DSM2 Bay-Delta Tutorial 3: Source Tracking (Fingerprinting)

Purpose: The purpose of this tutorial is to use the source tracking capabilities of the model to create a fingerprinting study. We will set up both volumetric and concentration-based fingerprinting and visualize the results.

1. **Reopen the historical tutorial**
   a. In windows, navigate to *{DSM2_home}**tutorial**historical*.
   b. In the GUI, open historical_tutorial.

2. **Create a model for source tracking:**
   In the background, source tracking imposes a computational cost on QUAL that is the same as one additional constituent per source. For this reason, it is courteous to create an entirely separate model for source tracking.
   a. In the GUI, navigate to the simulation.
   b. Right click and create a new model. Name it *historical_tutor_qual_fingerprint*.
   c. Add the layer *qual_standard_parameters.*
   d. Add the standard historical EC model layers. Go to the Boundary Concentration page. Add the *delta_historical_qual* and *dicu_ec* layers.

3. **Define the source groups.**
   a. Groups are defined in the QUAL Groups View. Group matching criteria reference the same boundary names that are created in hydro and matched in the boundary concentration assignments.
   b. Create a layer called tutorial_fingerprinting. Look at the boundary inputs and devise patterns that will isolate:
      1) mtz: Martinez tidal boundary
      2) sjr: Vernalis on the San Joaquin River
      3) sac: match Sacramento River and Yolo. You can use two group members or a single member with the (sac|yolo) syntax.
      4) ag: All the DICU – don't forget BBID in the reservoir source-sinks. You will find the dot-star wildcard useful for this (dicu_.* or dicu_drain_.*).

5) east: match the eastside streams such as calaveras, moke, consumnes.

4. **Define volumetric inputs**
   a. Create a layer called *tutorial_volumetric_fingerprint* in the Boundary Concentration view. Go through each of the time series input panels for QUAL and create an equivalent input that has a constant value of 100. Call the constituent *volume.* Hint: for the ag sources, you will want to do some of your work in Excel so that you can cut and paste.
5. **Define the fingerprinting output**
   a. Specify Clifton Court concentration output for each of the source groups that you defined for both EC and *volume*. The name should be clifton_court, the concentration should be ec or volume and the interval should be 1day. Avoid redundancy -- you do not need to put the constituent name or the source into the output name: ie, use “clifton_court” for the name, not “clifton_ag” or “clifton_ec”.
6. **Run HYDRO and QUAL for One Year**
   a. Change the model name in qual_ec.inp and run HYDRO and QUAL for one year in 2002. Start QUAL a day later to avoid mass conservation errors in the first hour. Make sure the init_conc variable is set to zero so that there will be no initial condition contribution for any variables (note: this is not always the case -- for a volumetric fingerprint, it may be useful to make this concentration 100 if you want to include initial conditions in the fingerprint analysis).
7. **Process the output**
   a. Use VISTA or HEC-DSSVUE to open up the output file. Copy May-September concentrations for each location. Paste the output into a new sheet in the Excel provided called excel_fingerprint.xls, which you can use as a reference. Use the “stacked area plot” in Excel (one of the standard Excel plot types) to plot up the fingerprint results.