CLIP Cookbook

Part 1: Basic Splicer Operations for use on a UNIX platform

A. Prepare Data

Use a browser to open the chosen data file from JANUS (see http://www-odp.tamu.edu/database/).

Once the data file has been opened in your browser, download the data to your selected folder; use the "Save as…" command in your browser. Remember to change the name of the data to indicate which hole and type of data you are saving.

Open the data file in a text editor. Delete all the extraneous information (e.g., html code, column headers). Do not forget that there is also extraneous information at the bottom of the data table. Once the data file has been modified, save it. The file is now ready to open in Splicer.

Run Splicer. Once in Splicer, all commands are executed with the left mouse button unless otherwise stated. The "dismiss" button at the bottom of any dialog window will close the window.

B. Opening data in Splicer

In the File menu choose: "Open" and then "Data file… (Ctrl+O)"

A dialog box will appear (see Figure 1, next page). Use the "Directories" section to locate the folder that contains your data files.

In the "Files" box highlight the data files of one type (e.g. susceptibility) for as many holes as you wish to compare. You must open all the holes you want to compare at once.

After highlighting the files use the "→" to move them to the "selected" files window (deselect with the "←" arrow).

Using the "File Format" button, choose the format which fits your data.

Hint: An incorrectly chosen file format, or wrongly formatted data, will result in an error opening data. If you are unsure of the data format, "preview input" in the File menu to view the column and header format in your data files. If you get an error message reading "Bad JANUSCLEAN….", then there is a problem in the data file, such as missing values. You should re-open the file in Text Editor and examine it closely for missing values (especially mbsf values). The file needs to be corrected before it will open.
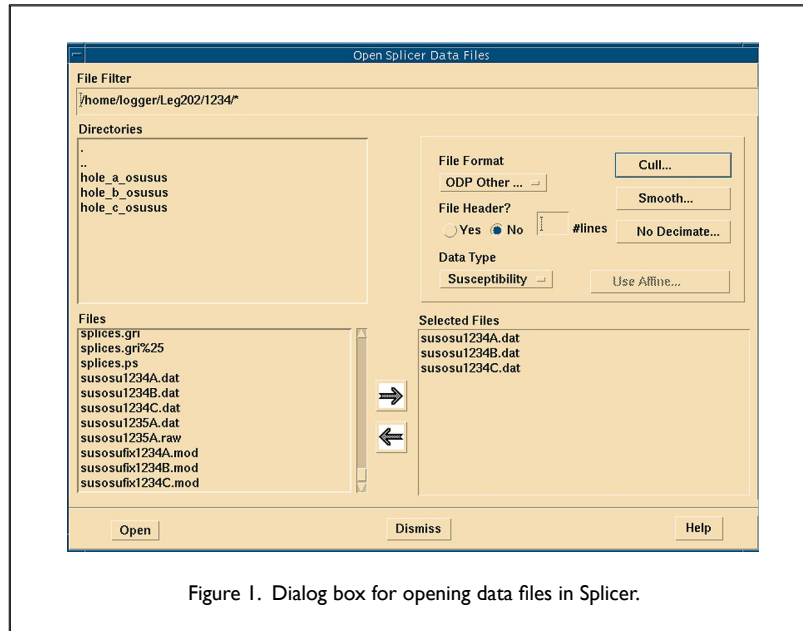
Figure 1. Dialog box for opening data files in Splicer.

Use the "Data type" button to select the type of data you are opening. For the method described above this will be "JANUS standard – all extraneous information removed." If it is a non-standard data type choose "other," enter the column number where the data values are, and if there are headers, click "yes" and enter the number of rows.

Click the "Open" button when you are ready to open the files. Optional: You may use the "Cull," "Smooth" and "Decimate" buttons to (de)activate or change the parameters for these operations when opening data. To apply a preexisting composite table (affine table) click on the "use affine" button, navigate to, and select the affine table you wish to apply. For more detailed help click on "Help" at the bottom right of the dialog box.

Producing a common depth scale between holes (Meters Composite Depth/mcd) :

In the Process menu choose "Composite…"

A "Composite" dialog appears (see Figure 2, next page) which allows you to assess the cross correlation in a defined window around the chosen tie points between the cores you are comparing, and then apply the chosen depth shift to the core(s). **Hint:** Always composite from the top down.

To make a tie use the middle mouse button to select a point on the reference curve, and the right button to place a tie point on the floating (non-composited) curve. Holding either button down and moving up or down over the respective curve allows you to slide one core relative to the other while viewing the correlation in the "Composite" dialog window.
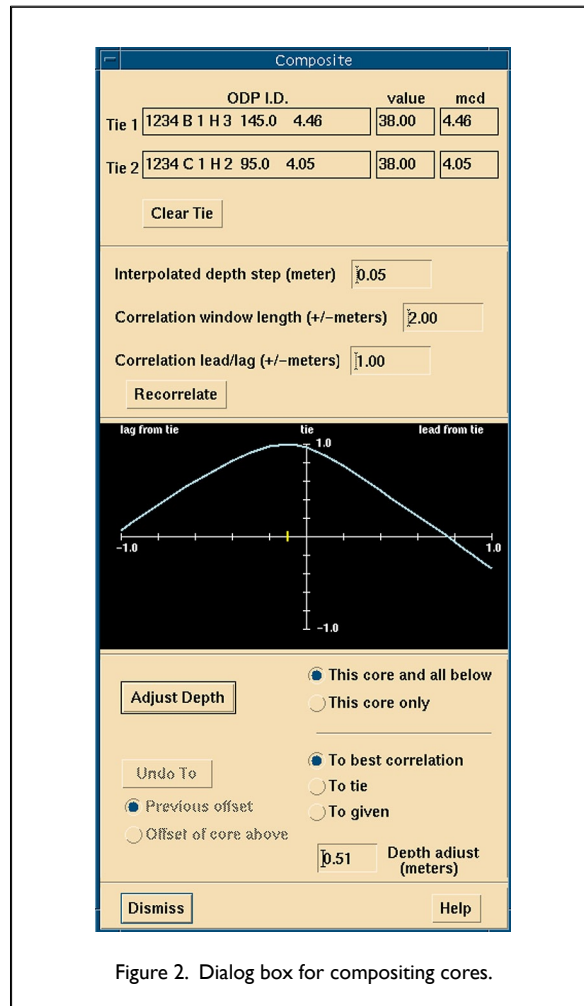
Figure 2. Dialog box for compositing cores.

To apply the tie point and adjust the core and all below it (unless you click on "this core only" in the "composite" window), click the "Adjust Depth" button in the "Composite" window. Note that by default Splicer adjusts the depth to create the best correlation between the compared cores; to override this you must click on "To tie" instead of "To best correlation" within the "Composite" window before clicking adjust depth.

To remove the tie, or deselect the chosen cores, click the "Clear Tie" button.

To save a table of composite tie points (the affine table), go to the File menu and select "Save…" followed by "Affine table… (Ctrl+A)."

To save your data files with MCD depths, go to the File menu and select "Save…," followed by "Data file…"

C.   Producing a continuous sediment section by "splicing" overlapping cores:

Open the depth adjusted data files (i.e. the data files saved with MCD depths) you wish to splice together.

In the Process menu choose "Splice" followed by "Constrained…" A splicing dialog window appears (Figure 3) which allows you to select cores for the splice and shows the cross correlation between curves at potential tie points.
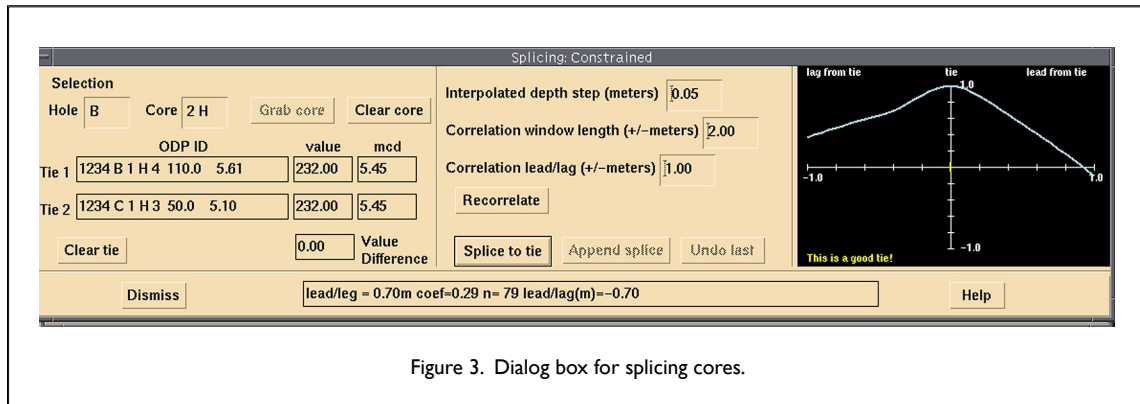
Figure 3. Dialog box for splicing cores.

To select a core to add to the splice, go to the main window and click on the curve you want. Go to the "Splicing: Constrained" dialog window and click on the "Grab core" button. The core will appear in the right hand panel of the main window (the Splice panel). To remove the core, click the "Clear core" button.

To choose a splice tie point to jump to another core, select the core you wish to jump to, go to the splice panel of the main window (right column) and hold the middle mouse button down, moving up and down over the splice curve to find a good tie point. Once you have decided on a tie point, release the middle mouse button and click the "Splice to tie" button in the "Splicing: Constrained" dialog window.

To save your Splice table (your table of splice tie points) go to the File menu and choose "Save…" followed by "Splicer table Ctrl+S." To save your spliced data files, go to the File menu and select "Save…" followed by "Spliced Data Record."

Questions and problems should be directed to stuartr@ldeo.columbia.edu

Part 1I: Basic Sagan Operations for use on a UNIX platform

After opening core and log data sets, there are two ways to map core data into the log data, automatically and manually.

A.   Automatically

This method must be done before any manual ties are chosen.

In the Process menu choose "Core-Log Auto Correlate…"

A "Core-Log Depth Matching" dialog window will appear (see Figure 4).
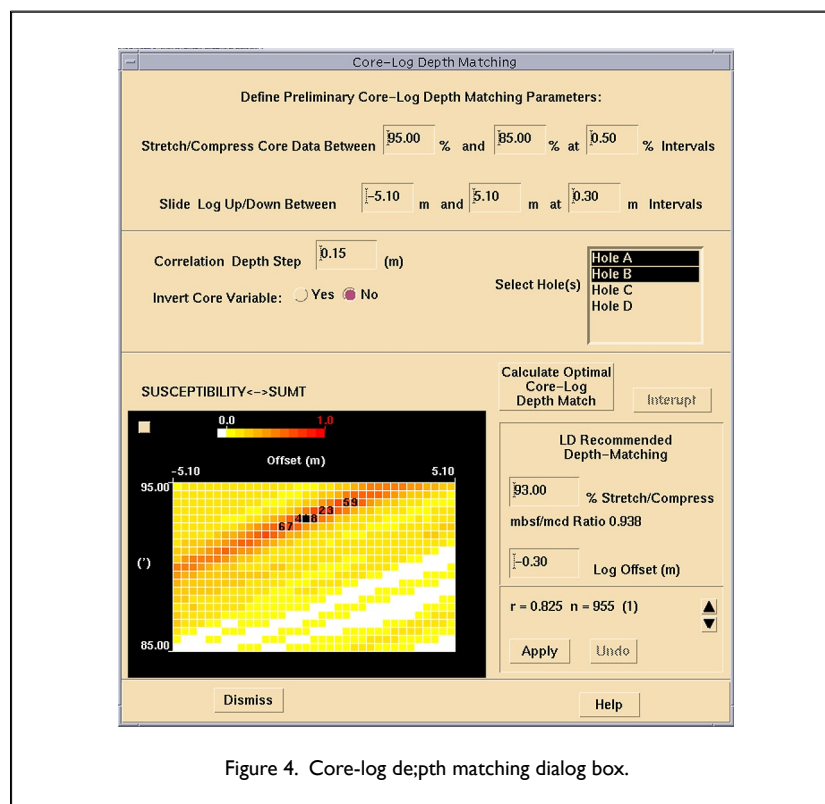

Figure 4. Core-log de;pth matching dialog box.

The autocorrelation routine will calculate the correlation matrix between core and log data for a user defined set of core data compressions and secular log data adjustments. Since the mcd depth scale is usually expanded by ~10%, the default compression window

(95%-85%, 0.5% steps) is a good starting point. The log adjustment corrects for offsets between drillers and logging depths which are commonly less than a couple of meters.

Click on the hole(s) you wish to correlate with the log data (usually the hole you logged in) and click on the "Calculate optimal core-log depth match" button to generate the cross-correlation matrix.

Apply the compression and log adjustment by clicking the "Apply" button at the bottom of the dialog window.

Hint: This routine will apply one compression factor to all core data and is a good starting point but will not provide a meter scale depth map for core-log integration. Manual ties can be added to refine the core log integration.

B. Manually

Allows the application of any number of tie points to map (stretch/compress) the core data to the log reference.

Double click on the core you want to tie to the log. The core will appear in the right hand window next to the log curve.

To choose a tie point on the core, click on the point with the middle mouse button.

To choose the equivalent point on the log reference curve, click on the log curve with the right mouse button. The core will project onto the log curve and the cross correlation between the two curves within a user defined window appears to the far right of the Sagan window. Hold down the right mouse button and slide up and down with the mouse to assess different matches.

To add the tie to the tie-list click "Add tie to list."

Choose more tie points the same way until you have as many tie points as you wish for the core. Then click the "Apply Ties" button to apply the ties to the chosen core.

C. To save your ELD table (your table of core-log tie points)

In the File menu select "Save…" followed by "Equivalent Log Depth Table…Ctrl+E"

To save your data files with MBSF, MCD, and ELD depth scales go to the File menu and select "Save…" followed by "Core data mbsf → [mcd] → eld Ctrl+D"

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Part III: How to run CLIP from Mac OS X (assuming CLIP is already installed on UNIX)

Notes: The following description should allow you to run CLIP software on a Macintosh that uses OS X. Text in `Courier font` represents various Unix commands and paths. In this description, `brg0` is the name of my UNIX machine whereas `logger` is the name of my Mac. `%` represents the OS X unix prompt in an X11 window. `*%` represents the prompt when you are logged into a UNIX server through X11.

Stages 1 and 2 are only necessary for users who do not have X11 or Fetch installed.

1. Download X11 from the apple website (http://www.apple.com/macosx/x11/)

2. Ensure you have a method of uploading files from your Mac to your home directory on your Unix system. A common method of doing this is to use a program called Fetch. More information about Fetch can be found at http://fetchsoftworks.com. Alternatively, contact your system administrator and ask about the best way to upload files from your Mac to your home directory.

3. Using your internet browser, download the desired data from JANUS (http://www-odp.tamu.edu/database/) or the logging database (http://www.ldeo.columbia.edu/BRG/ODP/DATABASE/index.html). Remember to ensure the file name indicates the correct hole or site.

4. Transfer these files directly to your Unix home directory (using Fetch or a similar application).

5. Open X11. Be sure to set the preferences to "emulate three button mouse" (otherwise you will not be able to use the CLIP software!).

6. To allow an external CPU to display on your Mac screen you need to type either:
   `% xhost +`

   or:

   `% xhost nameofunixmachine`
   (i.e `% xhost brg0`)

   at the prompt in the *X11* terminal window.

7. Now connect to your UNIX machine using the ssh command:

   `% ssh brg0`

8. You will probably be asked to enter your password.

9. Now you need to enable the UNIX machine to display on your Mac by typing :

    ```
    *% setenv DISPLAY macname:0.0
    ```

    (i.e. for a computer called logger:)

    ```
    *% setenv DISPLAY logger:0.0
    ```

10. Open a UNIX text editor by typing:

    ```
    *% dtpad
    ```

    If this fails to open a text editor then:

    ```
    *% set path = ($path /usr/dt/bin)
    ```

    Then type:

    ```
    *% dtpad
    ```

11. Use the text editor to open, edit and save your files (as described in Part I of this document).

12. To run Splicer or Sagan simply type:

    ```
    *% splicer
    ```

    or

    ```
    *% sagan
    ```

    at the prompt in the X11 terminal window.

13. Open the required data files, as per the procedure described in CLIP Manual Parts 1 & 2.

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