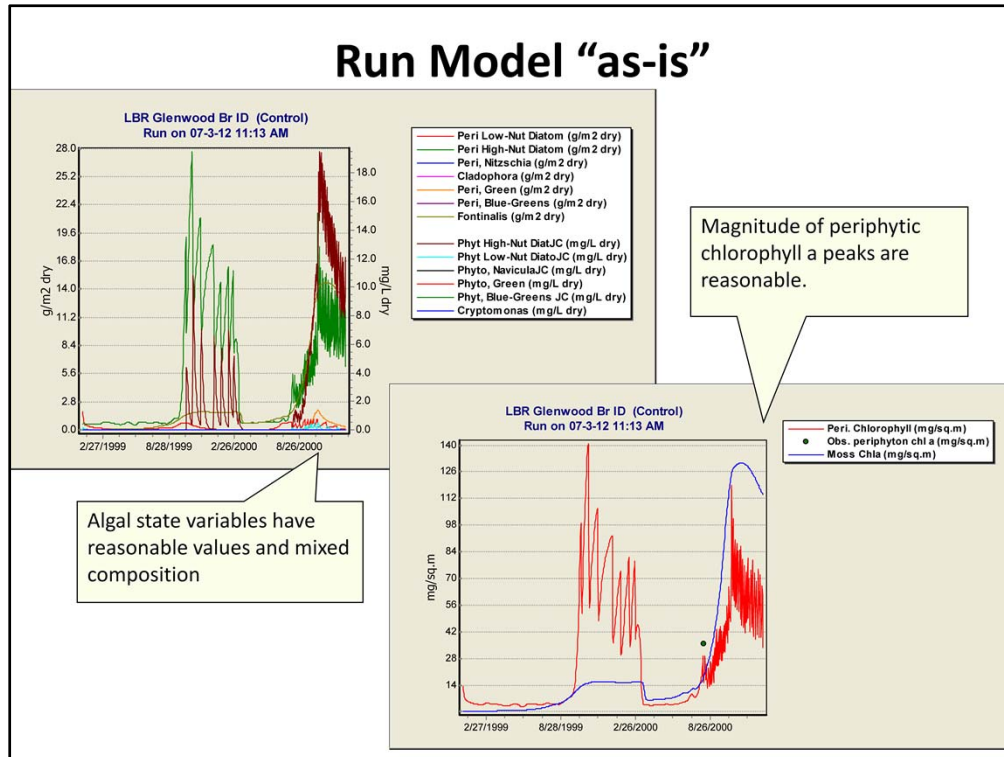**Lab 3: Choice of Biota, Calibration of Glenwood Bridge, Lower Boise River, ID**

- Check initial run with Rum River state variables
- Change Total Length for phytoplankton
- Change fish to reflect Boise R. species
- Minor calibration
- Discussion of model calibration goals

Open **LBR Glenwood Br ID.aps**, which you ran in Lab 2.

Our initial examination of results is somewhat encouraging. The observed composition consists of abundant centric (high-nutrient) diatoms.

The periphyton are going through buildup that is likely too rapid and sloughing events that are too frequent, however.

But are observed chlorophyll *a* levels comparable to those predicted? Let's examine predictions against observed data now.

These results have also been saved as **LBR Glenwood 1b.aps**

Loading Observed Data
"menu" "external data"

The AQUATOX model now has the capability to load observed data directly into the model for comparison against predictions.
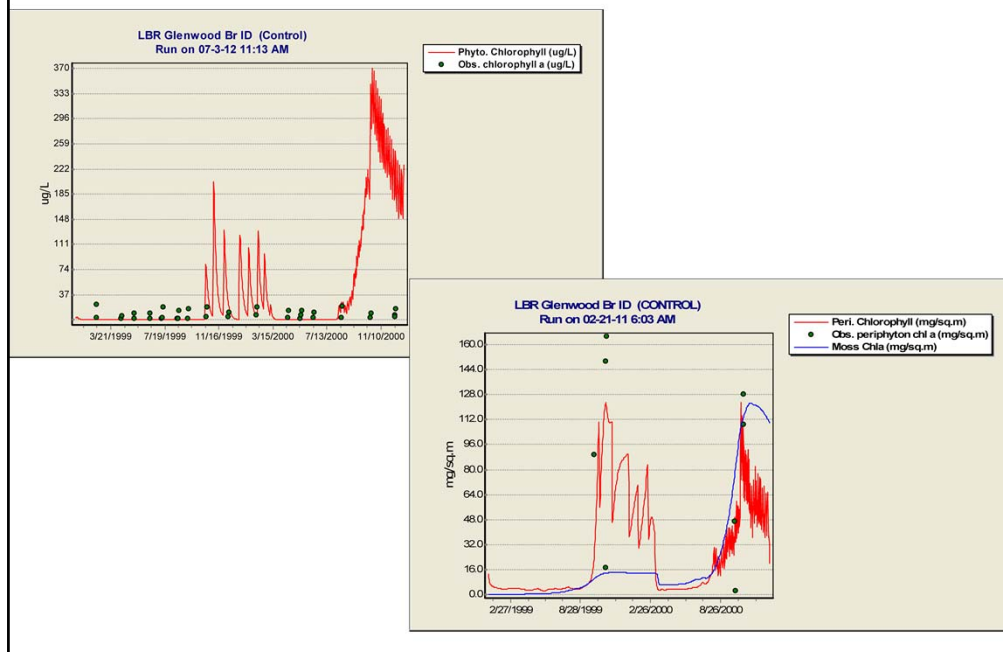
To load observed data, press the Output button in the main window. In the pull-down menu on the right side of the output window, select "External Data".

Overwrite the observed data associated with the Rum River.

Select "Obs. Chlorophyll a" and "Import Data" and then select the file "LBR_Glenwood_Chla_Observed.xls"

Select "Obs. Periphyton chl a" and "Import Data" and then select the file "LBR Glenwood Peri Chla Obs.xls"

The AQUATOX model now has the capability to load observed data directly into the model for comparison against predictions.

The imported "external data" will now appear at the end of the results list shown when you edit or create a new simulation.

The periphyton chlorophyll *a* simulation looks reasonable. Note that the data represent multiple measurements taken on the same day so the AQUATOX simulation (representing an average condition) could not hit all of those data points.

The chlorophyll *a* in the water column is unreasonably high at the end of the simulation so some additional calibration is warranted.

Change Length in Site Screen

For Calculating Phytoplankton Retention / Washout:

☑ Enter Total Length — (enter zero if NA) **40** km — **Lucky Peak dam is 16 km upstream**

or Estimate Total Length from Watershed Area — 3522 km² — SITE SUMMARY.xls mi2 converted to km

Site Notes: **Glenwood Bridge, Lower Boise River, Boise, Idaho.**

Length is used to calculate phytoplankton and zooplankton retention time

From the main window, go to "Site" then "Edit Underlying Site Data." Set the total length to 40 km (at the very bottom of the screen), which accounts for longer residence time (~length) due to Diversion and Barber impoundments.

Phytoplankton and zooplankton can quickly wash out of a short reach, but they may be able to grow over an extensive reach of a river, including its tributaries. Somehow the volume of water occupied by the phytoplankton needs to be taken into consideration. To solve this problem, AQUATOX takes into account the "Total Length" of the river being simulated so that phytoplankton and zooplankton production upstream can be estimated. Then, to simulate the inflow of phytoplankton from upstream reaches phytoplankton upstream loadings are estimated.

An integral assumption in this approach is that upstream reaches being modeled have identical environmental conditions as the reach being modeled and that plankton production in each mile up-stream will be identical to plankton production in the given reach.

Modify biotic assignments

(Remove Macrophyte Fontinalis)

Rum River MN

- **shiner**
- **bluegill** ⟶
- **sculpin**
- **catfish**
- **carp**
- **white sucker**
- **smallmouth bass (2)** ⟶
- **walleye** ⟶

Lower Boise R. ID

- **chiselmouth**
- **dace**
- **shiner**
- **pikeminnow**
- **sculpin**
- **catfish**
- **carp**
- **white sucker**
- **largemouth bass (2)**
- **rainbow trout (2)**
- **mountain whitefish (2)**

Fish species may change considerably from one watershed to another, so one should always check the assignments when modeling a new site.   We will demonstrate both how to add new species, as well as replace or modify existing spp in an application.

We can keep the algal and invertebrate designations the same for the most part. However, be alert for invasive species; the New Zealand mud snail is one that first appeared at Glenwood Bridge in 2003.

Also, as shown above, remove Fontinalis from the MN Rivers simulation. This is not well calibrated for the Lower Boise river and its rapid growth is contributing to the rapid growth of periphyton.

Add fish

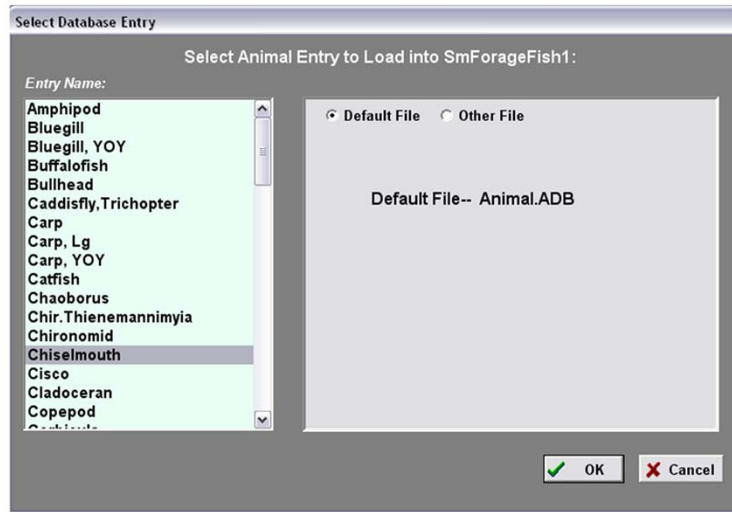There are three ways to modify the types of biota in the system.

1. Add a species "manually" through the main interface.
2. Replace an existing species with a different set of "underlying data"
3. Modify the species using the wizard (usually easiest).

We will demonstrate all three procedures within this exercise.

To add a fish "manually" click on **Add** and select the **State Variable to Insert**. We have another bottom fish to add, chiselmouth. We already have 4 bottom fish so we will add a small forage fish and assign chiselmouth to that designation. This illustrates an important point: the guild labels are just to help you organize the state variables; chiselmouth is a bottom fish, and it is large; however, these characteristics are imparted by the parameters that we use, not by the nominal guild name. The only exception is that dietary assimilation of toxicants by large game fish is more efficient than for other fish.

The choice of Animal Type (found on the parameter screen) can be important for invertebrates, however, because some of the ecological processes that affect them differ slightly. See p. 4-1 in the **Technical Documentation** for the differences in processes for the different plant and animal types.

Choose fish from list of animals in Library

Once you have added an organism, **double-click** on the name to open the loading screen and **set the initial condition**. Initial conditions are not important for plants and invertebrates, but fish respond slowly and the initial condition may require a "spin-up" period to obtain a stable value.

We will start with a value of 0.1 for chiselmouth.

To add a species not in the Library

mountain whitefish:
- load a similar species or group (trout in this case)
  – use GridMode to find best match in Library
- go to a parameter source, such as FishBase.Org, to check food preferences, temperature preferences, mean weight
- Google species to find more specific information online
  – changed TOpt based on Essig, 1998; TMin based on Sauter et al. 2001

New Zealand mud snail (Potamopyrgus):
- used gastropod as template
- all additional information in Hall et al., 2003

Always start with the closest species or group because many parameters extend across groups. In a later lecture we will cover examples of general sources of parameters. The Internet is a great source if general information and specific parameter values, and it is improving daily.
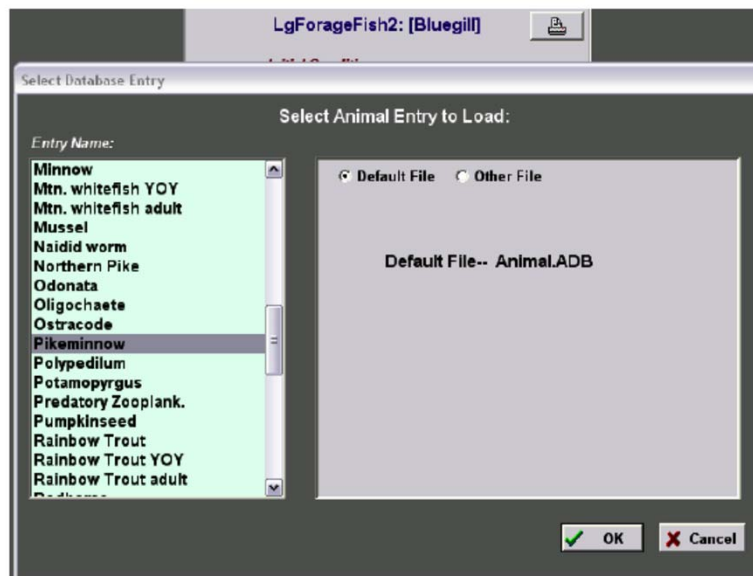
We will add these species to the simulation in the upcoming slides

In Library can choose GridMode to see all species at once

	Max Consumpt	Max Consumpt Reference	Min Prey	Min Prey Reference
Mtn. whitefish YOY	0.01	calc. from Hewett & Johnson '92, l. trout	0.25	
Mtn. whitefish adult	0.01	calc. from Hewett & Johnson '92, l. trout	0.1	bottom feeder
Mussel	0.05	Anadonta (Pusch et al., 2001, p. 320)	0	filter feeding mollusc
Naidid worm	0.25	prof judgment, calibrated	0.1	
Northern Pike	0.05	calc. from Hewett & Johnson '92 prms.	0.25	prof. judgement
Odonata	0.09	Leidy and Ploskey, 1980	0.1	prof. judgment
Oligochaete	0.5	prof judgment	0	
Ostracode	1.2	est. to be 1/2 cladoceran	0.06	twice cladoceran
Pikeminnow	0.05	Collins & Wlosinski 1983	0.25	prof. judgment
Polypedilum	0.7	McIntire & Colby p. 172	0.1	prof. judgment
Potamopyrgus	0.17	Hall et al., 2003, Frontiers in Ecology 1:8	0.7	(McIntire et al. 1996 = 0.7)
Predatory Zooplank.	1.1	Leidy & Ploskey, '80, p. 87	0.1	est. from Leidy & Ploskey, '80, p. 86
Pumpkinseed	0.05	Hewett & Johnson '92 calc. (Dace)	0.25	prof. judgement
Rainbow Trout	0.01	calc. from Hewett & Johnson '92, l. trout	0.25	
Rainbow Trout YOY	0.01	calc. from Hewett & Johnson '92, l. trout	0.25	
Rainbow Trout adult	0.01	calc. from Hewett & Johnson '92, l. trout	0.25	
Redhorse	0.06	Leidy & Jenkins '77	0.25	prof. judgment
Riffle beetle, Sten	0.5	McIntire & Colby p. 172	0.2	prof judgment
Rotifer, Brachionus	3.4	from sev. papers, extrapolated from growth	0.3	Walz, 1995, p. 441
Rotifer, Keratella	3.438	Collins & Wlosinski 9183, p. 45 (B.r.)	0.06	Walz, 1995, p. 441

To quickly scan (and edit) a Library click on **GridMode** at the top of the Library screen.

Replacing One Fish Species with Another
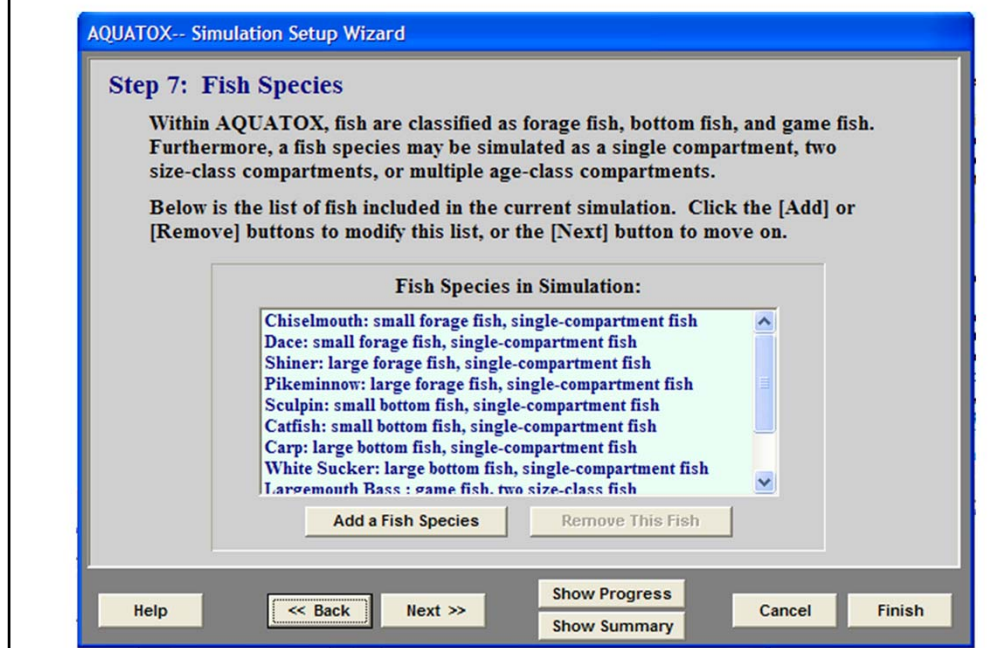
To replace an existing animal in the simulation with another, open the loading file for the original species and click on **Load Data** to bring up the screen to select the animal or plant entry, then choose the alternate species or group **and click OK**. We will do this to replace bluegill with pikeminnow.

Load **Pikeminnow** into existing LgForageFish2 (previously bluegill)

Using the Wizard to Modify Biota

AQUATOX-- Simulation Setup Wizard

Step 7: Fish Species

Within AQUATOX, fish are classified as forage fish, bottom fish, and game fish. Furthermore, a fish species may be simulated as a single compartment, two size-class compartments, or multiple age-class compartments.

Below is the list of fish included in the current simulation. Click the [Add] or [Remove] buttons to modify this list, or the [Next] button to move on.

Fish Species in Simulation:

Chiselmouth: small forage fish, single-compartment fish
Dace: small forage fish, single-compartment fish
Shiner: large forage fish, single-compartment fish
Pikeminnow: large forage fish, single-compartment fish
Sculpin: small bottom fish, single-compartment fish
Catfish: small bottom fish, single-compartment fish
Carp: large bottom fish, single-compartment fish
White Sucker: large bottom fish, single-compartment fish
Largemouth Bass : game fish, two size-class fish

Add a Fish Species   Remove This Fish

Help   << Back   Next >>   Show Progress   Show Summary   Cancel   Finish

Double-click on step 7 in the Wizard Progress window to jump to the fish entry screens.

1. Remove smallmouth bass (2 lines).
2. Remove walleye.
3. Add **Largemouth Bass** as a size-class gamefish (**Largemouth Bass YOY** and **Largemouth Bass, Lg**). Add the Lg class by selecting Yes at the dialog window that asks "Do you wish to load a different set of species data for the large size-class fish?"
4. Add **Mountain Whitefish** as a size-class gamefish (**Mtn. whitefish YOY** and **Mtn. whitefish adult**)
5. Add **Rainbow Trout** as a size-class gamefish (**Rainbow Trout YOY** and **Rainbow Trout adult**)
6. Add **Dace** as a single-compartment small forage fish

Set Fish Initial Conditions

AQUATOX-- Simulation Setup Wizard

Step 7: Fish Initial Conditions:

Enter initial conditions for these fish in this simulation:

SmForageFish1: [Chiselmouth]	0.1	g/m2 dry
SmForageFish2: [Dace]	0.1	g/m2 dry
LgForageFish1: [Shiner]	0.1	g/m2 dry
LgForageFish2: [Pikeminnow]	0.1	g/m2 dry
SmBottomFish1: [Sculpin]	0.1	g/m2 dry
SmBottomFish2: [Catfish]	0.1	g/m2 dry
LgBottomFish1: [Carp]	0.1	g/m2 dry
LgBottomFish2: [White Sucker]	0.1	g/m2 dry

SmGameFish1: [Largemouth Bass,	0.1	g/m2 dry
SmGameFish2: [Mtn. whitefish YOY]	0.1	g/m2 dry
SmGameFish3: [Rainbow Trout YOY]	0.1	g/m2 dry
LgGameFish1: [Largemouth Bass,	0.1	g/m2 dry
LgGameFish2: [Mtn. whitefish adult]	0.1	g/m2 dry
LgGameFish3: [Rainbow Trout adult]	0.1	g/m2 dry

Help   << Back   Next >>   Show Progress   Show Summary   Cancel   Finish

Using the wizard interface allows us to enter initial conditions for all fish species on a single screen.

We'll set all initial conditions to 0.1 for use in a spin-up.

We will revisit these initial conditions later.

Examine Trophic Interactions

Select "Edit Trophic Interactions" from the Study Menu:

	Dace	Shiner	Pikeminnow	Sculpin	Catfish	Carp	White Sucker	Largemouth	Mtn. whitefish	Rainbow Trout	Largemouth	Mtn. whitefish	Rainbow Trout
Cryptomonas													
Crayfish			11.1										
Rotifer, Brachionus													
Chironomid	25.0	7.1	5.6	81.2	31.6	11.1	6.1	36.5	62.4	13.2	0.7	6.2	14.6
Tubifex tubifex					33.3		6.1	36.5	1.1	13.2	0.7	4.5	14.6
Caddisfly,Trichopter	50.0	21.4	5.6	8.9	2.0		8.1	25.0	0.4	6.6	0.7	5.1	7.3
Daphnia		21.4							8.8	6.6		1.1	7.3
Sphaerid						11.1	6.1						
Mussel							6.1						
Stenelmis		14.3					8.1		2.2		3.4	1.1	
Mayfly (Baetis)	25.0	21.4	5.6	8.9					25.2	13.2		37.6	
Gastropod												16.9	
Chiselmouth		11.1								10.4	5.4	1.1	
Dace		11.1								10.4	3.1	1.1	
Shiner		11.1		1.0	31.6					10.4	37.1	1.1	11.6
Pikeminnow											37.1	1.1	11.6
Sculpin		11.1								10.4		1.1	
Catfish												0.6	
Carp											7.4	0.6	5.5
White Sucker												0.6	5.5
Largemouth Bass, YOY				31.6							5.5	6.7	7.3
Mtn. whitefish YOY			11.1									6.7	7.3
Rainbow Trout YOY			11.1									6.7	7.3
Largemouth Bass, Lg													
Mtn. whitefish adult											4.2		
Rainbow Trout													

An examination of trophic interactions is usually a wise step.

Remember that predators are listed across the top (x-axis) of the Trophic interactions grid, and prey down the right-hand side (y-axis).
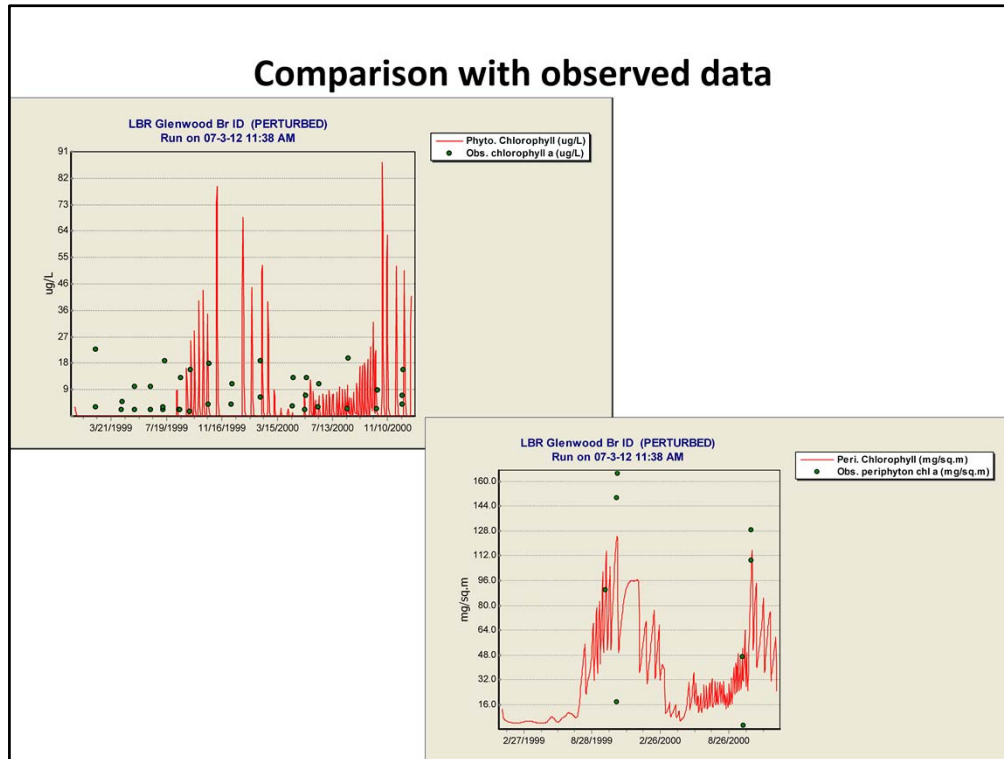
This has some suspicious entries (such as sculpin only being preyed upon by pikeminnows and mountain whitefish) , but we will let it go for now.

Back in the main menu, select LargeMouth Bass, Lg and edit its underlying characteristics, setting the preference for riffle as 10% and pool as 80% - otherwise these become excluded.

We are ready to run

We may not actually run this simulation during the workshop, because it is just an intermediate step and will take roughly 25 minutes to execute. If you'd like to run the simulation on your own now or later, please save the file now as an intermediate step. (We will be modifying the existing study and running it shortly.)
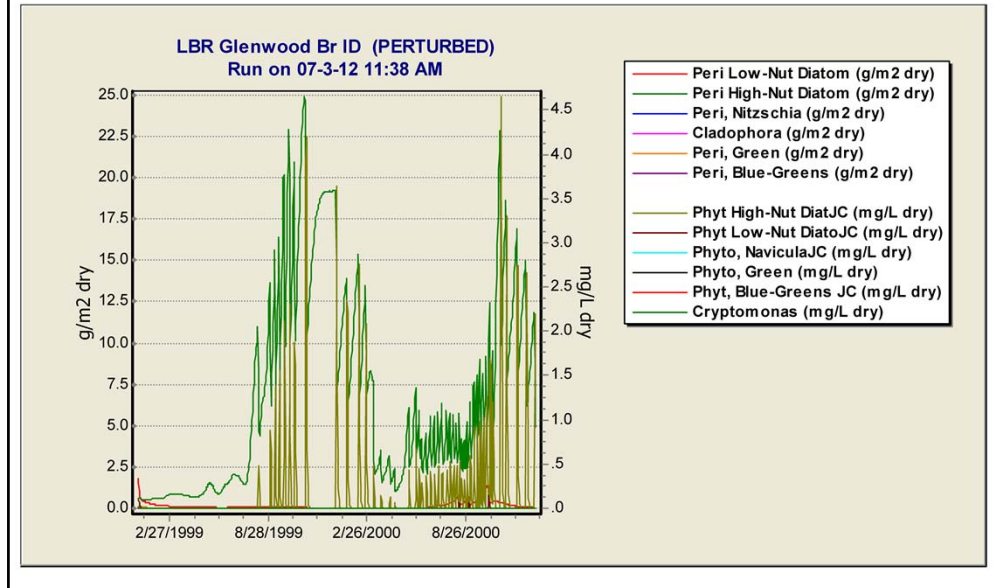
Your simulation now should match the file **LBR Glenwood 2.aps**"

Comparison with observed data

Same procedure performed previously. The results have changed as a result of top-down control. Chlorophyll *a* in the water column is significantly improved. Periphyton remains in a reasonable range.

The extreme variations in biomass due to periphyton buildup and sloughing are somewhat reduced which is also a good thing.
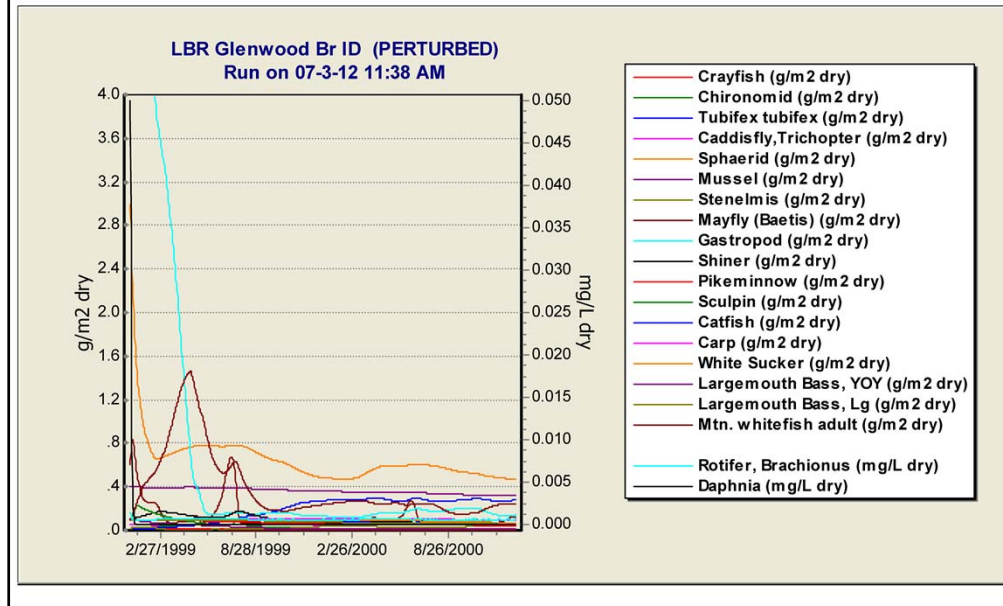
High-nutrient diatoms dominate

LBR Glenwood Br ID (PERTURBED)
Run on 07-3-12 11:38 AM

As observed in this graph, there is a linkage between periphyton and phytoplankton.
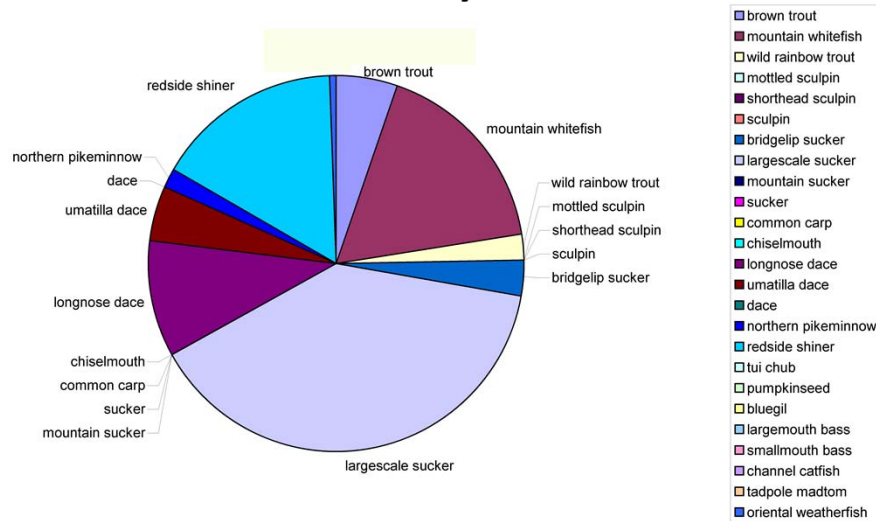
When periphyton are sloughed from surfaces and subsequently suspended in the water column, they then contribute to the suspended chlorophyll a and are "counted" as phytoplankton. By the same token, when phytoplankton settle on surfaces, they are incorporated into the periphyton and treated as such. The overall amount of biomass does not change, only its location.

Fish show transient dynamics

The initial condition for snails is 9 g/m2, which is obviously too high.

Observations on fish consist of numbers and these cannot be converted to biomass directly

We have percentage distributions for fish at Glenwood Bridge from USGS; these cannot be used directly to calibrate the model. However, allowing for differences in mean weight, the community is dominated by suckers, minnows, and mountain whitefish; brown trout, which we have not modeled, seem to exceed rainbow trout. We should probably add brown trout, but at this time let's consider them as lumped with rainbow trout and add gastropods (a prey item for brown trout) to the rainbow trout preference matrix for this study.

Reexamine Trophic Interactions

Select "Edit Trophic Interactions" from the Study Menu:

	Dace	Shiner	Pikeminnow	Sculpin	Catfish	Carp	White Sucker	Largemouth	Mtn. whitefish	Rainbow Trout	Largemouth	Mtn. whitefish	Rainbow Trout
Cryptomonas													
Crayfish			11.1										
Rotifer, Brachionus													
Chironomid	25.0	7.1	5.6	81.2	31.6	11.1	6.1	36.5	62.4	13.2	0.7	6.2	14.6
Tubifex tubifex					33.3		6.1	36.5	1.1	13.2	0.7	4.5	14.6
Caddisfly,Trichopter	50.0	21.4	5.6	8.9	2.0		8.1	25.0	0.4	6.6	0.7	5.1	7.3
Daphnia		21.4							8.8	6.6		1.1	7.3
Sphaerid						11.1	6.1						
Mussel							6.1						
Stenelmis	(yellow)	14.3	(yellow)				8.1		2.2		3.4	1.1	
Mayfly (Baetis)	25.0	21.4	5.6	8.9					25.2	13.2		37.6	
Gastropod												16.9 (yellow)	
Chiselmouth		11.1								10.4	5.4	1.1	
Dace		11.1								10.4	3.1	1.1	
Shiner		11.1		1.0	31.6					10.4	37.1	1.1	11.6
Pikeminnow											37.1	1.1	11.6
Sculpin		11.1								10.4	(yellow)	1.1	(yellow)
Catfish												0.6	
Carp											7.4	0.6	5.5
White Sucker												0.6	5.5
Largemouth Bass, YOY				31.6							5.5	6.7	7.3
Mtn. whitefish YOY		11.1										6.7	7.3
Rainbow Trout YOY		11.1										6.7	7.3
Largemouth Bass, Lg													
Mtn. whitefish adult											4.2		
Rainbow Trout													

Going back to the trophic interactions matrix we see that there are alternate predators for stenelmis. Snails are preyed on too heavily by mountain whitefish, but should also have some predation pressure from rainbow trout—although the true snail predator is brown trout, which we are not modeling. Finally, sculpin should be subject to predation by bass and rainbow trout.
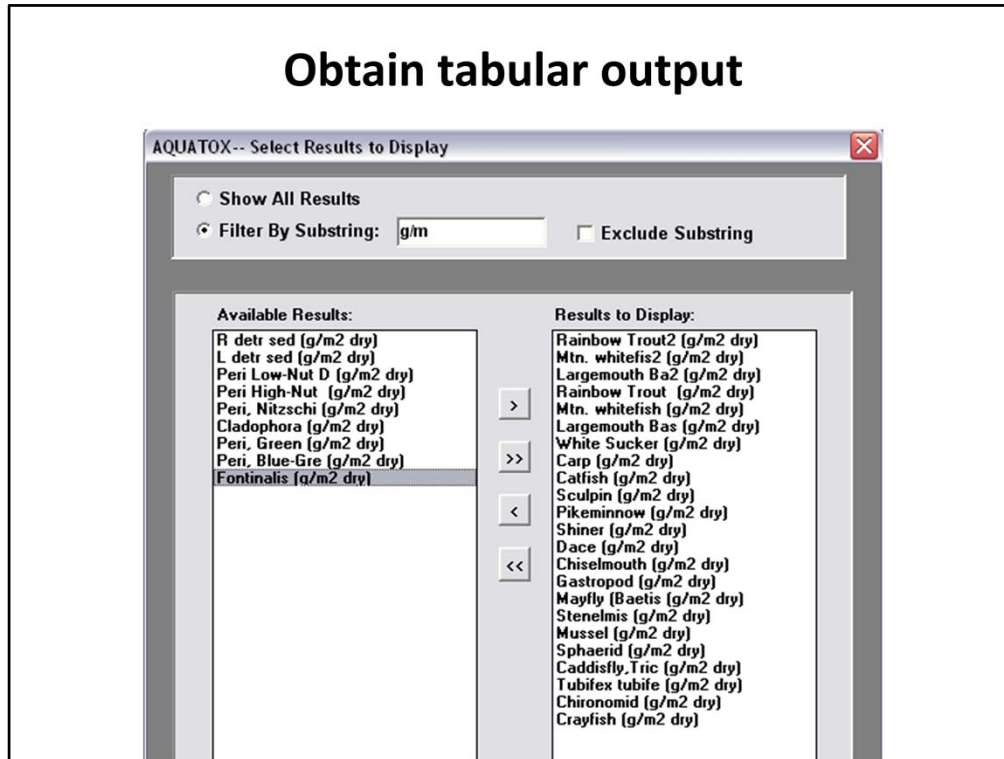
Suggested changes to preference values

- Dace: stenelmis = mayfly value
- Pikeminnow: stenelmis = mayfly
- Bass (adult): sculpin = bass: shiner
- Mtn. whitefish (adult): gastropod = 5.0
- Rainbow trout (adult): gastropod = 10
- Rainbow trout (adult): mayfly = caddisfly
- Rainbow trout (adult): sculpin = shiner

We will make those changes to the preferences. To calibrate the model, we would not make so many changes at once, but the fish matrices have not been set up since adding the fish to the simulation. (If you don't agree with our changes, feel free to make your own.)

Your simulation should now match **LBR Glenwood 3.aps**
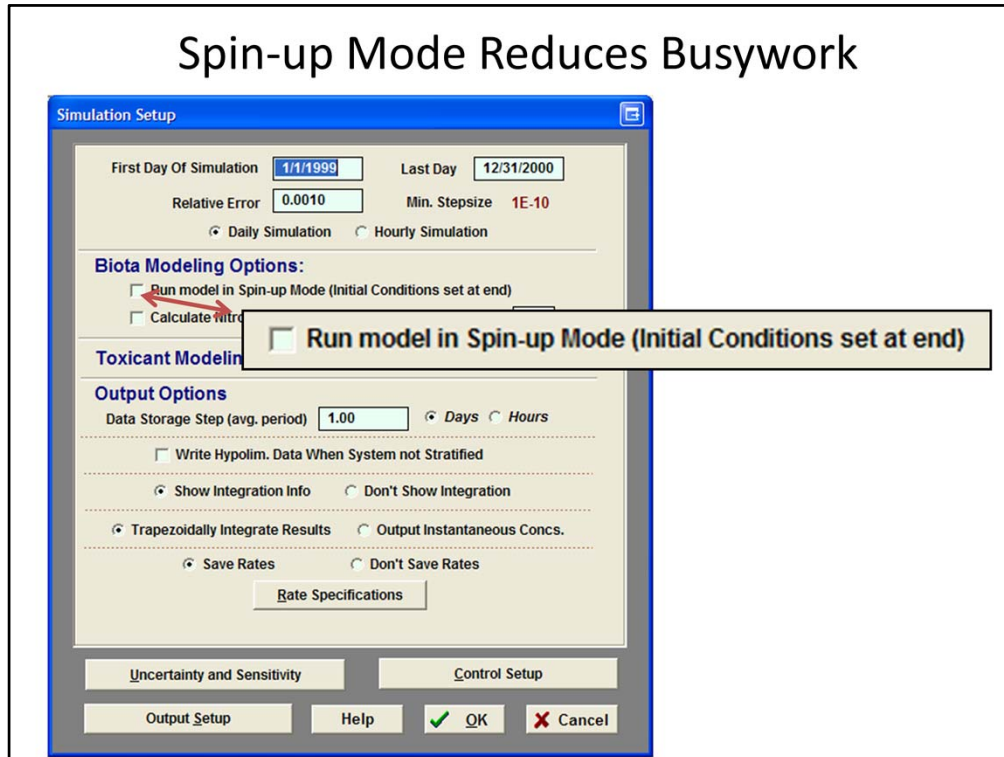
Obtain tabular output

Often times, in the absence of biomass data, it is useful to allow organism's biomasses within the model to equilibrate and then initialize the model with biomasses calculated on the last time-step of the previous simulation. This is known as "spinning up" the model.

To view the biomass values from the previous simulation as tables (rather than the graphs we usually use) you can use the "tabular output" tabs to the left of the output screen.

While still in the Output window, click on the **Perturbed Simulation** tab. Click on **Choose Variables**, use "g/m" as a filter substring to limit the list. Choose the invertebrates and fish for tabulation.

The biomass values in the last time-step could be used to initialize the next model run thus avoiding transient conditions resulting from biomass initial conditions. Instead of writing all of these parameter values down and typing them into the interface, an automated tool exists to "spin up" the model as shown in the next slide.
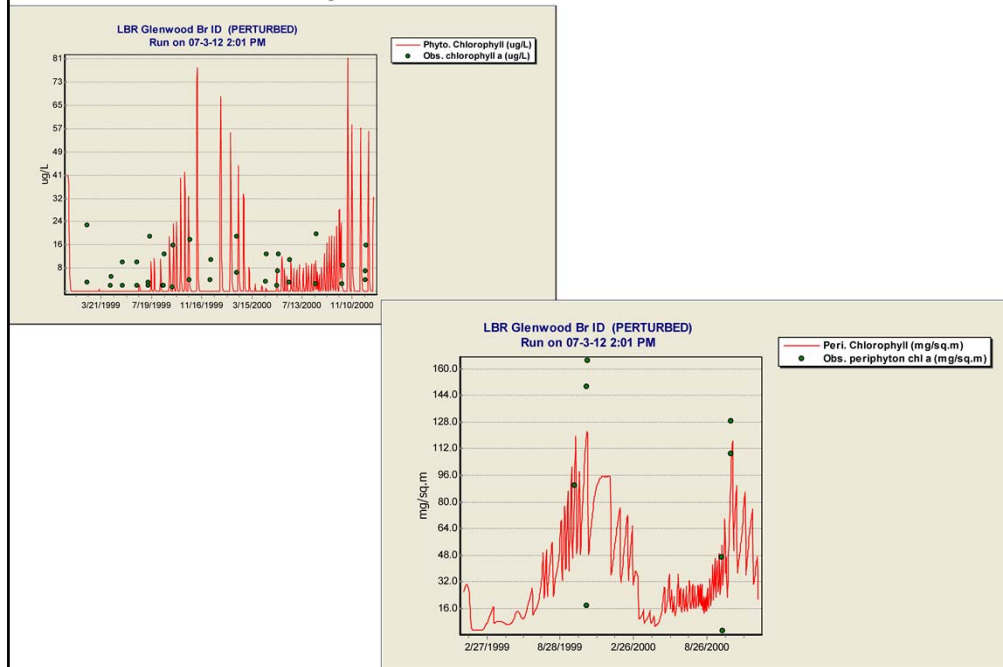
If the model is run in "**Spin-up Mode**" initial conditions for biota will be set based on the model results on the last time-step of the simulation. This can be useful in setting biotic initial conditions when there are insufficient available data. As initial conditions will be automatically overwritten it is best to first save a simulation before running in "spin-up mode.“

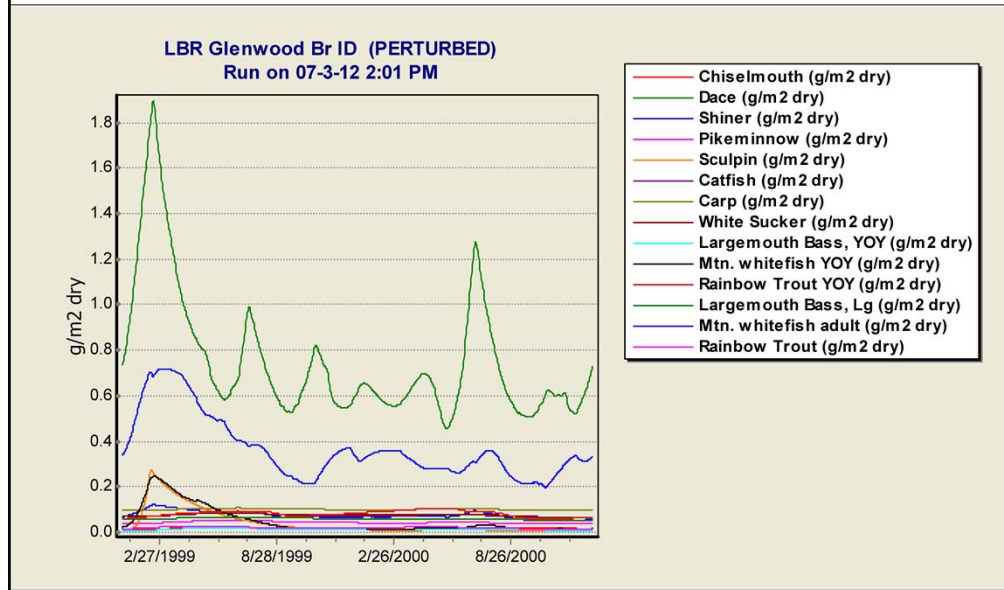We have several options as to how to proceed in this laboratory now

1. Run the model in spin-up mode and reset the biotic initial conditions automatically. This will take 20 minutes (note: for this lab, uncheck the "Also spin-up nutrients, suspended, and bed sediments). **Then run the model again using the newly defined initial conditions.**
2. Enter in biotic initial conditions by hand. 5-10 minutes of "busy work."
3. Load the spun up model saved in your "Data" folder. "**LBR Glenwood 3 Spinup.aps**"
4. Continue to run the model without spinning up. Compare results to what we derived after the spin up.
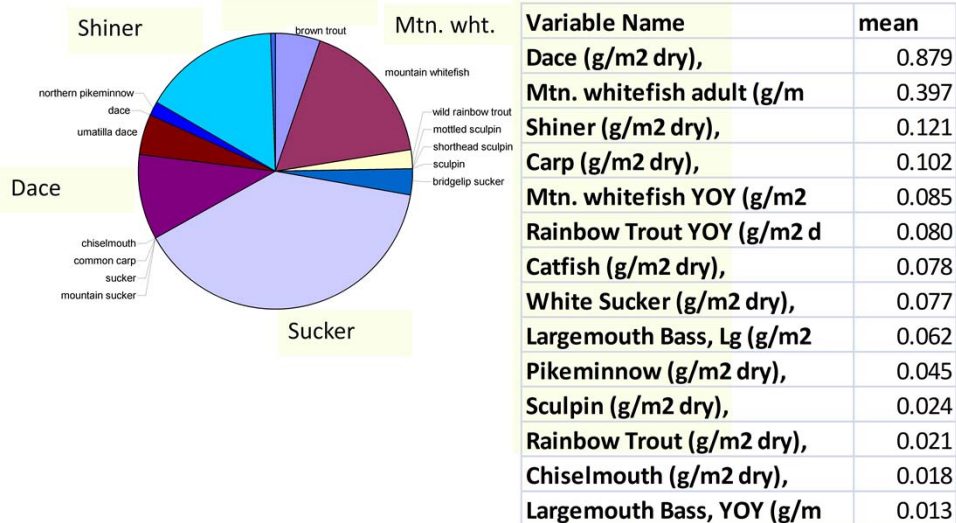
Comparison with observed data

Results are quite similar to what we saw previously.

Fish no longer exhibit explosive increases in biomass

Save the results. They are also saved in your directory as **LBR Glenwood 3 Results.aps**.

Simulation of fish suggests suckers are still too low

Variable Name	mean
Dace (g/m2 dry),	0.879
Mtn. whitefish adult (g/m	0.397
Shiner (g/m2 dry),	0.121
Carp (g/m2 dry),	0.102
Mtn. whitefish YOY (g/m2	0.085
Rainbow Trout YOY (g/m2 d	0.080
Catfish (g/m2 dry),	0.078
White Sucker (g/m2 dry),	0.077
Largemouth Bass, Lg (g/m2	0.062
Pikeminnow (g/m2 dry),	0.045
Sculpin (g/m2 dry),	0.024
Rainbow Trout (g/m2 dry),	0.021
Chiselmouth (g/m2 dry),	0.018
Largemouth Bass, YOY (g/m	0.013

The observed composition we saw previously may be compared with statistics from the AQUATOX simulation.

We will go through the output window to show how to output statistics from a graph. The steps are

1. Produce the graph that you are interested in statistics from. In this case, all fish in the simulation.
2. Use the Menu or "right click" on the graph and select "Statistics from Graph"
3. Export to Excel if you want to change formatting or sort

These results show that the top biomass for fish in the simulation are Dace, Mountain Whitefish , then Shiner, Carp, Catfish and White Sucker.

The observed data suggest that the top numbers observed were Sucker followed by Shiner, Mountain Whitefish, and Dace.

So the modeled composition is not bad but could be improved, especially by calibrating to increase Sucker biomass. Steps to take could be to examine the feeding preferences for this category, examine abundance of prey, examine other parameters in "underlying data."

Additional Calibration?

- We have now completed the first set of steps that enable you to apply an AQUATOX simulation to your new site.
  - Physical Characteristics
  - Nutrient and Organic Matter Loadings
  - Biotic Composition & Food Web
  - Comparison to Data
- If you have a site to model with AQUATOX, you would be well served to follow the steps in Labs 2 and 3 closely.

We will stop fiddling with the Glenwood Bridge study, but you are welcome to continue in your spare time.

Within these labs we have set up your site's physical characteristics, its nutrient and organic matter loadings, and we have set up your site's biotic composition as well.
The next steps you might take would be comparing your simulation against observed data in an iterative calibration process (if necessary). If you have an independent set of data you could then validate your calibrated model against those data points. Finally, you can use the calibrated (or validated) model to play "what if" games or forecast what the effects of changing conditions might be in your system. Of course, you can also examine the effects toxicants might have on the system as we will discuss in detail on day three.