f1.model <- "1,15000;20,5000;30,2000;"
f1.title <- "Breed.dat"
#Combine f1 components for writing
f1.comp <- c('<flow title="F1 Component">',
             paste0('<file value=""', f1.file, '" />'),
             paste0('<bypgone value=""', f1.bypgone, '" />'),
             paste0('<time0 value=""', f1.time0, '" />'),
             paste0('<goal0 value=""', f1.goal0, '" />'),
             paste0('<threshLo value=""', f1.thlo, '" />'),
             paste0('<threshHi value=""', f1.thhi, '" />'),
             paste0('<goalPlus value=""', f1.goalplus, '" />'),
             paste0('<goalF value=""', f1.goalf, '" />'),
             paste0('<slope value=""', f1.slope, '" />'),
             paste0('<weightF value=""', f1.weightf, '" />'),
             paste0('<weight0 value=""', f1.weight0, '" />'),
             paste0('<model value=""', f1.model, '" />'),
             paste0('<title value=""', f1.title, '" />'),
             '<bounds height="330" width="366" x="553" y="443" />',
             "</flow>")

#Info for f2 component ----
f2.file <- paste0(wd, "Harv_P_Pulp_Tons.dat")
f2.bypgone <- ""
f2.time0 <- "1000"
f2.goal0 <- "0.1"
f2.thlo <- "2000"
f2.thhi <- "100000"
f2.goalplus <- ".05"
f2.goalf <- "0.5"
f2.slope <- "0.0"
```

```

f2.weightf <- "1.0"
f2.weight0 <- "1.0"
f2.model.1 <- "1,100;20,2000;30,2000;"
f2.title <- "Harv_P_Pulp_Tons.dat"
#Combine f2 components for writing
f2.comp <- c('<flow title="F2 Component">',
  paste0('<file value=""', f2.file, '" />'),
  paste0('<bygone value=""', f2.bypgone, '" />'),
  paste0('<time0 value=""', f2.time0, '" />'),
  paste0('<goal0 value=""', f2.goal0, '" />'),
  paste0('<threshLo value=""', f2.thlo, '" />'),
  paste0('<threshHi value=""', f2.thhi, '" />'),
  paste0('<goalPlus value=""', f2.goalplus, '" />'),
  paste0('<goalF value=""', f2.goalf, '" />'),
  paste0('<slope value=""', f2.slope, '" />'),
  paste0('<weightF value=""', f2.weightf, '" />'),
  paste0('<weight0 value=""', f2.weight0, '" />'),
  #paste0('<model value="1,', f2.target, ';', f2.next.year, ',',
  #      f2.next.target, '" />'),
  paste0('<title value=""', f2.title, '" />'),
  '<bounds height="331" width="368" x="1260" y="440" />',
  "</flow>")
```

```

#Provide each of these flow component objects to the function and run
writeProj(f1.comp = f1.comp, f2.comp= f2.comp)
```

Now we have a project file saved to our working directory. Let's open habplan and see if this has worked.

```

#Open Habplan (if run from here, R functionality will cease until Habplan is closed)
shell("h", wait=TRUE)
```

Function: plotting an individual flow output - *FlowPlot*

After running Habplan, we will have several flows saved to our working directory. The option still exists to interactively watch the charts in a Habplan window. However, we provide a function to visualize each flow individually.

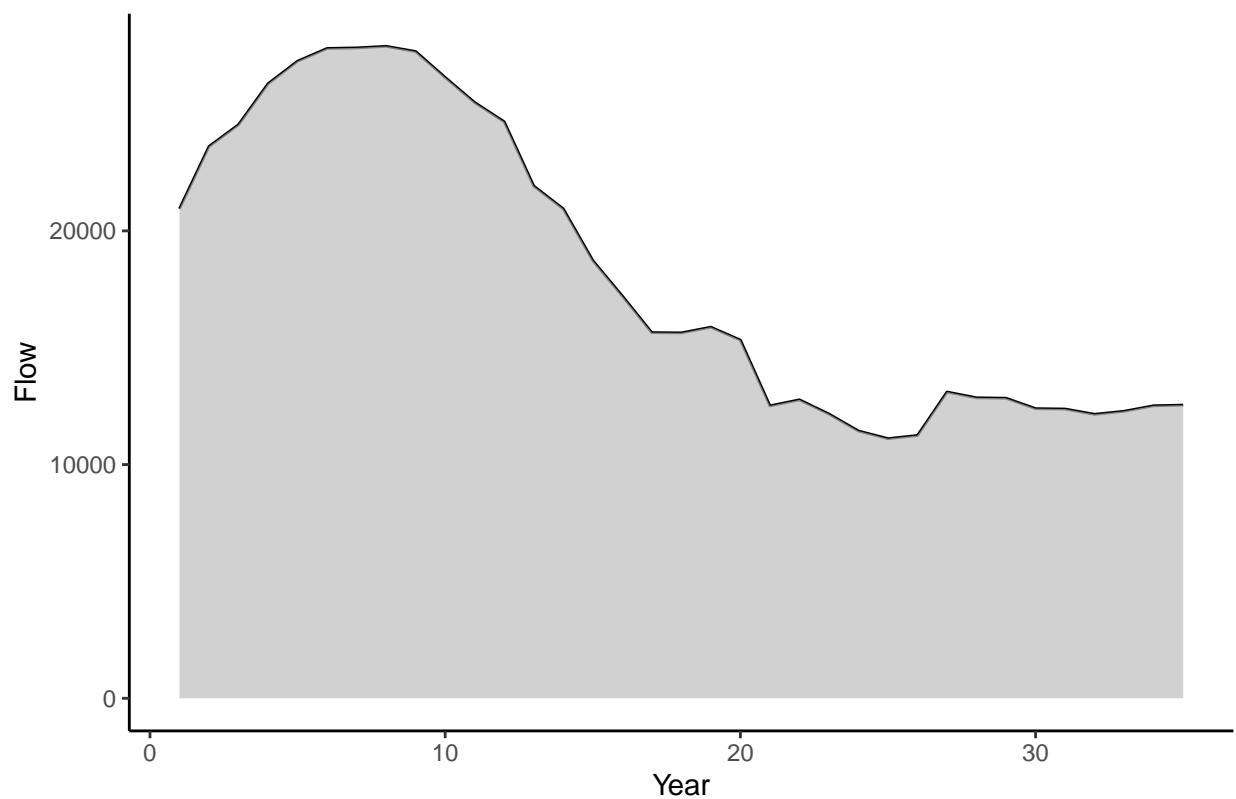
First read in the flow output file, and then feed this file into the function.

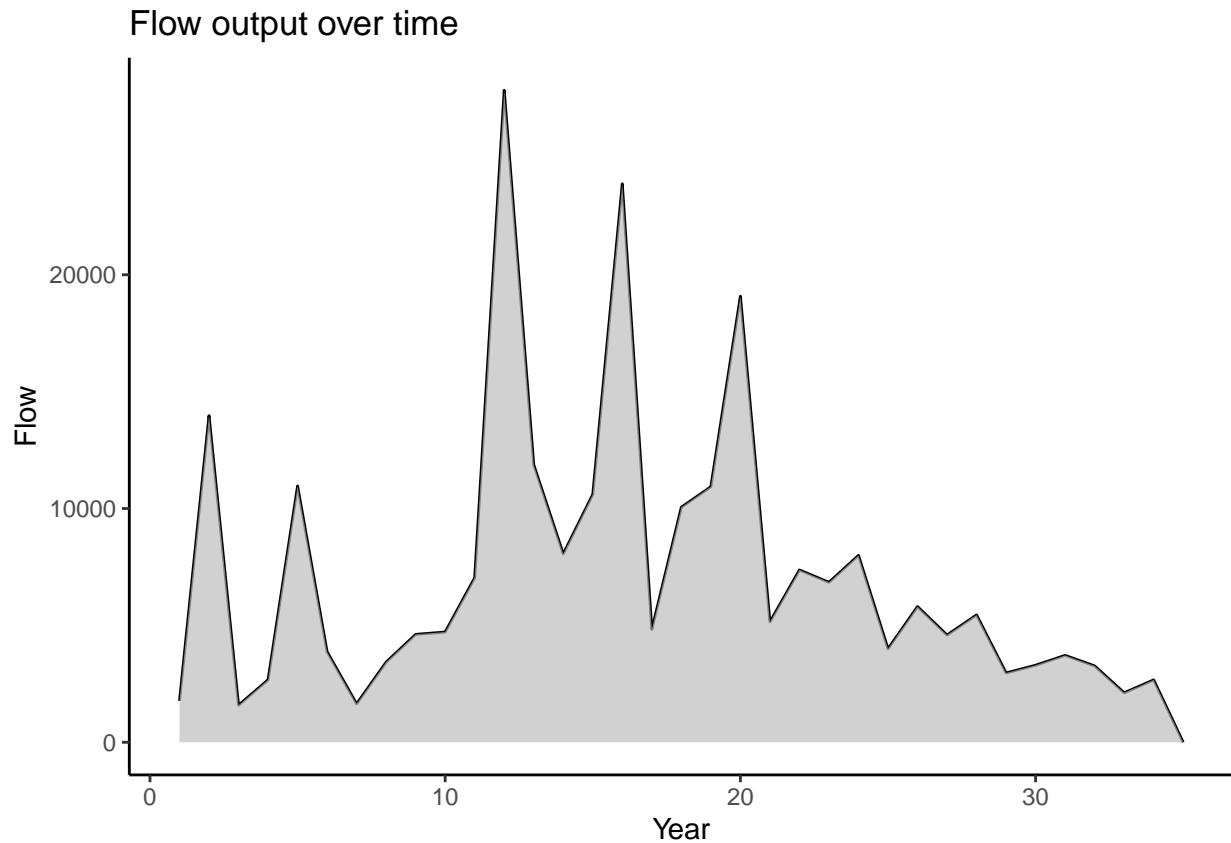
```

#Read in one of the flow files
flow1 <- read.csv("./saveFlow1", sep="")
flow2 <- read.csv("./saveFlow2", sep="")

#Input the flow file into the function, and number of years
flowPlot(flow.data = flow1, nyear = 35)
flowPlot(flow.data = flow2, nyear = 35)
```

Flow output over time





Again, the first figure above shows the output flow from our HSI component throughout our study period, and the second shows the hard pulpwood yield. These appear to have provided much larger yields for both HSI and hard pulpwood.

We can now run the final iteration of *HabSpace* to assess the spatial component. Even if the flow components are much better, it is still important to ensure that we have not compromised the spatial contiguity and suitability of the landscape for at risk species.

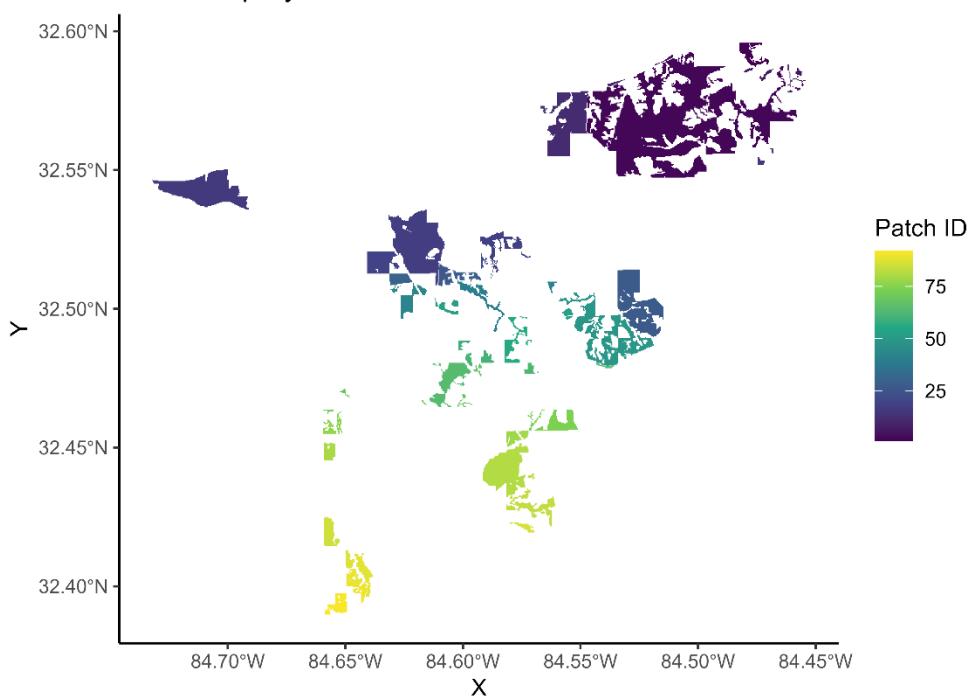
Function: spatial contiguity assessment - *HabSpace*

The HabSpace function may take several minutes to complete!

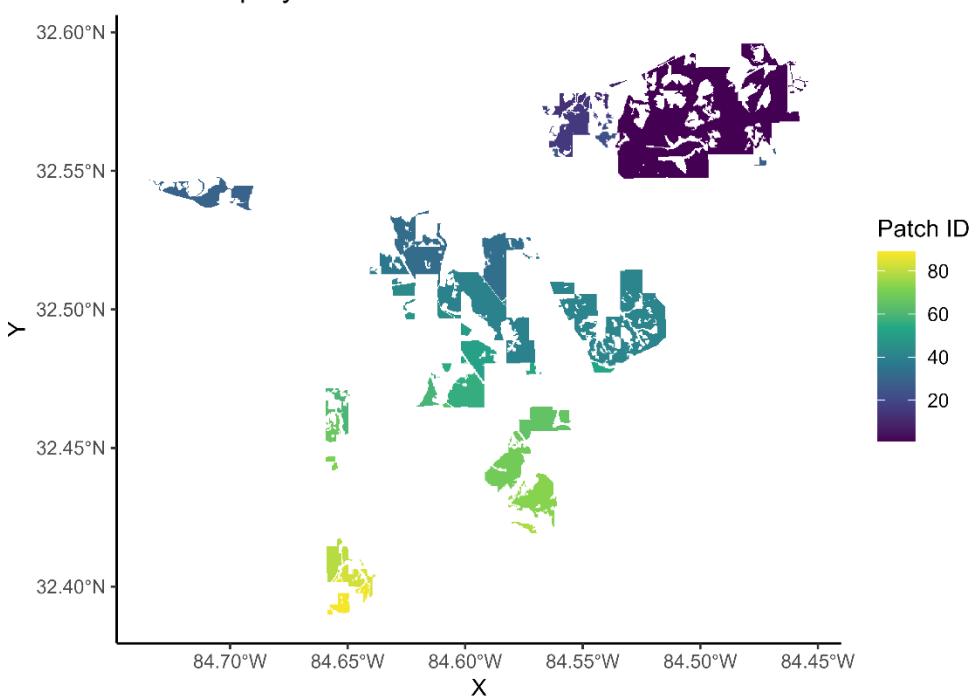
```
#Want to create a shapefile output for each year, to look at change
#of regime for each stand over time.
```

```
space.test <- HabSpace(site.shp = site.shp, flow = flow, nyear = 35,
                        mode = "terrestrial", dist = 500, level = "patch")
```

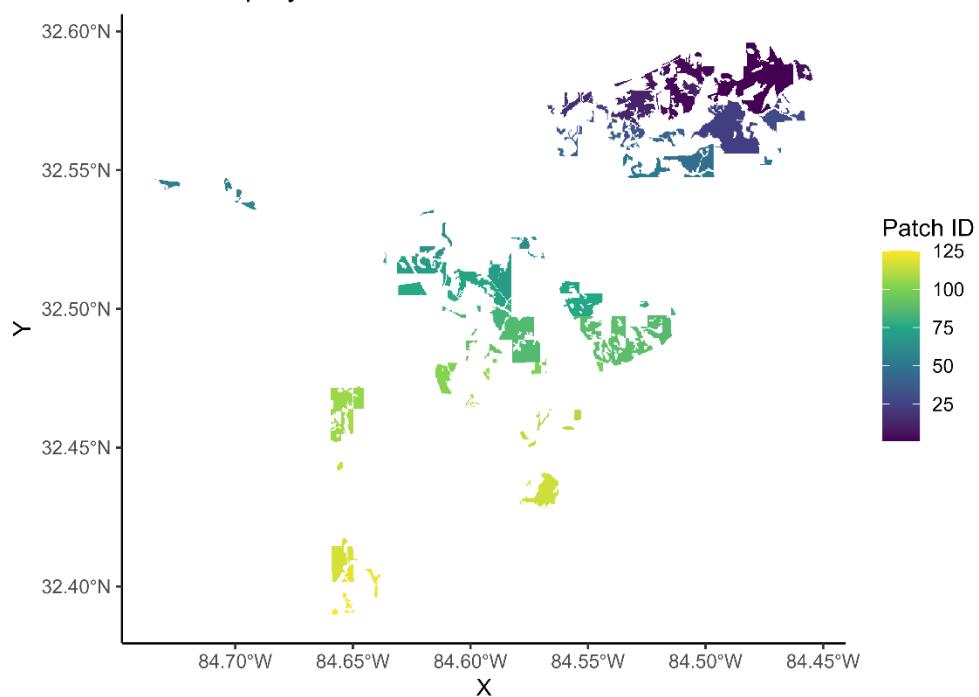
Patch map - year 1



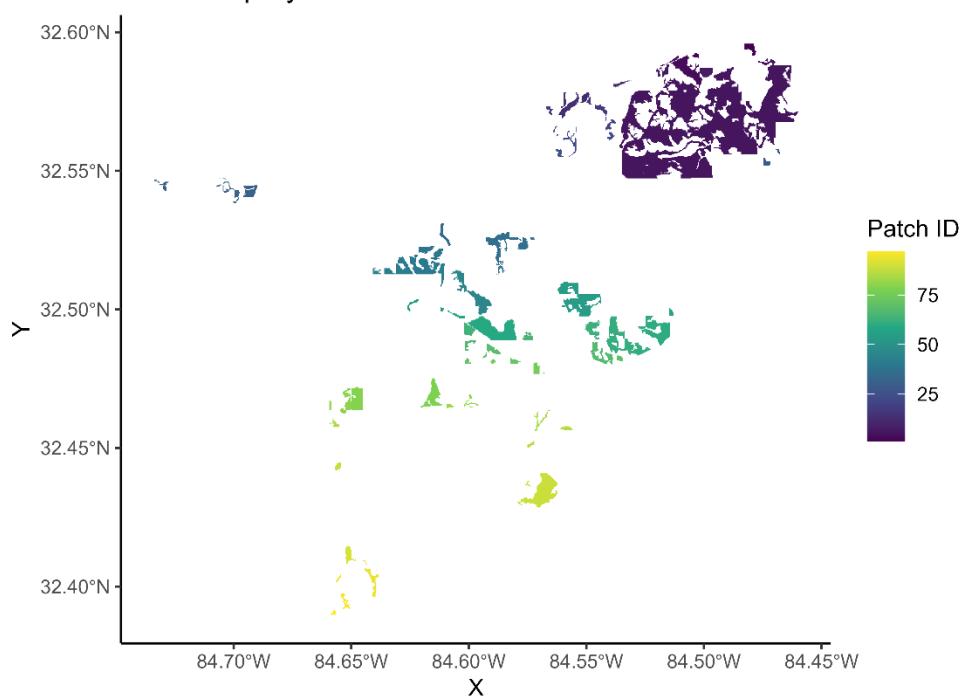
Patch map - year 10

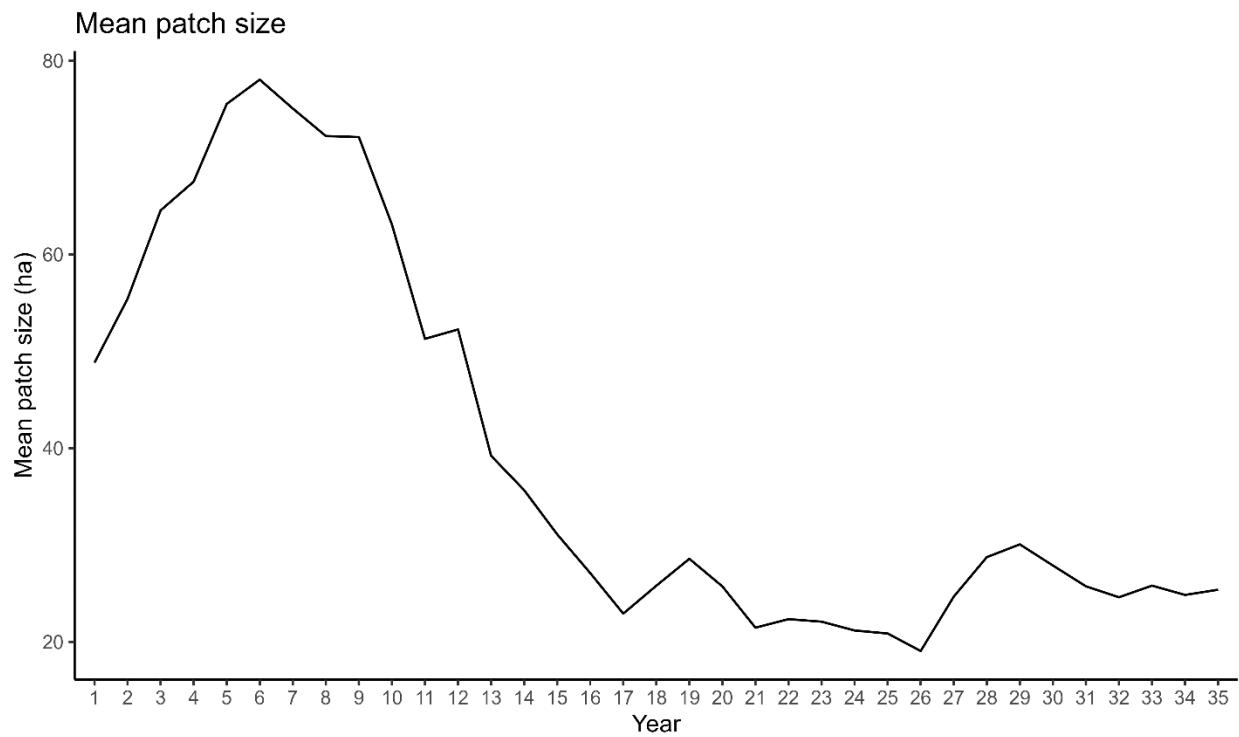
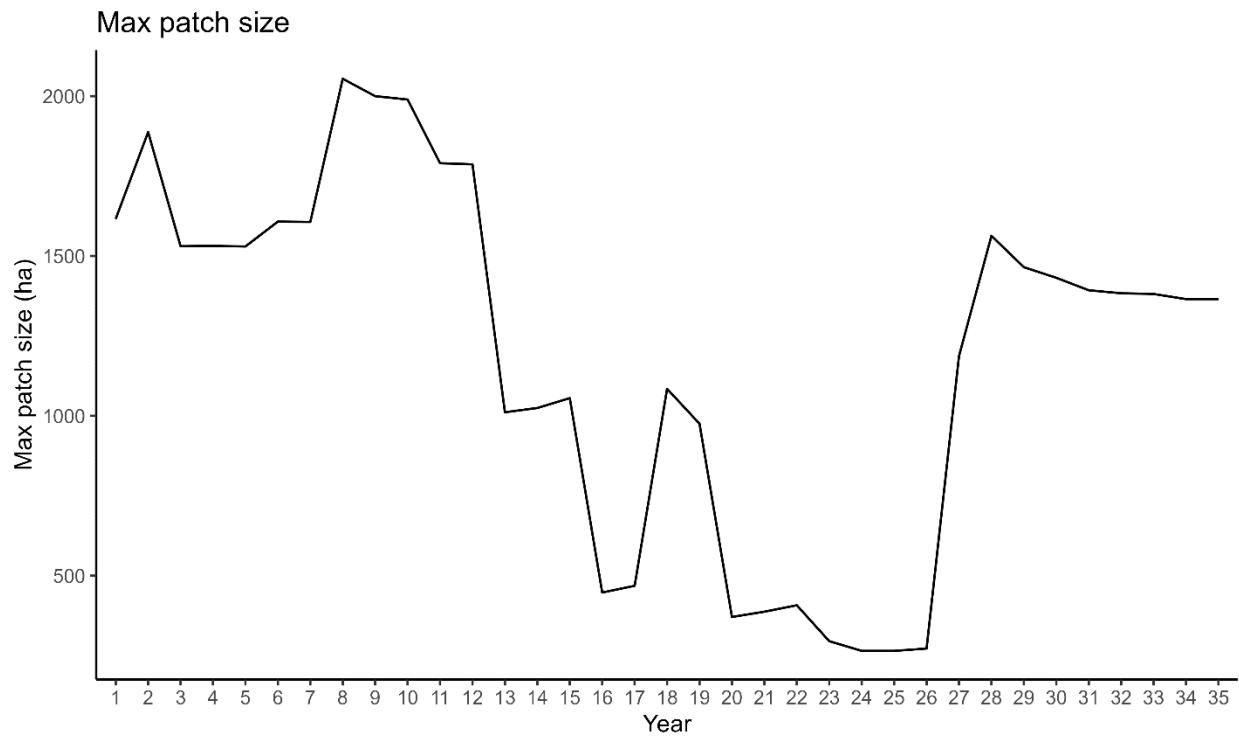


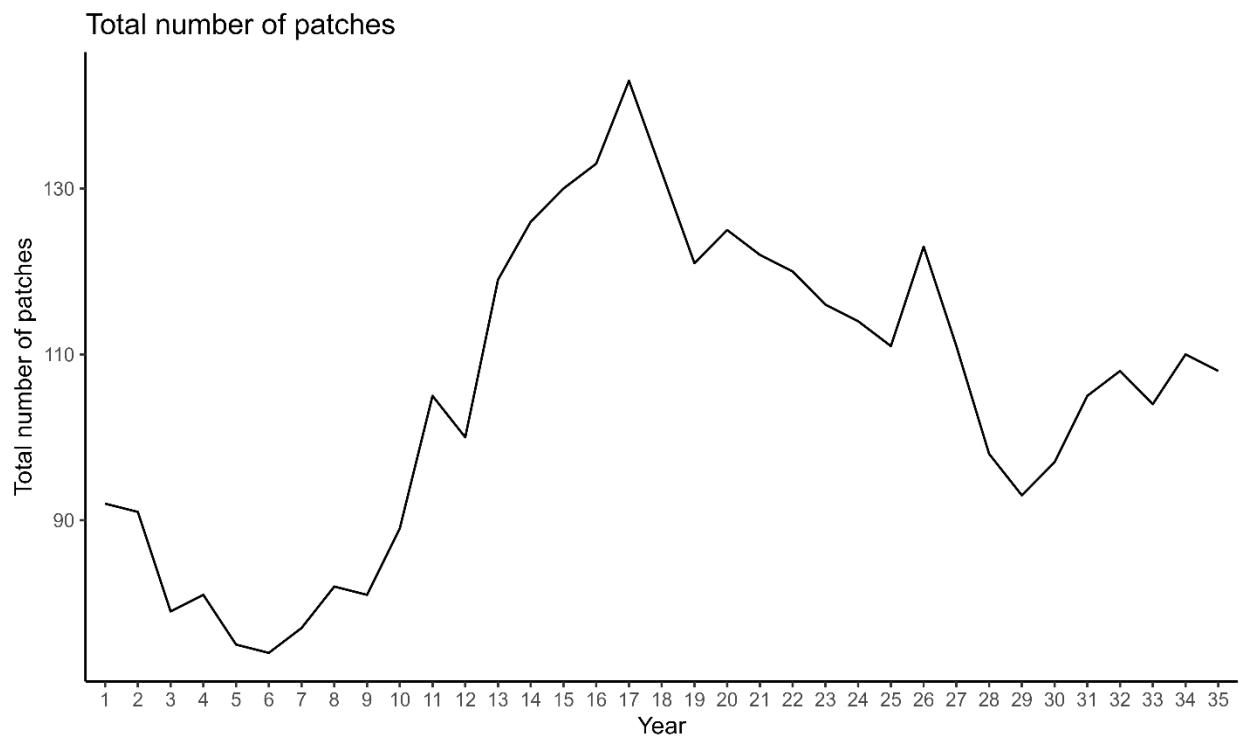
Patch map - year 20



Patch map - year 30







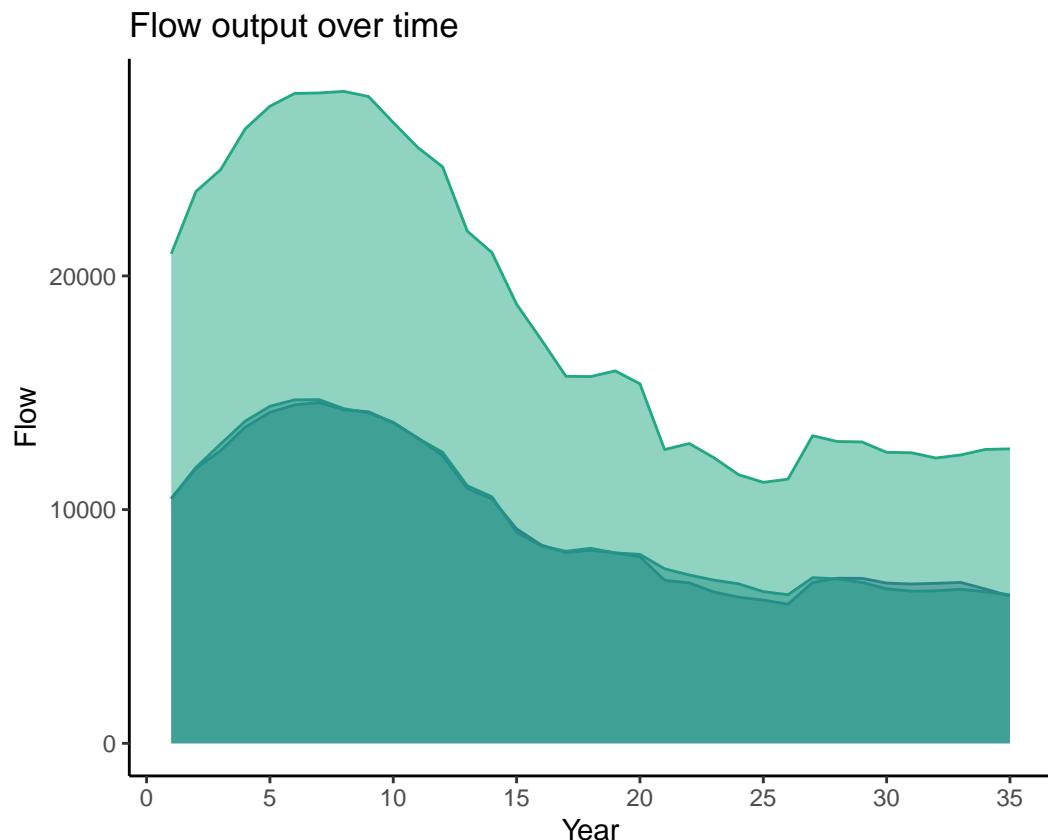
We can compare each run to see how the yields have changed with each change we have made.

Function: multiple flow outputs - *ComPlot*

The above will create a chart for one of the flows. However, it is also useful to be able to visualize the flows in relation to one another. We therefore provide another function: comPlot.

This requires the same input as before, but this time we will introduce some of the other flows outputs. Current maximum of 3 flows.

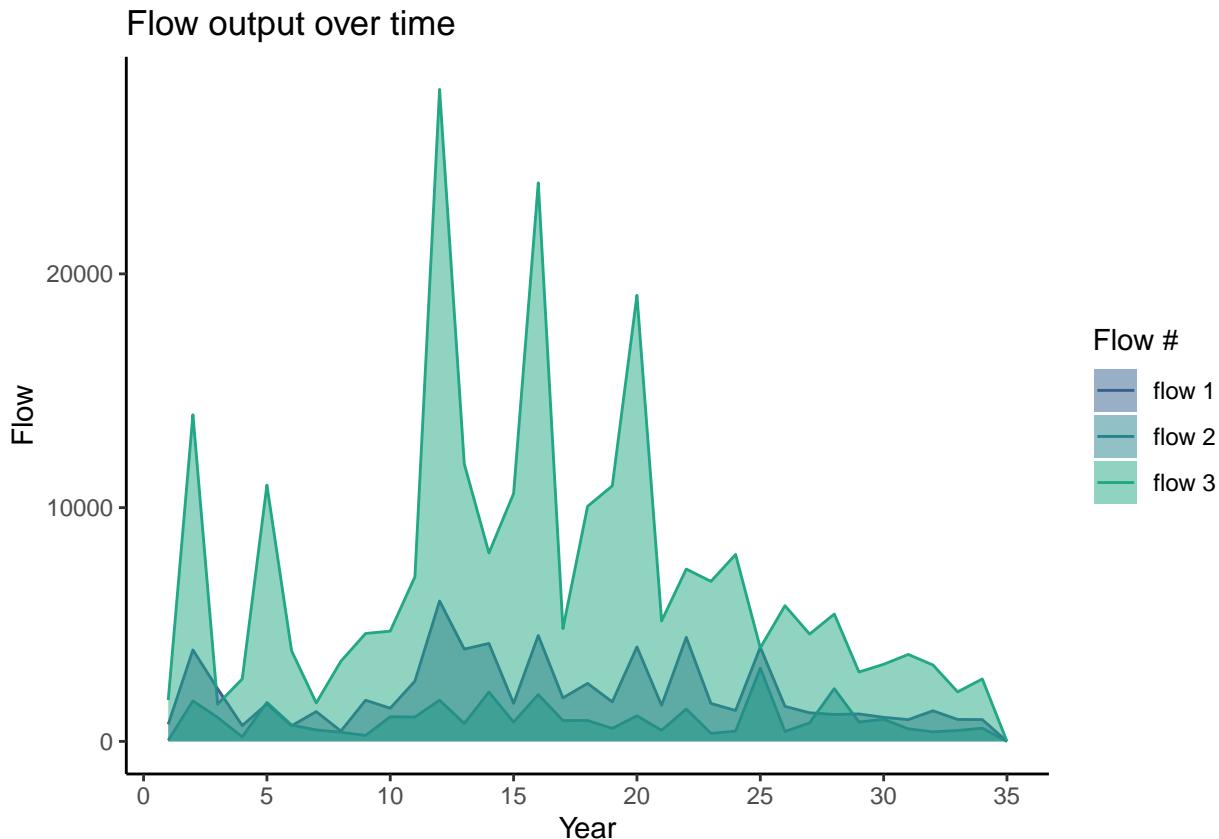
```
#Read in the example flows:  
flow1 <- read.csv("./Run_1/saveFlow1", sep="", header = F) #Files have been saved in separate folders  
flow2 <- read.csv("./Run_2/saveFlow1", sep="", header = F)  
flow3 <- read.csv("./Run_3/saveFlow1", sep="", header = F)  
#flow4 <- read.csv("./saveFlow4", sep="")  
  
#Run function with new flows  
comPlot(flow.data.1 = flow1, flow.data.2 = flow2,  
        flow.data.3 = flow3, 35)
```



```
#Read in the example flows:  
flow1 <- read.csv("./Run_1/saveFlow2", sep="") #Files have been saved in separate folders  
flow2 <- read.csv("./Run_2/saveFlow2", sep="")  
flow3 <- read.csv("./Run_3/saveFlow2", sep="")
```

```
#flow4 <- read.csv("./saveFlow4", sep="")

#Run function with new flows
comPlot(flow.data.1 = flow1, flow.data.2 = flow2,
        flow.data.3 = flow3, 35)
```



By visualizing the flows in comparison to one another from each run, we can now clearly see the little differences found between the first and second run, but the changes we made to the third run have greatly increased our average HSI and harvested hard pulpwood - ultimately providing more habitat for our species of interest, but maximizing yield and profits also.

Function: saving the top schedule to shapefile - *StandSched*

From this example, we are happy with the final run and will apply the recommended regime to each stand based on the output schedule from Habplan. Our next function pulls the information from the best schedule saved in the working directory (from Habplan), and attaches this to the stand shapefile.

As long as the file is still in the working directory (saveSched), then all we need to do is input the stand shapefile and run the function.

```
#Run function to add schedule to shapefile
standSched(site.shp)
```

A new .shp file can now be found in the working directory titled Site_with_schedule.shp.

For the purposes of creating flow files, running Habplan, and comparing possible management schedules output from Habplan, you can now stop at this point of the vignette. However, next we provide two additional functions for creating custom HSI flow files, and including a a blocksize flow subcomponent to the Habplan run.

Function: HSI calculation - *HSIcalc*

We are going to work through two examples of using the basal area (BA) to calculate HSI. We have provided a function that will compute an HSI based on a user-specified formula, and combine this with our stand data. We provide examples of simple HSI formulas, but any formula can be used, so long as the inputs are present in the std.data dataset. We use a single independent variable (BA), but function of multiple independent variables can be used.

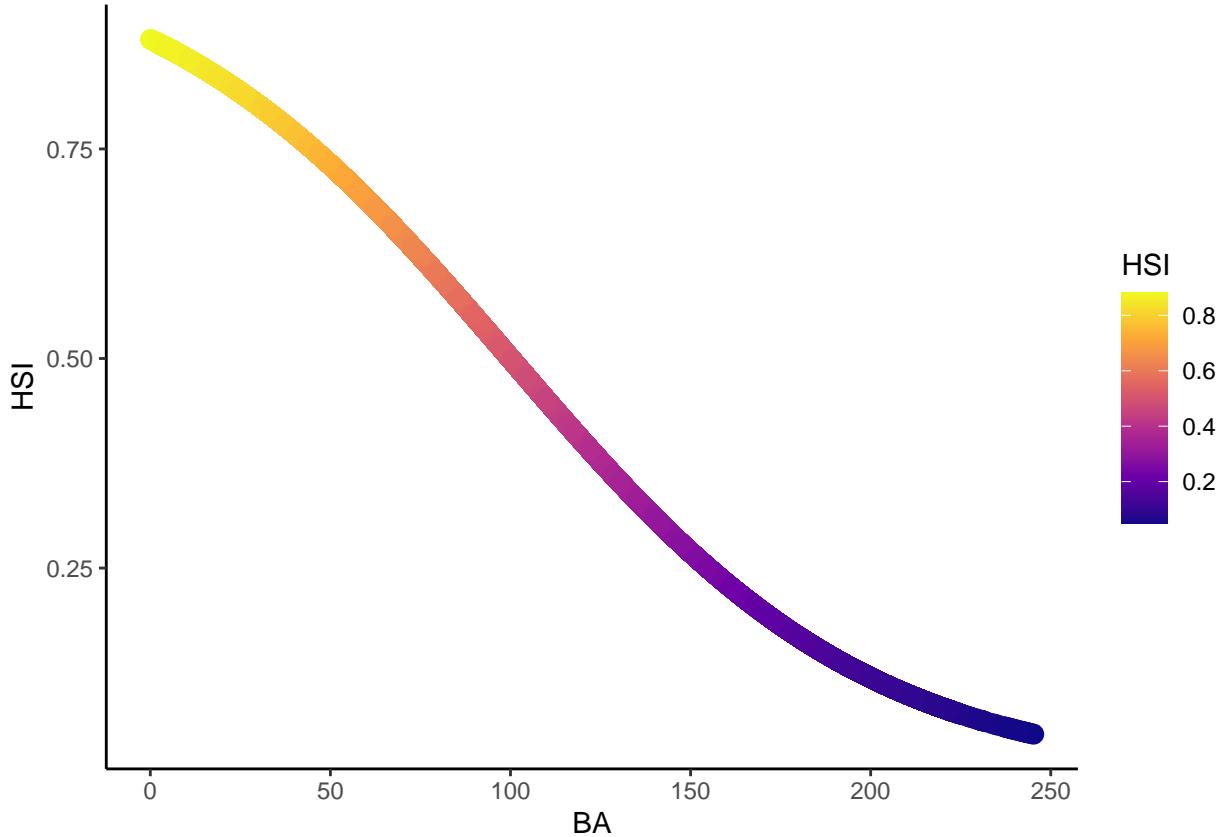
Our first example looks at a negative linear effect of BA on HSI. The equation will need to be provided in form of an R function.

```
#Create function to apply equation for HSI
#Define the independent variable (x), slope (m), and y-intercept (b) of the linear equation
hsi.func <- function(x = std.data$BA, m = -0.02, b = 2) {
  return(m * x + b)
}
```

We can now insert this equation into the *HSIcalc* function, which calculates HSI from the minimum to the maximum values of all x values in the std.data dataset, and then adds a new data column to our stand data for HSI values.

```
#The function will create a new column with the HSI values
new.data <- HSIcalc(std.data, hsi.func)

#Summarise the HSI data
summary(new.data$HSI)
#>   Min. 1st Qu. Median Mean 3rd Qu. Max.
#> 0.05188 0.40419 0.61323 0.54688 0.73023 0.88072
#Plot data against BA to show relationship
ggplot(data = new.data) +
  geom_point(aes(x = BA, y = HSI, color = HSI),
             size = 3) +
  scale_color_viridis_c(option = "plasma") +
  theme_classic()
```



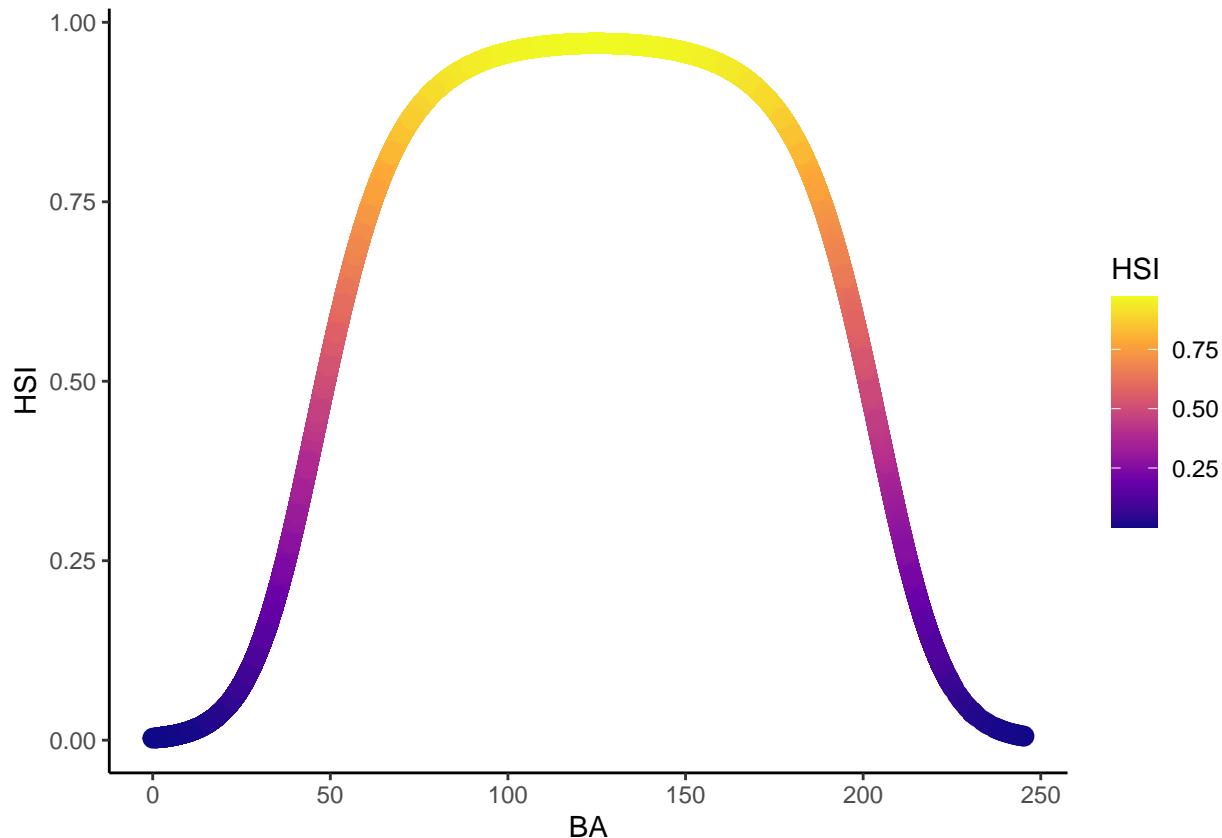
Our second example looks at a quadratic relationship of BA on HSI. Again, the equation will need to be provided in form of an R function:

```
#Create function to apply equation for HSI
#Use a, b, and c to change shape of graph
hsi.func <- function(x = std.data$BA, a = -0.0006, b = 125, c = 3.5) {
  return(a * (x - b)^2 + c)
}
```

We can now insert this equation into the *HSIcalc* function to add a column to our stand data for HSI values.

```
#The function will create a new column with the HSI values
new.data <- HSIcalc(std.data, hsi.func)

#Summarise the HSI data
summary(new.data$HSI)
#>      Min. 1st Qu. Median Mean 3rd Qu. Max.
#> 0.002816 0.394109 0.774463 0.661753 0.938009 0.970688
#Plot data against BA to show relationship
ggplot(data = new.data) +
  geom_point(aes(x = BA, y = HSI, color = HSI),
             size = 3) +
  scale_color_viridis_c(option = "plasma") +
  theme_classic()
```



Function: create block data - *HabBlock*

We will not be including the block data for the purpose of this vignette due to processing time. However, below we provide instructions for including a block size constraints to the Habplan run. Block size constraints are a sub-component of flow components. For a comprehensive guide to the purpose of block size constraints, please see section 9 of the Habplan user manual.

We can now run the function *HabBlock* from the HabplanR package. This takes the SpatVector shapefile, and stand data/info from earlier in the vignette and creates block data (defines which polygons are adjacent to each other). The block data will save directly to the working directory.

```
#HabBlock will create a block data file in the working directory
HabBlock(std.data = std.data, std.info = std.info, site.shp = site.shp,
         block.title = "block1")

#Since this block size component file is within the working directory already,
#we just need to specify the file name below (b1.file), and input the
#specific parameters for the component.

#Info for f1 block size component (green up) ----
b1.file <- "block1.txt"
b1.notBlock <- "1-4" #which regimes do NOT contribute to block sizes
b1.greenUp <- "3" #3 year green up period
b1.min <- "1" #minimum allowable block size
b1.max <- "1000" #maximum allowable block size
```

```

b1.goal <- "1" #a value of 1.0 means all blocks must comply
b1.weight <- "1.0" #good practice to start this at 1
b1.title <- "block1.txt"
#Combine f1 components for writing
block1 <- c('<block title="BK1(1) Component">',
            paste0('<file value=""', b1.file, '" />'),
            paste0('<notBlock value=""', b1.notBlock, '" />'),
            paste0('<greenUp value=""', b1.greenUp, '" />'),
            paste0('<min value=""', b1.min, '" />'),
            paste0('<max value=""', b1.max, '" />'),
            paste0('<goal value=""', b1.goal, '" />'),
            paste0('<weight value=""', b1.weight, '" />'),
            paste0('<title value=""', b1.title, '" />'),
            '<bounds height="330" width="366" x="553" y="443" />',
            "</block>")
```

You can include as many block size components as there are flow components, which can be included as above but changing the block title and file to match the number of the flow component.

We can then include block size constraints to the project file using the *writeProj* function.

```

#Provide each of these flow component objects to the function and run
writeProj(f1.comp = f1.comp, block1 = block1, f2.comp= f2.comp)
```

Summary

This is the end of the HabplanR vignette. Above we have provided a very simple example of how to use HabplanR to run a multi-objective forestry issue in Habplan. The values provided within the vignette are for demonstrative purposes only and do not represent real data. Real-world examples will likely have many more objectives to evaluate, alongside complex spatiotemporal considerations. If you encounter any issues with the HabplanR package, or require help with applying the functions to a novel dataset, feel free to contact Max Jones at maxdoltonjones@vt.edu

Acknowledgements

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