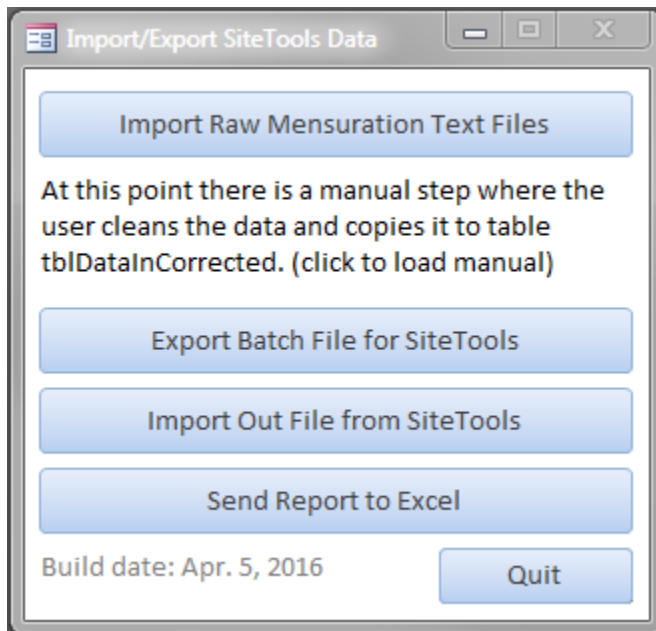


## Working Creating and Working with Batch files for SiteTools.

A step-by-step set of procedures has been created to help you generate site index summaries. The menu is laid out in the order which you will work, from raw files to finished product.



### *Tables included in this database*

tblDataFromSiteTools – this table contains the data that SiteTools output

tblDataIn – contains the data from the raw mensuration files

tblDataInCorrected – there will be errors in the tblDataIn table that need to be corrected. Put your clean data in this table

tblSiteData – this data came from BECMaster28Feb2013\_Env and can be changed by the user. The link to the site index data is the field PlotNumber

tblStandAge – is generated for you by a function in the program

tblTableNames – is a list of tables kept for documenting the data imported. It has no active roll in generating output

### *Importing raw mensuration text files*

Clean files that follow a set format will produce nice clean data. It is best to take the time now to clean your raw data files to the following specifications:

FIZ: 1 to 2

Plot number: 3 to 9

Mensuration ID: 10 to 16

BAF: 17 to 18

Height: 19 to 21

Species: 22 to 23

DBH: 24 to 27

Tree condition: 28

Pathology 1: 29

Pathology 2: 30

Pathology 3: 31

Pathology 4: 32

Pathology 5: 33

Pathology 6: 34

Pathology 7: 35

Columns 19 to 34 are repeated 4 times across the line. i.e. 36 to 53.

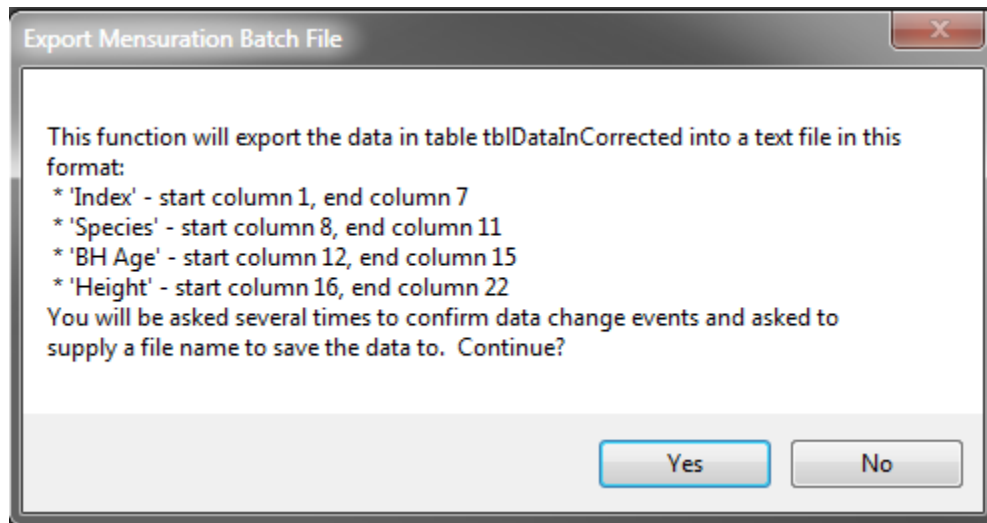
Age: 87 to 90.

### *Cleaning up your imported data*

You're probably not going to catch all the errors in editing the raw files. The data imported from the raw mensuration text files will have errors ranging from misaligned fields to unknown species codes. It is your job to review and correct this data, ensuring that the data is accurate and recognizable by SiteTools. SiteTools is flexible with regards to column start and end specifications, also species lists are customizable in SiteTools. Be careful when working with species codes because these codes determine the site index curves that will be applied to your data. Copy your clean data to the table aptly named "tblDataInCorrected".

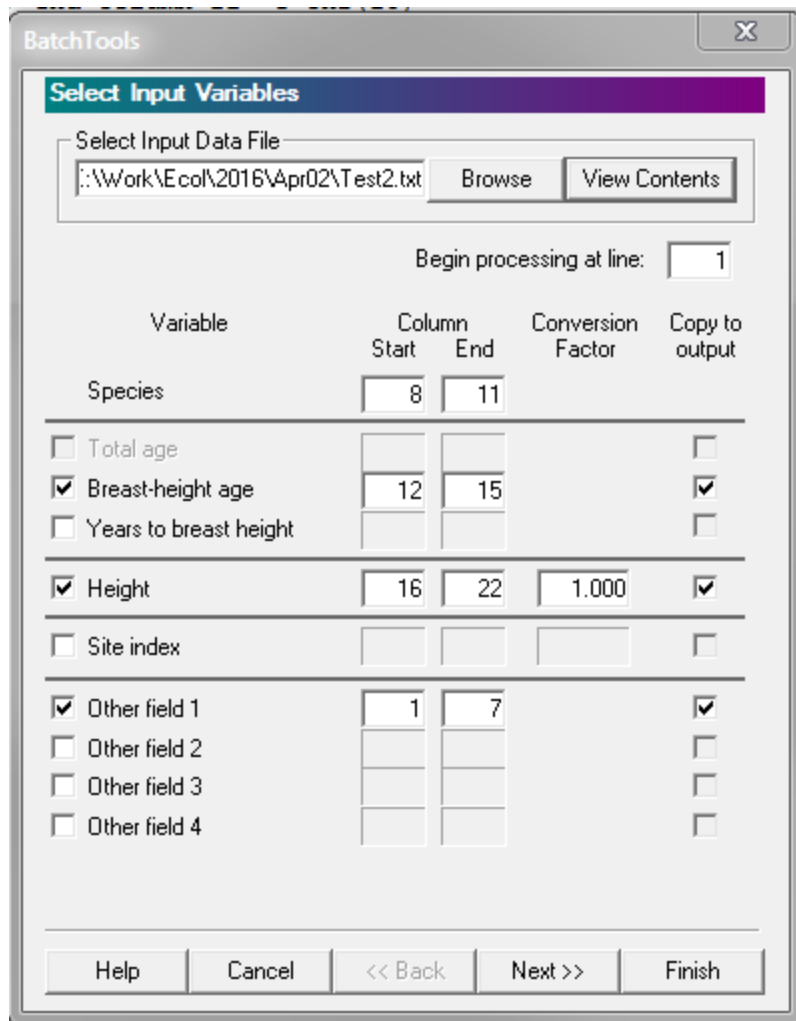
### *Exporting a batch file to SiteTools*

You should now be ready to export your data in a format palatable for SiteTools. Clicking the button will produce a little dialog box stating the format of the file to be exported to the batch file. The index will be automatically generated for you. The BH age is the maximum age found in the plot. Only records that contain species, age and height data will be included in the export.



### Using your batch file in SiteTools

Opening SiteTools (btools.exe) and clicking New in the file menu will get you started. In this first form you will enter the name of the input file you created in the previous step. It is important at this stage not to enter the location of the site index.



The image shows a Windows-style dialog box titled "BatchTools" with a close button (X) in the top right corner. The main title bar is purple and says "Select Input Variables". Below this is a section for "Select Input Data File" with a text box containing "C:\Work\Ecol\2016\Apr02\Test2.txt", a "Browse" button, and a "View Contents" button. Below that is a "Begin processing at line:" label with a text box containing "1". The main area is a table with columns: "Variable", "Column Start", "Column End", "Conversion Factor", and "Copy to output". The table has several rows with checkboxes in the "Copy to output" column. The rows are: "Species" (checked), "Total age" (unchecked), "Breast-height age" (checked), "Years to breast height" (unchecked), "Height" (checked), "Site index" (unchecked), "Other field 1" (checked), "Other field 2" (unchecked), "Other field 3" (unchecked), and "Other field 4" (unchecked). At the bottom are five buttons: "Help", "Cancel", "<< Back", "Next >>", and "Finish".

Variable	Column Start	Column End	Conversion Factor	Copy to output
Species	8	11		<input checked="" type="checkbox"/>
<input type="checkbox"/> Total age				<input type="checkbox"/>
<input checked="" type="checkbox"/> Breast-height age	12	15		<input checked="" type="checkbox"/>
<input type="checkbox"/> Years to breast height				<input type="checkbox"/>
<input checked="" type="checkbox"/> Height	16	22	1.000	<input checked="" type="checkbox"/>
<input type="checkbox"/> Site index				<input type="checkbox"/>
<input checked="" type="checkbox"/> Other field 1	1	7		<input checked="" type="checkbox"/>
<input type="checkbox"/> Other field 2				<input type="checkbox"/>
<input type="checkbox"/> Other field 3				<input type="checkbox"/>
<input type="checkbox"/> Other field 4				<input type="checkbox"/>

After clicking the Next button, you will get the output form. This is the form where you'll enter the site index location. Don't forget to enter the location and name of the output file.

**BatchTools**

**Select Output Variables**

Output Data Filename

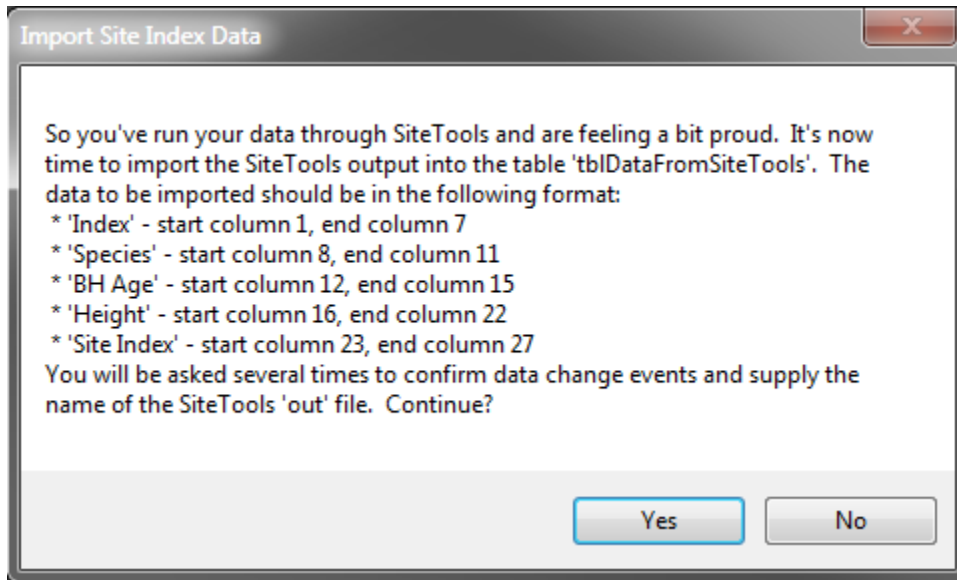
Variable	Column Start	Column End	Conversion Factor
Species	8	11	
<input type="checkbox"/> Total age			
<input checked="" type="checkbox"/> Breast-height age	12	15	
<input type="checkbox"/> Years to breast height			
<input checked="" type="checkbox"/> Height	16	22	1.000
Site index from			
<input checked="" type="checkbox"/> Site index equations	23	27	1.000
<input type="checkbox"/> Growth intercept models			
<input checked="" type="checkbox"/> Other field 1	1	7	1.000
<input type="checkbox"/> Other field 2			
<input type="checkbox"/> Other field 3			
<input type="checkbox"/> Other field 4			

☐ Include header    ☐ Include input file   

Clicking the Finish button will complete your work in SiteTools.

### *Importing the output from SiteTools*

You will again be reminded of what is going to happen. It is important to note that any previous import from SiteTools will be deleted and replaced with the import.



### *Sending your data to Excel*

Okay, you've stuck with it for these past steps and are dying to see the results. Go ahead, click that button.

Zone	SubZone	SiteSeries	Spp	n	Mean SI	SD	SE
BWBS	dk1	01	BL	4	11.43	1.38	0.69
BWBS	dk1	01	SW	12	10.62	1.80	0.52
BWBS	dk1	06	SW	15	8.38	2.48	0.64
BWBS	dk1	07	BL	7	7.38	7.37	2.79
BWBS	dk1	07	SW	7	5.01	1.04	0.39
CWH	mm1	01	BA	11	17.58	5.62	1.69
CWH	mm1	01	HW	4	21.28	1.63	0.81
CWH	mm1	05	BA	26	16.90	4.83	0.95
CWH	mm1	05	HW	5	14.40	4.46	1.99
CWH	mm2	04	BA	9	21.54	2.34	0.78
CWH	mm2	04	HW	6	16.83	2.46	1.01
CWH	vm1	07	BA	6	25.74	2.67	1.09