

Screen 1: There is no json file read from screen 1. At screen 1 you select a tree-ring network from a dropdown menu. TRISH is assumed to have the tree-ring chronologies and metadata for available networks. Once you select a network, TRISH used the metadata to set initial values to fill in the years in the edit boxes “First and last year” and “All cover.” The all-cover period will not be very long because all chronologies in the full network must cover that. You can then proceed to optional time screening and then to spatial screening. What TRISH does from screen 1 is to 1) build the trimmed (years and chronologies) tree-ring time series matrix, build the default predictand time series matrix (Runoff, water year, averaged over highlighted basin); and call ReconAnalog with the initial default init01.json. Finally, pressing “Go” at the bottom of the screen will run an initial default reconstruction, and bring you to screen 2, where you can revise settings and explore reconstruction.

Screen 2: When you change specifications and press “Re-run” at screen 2, the default init01.json is modified to a changed file init02.json. Then when you press “Re-run,” ReconAnalog is called and reads the revised json input file. Here I describe the relation of item in the json input file to objects on screen 2 and variables in ReconAnalog.

There are 27 input lines in the json input file. When you change setting of radio buttons, etc., on screen 2 and press “Re-run”, settings are changed in the json file and ReconAnalog is called to read that json and do a revised reconstruction. Following is a list of the json variables with details on relationship to screen 2 and to ReconAnalog. Refer to the screen 2 mock-up in file Screen2_TRISH.pdf and to the json file init01.json to understand the relationship between variables set in the json input and selection made in TRISH at screen 2.

Yellow highlight: specific to Meko’s laptop

Rust highlight: filenames assumed by ReconAnalog – maybe UNH also used those; if not, must change

Purple highlight: suggestions to UNH

Green highlight: corresponding item on TRISH screen 2, if applicable

First line of each item gives json init file item and the default settings for initial reconstruction. items are listed in order as in json file

1. **"code_dir" : "/home/dave/Data/RlibraryMeko/",**
The system folder where all the Meko-written functions called by ReconAnalog are stored on Meko’s laptop. He runs ReconAnalog from another working folder that contains ReconAnalog.R and tab-separated files of tree-ring time series, tree-ring metadata, and a predictand hydroclimatic time series.
2. **"pdf_dir" : "/home/dave/Projects/ba2/TRISHvisual/",**
The system folder from which TRISH copies the pdf file describing reconstruction method
3. **"tr_file" : "treeData.txt",**
Tab-separated file of input tree-ring chronologies. On Meko’s laptop, he built this himself. In TRISH, this file would be built at screen 1 based on the tree-ring network you select and the screening for time coverage and spatial domain. So, it is assumed that TRISH provides this time-and-space trimmed version of the tree-ring chronologies.
4. **"trM_file" : "treeMeta.txt",**
Tab-separated file of tree-ring metadata, trimmed accordingly so that included metadata just for those chronologies in treeData.txt. TRISH is assumed to provide this.
5. **cl_file" : "hydroData.txt",**
Tab-separated file of hydrologic predictand. This is two-column, with a year and a seasonalized hydrologic variable. By default for the initial reconstruction this variable is runoff (RO) expressed as an equivalent average depth over the basin, and is the sum for the water year. By default CRU is the basic climate input for the WBM providing runoff. The “basin” is the area that was highlighted on screen 1 upstream of the point the user clicked on the map.

The contents of this file could change in response to choices on screen 2. There you could pick a different source climate data than CRU, a different hydrologic variable than RO, and a different season than water year. TRISH must then produce the desired seasonalized hydrologic variable and store it as hydroData.txt

6. **"outputDir" : "/home/dave/AAATrish2/test_out/"**,
The system folder to which ReconAnalog writes all graphics files, tables, time series, and auxiliary files. I think this is where TRISH also gets graphics files to display on the screen 2 graphics window and statistics window.
7. **"NameNetwork": "Kyzyl", Screen 2: Network: Kyzyl**
Name of the selected tree-ring network. You select this from a dropdown menu at screen 1. I have a tailored network call "Kyzyl" that I used for developing ReconAnalog, but no such network exists right now on TRISH.
8. **"PrewrittenOrder" : 0, Screen 2: Prewritten chronologies? ☐ Y ☒ N; AR order: 1, 2, or 3**
The order of autoregressive model to use in prewhitening tree-ring chronologies. Order 0 corresponds to no prewhitening. Allowable orders of AR models for prewhitening are 1, 2, or 3. At screen 2, you answer Y or N to "prewhiten chronologies." If Y, you enter the AR order (1, 2 or 3) from a dropdown menu. If you choose "N", the AR order is ignored. TRISH needs to store the tree-ring matrix before any prewhitening so that you can revert to order 0 or to any other order after trying prewhitening with some other order.
9. **LallowLags" : true, Screen2: allow lags? ☒ Y ☐ N**
Whether to allow SSR model to include lags. If "true", the pool of potential predictors includes the tree-ring chronology lagged t-2 to t+2 from the predictand. If "false," only lag-0 tree-ring chronology is in the pool.
10. **NsitesUserNetwork" : 274, Screen 2: # Sites: 274**
Number of sites in the user-supplied tree-ring network. This is constant, depending on the network the user uploaded to TRISH. The network is selected at screen 1 and there is year-screened and space-screened (e.g., polygon), to product the trimmed tree-ring data for the initial reconstruction and for re-runs with different setting from screen 2.
11. **"YearScreen" : [1700,1997], Screen 2: Year screen:: 1700-2019**
You specify this at screen 1 by "Year screen" and "Mandatory coverage." By default, if you call for no screening, TRISH will use the period in common to all chronologies in the full network. This could be a very short period, and so may not be a good idea. At screen 1, you see that TRISH provides "First and last year," which gives you outer bounds on the possible years you might select for YearScreen.
12. **"NafterYearScreen" : 36 Screen 2: After year screen: 36**
The number of chronologies left after screening for "YearScreen." Internally computed by TRISH (no user setting) based on your selections for "YearScreen."
13. **"NafterPolygon" : 28 Screen 2: After polygon screen:: 28**
After screening by "YearScreen," the network could be further reduced in size (number of chronologies) by the spatial screening when you draw the polygon for the allowable region enclosing tree-ring sites to be used in the analysis. TRISH computes this from whatever polygon you draw.

The above items, except for the contents of HydroData.txt and TreeData.txt do not change once you leave screen 1. TreeData.txt time series can change later if you choose to try prewhitened chronologies in reconstruction. HydroData.txt will generally change because you will be picking different basic input climate sets (e.g., CRU vs others), hydrologica variables (e.g., RO vs Precipitation) and different seasons (e.g., summer vs water-year). Remaining items in the json input file are changeable from edit boxes and dropdown menus of screen 2

14. **"HydroVariable" : "RO", Screen 2: Predictand: RO**
Abbreviation for the the target hydrologic or climatic variable to be reconstructed. This is also called the

“predictand” of the MSR model.

There are currently has four options: ('RO','P','T','Q'). These correspond to ('Runoff','Precipitation','Temperature','Discharge'), with units (('mm'),('mm'),('Deg C'),('cms')). These variables are assumed to be average over the “basin” that is highlighted by TRISH at screen 1. For example, RO is the average depth of runoff basin, summed over the season specified in another menu item. Likewise, T is average mean monthly temperature; and Q is the discharge from the highlighted basin area. I think Q is a computed discharge, rather than discharge measured at a gage, and so is equivalent to RO time basin area. If so, this is redundant, as the reconstruction would differ in units only. I would favor an alternative variable. Model output soil moisture, for example, would be a good one, considering physical link to moisture sensed by trees. Should discuss with UNH. But first we should get TRISH working even with the RO, P and T.

15. **"ClimDatSet" : "CRU",** **Screen 2: Source climate: CRU**
The climate data to be used as input to UNH WBM in producing the predictand variable. You get to select from the following: ('CRU','Delaware','Reanalysis'). Nothing in ReconAnalog is done differently, whatever source is select. Need to discuss which climate data sets are actually available to WBM.
16. **"HydroSeason" : [9,12],** **Screen 2: Season: 12 mos Ending in 9**
The ending month and number of months in the “season” for which the predictand is to be seasonalized. the predictand. For example, [9,12] means 12 month period ending in September, which is usually defined as the “water year.” Screen 2 allows these to be set with edit boxes “Season: ?? mos Ending in ??” You enter your choices. Alternatively, these could be entered with dropdown menus (1-12 for ending month, and 1-12 for number of months).
17. **"yrgoc" : -99999,** **Screen 2: Cal. Years: 1954-2015, Maximum Possible X**
First year of predictand (e.g., water-year RO) allowed to be used in calibrating any single-site reconstruction (SSR) models. The screen 2 items here actually set both yrgoc and yrspc. If you choose radio button “Maximum possible,” TRISH should list the first and last years of available predictand in the “Cal. Years” edit box. If you do not choose the maximum possible, you should be allowed to enter two years in the edit box, and TRISH should make sure those years are within the coverage of the predictand. The default json entry -99999 here really means “NA,” which is not handled by json, and means the user selected the maximum possible calibration period.
18. **"yrspc": -99999,** **Screen 2: Cal. Years: 1954-2015, Maximum Possible X**
Last year of predictand (e.g., water-year RO) allowed to be used in calibrating any single-site reconstruction (SSR) models. Analogous to yrgoc.
19. **"ktran" : 1,** **Screen 2: Transform::None**
Numeric code for transformation to be applied to predictand before any reconstruction modeling. Codes are: none (1), square root(2) or log10 (3). The requested transformation may be incompatible with the data. For example, negative temperature values are incompatible with square root and log10 transformations and zero precipitation is incompatible with a log10 transform. ReconAnalog checks compatibility writes error message to system when bombing out if needed.

On screen 2, ktran is changeable through a dropdown menu “Transform::None.” Suggest for clarity that the menu on screen 2 use words rather the code numbers, though 1, 2, or 3 is written when revising the json init file.

20. **"methMSR" : 2,** **Screen 2: Method: MLR-PC**
Numeric code for method to be used for multi-site reconstruction (MSR). Options are (1) simple linear regression (SLR), (2) MLR on SSRs or their PCs, and (3) analog nearest neighbor PCA.

On screen 2, this is a bit tricky. Whatever you choose from the dropdown menu for “Method” on screen 2 will have the effect of seeing both methMSR and PCApredictors in the json input file. Suggest giving dropdown choices [“SLR”, “MLR-PC”, “Analog”]. The effect of each is as follows:

SLR: methMSR=1, PCApredictors=0

MLR-no PCA: methMSR=2, PCApredictors to "false"

MLR-PCA: methMSR=2, PCApredictors = "true"

Analog: methMSR=3, PCApredictors = "true"

21. **"PCApredictors" : true,** **Screen 2: ... this is set by methMSR (see above)**

Whether predictors are to be principal components (PCs) of the original chronologies (true), or the chronologies themselves (false). From the json file, both methMSR and PCApredictors are needed to fully specify the reconstruction method in the call to ReconAnalog when methMSR=2.

A whole sub-panel of screen 2 deals with PCA settings and options. The panel contents should appear only if PCApredictors="true." Otherwise, there is no PCA to be done, and no need for PCA settings

22. **"kHowPCA" : 2,** **Screen 2: PCA on: Corr Mtx O Covar Mtx X**

Whether the PCA of SSRs is to be done on the correlation matrix (1) or covariance matrix (2) of the SSRs. On screen 2 kHowPCA is set by your choice of radio button. If you pick "Corr Mtx," kHowPCA=1. If you pick "Covar Mtx," kHowPCA=2.

23. **"PCoption" : 2,** **Screen 2: # PCs to keep: Specify O, Highest r with RO X**

In any of the reconstruction methods using PCA, that is, methMSR=2 and PCApredictors=true, or methMSR=3, PCoption dictates how many and which of the PCs of SSRs is available to the final reconstruction. PCoption=1 indicates include the m PCs with highest eigenvalues, where m is set by json input nPCsKeep (see below). If PCoption=2, the PCs to keep are those whose absolute correlation with the predictand are highest. With this choice, exactly how many are included in the pool depends on your setting for the factor f (see below). For example f=0.10 means the size of the pool (number of PCs in it) must be smaller than f*N, where N is the length of the calibration period of the reconstruction model. Therefore, N=100 years and f=0.1 dictates that no more than 9 PCs can be in the pool.

Two radio buttons are available for PCoption. Clicking "Specify" sets PCoption=1 in the json file. Clicking "Highest r with ??" sets PCoption=2 in the json file.

24. **"nPCsKeep" : 1,** **Screen 2: "nPCsKeep" : 1,**

Number of PCs to keep in pool. This setting is ignored unless PCoption=1. , the "Specify" edit box should appear on screen 2, and you can enter a number indicating to use that number of PCs. If PCoption=2, there is no need to enter a number of PCs to use, and I suggest the edit box for "Specify:" not even appear on screen 2.

25. **"f" : 0.10,** **Screen 2: f ratio: 0.10**

The factor "f" constrains the number of variables in pool of potential predictors for the MSR stepwise regression models, and may also constrain the number of PCs used for analog identification with the combination methMSR=3 and PCoptions=2. The factor "f" is intended to help guard against overfitting and chance relationships. Depending on some other settings, the size of the pool of potential predictors for the MSR is restricted to be less than a decimal fraction f of the number of observations in the calibration period. So, if 100 years in the calibration period and f=0.1, no more than 9 variables would be

allowed in the pool of potential predictors. This fraction f is ignored with the following combinations of other settings:

1. methMSR=1
2. methMSR=2 and Pcpredictors=true and PCoption=1
3. methMSR=3 and PCoption=1

26. **"alphaR" : 0.05,** **Screen 2: α 0.05**

Threshold alpha-level for screening of PCs when using analog reconstruction method (methMSR=3) with PCoption=2. Only those PCs whose scores are significantly correlated with predictand at this alpha level (two-tailed test, no adjustment for autocorrelation). For any other settings of methMSR and PCoption, alphaR is ignored by ReconAnalog. The only acceptable levels for alphaR are members of the set {0.05, 0.01, 0.001}. Suggest that TRISH restrict user to picking one of those three values for alphaR.

27. **"Lcausal" : true** **Screen 2: Reject non-causal: Y**

Whether to require that lagged SSR models make sense causally to be accepted. If Lcausal=true, the SSR model is rejected if the only predictor(s) in the model are negative, implying that the current year's predictand can be reconstructed from previous years' tree rings only (illogical). The setting "true" is generally appropriate, but Lcausal is allowed to be changed for exploratory sensitivity analysis.

GRAPHICS WINDOW ON TRISH SCREEN 2

In the lower of TRISH screen 2 is the word **Graphics**, with six associated radio buttons. Each of those buttons is a dropdown menu at which you select a graphics file. The dropdown items should select specific graphics png files that are stored by ReconAnalog. The dropdown items and corresponding file names may be different depending on the setting for methMSR. So each of the four possible methods is associated with graphic filenames that must link properly with dropdown choices. The outline below gives the linkages.

- **methMSR=SLR**
 - SSR
 1. Chronology screening Figure01-SSR1.png
 2. Histograms of lags Figure02-SSR2.png
 3. Recent-end signal drop Figure03-SSR3.png
 4. Signal in mean SSR Figure04-SSR4.png
 - Calibration
 1. Summary Figure05-Calibration1.png
 2. Histograms and ACFs Figure06-Calibration2.png
 - Validation
 1. Time plots Figure10-Validation1.png
 2. Statistics Figure11-Validation2.png
 - Reconstruction
 1. Time plot Figure12-Reconstruction1.png
 2. Histograms and ACFs Figure13-Reconstruction2.png
 - Resids Analysis
 1. Normality and Constancy of Variance Figure07-AnalysisResiduals1.png
 2. Trend Figure08-AnalysisResiduals2.png
 3. Autocorrelation Figure09-AnalysisResiduals3.png
 - **PCA: No PCA is done when methMSR=SLR. If the radio button for PCA is clicked, users should be told “PCA does not apply for this method.”**

- **methMSR=MLR-noPCA**
 - SSR
 1. Chronology screening Figure01-SSR1.png
 2. Histograms of lags Figure02-SSR2.png
 3. Recent-end signal drop Figure03-SSR3.png
 4. Signal in mean SSR Figure04-SSR4.png
 - Calibration
 1. Corr of SSRs with y Figure05-MSRrcalibration1.png
 2. Summary Figure06-MSRcalibration2.png
 3. Histograms and ACFs Figure07-MSRcalibration3.png
 - Validation
 1. Time plots Figure11-Validation1.png
 2. Statistics Figure12-Validation2.png
 - Reconstruction
 1. Time plot Figure13-Reconstruction1.png
 2. Histograms and ACFs Figure14-Reconstruction2.png
 - Resids Analysis
 1. Normality and Constancy of Variance Figure08-AnalysisResiduals1.png
 2. Trend Figure09-AnalysisResiduals2.png
 3. Autocorrelation Figure10-AnalysisResiduals3.png
 - **PCA: No PCA is done when methMSR=MSR-noPCA. If the radio button for PCA is clicked, users should be told “PCA does not apply for this method.”**

- **methMSR=MLR-PCA**
 - SSR
 1. Chronology screening Figure01-SSR1.png
 2. Histograms of lags Figure02-SSR2.png
 3. Recent-end signal drop Figure03-SSR3.png
 4. Signal in mean SSR Figure04-SSR4.png
 - Calibration
 1. Corr of PC scores with y Figure07-MSRrcalibration1.png
 2. Summary Figure08-MSRcalibration2.png
 3. Histograms and ACFs Figure09-MSRcalibration3.png
 - Validation
 1. Time plots Figure13-Validation1.png
 2. Statistics Figure14-Validation2.png
 - Reconstruction
 1. Time plot Figure15-Reconstruction1.png
 2. Histograms and ACFs Figure16-Reconstruction2.png
 - Resids Analysis
 1. Normality and Constancy of Variance Figure10-AnalysisResiduals1.png
 2. Trend Figure11-AnalysisResiduals2.png
 3. Autocorrelation Figure12-AnalysisResiduals3.png
 - PCA:
 1. Scree of Eigenvalues Figure05-PCA1
 2. Loadings on SSRs Figure06-PCA2

- **methMSR=Analog**
 - SSR
 - 1. Chronology screening Figure01-SSR1.png
 - 2. Histograms of lags Figure02-SSR2.png
 - 3. Recent-end signal drop Figure03-SSR3.png
 - 4. Signal in mean SSR Figure04-SSR4.png
 - Calibration
 - 1. Corr of PC scores with y Figure07-MSRrcalibration1.png
 - 2. Summary Figure08-MSRcalibration2.png
 - 3. Histograms and ACFs Figure09-MSRcalibration3.png
 - Validation
 - 1. Time plots Figure13-Validation1.png
 - Reconstruction
 - 1. Time plot Figure14-Reconstruction1.png
 - 2. Histograms and ACFs Figure15-Reconstruction2.png
 - Resids Analysis
 - 1. Normality and Constancy of Variance Figure10-AnalysisResiduals1.png
 - 2. Trend Figure11-AnalysisResiduals2.png
 - 3. Autocorrelation Figure12-AnalysisResiduals3.png
 - PCA:
 - 1. Scree of Eigenvalues Figure05-PCA1
 - 2. Loadings on SSRs Figure06-PCA2