

Linking R and JUICE

Software tool for analysis and visualization of vegetation data

David Zelený & Lubomír Tichý

Institute of Botany and Zoology, Masaryk University
Kotlářská 2, CZ-61137 Brno, Czech Republic
e-mail: zeleny@sci.muni.cz, tichy@sci.muni.cz

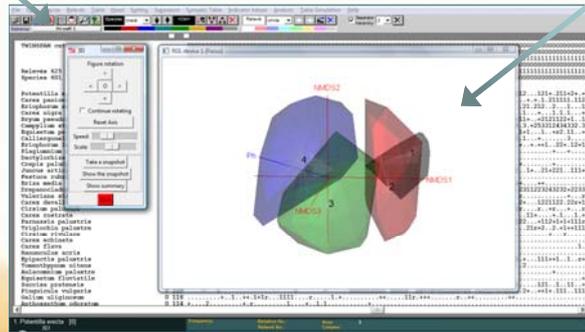


R-project



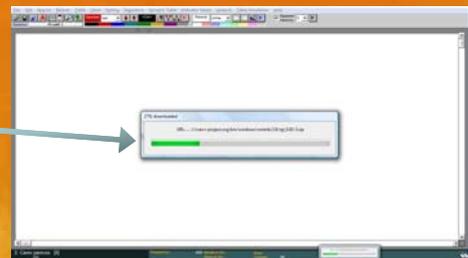
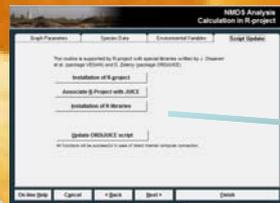
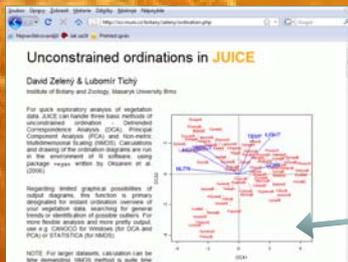
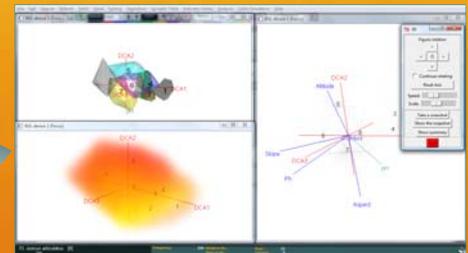
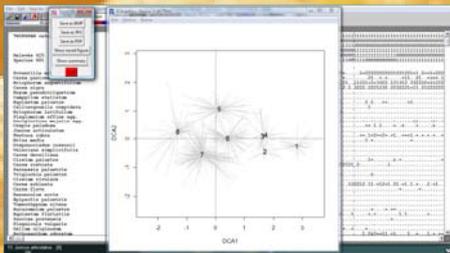
JUICE 7.0

is a stand-alone Windows application for editing, classification and analysis of large phytosociological tables and other ecological data. It has been developed by Lubomír Tichý (Masaryk University Brno) since 1998, written in Visual Basic and optimized for Windows OS (but operating also under Linux via Wine emulator). JUICE can also automatically or semi-automatically operate other commercial or freeware softwares, such as PC-ORD, CANOCO, SYNTAX or Mulva. For more information and free download, visit <http://www.sci.muni.cz/botany/zeleny/> or <http://www.juice.muni.cz/>.



Linking JUICE and R offers quick and effective availability of selected R analytical and visualization functions: JUICE offers user friendly environment of vegetation data handling and import, R works as an engine for analysis and visualization. Recently implemented functions are multivariate analysis of vegetation data (DCA, PCA, NMDS) and modeling of species response curves (GLM, GAM, Gaussian and HOF models).

- Following R packages are used by JUICE:
- **vegan** (Oksanen, Kindt, Legendre, O'Hara et al.) - number of tools for analysis of ecological communities, diversity and multivariate analysis;
 - **gravy** (Oksanen) - modeling of species response curves along environmental gradients;
 - **rgl** (Adler & Murdoch) - 3D interactive ordination diagrams;
 - **geometry** (Grasman & Gramacy) - calculation of convex hulls;
 - **tcltk** and **tkrgl** (Murdoch & Chen) - user interface for interaction with figures;
 - **ordjuice** and **srcjuice** (Zelený) - connecting JUICE and R and offering some additional analytical and visualization tools.



Technical solutions

Link between JUICE and R is mediated by sharing the files via R/bin directory and using libraries *ordjuice* (for unconstrained ordinations) and *srcjuice* (for species response curves). JUICE offers wizard for selection of appropriate analysis parameters and type of graphical output. Data are saved into R/bin file, and R is initialized to run in a batch mode by sending the script with selected parameters into Windows command line. R draws the figure onto graphical device (X11 or rgl) and opens Tcl/Tk panel; after either the device or Tcl/Tk bar is closed, R is terminated. This design allows several R session to run simultaneously using the same data, but different parameters. Other option is R running in silent mode: the result of analysis and figures are saved back to R/bin directory, where it's awaited by JUICE, and R is terminated.

Updates of *ordjuice* and *srcjuice* libraries are available from R repository in <http://www.sci.muni.cz/botany/zeleny/R>. If in use, once per day is checked for new updates and user is notified about the need to update.

