

**tpsUtil**

# **USER MANUAL**

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# Introduction

## 1 Introduction

### 1.1 Contents

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### 1.2 How to get started using this software

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The purpose of this program is to provide various file conversion and other utility functions to help one manipulate the TPS files that are used in my tps series of morphometric programs.

From the [main dialog window](#), one should first select an operation to be performed because this influences the types of input and output files that can be selected. Then select an input and an output file. Note that for some operations only the input directory name is needed. In this case *select any file* in that directory. Because this program performs such a miscellaneous collection of operations, they are hard to describe here in summary form. Browse this help file to find the descriptions of the things this program can do.

Next click on the button labeled either "Create" or "Compute". If the button is labeled "Create" then that means that the output file will be produced immediately. For most of the operations the button will be labeled "Compute" and another window will open that will allow you to select various options before you click on its "Create" button to actually produce the output file.

Both 32 bit and 64 bit versions of the program are available (though 64 bit are probably seldom needed by this software).

On some computers there may be a problem when the program attempts to save configuration information in an INI file. You can add the -E parameter to the Windows shortcut icon to force the program to save the INI file in the same directory as the program itself.

I hope you find this program useful. Please contact me if you would like additional features.

# Program windows

## 2 Program windows

### 2.1 Main dialog window

---

This window consists of four sets of controls and a menu.

In the operation region there is a drop-down list in which one can select the desired operation to be performed.

#### **Build, append, split, or rearrange specimens in a file:**

1. "Build tps file from images" will open a new [window](#) with all of the graphic files in the input directory presented in a list box. Select one or more of them and click the "Create" button to create a new TPS file. The new file will contain only a "LM=0" field and an "image=" field corresponding to each of the selected graphics files. An option is available to store just the image file name or the complete path to the image file.
2. "Randomly order specimens" will scramble the order of the specimens in a TPS file. It will store the original sequence number in the variables field for each specimen using the keyword "OrigNum".
3. "Restore original order" will reorder the specimens in a TPS file back into their original order using the "OrigNum" keyword in the variables field.
4. "Delete/reorder landmarks" will open a new [window](#) listing the landmarks (landmark numbers). You can delete landmarks and/or reorder them. All specimens *must* have the same number of landmarks.
5. "Split NTS file" will open a [window](#) that will allow you to separate an NTS rectangular matrix into a series of separate matrices all in the same file. The purpose of this is, for example, to break apart a combined partial warp scores matrix into separate matrices for each original group.
6. "Split TPS file" will take a TPS file apart and write each specimen to a separate file with the same name as its image file (but with an extension of .TPS).
7. "Append files" will open a new [window](#) with the names of all the TPS or NTS files in the selected directory. You can change the order of the files and exclude files. The remaining files will be combined and saved in the output file. Optionally, you can also produce a group ID file (an NTS file with the group number of each specimen in the combined file) and a group N file (an NTS file with the sample sizes of each group).

#### **Convert file format, add or create file of variables:**

8. "Convert tps/nts file" will convert landmark coordinates into different file formats. Input TPS files can be converted to NTS files and NTS files can be converted to TPS, M (Matlab), or CSV (Excel) file formats. It will open a [new window](#) to provide options. Note: for this conversion all specimens must have the same number of landmarks and dimensions except for the conversion of TPS files to NTS files if the "Separate matrices" checkbox is checked. Curve and outline points are ignored.
9. "Add variable" opens a [window](#) in which one can specify a keyword and a value to be entered in the variables field for every specimen in the input file.
10. "Build variable matrix" will create a output file compatible with the NTS, M, or CSV formats. The file will contain a row for each specimen and a column for each keyword in the variables field of the input TPS file. The values (which should be numeric) will be stored as elements of this matrix. The operation is useful, for example, to automatically build a matrix of independent variables for use by the tpsRegr program. The order of the variables in the first specimen is used as the order of the columns in the output matrix. The program will check for variables used in subsequent specimens that were not used in the first specimen. Variables used in the first specimen but not in some of the subsequent specimens will be given a value of 999.

#### **Delete or reorder landmarks, convert curves and outlines:**

11. "Delete/reorder landmarks" opens a window where you can delete or reorder landmarks. The change applies to all specimens.

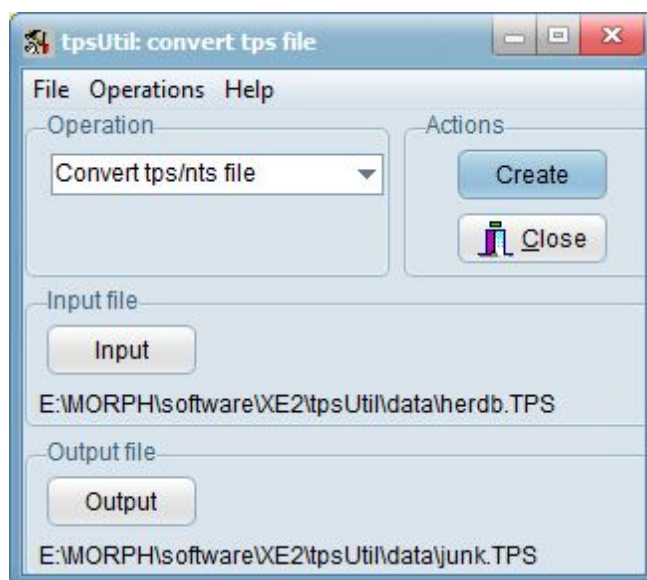
12. "Delete outlines & curves" will remove any outlines or hand drawn curves from a tps file.
13. "Convert tps XY outline to landmarks" will delete any landmarks present and treat the outline x,y coordinates as the coordinates of landmarks.
14. "Append tps curves to landmarks" will append points along curves (points marked with the pencil tool in tpsDig) as landmarks in addition to any existing landmarks. The number of curves must be the same for all specimens. In addition, the number of points on the corresponding curves must be the same for all specimens (e.g., the number of points on the 2nd curve must be the same on all specimens).

## Miscellaneous operations:

15. "Make landmark pairs file" will create an NTS file listing the paired landmarks. I can also save a file in which the landmark configurations have been reflected (needed as one step in further analysis).
16. "Make links file" will display a window in which one can specify pairs of landmarks to be connected by a link in the visualization windows of some of the tps programs.
17. "Make sliders file" will display a window in which one can specify which landmarks are to be treated as semilandmarks by letting them slide between two other points.
18. "Unbend specimens" performs a specialized operation that is not expected to be appropriate for most datasets. It will open a [window](#) in which you can define a set of points to be fit by a quadratic curve. Then a matrix of transformed coordinates is produced using perpendicular projections of the landmarks onto this curve. Curve and outline points are ignored.
19. "[Compute area & perimeter](#)" computes the area enclosed by a set of selected landmarks and the perimeter. These will be in pixels unless a scale factor is present and selected. Circularity,  $4\pi A / P^2$ , is also computed.
20. "List images in TPS file" will simply list the names of all the images in the selected TPS file in the output listing window as well as writing it to a CSV file that can be imported into Excel.
21. "Remove path from image name" will change the IMAGE= field in a tps file to just the file name rather than the full path to the file. In order to use the resulting file with tpsDig or tpsSuper this .TPS file will have to be located in the same directory as the image files.

In the Input file region there is a button to allow one to specify the name of the input TPS file. For the "Build TPS file from images" option one should select any file in the desired directory. In the Output file region there is a button for the specification of the name to be given to the output file.

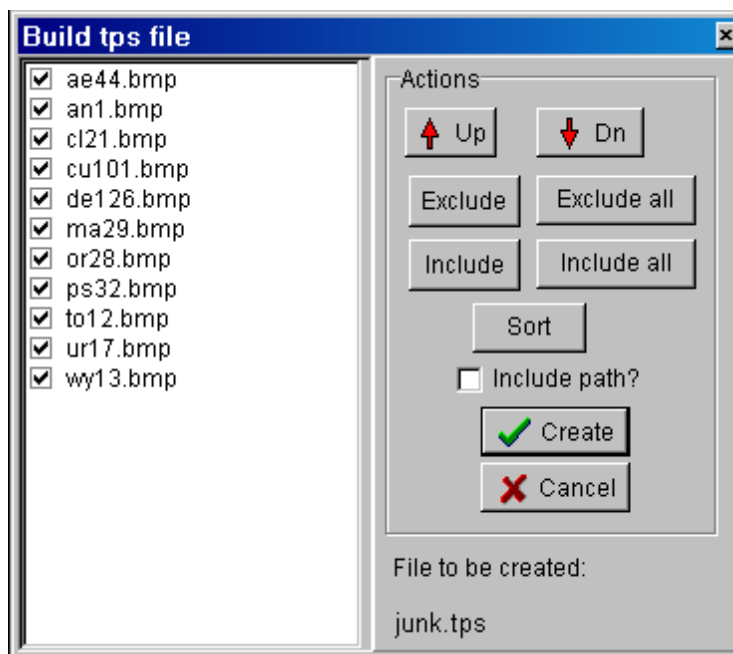
In the actions region one can select "Compute" to actually carry out the operation or "Close" to exit the program.



## 2.2 Image files window

This window displays the names of all of the graphics file. Initially they are all have their checkboxes checked. You can uncheck the boxes of files you do not want to include. The “Select all” and “Select none” buttons allow one to quickly check or uncheck all of the names. To select a range of file names, click on one file name and then hold down the shift key and then select another file name. To select an arbitrary combination of files hold down the Control key and then click on the desired files. The “Sort” button can be used to sort the names in alphabetical order. When done, click the “Create” button to create a new *TPS* file listing the names of all of the selected graphics files.

For each selected image file, two lines will be added to the file. The first line is “LM=0”. The second line will be “IMAGE=xxx”, where “xxx” is the name of an image file. If the “Include path?” box is checked then the complete path to the image file will be stored in the *TPS* file.



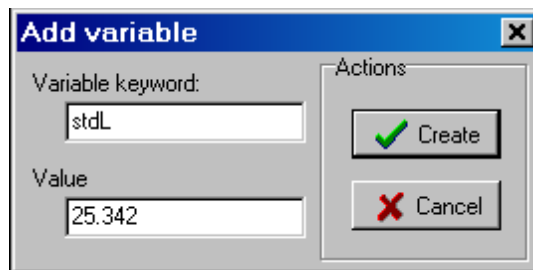
## 2.3 Add variable window

This window allows you to specify a keyword and its value to add to the variables field for every specimen in a *TPS* file. While not required by this software, the value should be numeric for processing by software such as *tpsRegr* or *NTSYSpc*. Note that only one keyword=value entry can be added each time this operation is performed. One can, of course, run the *tpsUtil* program several times.

Of course to be useful, different specimens should have different values for the variables. One may wish to first build *TPS* files with the groups in separate files and then combine them into a single file after using this software to add the appropriate variable fields.

Click on the “Create” button to actually make the addition or the “Cancel” button to close this window with no changes made.



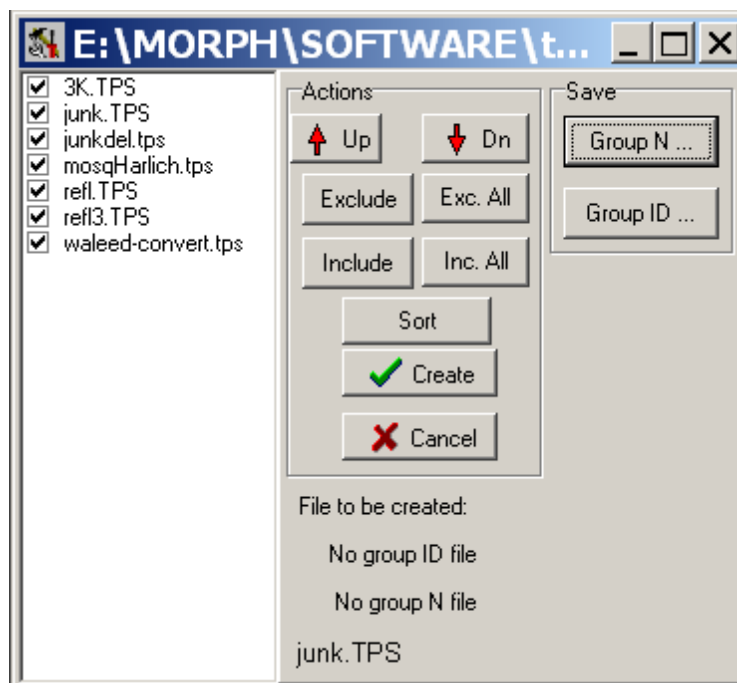


## 2.4 Append files window

This window lists all of the `TPS` or `NTS` files in the specified directory (depending on the extension given for the name of the output file). Using the buttons at the right you can change the order of the files (select a file with the mouse and then move it up or down in the list). Files can also be excluded from the output file by unchecking them or by selecting them with the mouse and then clicking on the “Exclude” button. You can include a file again by clicking on the checkbox or by selecting it and then clicking on the “Include” button. The “Exc. All” and “Inc. all” buttons can be used to exclude or include all files. The “Sort” button can be used to sort the names in alphabetical order. The input file type can be either `TPS` or `NTS` but the output file must be the same type as the input.

Optionally, one can click on the “Group N” button to specify the name for a file in which the sizes of each file being combined will be stored. This can be used by the [“Split NTS file”](#) operation to recover the original groups of specimens. The “Group ID file ...” button can be used to specify the name for a file in which group ID numbers will be placed. This will be an `NTS` file with one column and as many rows as there are specimens in the combined files. For each specimen an integer number will be stored giving the number of the file to which it originally belonged. This file can be used, for example, in `NTSYSpc` to give different plotting symbols to specimens from different groups.

An example is shown below. Two files have been excluded. The files have not yet been arranged in the desired order. A name for a group N file has been specified.

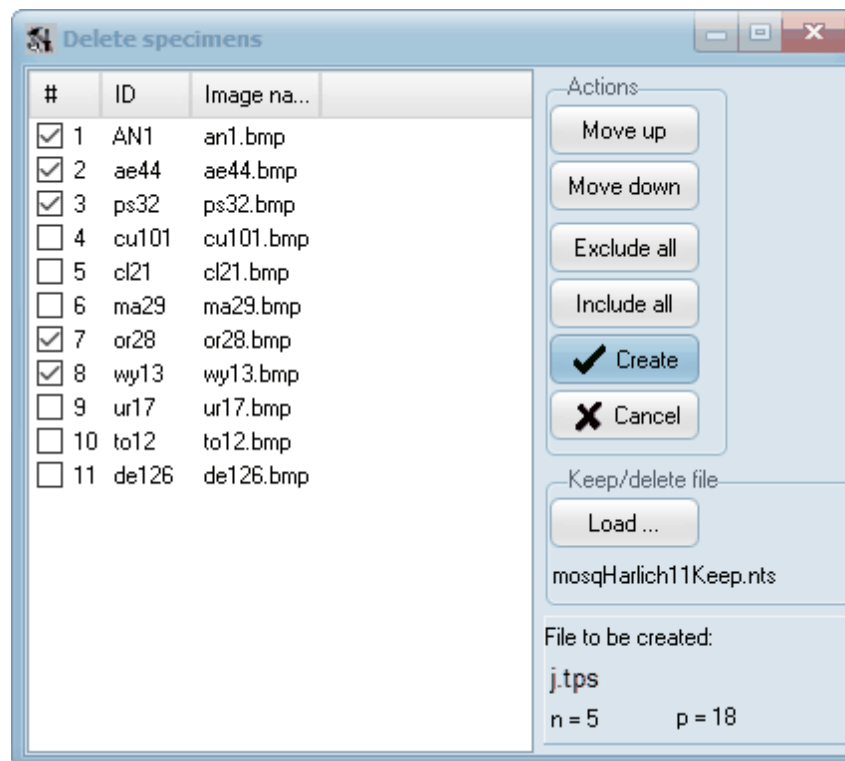


Click on the “Create” button to actually create the output file or the “Cancel” button to close this window with no output file created. If a groupN or groupID file was specified then it is created at the same time as the appended file.

## 2.5 Delete or reorder specimens

This window lists the specimen numbers, ID codes, and image file names (if present in the tps file) for the specimens in the input file. You can highlight a specimen and then using the buttons at the right to move the selected specimen up or down in the list. Specimens can be excluded from the output file by unchecking them. You can include a landmark again by clicking on its checkbox. The input file type can be either tps or nts but the output file must be the same type as the input.

An example is shown below. Specimens 4, 5, 6, 9, 10, and 11 will not be included in the output when the “create” button is clicked. In this example the selection of specimens was taken from the file moqHarlich11Keep.nts. That file is shown below.



Click on the “Create” button to actually create the output file or the “Cancel” button to close this window with no output file created.

The Keep/delete file for the example given above.

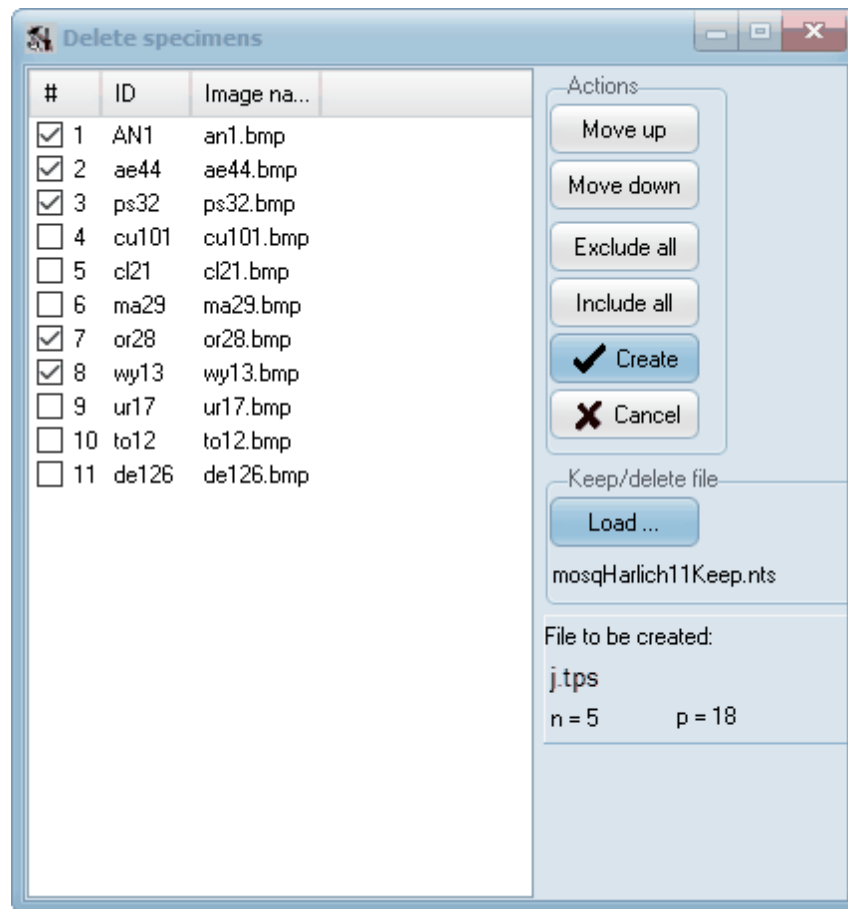
```
1 11 1 0
1
1
1
0
0
0
1
1
0
0
0
```

In this file the first line is a header line. The first and third values must be a '1', the second is the number of specimens in the data file, and the fourth value must be a zero. The remaining lines (one for each specimen) contain a '1' if that specimen is to be kept in the output file or a "0" if not. At the bottom panel the number of specimens remaining and the number of landmarks is displayed.

## 2.6 Delete/reorder landmarks

This window lists the identification numbers of the landmarks in the input file. You can highlight one or more landmarks (holding down the shift or control keys while clicking with the mouse) and then using the buttons at the right to move the selected landmarks up or down in the list. Landmarks can also be excluded from the output file by unchecking them or by highlighting them with the mouse and then clicking on the "Exclude" button. You can include a landmark again by clicking on its checkbox or by selecting it and then clicking on the "Include" button. The input file type can be either *tps* or *nts* but the output file must be the same type as the input.

An example is shown below. Landmarks 4 and 5 will be excluded from the output file and landmarks 6, 7, and 8 will become landmarks 4, 5, and 6.



Click on the “Create” button to actually create the output file or the “Cancel” button to close this window with no output file created.

## 2.7 Convert tps/nts files

This operation allows one to convert a TPS file into NTS, CSV (comma separated variables file compatible with Excel), or M (Matlab) files or an NTS file into TPS, CSV, or M files.

This window provides two options when the input is a TPS file: use the ID field or the name of the image file for each specimen as the row label of the output file. One can also choose whether to apply the scale factor to the landmark coordinates. For TPS files any outlines or curves are ignored and not copied to the output.

When the input is an NTS file the program may not be able to automatically determine whether 2D or 3D coordinates are appropriate. That can be selected manually.

Click on the “Create” button to actually create the output file or the “Cancel” button to close this window with no output file created.

Options

☐ Use scale factor

No. dimensions

☒ 2D landmarks

☐ 3D landmarks

NTS row labels

☒ Image name

☐ ID field

Actions

NTS files

☐ Separate matrices

☐ One landmark/line

File to be created:

**junk.NTS**

Number of specimens = 55

Number of landmarks = 8

The “NTS file” controls can also be used to write each specimen as a separate NTS matrix within the output file and/or write the coordinates for each landmark on a separate line in the output file (that is why the program allows one to “convert” from an NTS file to an NTS file).

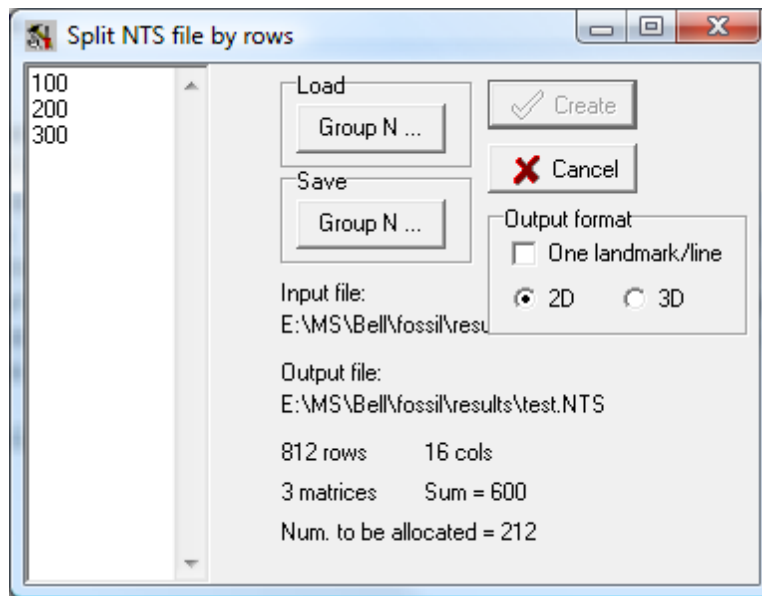
If the input file is an NTS file and the output file is a TPS file then one may have to select the correct number of dimensions (2D or 3D) for proper output as this sometimes cannot be determined out from the input file.

## 2.8 Split NTS file by rows

This window allows one to specify the sizes of the matrices to be produced from the input NTS matrix. Initially, the total number of rows in the matrix will be displayed at the left. To break a matrix of 100 rows into three matrices of sizes 25, 25, and 50 simply replace the 100 by 25, 25, and 50 (with each value in a separate row). As you make changes the status display will change to indicate the current number of groups, the sum of their sample sizes, and the number of rows not yet allocated to a group. The “Create” button will not be enabled unless the sum of the sample sizes is equal to the original number of rows (and hence the number to be allocate is zero).

The buttons for loading and saving “Group N” allow one to save and restore this list of group sizes. Such a file can be produced by the [“Append files”](#) operation. This will allow one to easily combine and then separate datasets (e.g., when extracting separate W matrices for each group after having performed an overall GPA).

An example is shown below. Only 600 of the 812 rows have been allocated so far and thus the “Create” button is disabled until another 212 are allocated.



Click on the “Create” button to actually create the output file or the “Cancel” button to close this window with no output file created.

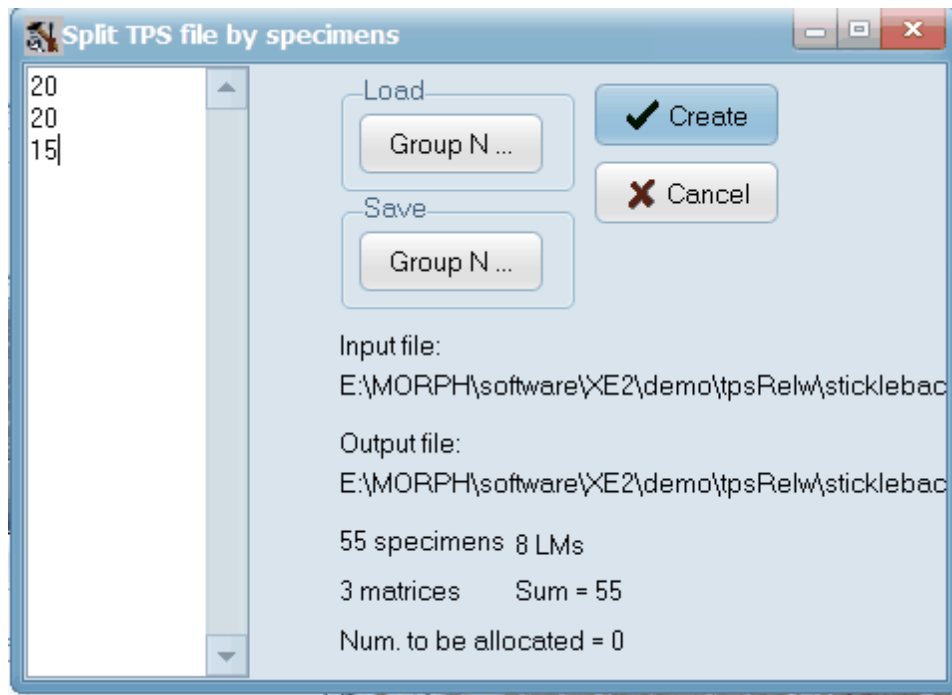
The “Output format” controls can be used to output the file with the coordinates for just one landmark on each line. In order to do this the program needs to know whether there are two or three coordinates per landmark.

## 2.9 Split TPS file by specimens

This window allows one to specify the sizes of the matrices to be produced from the input *NTS* matrix. Initially, the total number of rows in the matrix will be displayed at the left. To break a matrix of 100 rows into three matrices of sizes 25, 25, and 50 simply replace the 100 by 25, 25, and 50 (with each value in a separate row). As you make changes the status display will change to indicate the current number of groups, the sum of their sample sizes, and the number of rows not yet allocated to a group. The “Create” button will not be enabled unless the sum of the sample sizes is equal to the original number of rows (and hence the number to be allocate is zero).

The buttons for loading and saving “Group N” allow one to save and restore this list of group sizes. Such a file can be produced by the [Append files](#) operation. This will allow one to easily combine and then separate datasets.

An example is shown below. All 55 of the specimens have been allocated to three groups so the “Create” button is enabled.



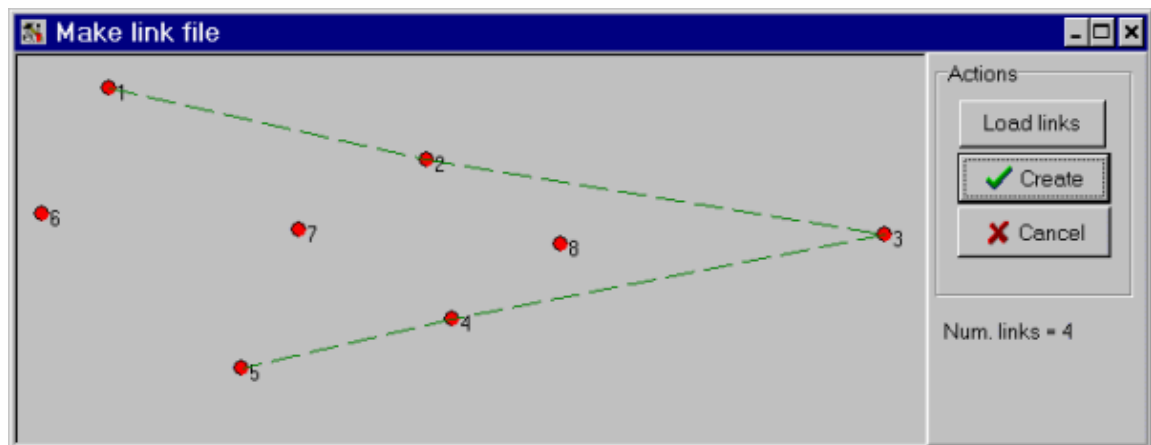
Click on the “Create” button to actually create the output file or the “Cancel” button to close this window with no output file created.

## 2.10 Make link file

This utility is to enable one to build a link file graphically. The locations of the landmarks on the first specimen in a TPS or NTS file is displayed. With the mouse, one can draw links between any pairs of landmarks. When drawing the program will display a “rubber band” line and will beep when you are sufficiently close to another landmark so that one can lift the left mouse button to end the current link.

To delete the last link drawn, right-click on an unused portion of the background. To delete a specific link, right-click on it.

An example is shown below.



The “Load links” button can be used to load an existing NTS link file if you wish to make minor changes rather than starting all over. Note the links file is just an ASCII file so you can also just edit it directly.

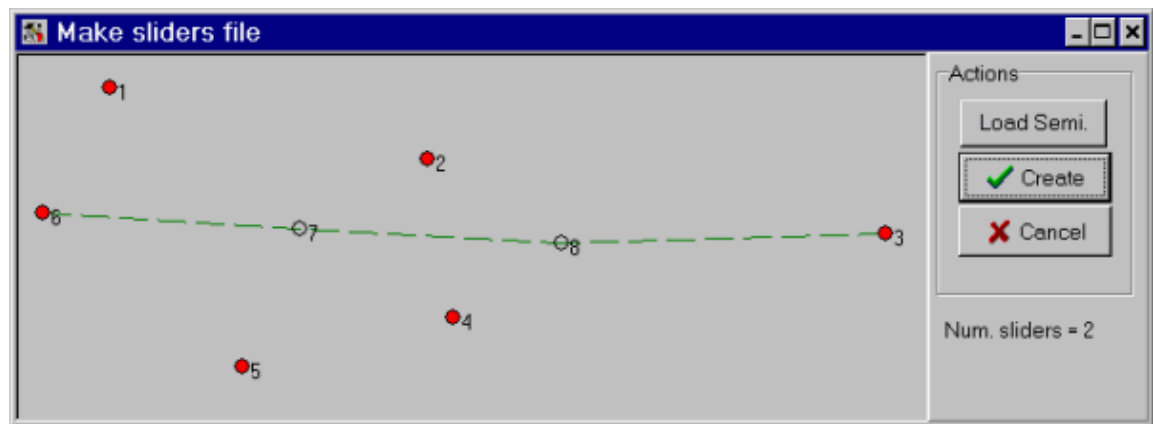
## 2.11 Make sliders file

This utility is to enable one to build a “sliders” file graphically. This file defines how semilandmarks can be slide so as to minimize bending energy during a generalized Procrustes analysis (GPA) superimposition. The locations of the landmarks on the first specimen in a `TPS` or `NTS` file are displayed. With the mouse, one can draw links between any triplets of landmarks. The middle landmark of a triplet is then considered a semilandmark (it will be displayed using an open circle) and it will be allowed to slide in a direction parallel to the difference between the other two landmarks.

When drawing the program will display a “rubber band” line and will beep when you are sufficiently close to a second landmark and that link will turn yellow and a new “rubber band” line will be displayed. The program will beep again when you are sufficiently close to a third landmark so that one can lift the left mouse button to end the current link. To define a curve made up of many semilandmarks, simply define a series of overlapping triplets of points. While one can draw these links in any way that makes sense, a point can only be defined once as a semilandmark, i.e., it can only be used once as the middle point of a triplet.

To delete the last link drawn, right-click on an unused portion of the background. To delete a specific link, right-click on it.

An example is shown below.

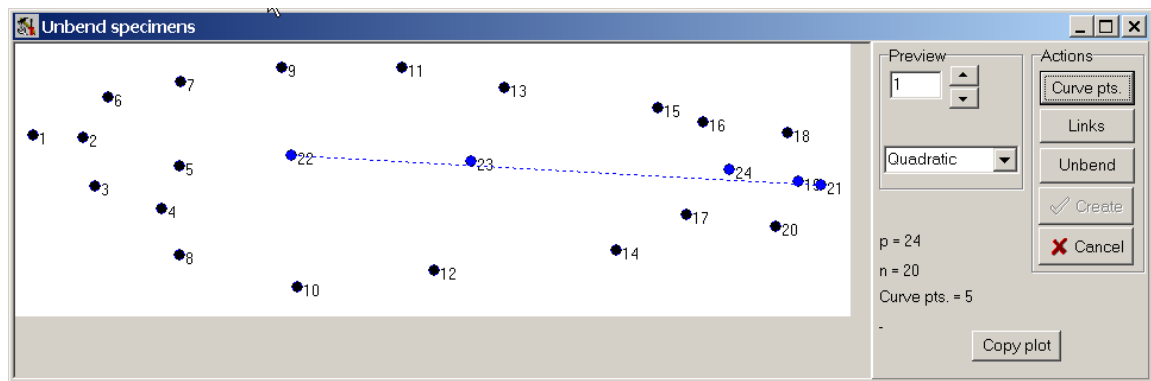


The “Load Semi.” button can be used to load an existing sliders `NTS` file if you wish to make minor changes rather than starting all over. Note the sliders file is just an ASCII file so you can also just edit it directly.

## 2.12 Unbending specimens

This module performs a simple transformation of a configuration of landmarks that may be useful in some special situations. What it does is to fit a quadratic curve through a designated set of landmarks and then “unbends” the entire configuration so that the estimated quadratic curve becomes a horizontal straight line. This module was written to adjust for the fact that some fish tend to curve when they die – especially when by suffocation. This condition is also found in fossil fish where one cannot physically straighten them before measurement. An example is shown below.





In this example, the four blue points (along the backbone) were used to fit the quadratic curve and the remaining landmarks are shown as black points. The first and last points used for the curve are used to rotate the configuration (horizontal dotted line). The blue dotted curve shows the fitted function. For these data the points fit the curve remarkably well. The new x-coordinates are the perpendicular projections of each point and the y-coordinates are the perpendicular deviations of each point from the curve. The transformed coordinates are shown as red points. Note: the points used to define the curve will not be perfectly aligned after the transformation unless they perfectly fit the quadratic curve. There are also arrows between the original points and their new positions but they are hard to see unless the displacement is very large. In some cases, such as the present example, no fixed landmarks are available along the backbone. In such cases one can enter sliding semilandmarks that can be adjusted later (using the *tpsRelw* program) or perhaps even deleted from the dataset once an appropriate unbending has been achieved for the other landmarks.

The “Curve pts.” button is used to load an *NTS* file that lists the landmarks to be used to define the curve. An example is shown below. In this example, four landmarks (6, 7, 8, and 3) were used to define the curve. The first and last points should define the two ends of the curve (left to right). The order of the other points does not matter.

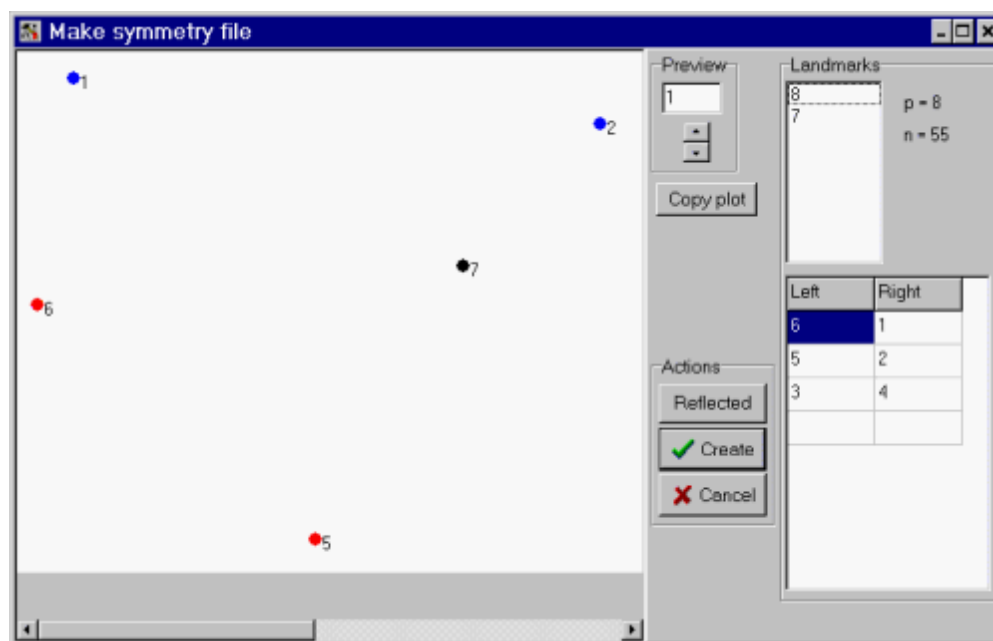
```
" 3k backbone file
1 4 1 0
6
7
8
3
```

Once the curve points have been defined, the “Unbend” button will be enabled. Clicking on it performs the computations. The “Preview” control allows you to scroll through the specimens to determine whether the unbending operation was reasonable for your data. You may need to resize the window in order to see the entire plot. The *R*<sup>2</sup> value near the bottom right gives a measure of the fit of the quadratic regression. Values near 1 imply a good fit but do not mean much if the curve is very straight initially. A value of 0.0 will be given if the points are already in a perfect straight line. The listing file gives more details about the fit. The “ID” value is taken from the ID field of a *TPS* file or the row label of an *NTS* file.

The “Copy plot” button can be used to copy the current plot to the Windows clipboard as a metafile that can be pasted into programs such as Word.

## 2.13 Make paired landmarks file

This module can be used in studies of symmetry and fluctuating asymmetry for both 2D and 3D data. The main use of this module is to simply prepare a file in *NTS* format that lists the pairs of landmarks. It can also output a file in which the landmark configurations have been reflected. A screen shot is shown below.



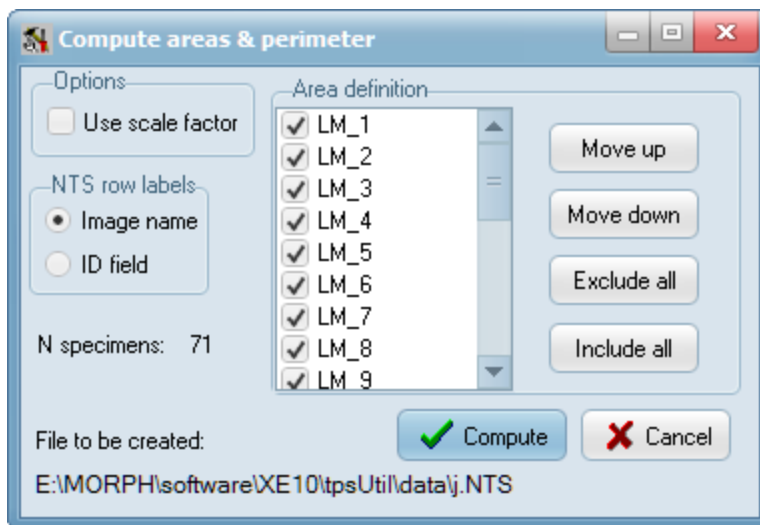
In this example there are 8 landmarks and 55 specimens. The pairs defined so far are 6 – 1, 5 – 2, and 3 – 4. At the left is a preview plot of the landmarks for the first specimen in the file (this plot is available only for 2D data, its purpose is to provide feedback that you have defined the intended pairs of landmarks). Landmarks on the left are shown in red and those on the right are shown in blue. Unpaired landmarks are shown in black. The pairs are defined by dragging them from the upper list to their appropriate location in the table of pairs. One can also drag them back to the upper list or between cells in the table. Blank rows in the table will be automatically removed.

The "Reflected" button creates a file with the coordinates of the paired landmarks reflected (for 2D data the y-coordinate is multiplied by  $-1$  and for 3D data the z-coordinate is multiplied by  $-1$ ).

The "Copyplot" button copies the current plot to the Windows clipboard as a Windows metafile that can be pasted into Word or many graphics programs.

## 2.14 Area & perimeter

Computes the area and perimeter of a region enclosed by selected landmarks. The units will be in pixels unless the use of a scale factor is selected. The output will be an .nts file.



The landmarks need to be ordered consecutively around the area of interest. Selected landmarks can be moved up or down in the list to put them in an appropriate order. Irrelevant landmarks can be excluded from the computations by removing their check mark.

A measure of circularity,  $4\pi A / P^2$ , is also computed, where  $A$  and  $P$  are the area and perimeter.

The first few lines of an output file are shown below.

```
" Areas
1 71 3L 0
Area Perimeter circularity
1.54424500000000E+0005 2.82113963467422E+0003 2.43824253336292E-0001
7.15635000000000E+0004 2.02402832673603E+0003 2.19517053267018E-0001
1.13364000000000E+0005 2.51633744054511E+0003 2.24981737473655E-0001
7.87740000000000E+0004 2.11843742681707E+0003 2.20577637838290E-0001
1.22688500000000E+0005 2.61224214040902E+0003 2.25936740182898E-0001
1.00487500000000E+0005 2.31073593237982E+0003 2.36494622573208E-0001
3.93191500000000E+0005 4.57022745855463E+0003 2.36558389128092E-0001
```

Note that "E+0005", for example, means to multiply the value at its left by 10 raised to the 5th power. E-0001 means to divide by 10.

**Technical support**

## 3 Technical support

### 3.1 Credits

---

This software was developed by

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The development of this software has been supported in part by a series of grants to F. James Rohlf from the National Science Foundation.

Waleed Gharaibeh inspired the initial creation of this program. Numerous users have offered suggestions for new features.

To cite the use of this software in a publication, please list it in your bibliography in the following form (inserting, of course, the appropriate year and version number for your copy of the software):

Rohlf, F. J. 2015. tpsUtil, file utility program. version 1.61. Department of Ecology and Evolution, State University of New York at Stony Brook.

One can also cite the entire tps series of software as follows:

Rohlf FJ. 2015. The tps series of software. Hystrix, the Italian Journal of Mammalogy, 26:1-4.

The paper can also be downloaded from the journal at:

<http://www.italian-journal-of-mammalogy.it/>

### 3.2 Technical support

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For help with this program contact

**F. James Rohlf**, Department of Ecology & Evolution and the Department of Anthropology, Stony Brook University, NY 11794-4364.

e-mail: [f.james.rohlf@stonybrook.edu](mailto:f.james.rohlf@stonybrook.edu) e-mail

You may also be able to get help by posting questions to the morphmet listserver: [morphmet@wfubmc.edu](mailto:morphmet@wfubmc.edu). This list is maintained by Dr. Dennis Slice.

### 3.3 Updates

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Updates of this program will be made available from the morphmet directory of the server at Life.Bio.SUNYSB.edu. The most convenient way to access this server is via the morphometrics WWW home

page at <http://life.bio.sunysb.edu/morph> WWW (this will also give you a chance to see other morphometric software currently available).

Announcements of bug fixes and other significant changes in the program will be distributed via the morphmet listserver at [morphmet.org](mailto:morphmet.org). This list is maintained by Dr. Dennis Slice.

**Changes:**

- Version 1.74:** The list of specimens to be kept or deleted can now be read from a file.
- Version 1.73:** Recompiled using Delphi DX10.1 and add computation of perimeter and circularity in addition to areas.
- Version 1.61:** Recompiled using Delphi XE8 and created both 32 bit and 64 bit versions.
- Version 1.58:** Added more support for output as .CSV files.
- Version 1.56:** Added image file names to the delete/reorder specimens dialog box.
- Version 1.51:** Rewrote the convert tps/nts option so that it will now actually perform the conversions.
- Version 1.48:** Recompiled using Delphi XE2, fixed problem with conversion of NTS to TPS files, and added a new color theme.
- Version 1.46:** Allowed for more than one curve to be appended to the landmarks.
- Version 1.40:** Added the list images and split TPS file options. Also fixed a bug in the unbending option when the points happened to align perfectly before the unbending was attempted.
- Version 1.34:** Added Mand CSV output to the build variable matrix operation.
- Version 1.33:** Fixed a number of small problems and changed several listboxes into checkboxes. Added "Sort" buttons to the build tps file and append windows.
- Version 1.24:** Added module to define pairs of landmarks and enhanced several other modules such as the one to delete and/or reorder landmarks.
- Version 1.22:** Added modules to treat outlines or curves as landmark points.
- Version 1.18:** Added module to unbend a configuration. Also made some changes to the input and output of the append, split, and convert modules.
- Version 1.16:** Added modules to create link and sliders files. Also extended the convert and the split modules.
- Version 1.12:** Added "Split NTS file" option. Added "create group ID file" to the append window.
- Version 1.11:** Added option to save tps files in NTS, M, or CSV formats.
- Version 1.10:** Added option to delete outlines and curves.
- Version 1.06:** Fixed several bugs.
- Version 1.02:** Added options to add a keyword to the variables field, create an NTS matrix from the information in the variable field, and to create a combined file by appending TPS files.
- Version 1.01:** Added option to build tps file from directory containing image files.
- Version 1.00:** Initial release, October 2000.

## 3.4 Uninstalling this program

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You can use the Windows Add/Remove icon in the Control Panel to uninstall this program. or else the uninstall icon. Data files will not be removed.

# Glossary

## 4 Glossary

### 4.1 Glossary

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Bookstein (1991)

See the more extensive glossary available from the web pages at <http://life.bio.sunysb.edu/morph>.



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