

py_tm2tnt 4.0 User Manual

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1. Introduction

py_tm2tnt is a Python-based graphical application designed for users who need to convert traditional morphometric data into [TNT](#) format for parsimony analysis. This software includes tools for calculating intervals, performing statistical analyses, and exporting data in formats suitable for phylogenetic analysis.

For detailed theory and instructions to perform parsimony analysis with continuous data, please see Catalano & Goloboff, (2018).

2. System requirements

Python 3.8 or later

Required libraries: pandas, tkinter, numpy, csv, scipy, itertools, collections

3. Installation

1. Install Python 3.8 or later if not already installed.
2. Install the required libraries via pip*:

```
pip install pandas, tkinter, numpy, csv, scipy, itertools, collections
```

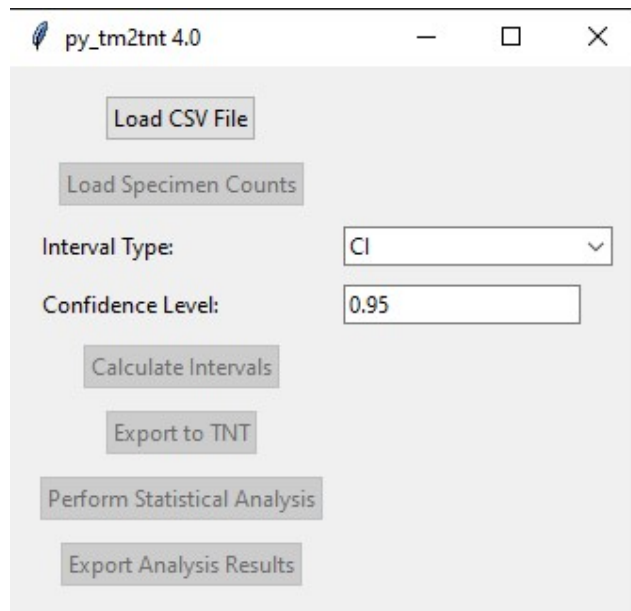
3. Download the py_tm2tnt script and save it to a local directory.

(*) If you installed Python from source, with an installer from python.org, you should already have pip. If you're on Linux and installed using your OS package manager, you may have to install pip separately, see

<https://packaging.python.org/en/latest/tutorials/installing-packages/>

4. Interface Overview

The interface of `py_tm2tnt` includes buttons and entry fields to load files, specify parameters, calculate statistical results, and export data. Each button is clearly labeled and designed to guide users through each step.



5. General Instructions

Loading Data Files

1. Load CSV File

- Click **Load CSV File** to select a CSV file containing species measurements (morphometric data). Each row should start with a species name followed by numerical measurements:

```
Species1,0.373,0.423,0.618,0.463,0.758,0.564,0.379,0.23, ..
```

```
Species1,1,0.233,0.484,0.395,0.476,0.451,0.384,0.43,0.333, ..
```

```
Species1,0.309,0.292,0.496,0.321,0.708,0.548,0.433,0.297, ..
```

```
.
```

- The application will parse and store these values for subsequent analysis.

2. Load Specimen Counts

- After successfully loading a CSV file, click **Load Specimen Counts** to specify a text file containing the count of specimens for each species. Each line should include a species name and a count:

Species1 29

Species2 44

Species3 30

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Setting Parameters

1. **Interval Type**
 - Choose between **CI** (Confidence Interval) and **Mean \pm SE** (Standard Error) to set the type of interval calculation.
2. **Confidence Level**
 - Enter a confidence level for interval calculations (default is 0.95).

Calculating Intervals

1. After setting the parameters, click **Calculate Intervals**.
2. The application will display calculated intervals based on the chosen interval type.
3. After calculation, the **Export to TNT** button becomes active for exporting the intervals.

Performing Statistical Analysis

1. Click **Perform Statistical Analysis** to begin analysis on the loaded data.
2. The application will automatically choose between the ANOVA or Kruskal-Wallis test based on the following criteria:
 - Normality of the data is evaluated using the Shapiro-Wilk test.
 - Homoscedasticity (equal variances) is assessed using Levene test.
 - If data is normally distributed and variances are equal across groups, ANOVA will be used; otherwise, Kruskal-Wallis test will be applied.
3. The program applies the **Bonferroni correction** to adjust significance values for multiple comparisons, ensuring robust statistical interpretation.
4. Once the analysis is complete, the **Export Analysis Results** button becomes active, allowing you to save the statistical results to a CSV file.

Exporting Results to TNT

1. Click **Export to TNT** to save the calculated intervals in TNT format.
2. The TNT file will include species names (with spaces replaced by underscores) and the formatted interval data.

It is important to note that TNT software support only recognizes continuous characters with 65.000 states. However, the program scales all continuous values. To display the original states, it is necessary to utilize the command `nstates` [

6. References

- Catalano, S., Goloboff, P.A. (2018). A guide for the analysis of continuous and landmark characters in TNT (Tree Analysis using New Technologies). 10.13140/RG.2.2.23797.27360
- Goloboff, P.A., Morales, M.E. (2023). TNT version 1.6, with a graphical interface for MacOS and Linux, including new routines in parallel. *Cladistics*, 39: 144-153.
<https://doi.org/10.1111/cla.12524>