***Align* Documentation**

**1. Downloading & Preparation**

First, download the ZIP archive named Align. Unpack the ZIP on your Desktop to create a new directory with the same name. *Note that Align will save files to this directory*. Also, check that you have installed R on your computer. Additional required R packages include shiny, dplyr, ggplot2, ggtext, viridis, and align (an R package that we wrote that hosts the Hay et al. (2019) algorithm translated into R; available through Cran R Project: https://cran.r-project.org/web/packages/align/index.html). For those who are not already experienced with R, we strongly recommend using RStudio as your coding environment.

**2. Starting the DTW GUI**

Double-click on Align.r, which will open the entire script in RStudio. Click the small green triangle near the center-top of the RStudio window to run the GUI script. This will open a separate window (the GUI) that you will use exclusively in the remainder of this guide. We do not recommend modifying any portion of the code unless you have prior experience with R and Shiny.

**3. Preparing your data**

Before you can utilize *Align*, you must first format your data correctly. Two example datasets (Jiang et al., 2012; Husson et al., 2015) are included in the correct data format, which we recommend you mimic in the preparation of your own data.

Your target dataset should be saved in a .csv file with two data columns: δ13Ccarb in A, and stratigraphic height in B (include header labels). Your candidate dataset(s) should be saved in a .csv file with two data columns for each candidate record and a blank column between candidate datasets. For example, δ13Ccarb data from Candidate #1 in A, stratigraphic height from Candidate #1 in B, column C is left blank, δ13Ccarb data from Candidate #2 in D, stratigraphic height from Candidate #2 in E, and so on (include header labels for each data column). You can include up to 3 candidate datasets in your candidate data file.

**4. Running the DTW algorithm with the GUI**

Once you have downloaded the necessary programs and packages, and prepared your data, you are ready to use *Align*. For these steps, remain in the “Generate New Alignments” tab at the top of the GUI window.

**4.1 Uploading your data**

First, using the “Browse…” button, upload your target dataset file and give it a name in the textbox below (e.g., Target). Second, using the next “Browse…” button, upload your candidate dataset(s) file. Indicate the number of candidate datasets in your file in the next textbox and name each of the candidate datasets in the last textbox. Note that candidate names should be separated by commas but no spaces (e.g., Candidate1,Candidate2,…).

**4.2 Viewing your data**

Once you have uploaded and named your data, click the green “Plot” button to verify that your data look correct. You can use the “Candidate record” drop down menu to select which candidate record you would look to view plotted next to the target record. You must plot these data before moving on to the next step.

**4.3 Running the algorithm**

Once you have uploaded and plotted your data, click the green “Run DTW algorithm” button to run the DTW algorithm and generate the alignment libraries for these target–candidate pairings. Look for notifications in the lower right hand of the window indicating algorithm progress. Plots of each target–candidate alignment, as well as accompanying .csv files, are output in the “Output\_Data” and “Output\_Images” directories within your [*candidate name*-*target name*] directory.

**5. Alignment library viewer**

The alignment libraries for each target–candidate pairing can be viewed using the GUI viewer tool. Navigate to the “Alignment library viewer” tab at the top of the GUI window to use this tool.

**5.1 Narrowing alignment libraries**

First, use the “Candidate record” drop down menu in the upper left corner of the window to select the candidate record of interest. Next, use the two slider bars to *narrow* the alignment library as desired. The xc cutoff sets the correlation coefficient threshold for inclusion in the library (default is set to 0.80). The overlap cutoff sets the percent overlap threshold for inclusion in the library, where a 10% overlap threshold indicates that the aligned candidate record overlaps with at least 10% of the target record (default set to 10%). Lastly, type a nickname for these criteria: this will be used to save your narrowed alignment library data so you can experiment with different narrowing criteria without ‘losing’ previous libraries. Once you have selected your criteria and provided a nickname, click the green “Narrow alignment library” button to generate the narrowed library.

**5.2 Plotting different candidate record alignments**

Once you have clicked the green “Narrow alignment library” button, the alignments that fit the indicated criteria will populated the lower “Candidate record” drop down menu. To display these alignments, select the alignment of interest from the drop-down menu and click the green “Plot alignment” button. Each plot is output to the “Output\_Images” directory in a new directory named according to the criteria nickname you provided above.

**Additional Resources**

This documentation provides a simple walk-through for using *Align*, as detailed in Hagen et al., 2023. For additional details, please refer to the publication.