CONIFERS package in R: `rconifers`

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Abstract

CONIFERS is a model for young stand growth developed by personnel at the USFS Pacific Southwest Research Station in Redding, California. Although originally developed with a graphical user interface (GUI), currently only the dynamic linked library (dll) and an R package are supported and updated. The current version of the software includes four variants. The original version (SWO) of the project is for growth of mixed-conifer plantations in Southern Oregon and Northern California (SWO). The second is a Stand Management Cooperative (SMC) variant for northwest Oregon and western Washington, developed using data from research cooperatives. Variant 3 is a process/hybrid version of SWO. The final Variant was developed by Doug Maguire and Doug Mainwaring of the Center for Intensive Planted-Forest Silviculture (CIPS) at Oregon State University.

1 Introduction

Forecasts of forest growth and yield are critical elements used in the management of forested lands. Managers rely on forecasts of stand development to evaluate anticipated silvicultural prescriptions, and as a guide in forest-level planning of timber harvests and other management activities. Ideally, simulators should be able to provide users with a means to forecast development of stands across the full range of anticipated stand conditions. In general, simulators for established stands are ineffective at simulating the growth of very young stands, or any stand in which non-tree vegetation contributes significantly to the level of competitive stress to which trees are exposed. Examples of established stand simulators for application in the western United States include FVS (Wykoff et al., 1982), ORGANON (Hann, 2006) and CACTOS (Wensel et al., 1986).

Young stand simulators, designed to handle young plantations include SYSTUM-1 (Ritchie and Powers, 1993), RVMM (Knowe et al., 2005), and CONIFERS (Ritchie and Hamann, 2006). CONIFERS has been through numerous updates and was originally implemented with a graphical user interface (GUI). However maintenance of the GUI presented a significant drain on limited resources, so it is no longer updated or supported (although still available). Therefore, the growth and other key functions have been ported to a dll and the `rconifers` package.

CONIFERS is currently supported in two formats. The functionality of the model can be accessed using the `dll` or with an R package (`rconifers`) that calls the `dll`. Direct application of the `dll` is for advanced users and is not the subject of this presentation.

1.1 Why R?

The easiest way to access the CONIFERS model is through the R analysis system (R Development Core Team, 2012). Although unfamiliar to many foresters, R is a powerful analysis package and the steps required to load and run the CONIFERS Variants are fairly simple. This is done is by first installing R then the `rconifers` package into the R system. Once installed the complete functionality of CONIFERS is at available as will be demonstrated in examples.

There are two advantages to using `rconifers`. First, with R the user has powerful analyitical tools, including the abilty to develop many types of graphical images for analyses. Second, most of the supporting R functionality is maintained independently, thus reducing code maintenance for CONIFERS. There are fewer problems with code maintenance needed to mantain currency with the Microsoft operating system. We avoid, to a large extent, the problem of software obsolescence which has been a chronic problem with simulator development over the last 30 years.

We should mention that R is freely available to anyone with connection to the internet. Thus software distribution is simplified as well.

1.2 Installing R

The installation process is not time consuming but it does require a few steps. The first thing a user will need to do is install R. This is a simple process which is initiated by opening a browser and accessing the CRAN web site (`http://cran.r-project.org`). At this website there is a lot of information that you really don't need for the task at hand. To obtain a Windows executable, the user should choose to download R for Windows. If you have another operating system choose accordingly; we will continue with the installation example for Windows.

The next step is to select: install R for the first time. And, finally: Download R for Windows. In this last link there will be a version number and this will update from time to time. When prompted, save the installation file to a handy location and then install as you would any Windows software. If you wish to upgrade at any time to the most current version of R, simply repeat this process.

During the installation, we recommend beginners just choose the defaults. For Windows you will be prompted to choose a 64 or 32 bit installation. If you have a 64 bit version of Windows, choose the 64 bit installation. If you have 32 bit or are not sure, choose the 32 bit installation. Once installed you should find the icon on your desktop for R. Double-click and R will open providing a command-line prompt and an array of drop down menus across the top.

1.3 Installing `rconifers`

Step 2 is to install the `rconifers` package. From within R many packages for various types of analysis are available. The rconifers package is just one of many to choose from. To install the `rconifers` package, choose Packages:Install Package(s). Then choose a nearby mirror and select OK. Finally you will see a long scrollable list presenting packages alphabetically. Choose `rconifers` by scrolling down and select OK. This completes installation of R and the `rconifers` package.

This step need only be executed once unless there is an update or you change to a newer version of R.

1.4 Loading `rconifers`

One of the confusing aspects of R, for beginners, is the difference between installing and loading a package. The simple version of this is that installing is done once. Loading, however, is done every time you open R, if you choose to run `rconifers` in that particular session. One way to think of this is that installing places the package on your machine. Whereas loading makes that particular package available for any particular session in R. To load the package, type `library(rconifers)` at the R prompt.

2 Application of `rconifers`

We will illustrate the use of `rconifers` with the r-script below. We will use the SWO variant (set.variant=0) and the sample plant list for swo that comes with the `rconfiers` package (`plants.swo`). The first line is a comment for the user's benefit. R will ignore lines starting with #. You will notice the first executable step is the `library` command. This loads the `rconifers` package for this run. It is good form to load any packages you might need right up front just to get this step out of the way. Notice the form of the statement: `library(rconifers)`. The first part, `library`, is a function call recognized by R. It means simply go fetch a package that we have already installed. Inside the brackets is the *argument* for the function: `rconifers`. Some function calls will have more than one argument, separated by commas.

You will notice a data function call a few steps down. This function works much like `library`, in that it retrieves data that has been installed. When `rconifers` was installed, several test data sets were included. One of these is called `plots.swo`, another is `plants.swo`. These are respectively: (1) a file with the list of plots sampled with some additional information, and (2) the associated plants that were sampled on these plots. It is rather important that these two files match up.

```
> ## load the rconifers library
> library( rconifers )
> ## set the number of digits for the output to five (5)
> options(digits=5)
> ## set the variant to the SWO variant (variant=0)
> set.variant(0)
```

```
Initialized 19 functional species coefficients for variant # 0 CONIFERS_SWO
The code label for the variant is CONIFERS_SWO
The coefficients version is 4.140000
The model version is 4.140000
[1] 0
```

```
> ## set the species map as swo for this run
> data( species.swo )
> set.species.map( species.swo )
> # load CONIFERS SWO example plots
> data( plots.swo )
> # load CONIFERS SWO example plants
> data( plants.swo )
```

At this point we have set the variant to 0 (`set.variant(0)`). It may seem confusing that the first Variant is called with `set.variant(0)`. This is a programming issue related to the native language of CONIFERS, which is ANSI C. In the C language indexing begins at zero by default. The four CONIFERS Variants thus are are indexed then from 0 to 3.

Next, for this example, we are going to modify the data a bit. We have a tree in this file that is a large white fir overstory tree that I wish to remove from this run. The big white fir happens to be the third plant in the list. If you want to see it, type `plants.swo[3,]` at the R prompt. This serves the purpose of illustrating the indexing of data frames in R. Data frames are indexed by rows and then columns so `plants.swo[3,]` tells R that you wish to view row 3 and all columns of the data frame. If you want to view the entire plant list type `plants.swo` at the R prompt and you will see a print out of the entire sample. If you leave it in, CONIFERS will attempt to grow this tree, but it may not do a very good job of it. It is, after all, a simulator for young plantations so this represents an extrapolation of our data. For now, we will remove it with a powerful little R command that may seem confusing.

```
> ## modify so we eliminate any overstory >40 inches
> plants1.swo <- plants.swo[plants.swo$d6<40.0,]
```

First notice the assignment operator: `<-`. This tells R to assign what is on the right into what is on the left. In other words, make a new version of plants.swo called plants1.swo. These are structured data objects called data frames in R. As such, they are two dimensional arrays with column headings. They may be used as a template format for any sample data to be used in `rconifers`. So `plants.swo` has rows and columns specified to conform to that required by `rconifers`.

To confirm this format type `dim(plants.swo)` at the command prompt to obtain the number of rows and columns in this particular file (60 and 9). If you type `names(plants.swo)` you will see a list of the fields in the data frame that `rconifers` wants to see. These are the plot, species code (sp.code), basal diameter (d6) in inches, breast height diameter (inches), total height (feet), live crown ratio (cr), number of stems per plant (n.stems), the per-acre expansion factor (expf) and the crown width (crown.width) in feet. The expansion factor is a transformation of the plot area in square feet:

$$expf = \frac{43560}{plot\ area}. \tag{1}$$

To view a single element of the sample plants data frame, type `plants.swo[3,4]` at the command prompt in R. R will return a value of 35.2. This is the diameter of the 3rd plant (row three) in the original plant list. The dbh happens to be the fourth column in the data frame called `plants.swo`. So in the line of code assigning `plants1.swo` above, since we didn't specify a column, all columns are moved into `plants1.swo`. However because we specified which rows on the right side to include, the new file only includes those in which d6 (basal diameter) is less than 40 inches. So the new file `plants1.swo` doesn't include that big white fir because the basal diameter exceeded 40.0.

One other litte exercise is to type `plants.swo[3,2]` at the command prompt. You will notice this returns column two of the third tree in the list: the species code. Additionally, R throws in something else: the list of all species found in the file.

If we want to confirm that there aren't any other giant trees in the file, we can tell R to display all the individuals in the `plants1` data frame that have a height less than 7.0 feet. You will notice the big white fir is not in the list and there are no other large trees.

```
> ## view trees bigger than 7.0 feet in height
> plants1.swo[plants1.swo$tht>7.2,]

   plot sp.code   d6  dbh   tht    cr n.stems expf crown.width
1     1      PP 4.80 2.91 11.50 0.852       1  100        7.55
12    3      PM 1.56 0.98  8.80 0.852       6  100        5.25
13    3    COCO 0.68 0.00  7.40 1.000      15  100        6.10
57    4      PP 4.00 2.80 10.58 0.811       1  100        7.49
58    4      PM 2.63 0.97  7.80 0.705       3  100        4.45
```

Finally, we are going to create what is called a `sample.data` list object. This object encapsulates all the information about a stand needed to forecast growth and do the associated bookeeping. There are five arguments in the list. In addition to the plants and plots we assigned a stand age (0) and the number of years of growth we have simulated at this point (also 0) as well as *x0*. This last value helps determine the rate of mortality and for young stands we start it out at zero (Hann and Wang, 1990).

```
> ## create the sample.data list object
> sample.swo <- list( plots=plots.swo, plants=plants1.swo, age=3, x0=0.0, n.years.projected=0 )
> class(sample.swo)  <- "sample.data"
> ## display the sample list object summary
> sample.swo

sample contains 4 plots records
sample contains 59 plant records
```

```
n.years.projected =  0
age =  3
x0 =  0
max sdi =  375.8
        qmd   tht      ba bhexpf texpf
CEIN 0.0000 4.700 0.00000    250   250
COCO 0.0000 5.491 0.00000    375   825
DF   0.3350 3.163 0.06121    100   425
IC      NaN 1.179 0.00000      0   500
PM   0.6885 6.738 1.61593    625   650
PP   2.4165 7.425 2.38866     75   100
WF   0.3100 2.375 0.01310     25   275
```

This summary shows that we have a 3 year old plantation which has some competing vegetation. CEIN (deerbrush) is at 250 stems per acre and COCO (California hazel) is at 825 stems per acre total and of these 375 stems per acre are greater than 4.5 feet in height. In addition this stand has PM (Pacific madrone) at 650 per acre (625 abh). The conifers in this stand include WF and PP (white fir and ponderosa pine) at 275 and 100 trees per acre respectively. There is also some DF (Douglas-fir) and IC (incense-cedar).

We can also quickly plot a summary of this stand by calling the `plot` function which produces a four panel plot(Figure 1):

```
> ## plot the sample
> plot(sample.swo)
```

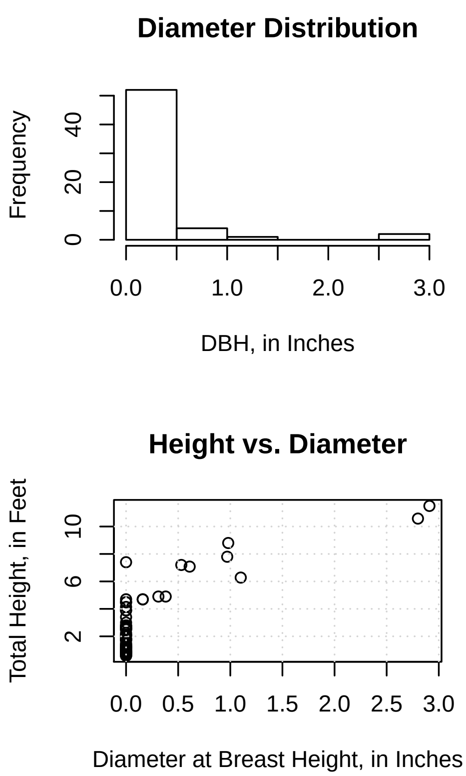

Figure 1: Summaries of the initial observed stand conditions (age 3).

Some closing notes on executing R code. R documentation, such as this typically contains executable code snippets that the user may cut and paste into the R prompt at any time. If you do so, your results should match those in the documentation. For more complicated projects a series of commands are often created in a plain text editor. Many text editors are availiable online and some of these will provide helpful highlighting for documents with a .r extension as is the convention for R scripts.

If you ever find yourself lost in R, help can be found by typing `help.start()` at the command prompt. This will provide a reference page. Help for any installed packages may be accessed by selecting packages on the reference page.

3 Growth

Forecasting growth with conifers is done with the project command. It is possible to grow in individual annual increments or you can choose to grow for a longer time span and return the results. While CONIFERS places no limits on maximum age, any projection beyond about 25 year of age is not advised. For this example we first set random error component off (rand.err=0) and set the random seed to an arbitrary integer (107). Mortalilty is turned off and we selected a 15 year growth projection.

```
> # now, project the sample forward for 15 years, no mortality
> # with all of the options turned off
> sample.swo.18 <- project( sample.swo, 15,
+           control=list(rand.err=0,rand.seed=107,endemic.mort=0,sdi.mort=0))
> sample.swo.18
```

```
sample contains 4 plots records
sample contains 59 plant records
n.years.projected =  15
age =  18
x0 =  0
max sdi =  397
        qmd    tht      ba bhexpf texpf
CEIN 0.0000  8.358  0.0000    250   250
COCO 0.0000  9.877  0.0000    825   825
DF   2.5116 20.840 14.6221    425   425
IC   0.9036  4.554  0.6680    150   500
PM   4.4825 29.638 71.2340    650   650
PP   8.7337 32.367 41.6025    100   100
WF   0.5542  4.909  0.2512    150   275
```

We can also plot a summary at age 18 by calling the plot function as we did earlier (Figure 2).

```
> ## plot the sample
> plot(sample.swo.18)
```

4 CONIFERS Variants

4.1 Southwest Oregon Variant

The SWO variant (`set.variant=0`) was the first variant of CONIFERS (Ritchie and Hamann, 2008). It was developed, using data from stands in southwest Oregon and northern California (Figure 3). Stands were mixed-conifer, heavy to Douglas-fir in southern Oregon and heavy to ponderosa pine in northern California. The age range for these plantations was from 3 years to about 23 years however there were few stands above 18 years of age. This variant does not

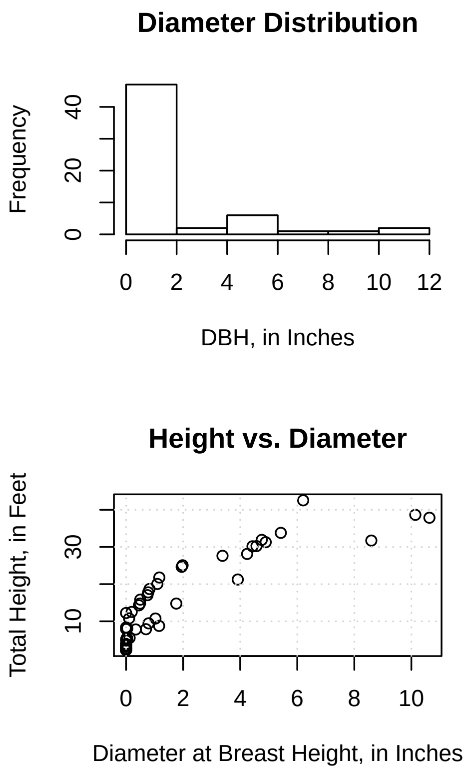

Figure 2: Summaries of the stand conditions forecast at age 18.

use site index but does require water holding capacity (in inches) in the `plots` file. Competing vegetation is handled on an individual-plant basis (Ritchie and Hamann, 2006).

The CONIFERS simulator was built on the foundation laid by the SYSTUM-1 project. The primary weakness of SYSTUM-1 was that very little data were available for young stands in which competing vegetation was quantified. If a robust system of equations was to be developed for a simulator, it would necessitate a data collection effort specifically for that project. In 1994 a data collection effort for the Klamath province was initiated with the intent of building a suite of functions for a young stand simulator. Data were collected on each selected stand on a two year interval. The initial measurement was followed by a re-measurement two years later. The remeasurement was conducted on a date as near to the original as possible so that the result provided two full growing seasons for each site. On most stands the remeasurement was within one week of the original date of initial measurement.

Stands were sampled in northern California and southern Oregon, from southern Trinity county in the south, to Douglas County in the north. Sites were selected from National Forest Land and sites on BLM land in Oregon. In addition, a limited number of sites under private ownership were sampled in northern California. All sites were plantations less than 26 years of age at the time of the initial measurement, and very few were older than 18 years initially. Some sites had some overstory trees from a previous stand. About 21 percent had greater than 20 square feet of basal area per acre on one or more plots in trees $>$ 12 inches in diameter at breast height. Only about 11 percent had greater than 20 square feet of basal area per acre on two or more plots.

Candidate stands were selected from across a range of ages and elevations by first stratifying all potential stands into age and elevation classes. It should be noted, however, that budgetary and time constraints limited the number of stands sampled to 109, the last of these were established in 1998 and remeasured in 2000 at the southern end of the sampled area.

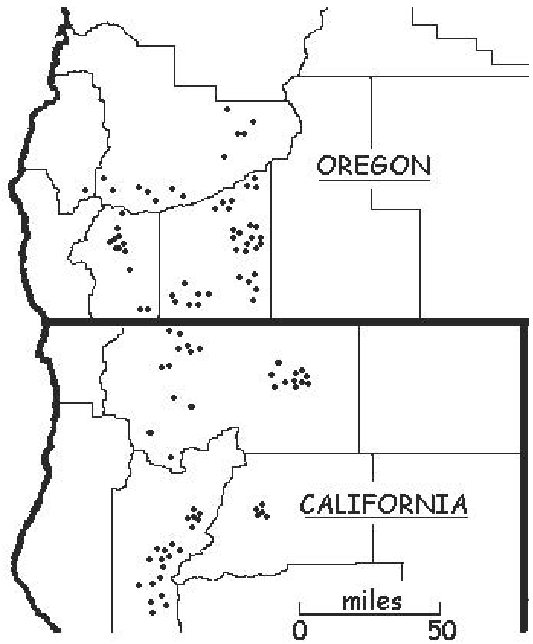

Figure 3: Plot locations for SWO variant of CONIFERS.

4.2 Stand Management Cooperative Variant

The SMC variant (`set.variant=1`) was developed by Nicholas Vaughn and Martin Ritchie and released in 2008 (Vaughn, 2007; Vaughn et al., 2010). Funding was provided by Agenda 2020. Data were contributed from the Stand Management Cooperative at the University of Washington and the RVMM project courtesy of Steve Radosevich at Oregon State University. The combined data set included 220 separate sites primarily in Oregon and Washington (Figure 4). Top height varied from 1 to 47.2 feet with a mean of 19.6. Although this distribution is highly skewed and most observed tree heights were less than 14 feet.

This variant only grows Douglas-fir trees and competing vegetation is handled differently than the original SWO variant. There was a limited amount of data for western hemlock, but these were not included in the development of the SMC variant.

Whereas in the SWO variant competing vegetation is grown as individual plants, in the SMC variant competing vegetation is modeled as an aggregate cover and height, much as it was in the original SYSTUM-1 model (Ritchie and Powers, 1993). Site productivity is reflected in site index at base age 30 provided in the `plot file` (Flewelling et al., 2001). The original GUI provided a conversion from base age 50 (Flewelling et al., 2001), but users must make this conversion on thier own for the SMC variant of `rconifers`.

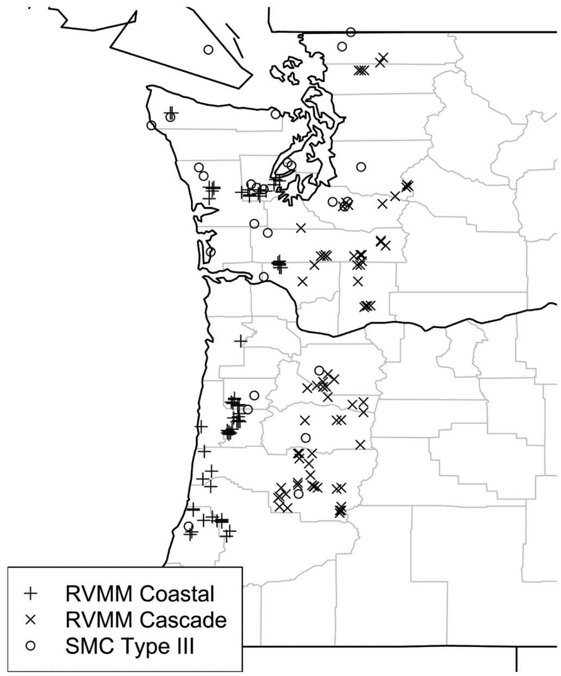

Figure 4: Plot locations for SMC variant of CONIFERS.

4.3 Hybrid SWO Variant

The hybrid variant (`set.variant=2`) is based on the same data as SWO but uses a different approach for quantifying site productivity. Whereas SWO uses water holding capacity, this Variant uses temperature and precipitation (growing season) to power growth forecasts. We essentially employed the lightsum approach in developing primary predictive equations (Mason et al., 2011). The only modified growth functions in this variant are for Douglas-fir and ponderosa pine. At this time there are no functions for competing vegetation.

At this point in time the hybrid variant should be viewed as a prototype as it is largely untested.

4.4 CIPS Variant

The CIPS/VMRC variant (`set.variant=3`) was developed to simulate the response of young Douglas-fir trees in western Oregon and Washington to varying levels of competing vegetation (Figure 5). The modeling database was drawn from the Vegetation Management Research Cooperative (VMRC) and the Pacific Northwest Research Station. Growth data were from 16 different sites distributed among six different studies. There were four VMRC data sets: the Critical Period Threshold Study (CPT) (Maguire et al., 2009), the HERB1 study (Rose and Rosner, 2005), Evaluating Common Regimes (ECR), and Two Meters in Two Years (TMTY). Data from two additional studies, the Matlock/Moalla field trials, and the CRAFTS B study, were provided by PNW Reasearch Station. This variant also uses site index (Flewelling et al., 2001).

Growth trends described by this database represented responses to a wide range of experimentally manipulated levels of competing vegetation. The field trials were designed specifically to test the efficacy of different intensities of competing vegetation control on Douglas-fir growth and survival. The database included 102,573 observations on 15,821 trees from 354 plots. Initial tree heights ranged from 0.3 feet to 13.6 feet.

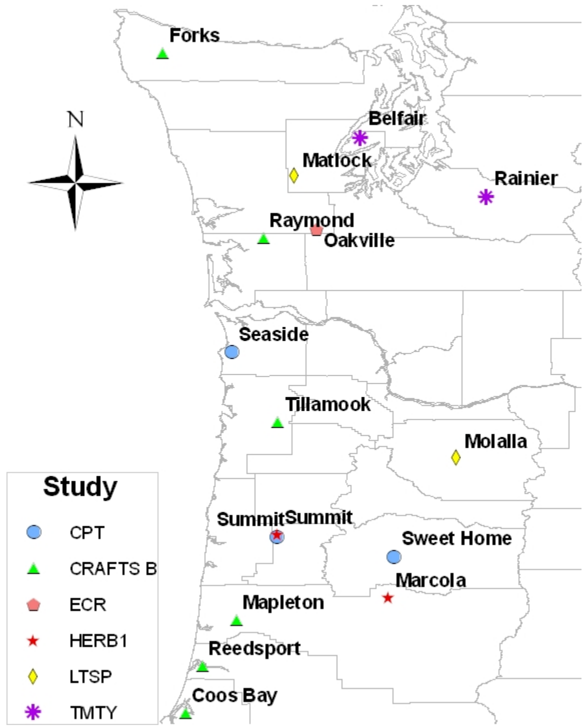

Figure 5: Plot locations for CIPS/VMRC variant of CONIFERS.

The field trials from which data were compiled to construct the CIPS/VMRC equations were large and often complex study designs, so only a limited number of sites were represented. Site quality was generally higher than average for the region, but the geographic range was similar to that of the database for the SMC variant of CONFERS.

The CIPS/VMRC variant was made possible by financial support from the Center for Intensive Planted-Forest Silviculture (CIPS) and generous contribution of data and expertise from Robin Rose, Eric Dinger and Tim Harrington. similar to that of the database for the SMC variant of CONIFERS (Figure 5).

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Appendix

A1. Plants Data

1. plot = Plot number (positive integer value)
2. sp.code = Species Code (text string) e.g. "DF" or "WF"
3. d6 = basal diameter (inches)
4. dbh= breast height diameter (inches)
5. tht = total tree height (feet)
6. cr = live crown ratio, crown length divided by total tree height
7. n.stems = number of stems per plant
8. expf = expansion factor (plants per acre represented by this tree)
9. crown.width = crown width (feet)

The simulator does requires that these values are all present for growth but some may be imputed through the `impute` function supplied with `rconifers`. Height is required input but diameters and crown widths may be imputed.

Species Codes

SWO and SWO hybrid Primary Species Codes in the plants data frame

1. DF = Douglas-fir
2. PP = ponderosa pine
3. WF = white fir
4. SP = sugar pine
5. IC = incense-cedar
6. RF= California red fir
7. WH = western hemlock
8. OC= other conifer
9. PM = Pacific madrone
10. GC = golden chinkapin
11. BM= bigleaf maple
12. TO = tanoak
13. ARPA = greenleaf manzanita
14. CEVE = snowbrush
15. CEIN = deerbrush
16. NS = Not stocked

These and more can be found in `data(species.swo)`
SMC and CIPS Species Codes for the plants data frame plot

1. DF = Douglas-fir
2. CV = competing vegetation
3. NS = Not stocked

SWO hybrid Species Codes for the plants data frame

1. DF = Douglas-fir
2. PP = competing vegetation
3. NS = Not stocked

Note that SWO hybrid does not handle competing vegetation at this time.
NS is used as a placeholder for a plot with no observed plants