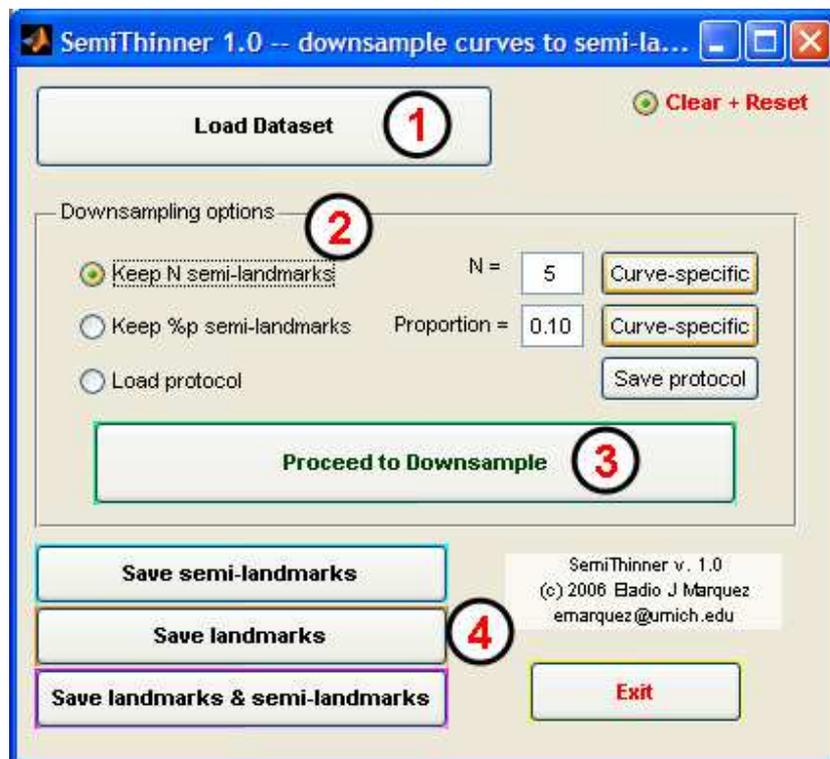


SemiThinner: Utility to downsample curves to sets of equal numbers of semi-landmarks, version 1.02 (compiled 03/11/14)

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Reference Guide

All functions in SemiThinner (semithnr) are accessible from the main panel. An overview of the main functions available in this program is schematized in the following figure and explanation:



Description of functions:

- 1. Load Dataset** button: before a dataset is loaded, all buttons (but Exit) are disabled. As of August 2006, SemiThinner accepts only 2-D landmark data in James Rohlf's TPS format, in which curves are grouped under CURVES and POINTS statements. All specimens in the dataset must have the same number of CURVES. SemiThinner downsamples each curve so that the number of POINTS (semi-landmarks) is the same for each curve across all specimens. It also allows

different curves to produce different numbers of points. A sample dataset is packaged with this release.

- 2. Downsampling options:** in order to activate the Proceed to Downsample button, at least one option must be selected. These options are used to determine the number of points (semi-landmarks) that each curve will have after downsampling. The first option, Keep N semi-landmarks, allows defining the actual number of points to retain per curve. This number can be constant for all curves (N= box) or curve-specific (via dialog box). The second option, Keep %p semi-landmarks, allows defining the number of points to downsample to as a proportion of the number of points in a curve. Since the number has to be constant for each curve across specimens, the actual number used is the specified proportion of the smallest number of points in a curve sampled over all specimens, rounded to the next (upper) integer. As in the first case, proportions can be specified on a per-curve basis, via dialog box.

The last option allows loading a previously saved protocol. A protocol is a simple text file containing a vector (either row or column) of counts or proportions that indicate the program how many points to retain for each curve. The protocol has to have one number per curve in order to be successfully imported. If these numbers are higher than one, they are interpreted as actual counts of points. If they are above zero and below one, they are interpreted as proportions.

Irrespective of the downsampling method, SemiThinner internally forms a protocol of absolute (rounded if necessary) counts of semi-landmarks. This internal protocol can be saved by pressing Save protocol, for future use. This button is enabled as long as there is a valid protocol in use, and it saves the most recently edited protocol. Two sample protocols are packaged with this release.

- 3. Proceed to Downsample:** the most recently edited protocol will be used for downsampling.
- 4. Save buttons:** SemiThinner does not modify the coordinates in the input dataset in any way, but merely reorganizes them into columns of equal length. You can choose to save only the semi-landmarks obtained from downsampling curves, the landmarks originally input, or both landmarks and semi-landmarks. In all cases, ordering in input file is preserved, with landmarks occupying columns at the left of semi-landmarks if both are included. A sample output file containing both landmarks and semi-landmarks is packaged with this release.

Note: if you need a format different from TPS, or if you need a version of SemiThinner for 3-D landmark data, you can send me an annotated sample data file so that I could include it among the formats compatible with SemiThinner.