FFI Workshop – Query Builder and External Data Analysis

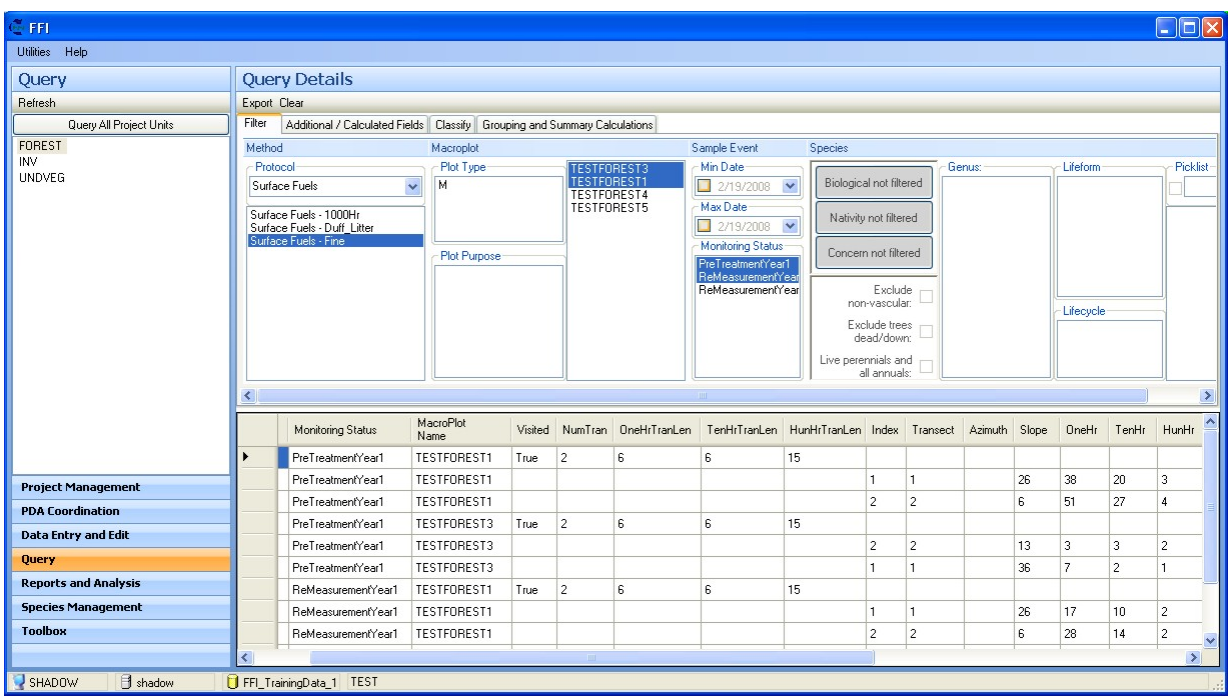
1. FFI – Query Builder: Filtering Data and Adding Fields

The first two tabs on the Query Builder allow users to filter data for the selected sampling method and to add fields from other FFI data tables. Data can be filtered by Macroplot, Monitoring Status, Sample Event, and Species attributes. Fields may be added to the query from the Macroplot, Sample Event, Monitoring Status, and Master Species List tables.

Data for the selected method is displayed in the Query Builder data grid. For each Macroplot and Sample Event, the sample attribute data are displayed in the first row followed by one or more rows of method attribute data.

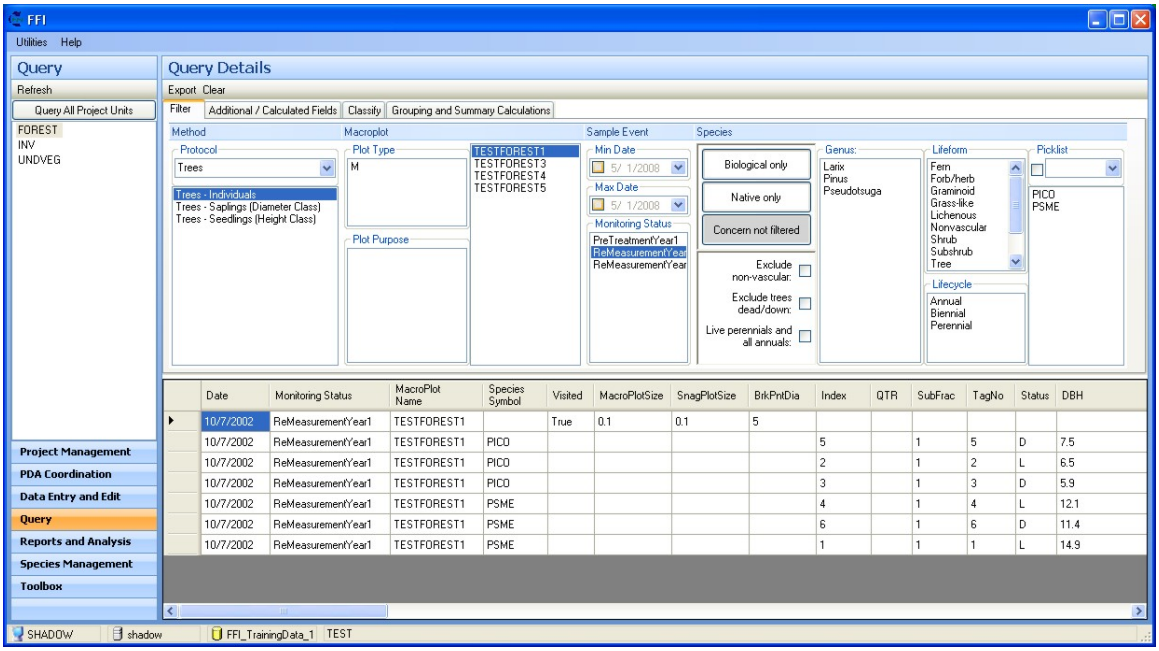
Exercise 1.1: Use Query Builder to view data for the Surface Fuels – Fine method.

1.1a) Select the Surface Fuels Protocol and the Surface Fuels - Fine method on the *Filter* tab. Next, select plots TestForest1 and TestForest3. Select monitoring statuses PreTreatment and ReMeasurementYear1.

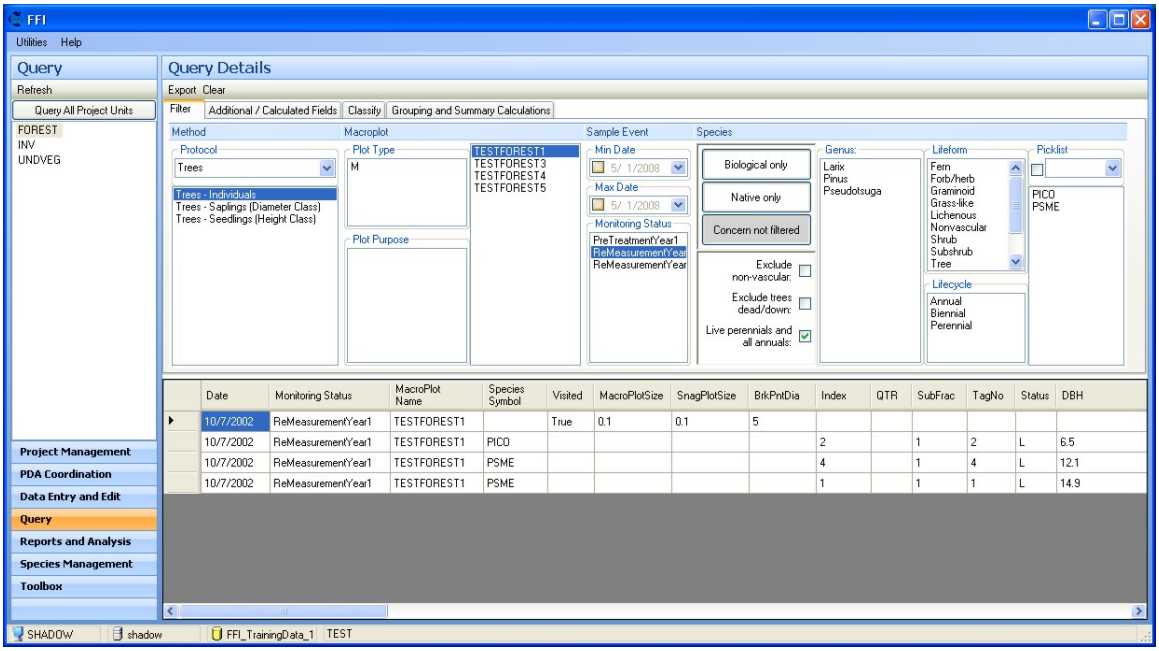


Exercise 1.2: Use Query Builder to view data for the Trees - Individuals method.

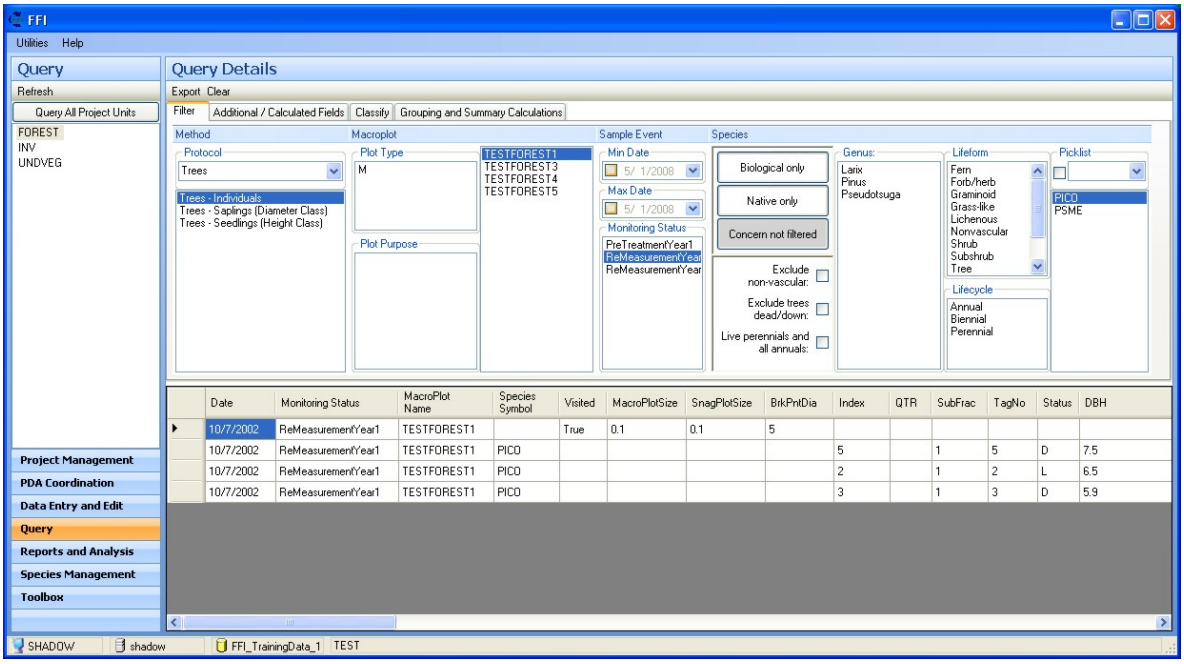
1.2a) Select the Trees protocol and the Trees - Individuals method on the *Filter* tab. Next, select plot TestForest1 and monitoring status ReMeasurementYear1.



1.2b) Check the *Live perennials and all annuals* checkbox. This filters the tree data to display only live trees.

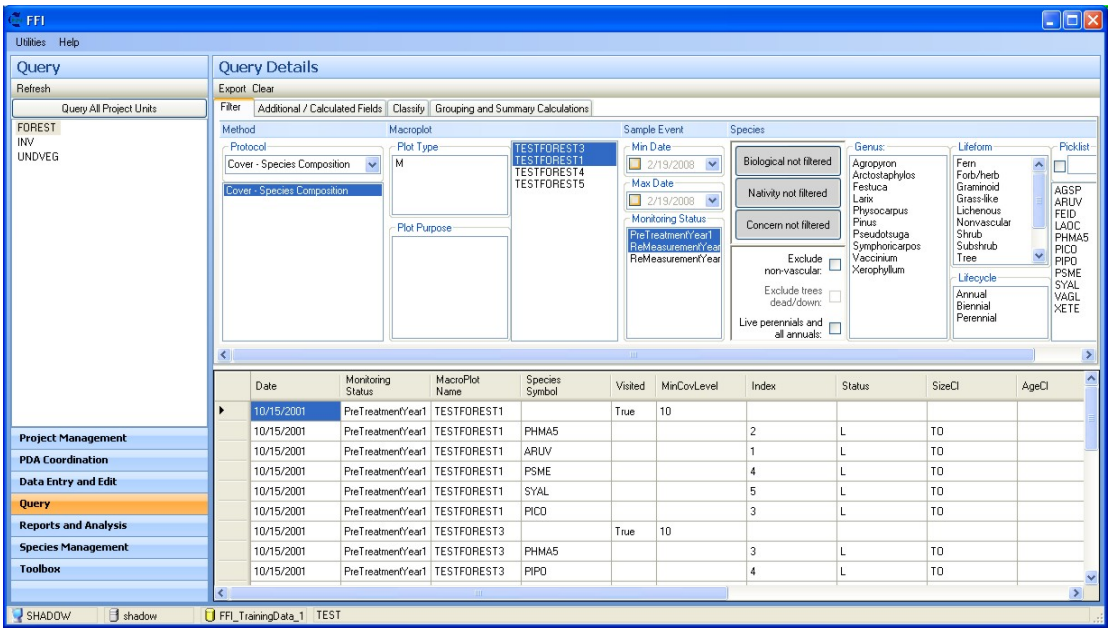


1.2c) Uncheck the *Live perennials and all annuals* checkbox. Select "PICO" in the species list. This filters the tree data to display only data for Lodgepole pine (PICO).

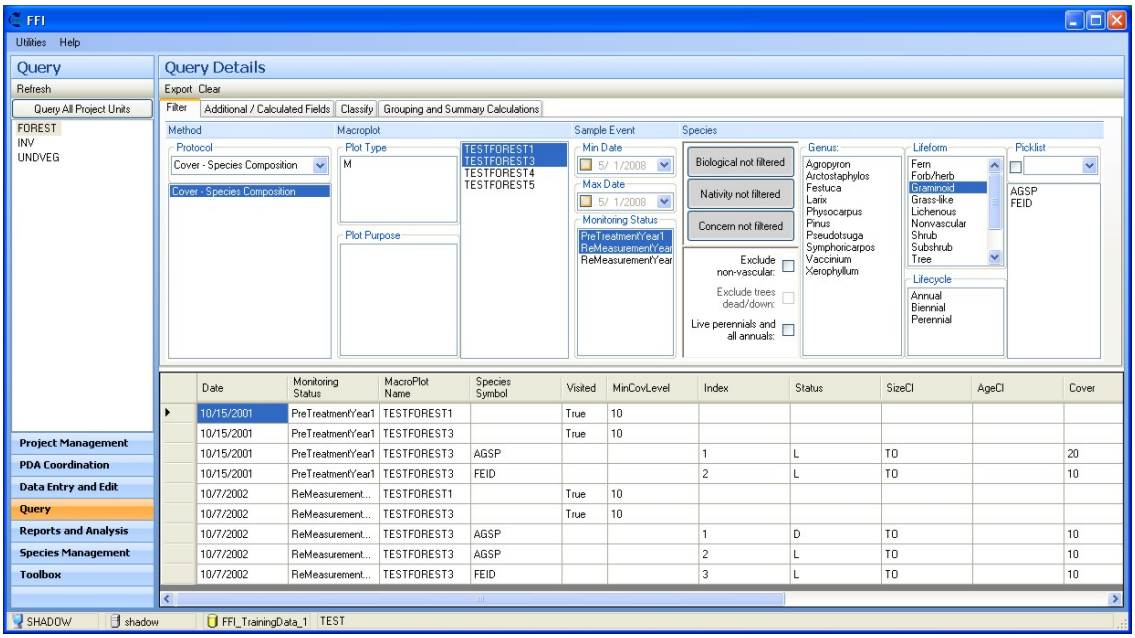


Exercise 1.3: Use Query Builder to view data for the Cover – Species Composition method. Add fields from the macroplot table and master species list to the query.

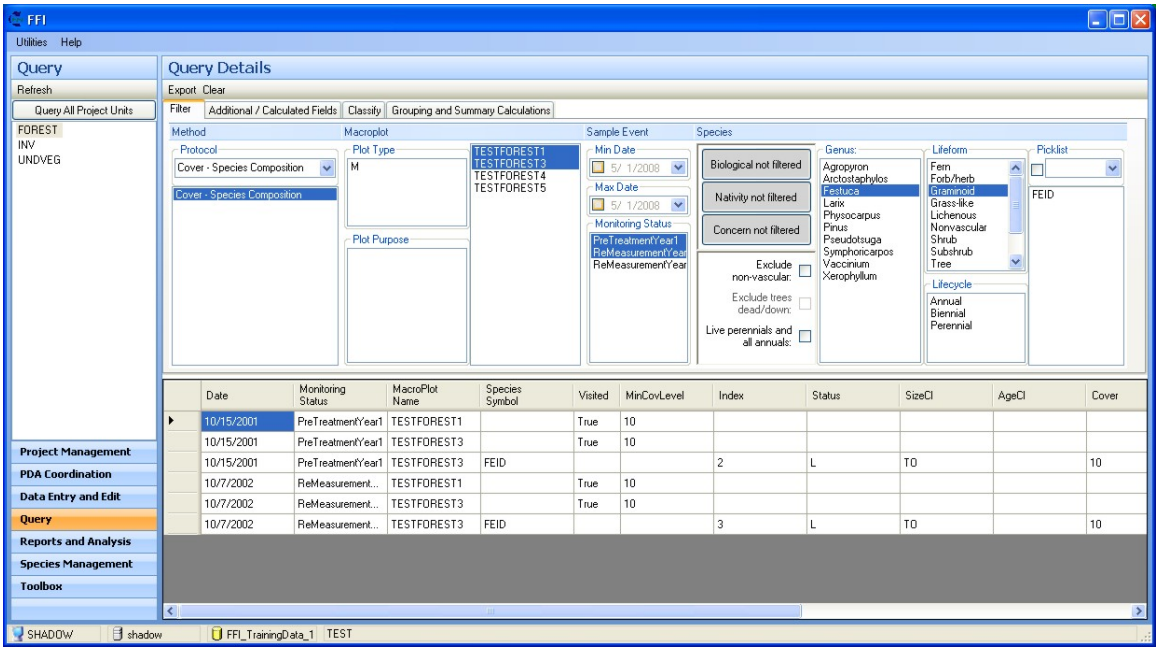
1.3a) Select the Cover – Species Composition protocol and method on the *Filter* tab. Next, select plots TestForest1 and TestForest3 and monitoring statuses PreTreatment and ReMeasurementYear1.



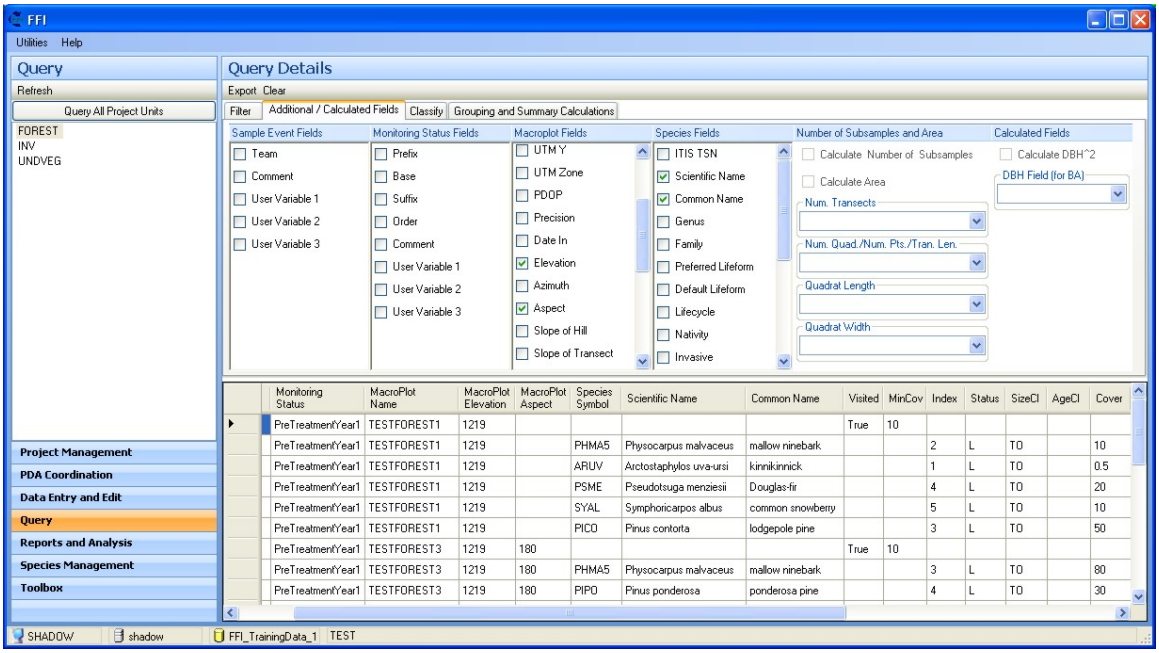
1.3b) Select "Graminoid" in the *Lifeform* list box. This will filter the data to display only graminoids.



1.3c) Select “Festuca” in the *Genus* list box. This will filter the data to display only grasses in the genus Festuca; in this case only *Festuca idahoensis* (Idaho fescue).



1.3d) Unselect “Festuca” and “Graminoid”. Click on the *Additional/Calculated Fields* tab. Add Elevation and Aspect from the *Macroplot Fields*. Add Scientific Name and Common Name from the *Species Fields*.



2. FFI – Query Builder: Calculations

Query Builder provides calculations for density, cover, frequency, and basal area. These calculations work for all the sampling methods provided with the FFI software. They will also work with any new sampling methods created by FFI users provided the new methods contain the appropriate sample and method attributes. Because they offer the flexibility to work with existing and new sampling methods, the query builder calculations require users to input the appropriate fields for each calculation. Users must have some familiarity with how the appropriate sample attributes and method attributes are used to summarize the data.

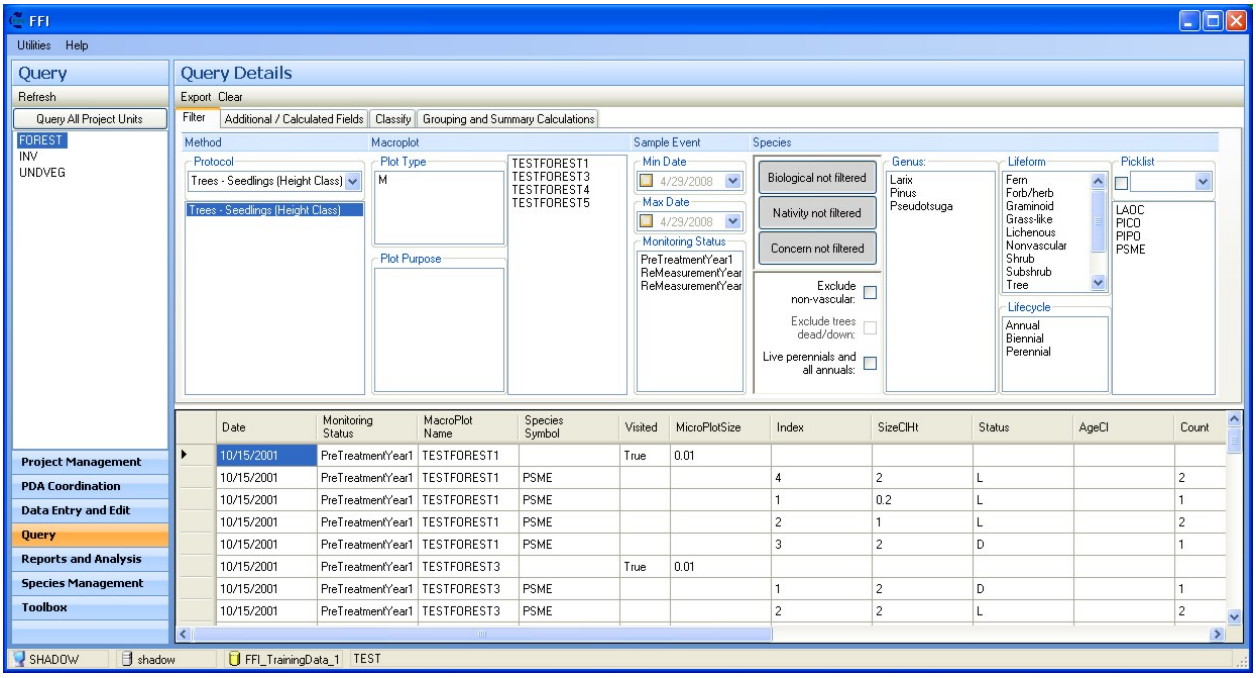
The following exercises provide examples of how to use the calculations for cover, density, frequency, and basal area with various FFI sampling methods. They also emphasize the classification and grouping options in query builder, which offer additional data summary capabilities than are available using the standard data summary reports. Finally, these exercises demonstrate how to export Query Builder data for input into the FFI External Data Analysis Tool. Using Query Builder results with the External Data Analysis Tool allows users to analyze data summarized differently than in the standard data summary reports.

Exercise 2.1: Use Query Builder to calculate seedling density by status (live / dead) using the Trees – Seedlings (Height Class) method. Export the query results as a CSV file.

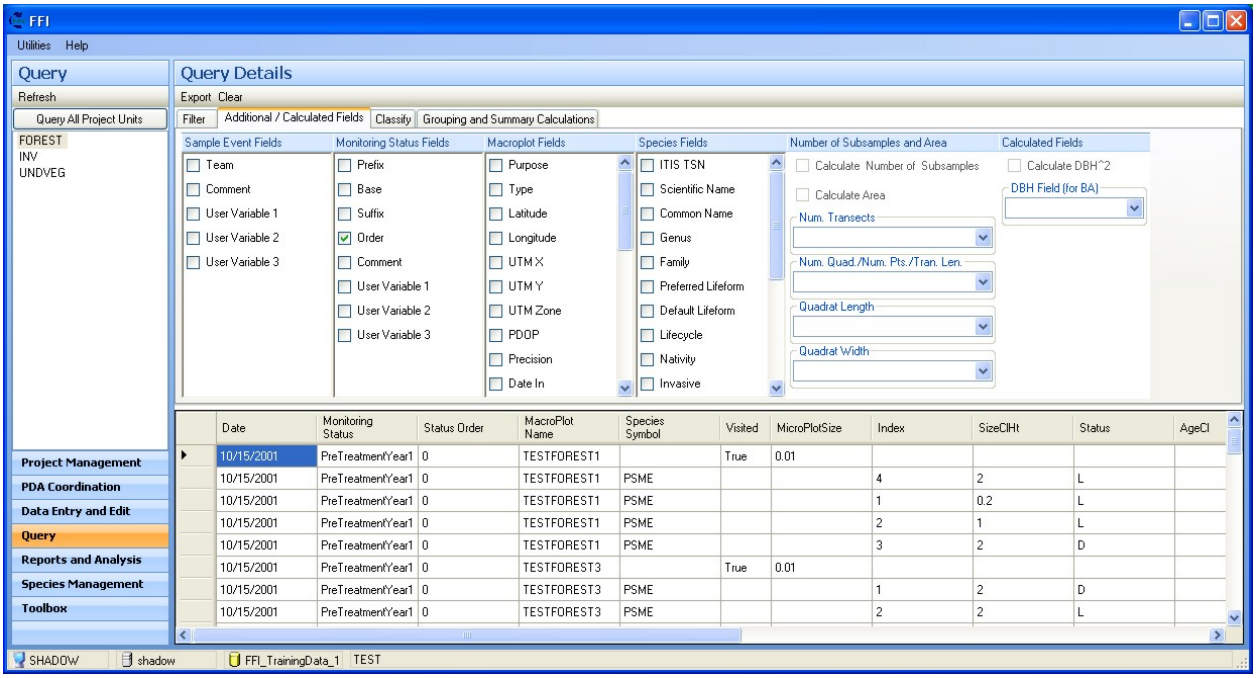
In order to calculate density by status, we first need to group the seedlings by status (live or dead). Next, we must sum the number of seedlings in each

status. Then we can calculate density by dividing the number of seedlings in each status by the area sampled. The area sampled is the macroplot area if grouping data by macroplot and sample event or the sum of macroplot areas if grouping data for multiple macroplots and/or sample events. Finally, we need to provide a conversion factor to display the data in the desired units (per acre or per hectare).

2.1a) Select the Trees protocol and the Trees - Seedlings (Height Class) method on the *Filter* tab.



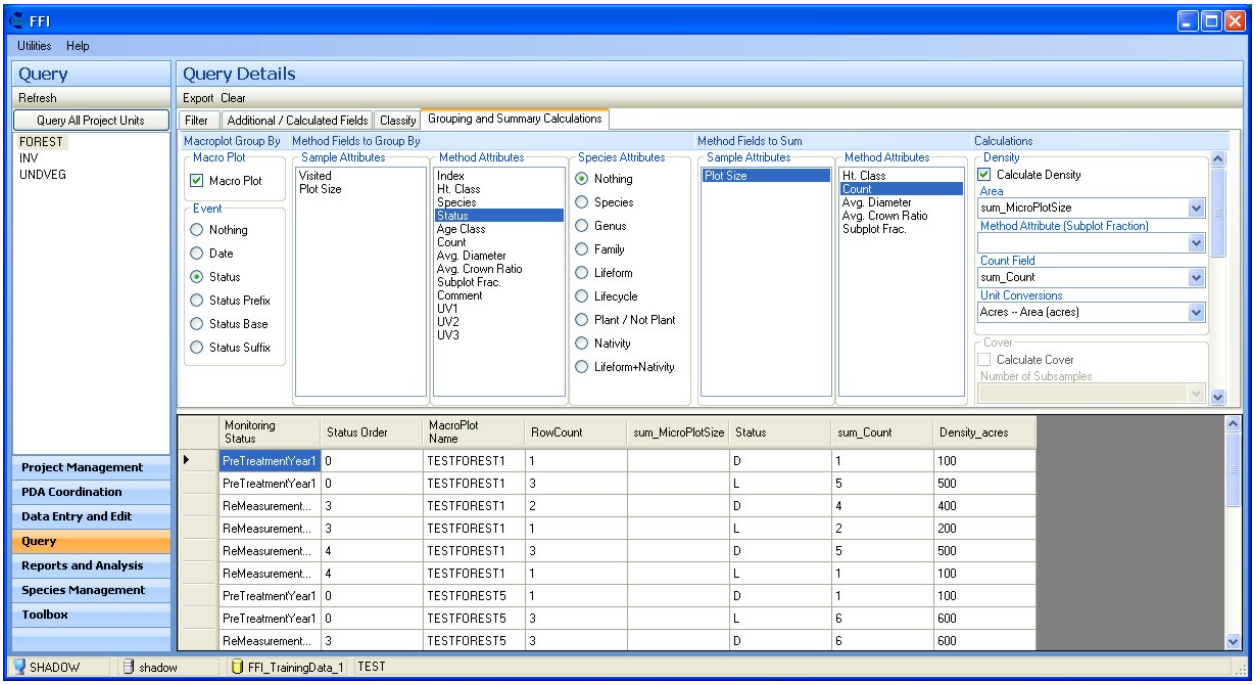
2.1b) Select monitoring status order on the *Additional/Calculated Fields* tab. Monitoring status is necessary when exporting data for input into the FFI External Data Analysis Tool.



2.1c) Calculate density by tree status on the Grouping and Summary Calculations tab. First, group the data by Macroplot and Monitoring Status. Next, group the data by Status (tree status) under *Method Attributes*. Then select Plot Size and Count under *Method Fields to Sum*. These fields are required to perform the density calculation.

Now fill in the appropriate fields for the *Density* calculation text boxes. Select the field “sum_MicoPlotSize” in the *Area* textbox. MicroPlotSize is the sampled area for seedlings for each macroplot and sample event. The *Method Attribute (Subplot Fraction)* is optional here. It is only required when some seedlings are sampled within a fraction of the sampling area. Select “sum_Count” in the *Count Field* text box. This field sums the number of seedlings in each status (live or dead). Finally, select “Acres – Area (acres)” in the *Unit Conversions* text box. This conversion factor will calculate density as the number of seedlings per acre given that the sampling area was recorded in acres. Check the *Calculate Density* checkbox and the density values are added to the data grid.

Export the Query Builder results as a CSV file.

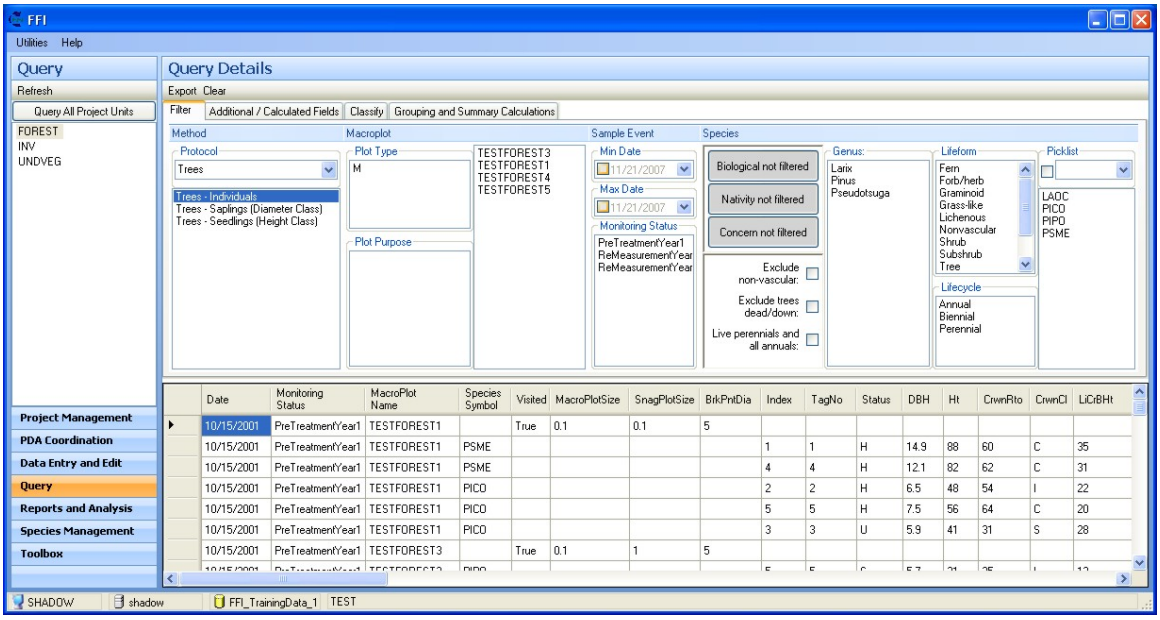


Exercise 2.2: Use Query Builder to calculate basal area by dbh classes using the Trees – Individuals method.

In order to calculate basal area by dbh classes we need to know the dbh^2 value of each tree so we can calculate the basal area of each tree as a constant * dbh^2. The constant is derived from the equation area = $pi*(dbh/2)^2$. The constant differs depending on basal area units (sq. ft. / acre or sq. m / ha) and whether you recorded dbh in inches or cm.

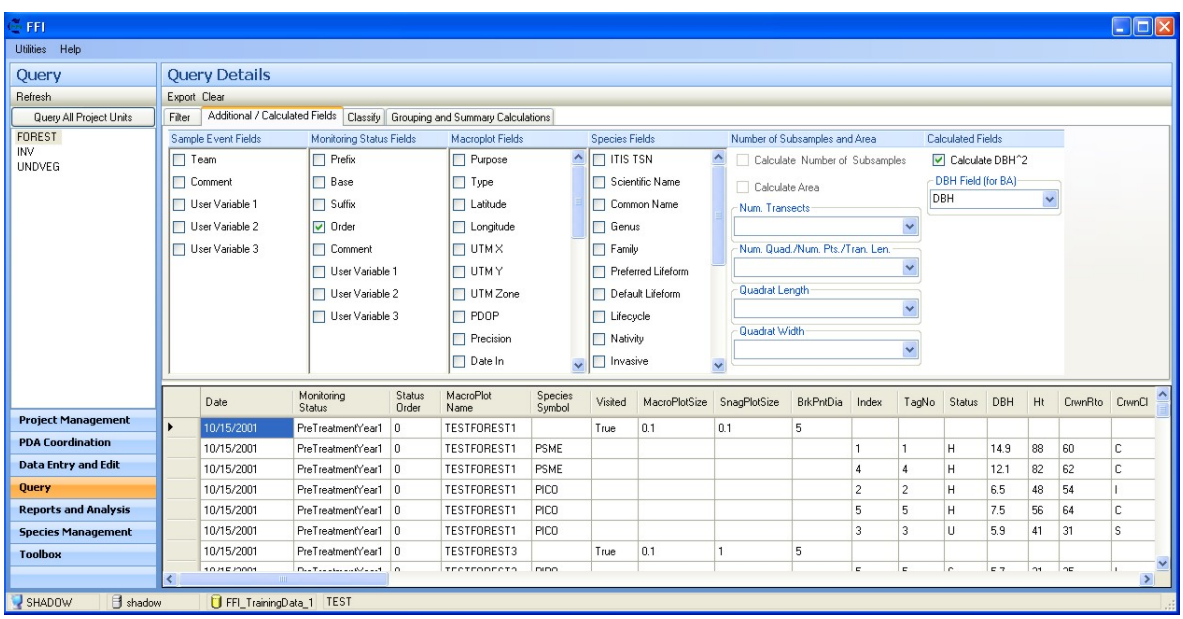
Next we must classify the actual dbh values into our desired classes. Then we can sum the basal area by dbh classes. Now, we can calculate basal area by our dbh classes by dividing the sum of basal area for each dbh class by the area sampled. The area sampled is the macroplot area if grouping the data by macroplot and sample event or the sum of macroplot areas if grouping data for multiple macroplots and/or sample events. Finally, we need to provide a conversion factor to display the data in the desired units (sq. ft. / acre or sq. m. per ha).

2.2a) Select the Trees protocol and Trees-Individuals method on the *Filter* tab.



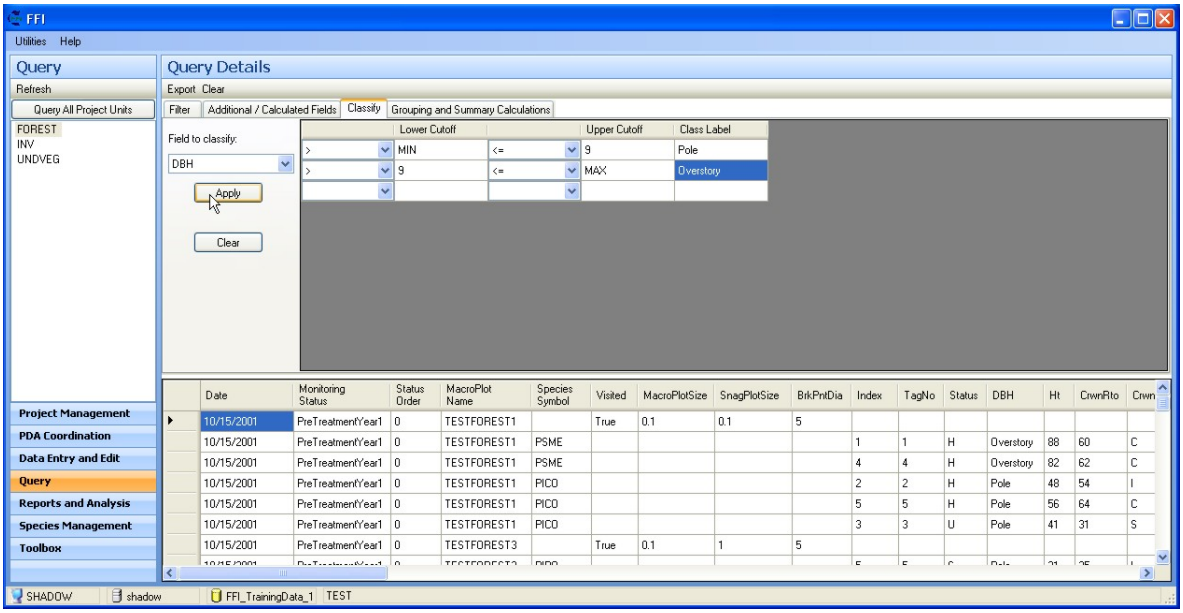
Date	Monitoring Status	MacroPlot Name	Species Symbol	Visited	MacroPlotSize	SnagPlotSize	BrkPntDia	Index	TagNo	Status	DBH	Ht	CrwnRto	CrwnCl	LiCrBHt
10/15/2001	PreTreatmentYear1	TESTFOREST1		True	0.1	0.1	5								
10/15/2001	PreTreatmentYear1	TESTFOREST1	PSME					1	1	H	14.9	88	60	C	35
10/15/2001	PreTreatmentYear1	TESTFOREST1	PSME					4	4	H	12.1	82	62	C	31
10/15/2001	PreTreatmentYear1	TESTFOREST1	PICO					2	2	H	6.5	48	54	I	22
10/15/2001	PreTreatmentYear1	TESTFOREST1	PICO					5	5	H	7.5	56	64	C	20
10/15/2001	PreTreatmentYear1	TESTFOREST1	PICO					3	3	U	5.9	41	31	S	28
10/15/2001	PreTreatmentYear1	TESTFOREST3		True	0.1	1	5								

2.2b) Select Monitoring Status Order and calculate dbh^2 on the *Additional/Calculated Fields* tab. We need the Monitoring Status Order if we are going to import the data into the External Data Analysis Tool. We need to calculate dbh^2 for calculating basal area.



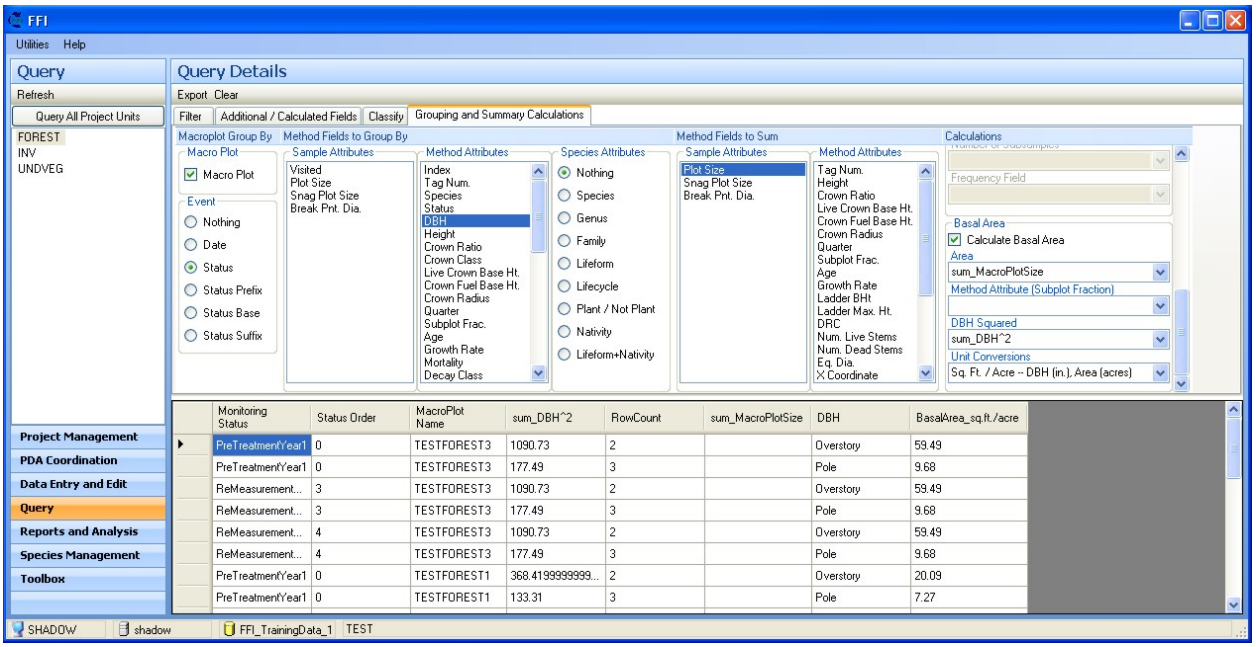
Date	Monitoring Status	Status Order	MacroPlot Name	Species Symbol	Visited	MacroPlotSize	SnagPlotSize	BrkPntDia	Index	TagNo	Status	DBH	Ht	CrwnRto	CrwnCl
10/15/2001	PreTreatmentYear1	0	TESTFOREST1		True	0.1	0.1	5							
10/15/2001	PreTreatmentYear1	0	TESTFOREST1	PSME					1	1	H	14.9	88	60	C
10/15/2001	PreTreatmentYear1	0	TESTFOREST1	PSME					4	4	H	12.1	82	62	C
10/15/2001	PreTreatmentYear1	0	TESTFOREST1	PICO					2	2	H	6.5	48	54	I
10/15/2001	PreTreatmentYear1	0	TESTFOREST1	PICO					5	5	H	7.5	56	64	C
10/15/2001	PreTreatmentYear1	0	TESTFOREST1	PICO					3	3	U	5.9	41	31	S
10/15/2001	PreTreatmentYear1	0	TESTFOREST3		True	0.1	1	5							

2.2c) Using the *Classify* tab, classify the dbh field into pole (> breakpoint dbh and <=9 inches) and overstory (>9 inches) classes. When you apply the classification, the numeric dbh values will be replaced with their classified value. This classified value will be carried over to the *Grouping and Summary Calculations* tab.



2.2d) Calculate basal area by dbh classes using the *Grouping and Summary Calculations* tab. We will calculate basal area by dbh class for each Macroplot and Monitoring Status. First, group the data by Macroplot, Monitoring Status, and DBH class. Next, select Plot Size under *Method Fields to Sum*. These fields are required to perform the basal area calculation.

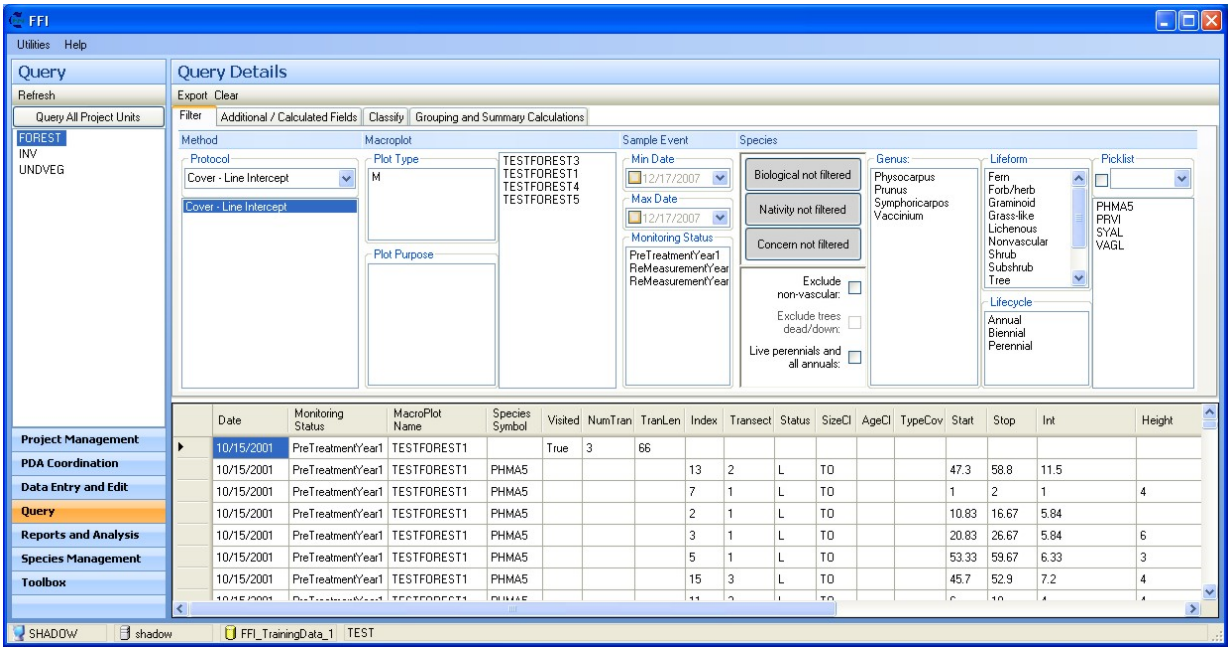
Now fill in the appropriate fields for the *Basal Area* calculation text boxes. Select the field “sum_MacroplotSize” in the *Area* textbox. This will give us the total plot area sampled. The *Method Attribute (Subplot Fraction)* is optional here. It is only required when some trees are sampled on a fraction of the macroplot area. Select “sum_DBH^2” in the *DBH Squared* text box. This field will provide the sum of dbh^2 for calculating basal area. Finally, Select “Sq. Ft. / Acre – DBH (in), Area (acres)” for the Unit Conversion. This will apply the appropriate unit conversion to calculate basal area in Sq. Ft. / Acre given that dbh was recorded in inches and macroplot area was recorded in acres. Check the *Calculate Basal Area* checkbox and the basal area values are added to the data grid.



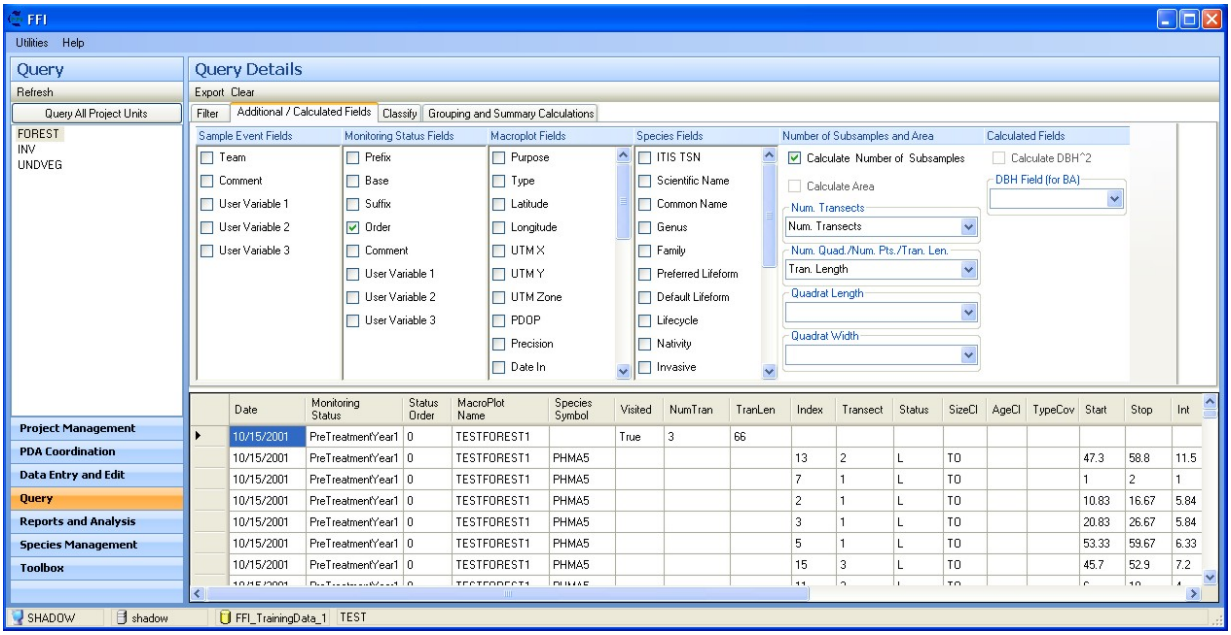
Exercise 2.3: Use Query Builder to calculate cover by life form using the Cover – Line Intercept protocol.

In order to calculate cover using the Cover – Line Intercept protocol, we must know how many inches (cm) of transect were sampled for each macroplot. We can calculate the total length of line sampled per macroplot by multiplying the number of transects by the length of each transect. Next we can sum the total intercept for each species on a plot. We can calculate cover by dividing the sum of intercepts for each species by the total length of transects sampled and multiply by 100. If we are interested in calculating cover by life form, we can group species into life forms before we perform the cover calculation.

2.3a) Select the Cover – Line Intercept protocol and method on *Filter* tab.



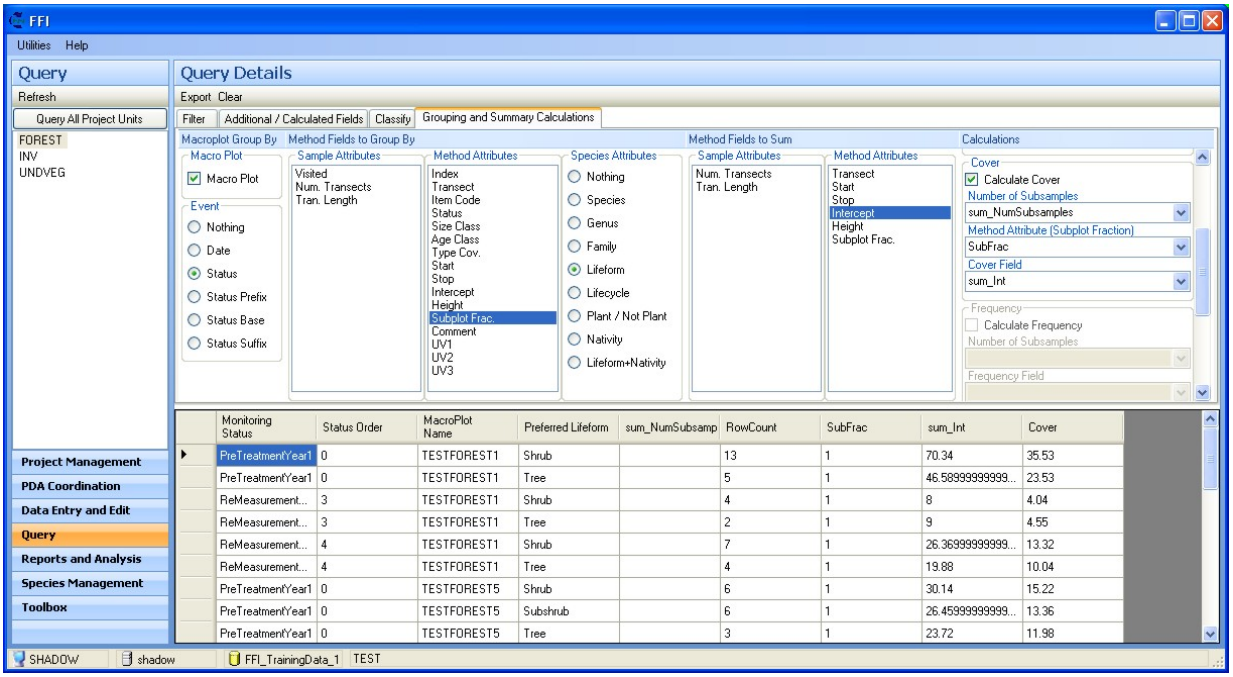
2.3b) Select Monitoring Status Order and Calculate Number of Subsamples on the *Additional/Calculated Fields* tab. The number of subsamples is the total number of inches (cm) of tape sampled for each macroplot and sample event. Select the field “Num. Transects” in the *Num. Transects* text box and the field “Tran. Length” in the *Num. Quad./Num. Pts./Tran. Len.* textbox. When you calculate the number of subsamples the total number of inches (cm) sampled is calculated by multiplying the number of transects by the transect length.



2.3c) Calculate cover by life form on the *Grouping and Summary Calculations* tab. First, group by Macroplot, Monitoring Status, Subplot Fraction, and Lifeform. Subplot fraction is optional here since it is always equal to 1, meaning that all species on a macroplot were sampled along the same length of transect. Next, select Intercept under *Method Fields to Sum.* These fields are required to perform the cover calculation.

Now fill in the appropriate fields for the *Cover* calculation text boxes. Select the field “sum_NumSubsamples” in the *Number of Subsamples* textbox. This will give us the total length (in. or cm) of line transects

sampled. The *Method Attribute (Subplot Fraction)* is optional here, but we will use it just as an example. Select the field “SubFrac” for this textbox. Select “sum_Int” in the *Cover Field* textbox. This field will provide the sum of intercept sampled by life form. Check the *Calculate Cover* checkbox and the cover values are added to the data grid.

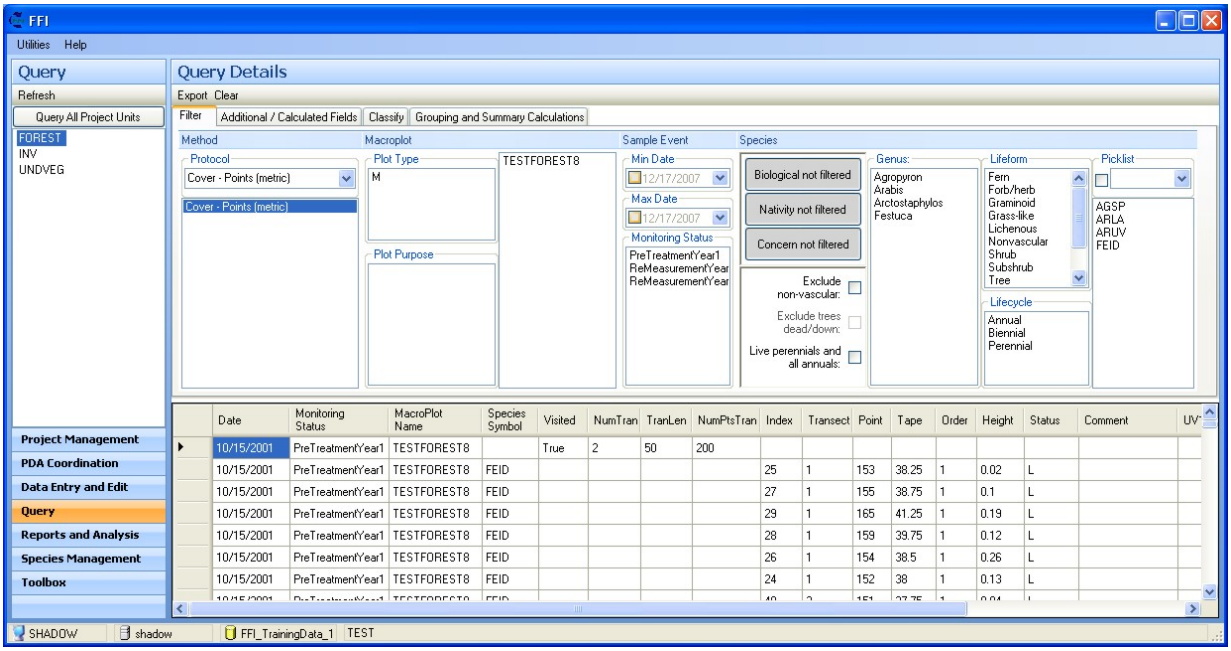


Exercise 2.4: Use Query Builder to calculate cover by life form for the Cover – Points protocol.

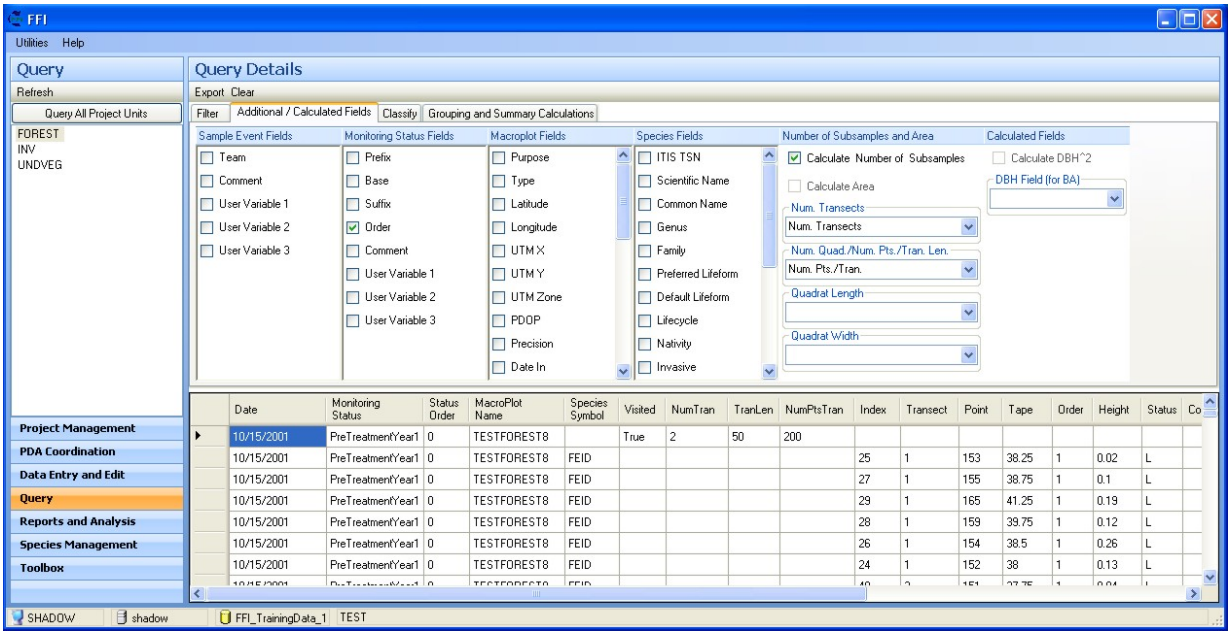
In order to calculate cover using the Cover – Points protocol, we must know how many points were sampled for each macroplot. We can calculate the total number of points sampled per macroplot by multiplying the number of transects by the number of points sampled along each transect. Next we can sum the total number of unique “hits” at each point for each species. Unique hits are recorded once per species at a point, thus multiple hits at a point for a species are only counted as one. We can calculate cover by dividing the

number of unique hits for each species by the total number of points sampled and multiply by 100. If we are interested in calculating cover by life from, we can group species into life forms before we perform the cover calculation.

2.4a) Select the Cover – Points (metric) protocol and method on *Filter* tab.



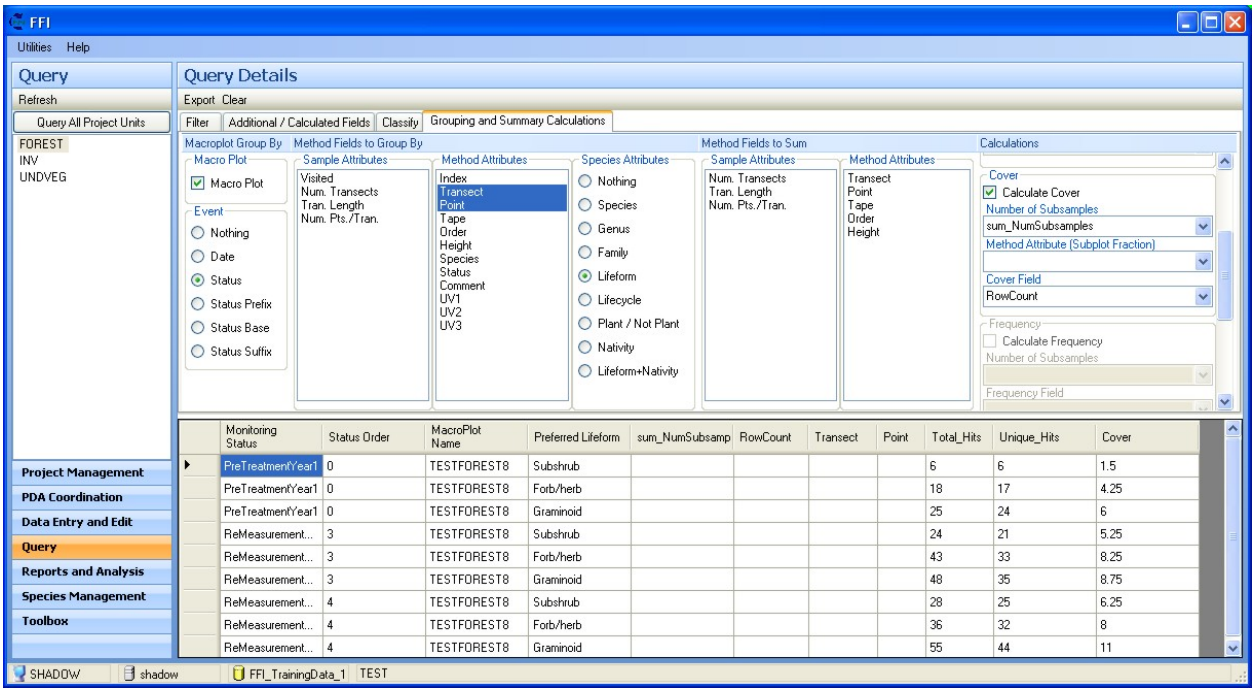
2.4b) Select Monitoring Status Order and calculate Number of Subsamples on the *Additional/Calculated Fields* tab. The number of subsamples is the total number of points sampled for each macroplot and sample event. Select the field “Num. Transects” in the *Num. Transects* text box and the field “Num. Pts./Tran.” in the *Num. Quad./Num. Pts./Tran. Len.* textbox. When you calculate the number of subsamples the total number of points sampled is calculated by multiplying the number of transects by the number of points per transect.



2.4c) Calculate cover by life form on the *Grouping and Summary Calculations* tab. First, group by Macroplot, Status, Transect, Point, and Lifeform. Grouping by Transect and Point is necessary for this method in order to determine which points have multiple hits per species. Cover is calculated using only unique hits at each point. These fields are required to perform the cover calculation.

Now fill in the appropriate fields for the *Cover* calculation text boxes. Select the field “sum_NumSubsamples” in the *Area* textbox. This will give us the total number of points sampled. The *Method Attribute (Subplot Fraction)* is optional here. It is only required if some species on a

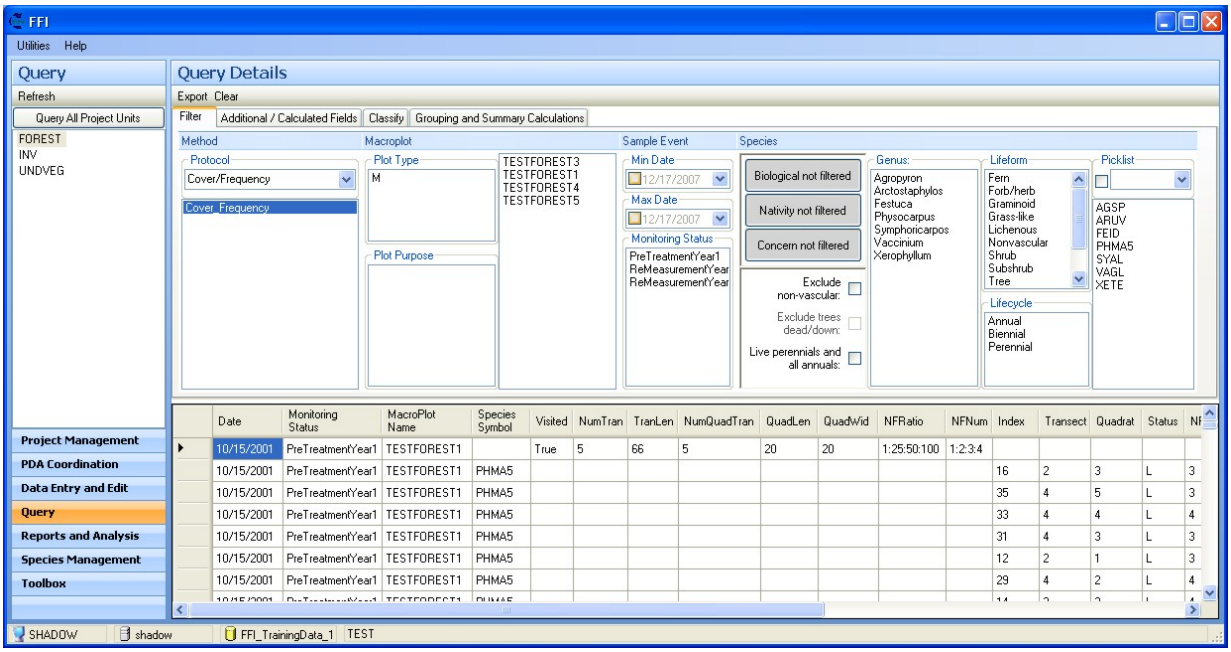
macroplot were sampled with fewer points. Select “RowCount” in the *Cover Field* textbox. This field will provide the number of unique hits for a species along each transect. Check the *Calculate Cover* checkbox and the total hits, unique hits, and cover values are added to the data grid below.



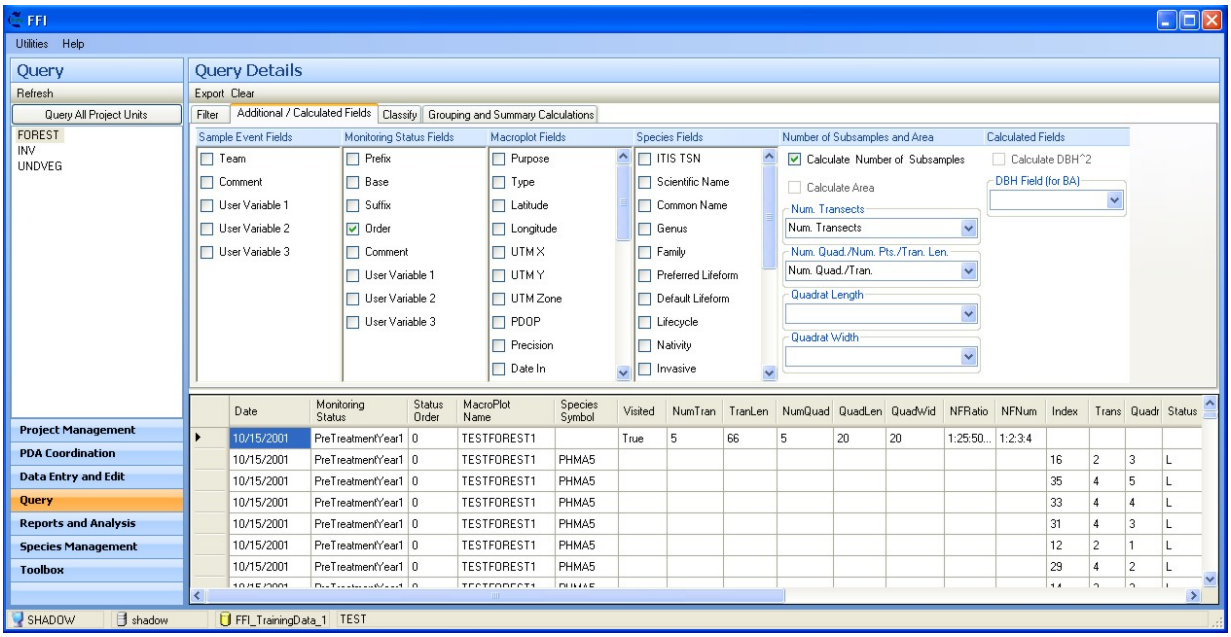
Exercise 2.5: Use Query Builder to calculate frequency by species using the Cover/Frequency protocol.

In order to calculate frequency using the Cover – Frequency protocol, we must know how many quadrats were sampled for each macroplot. We can calculate the total number of quadrats sampled per macroplot by multiplying the number of transects by the number of quadrats sampled along each transect. Next we can sum the total number of quadrats in which a species occurs. We can calculate frequency by dividing the number of quadrats in which a species occurs by the total number of quadrats sampled and multiply by 100.

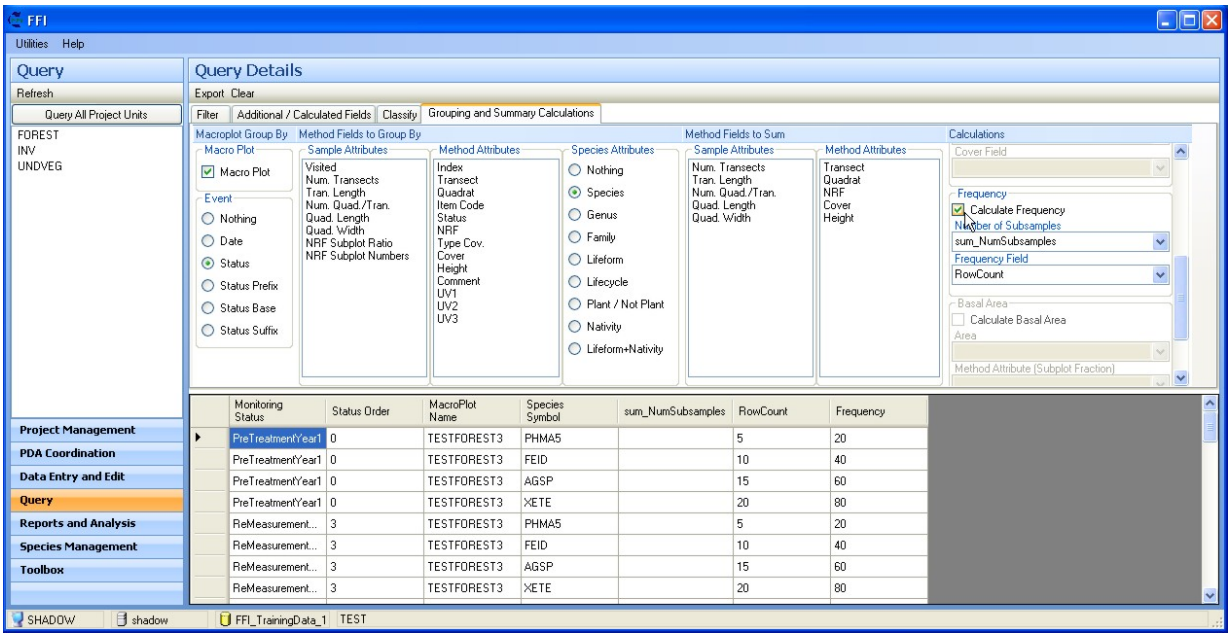
2.5a) Select the Cover/Frequency protocol and method on the *Filter* tab.



2.5b) Select Monitoring Status Order and calculate Number of Subsamples on the *Additional/Calculated Fields* tab. The number of subsamples is the total number of quadrats sampled for each macroplot and sample event. Select the field “Num. Transects” in the *Num. Transects* text box and the field “Num. Quad./Tran.” in the *Num. Quad./Num. Pts./Tran. Len.* textbox. When you calculate the number of subsamples, the total number of quadrats sampled is calculated by multiplying the number of transects by the number of quadrats per transect.



2.5c) Calculate frequency by species on the Grouping and Summary Calculations tab. First, group by Macroplot, Status, and Species. Now fill in the appropriate fields for the *Cover* calculation text boxes. Select the field “sum_NumSubsamples” in the *Area* textbox. This will give us the total number of quadrats sampled. Select “RowCount” in the *Cover Field* textbox. This field will provide the number of quadrats in which a species occurs. Check the *Calculate Frequency* checkbox and the frequency values are added to the data grid.



3. FFI – External Data Analysis

Exercise 3.1: Import the Query Builder results for seedling density by status (live / dead) and view an analysis report and graph.

3.1a) Open the CSV file from the Query Builder results in Excel and save it in an Excel spreadsheet format (.xls).

3.1b) Import the Excel spreadsheet into the External Data Analysis tool. Open the spreadsheet and select the worksheet.

3.1c) Select the Analysis Variables.

- Strata = Status
- Monitoring Status Order = Status Order
- Monitoring Status = Monitoring Status
- Macroplot = MacroPlot Name
- Data Attribute = Density_acres

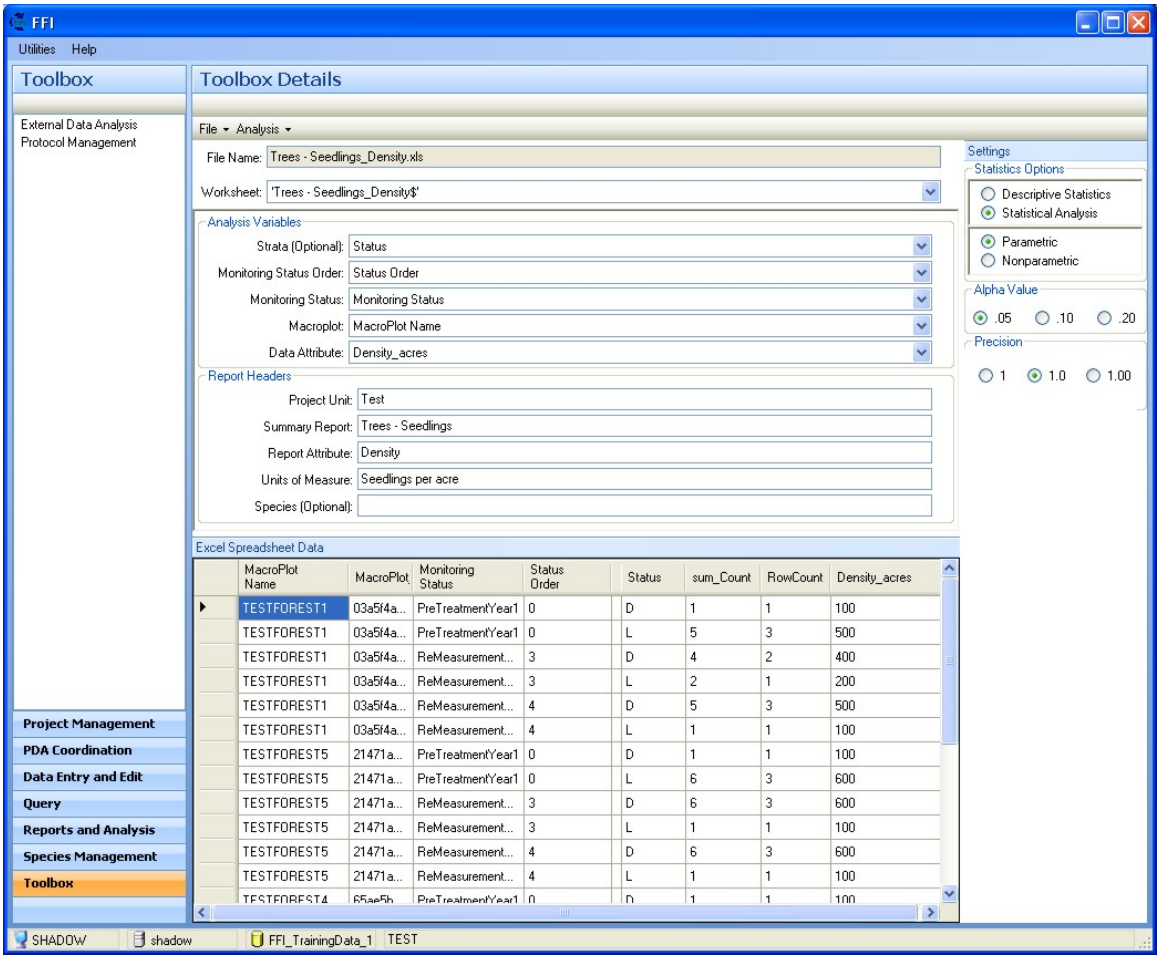
3.1d) Type in the Report Headers.

- Project Unit = Test
- Summary Report = Trees - Seedlings
- Report Attribute = Density
- Units of Measure = Seedlings per acre

3.1e) Select the Analysis Settings.

- Statistical Analysis
- Parametric
- Alpha Value = 0.5
- Precision = 1.0

External Data Analysis Settings



3.1f) View the Analysis Report.

Analysis Report

Save Copy

Project Unit_____**Test**
Summary Report_____**Trees - Seedlings**
Report Attribute_____**Density**
Units_____**Seedlings per acre**

Strata: D

	PreTreatmentYear1	ReMeasurementYear1			ReMeasurementYear2		
Plot	Attr	Attr	Diff	%Diff	Attr	Diff	%Diff
TESTFOREST1	100.0	400.0	300.0	300.0	500.0	400.0	400.0
TESTFOREST3	100.0	400.0	300.0	300.0	500.0	400.0	400.0
TESTFOREST4	100.0	500.0	400.0	400.0	500.0	400.0	400.0
TESTFOREST5	100.0	600.0	500.0	500.0	600.0	500.0	500.0
Mean	100.0	475.0			525.0		
SDev	0.0	95.7			50.0		
N	4.0	4.0			4.0		
CI-Lower	100.0	322.7			445.5		
CI-Upper	100.0	627.3			604.6		

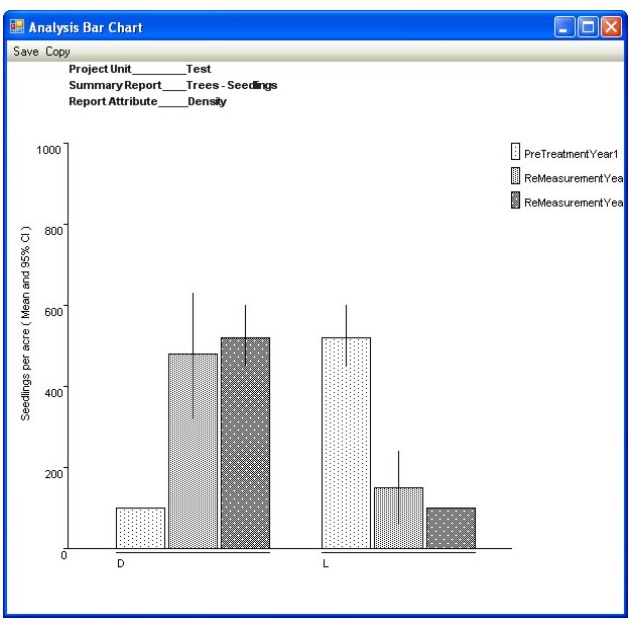
F-Value = 55.50 Prob = 0.0000 Alpha =.05 (Settings Dialog Box)

PreTreatmentYear1 to ReMeasurementYear1: p <= .01
PreTreatmentYear1 to ReMeasurementYear2: p <= .01

Strata: L

	PreTreatmentYear1	ReMeasurementYear1			ReMeasurementYear2		
Plot	Attr	Attr	Diff	%Diff	Attr	Diff	%Diff
TESTFOREST1	500.0	200.0	-300.0	-60.0	100.0	-400.0	-80.0
TESTFOREST3	500.0	200.0	-300.0	-60.0	***	***	***
TESTFOREST4	500.0	100.0	-400.0	-80.0	100.0	-400.0	-80.0
TESTFOREST5	600.0	100.0	-500.0	-83.3	100.0	-500.0	-83.3
Mean	525.0	150.0			100.0		
SDev	50.0	57.7			0.0		
N	4.0	4.0			3.0		
CI-Lower	445.5	58.1			100.0		
CI-Upper	604.6	241.9			100.0		

Missing plot data - no statistical analysis run

.

3.1g) View the Analysis Graph.