

Draft template for Applications in Plant Sciences - Software Note

Short Title for Running Head: Surname of the first author, followed, as appropriate, with the surname of a sole co-author, or et al. (if there are three or more authors) - 2 to 4 descriptive words [e.g., Chippendale & Henson - TreeNut software]

TreeNut: A visual recognition software application to identify fruits of woody angiosperms¹

[no more than 125 characters; after a species name, include family name in parentheses]

Thomas Chippendale² and William Henson^{3,4}

²Department of Forestry, University of London, Senate House, Malet Street, London, WC1E 7HU,
United Kingdom

³Department of Biological Sciences, University of Texas at Dallas, 800 W. Campbell Road,
Richardson, Texas 75080-3021 USA

Email addresses: TC: chipndale@test.edu

WH: hensontex@test.edu

Number of words: YYYY *[3500 or fewer, consisting of Introduction, Methods and Results, and
Conclusions sections].*

¹Manuscript received _____; revision accepted _____.

⁴Author for correspondence: hensontex@test.edu

Acknowledgments should be limited to no more than 75 words.

ABSTRACT

The abstract should capture the interest of the general botanical community as well as specialists within the area. The abstract is 150 words or less, written in a structured format:

- Premise of the study (why the work was done)
- Methods and Results (how the software was developed and tested)
- Conclusions

Avoid references; if essential, cite parenthetically with journal name, volume number, pages, and year.

Here is a sample abstract:

- *Premise of the study:* Identification of woody tree species through fruit morphology has traditionally been difficult, but modern applications of electronic handheld devices open up new avenues for botanical identification. TreeNut was developed to enable plant scientists to easily and reliably identify angiosperm trees in the field using smartphone technology.
- *Methods and Results:* A visual recognition algorithm instituted on both iOS and Android operating platforms was used to identify over 40 different tree species in 10 geographic locations. The application was 94% accurate in identifying fruits to species, with failures largely due to substantial fruit herbivory.
- *Conclusions:* Compared with traditional identification techniques, the software application described here offers greater portability, flexibility, ease of use, and accuracy for visually identifying angiosperm tree species.

Key words: APX; visual recognition.

[List 3 to 6 key words here in alphabetical order, separated by semicolons.]

INTRODUCTION

This section should consist of no more than two paragraphs explaining the development of the new software program and why it is novel within the plant sciences community. A substantial update of an existing program is also acceptable, provided that the authors clearly show that it is a significant improvement over the existing version; for example, an updated program might incorporate new types of data, data formats, and/or improved statistical analyses that substantially advance the capabilities of the program. In addition, software applications for the analysis, filtering, or modification of data, or mining of large data sources are also welcome. For all types of software, authors must clearly and succinctly describe the need for the program or application, and describe its importance within the plant sciences.

METHODS AND RESULTS

The combined **Methods and Results** section will consist of up to seven paragraphs. In the first one to four paragraphs of this section, the rationale used to design the software program or update should be presented. This should contain enough detail to allow readers to understand the theory, processes, and functions behind the program, including as appropriate any mathematical algorithms. Authors may also include optional multimedia content (e.g., an animated video) to clarify difficult concepts. Any assumptions and limitations associated with the software must be clearly presented. Examples of appropriate types of input data and output formats are strongly encouraged, placed either here within the text or as an appendix (see below). Software that uses standard import/output file formats (such as Arlequin, GenAlEx, or GENEPOP) are especially

desired. An interpretation of the output itself should be provided along with the examples.

Within this section, authors must also provide compatibility information for operating systems associated with stationary and portable computing devices. We encourage programmers to consider multiple platforms when at all possible and to make source code available under the terms of a free software license (e.g., GNU General Public License, MDS License, or Apache License). The complete user manual must be included as supplementary material, and authors must provide a link to a permanent website where the software program and user manual can be downloaded free of charge. The software and manual can also be provided as multimedia content as appropriate (see Instructions for Authors).

In the final one to two paragraphs of this section, the authors must clearly demonstrate the feasibility and utility of the software. This can be done, for example, by evaluating the program against existing software programs or versions. Alternatively, a new software program or data mining application can be used to analyze different data sets to demonstrate its usefulness. Supporting data resulting from the analysis may be presented in text, tabular, or figure format. During the submission process and to assist review, authors must provide the software program (preferably as a zipped executable file, including any ancillary files) and example data set(s) along with a description of expected results. Any software programs that do not perform as stated when tested will result in rejection of the manuscript.

CONCLUSIONS

In this section, the author(s) should clearly state in one to two paragraphs the main conclusions that have been reached, focusing on the effectiveness and applicability of the software in comparison to other existing programs or versions. In addition, the authors may address potential advances that would be gained through the application of this software, as well as any drawbacks that may exist.

LITERATURE CITED *[no more than 30]*

- GOUDET, J. 1995. FSTAT: A computer program to calculate F statistics, version 1.2. *Journal of Heredity* 86: 485–486.
- STEBBINS, G. L. 1974. Flowering plants: Evolution above the species level. Belknap Press, Cambridge, Massachusetts, USA.
- STEVENS, P. F. 2001 onward. Angiosperm phylogeny website, version 8, June 2007 [more or less continuously updated]. Website <http://www.mobot.org/MOBOT/research/APweb/> [accessed 00 Month Year].
- TURNER, B. L., AND R. M. KING. 1977. Chromosome numbers in the Compositae. VIII. Mexican and Central American species. *Southwestern Naturalist* 9: 27–39.
- WHITE, T. J., T. D. BRUNS, S. B. LEE, AND J. W. TAYLOR. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In M. A. Innis, D. H. Gelfand, J. J. Sninsky, and T. J. White [eds.], *PCR protocols: A guide to methods and applications*, 315–322. Academic Press, San Diego, California, USA.

Tables

Tables are optional but up to two tables can be included if necessary in software note papers. They must follow the general format of all APPS manuscripts in which each table has a brief legend, with footnotes explaining any abbreviations within the table itself.

Figure and Legend

[limited to two optional figures, which should be uploaded as separate files; the legend should be included in the text file]

Appendix

As appropriate, information can also be placed within an appendix (“Appendix 1”).