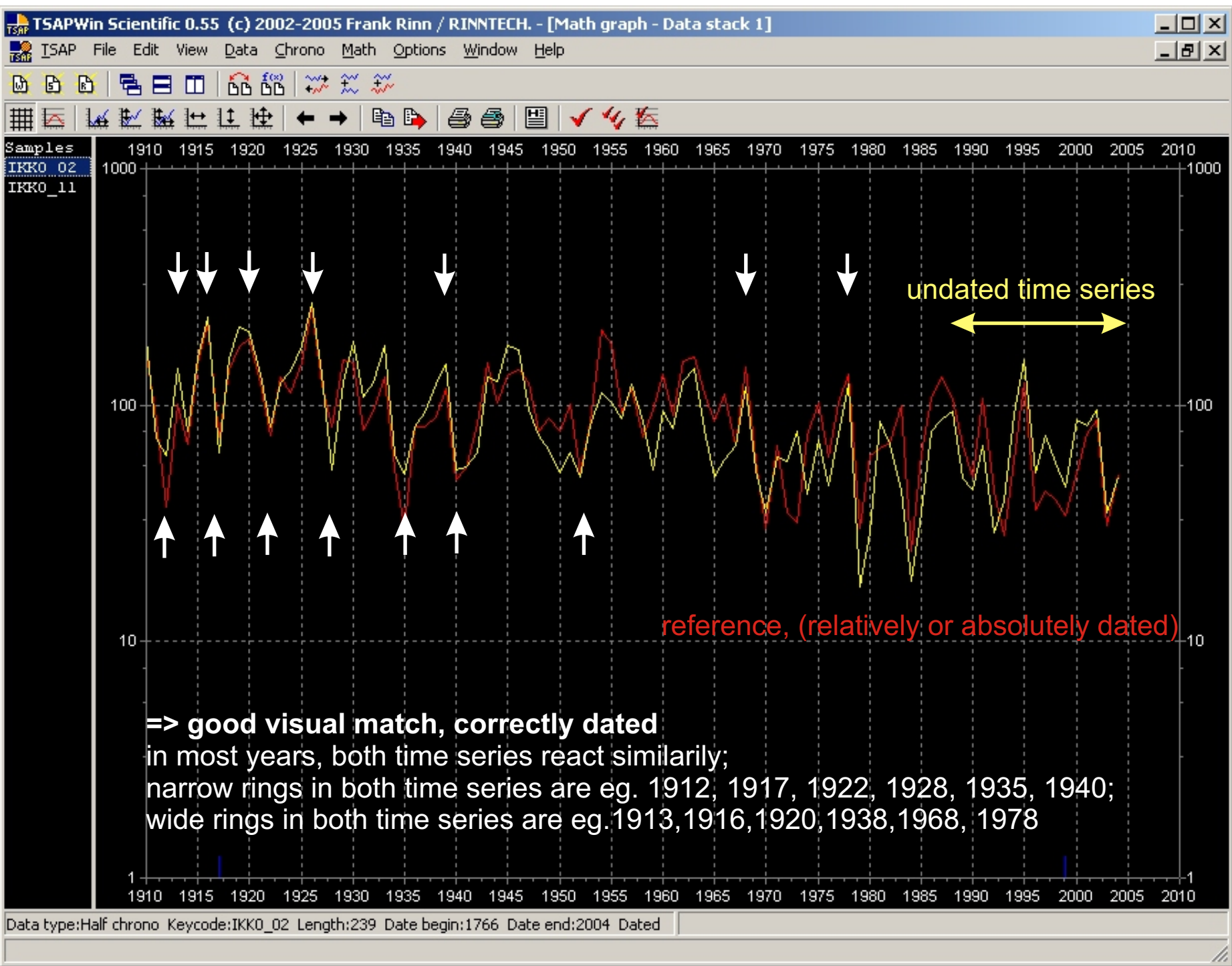
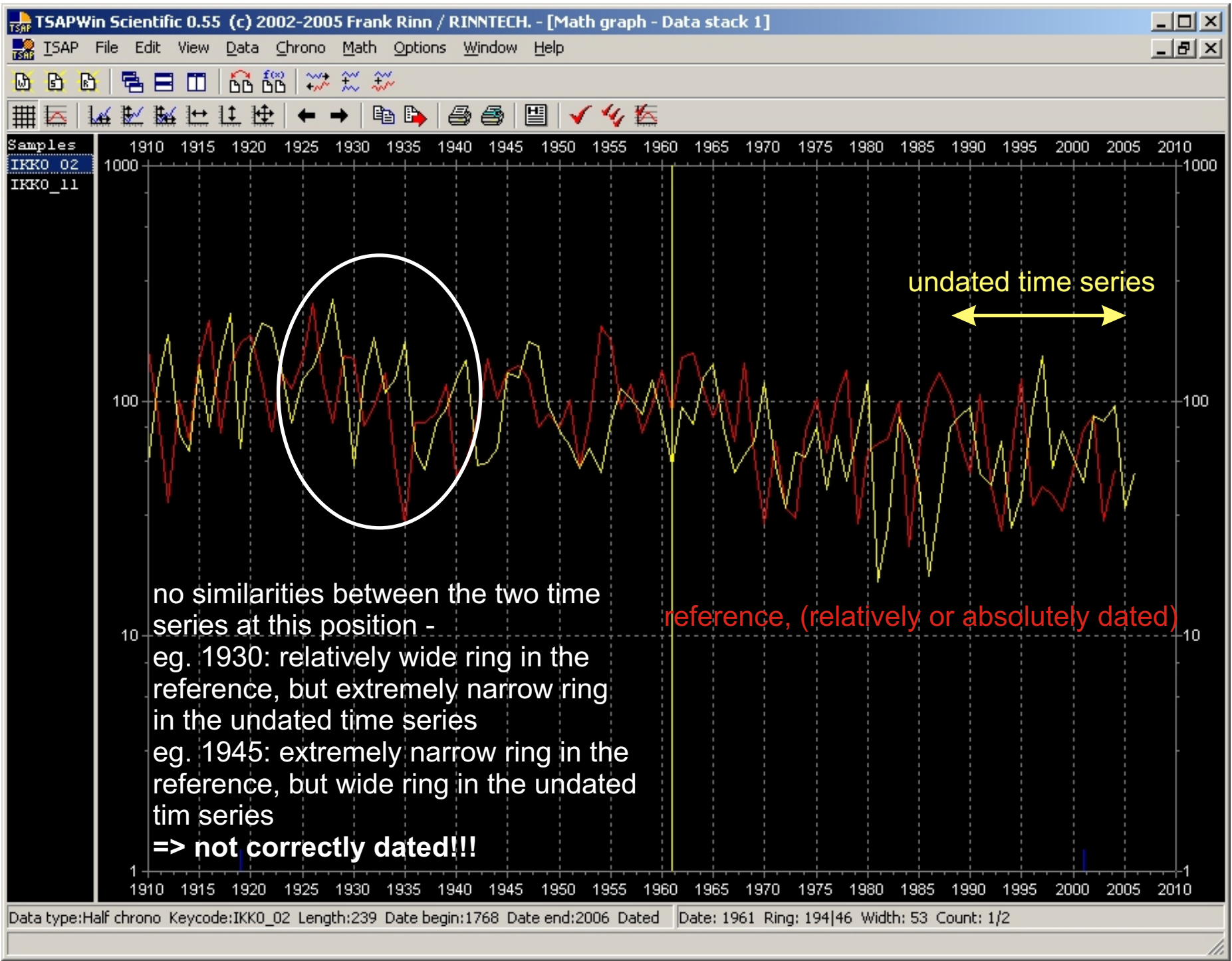


Working in the dendro lab: crossdating

Visual crossdating:

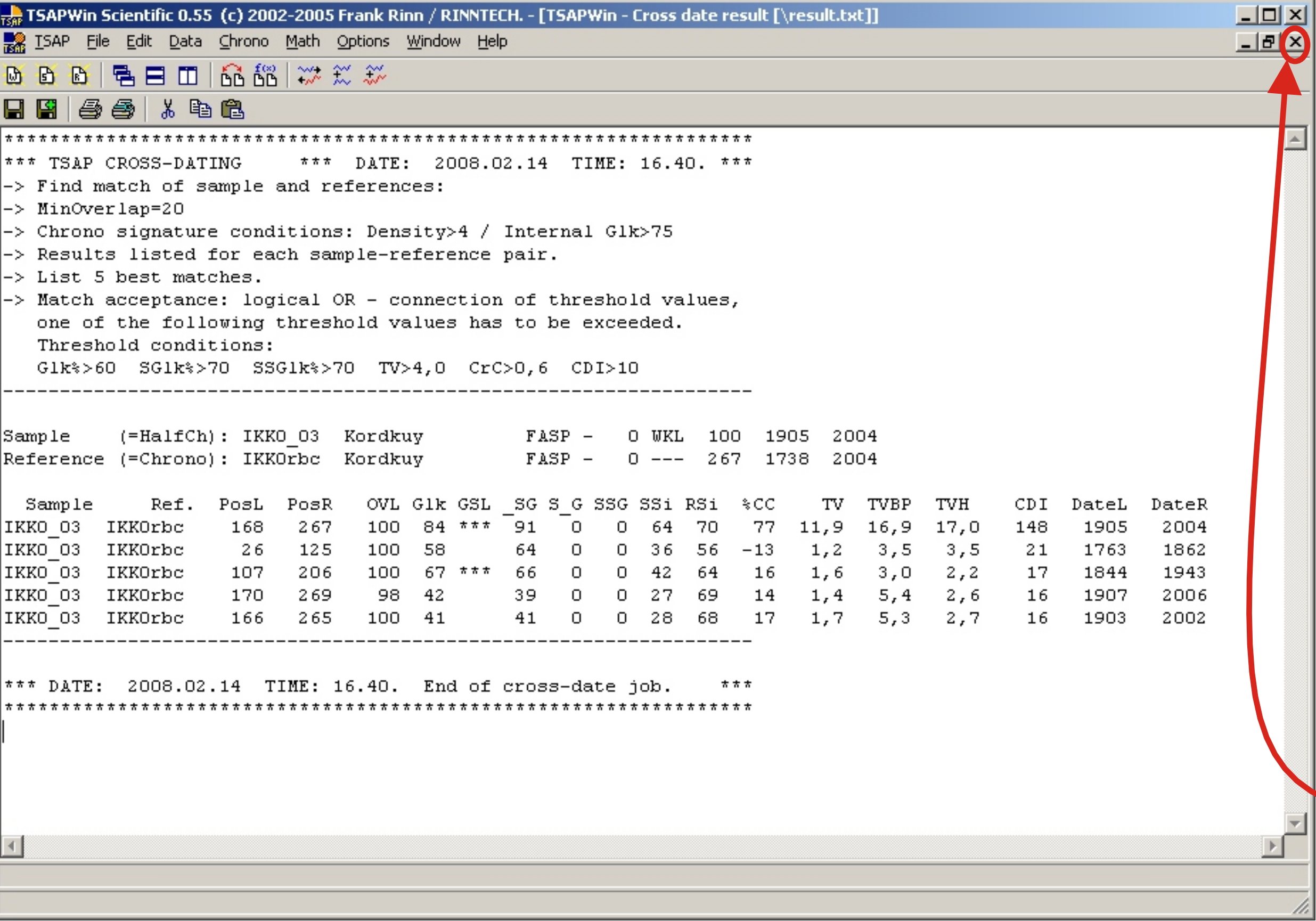
Trees of the same species growing in one site are influenced similarly by local site conditions. Therefore, time series of annual growth increments of stems (aka tree rings) from different trees share a **common pattern** of wide and narrow tree rings, which can be used to identify the exact year in which each tree ring was formed. Thus, accurate dating of wood of unknown age against a previously established ring width series of known age is possible.



Before the advent of computers, crossdating was performed optically. A reference was put on a light table and the undated time series was shifted along the whole length of the referene, until a matching position was found. Visual crossdating and data editing in TSAP can be performed in math graph:

Statistically aided crossdating:

In TSAP, performs statistically aided crossdating. After selecting which datastacks are used for samples and references, TSAP automatically calculates several statistical parameters for all possible match positions and sorts them according to the highest relevance. The 5 best positions are listed in a new window as a text file.

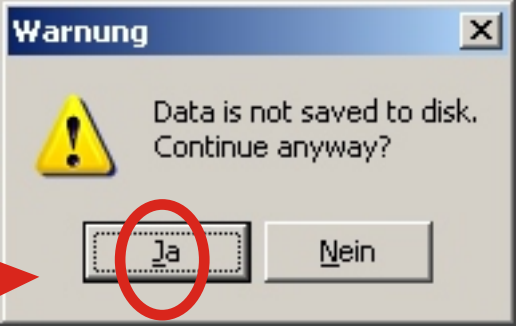


Sample / Ref. : keycode (name) of sample and reference, respectively
PosL / PosR: relative position of the first and the last year of the sample on the reference
OVL: overlap between sample and reference (number of common years)
GLK: “Gleichläufigkeit” = sum of equal slope intervals in % (= percentage of years, where both time series show identical growth patterns (decreasing or increasing ring width compared to the previous year)
GSL: significance level for “Gleichläufigkeit”, *: 95%, **: 99%, ***: 99,9%, depends very much on the length of overlap.
CC: cross correlation
TV: standard t-value
TVBP: t-value Baillie and Pilcher (1973), t-value calculated after detrending with a 5-year moving average and logarithm to base e.
TVH: t-value Hollstein (1980), t-value calculated after detrending with “Wuchswert”
CDI: cross date index - combined index, including t-values and Gleichläufigkeit

GLK is a very good indicator for the year-to-year similarity of growth. For completely independent time series, a GLK value of 50 would be expected. For dating purposes, GLK should be at least close to 60.
TVBP and TVH both are good indicators for the similarity of growth trends (decadal and longer). Both t-values should reach at least 3.5.
Always keep in mind: statistics only aid crossdating. There are no thresholds to “prove” correct dating. Even very good statistical results may be misleading, especially if a false or missing ring occurs in the first or last rings of a time series.

.Therefore, always check manually, if the dating is correct! - The last decision is yours!

To close the statistics window, press X. You will be asked whether you want to close the window or to save your data. Close the window



This will open the crossdating window. It is identical to the math graph, except for the crossdating statistics displayed in the lower part of the window. The five statistically best positions will be shown in the left side of the crossdating window.

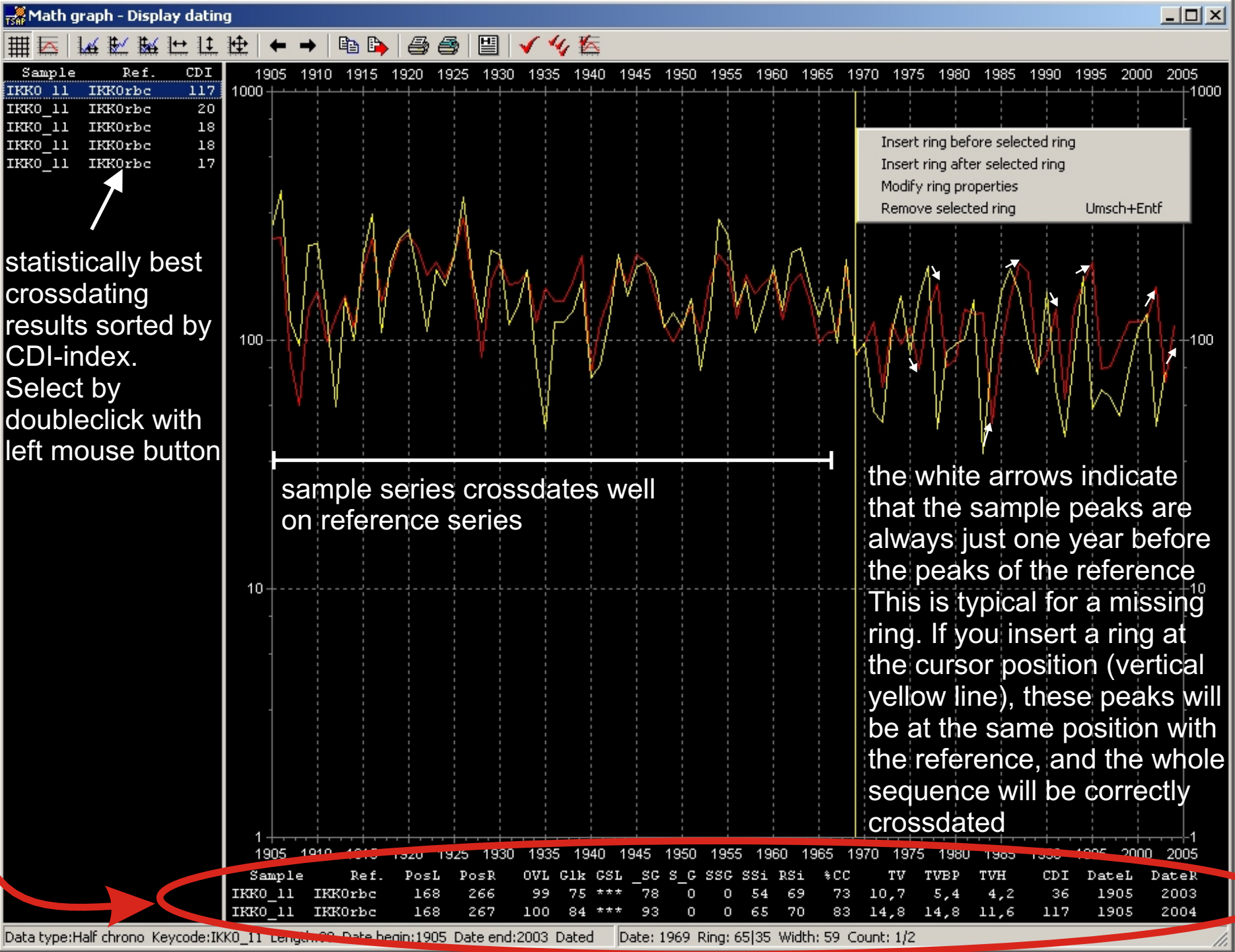
In this view, only the sample can be moved, using the arrow keys on your keyboard (↑ ↓ → ←). The lower line of the crossdate statistics will still show the selected crossdating results. The upper line will show the actual crossdating statistics after moving or editing the sample series. For editing, use the right mouse button. It will open the editing window, where you can insert, delete or modify single rings. Don't forget to make any changes in your tree ring series permanent by using !

Samples, where the sampling date is known and that possess “Waldkante” (complete outermost ring before the cambium / bark) can be dated by inserting the year of the last growing season into the “Date end” field in the data header.

Problems with crossdating:

How to find missing or false rings? If you have samples of known age (eg a set of cores from living trees) and crossdating results are no good, you have to check for missing or false rings. First, check manually, if you can find a position, where at least part of the sample series fits to the reference series. Use the arrow keys to move the sample. Quite often you will find that the rest of the series will fit, if you move the series for one or two years from the first position. Repeat, until you find the exact position, where the problem lies. **Take your sample and check** the problematic rings for measurement errors, or surface problems, or wounds, or problematic parts of your sample that may be a missing or wedging ring. If you don't have a good chronology, but want to compare radii of trees, always check both radii - you never know, whether the problem is one missing ring in one radius, or one false ring in the other radius.

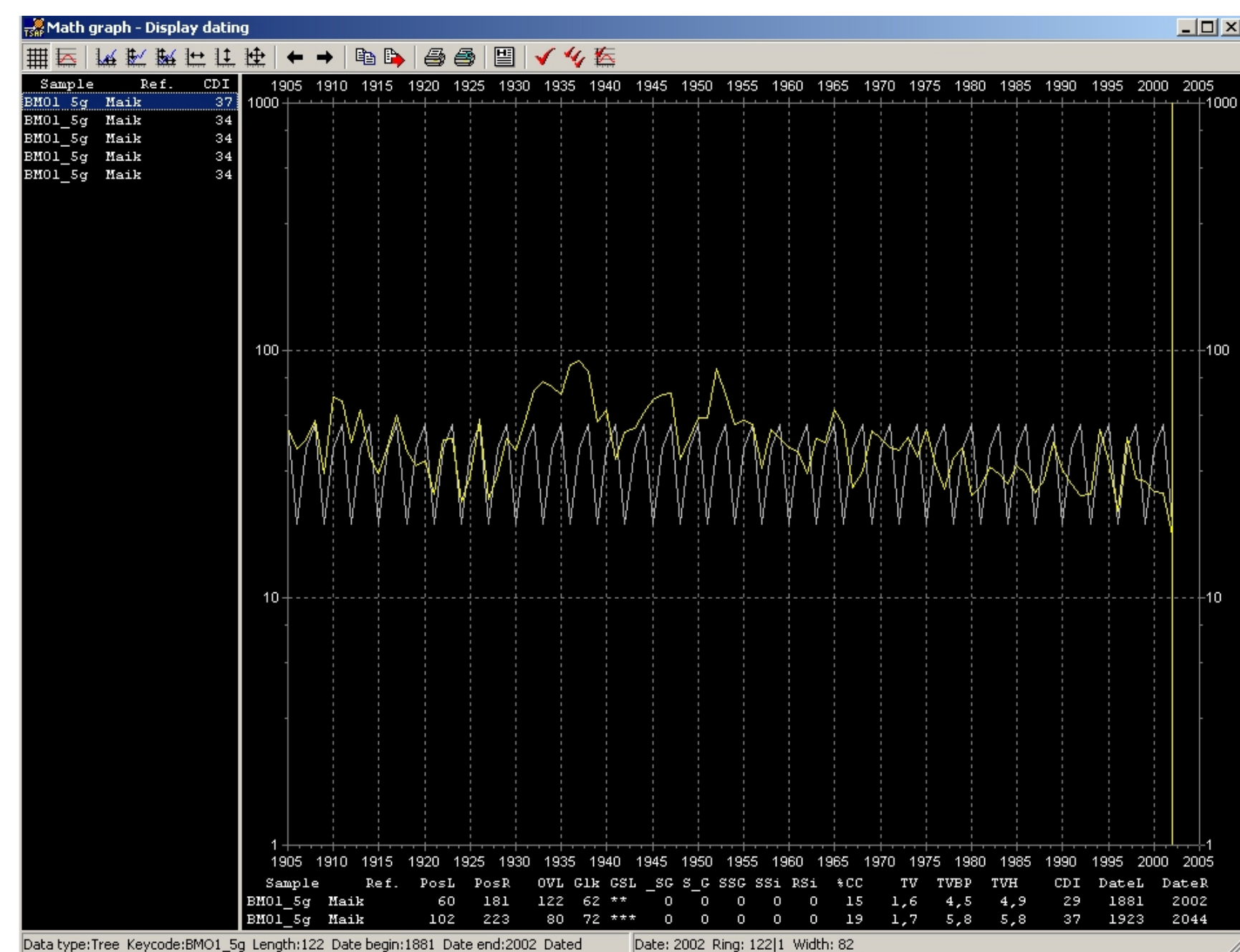
If you find the problem, simply remeasure the area, write down the correct ring widths and use the editing function to insert a new ring or delete a false ring, and, if necessary, modify the ring width of the preceeding or following ring. If you you don't find any problems, but you have a very good reference and there are still missing rings, you can insert rings, even if you don't see anything on the wood - but use this only if you are completely sure that there are missing rings - **bad crossdating will invalidate any conclusions from your data!**



This is also a good example why you cannot trust statistical crossdating alone: Even though there is a definitely a ring missing, the GLK is 75 and the t-values are 5,4 (Baillie-Pilcher) and 4,2 (Hollstein), respectively. **Therefore always recheck your crossdate results manually and optically!**

Working in the dendro lab: problems with crossdating

Some typical crossdating problems are shown below to help getting a feeling for what crossdating can and cannot do:

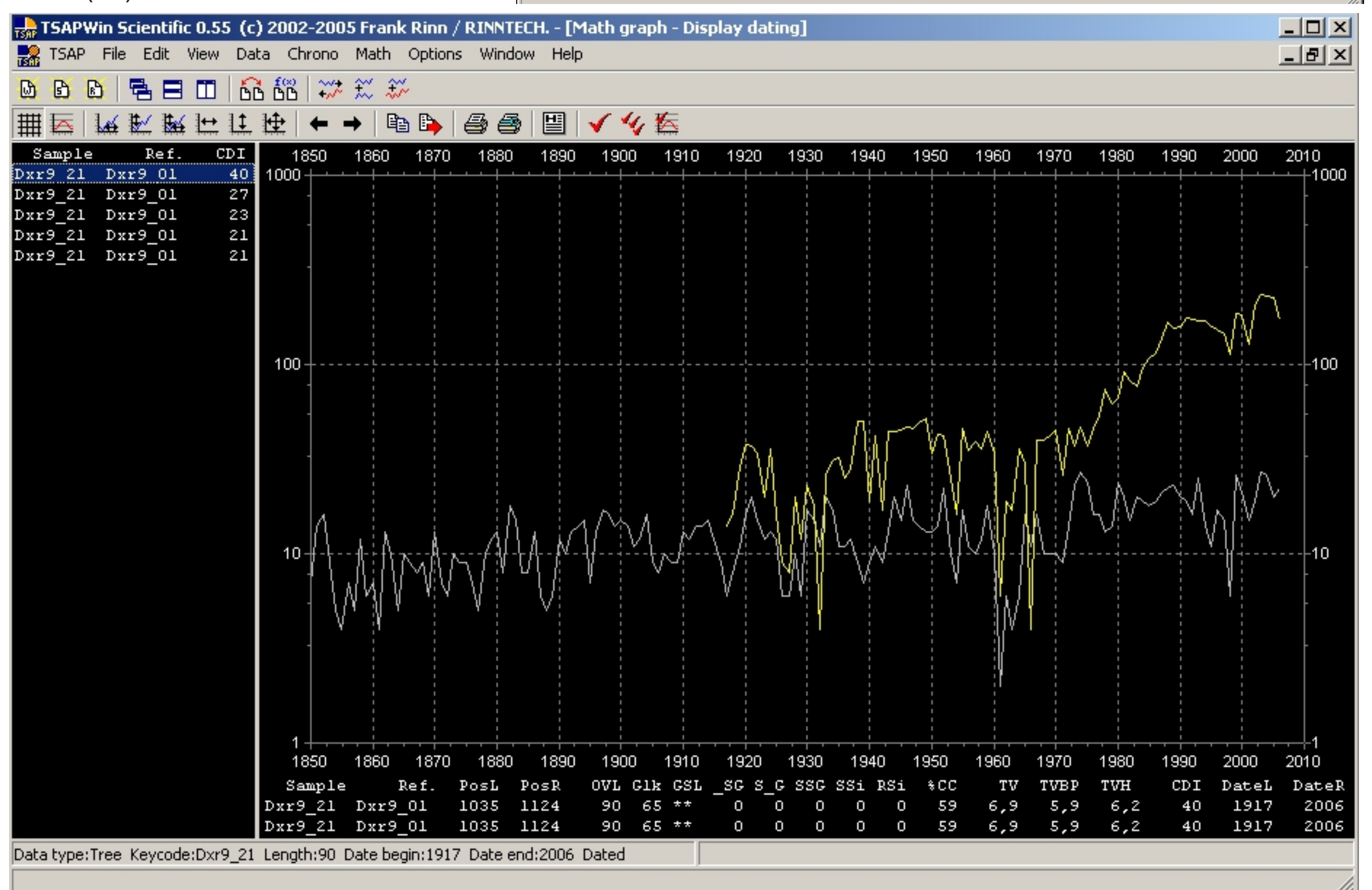
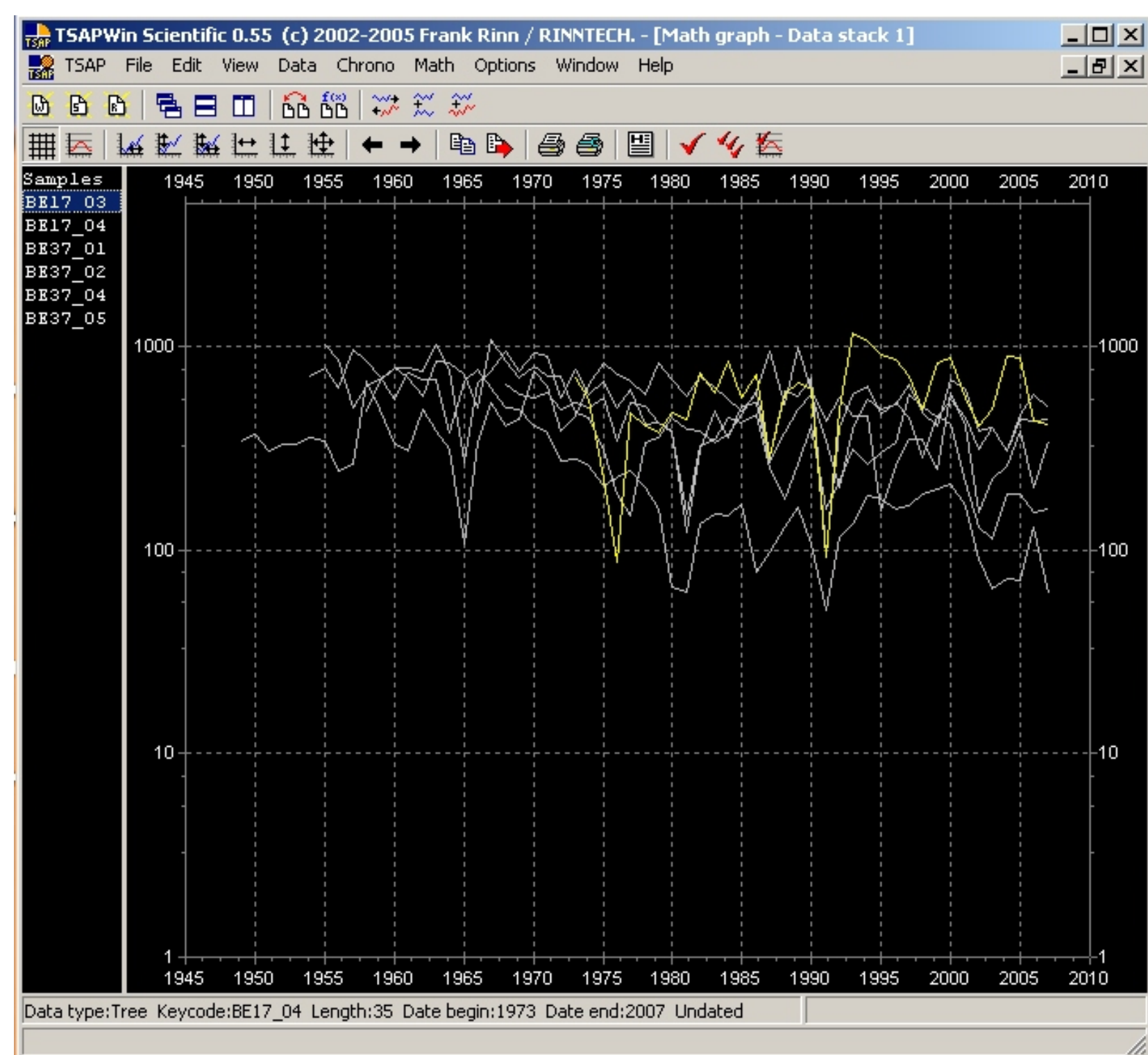
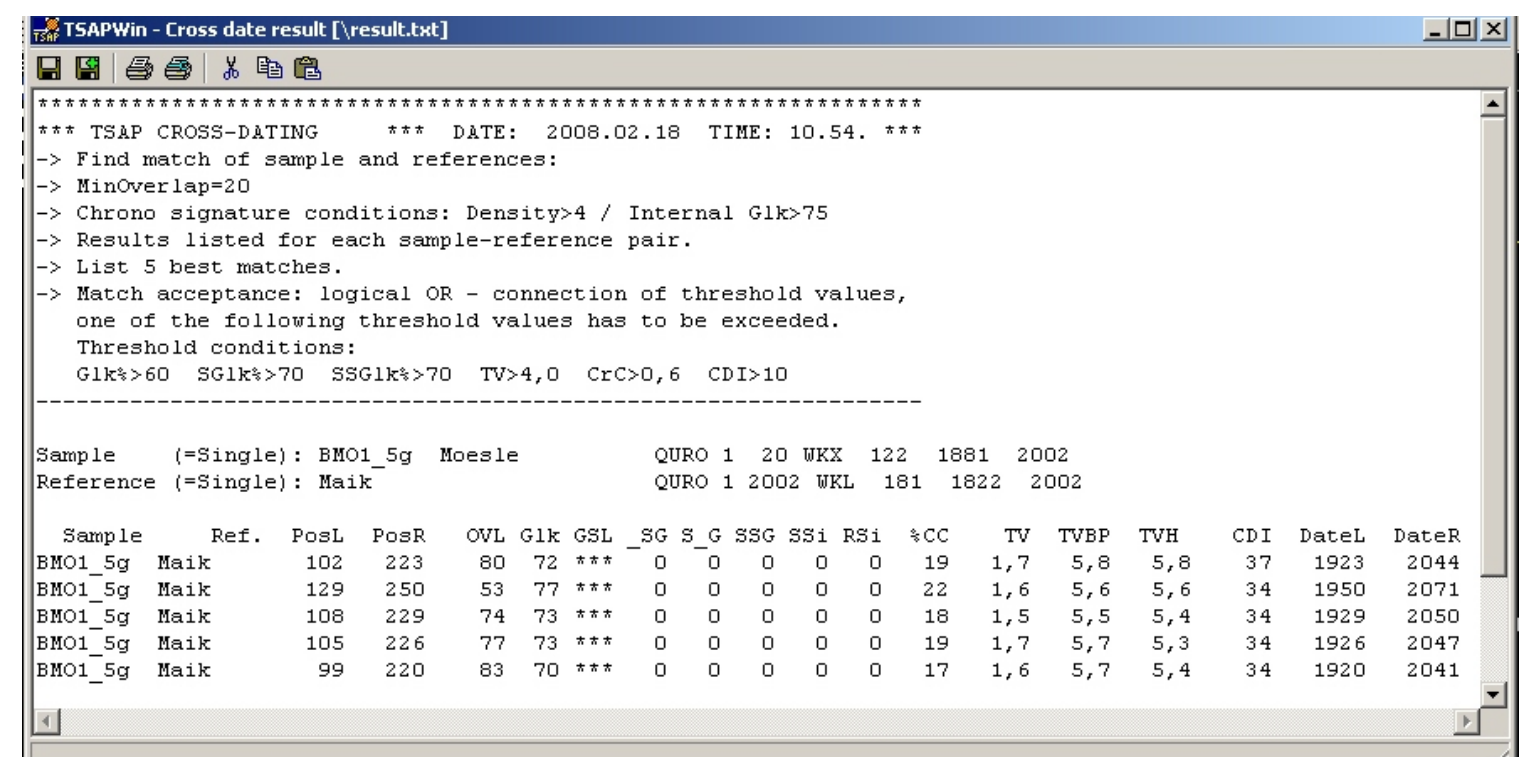


This is a case where crossdating will not work. The tree (*Quercus robur*) is influenced by periodical insect infestations by a bug named cockchafer (*Melolontha melolontha*). Every three to five years, the bugs will mature from their larval stadium and damage the trees.

The grey time series is an artificial representation of this cycle: one very narrow “ring”, representing the year of infestation, and two bigger “rings”, representing two years of recovery. The crossdate statistics show the strong influence of this cycle on the time series. It superposes all climatic influence. Crossdating is not possible because there will be false positive dates every three years. By sampling date, 2002 is the correct end year for this tree, but check the lower line of the crossdating statistics to see the statistical results for the end year of 2044: GLK > 70%, t-values of 5,8!

Trees that exhibit such strong cyclicity are unsuitable for crossdating and analysis. Other examples for periodic bug infestations include larch budmoth (*Zeiraphera diniana*).

A good indicator for this type of problems is the table for crossdate results: as you see in the figure on the right sind, you find many possible dates for your sample, all in a three years interval: 2041, 2044, 2047, 2050, all with similar GLK (>70) and similar t-values (>5).



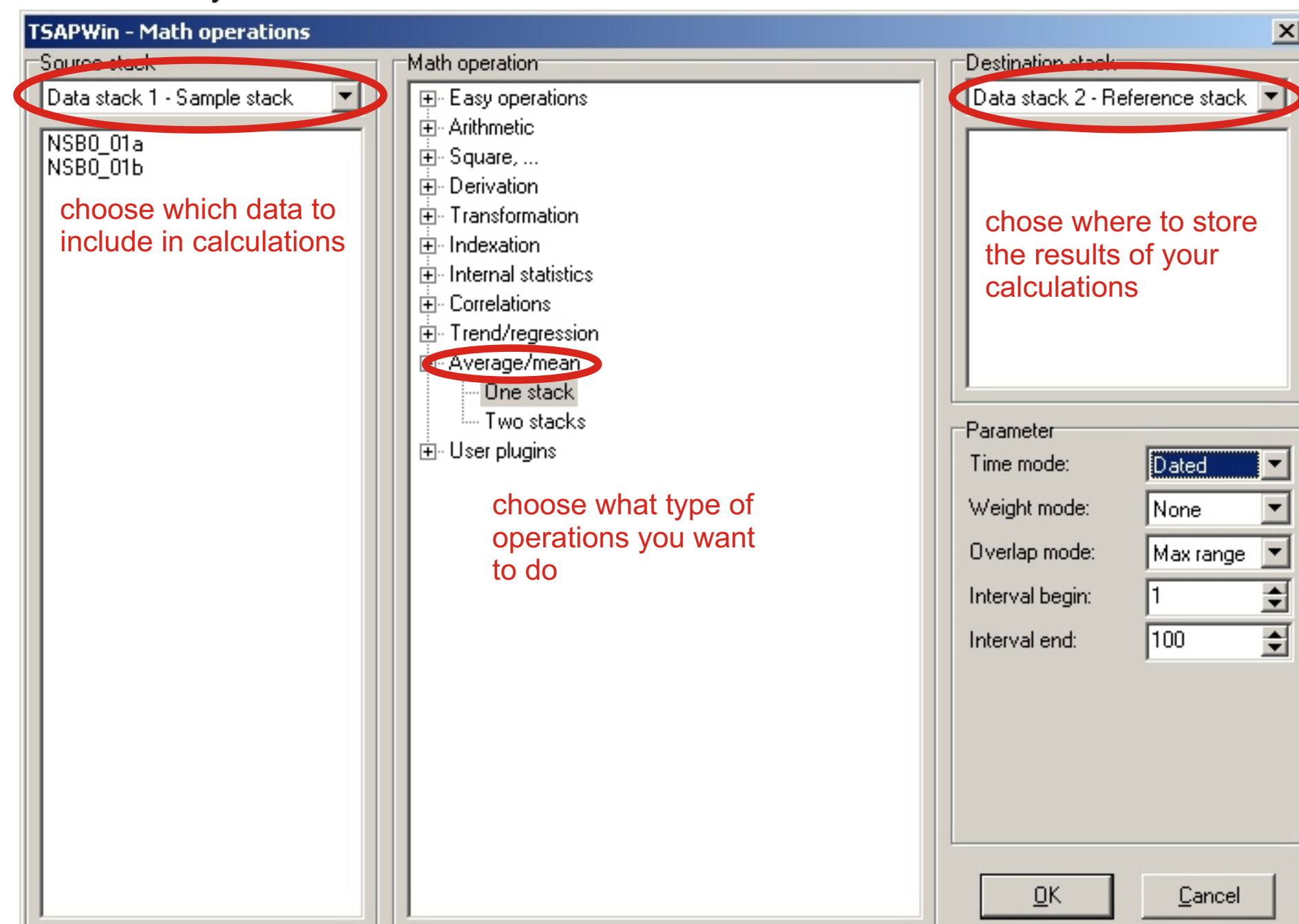
Another type of crossdating problems exists with very short time series and/or time series with very little common signal. Statistics will not help you in this case, since all parameters need a large number of samples (aka years) to be statistically significant.


The samples in the figure on the upper left side are from willow trees (*Salix sp.*) from southern Germany. The trees grow very well, sometimes even more than 1 cm / year. Also, tree ring series usually exhibit some autocorrelation. The ring width of one year is influenced by the previous year(s). One reason for this lies in reserves of sugars and other substances stored in the tree during winter. Therefore, it is not very likely that these trees show completely missing rings after growing so very well in the previous year. These trees are unsuitable for temperature or precipitation reconstruction since in most years, usual temperature or precipitation variations are obviously not very limiting to growth and all trees show only a weak common signal. The only exception are several event years. Here, all or most trees show distinct growth reductions. Examples for such years are: 1965, 1976, 1981, 1991 and 2002. These event years can be used for dating. Sample BE17_03 was dated to the end year of 2007, using the event years 1981, 1991, and 2002. In addition, the sample was complete with bark and was sampled in 2007. In this case, crossdating does not mean "independent statistical verification of crossdating for >100 year time series". But this method of dating is still valid - even if there is not much common signal - because for ecological reasons the probability of missing rings, especially outside of event years, is very low.

Time series shorter than 20 years cannot be crossdated statistically. The only way to deal with these extremely short series is to place them according to sampling date and “Waldkante” (end of series complete until beginning of cambium) and to accept them if at least both radii crossdate well on themselves and show no indication of missing or false rings and the resulting mean curve doesn't contradict your chronology. Sometimes, there are also difficulties with differing growth trends. Growth trends are either caused by age trends, or, in dense stands, by interaction between trees (eg. suppression of growth in the shade of dominant trees and growth release in the understory after a dominant tree fell down. A typical example for different age trends is shown in the upper right graph. A very jung juniper tree (yellow graph) is plotted together with a very old tree (>800 years, grey graph). The different trends negatively influence the t-values, but GLK is not affected.

Averaging time series and chronology building

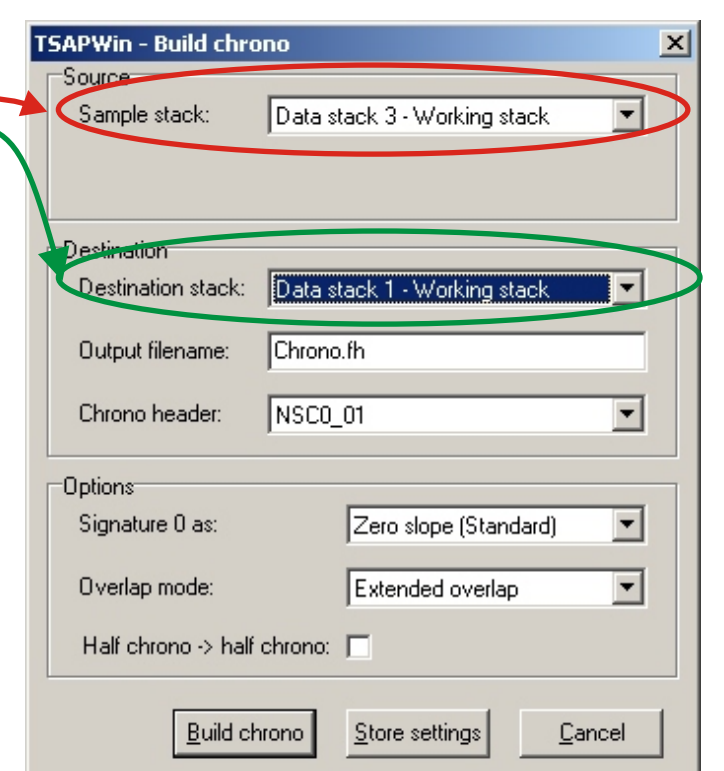
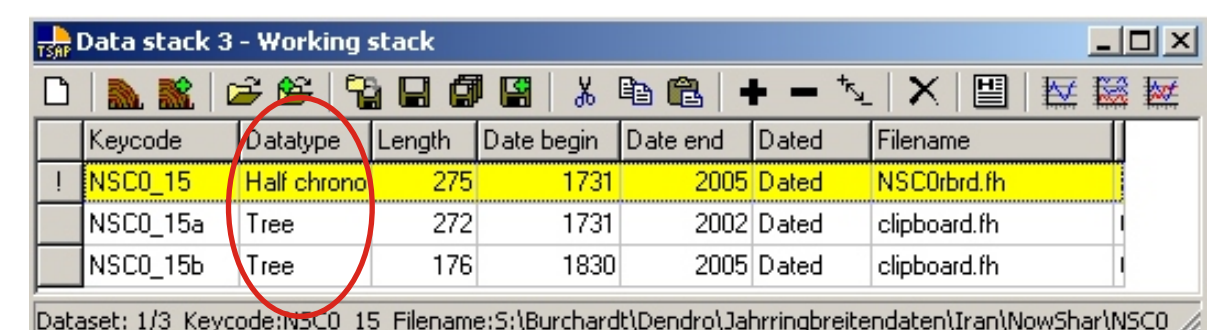
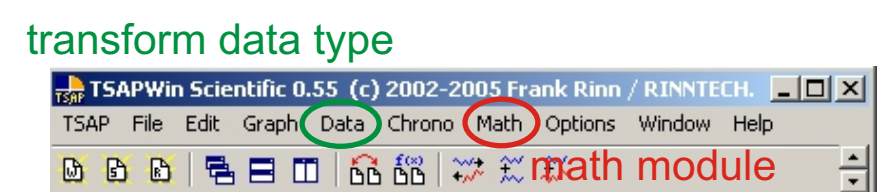
After crossdating two or more radii from one tree, an average time series for each tree can be calculated by using TSAP's math module. All of TSAP's mathematical features are operated similarly. First, choose what type of operations you want to do in the central window. In this case, I want to calculate an average of two radii from one tree. Next, choose on which stack your data can be found. Here, both radii are on data stack 1. All active (red) data on the selected data stack will be included in your calculations. The keycodes of your active data sets are shown in the window on the right side. In the window on the upper left side, you can specify where the results of your calculations shall be stored.



Mean curves in TSAP will be stored as “half chrono”. Thus, the number of radii used to calculate the mean curve will be stored, too. For chronology building, it is important that each tree included in the chronology has the same statistical influence, no matter if it consists of one radius, or is a mean curve of 10 radii. Therefore, the menu point “Data” can be used to transform the data type transform - to single series” command. Crossdated improve an existing chronology .

As in “Math operations”, you will be asked to specify both the stack with the source data and the stack to store the resulting chronology. The new chronology will take its data header from one of the trees from the source data, so make sure to change the name of the chronology.

A chronology basically is an arithmetic average of its source trees. Therefore, the common signal will be amplified and the effect of events influencing only individual trees will be weakened. Thus, crossdating is much easier with a chronology than with individual trees. As soon as there are more than two crossdated trees from one site, it is helpful to create a simple chronology as an aid for crossdating the rest of the samples. The quality of a chronology improves with the number of samples in it - so make sure to add all newly dated samples into your chronology and then go back and try to date the rest of your samples.



Check back to wood all the time!

Don't just believe in the statistics, always in wood!

FR (false ring)/MR (missing ring)/i (inserted ring)

