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### Data S3

### Estimate stream metabolism for all site years

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### File list

run\_streamMetabolizer\_raymond\_K600.R

inspect\_model\_fits.R

compile\_sm\_models.R

compile\_all\_model\_results.R

compare\_cbp\_met\_with\_different\_depths.R

**Description**

These files run metabolism models on all the data and compile, inspect and plot outputs. They require that the steps in DataS2 have been executed and they reference the NHCsite\_metadata.csv file. Comparisons to historical data rely on data from Hall 1970 and 1972, which has been compiled and included in DataS1 for user convenience.

run\_streamMetabolizer\_raymond\_K600.R – Runs stream metabolizer models on the prepared datafiles (see DataS2) using a Bayesian partially pooled model with both observation and process error. Models are run on individual site years of data.

inspect\_model\_fits.R – Functions for evaluating, reformatting, and plotting stream metabolizer output objects. This script can be sourced at the beginning of a file and doesn’t need to be opened.

compile\_sm\_models.R – Compiles and filters all model output objects removing bad data fits, out of bounds solutions and days with flow conditions that violate model assumptions. Plots model fit information for the supplementary materials.

compile\_all\_model\_results.R – Compiles metabolism estimates from stream metabolizer with reported values from Hall 1970 and 1972. Converts all data into units of g C from g O2. Calculates summary metrics including peak metabolic windows and cumulative annual metabolism. Generates data included in Table 1.

compare\_cbp\_met\_with\_different\_depths.R – Compares the metabolism estimates from site NHC\_5 calculated with modern depths to those re-estimated using adjusted depths to match those reported in Hall 1970.