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HabplanR Vignette

A complementary 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.

Max D. Jones

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Introduction to HabplanR

The *HabplanR* package was developed to complement 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. *HabplanR* broadens applicability of Habplan and make file-formatting and data input easier for more efficient program use.

The main functions of *HabplanR* are to provide important ecological context to the multi-objective optimization performed by Habplan, and streamline program use. 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. We demonstrate the utility of *HabplanR* using flow objectives derived from Forest Vegetation Simulator (FVS; <https://www.fs.usda.gov/fvs/>) growth model data. Specifically, we explore two objective flows: harvested tons of pine pulpwood (acres), and habitat area (acres; based on predetermined Habitat Suitability Index [HSI]). We use these flows as proxies for economic and ecological goals, respectively, highlighting the range of objectives that Habplan can accommodate. There can be any number of objectives used within a multi-objective problem, and this vignette serves as an example on how to incorporate and adjust two objectives, which can be expanded across several user-defined objective functions.

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("NCASI/Habplan_Memberonly/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):

```
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. If there are any issues installing/using the spdep package, there may be an issue relating to the terra package, and/or the package raster may be needed. See <https://github.com/r-spatial/spdep/issues/78> for further information.

```
#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.0.3.2  
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.

All of the necessary files and software for this vignette can be found at https://github.com/NCASI/Habplan_Memberonly. Download both the “HabplanR” and “Habpan_software” folders, and then copy all of the files from the Habpan_Software folder into the HabplanR folder. The HabplanR folder should then be set as the working directory for the purpose of this 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 of interest. 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

IMPORTANT The publicly available version of Habplan only supports data with up to 500 polygons (stands). For larger data needs, please contact NCASI to obtain access.

```
#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 × 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 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 × 18
#>   RegimeKey `Regime Activity` StandID Year   Age     BA    TPA
#>   <dbl> <chr>           <chr>   <dbl> <dbl> <dbl> <dbl>
#> 1 1.35      4 Thin 1 at 120 BA to ... 15588_1 2017     9  5.53  266.
#> 2 1.83      4 Thin 1 at 120 BA to ... 15588_1 2020    12  8.82  265.
#> 3 2.10      4 Thin 1 at 120 BA to ... 15588_1 2023    15  8.17  169.
#> 4 2.79      4 Thin 1 at 120 BA to ... 15588_1 2026    18 10.8   168.
#> 5 3.43      4 Thin 1 at 120 BA to ... 15588_1 2029    21 14.0   168.
#> 6 3.42      4 Thin 1 at 120 BA to ... 15588_1 2032    24 17.6   167.
#> # [i] 10 more variables: Pine_CNS_Tons <dbl>, Pine_Saw_Tons <dbl>,
#> # Hwd_Pulp_Tons <dbl>, Hwd_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>, HSI <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 appropriate data column 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"   "HSI"
```

From the column names, we are interested in “Harv_P_Pulp_Tons” (pulp pinewood harvested [tons/acre]) and “HSI” (stands with a higher HSI value than a specified value), which are column number 13 and 18 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 are of interest (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 = 18,
                         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 and output files are to be stored, and all data and software are maintained. The working directory is user-defined.
- 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,  
#but include  
#the "/" at the end as shown here  
#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.bypgone <- ""
f1.time0 <- "1000"
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('<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 <- "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.bystone, '" />'),  

  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)

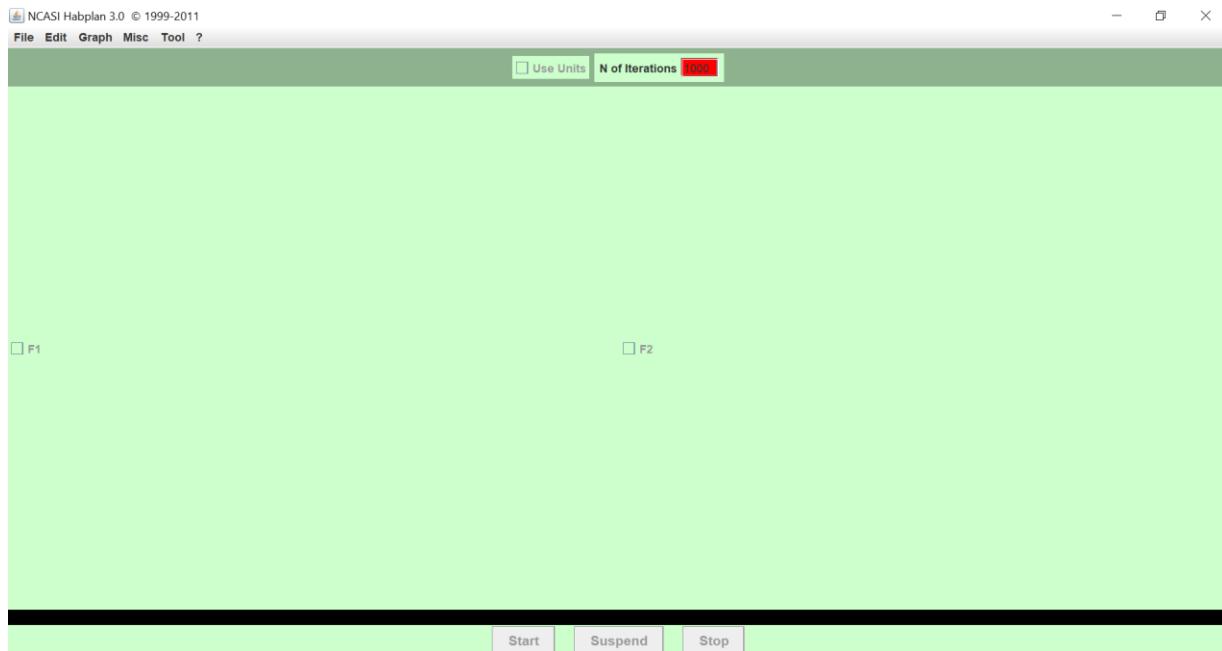
Now we have a project file saved to our working directory. Let's open Habplan and see if this has worked. The Habplan program needs to be stored in the working directory that was assigned earlier, so that it can be run from RStudio below.

IMPORTANT Java must be installed for Habplan to run, otherwise execution of the following code will fail.

```

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

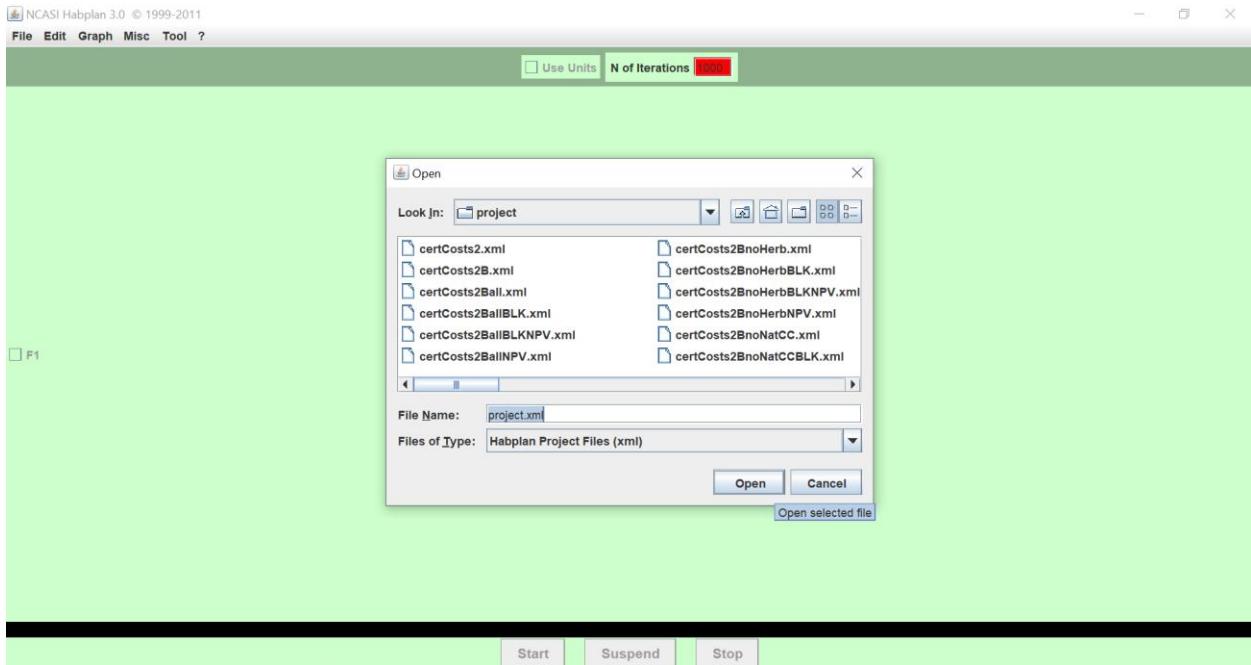
When you first open Habplan from the R script, the following window will open. Note that you will be unable to run anything in your R session when Habplan has been opened via R. Additionally, your start-up screen may look slightly different – this is ok!



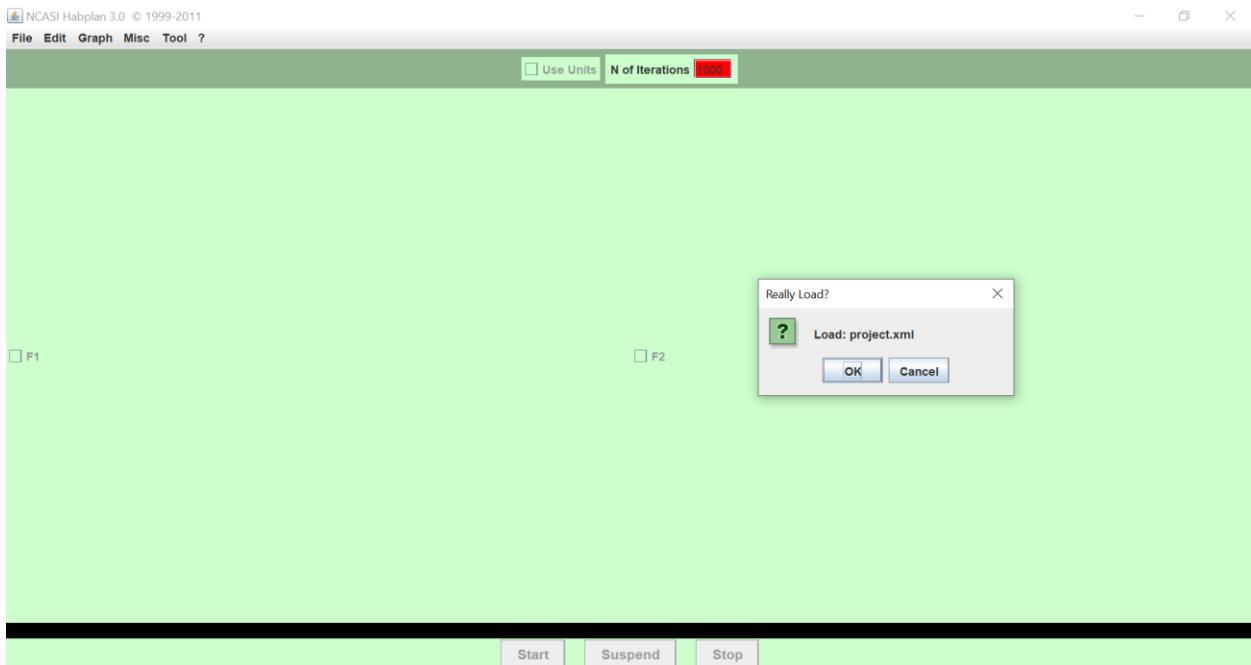
To open the project file we have just created, we can navigate to File > Open... Make sure to navigate to the correct project file (the one created via the R script) if there are multiple saved on your computer.



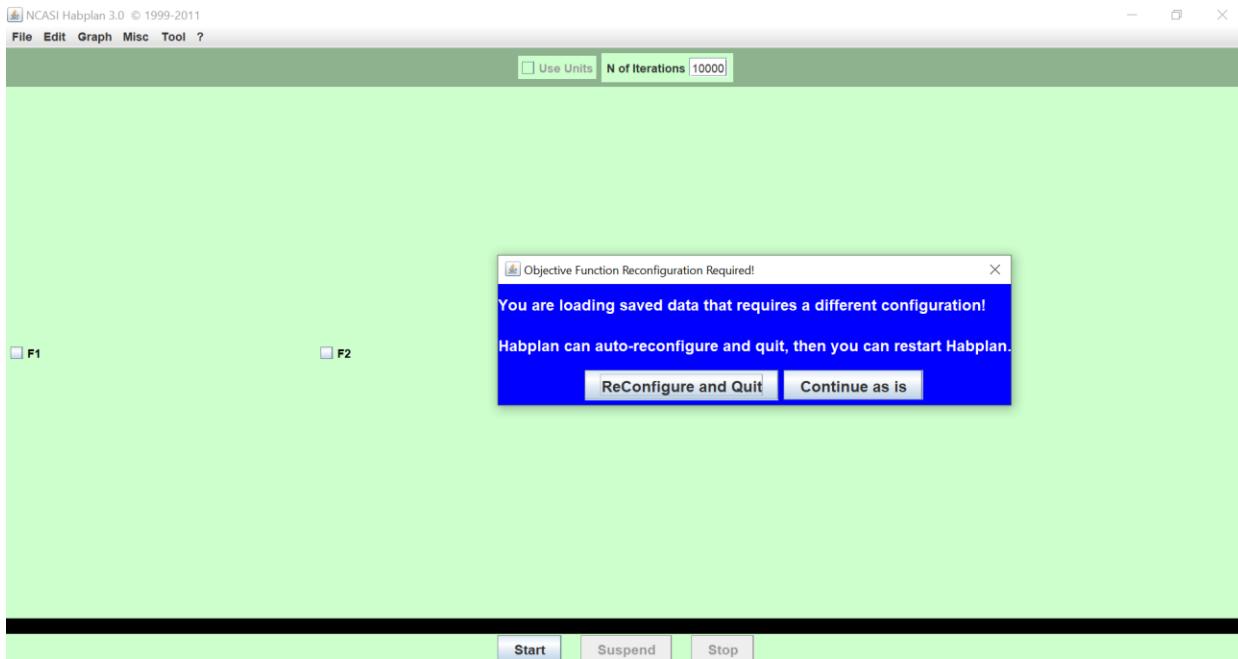
A new window will open to select the appropriate file, which will have saved in the set working directory as project.xml. Navigate to the project.xml file that was just created in R, select that file and click Open.



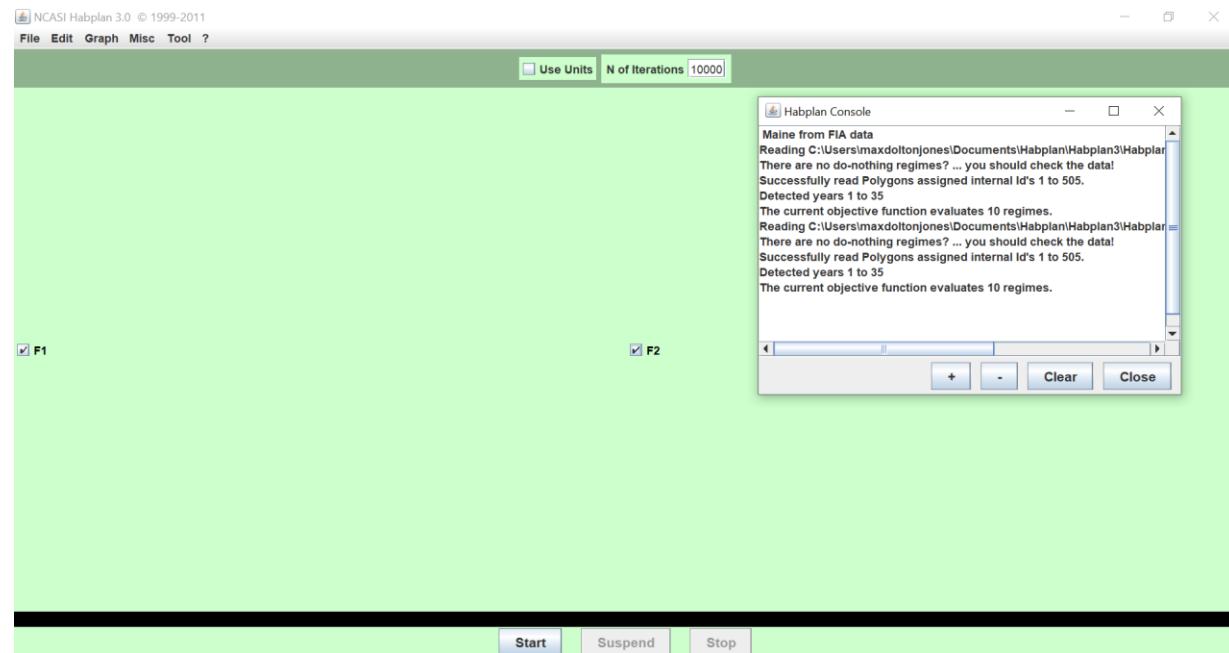
A new window will then open. Click OK to load the project file.



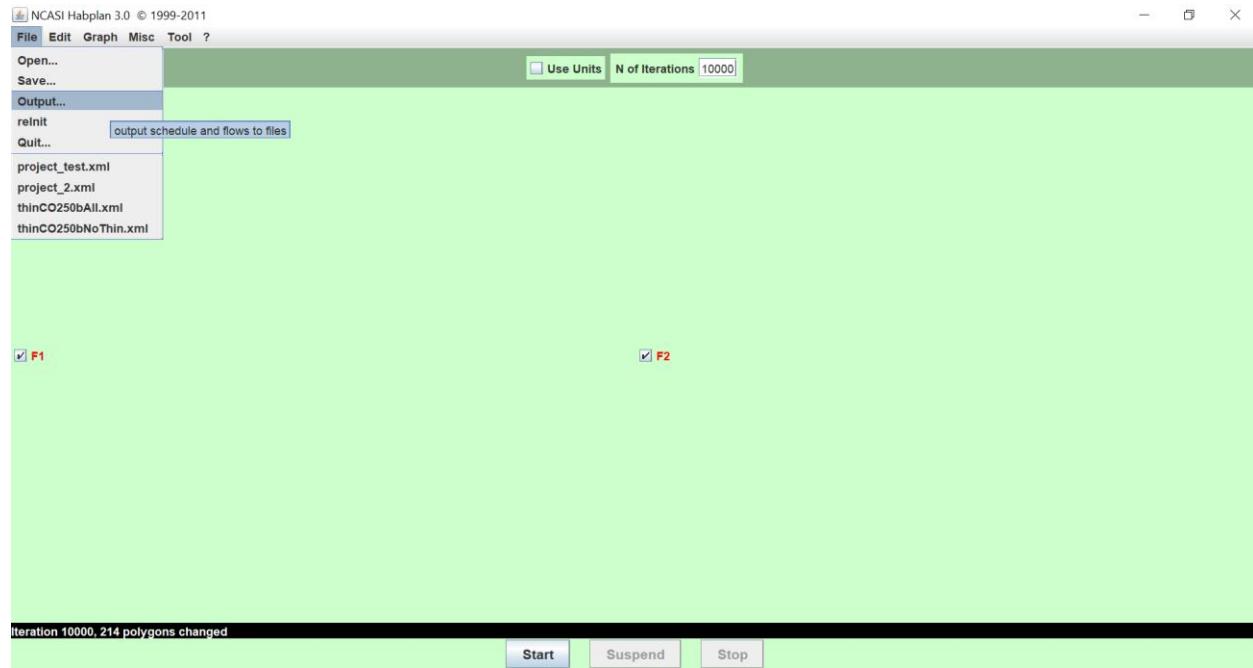
When opening the project file, you may encounter the following pop-up window. This means that the configuration file has a different configuration than the project file. In this circumstance, select ReConfigure and Quit, which will close Habplan. Once that happens, re-run the R code `shell("h", wait=TRUE)`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



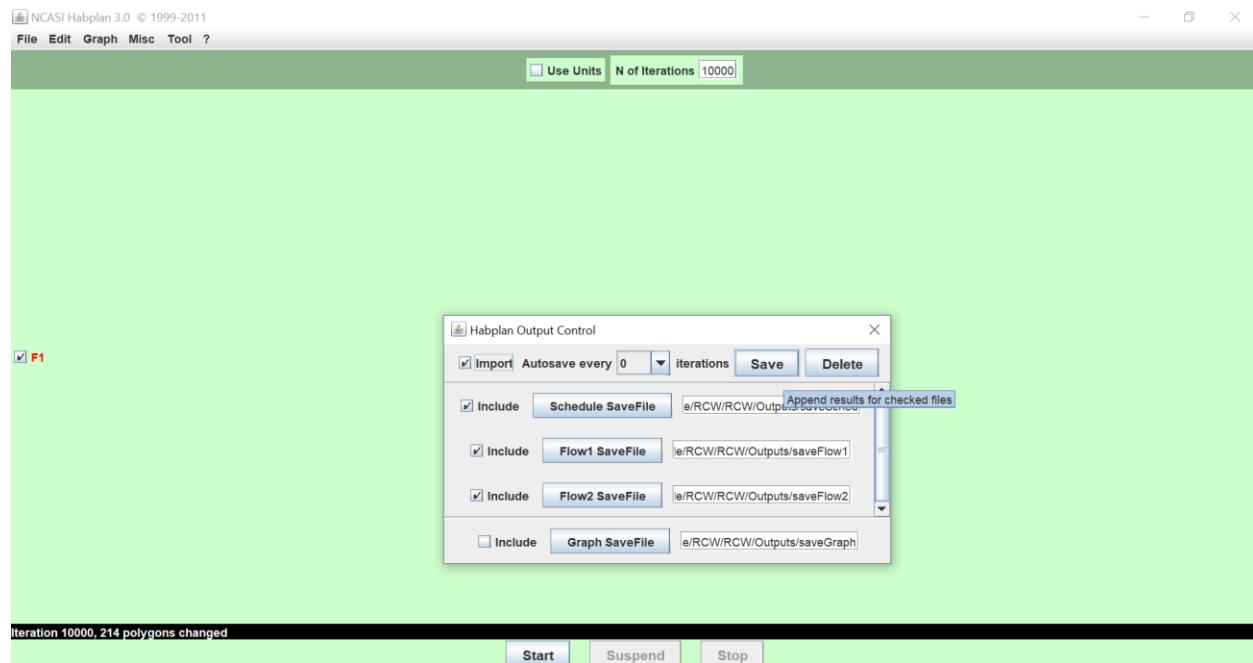
Another new window will now be available titled Habplan Console, where the program will provide updates and errors. We will also have the opportunity to select the flow components on the main window, named F1 and F2 in our example. Including other flows in the project file will add new component check 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. If an error is encountered when attempting to save, check the file directory in the Habplan Output Control window.



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 details:

- File Bar:** File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help.
- Project Bar:** HabplanR - RStudio, Habplan_workflow_v3.R, HabplanR.vignette.v2.Rmd.
- Code Editor:** Shows the code for the vignette, including setting the working directory, writing project files, and running Habplan.
- Environment Tab:** Global Environment is empty.
- Console Tab:** Shows the R session output, including the loading of the 'usethis' package and the execution of the vignette code.
- Bottom Status Bar:** C:\Users\maxdoltonjones\Documents\Habplan\Habplan3\Habplan3>java -mx1012m Habplan3

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)
```

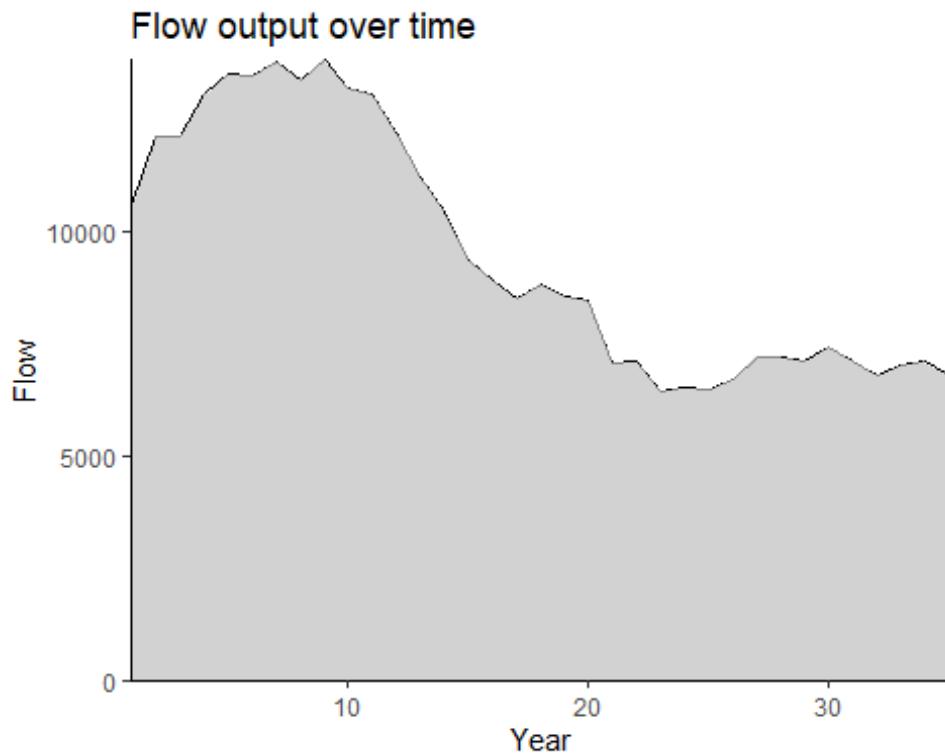


Figure 1. The amount of flow (habitat area) attained over time as a result of the suggested Habplan management schedule.

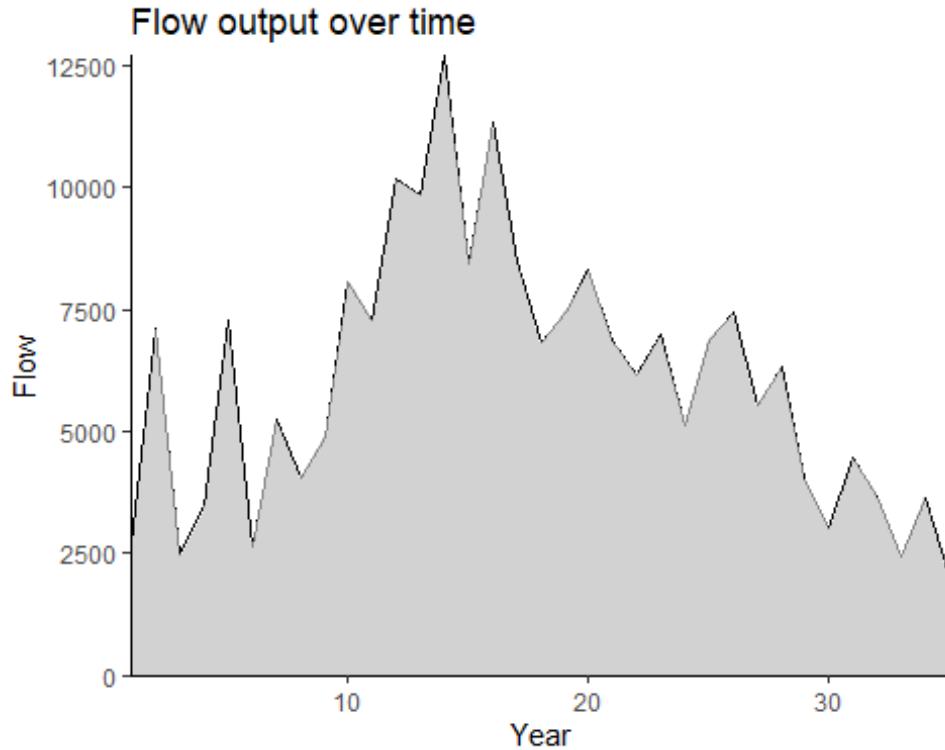


Figure 2. The amount of flow (harvested pine pulpwood) attained over time as a result of the suggested Habplan management schedule.

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

We are going to create 3 runs of Habplan for this vignette. To compare the flow outputs of each of these Habplan runs, we will need to save the output in separate folders. For the vignette, we created 3 folders named Run_1, Run_2, and Run_3. Save the "saveFlow1" and "saveFlow2" files into the Run_1 folder and repeat on the following runs.

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 additional 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 examine 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 saves 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.

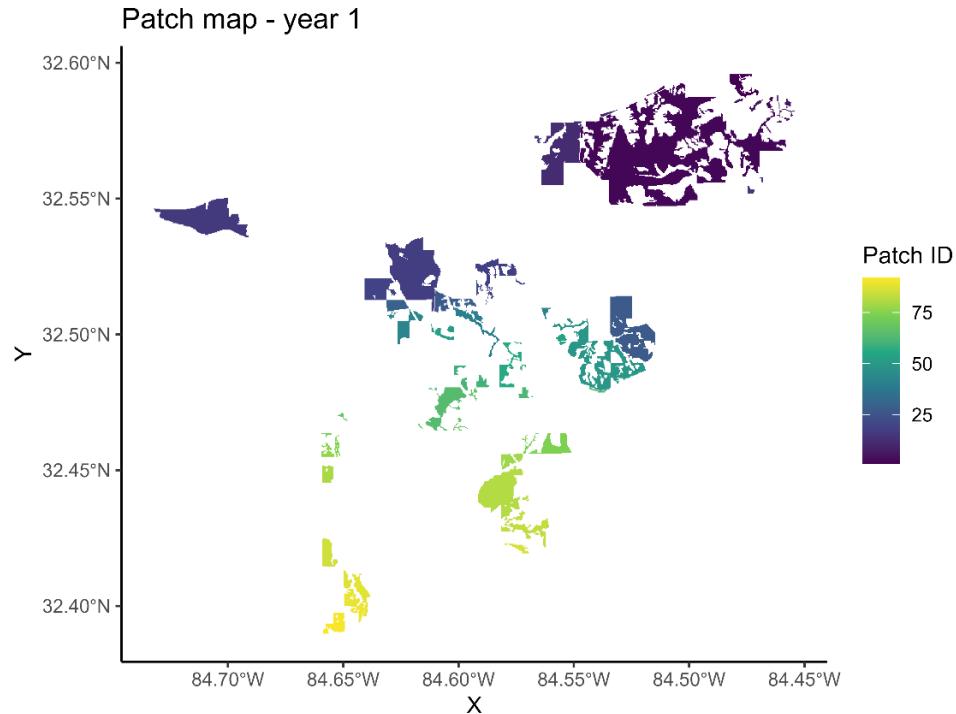


Figure 3. First year of landscape patches resulting from the Habplan management schedule.

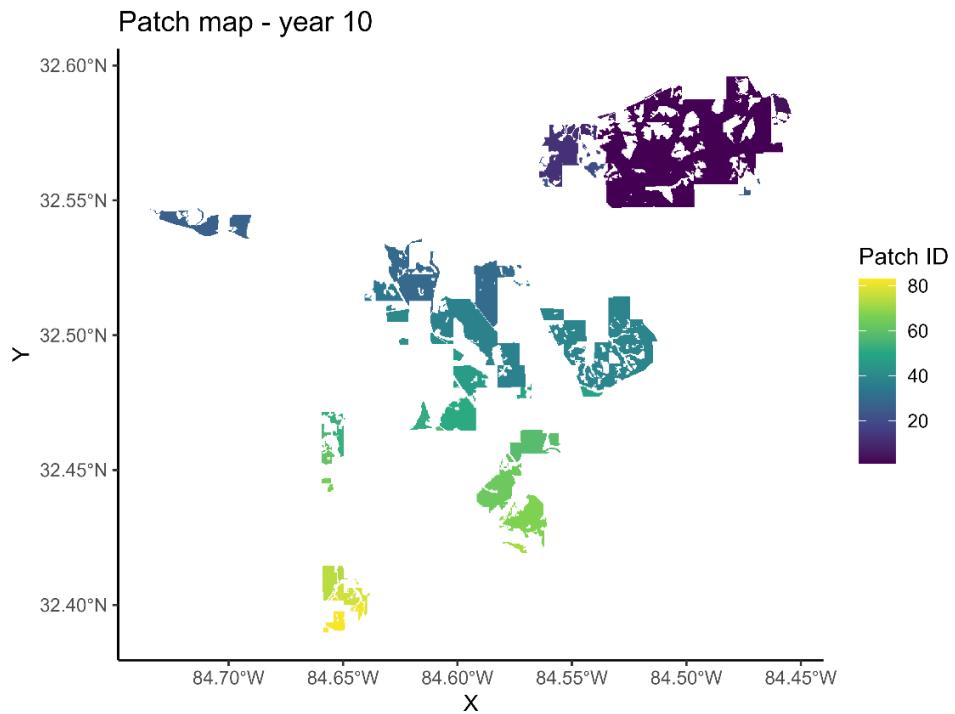


Figure 4. Tenth year of landscape patches resulting from the Habplan management schedule.

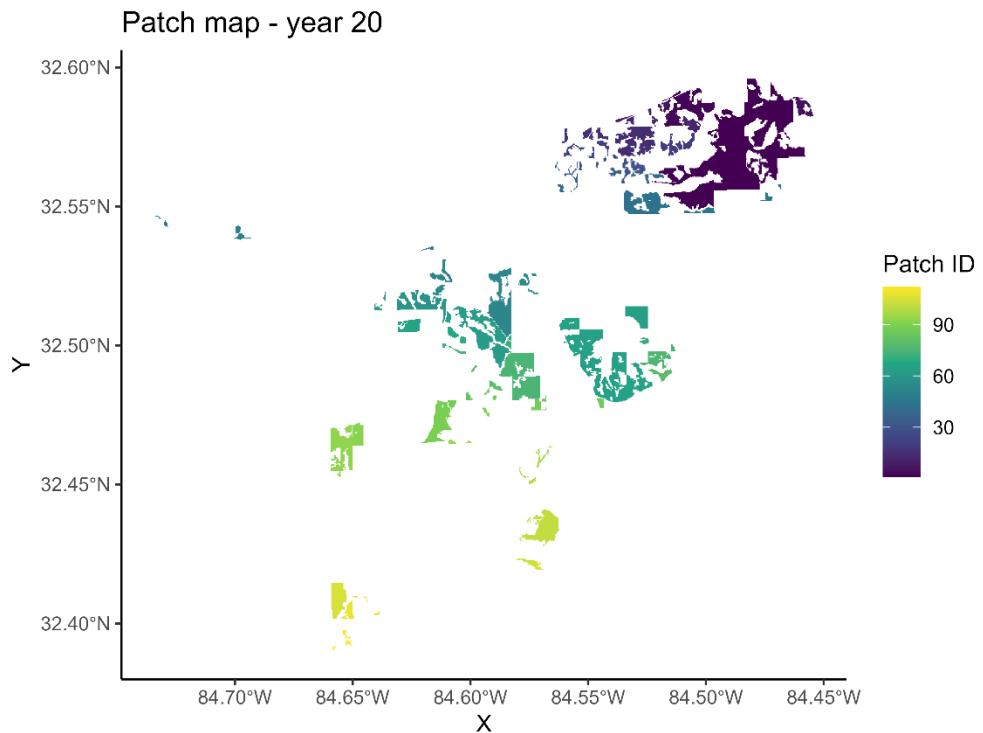


Figure 5. Twentieth year of landscape patches resulting from the Habplan management schedule.

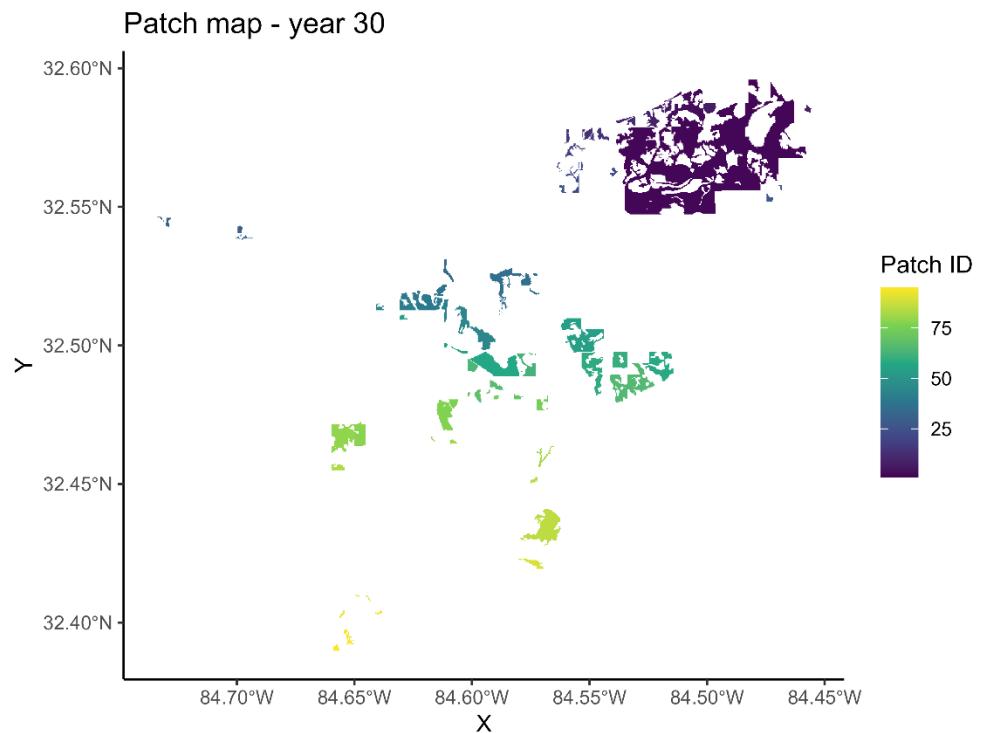


Figure 6. Thirtieth year of landscape patches resulting from the Habplan management schedule.

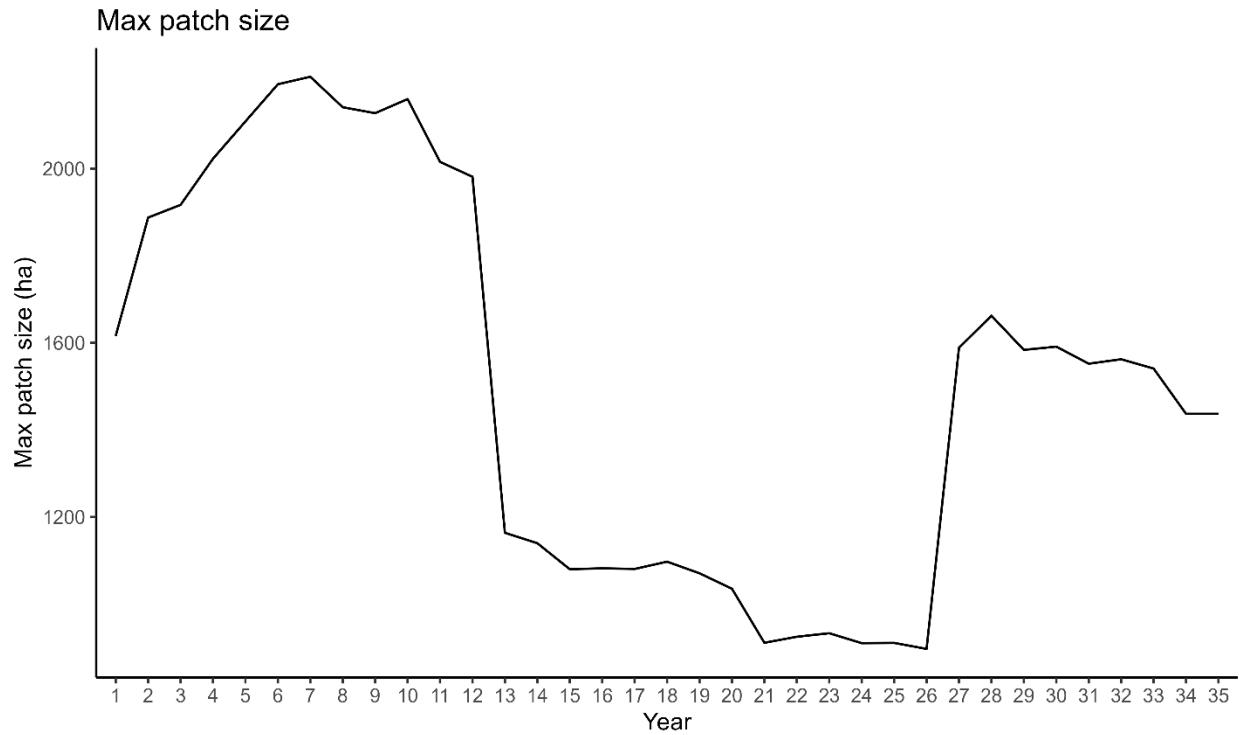


Figure 7. Size of the largest landscape patch across time resulting from the Habplan management schedule.

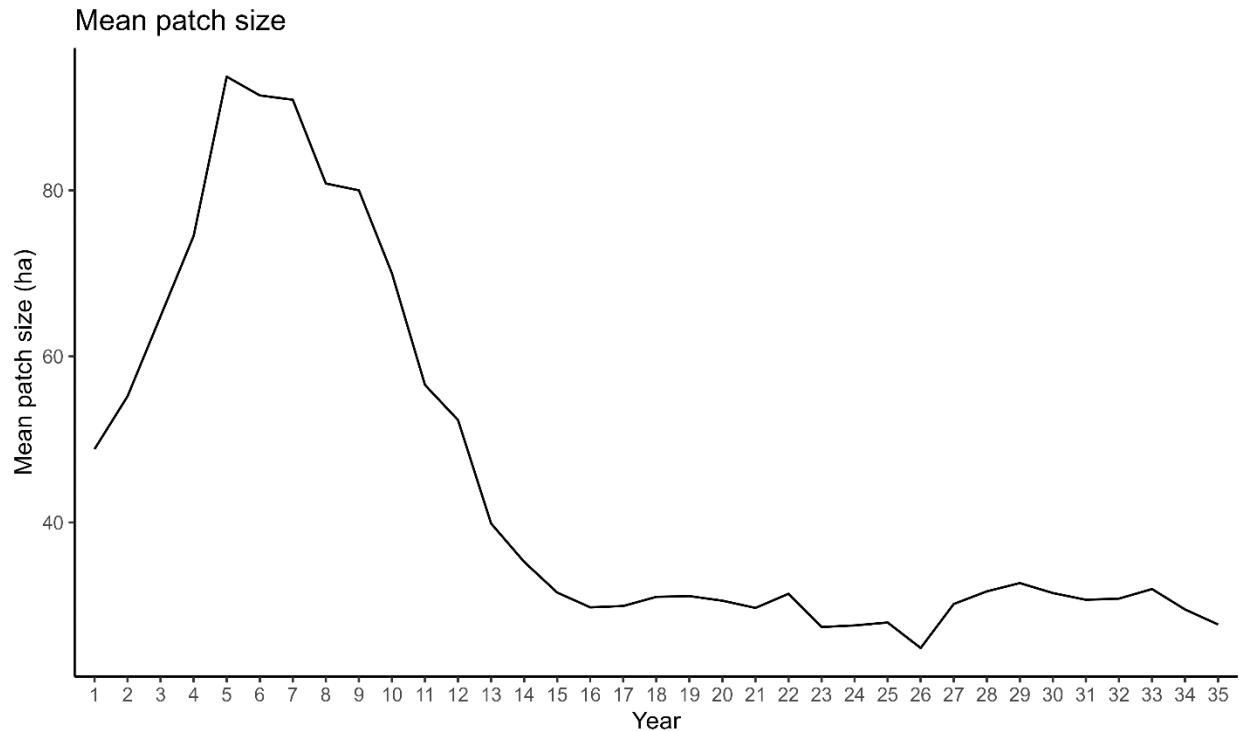


Figure 8. Average size of landscape patches across time resulting from the Habplan management schedule.

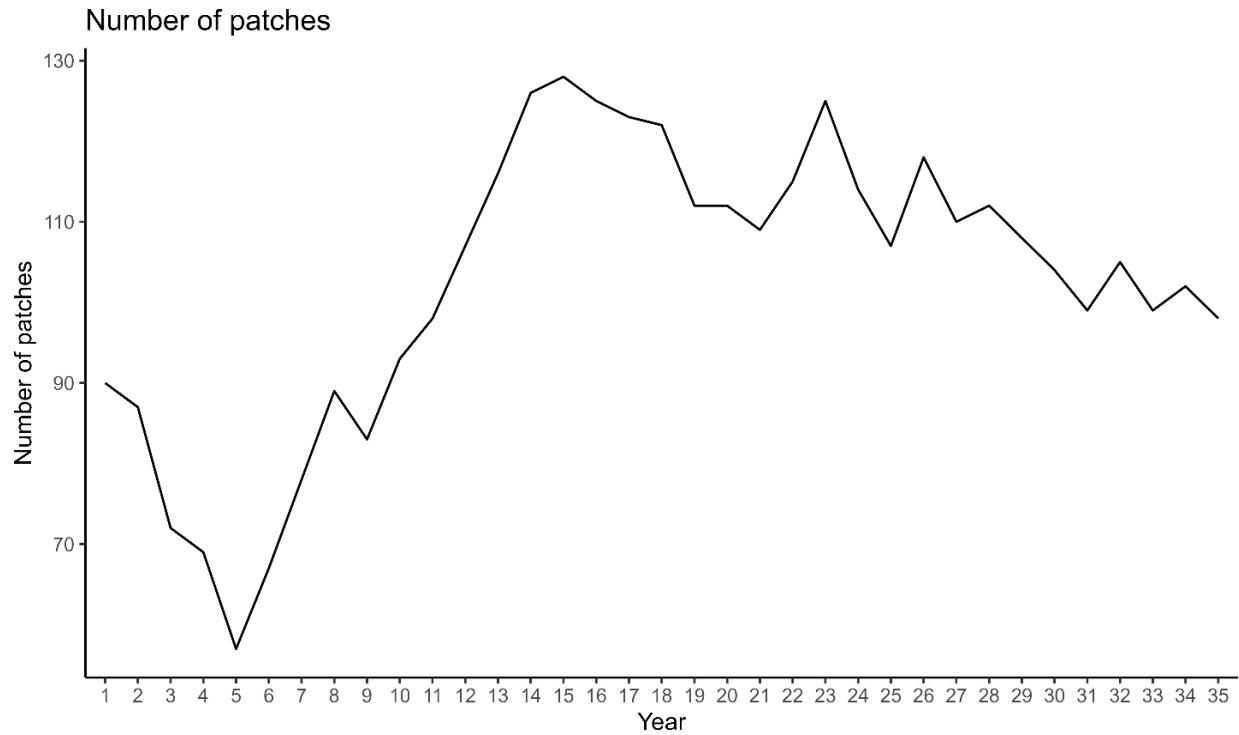


Figure 8. Number of landscape patches across time resulting from the Habplan management schedule.

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.bystone, '" />'),
  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.

IMPORTANT - USER MUST RENAME OR MOVE SAVEFLOW1 AND SAVESCHED FROM WORKING DIRECTORY IF THEY DO NOT WANT THE FILES TO BE DELETED

```

#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)
```

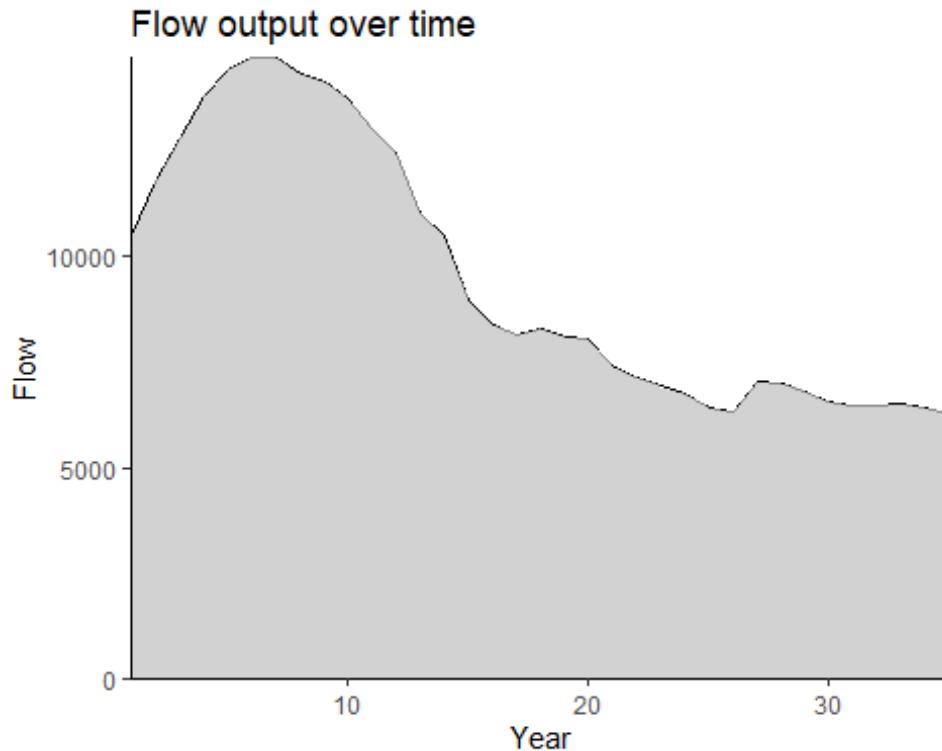


Figure 9. The amount of flow (habitat area) attained over time as a result of the suggested Habplan management schedule.

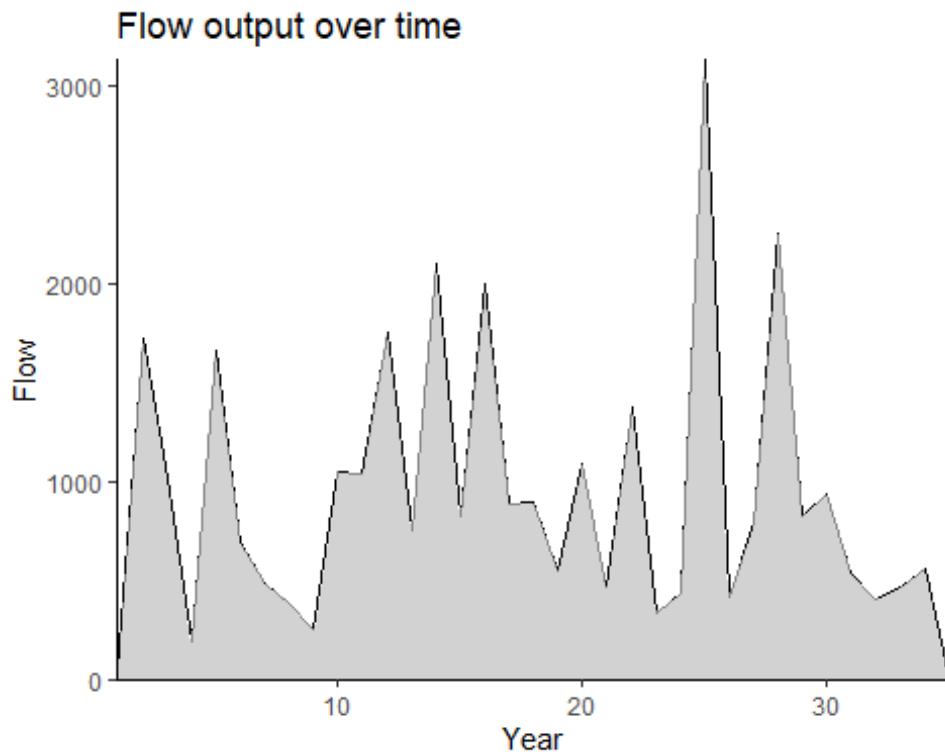


Figure 10. The amount of flow (harvested pine pulpwood) attained over time as a result of the suggested Habplan management schedule.

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 = flow1, nyear = 35,
                           mode = "terrestrial", dist = 500, level = "patch")
```

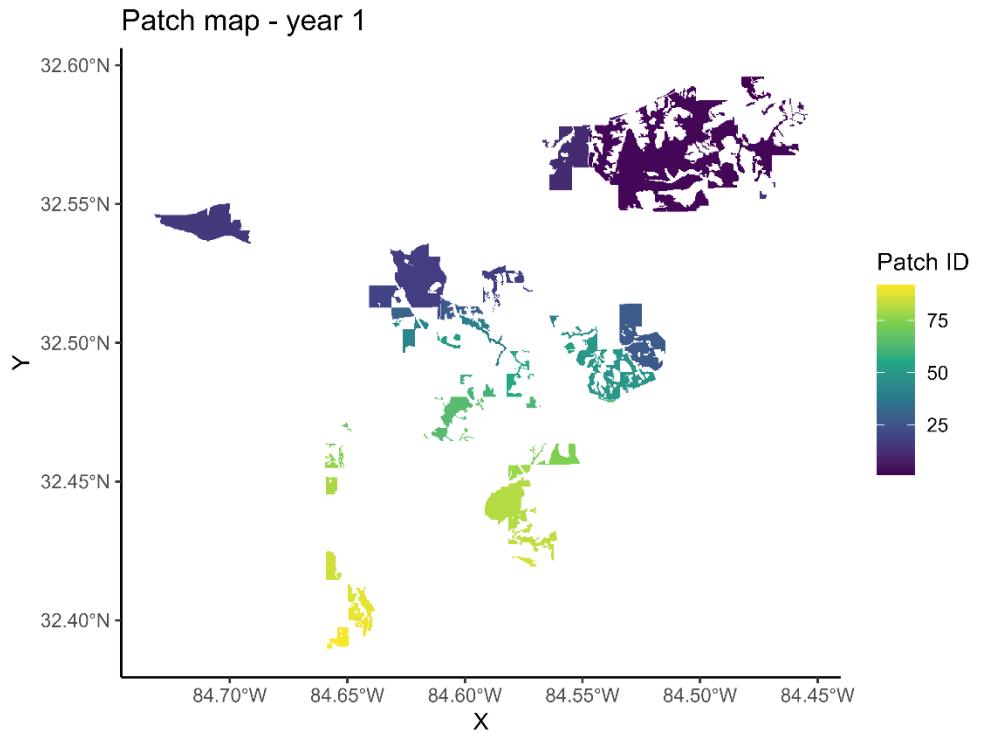


Figure 11. First year of landscape patches resulting from the Habplan management schedule.

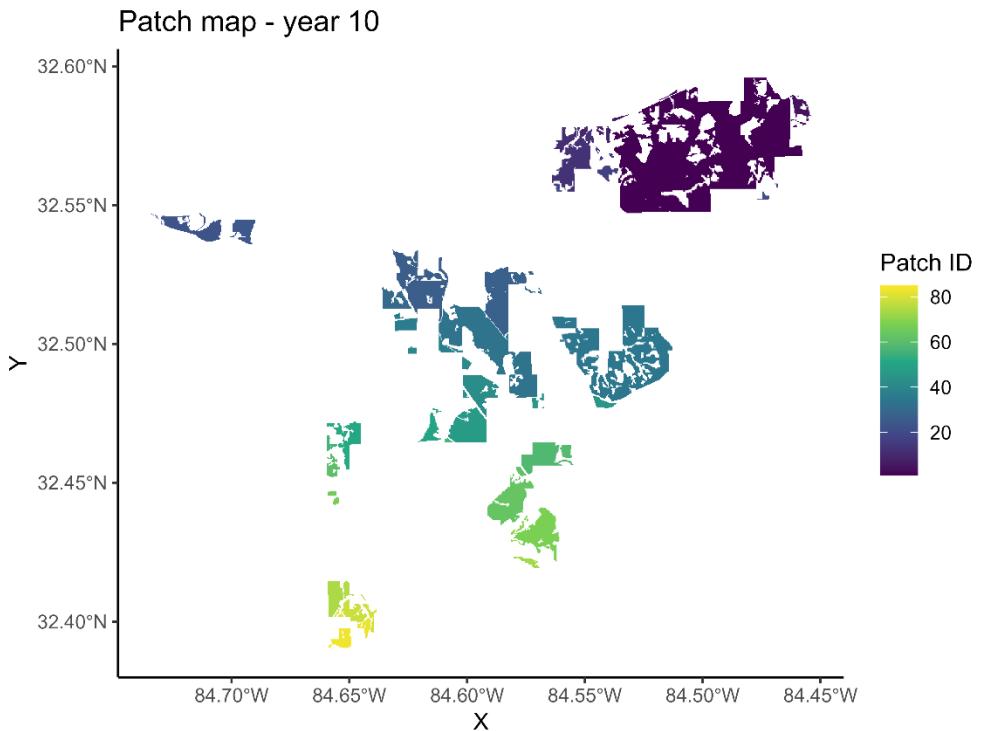


Figure 12. Tenth year of landscape patches resulting from the Habplan management schedule.

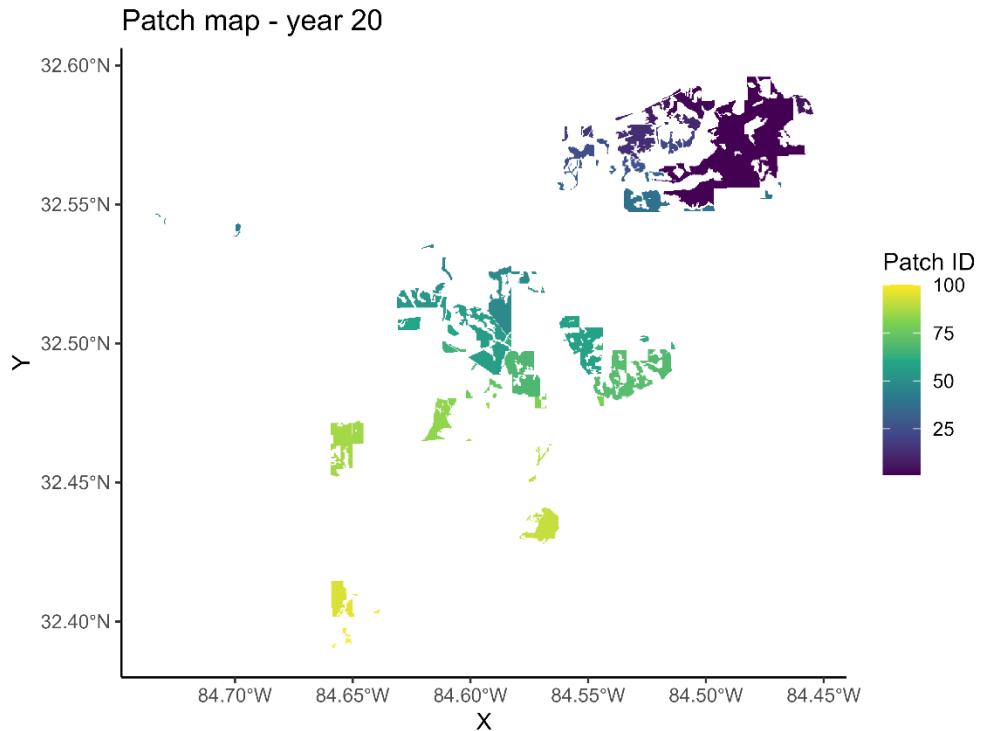


Figure 13. Twentieth year of landscape patches resulting from the Habplan management schedule.

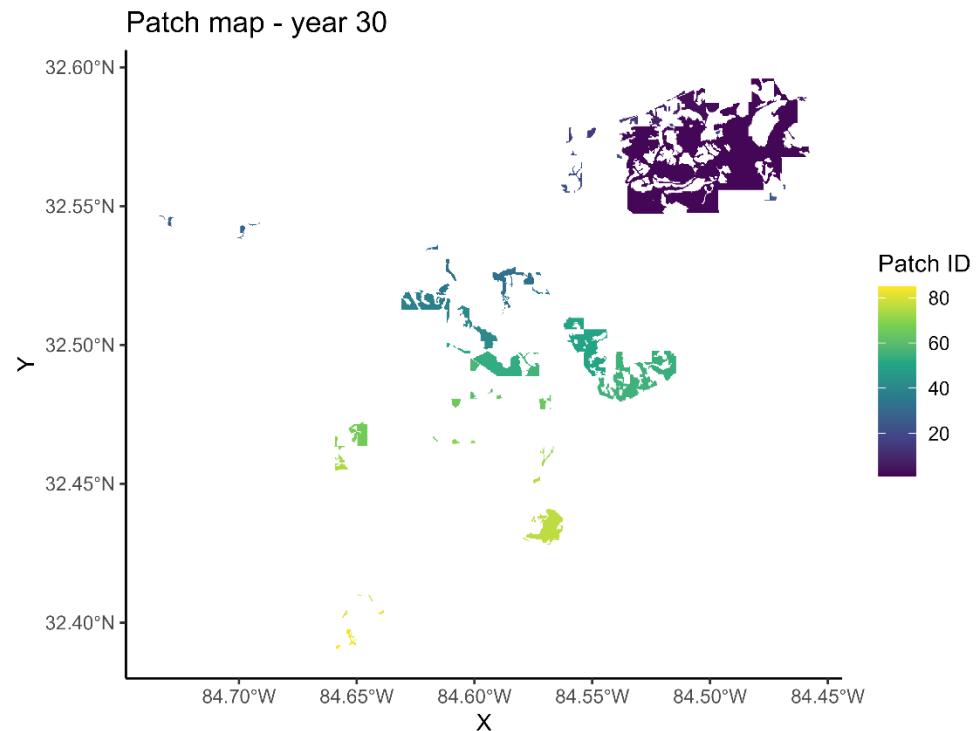


Figure 14. Thirtieth year of landscape patches resulting from the Habplan management schedule.

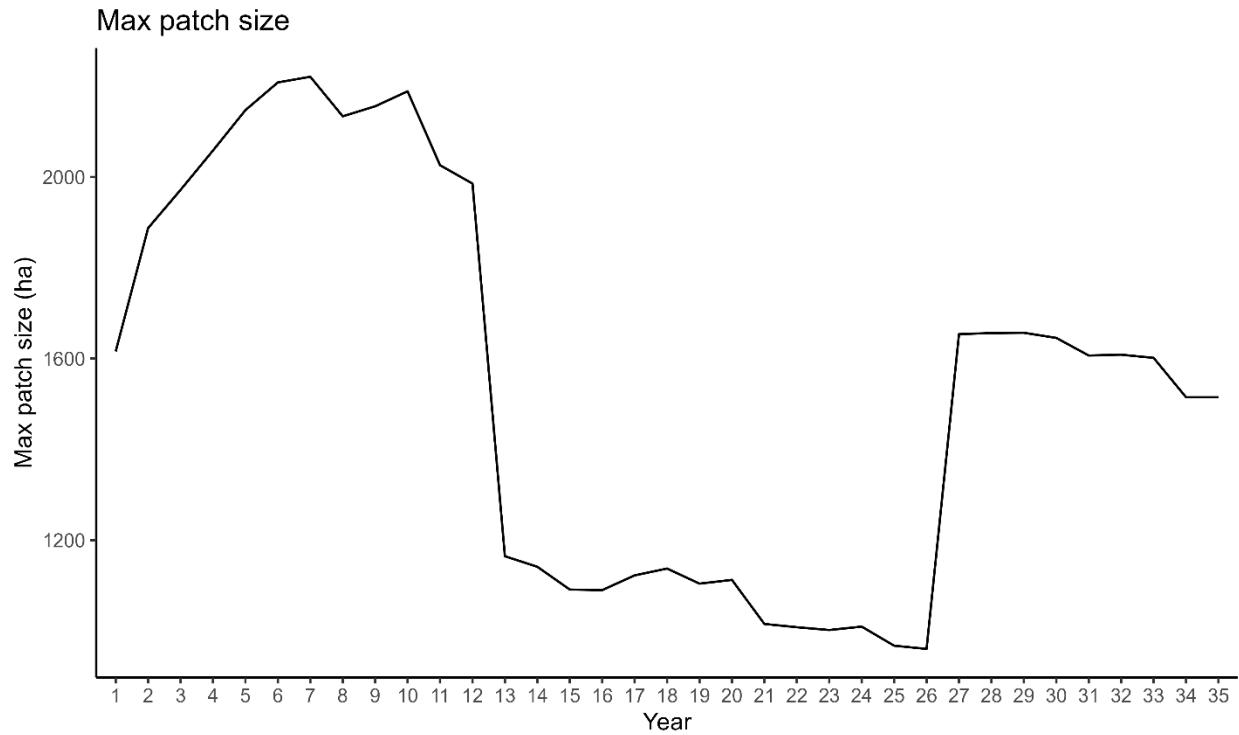


Figure 15. Size of the largest landscape patch across time resulting from the Habplan management schedule.

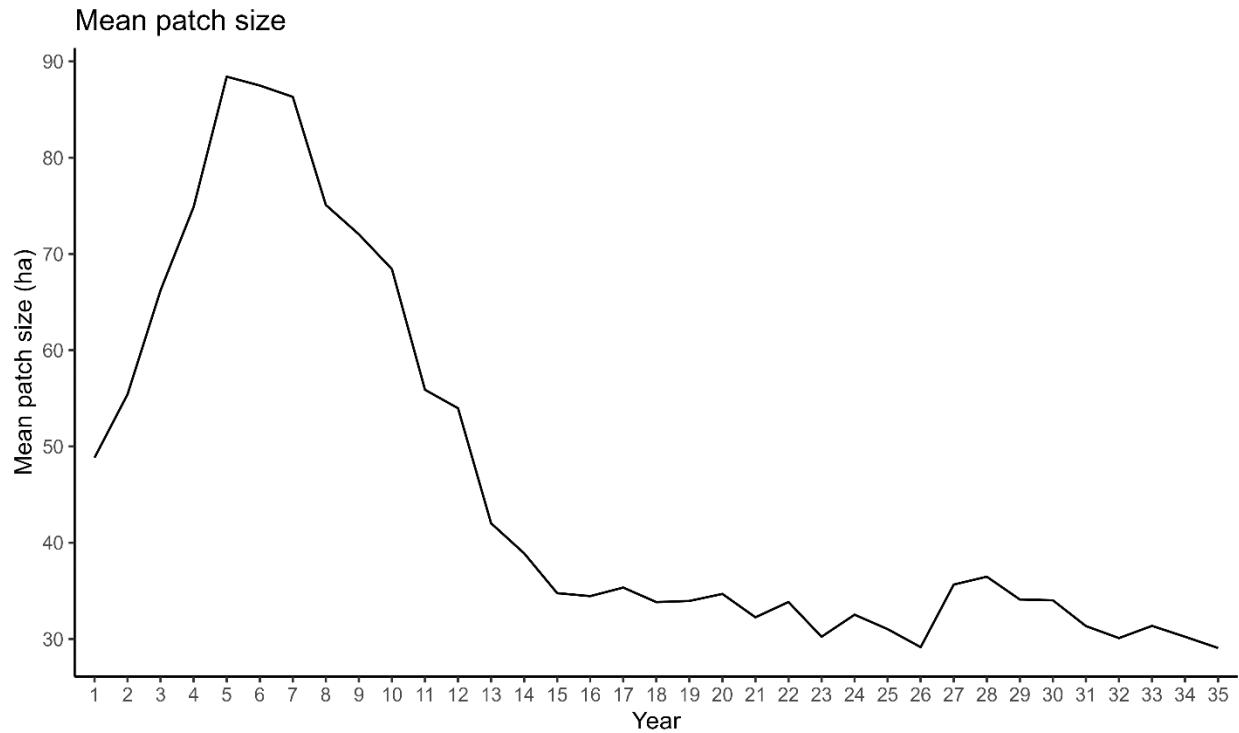


Figure 16. Average size of landscape patches across time resulting from the Habplan management schedule.

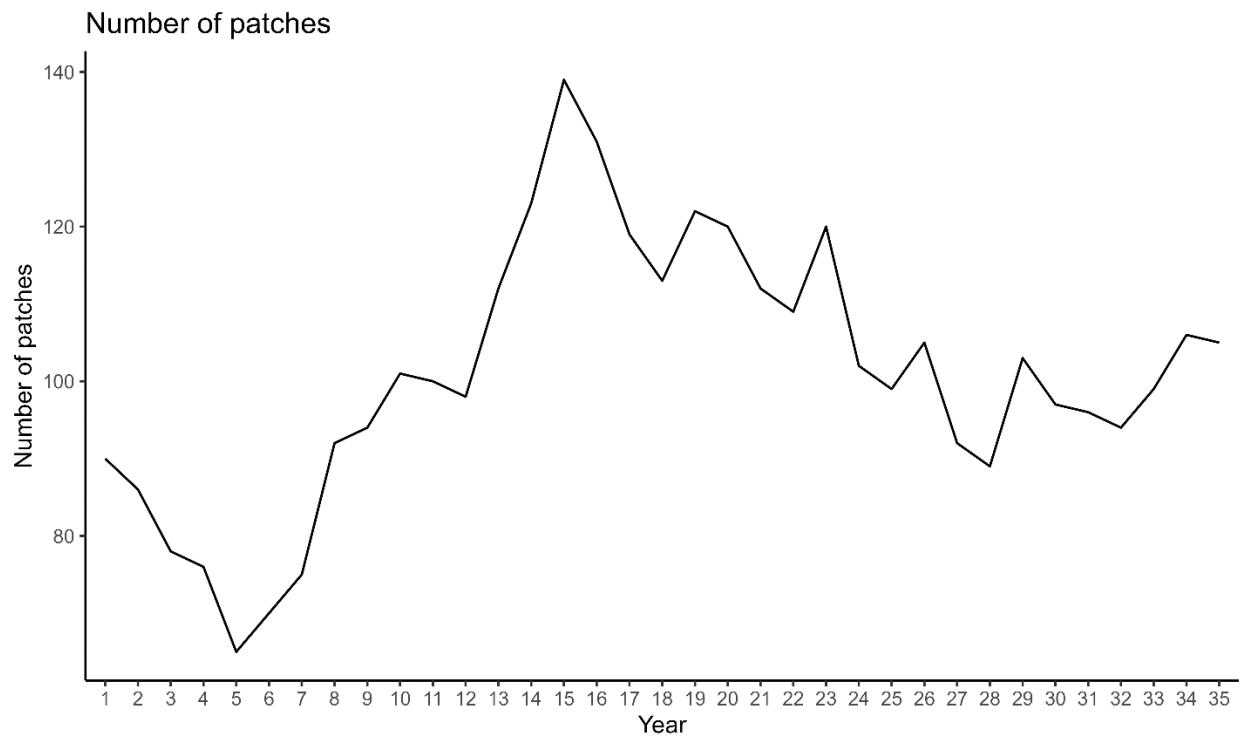


Figure 17. Number of landscape patches across time resulting from the Habplan management schedule.

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 pine pulpwood flow component, we believe we should be able to achieve much higher values. Therefore, we will set the thlo to 2000, but have the thhi be 100000. With such a large upper threshold, 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.bystone <- ""
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('<bystone value=""', f1.bystone, '" />'),
  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.bystander <- ""
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('<bystander value=""', f2.bystander, '" />'),
  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.

IMPORTANT - USER MUST RENAME OR MOVE SAVEFLOW1 AND SAVESCHED FROM WORKING DIRECTORY IF THEY DO NOT WANT THE FILES TO BE DELETED

```

#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)
```

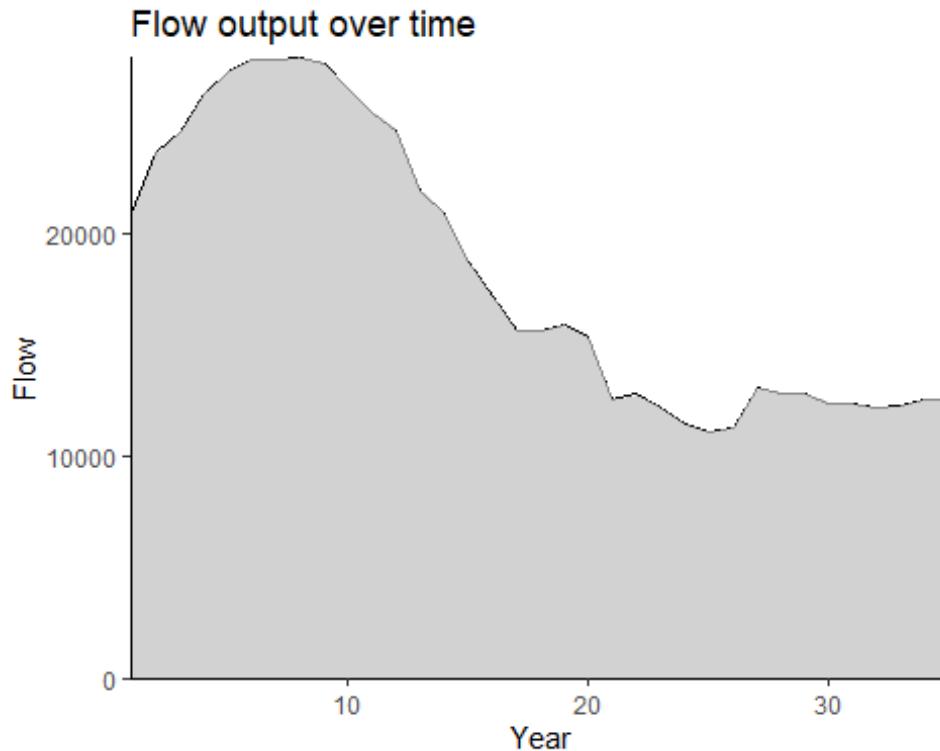


Figure 18. The amount of flow (habitat area) attained over time as a result of the suggested Habplan management schedule.

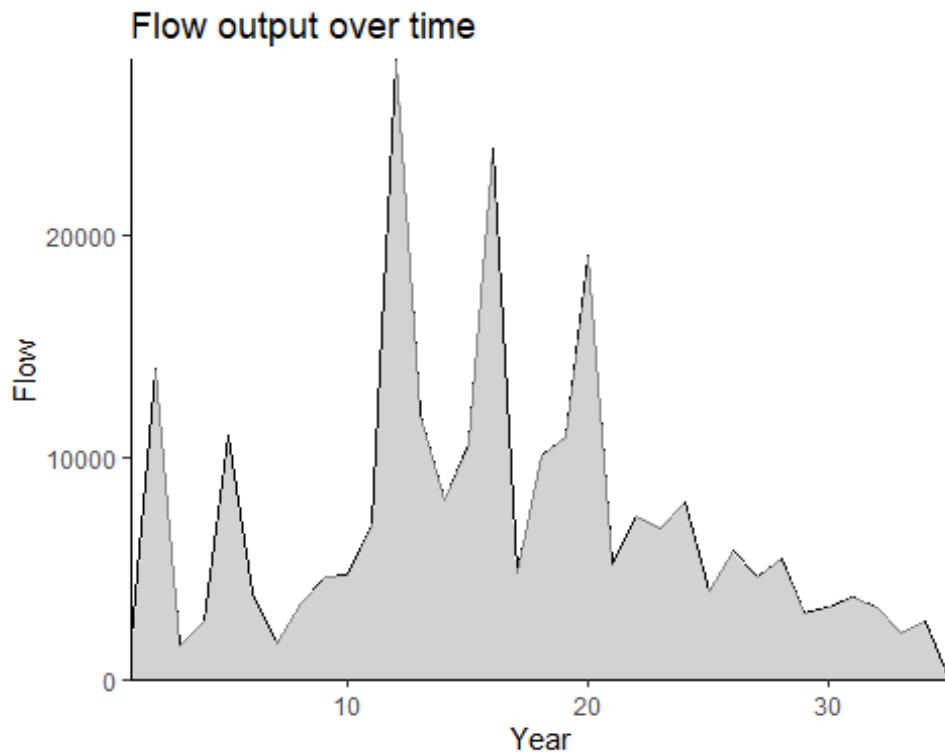


Figure 19. The amount of flow (harvested pine pulpwood) attained over time as a result of the suggested Habplan management schedule.

Again, the first figure above shows the output flow from our HSI component throughout our study period, and the second shows the amount of harvested pine pulpwood. 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 species of interest.

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 = flow1, nyear = 35,
mode = "terrestrial", dist = 500, level = "patch")
```

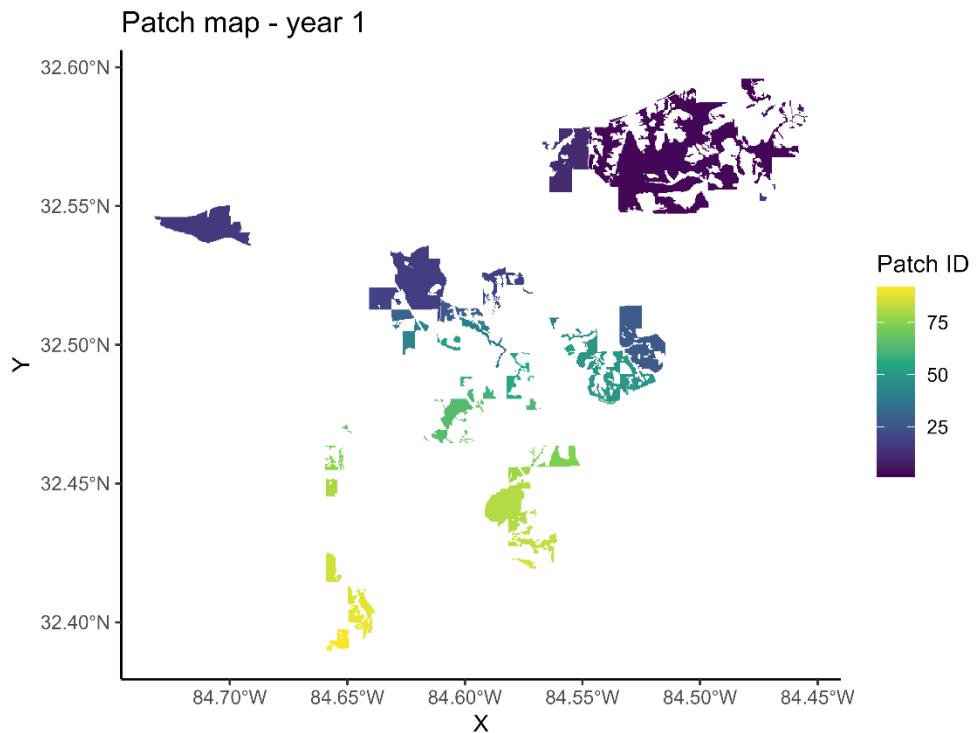


Figure 19. First year of landscape patches resulting from the Habplan management schedule.

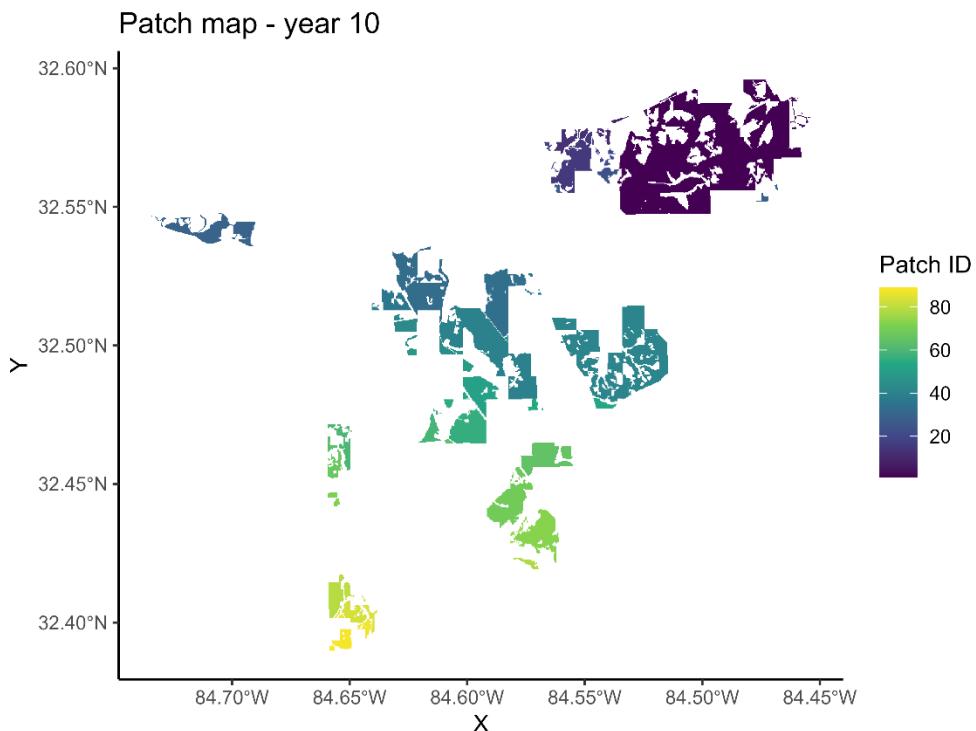


Figure 20. Tenth year of landscape patches resulting from the Habplan management schedule.

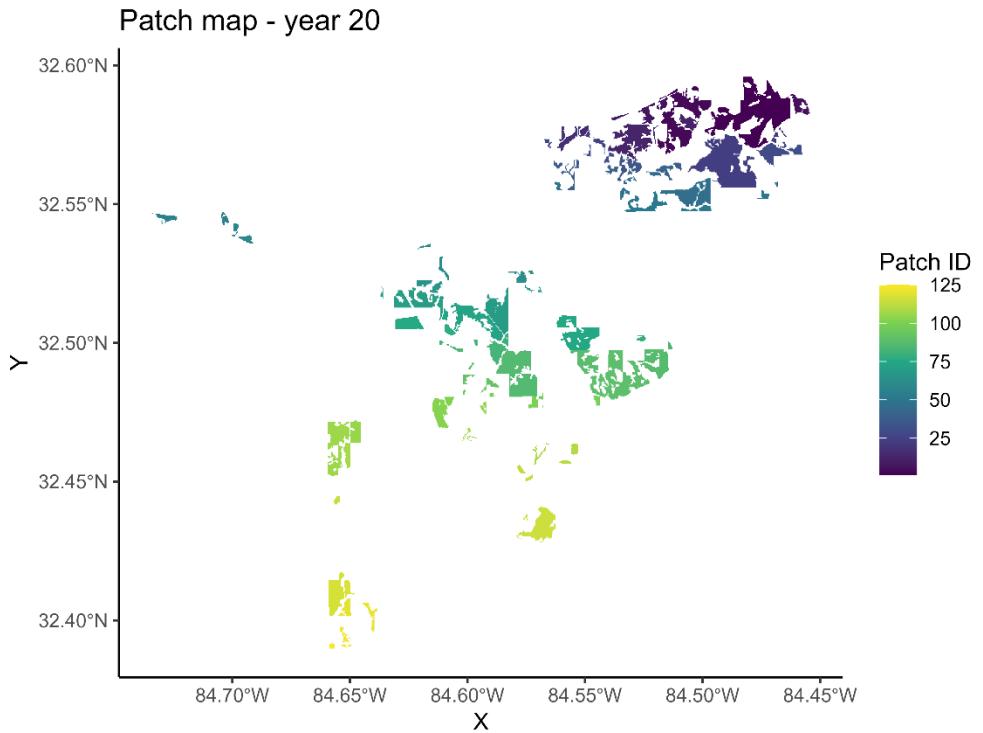


Figure 21. Twentieth year of landscape patches resulting from the Habplan management schedule.

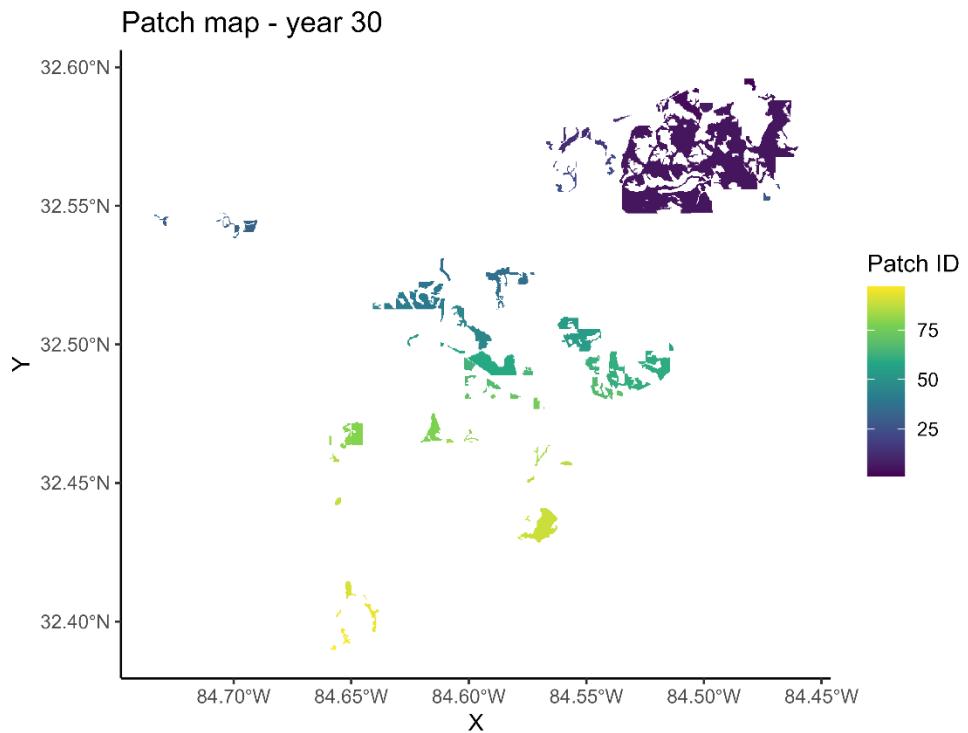


Figure 22. Thirtieth year of landscape patches resulting from the Habplan management schedule.

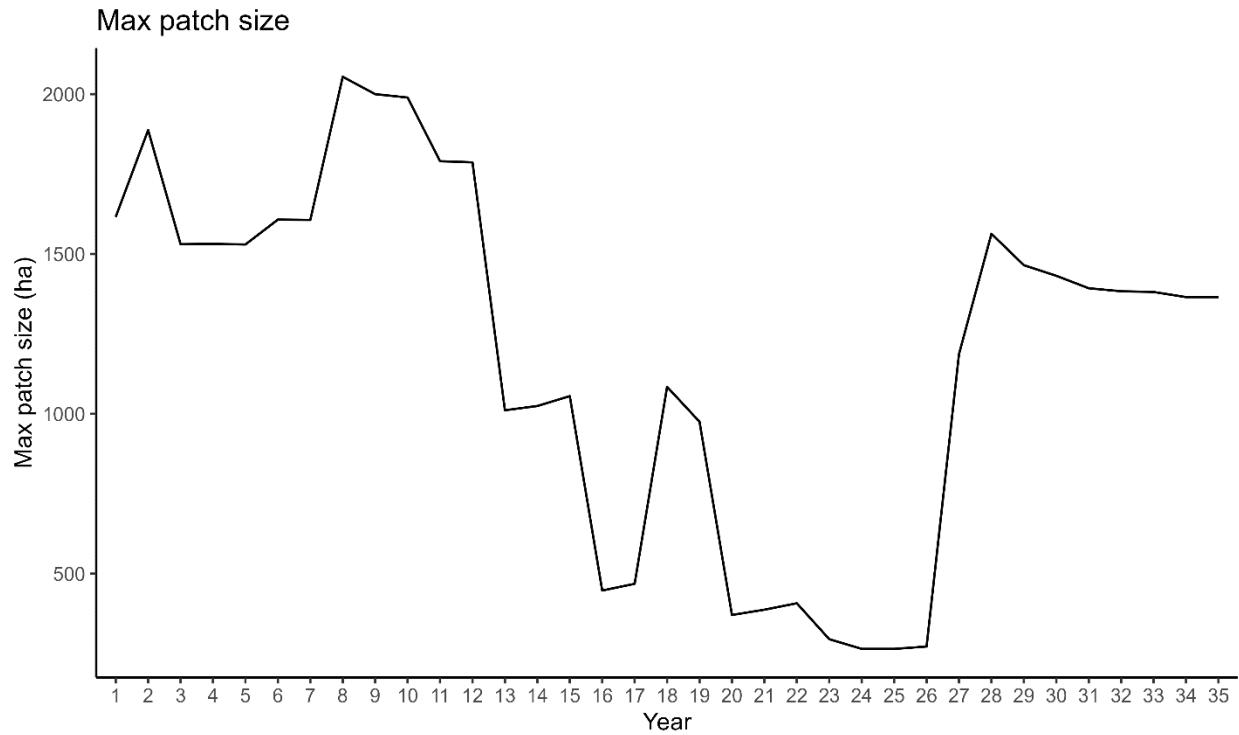


Figure 23. Size of the largest landscape patch across time resulting from the Habplan management schedule.

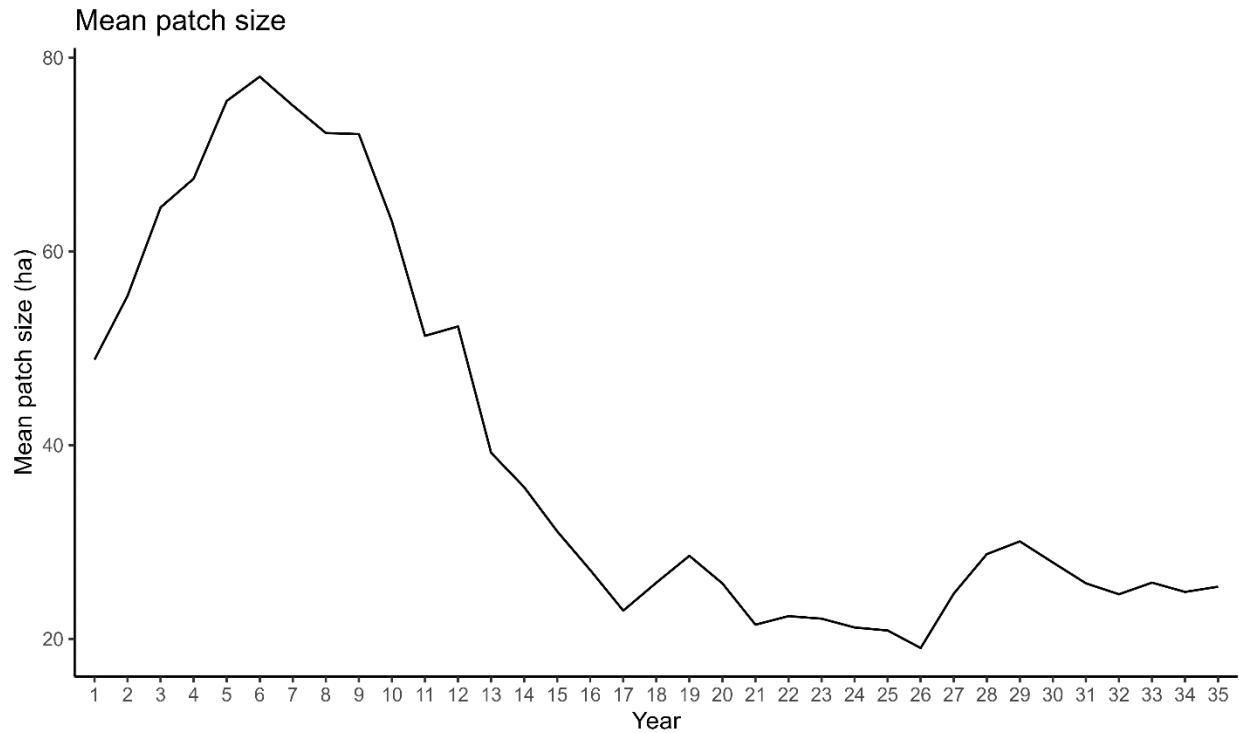


Figure 24. Average size of landscape patches across time resulting from the Habplan management schedule.

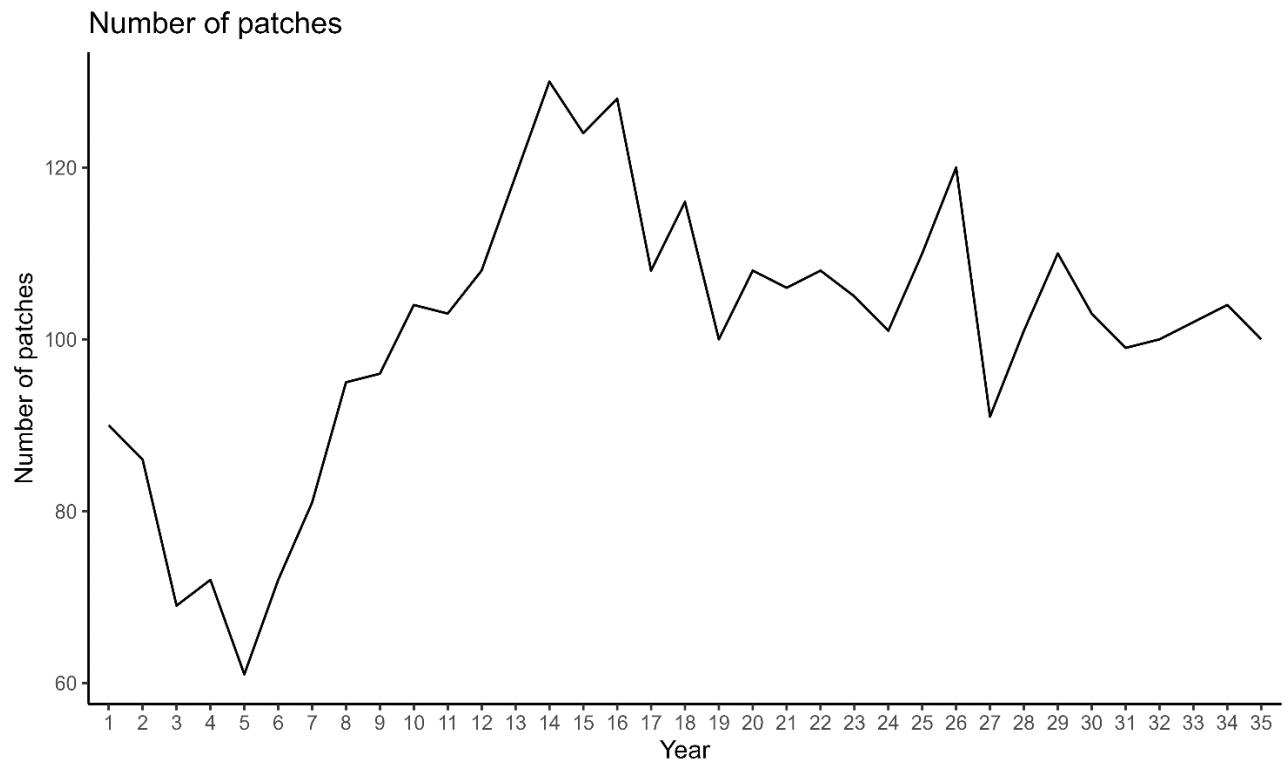


Figure 25. Number of landscape patches across time resulting from the Habplan management schedule.

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 flow outputs, which should have been saved into separate folders as described earlier. 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)
```

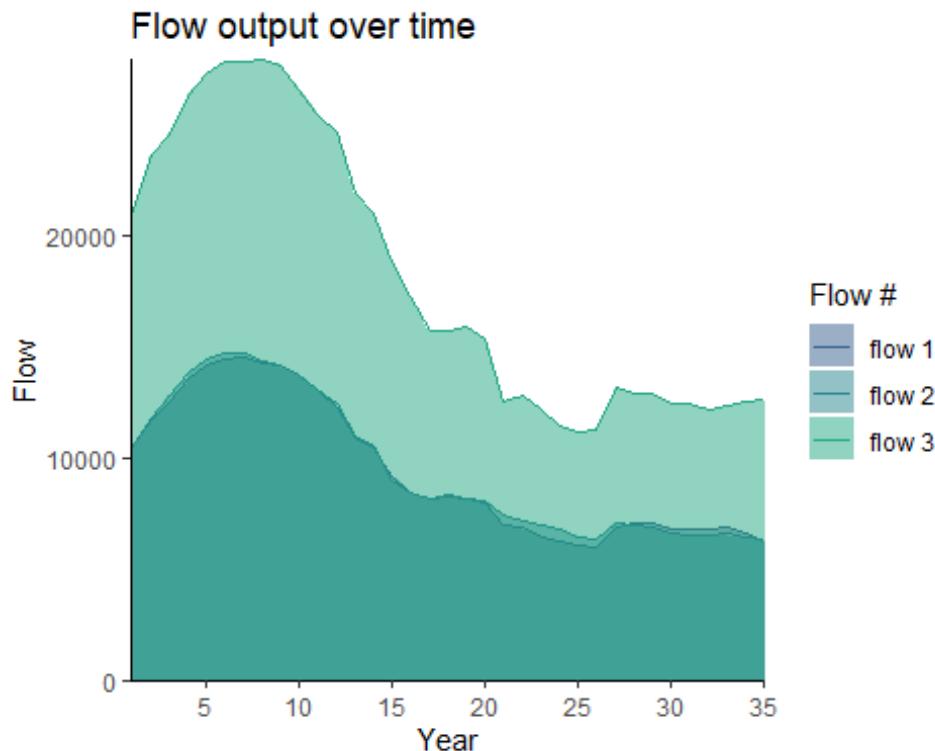


Figure 26. The amount of flow (habitat area) attained over time as a result of the three separate Habplan management schedule (flow1, flow2, and flow3). Each flow is represented by a different shade of blue.

```
#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)
```

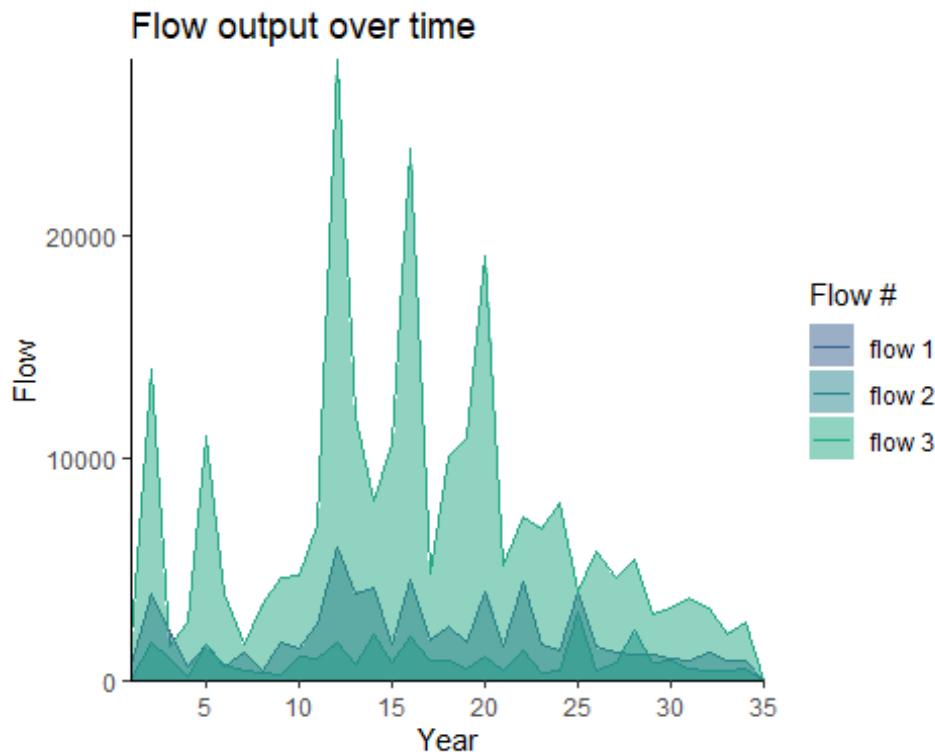


Figure 27. The amount of flow (harvested pine pulpwood) attained over time as a result of the three separate Habplan management schedule (flow1, flow2, and flow3). Each flow is represented by a different shade of blue.

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 pine 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)
```

If an error message comes up that states the following:

Error: unable to find an inherited method for function ‘writeVector’ for signature ‘x = “data.frame”, filename = “character”’

then run the next section in R to manually save the top schedule as a shapefile.

```
#Read in saved schedule from habplan run
sched <- read.csv("./saveSched")
#Change column headings so that it's easier to work with
colnames(sched) <- c("id", "StdID", "sched")
#Remove any blank spaces that may have been brought in from the import
sched$StdID <- gsub(" ", "", sched$StdID)
#Add the new column
new.shp <- merge(site.shp, sched, by = "StdID")
#Save to the working directory
writeVector(new.shp, "./Site_with_schedule.shp", filetype="ESRI Shapefile",
            overwrite=TRUE)
```

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 blocksize flow subcomponent to the Habplan run.

Function: HSI calculation - *HSIcalc*

We are going to work through two examples of using 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 a function of multiple independent variables can also 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 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()
```

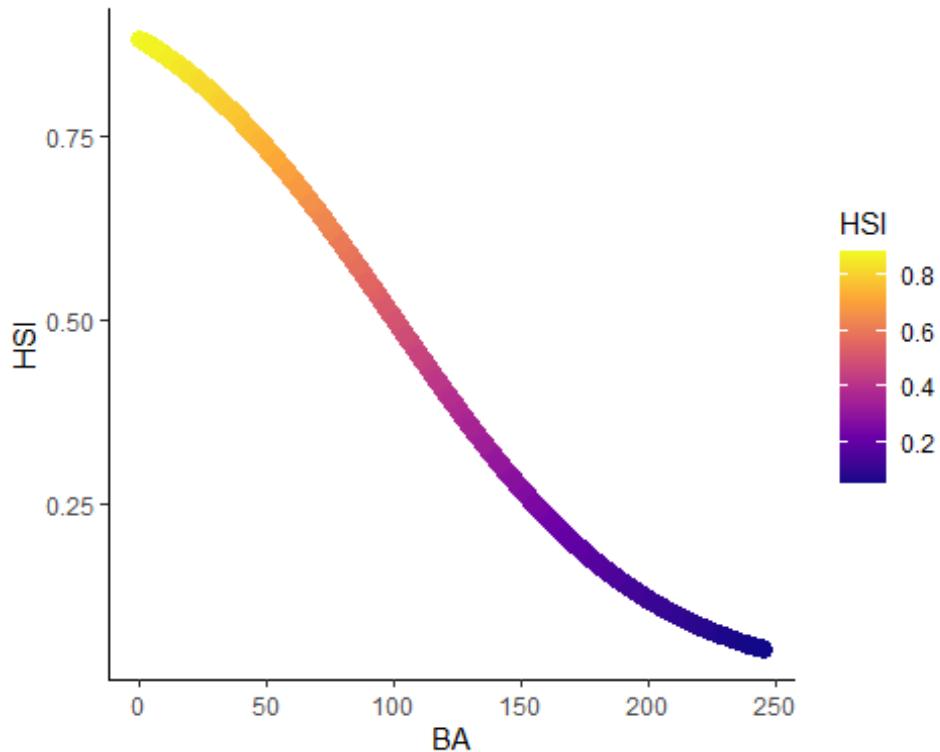


Figure 28. A negative linear effect of BA on HSI. Color represents change in HSI values.

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()
```

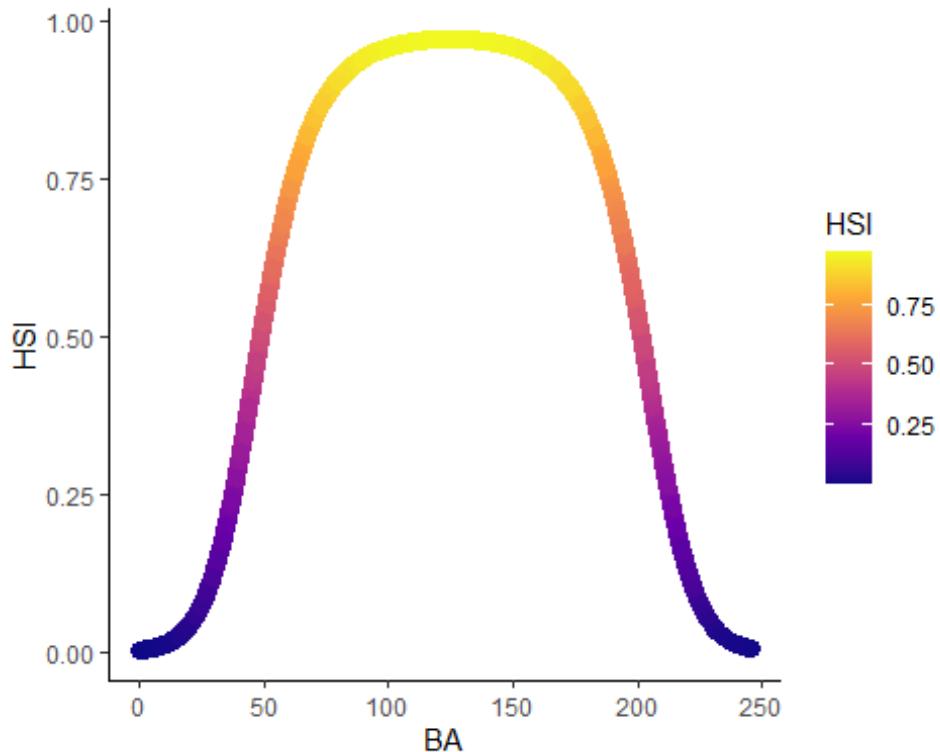


Figure 29. A quadratic effect of BA on HSI. Color represents change in HSI values.

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)
```

Member-only version

Using the linear programming component of Habplan

We will now use the parameters from our third Habplan run, and use the linear programming component of Habplan to compare management solutions.

Function: creating biological type II data - *HabBio2*

To move forward with using the linear programming model of Habplan, we first need biological type II data. For more information, see section 11 (page 36) of the Habplan manual. We have developed a function embedded within *HabplanR* to create one of these files.

The biological type II data works by assigning weights to each combination of stand ID and regime. A higher weighting on a regime for a specific stand will prioritize that regime for

that stand. The below function assigns an equal weight to each regime. For the function to run, we need to provide the std.data, and std.info file we have used previously.

```
#Run function to create Bio2 file
HabBio2(std.data = std.data, std.info = std.info)
```

We now have a new .dat file saved in the working directory called Biol2_data. If any regimes need to be weighted greater than others for specific stands, then the Biol2_data file should be opened with a note application, and the corresponding number 1 (right hand column of data file), should be replaced with a number 2.

This file can now be treated as an additional flow component for the Habplan run; however, the parameters to set in the project file are different than other flow components. We will go through a new run incorporating the biological type II data below. We will use the same parameters as the third run exampled above.

```
#Info for f1 component ----
f1.file <- paste0(wd,"HSI.dat")
f1.bystone <- ""
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('<bystone value=""', f1.bystone, '" />'),
             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.bystander <- ""
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('<bystander value=""', f2.bystander, '" />'),
  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>")

#Info for bio2 component ----
bio2.1.file <- "Flows/Biol2_test.dat"
goal.val <- "0"
weight <- "1"
sum.val <- "1"
max.val <- "1"
bio2.title <- "Biol2_test.dat"
#Combine bio2 components for writing
bio2.1 <- c('<biol2 title="Bio2-1 Component">',
  paste0('<file value=""', bio2.1.file, '" />'),
  paste0('<goalKind value="max" />'),
  paste0('<goal value=""', goal.val, '" />'),
  paste0('<weight value=""', weight, '" />'),
  paste0('<sum value=""', sum.val, '" />'),
  paste0('<max value=""', max.val, '" />'),

```

```
paste0('<title value=""', bio2.title, '" />'),  
"</biol2>")
```

The biological 2 component will be incorporated into a new project file for Habplan to read. To do this, we need to assign the component as a new argument in the *writeProj* function. Additionally, we need to set a new configuration. The new configuration now includes a 1 in the corresponding biological 2 component position.

```
#Need a new configuration to include bio2 component  
config <- "2,0,0,0,0,0,1,0" #now includes an additional 1 in second to last  
position  
  
#Provide each of these flow component objects to the function and run  
writeProj(f1.comp = f1.comp, f2.comp= f2.comp, bio2.1 = bio2.1)
```

We now have the configuration and project parameters ready for our linear programming run. However, we need an additional file for the linear programming solver.

Function: creating an MPS file for lp_solve - *lpMPS*

Habplan uses an additional free software for running the linear programming component, *lp_solve*, which works by reading MPS files. These files are difficult to interpret, but we provide a function below to create one of these files in preparation for the Habplan run.

For the function to work, we need to provide our std.data as many of the functions before, and the nyear (35). We have also provided the option to change the filename of the output MPS file via the filename argument. The two final arguments are th.hi (upper threshold), and th.lo (lower threshold). Both of these arguments are bounded between 0-100, and now represent a percentage of positive or negative deviation, respectively. In our example below, we are allowing a positive deviation of 50% for our model targets, and a negative deviation of only 10%.

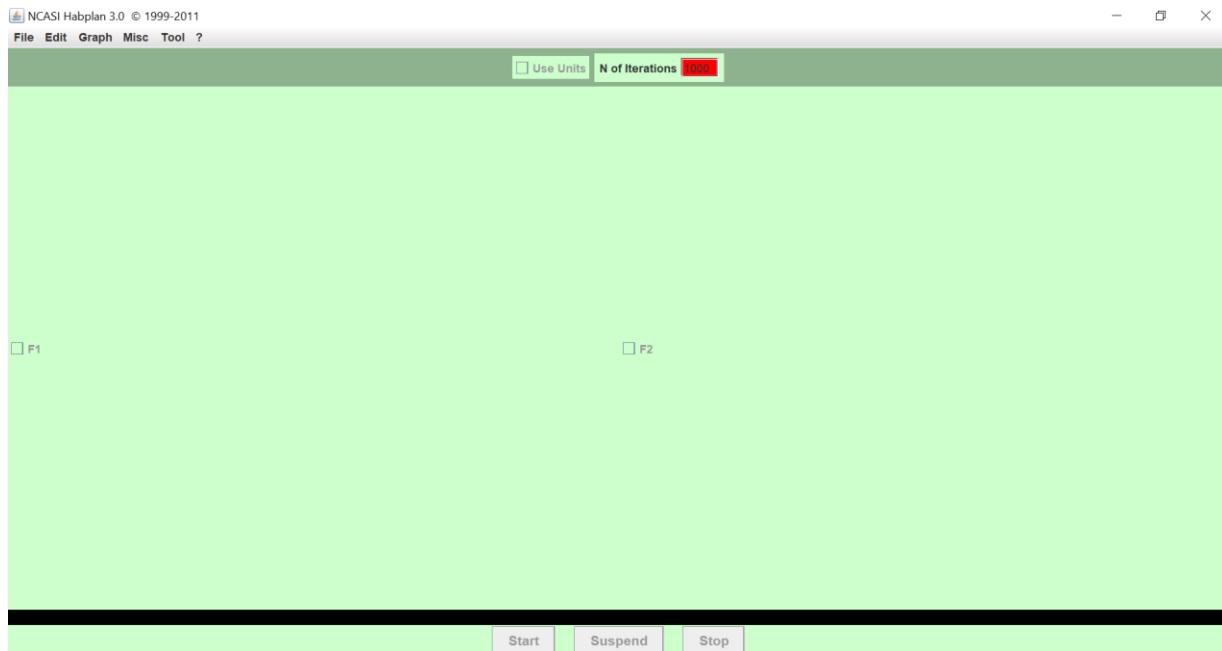
```
#Create an MPS file for Linear programming  
lpMPS(std.data = std.data, nyear = 35, filename = "lpMPS",  
       th.hi = 50, th.lo = 10)
```

Let's open habplan and run through the linear programming example.

IMPORTANT - MUST RENAME OR MOVE SAVEFLOW1 AND SAVESCHED FROM WORKING DIRECTORY IF YOU DO NOT WANT THE FILES TO BE DELETED

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

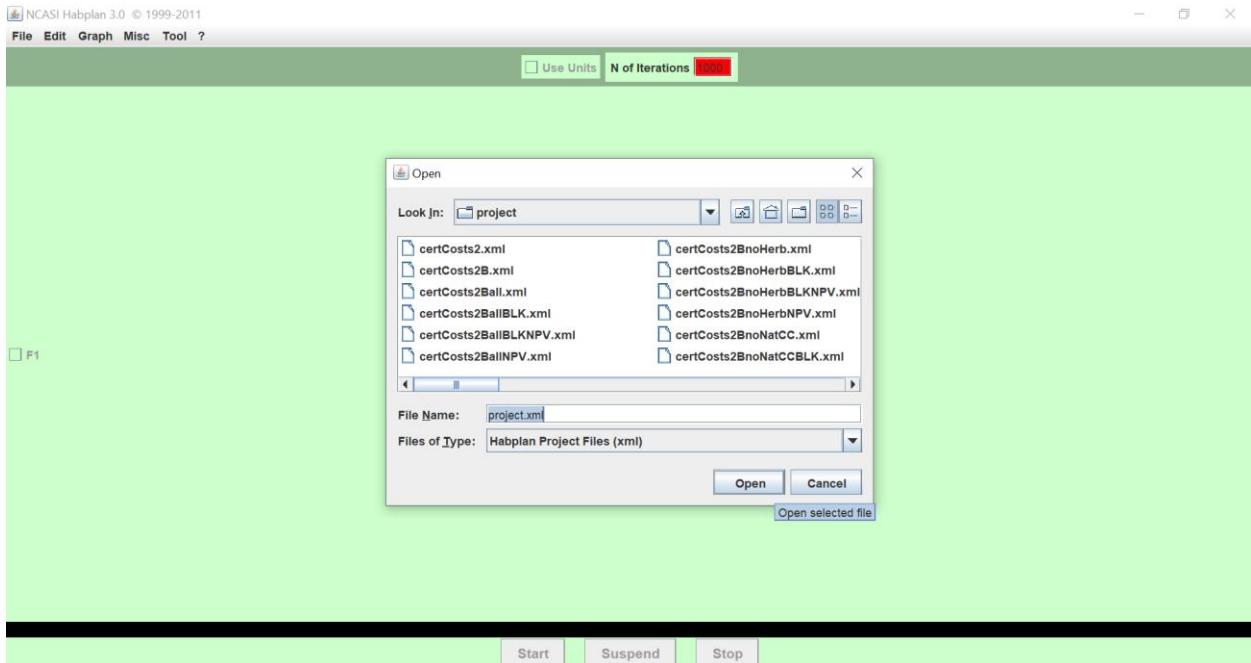
When you first open Habplan from the R script, the following window will open. Note that you will be unable to run anything in your R session when Habplan has been opened via R. Additionally, your start-up screen may look slightly different – this is ok!



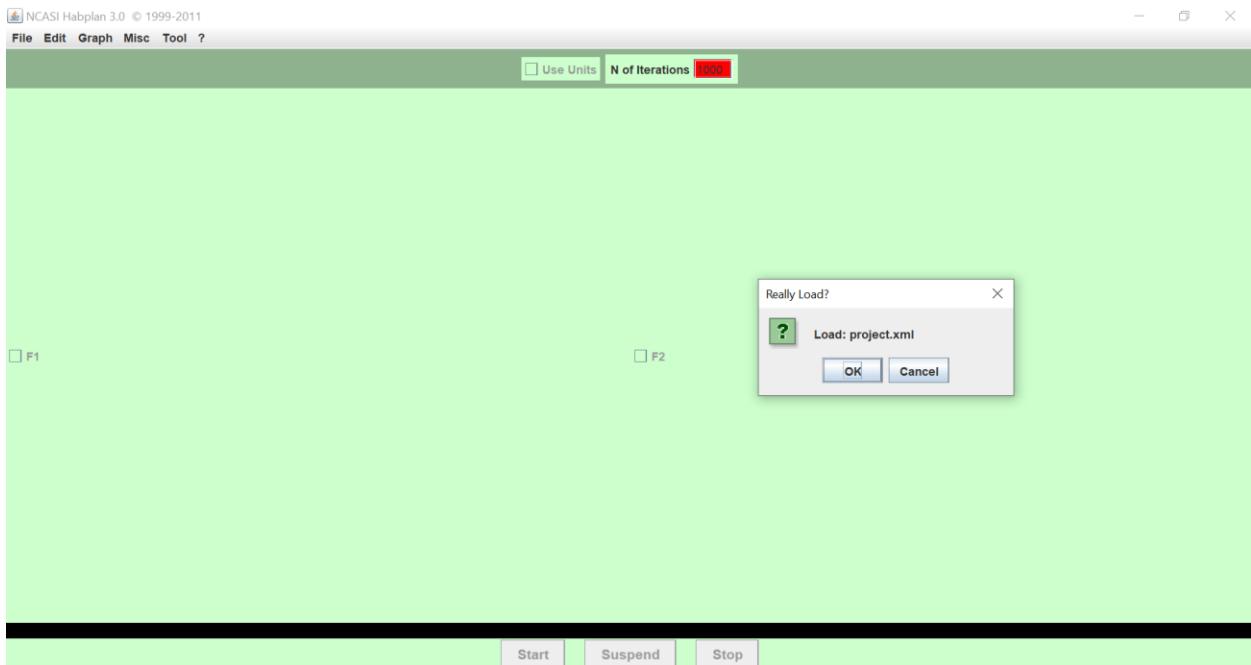
To open the project file we have just created, we can navigate to File > Open... Make sure to navigate to the correct project file (the one created via the R script) if there are multiple saved on your computer.



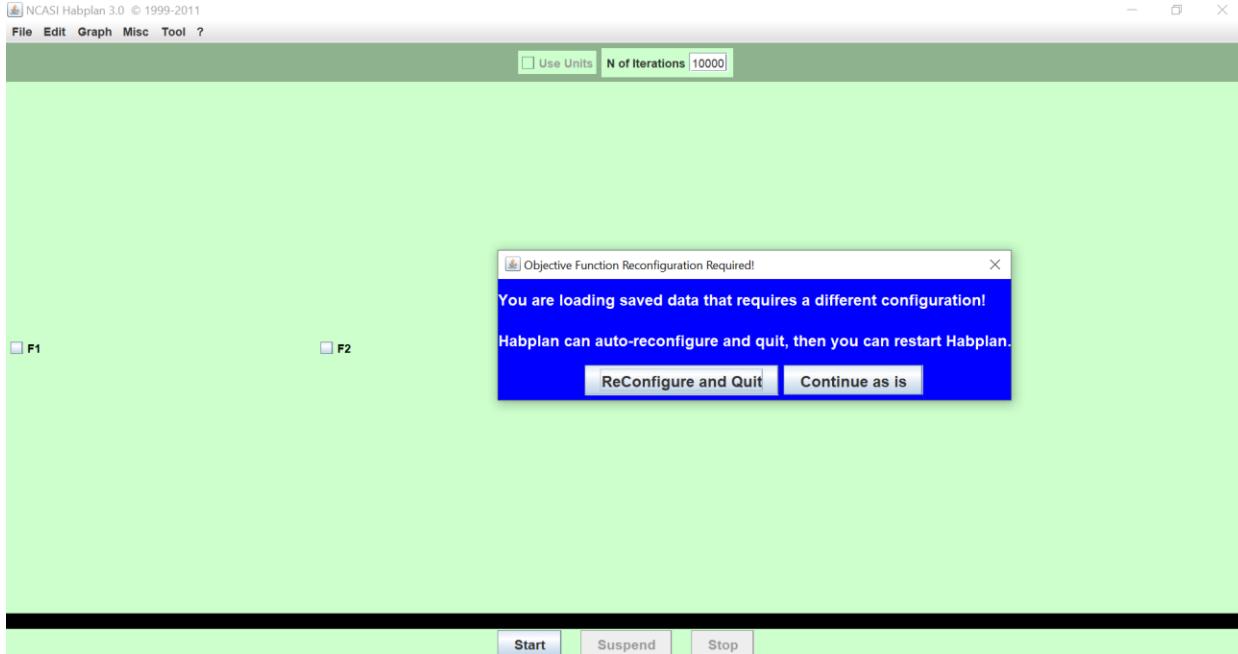
A new window will open to select the appropriate file, which will have saved in the set working directory as project.xml. Navigate to the project.xml file that was just created in R, select that file and click Open.



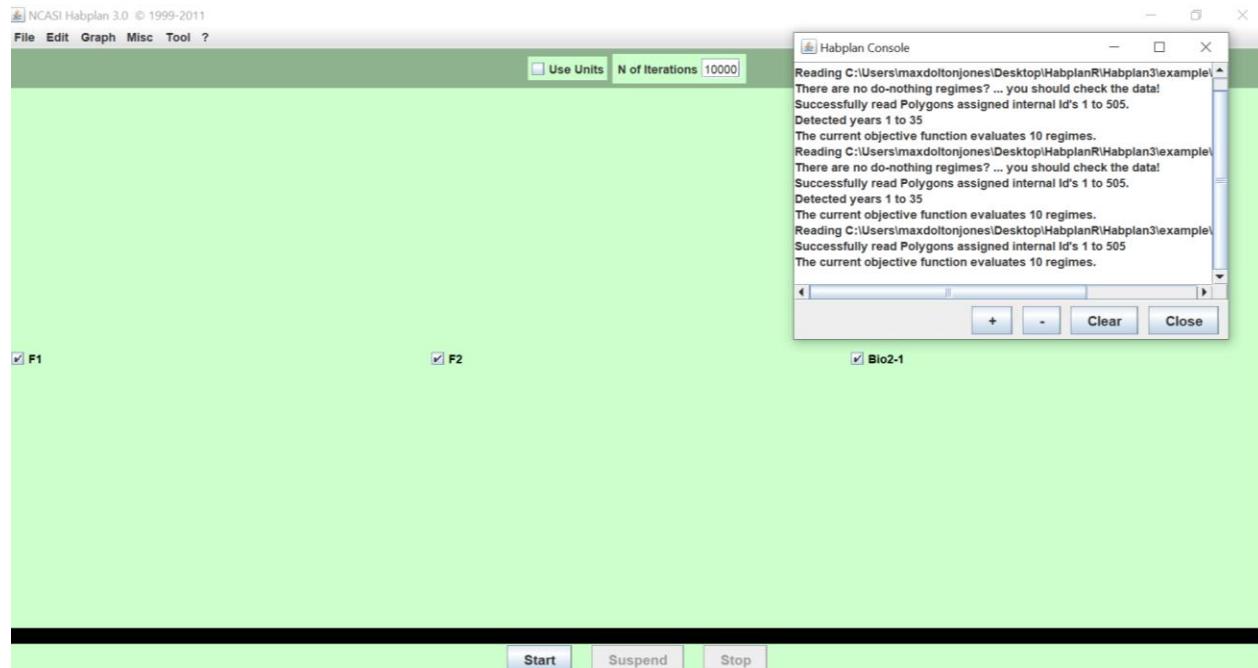
A new window will then open. Click OK to load the project file.



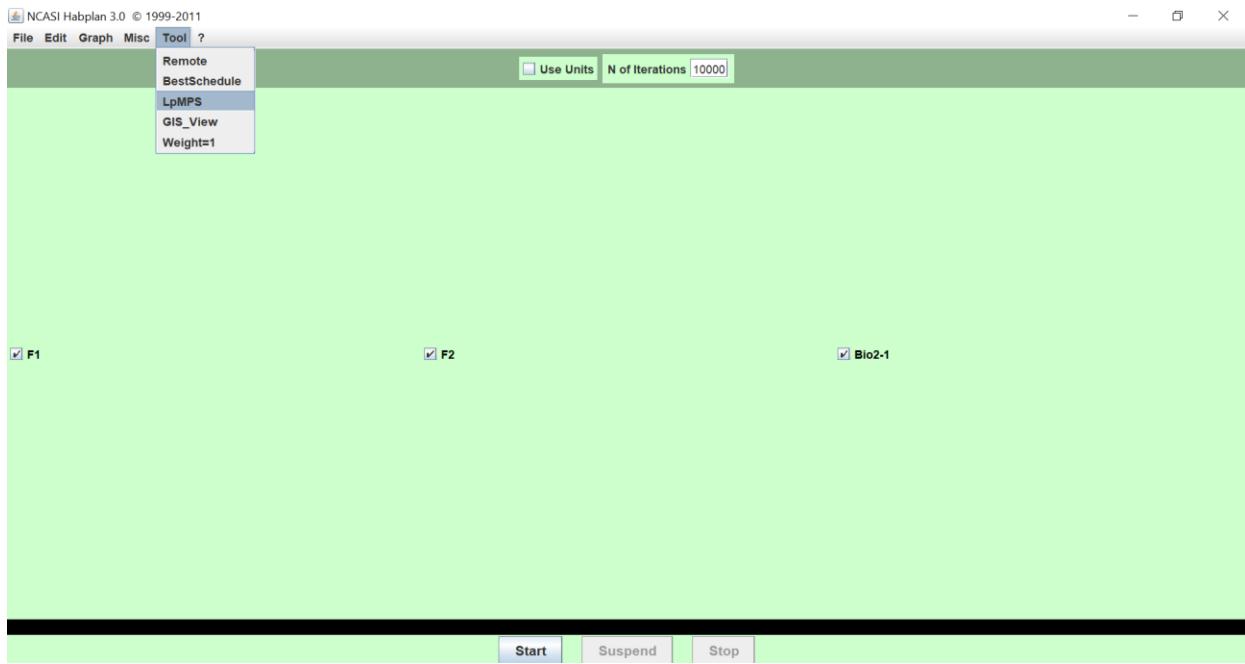
When opening the project file, you may encounter the following pop-up window. This means that the configuration file has a different configuration than the project file. In this circumstance, select ReConfigure and Quit, which will close Habplan. Once that happens, re-run the R code `shell("h", wait=TRUE)`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



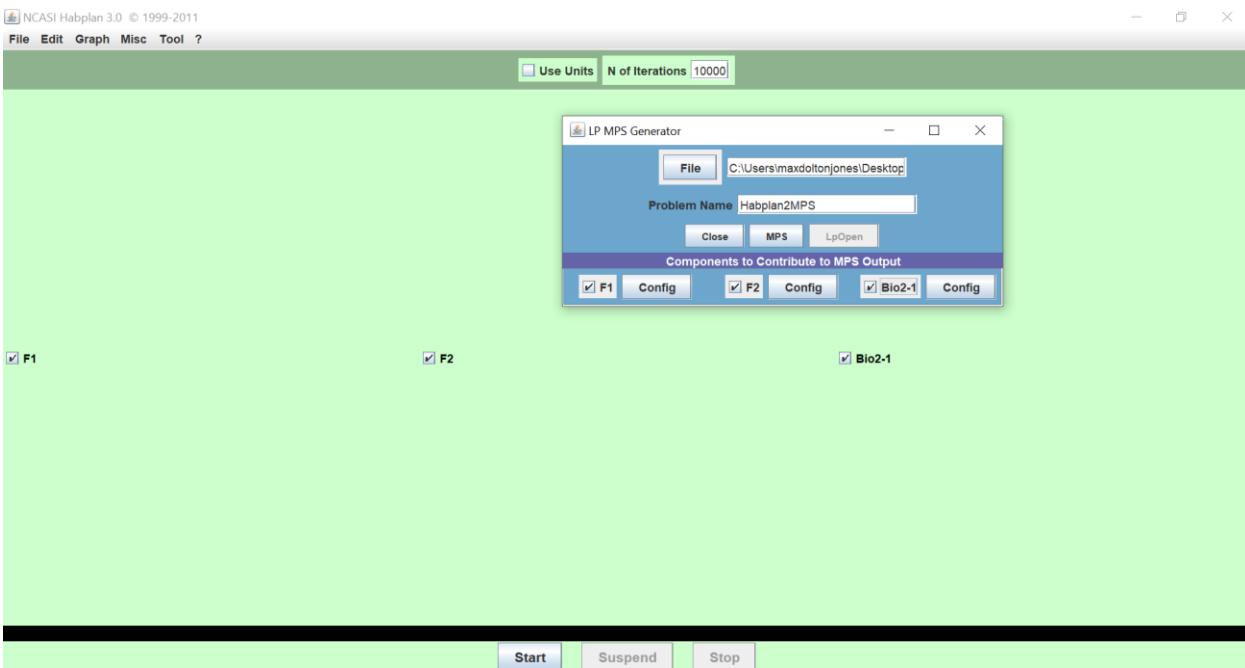
Another new window will now be available titled Habplan Console, where the program will provide updates and errors. We will also have the opportunity to select the flow components on the main window, named F1, F2, and Bio2-1 in our example. Including other flows in the project file will add new component check boxes. Go ahead and select the three check boxes on the main window so that they appear as below.



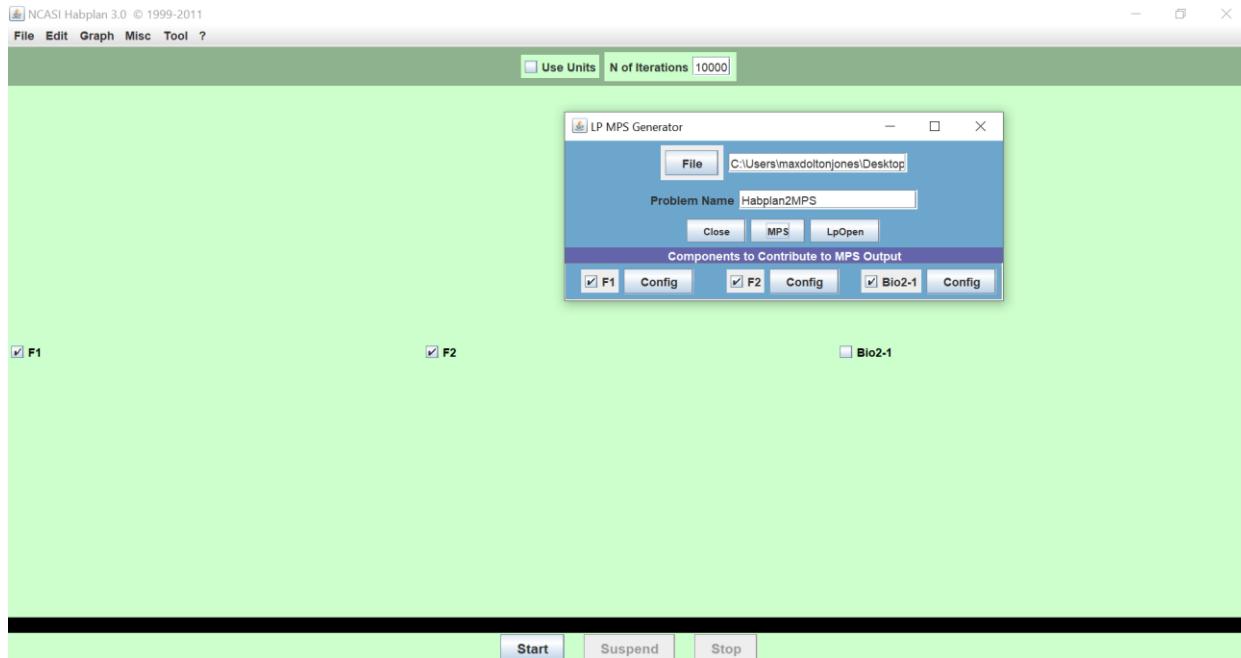
We will now navigate to Tool > LpMPS.



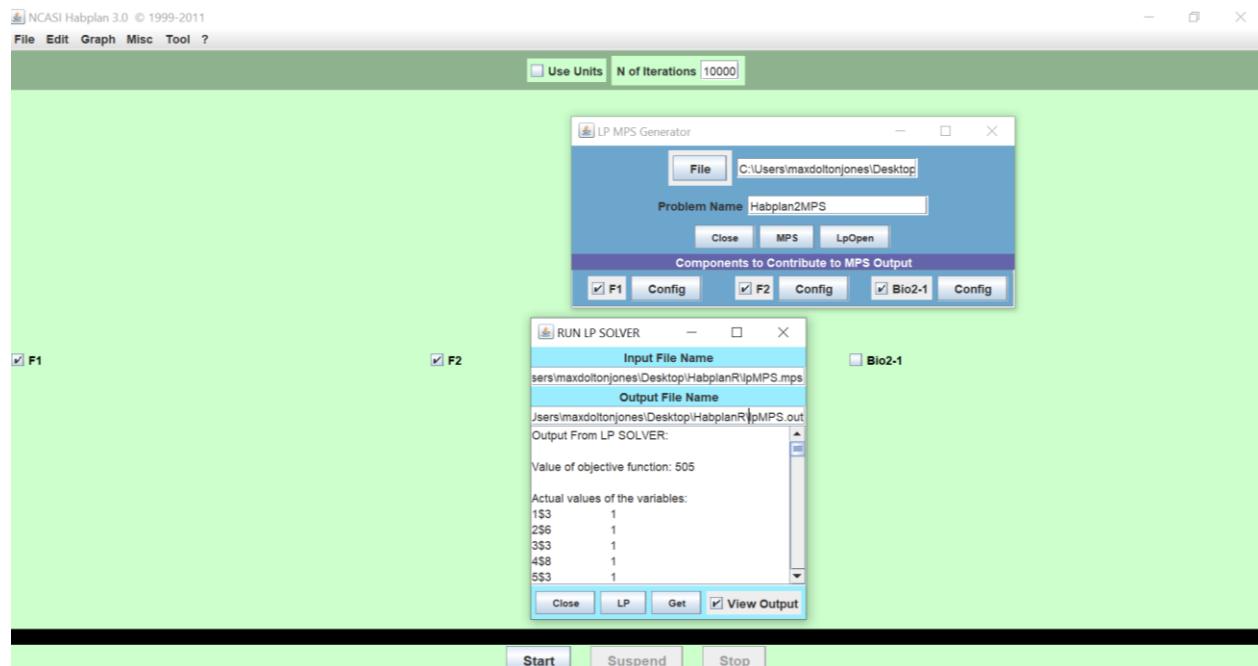
This will open a new window titled LP MPS Generator. As before, select the three check boxes on the new window so that they appear as below. To move forward we can click the “MPS” button, which will create a new MPS file based on the configurations that can be set using the three “Config” buttons. You can use these and create a new MPS file, which will be saved to the location in the top text box of the window. However, we have already created a file using the *lpMPS* function of **HabplanR**.



When the “MPS” button has been selected (which needs to be clicked to move forward), the “LpOpen” button will now become available, as shown below. Now click the “LpOpen” button.



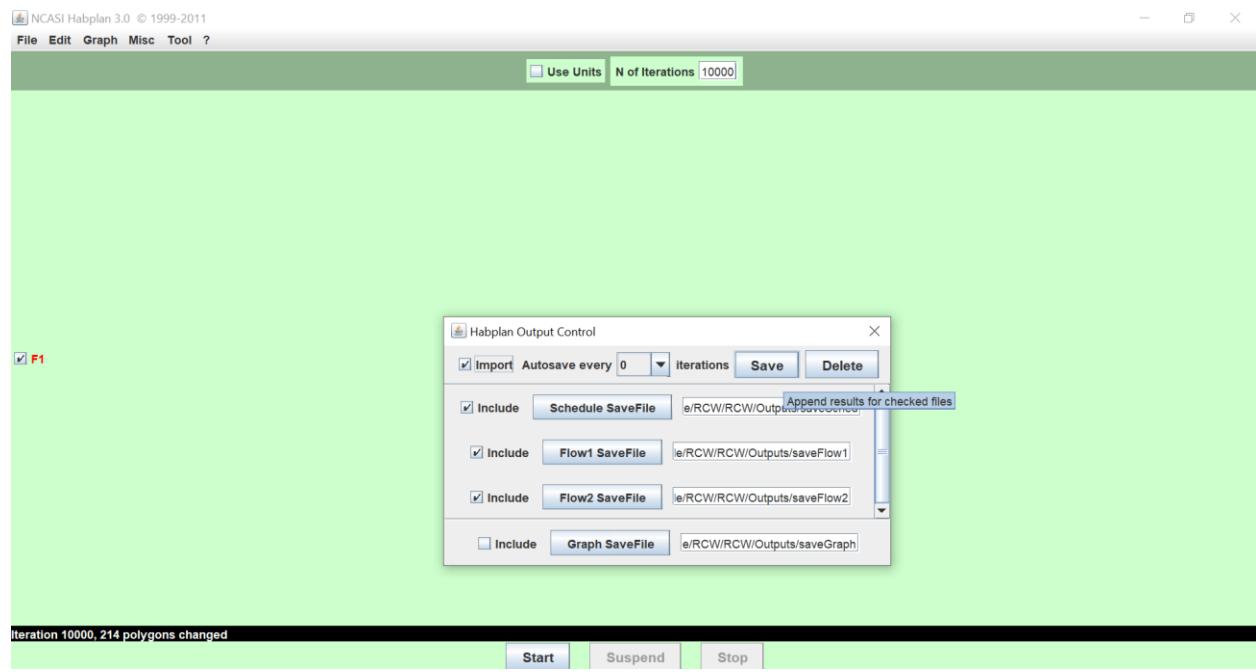
The “LpOpen” button will open a new window titled RUN LP SOLVER. When this first opens, there will be no information in the white space, and lp_solve will assign file inputs and outputs. We want to change the “Input File Name” to the MPS file we created in R, and then assign an “Output File Name” of your own preference. Click “LP” and this will run the LP solver. Once finished, click “Get” and this will transfer model results back into the Habplan main window.



We can now save the output as we have done before. 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. If an error is encountered when attempting to save, check the file directory in the Habplan Output Control window.



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.
- Project Explorer:** Shows two files: "Habplan_workflow_v3.R" and "HabplanR.vignette.v2.Rmd".
- Code Editor:** Displays the R code for the vignette, including comments and code snippets for setting the working directory, writing project files, and plotting flow outputs.
- Environment Tab:** Shows the Global Environment pane which is currently empty.
- Console Tab:** Shows the R session output. It includes the command to install the package from GitHub, the library loading message, and the command to run the Java application "Habplan3" with memory settings.
- Bottom Status Bar:** Shows the path "C:\Users\maxdoltonjones\Documents\Habplan\Habplan3\Habplan3>" and the Java command "java -mx1012m Habplan3".

Similar to our other outputs from Habplan, we can read in the output flow files and plot them. We are going to compare the results to those of the Metropolis Hastings algorithm from the third run above.

```
#Read in 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)
```

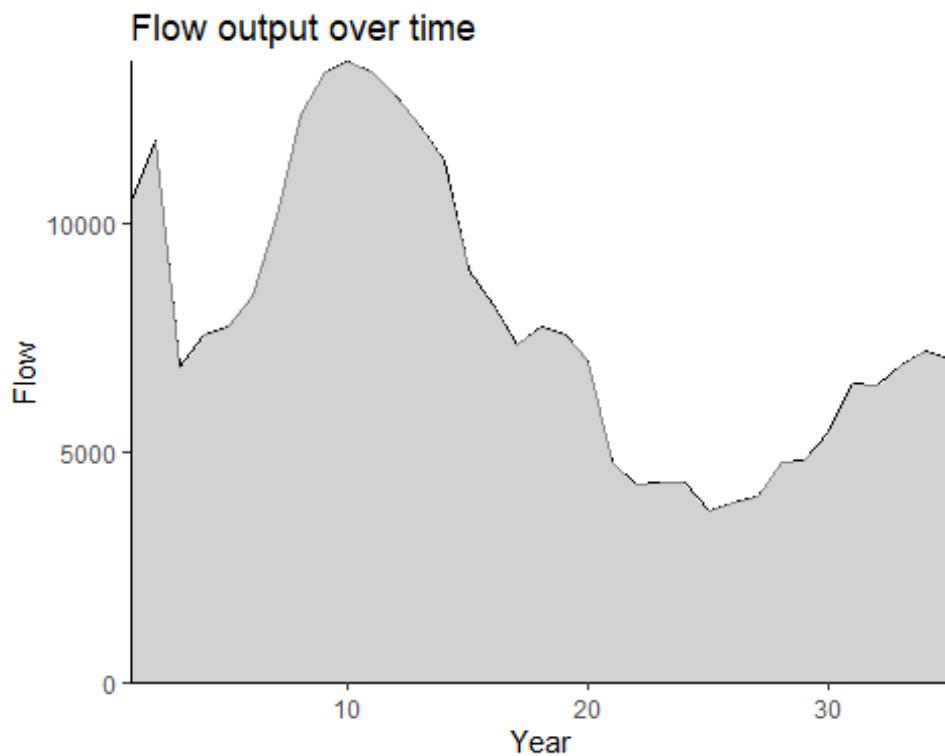


Figure 30. The amount of flow (habitat area) attained over time as a result of the suggested Habplan management schedule, based on Habplan linear programming.

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

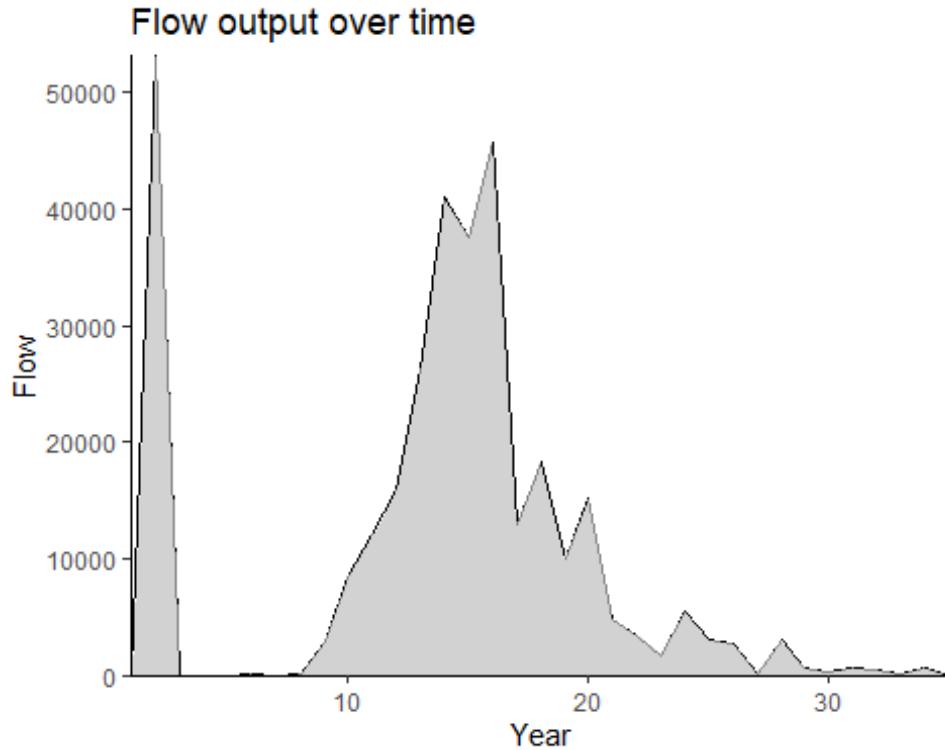


Figure 31. The amount of flow (harvested pine pulpwood) attained over time as a result of the suggested Habplan management schedule, based on Habplan linear programming.

Now that we have looked at the flows individually, we will use the *comPlot* function to compare the original Habplan runs with the LP Solver.

```
#Let's compare the flows across runs.
#For this example, we have saved the flow files in different folders
flow1 <- read_csv("./Run_2/saveFlow1", col_names = F)
#> Rows: 505 Columns: 73
#> — Column specification


---


#> Delimiter: ","
#> chr (1): X2
#> dbl (72): X1, X3, X4, X5, X6, X7, X8, X9, X10, X11, X12, X13, X14, X15,
X16, ...
#>
#> [i] Use `spec()` to retrieve the full column specification for this data.
#> [i] Specify the column types or set `show_col_types = FALSE` to quiet this
message.
flow2 <- read_csv("./Run_3/saveFlow1", col_names = F)
#> Rows: 1010 Columns: 73
#> — Column specification


---


#> Delimiter: ","
```

```

#> chr (1): X2
#> dbl (72): X1, X3, X4, X5, X6, X7, X8, X9, X10, X11, X12, X13, X14, X15,
X16, ...
#>
#> [i] Use `spec()` to retrieve the full column specification for this data.
#> [i] Specify the column types or set `show_col_types = FALSE` to quiet this
message.
flow3 <- read_csv("./Run_LP/saveFlow1", col_names = F)
#> Rows: 505 Columns: 73
#> — Column specification


---


#> Delimiter: ","
#> chr (1): X2
#> dbl (72): X1, X3, X4, X5, X6, X7, X8, X9, X10, X11, X12, X13, X14, X15,
X16, ...
#>
#> [i] Use `spec()` to retrieve the full column specification for this data.
#> [i] Specify the column types or set `show_col_types = FALSE` to quiet this
message.
#flow4 <- read.csv("./saveFlow4", sep="")

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

```

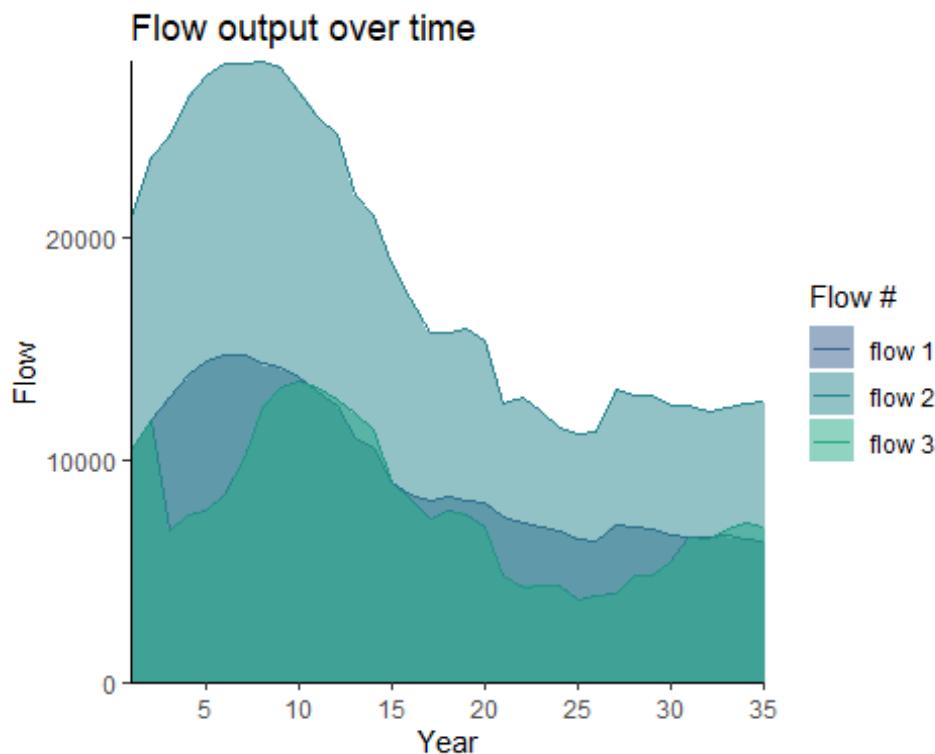


Figure 32. The amount of flow (habitat area) attained over time as a result of the three separate Habplan management schedule (flow1, flow2, and flow3 [linear programming]). Each flow is represented by a different shade of blue.

As can be seen from the above example, the suggested management regimes from the original Habplan run and the LP Solver can be very different. That's why it is important to look at each forestry problem using multiple methods and parameters, and plot them across time to find the "best" schedule.

Function: Carbon data conversion: *CarbConvert*

In the member-only HabplanR version, we have also incorporated a new function for converting Carbon data into Habplan flow files, similar to the *HabConvert* function introduced earlier in the vignette.

We need to provide the custom function with one argument only:

1. std.data: the flow information in csv format

We will read in the stand data with the carbon information embedded within.

```
#Load in stand and corresponding Carbon data
std.data <- read_csv("./HSM_OUT_FINAL_MerchStds_wCarbon.csv")
```

Now we can run the *CarbConvert* function. We only need to include our new std.data file for the function to run:

```
#Run function
carb.flow <- CarbonConvert(std.data = std.data)
```

The above function will save a flow file called "Carbon_data.dat" in our working directory

We will use a previously highlighted function of HabplanR, *WriteProj* to create a project file which can be loaded into Habplan to set parameters and other configurations. The only arguments needed for the actual function to work, are the object names for each flow component which needs to be included.

Since Habplan inputs allow for customization, we provide script which will allow users the same level of input manipulation. For our carbon workflow, we will only be working with one flow component: carbon.

```
#Overarching information for habplan run:
#Get the number of stands for later
npoly <- length(unique(std.data$StandKey))
#Configuration - see HabPlan Manual
config <- "1,0,0,0,0,0"
#wd is the working directory where HabPlan and data are stored
wd <- "FILEPATH HERE"
```

```

#iter is the number of iterations needed for the HabPlan run
iter <- "10000"

f1.file <- "Carbon_data.dat"
f1.bystander <- ""
f1.time0 <- "100"
f1.goal0 <- "0.1"
f1.thlo <- "100"
f1.thhi <- "500"
f1.goalplus <- ".05"
f1.goalf <- "0.5"
f1.slope <- "0.0"
f1.weightf <- "1.0"
f1.weight0 <- "1.0"
f1.model <- "1,100;10,100;20,100;30,100"
f1.title <- "Carbon.dat"
#Combine f1 components for writing
f1.comp <- c('<flow title="F1 Component">',
  paste0('<file value=""', f1.file, '" />'),
  paste0('<bystander value=""', f1.bystander, '" />'),
  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>")

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

IMPORTANT - MUST RENAME OR MOVE SAVEFLOW1 AND SAVESCHED FROM WORKING DIRECTORY IF YOU DO NOT WANT THE FILES TO BE DELETED

```

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

```

After running Habplan, we will have a carbon flow 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.

```
#Read in the Carbon flow file  
flow1 <- read.csv("./saveFlow1", sep="", header = F)
```

IMPORTANT - if the flow1 object has more rows than number of stands something went wrong. Most likely, the saveFlow1 file was not removed from the working directory before Habplan was run.

```
#Input the flow file into the function, and number of years  
flowPlot(flow.data = flow1, nyear = 36) #Carbon dataset has 36 years, not 35.
```

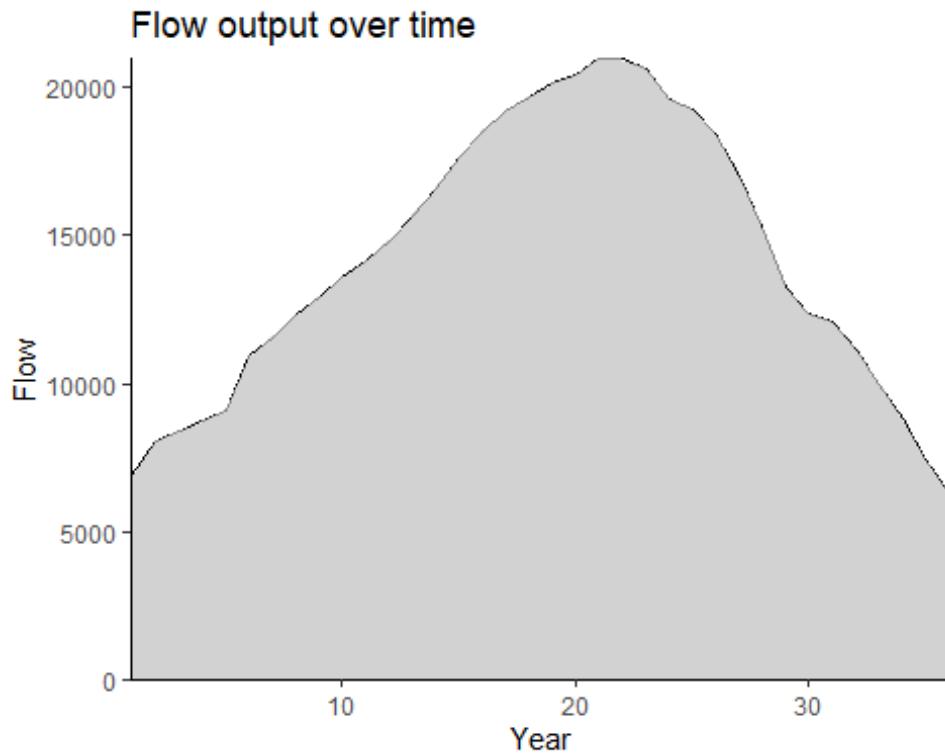


Figure 33. The amount of flow (sequestered carbon) attained over time as a result of the suggested Habplan management schedule.

Run 2

For this second run, we will maintain the overarching Habplan parameters, but will now change the upper threshold (thhi), lower threshold (thlo), and model values.

```
f1.file <- "Carbon_data.dat"  
f1.bystander <- ""
```

```

f1.time0 <- "5000"
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 <- "1,10000;10,12000;20,12000;30,12000"
f1.title <- "Carbon.dat"
#Combine f1 components for writing
f1.comp <- c('<flow title="F1 Component">',
  paste0('<file value=""', f1.file, '" />'),
  paste0('<bygone value=""', f1.bystone, '" />'),
  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>")

```

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

**IMPORTANT - MUST RENAME SAVEFLOW1 AND SAVESCHED FROM WORKING DIRECTORY
 IF YOU DO NOT WANT THE FILES TO BE DELETED**

```

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

```

After running Habplan, we will have a carbon flow saved to our working directory. The option still exists to interactively watch the charts in a Habplan window. However, we will visualize this flow using the flowPlot function.

```
#Read in the Carbon flow file
flow1 <- read.csv("./saveFlow1", sep="", header = F)
```

IMPORTANT - if the flow1 object has more rows than number of stands something went wrong. Most likely, the saveFlow1 file was not removed from the working directory before Habplan was run.

```
#Input the flow file into the function, and number of years
flowPlot(flow.data = flow1, nyear = 36)
```

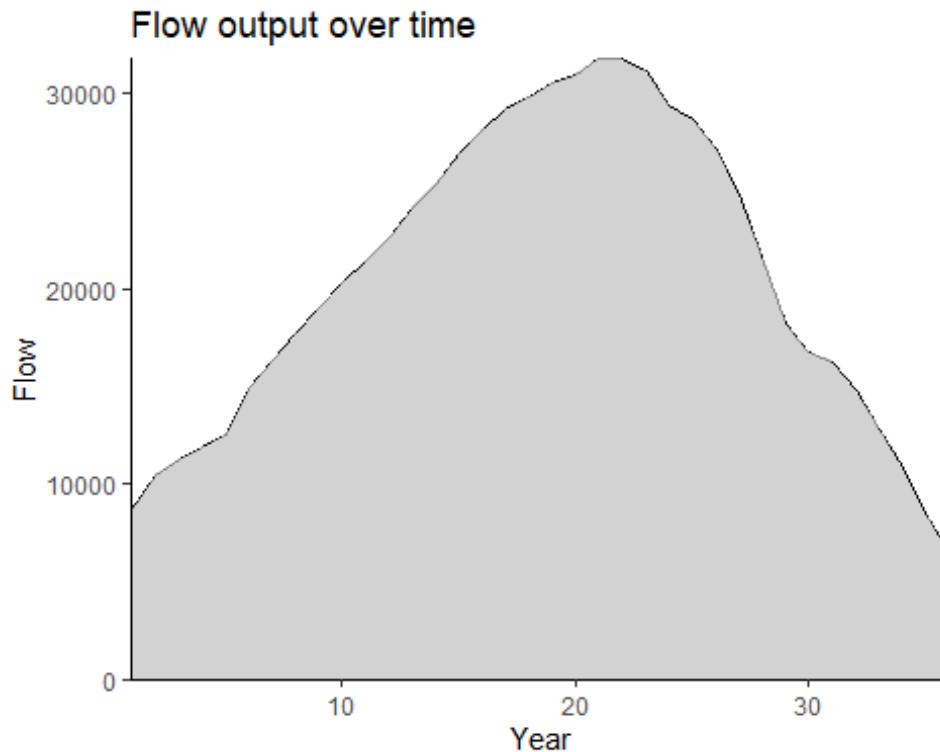


Figure 34. The amount of flow (sequestered carbon) attained over time as a result of the suggested Habplan management schedule.

Run 3

For this third run, we will maintain the overarching Habplan parameters, but will now change the upper threshold (thhi), lower threshold (thlo), and model values.

```
f1.file <- "Carbon_data.dat"
f1.bystander <- ""
f1.time0 <- "10000"
f1.goal0 <- "0.1"
f1.thlo <- "3000"
f1.thhi <- "15000"
```

```

f1.goalplus <- ".05"
f1.goalf <- "0.5"
f1.slope <- "0.0"
f1.weightf <- "1.0"
f1.weight0 <- "1.0"
f1.model <- "1,15000;10,15000;20,15000;30,15000"
f1.title <- "Carbon.dat"
#Combine f1 components for writing
f1.comp <- c('<flow title="F1 Component">',
  paste0('<file value=""', f1.file, '" />'),
  paste0('<bygone value=""', f1.bystone, '" />'),
  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>")

```

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

*IMPORTANT - MUST RENAME SAVEFLOW1 AND SAVESCHED FROM WORKING DIRECTORY
 IF YOU DO NOT WANT THE FILES TO BE DELETED*

```

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

```

After running Habplan, we will have a carbon flow saved to our working directory. The option still exists to interactively watch the charts in a Habplan window. However, we will visualize this flow using the flowPlot function.

```

#Read in the Carbon flow file
flow1 <- read.csv("./saveFlow1", sep="", header = F)

```

IMPORTANT - if the flow1 object has more rows than number of stands something went wrong. Most likely, the saveFlow1 file was not removed from the working directory before Habplan was run.

```
#Input the flow file into the function, and number of years
flowPlot(flow.data = flow1, nyear = 36)
```

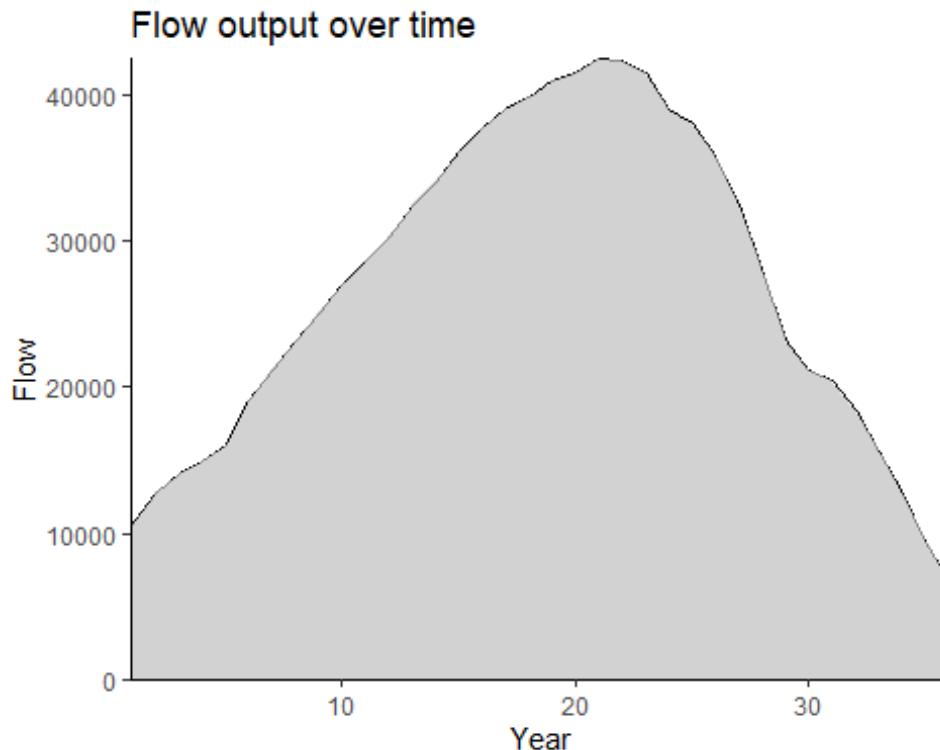


Figure 35. The amount of flow (sequestered carbon) attained over time as a result of the suggested Habplan management schedule.

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 will therefore use the comPlot function, as we have demonstrated earlier.

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

```
#Let's look at these flows together
flow1 <- read_csv("./saveFlow1_1", col_names = F)
flow2 <- read_csv("./saveFlow1_2", col_names = F)
flow3 <- read_csv("./saveFlow1", col_names = F)
#flow4 <- read.csv("./saveFlow4", sep="")

#Run function with new flows
```

```

comPlot(flow.data.1 = flow1, flow.data.2 = flow2,
       flow.data.3 = flow3, nyear = 36) # 36 years in new Carbon data

#> Rows: 454 Columns: 75
#> — Column specification


---


#> Delimiter: ","
#> chr (1): X3
#> dbl (74): X1, X2, X4, X5, X6, X7, X8, X9, X10, X11, X12, X13, X14, X15,
X16, ...
#>
#> i Use `spec()` to retrieve the full column specification for this data.
#> i Specify the column types or set `show_col_types = FALSE` to quiet this
message.
#> Rows: 681 Columns: 75
#> — Column specification


---


#> Delimiter: ","
#> chr (1): X3
#> dbl (74): X1, X2, X4, X5, X6, X7, X8, X9, X10, X11, X12, X13, X14, X15,
X16, ...
#>
#> i Use `spec()` to retrieve the full column specification for this data.
#> i Specify the column types or set `show_col_types = FALSE` to quiet this
message.
#> Rows: 908 Columns: 75
#> — Column specification


---


#> Delimiter: ","
#> chr (1): X3
#> dbl (74): X1, X2, X4, X5, X6, X7, X8, X9, X10, X11, X12, X13, X14, X15,
X16, ...
#>
#> i Use `spec()` to retrieve the full column specification for this data.
#> i Specify the column types or set `show_col_types = FALSE` to quiet this
message.

```

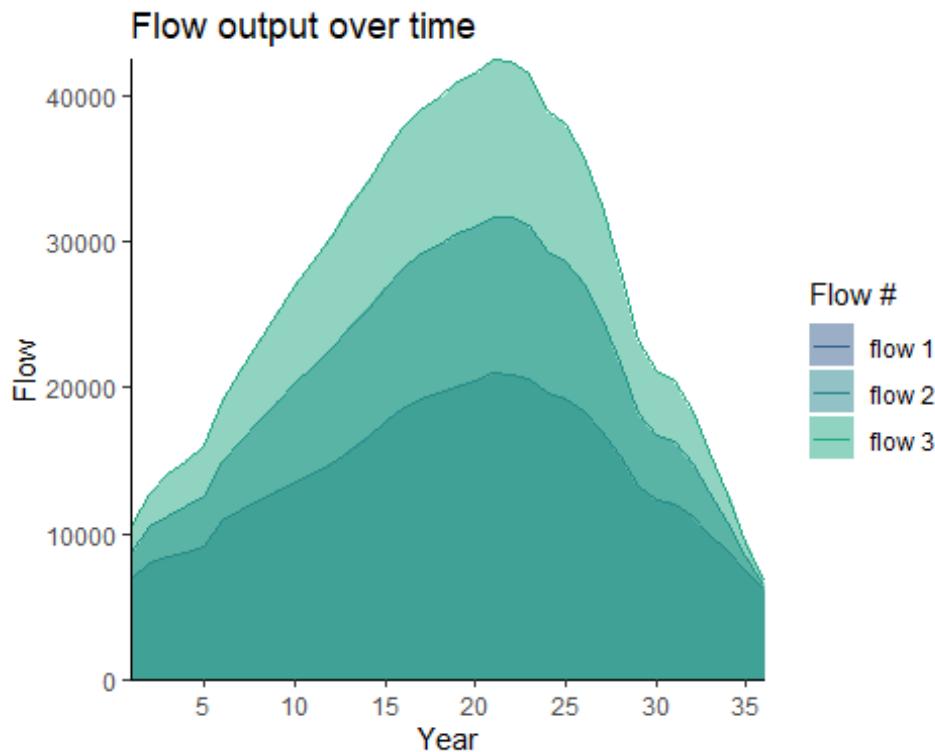


Figure 36. The amount of flow (sequestered carbon) attained over time as a result of the three separate Habplan management schedule (flow1, flow2, and flow3). Each flow is represented by a different shade of blue.

Summary

Above, we have provided very simple examples 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. To access the member-only version, or for additional help, please contact Holly Munro at hmunro@ncasi.org.

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Appendix 1 - FVS variable names and descriptions

- RegimeKey: Unique number used to identify a specific management regime.
- Regime Activity: Descriptions of management regimes used within the Forest Vegetation Simulator growth model to project stand conditions. BA: Basal Area, LL: Loblolly Pine (*Pinus taeda*), TPA: Trees Per Acre.

- StandID: Unique forest stand ID.
- Year: Projected year by the growth model for that combination of forest stand and regime.
- Age: Age of forest stand.
- BA: Basal area.
- TPA: Trees per acre.
- Pine_Pulp_Tons: Tons of pine pulpwood.
- Pine_CNS_Tons: Tons of pine chip-n-saw.
- Pine_Saw_Tons: Tons of pine sawtimber.
- Hdwd_Pulp_Tons: Tons of hardwood pulpwood.
- Hdwd_Saw_Tons: Tons of hardwood sawtimber.
- Harv_P_Pulp_Tons: Harvested pine pulpwood (tons/acre).
- Harv_P_CNS_Tons: Harvested pine chip-n-saw (tons/acre).
- Harv_P_Saw_Tons: Harvested pine sawtimber (tons/acre).
- Harv_H_Pulp_Tons: Harvested hardwood pulpwood (tons/acre).
- Harv_H_Saw_Tons: Harvested hardwood sawtimber (tons/acre).
- HSI: Habitat Suitability Index.

Appendix 2 - List of HabplanR functions and brief description

- HSIconc: Calculates HSI and inserts into dataset.
- HabConvert: Converts Forest Vegetation Simulator data (or similar) to Habplan flow file.
- WriteProj: Creates a project file with Habplan configurations/parameters.
- FlowPlot: Plots a single output flow file across time.
- ComPlot: Plots multiple flow files on a combined graph across time.
- StandSched: Adds the top schedule to stand shapefile.
- HabBlock: Creates block size constraint data (adjacency table).
- HabSpace: Spatial analysis of HSI flows.
- lpMPS: Create an MPS file to run the lp solver in Habplan.
- CarbonConvert: Converts growth model projection data with Carbon data to Habplan flow file.