Running_Instructions_ReconAnalog

This file tells you how to use downloaded Reconanalog.R and associated files (GitHub) to duplicate the sample illustration in section 4.0 of Prusevich et al. (submitted) on your laptop in RStudio. It is assumed you have downloaded a zip file with ReconAnalog.R and associated files from GitHub. It is also assumed you have R and RStudio installed and working on your laptop.The folder names "C:/trish/" folder name is arbitrary and is used just as an example.

1. Create empty folder C:/trish/ and subfolder C:/trish/test_out on your laptop.
2. Unzip the downloaded zip file into C:/trish/
3. Install the R packages require by ReconAnalog (see "PackagesNeeded.txt")
4. Edit the first 6 lines of the json file Recon_Katun.init so that the path names match the setup on your computer (do not change the filenames)
5. Save a copy of Recon_Katun.init as "Recon.init" overwriting the existing Recon.init. ReconAnalog expects input specification in a file with name "Recon.init." For meanings of the settings in Recon.init, see "Recon_init_explanation.pdf."
6. In RStudio, do the following
   ○ Create new project in C:/trish/
   ○ Open ReconAnalog.R
   ○ Run ReconAnalog.R
   ○ After successful run, you should see the output files in "C/trish/test_out/"

Tips

• <u>Tailored ".init" files</u>. If running multiple analyses, each with different reconstruction settings (e.g., lags vs no lags) or different input data (e.g., Katun River vs Yenisei River) you will want to have dedicated ".init" file -- for example, Recon_Katun.init and Recon_Yenisei.init. Be sure to copy the desired file for a particular run as "Recon.init" before running ReconAnalog, because ReconAnalog reads from "Recon.init"
• <u>Tailored paths</u>. For simplicity, the instructions above have all files needed for the analysis in "C:/trish/." With experience, you will generally want to arrange the input in different paths by modifying the first 6 lines of Recon.init. The only file that actually needs to be in the R project folder is Recon.init. ReconAnalog.R and functions it calls can be a separate folder, input data files can be in another folder, and output can be specified to go to some folder other than "C:/trish/test_out"
• <u>Tailored input chronology data and metadata</u>. Use **siteMeta_Katun.txt** and as **siteMeta_Katun.txt** as examples to make tab-separated files of the input tree-ring metadata and data. The headings in row 1 of the metadata must exactly match those in the example.
   ○ The "Id" field in the metadata must exactly match the chronology Ids in row 1 of the time series matrix.
   ○ Note that that the input files for standalone (in RStudio) ReconAnalog are a bit different from those you might have uploaded for TRISH. For standalone ReconAnalog:
      1. Data: no initial row of column numbers (row 1 is the Ids)
      2. Data: all series assumed to have data in the first year of matrix
      3. Meta: the numbers in column two allow you to cross-reference your chronologies to some numbering in an outside database. If no such cross-reference is needed, just duplicate column 1 (sequential numbers) as column 2.
      4. Meta: all column shown in the example **siteMeta_Katun.txt** are required. This means, among other things, that you need the columns of first and last years of chronologies

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- "Recon.init" -- You will need to build an ".init" file analogous to the one you downloaded for the sample data to specify reconstruction settings for your own data. The format of .init files must be exact. Use the existing "Recon_Katun.init" as a template and edit lines accordingly. See the instructions above about needing needing to rename your .init as "Recon.init" before running ReconAnalog, and about how to use .init files for easy running of multiple versions of a reconstruciton. All of the entries in this file are discussed in the opening comment section of ReconAnalog.init. Please search for the string "JSON INITIALIZATION FILE" and read the definitions

References (annotated, in chronological order)

- **Meko, D. (1997)**. Dendroclimatic reconstruction with time varying predictor subsets of tree indices. *J. Clim.*, 10 (4), 687–696. doi: 10.1175/1520-0442(1997)010 ⟨0687:DRWTVP⟩ 2.0.CO;2

  Describes the two-stage reconstruction method and presents mathematics of the method in the context of a reconstruction of precipitation in a southern Arizona river basin.

- **Meko, D. M., Woodhouse, C. A., Baisan, C. H., Knight, T. A., Lukas, J. J., Hughes, M. K., & Salzer, M. W. (2007).** Medieval drought in the upper Colorado River Basin. Geophys. Res. Lett., 34 (L10705). doi: 10.1029/2007GL029988

  Application of two-stage reconstruction method to reconstruction of annual flows of Colorado River, USA. Predates the development of ReconAnalog.R and TRISH, but uses one of the reconstruction methods included in ReconAnalog.R -- reconstruction by stepwise regression of flows on principal components of tree-ring chronologies transformed in a preliminary step to individual single-site reconstructions of flow.

- **Meko, D. M., Biondi, F., Taylor, A. H., Panyushkina, I. P., Thaxton, R. D., Prusevich, A. A., . . . Glidden, S. (2024)**. Runoff variability in the Truckee-Carson River Basin from tree rings and a water balance model. *Earth Interact*. (Early online version, 5 June 2024) doi: 10.1175/EI-D-23-0018.1

  *Introduces the R reconstruction program **ReconAnalog.R** in context of reconstruction of point runoff and other variables. Supplemental material includes ReconAnalog.R, functions it relies on, sample data, and instructions for running. Paper mentions that that ReconAnalog.R was developed with team of researchers as part of web-based TRISH tool, although this paper is based on running ReconAnalog.R outside TRISH in RStudio.*

- **Prusevich, A. A., Meko, D. M., Panyushkina, I. P., Shiklomanov, A. I., Lammers, R. B., Glidden, S., & Thaxton, R. D. (submitted)**. TRISH: Tree-Ring Inte- grated System for Hydrology, a web-based tool for reconstruction. *Environ. Model. Softw*. (Manuscript ENVSOFT-D-24-01458, submitted 29 October 2024; Irina Panyushkina corresponding author; under review as of 1 February 2025)

  *The main reference for the web-based **TRISH** tool. TRISH relies on R software ReconAnalog.R and associated user-written functions to do reconstructions, but includes a water balance model, mapping package, and interactive menus to generate the reconstruction predictand and specify reconstruction settings.*