

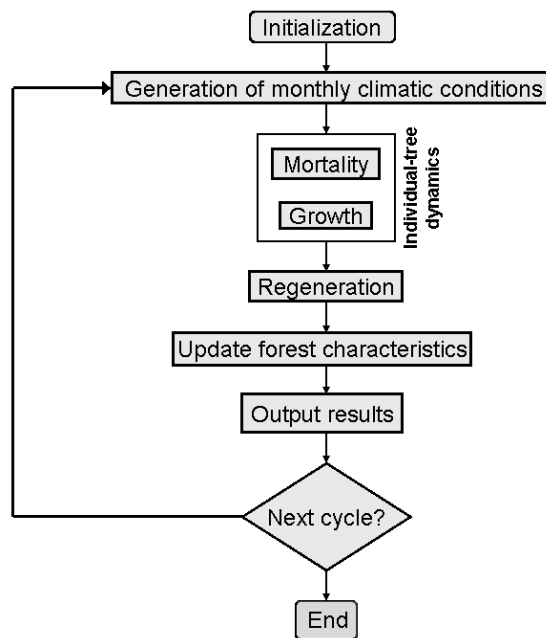
# Gap model ZELIG-CFS – User’s guide

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This user guide includes three appendices that describe applications related to ZELIG-CFS: (1) the program *ZELIG-Create\_Input\_Files.exe* to create input files (Appendix 2), (2) the program *ZELIG-Fertility\_Factor.exe* to estimate the fertility factor (Appendix 3) and (3) the program *PartialCut\_ZELIG-CFS.exe* to create intervention files for the simulation of partial cuts (Appendix 4).

ZELIG-CFS is a succession model (gap type) that represents the main processes of individual-tree and stand growth, including light interception, competition and environmental constraints on growth, regeneration establishment and mortality:



As it has a mechanistic basis, ZELIG-CFS possesses the appropriate model components to simulate the development of uneven-aged mixed forest types with complex structures. Input (Initialization) files to run simulations with ZELIG-CFS include species-specific ecological properties, monthly mean temperatures and precipitations, soil texture, species-specific potential annual germination rate (number of seedlings per m<sup>2</sup> and stocking), and list of tree numbers,

species code and dbh. New model components have been included to simulate the effects of climate change, including changes in mean monthly temperature and precipitation and increase in atmospheric CO<sub>2</sub>. More information about ZELIG-CFS may be found in Larocque et al. (2011), Elzein et al. (2020), Larocque and Bell (2021) and Searle et al. (2021).

The file “AmericanC\_Input\_RCP4\_5.csv” included on this web site is an example of a typical input file to run ZELIG-CFS. All the variables in the first line of this input file are defined in Appendix 1. Every input file may contain input data for several sample plots. The simulations for each sample plot are executed sequentially. The program *Zelig\_Create\_Input\_Files.exe* is used to create input files for ZELIG-CFS (see Appendix 2 for a description).

The simulations performed using ZELIG-CFS are managed by AMSIMOD, which is also available on this web site, along with a user’s guide (see *AMSIMOD\_User\_Guide\_Version\_8.pdf*). Models managed by AMSIMOD are defined within projects. An example of a project file can be seen on Figure 1.

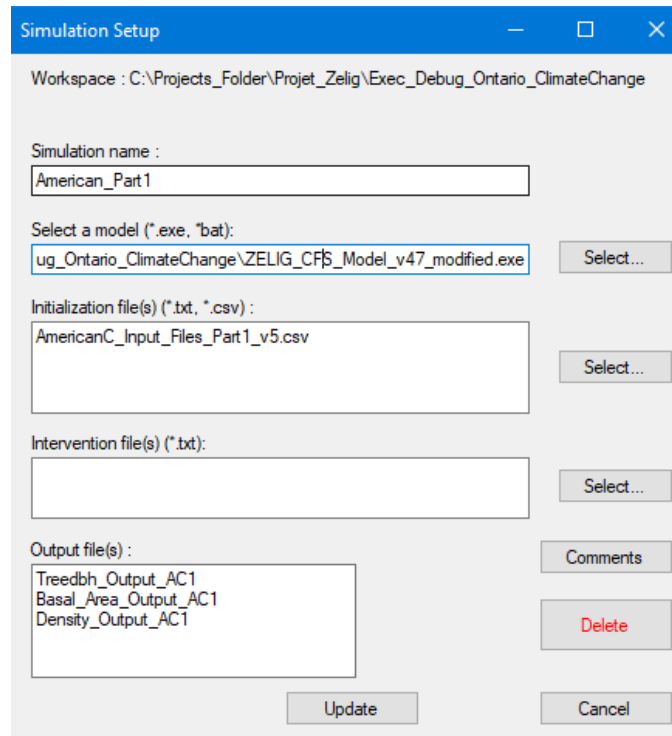


Figure 1: Window in an AMSIMOD project to enter or edit the different names of the files necessary to run ZELIG-CFS.

In the example of Figure 1, there are different edit fields to enter the name of the model, the input (initialization) file, the intervention file (if necessary) and simulation result text file(s) (the extension .txt is added automatically by AMSIMOD). The result files listed in the example of Figure 1 contain three types of simulation results:

- Treedbh\_output\_AC1.txt: Individual-tree growth results grouped by sample plot, species and simulation year;
- BasalArea\_Output\_AC1.txt: Basal area results grouped by sample plot, species and simulation year;
- Density\_Output\_AC1.txt: Number of trees grouped by sample plot, species, dbh class and simulation year;

### **Literature cited**

- Elzein, T., G.R. Larocque, L. Sirois and D. Arseneault, 2020. Comparing the predictions of gap model with vegetation and disturbance data in south-eastern Canadian mixed forests. *For. Ecol. Manage.* 455:117649.
- Larocque, G.R., L. Archambault and C. Delisle, 2011. Development of the gap model ZELIG-CFS to predict the dynamics of North American mixed forest types with complex structures. *Ecol. Modell.* 222:2570-2583.
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- Searle, E.B., F.W. Bell, G.R. Larocque, M. fortin, J. Dacosta, R. Sousa-Silva, M. Mina and H.D. Deighton.2021. Simulating the effects of intensifying silviculture on desired species yields across a borad environmental gradient. *Forests* 12: <https://www.mdpi.com/1999-4907/12/6/755>

**Appendix 1:** Definitions of the most important variables included in a typical input file to perform simulations with ZELIG-CFS.

Variable	Definition
Aire_observation	Name of the area where simulations are conducted
ParcNum	Plot number
ParcID	Plot identification (used to distinguish the different plots in an input file)
PlotArea	Area of the sample plot.
Plotshape	shape of a sample plot
LAT	Latitude
LONG	Longitude
Altitude	Altitude
NbYears	Number of years in the simulation
IntervalPrintout	Interval between printouts
AnTempInc	Annual increase in temperature (Deg. C)
AnChgPrecPrec	Annual change in precipitation (%)
CO2Level	Current CO <sub>2</sub> concentration (ppm)
ChgCO2ppm	Annual change in CO <sub>2</sub> (ppm)
NumYearsCO2Effects	Number of years of CO <sub>2</sub> effects
FieldCap	Field capacity (cm of water at 0.1 bar).
WiltPoint	Wilting point (cm of water at -15.0 bar)
SoilFert	Soil fertility expressed as maximum annual above-ground woody formation (Mg ha <sup>-1</sup> year <sup>-1</sup> )
Tjanvier to TDecembre	Average monthly temperatures (Deg. C)
TSDJanvier to TSDDecembre	Standard deviations for average monthly temperatures
Pjanvier to PDecember	Monthly precipitations (cm)
PSDJanvier to PSDDecember	Standard deviations for monthly precipitation
Seed	Potential number of seedlings per m <sup>2</sup> that originate from natural regeneration
Stocking	Proportion of the area that the seedlings of a species can occupy
Species	Species code used by ZELIG-CFS. They are converted to full name in the output files.
Dbh(cm)	Diameter at breast height (cm) of the trees in a sample plot

## **Appendix 2:** Program *ZELIG\_Create\_Input\_Files.exe* to create input files for ZELIG-CFS.

The program *ZELIG\_Create\_Input\_Files.exe* facilitates the creation of input (aka initialization) files for ZELIG-CFS. Every input file may contain input data for several sample plots. The simulations are run sequentially for each sample plot. It was adapted for different provinces, including Quebec, Nova Scotia, New Brunswick, Ontario and Alberta. Thus, users don't have to convert provincial species-specific codes into ZELIG-CFS species codes, as the conversion is handled by the program. As Canadian provinces, forest companies or other forestry organizations have different procedures or software applications to manage forest data, it would have been unproductive and impractical to develop an application that would meet every particular need. However, the application was developed in such a way that users can easily "copy and paste" tree and climatic data from common applications, such as Excel or Access, directly into the appropriate edit or data fields of the program, as long as each line of data is separated by a "carriage return". Figure 2 shows the main window of *ZELIG\_Create\_Input\_Files.exe*.

### Description of required information and data:

#### 1- Name of the file to create

This is the name of the input file that will be created. This file may contain data for several sample plots. A maximum of 30 alphanumeric characters, including the underscore character ("\_") if necessary, is allowed for the name of the input file. A new file to be created can be saved any folder and in two formats: ".csv" or ".txt", but the default format is ".csv".

#### 2- Forest area name

This is the name that identifies the area where a sample plot is located. Examples are "Mauricie", "Brightsand" or "FallingSnow". Alphanumeric characters are allowed, as well as the underscore character. Several sample plots can belong to the same forest area. The selection of this name is important because it is used as an attribute (stratification variable) for the identification of a sample plot to perform partial cuts or visualize sample plot results.

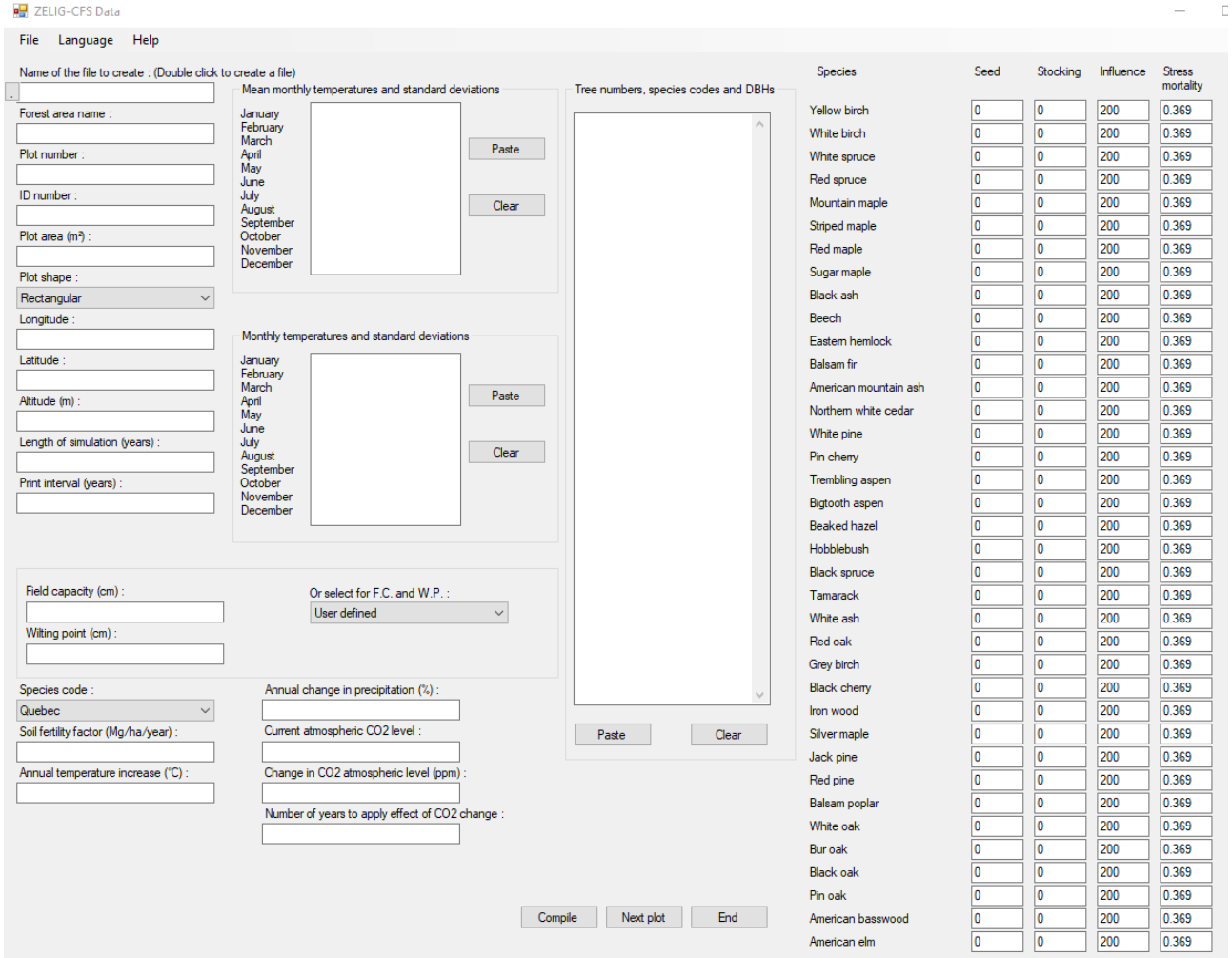


Figure 2: Main interface of the application ZELIG\_Create\_Input\_Files.exe to create input files necessary to execute the model ZELIG-CFS.

### 3- Plot number

For a given forest area, this is a number associated with a sample plot. Only integers are allowed. The same plot number can be used more than once in an input file, but as long as they belong to a different forest area.

### 4- ID number

This number is specific to each sample plot. Only integers are allowed. It is suggested to have a minimum of 4 digits.

#### 5- Plot area and shape

Plot area is entered in squared meter (m<sup>2</sup>). Two choices are possible for shape: rectangular or circular.

#### 6- Longitude, latitude and altitude for sample plots

For minutes and seconds for longitude and latitude, the information must be converted into decimals. If the information is not available, just enter “0.0”.

#### 7- Length of simulation (years)

For instance, 100 for 100 years. Decimals are not allowed because the simulation time cycle is one year.

#### 8- Print interval (year)

This information indicates the number of years between which data are stored in output files. For instance, the number “5” indicates that the results will be recorded every 5 years. Even though the simulation time cycle of ZELIG-CFS is annual, setting up a print interval value greater than the ZELIG-CFS time cycle may save considerable storage space on disk when many plots are simulated over a long time period.

#### 9- Field capacity and wilting point

The two values are expressed in centimeters. If these two values are not available, it is possible to indicate the following classes :

- Sand
- Sandy loam
- Loam
- Silt loam
- Clay loam

Values associated with each class will appear on the left.

#### 10- Species code (province)

Indicate the province where the sample plot data are located. The program will automatically convert species-specific provincial codes into ZELIG-CFS species codes.

#### 11- Fertility factor (Mg/ha/year)

This value is an estimate of maximum above-ground woody biomass productivity and is used to evaluate relative soil fertility. The program *ZELIG\_Fertility\_Factor.exe* (see Appendix 3) can be used to compute this number, which can be estimated using similar stand data, within the same region, that have not been affected by any disturbance.

#### 12- Effects of climate change

As previously mentioned, ZELIG-CFS can simulate the effects of climate change. The following information must therefore be provided in specific edit fields:

- Annual Temperature increase ((°C)
- Annual change in precipitation (%)
- Current atmospheric CO<sub>2</sub> level (ppm)
- Change in CO<sub>2</sub> atmospheric level (ppm)
- Number of years to apply effect of CO<sub>2</sub> change

This value indicates the length of the duration of CO<sub>2</sub> effects, as current literature suggests that CO<sub>2</sub> increase has a limited time effect.

#### 13- Monthly temperature means and standard deviations and monthly precipitations with standard deviations

Temperature and precipitation data are important for ZELIG-CFS. They can be obtained from local weather stations or Environment and Climate Change Canada. They can also be obtained from BioSIM (see <https://cfs.nrcan.gc.ca/projects/133> and [ftp://ftp.cfl.forestry.ca/regniere/software/ BioSIM/](ftp://ftp.cfl.forestry.ca/regniere/software/BioSIM/)). For realistic representation of normal variations in temperature and precipitations, it is suggested to use data for at least a 30 year period to compute means and standard deviations.

Data in a text file or an Excel sheet can be copied and pasted (Figure 3). (If there is an error, it is possible to clear the data and copy and paste them again). If data are copied from a text file,



the temperature and precipitation values and the standard deviation for each month must be separated by a space.

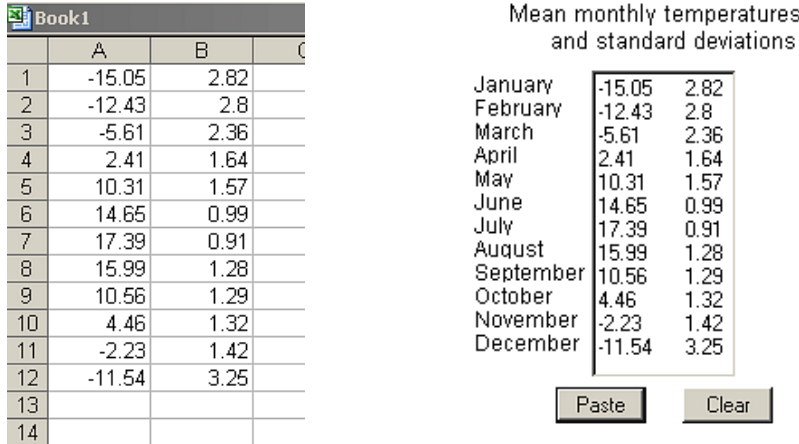


Figure 3: Illustration of the procedure to copy and paste data from a spreadsheet to *Zelig\_Create\_Input\_Files.ex*.

#### 14- Tree numbers, species codes and Dbh values (cm)

The procedure to enter data is the same as the procedure for temperature and precipitation, except that 3 columns of data must be entered: tree number, species code and dbh (cm). Data are copied and pasted from a text file or a spreadsheet. It is possible to clear the data and copy and paste them again. Tree numbers, species codes and dbh values must be separated by a space if they are copied and pasted from a text file.

#### 15- Data on potential germination rate, stocking, zone of influence and stress mortality

For each species listed on the right hand side of the main form, it is possible to enter data on potential germination rate (seed), stocking, zone of influence and stress mortality. (For now, it is not necessary to enter influence zone and stress mortality data. These two attributes were added for future developments). Germination rate (seed) is the number of seedlings per m<sup>2</sup> that can be expected in a given forest ecosystem. It is a potential number that can be estimated from regeneration data. Examples of realistic numbers are 0.0175, 0.028 or 0.44, which correspond to 175, 280 or 4,400 seedlings per ha. In the simulations, germination rates will be affected by light conditions at the soil level. For instance, in understory shade conditions, a shade tolerant species

such as sugar maple can have a high germination rate. On the other hand, a shade intolerant species, such as trembling aspen, can germinate well on open-fields or in gaps under full sunlight. The number of seedlings generated annually in the simulations eventually join the tree cohort, but the transition rate can be influenced by seedling mortality rate.

Stocking is the proportion of space occupied by the seedlings of a species. It varies between 0 and 1. When all the species are considered within a forest, stocking differences can be substantial. For instance, sugar maple sometimes occupy large areas within a forest. So, its stocking value may be very high, close to 1. Other species, such as yellow birch, occupy a small proportion of space, with a stocking that can be as low as 0.1.

Regeneration values are provided only for species that can potentially germinate and grow within a species-specific forest ecosystem.

Once all the data and information are entered, click on «Compile». The program will process the sample plot data. It is important to read the messages at the bottom left of the main window. If there are errors, specific error messages are displayed. If there are no error messages, click on “Next Plot”. All the edit and data fields will be initialized for another sample plot data entry session. When the data for all sample plots are entered, click on “End”. The file name with the extension (“.cvs” or “.txt”) provided when “Create\_InputFiles\_ZELIG-CFS.exe” was launched is created.

**Appendix 3:** Program *ZELIG\_Fertility\_Factor.exe* to estimate the Fertility factor.

One of the inputs required by ZELIG-CFS is a fertility factor (Mg/ha/year). This number is an estimate of potential biomass productivity for tree species in forest ecosystems. The program *ZELIG\_Fertility\_Factor.exe* can be used to compute this number. For each forest type, stand data from undisturbed forests located in the same region can be used. However, it is not necessary to estimate this value for each ecosystem under study, just for representative ecosystems.

*ZELIG\_Fertility\_Factor.exe* was adapted for Quebec and Ontario. So, users don't have to convert provincial species-specific codes into ZELIG-CFS species codes, as the conversion is handled by the application.

Description of required information and data:

1- Name of the file to create

Biomass productivity estimates will be saved in this file. This file may contain data for several sample plots. A maximum of 30 alphanumeric characters, including the underscore character “\_”, are allowed. When you click “Create”, you may save the file in two formats, .csv or .txt, in any folder.

2- Forest area name

This is the name that identifies the area where a sample plot is located. Examples are “Mauricie”, “Brightsand” or “FallingSnow”. Alphanumeric characters are allowed, as well as “\_”. Several sample plots can belong to the same forest area.

3- Plot number

For a given forest area, this is a number associated with a sample plot. Only integers are allowed. The same plot number can be used more than one time in a driver file, but as long as they belong to different forest areas.

#### 4- Plot area

Plot area is entered in square meter (m<sup>2</sup>).

#### 5- Species code (province)

Indicate the province where the data come from. The species codes will be translated by the application.

#### 6- Tree numbers, species codes and DBHs (cm)

Data can be copied and pasted from a text file or a spreadsheet (Figure 4). It is possible to clear the data and copy and paste again. If data are copied from a text file, tree numbers, species codes and dbh must be separated by a space (e.g., no comma or any other character).

#### Final steps

Once tree data are entered for a sample plot, click on “Compute” to estimate the fertility factor. It is important to read the messages in the middle of the left-hand side of the main window. If there are errors, specific error messages will be displayed. If there is no error message, click on “Next sample plot” to process another dataset or sample plot. All the edit boxes will be initialized for another sample plot data acquisition.

H	I	J
1	SAB	7.6
2	THO	7.6
3	THO	5.1
4	THO	5.1
5	THO	10.2
6	THO	10.2
7	SAB	5.1
8	SAB	7.6
9	SAB	7.6
10	THO	5.1
11	SAB	25.4
12	THO	5.1
13	EPR	5.1
14	EPR	5.1
15	EPR	5.1
16	EPR	5.1
17	EPR	5.1
18	BOP	12.7
19	BOJ	25.4
20	BOJ	5.1
21	BOP	7.6
22	BOP	7.6
23	BOP	7.6
24	BOP	5.1
25	BOP	7.6
26	BOP	10.2
27	BOP	5.1
28	BOP	12.7
29	BOP	12.7
30	BOJ	7.6
31	BOJ	7.6
32	BOJ	12.7
33	BOJ	12.7
34	EPR	7.6
35	BOP	7.6
36	SAB	17.8
37	SAB	5.1

Tree numbers, species codes and DBHs (cm)

1	SAB	7.6
2	THO	7.6
3	THO	5.1
4	THO	5.1
5	THO	10.2
6	THO	10.2
7	SAB	5.1
8	SAB	7.6
9	SAB	7.6
10	THO	5.1
11	SAB	25.4
12	THO	5.1
13	EPR	5.1
14	EPR	5.1
15	EPR	5.1
16	EPR	5.1
17	EPR	5.1
18	BOP	12.7
19	BOJ	25.4
20	BOJ	5.1
21	BOP	7.6
22	BOP	7.6
23	BOP	7.6
24	BOP	5.1
25	BOP	7.6
26	BOP	10.2
27	BOP	5.1
28	BOP	12.7
29	BOP	12.7
30	BOJ	7.6
31	BOJ	7.6
32	BOJ	12.7
33	BOJ	12.7
34	EPR	7.6
35	BOP	7.6
36	SAB	17.8

Figure 4: Illustration of the procedure to copy and paste tree data from a spreadsheet to *ZELIG\_Fertility\_Factor.exe*.

**Appendix 4:** program *PartialCut\_ZELIG-CFS.exe* to simulate partial cuts

ZELIG-CFS can simulate the effects of partial cuts on species-specific tree and stand growth and succession. The program *PartialCut\_ZELIG-CFS.exe* is used to develop partial cut scenarios for simulation with ZELIG-CFS. The input file consists of a tree list containing simulation results from ZELIG-CFS. A good example of an input file is *Treedbh\_Output\_Example.txt*, which is included on this web site. Normally, this file is located in a result folder of a project. Figure 5 shows the main window that appears when the program is launched.

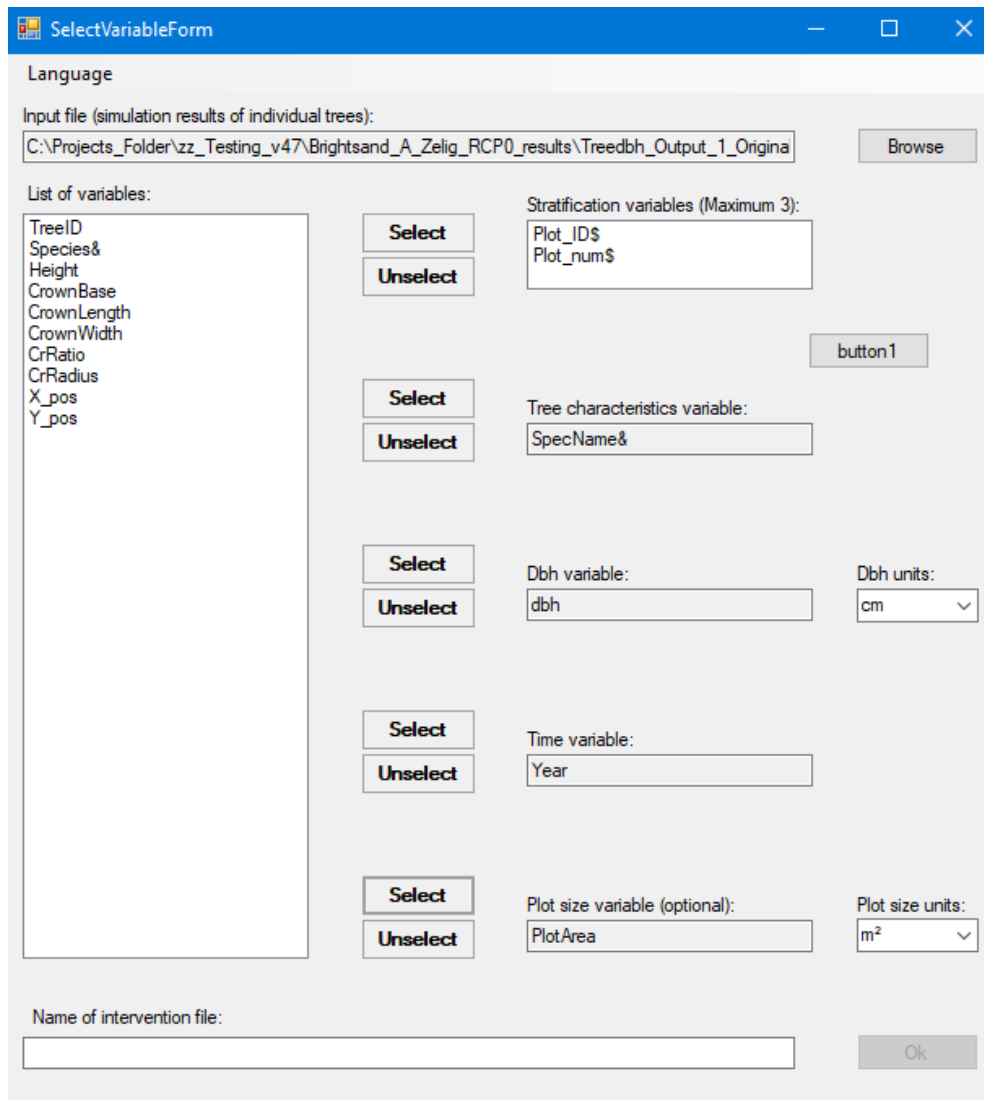


Figure 5: Main window of the program *PartialCut\_ZELIG-CFS.exe* that appears when it is launched.

The tree list must include one or two stratification variables to identify and differentiate sample plots (Plot\_ID\$ and Plot\_num\$ in Figure 5), a category variable to identify the tree characteristic variable (SpecName& in Figure 5. Species& could have been selected as well), a variable that represents dbh values (dbh), a variable to identify the time variable (Year) and a variable that contains the area of sample plots (PlotArea).

The final information to enter is the name of the output file that will contain the scenario of partial cuts. It is preferable to save this file in the same folder that contains the input file to execute ZELIG-CFS. Once the information is provided, a click on the *Next* button launches a second window to provide the rules of partial cut (Figure 6).

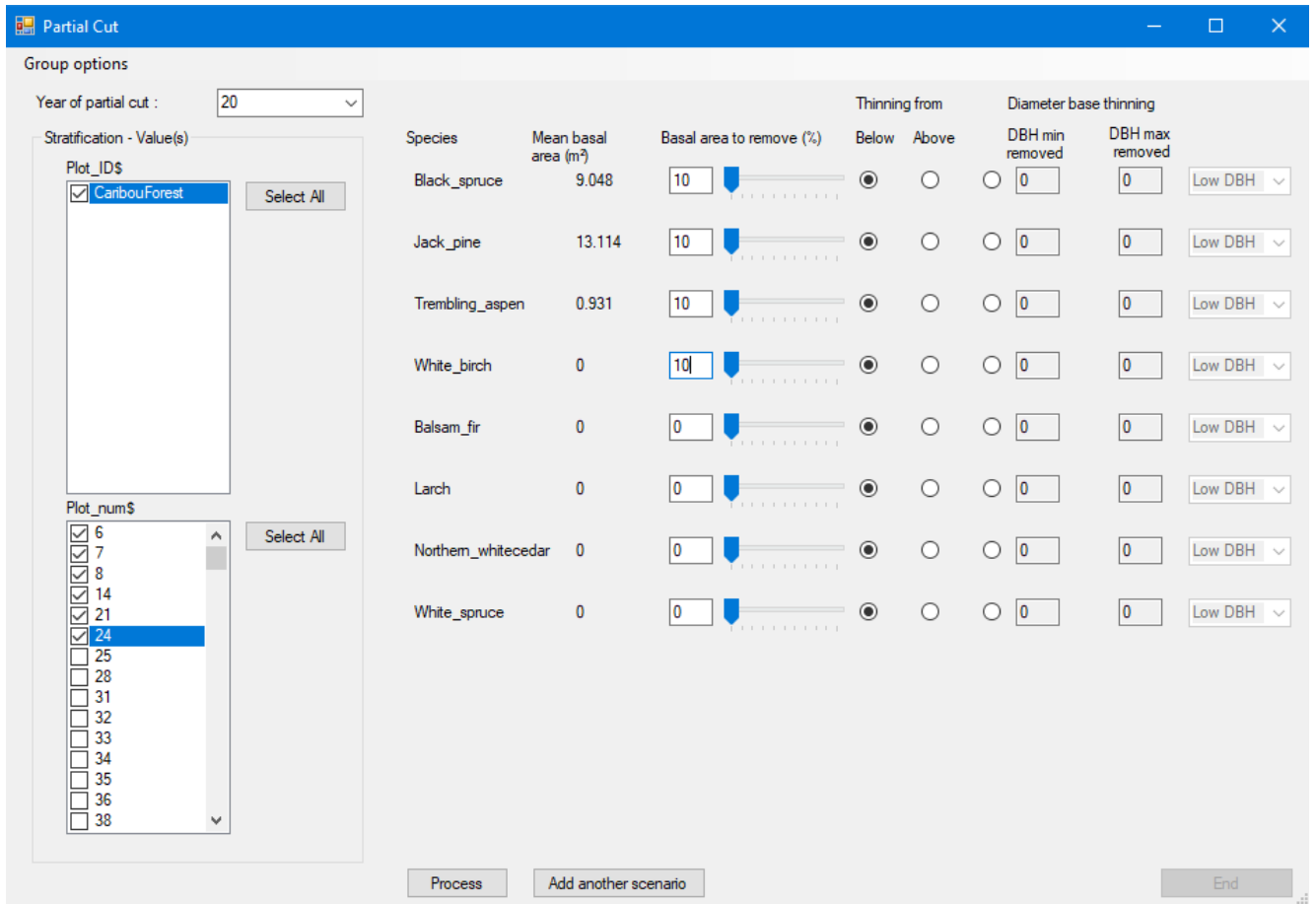


Figure 6: Second window of the program *PartialCut\_ZELIG-CFS.exe* to define the partial cut rules.

The program *PartialCut\_ZELIG-CFS.exe* allows the selection of specific sample plots on which to perform partial cuts. In the example of Figure 6, sample plots selected for the application of partial cuts are chosen by clicking on specific Plot\_ID\$ and Plot\_num\$. (In the example of Figure 6, there is only one Plot\_ID\$, but here could be several of them). Once the sample plots are selected, the age to perform partial cut must be specified in the box *Year of partial cut*. Then, the basal area for each species is computed and is shown under the heading *Basal area*. If only one sample plot is selected, the basal area that is computed is applicable for this sample plot. If several sample plots are selected, the average basal area values are computed for each species found in the different sample plots. Information on the rules of partial cut, which consist of the percentage of basal area to remove and the type of partial cut, including thinning from below or above or the range of dbh values to remove, must be provided. The percentages can be selected by using sliders or entering values in the edit box associated with a species. However, sliders vary between 0 and 50%, but it is possible to indicate values greater than 50% in the associated edit boxes.

Once the rules for selected sample plots are defined, a click on the *Process* button writes in the output file the following information on the rules of partial cut:

- Name of the first stratification variable (Plot\_ID\$ in the example of Figure 6);
- Name of the second stratification variable ((Plot\_num\$ in the example of figure 6);
- Simulation year when the partial cut is performed;
- Species;
- Percentage of basal area to remove;
- Type of partial cut;
- Minimum and maximum values of dbh to remove.

Then, other sample plots can be selected to define other partial cut rules by Clicking the *Add another scenario* button. When there is no more partial cut scenario to define, clicking on the *End* button creates the file for partial cut rules. This file must be included in the box *Intervention file(s)* in an AMSIMOD project.