SSD ANALYSIS TOOL

# DATA

This tool uses a simple copy-paste process for data input.  We recommend that data be set up in Excel or similar where the rectangular region containing the data are copied and then pasted into the input field.  An example is provided with a download button near the top next to the reset button.

1.     Provide a simple rectangular data table with results for each case/species arranged by rows.  Extra annotations, formatting, etc may need to be removed.  Do not copy whitespace, use the minimum possible region containing the data.

2.     The data block should have a header line with names.  The column names can be flexible, but they should be unique and useful for chosing the variables for analysis if there is any possibility for confusion.  The names are not used in the output except in a view of the input data and variable selections.

3.     The tool warns when multiple entries have the same species labels.  The analysis can still proceed.  The user is responsible for resolving, if appropriate.

4.     For the most reliable performance, paste only columns required for the analysis.  The tool is designed to allow for extra columns in the data, but we cannot guarantee that the program will not confuse columns versus the users intentions.

## VARIABLE ROLES:

Response/NOEC value:  Only numeric variables.  If more than one column of numeric data is supplied, the one with the most unique values is populated into this selection box.  If more than one variable meets the previous criterion, a normal goodness-of-fit test is used as a tie-breaker.  All numeric variables remain in the list of potential analysis variables, these rules only provide a guess to which variable is the one intended for analysis.

Species label:  To be most general, this could be numeric or character.  The first one with the most unique values is populated.  The program will respond with an error if the column chosen is not unique for every data value.

Grouping variable:  When the grouping checkbox is selected the column with the fewest unique values, but more than one, is populated.  Most groups should have at least two data values.  Any group label with a single value may invalidate the grouping statistical analysis.

The tool will allow variables to play dual roles (e.g., for a grouped analysis it may be of interest to label observations by taxonomic group instead of unique species labels).

# COMPONENTS OF THE ANALYSIS

The SSD analysis tool fits log-logistic and log-normal distributions.  In SSD literature other distributions are occasionally used, but at typical sample sizes it is very difficult to statistically differentiate distributions.

There will always be a best fitting distribution, but such a selection method has high error rates. We recommend evaluating distributions based on Anderson-Darling Goodness of Fit statistic, and if both distributions provide a suitable fit, select the more conservative HCx value as the SSD output. The output in MS Excel format provides the numerical results, while the PDF output provides graphical summaries.

The user may optionally request leave-one-out and add-one-in analyses to investigate the sensitivity of the fits to the data in hand, and the potential that a single new observation could move the HCx to various degrees. The user may also chose to complete a grouping analysis to determine if there are substantial patterns of differences in sensitivity with respect to trophic level/taxonomic groups.

For more information, please consult the User Guide

# DISCLAIMER

No warranty is made.  It is the responsibility of the user to ensure that the application of this tool is appropriate for the data being analyzed.