DSM2 Bay-Delta Tutorial 2: 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*. (folders and files are copied as described in the Delta tutorial 1)

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 useful to comment out source tracking as a standard course of running DSM2. But when you desire source tracking, you can uncomment it as follows:
   a. In *historical_qual_ec.inp*, locate the GROUPS include section.
   b. Uncomment the group definitions for source tracking (delete the # sign at the start of the line). You may wish to review the referenced file to see how the groups are identified.
   c. Similarly uncomment the two fingerprinting files – the ones that have "source_track" in their names.

3. **Define volumetric inputs**
   a. Create the QUAL volumetric input file. Copy *historical_qual_ec.inp* and rename as *historical_qual_vol.inp*.
   b. Modify the concentration blocks. Go through each of the node and reservoir concentration files for QUAL ec. Modify the constituent (variable) to *unit*, value (FILE) to constant, (PATH) to 100. This step is conceptually simple, but will produce a large file – feel free to break it into several files if you prefer. If you are using Notepad++, you may want to use its column delete/copying features (press alt while you make your selection).

c. Compare what you produced to the existing files in common_input that have “volumetric” in their names (node and reservoir concentration). Are they the same input? How could you test this using the echoed output?

4. Define the fingerprinting output

a. Specify Clifton Court concentration output for each of the source groups defined in the previous step, for both constituents: *ec* and *unit*, in block OUTPUT_RESERVOIR_SOURCE_TRACK. The name should be clifton_court, the concentration (variable) should be ec or volume and the interval should be 1day. Avoid redundancy or use of the source in the output name: i.e. use “clifton_court” for the name, not “clifton_ag” or “clifton_ec” . Because the source information is recorded in the F part of output dss file.

b. Similar specification could be defined for channel source track in block OUTPUT_CHANNEL_SOURCE_TRACK. Pick any channel you are interested and do the definition.

5. Run HYDRO and QUAL for One Year

a. Using *historical_hydro.inp, historical_qual_ec.inp, historical_qual_vol.inp* as the launch files, 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 (in SCALAR block) is set to zero so that there will be no initial condition contribution for any variables (note: for a volumetric fingerprint, it may be useful to make this concentration 100 if you want to include initial conditions in the fingerprint analysis).

b. Open the output file (*historical.dss*), and examine the results.

6. Process the output

a. Use VISTA or HEC-DSSVUE to open up the output file. Copy May-September concentrations source track of Clifton Court 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.