SM4: Polar Urals trees consistency and adjustment

PC1. Rescaling MXD samples for RCS processing

There is increasing evidence that while densitometric measurements made on the same machine at the same time are consistent, different machines and even measurements made on the same machine but at different times may be systematically different (Helama et al. 2008, Helama et al. 2012, Melvin et al. 2013 and Alex Kirdyanov pers. comm.). So while it is not necessary to rescale ring-width measurements on the grounds of measuring system bias, it may be necessary to compare and rescale MXD measurements made under different circumstances. It is necessary to explore whether the means and standard deviations of MXD measurements are unbiased and where it is found that they are biased it is necessary to rescale both the mean and standard deviation of the different MXD data sets prior to combining the data into one set for RCS processing. A detailed description of the adjustments applied to the Polar Urals data follows.

The RCS method presumes that under the same climate conditions proximal trees have similar growth rates and measured ring-width series display similar age-related-growth trends. When combining samples from different sites or samples obtained using differing selection techniques (e.g. living trees and sub-fossil trees) it is necessary to establish that they are sufficiently similar and that any differences are not sufficient to produce systematic bias if they are processed together. In order to compare growth rates in different samples, it is necessary to take account of any differences in ring age and in the common (climate) forcing signal at the time when that ring grew. If data from multiple sites (sub-samples) are combined and processed using one-curve signal-free RCS, separate plots of the means of signal-free measurements for each sub-sample will give an indication of the relative growth rates at each site. Signal-free tree-index series are created by dividing tree-index series by the common chronology signal. The overall mean value of signal-free indices for the combined sites will be approximately 1.0 and any difference between the means of signal-free indices for the sub-samples will indicate the value of any necessary rescaling. Rescaled data sets will be much more compatible and hence much more suitable for RCS processing. Here we rescale the samples of one sub-sample (usually the one with fewest trees) such that the samples of the second site have mean signal-free indices of 1.0. This rescaling using the mean value of signal-free indices needs to be made iteratively, because the different sites will have differing sample counts by age and by calendar year. See part PC2 for more details.

For TRW, measurement systems are generally accurate and provide data that are consistent, within “measurement error”. Therefore we do not consider it necessary to make adjustments but we still undertake the same comparisons between sub-samples of data as is done for MXD data. This allows direct comparison of the results and allows us to look for differences in the slope (as compared to magnitudes) of the sub-sample RCS curves. Notable differences would indicate the need to use different RCS curves to process these data. Due to the root-collar/stem problem (discussed in the main paper Section 6.1 and SM3 part PU3) in the case of the Polar Urals sub-fossil material it was necessary to examine various combinations of the Polar Urals data to discover which measurement series could reasonably be used (and combined) in RCS TRW chronologies. Figure PC02 demonstrates that it was not considered possible to "adjust" the TRW root-collar samples satisfactorily and these data were not used in subsequent analysis. The sub-groups developed and tests used here to assess the need for adjustment between sub-groups of data are illustrated in Figure PC01.

PC2. Rescaling Method

We designate the data set to be rescaled as sub-sample 1. This is to be rescaled so as to be consistent with the data for sub-sample 2. Measurements from the two sub-samples are first processed together using one-curve signal-free RCS. The counts of indices (nr1 and nr2) and means (mnsf1 and mnsf2) and standard deviations (sdsf1 and sdsf2) of signal-free indices (tree indices divided by chronology values) are calculated for both sub-samples. The values of all measurements of sub-sample 1 (M1) are rescaled as follows:

$$M1 = M1*(1.0 + (mnsf2-1.0)*(nr1+nr2)/nr1).$$

For MXD measurements, the standard deviation of sub-sample 1 is also adjusted: the mean (MnM1) is removed, the measurement anomalies are rescaled, and the mean (MnM1) is added back as follows:

$$M1 = (M1-MnM1)*sdsf2/sdsf1+MnM1.$$

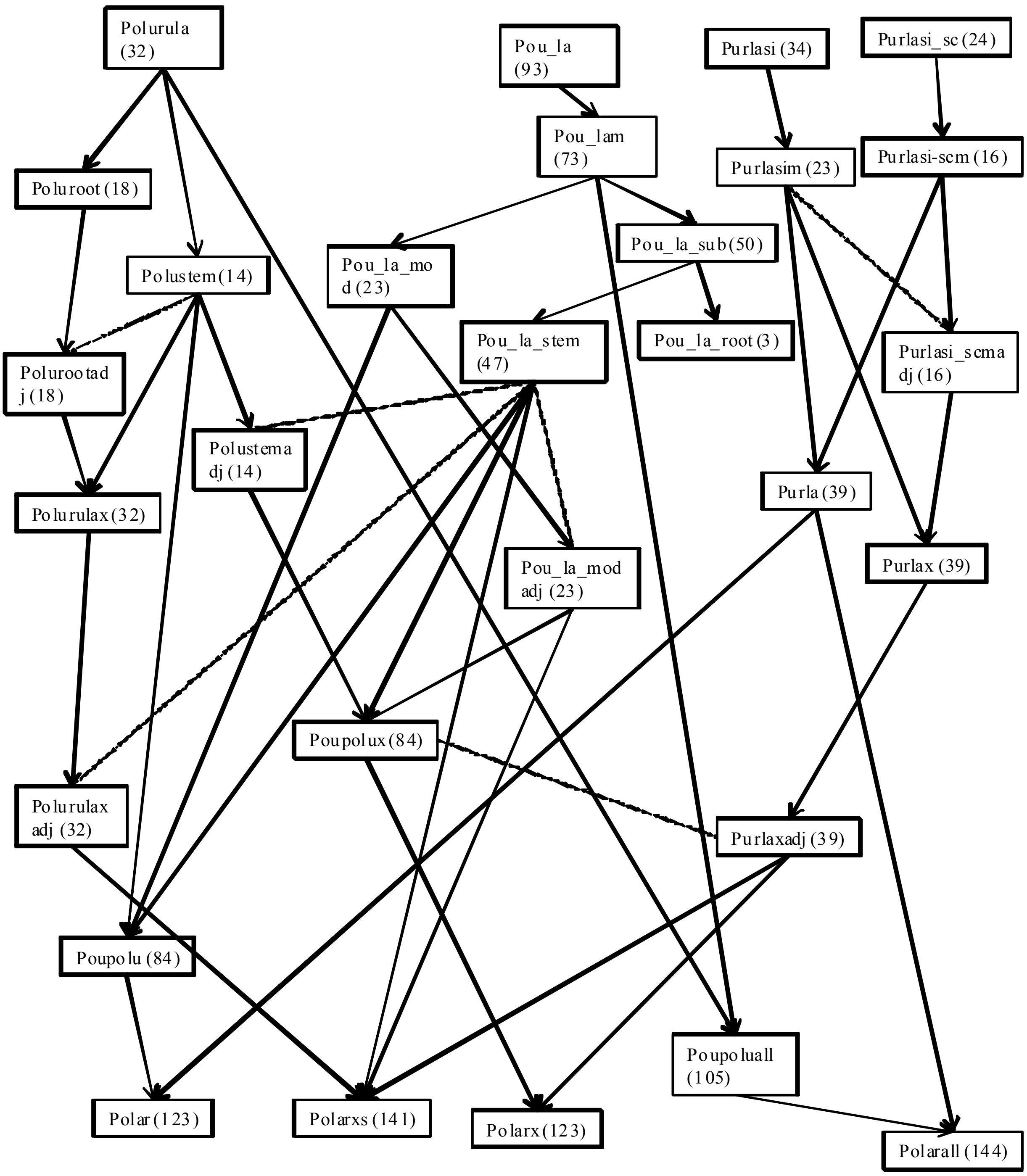
The process is repeated iteratively 3 times and the rescaled measurements of sub-sample 1 are saved.

The report "Rescale_Pol.prn" is produced by the program which calculates and creates adjusted data files and also creates the figures shown here. The program reports the file names of the file to be rescaled, the file used for comparison and the file of output data. For each of three iterations, the number of rings, number of trees, the mean of signal-free indices and standard deviation of signal-free indices are reported. Finally, the total adjustment to the mean value of measurements and (for MXD only) the subsequent adjustment to the standard deviation of measurements are reported.

Filename	**Count**	**Source of data**	
Polurula	32	Update sub-fossil samples	
Poluroot	18	Root-collar samples from Polurula	
Polustem	14	Stem samples from Polurula	
Polurootadj	18	Rescaled (against Polustem) Poluroot samples	
Polustemadj	14	Rescaled (against Pou_la_stem) Polustem samples	
Polurulax	32	Combined Polustem and Polurootadj sample	
Pou_la	93	Original sub-fossil and modern data	
Pou_lam	73	Mean-tree version of Pou_la	
Pou_la_mod	23	Living-tree samples from Pou_la	
Pou_la_sub	50	Sub-fossil samples from Pou_la	
Pou_la_stem	47	Stem samples from Pou_la-sub	
Pou_la_root	3	Root collar samples from Pou_la-sub	
Pou_la_modadj	23	Rescaled (against Pou_la_stem) Pou_la_mod samples	
Purlasi	34	Living samples up to 2001	
Purlasim	23	Mean-tree version of Purlasi	
Purlasi_sc	24	Living samples up to 2006	
Purlasi_scm	16	Mean-tree version of Purlasi_sc	
Purla	39	Combined Purlasim and Purlasi_scm samples	
Purlasi_scmadj	16	Rescaled (against Purlasim) Purlasi_scm samples	
Purlax	39	Combined Purlasim and Purlasi_scmadj samples	
Poupolux	84	Combined Polustem and Pou_la_modadj samples	
Polurulaxadj	32	Rescaled (against Pou_la_stem) Polurulax samples	
Purlaxadj	39	Rescaled (against Poupolux) Purlax samples	
Polar	**123**	**Combined Poupolu and Purla samples**	
Polarxs	**141**	**Combined Polurulaxadj, Pou_la_stem, Pou_la_modadj, and Purlaxadj samples**	
Polarx	123	Combined Poupolux and Purlaxadj samples	
Poupoluall	105	Combined Polurula and Pou_lam samples	
Polaresp	125	Combined pou_la and Polurula samples	
Polaresp_nor	104	Combined Pou_la and Polurula without root samples	
Polarall	144	Combined Poupoluall and Purlax samples	

Table PC1. The filenames and associated sample counts for the TRW and MXD datasets used in analyses described in the main paper and the Supplementary Material. The TRW and MXD data used in the final Polar Urals chronologies are indicated by bold font. The 123-tree (excluding roots) unadjusted “Polar.raw” data are used as the combined TRW data set and the 141-tree (including roots from the Polurula data set) adjusted “Polarxs.mxd” data are used as the combined MXD data set.

Figure PC01 Schematic representation of the development steps involved in assessing the need to rescale and in the actual rescaling of the data: starting from original data files (top row) to combined and adjusted data files on the lowest row. Solid lines show data used in creating file below and dashed line shows trees against which adjustments are calculated and made. The number of samples is shown in parentheses. The processing stages are summarised in PC3.



PC3 Polar Urals Larch MXD (and associated TRW) from WSL

1. Two files “pou_la” (93 cores) and “polurula” (32 trees) both with MXD, TRW and pith offset estimates.
2. Created “.pth” file for both in CRUST format (core name – year pith grew – missing radius cms).
3. Checked crossdating using combined data (“larch.raw” and “larch.mxd”) – see reports “larch_TRW_Corr.prn”, “larch_MXD_Corr.prn”, “larch_TRW_Stats.prn”, and “larch_MXD_Stats.prn”.
4. Created mean tree files by averaging core data from same tree to get “pou_lam” (73 trees) and see report “pou_la_sub_mean.prn”. Note that “polurula” data were already mean tree data.
5. Separated ”pou_lam” data into living samples “pou_la_mod” (23 trees) and sub-fossil samples “pou_la_sub” (50 trees).
6. Separated “pou_la_sub” samples into root “pou_la_root” (3 trees – 862249H, 86260H and 862510H) and stems “pou_la_stem” (47 trees).
7. Separated “polurula” samples into root “poluroot” (18 trees) and stems “polustem” (14 trees) files
8. Compared “poluroot” (18 trees) with “polustem” (14 trees) to look for (and adjust) any differences in means (Figures PC02 and PC03 and file “Rescale_Pol.prn”) creating adjusted files “polurootadj.raw” and “polurootadj.mxd” and reports “polurootadjMXD.prn” and “polurootadjTRW.prn”.
9. Combined “polurootadj” and “polustem” files creating adjusted file “polurulax” (32 trees).
10. For TRW, the “root” measurements are roughly twice as large as the “stem” measurements and the combined data cannot be sensibly used in RCS standardisation so only the stem data are used (“pou_la_root” and “polurrootadj” are discarded from further TRW analysis).
11. For MXD, root and stem measurements are not consistently different and their use together is tested. Insufficient “pou_la_root” trees (only 3) for sensible comparison so “pou_la_root” discarded for MXD.
12. Compared “pou_la_mod” (23 trees) with pou_la_stem (47 trees) to look for (and adjust) any differences in means (Figures PC04 and PC05). Created “pou_la_modadj” files.
13. Compared “polustem” (14 trees) with “pou_la_stem” (47 trees) to look for (and adjust) any differences in means (Figures PC06 and PC07) and created “polustemadj” files.
14. Created “poupolu” files (84 trees) from “pou_la_mod”, “pou_la_stem” and “polustem” which contains all of the WSL Polar Urals data extracted from stems.
15. Created “poupolux” files (84 trees) from “pou_la_modadj”, “pou_la_stem” and “polustemadj” which consist of all the adjusted versions the WSL Polar Urals data extracted from stems.
16. Created “poupoluall” files (105 trees) from “pou_lam” and “polurula”. This contains all of the WSL Polar Urals data from both stems and roots.
17. Compared “purlax” (39 trees) with “poupolux” (84 trees) to look for (and adjust) any differences in means (Figures PC08 and PC09) and created “purlaxadj” files.
18. Created combined files “polar” from “poupolu” and “purlax”.
19. Compared “polurulax” (32 trees) with “pou_la_stem” (47 trees) to look for (and adjust) any differences in means (Figures PC10 and PC11) creating files “polurulaxadj” and reports “polurulaxadjMXD.prn” and “polurulaxadjTRW.prn”.
20. Created combined files “polarx” (123 trees) from “poupolux” and “purlaxadj”.

21. Created combined files “polarxs” (141 trees) from “polurulaxadj”, “pou_la_stem”, pou_la_modadj” and “purlaxadj.raw”.
22. Created combined files “polarall” (144 trees) from “poupoluall” and “purlax”.

PC4. Polar Urals Larch MXD update (and TRW) from Krasnoyarsk

1. Two files for sites “purlasi” (34 cores) and “purlasi_sc” (24 cores) both with MXD, TRW and pith offset estimates
2. Created “.pth” files in CRUST format (core name – year pith grew – missing radius cms). Adjusted pith years for a few trees where cores from same tree had slightly differing pith years (also relabelled 2nd core 148 211 to 148 212 to avoid confusion).
3. Checked crossdating and all OK. See reports “purlasi_sc_TRW_Corr.prn”, “purlasi_sc_MXD_Corr.prn”, “purlasi_sc_TRW_Stats.prn” and “purlasi_sc_MXD_Stats.prn”.
4. Created mean tree files by averaging cores from same tree to produce files “purlasim” (23 trees) and “purlasi_scm” (16 trees).
5. Compared sites using “signal-free” indices to look for (and adjust) any differences in means (and standard deviation for MXD) (Figures PC12 and PC13) creating files “purlasi_scmadj” and report “purlasi_scm.prn”.
6. Created combined files “purla” (39 trees) from “purlasim” and “purlasi_scm”.
7. Created combined files “purlax” (39 trees) from “purlasim” and “purlasi_scmadj”.

PC5. Adjustment Report

The content and layout of the Figures PC02 to PC13 are similar. Two sub-samples ('1' and '2') of either TRW or MXD data are compared to identify systematic differences in means and (for MXD only) standard deviations, and to calculate the adjustments that could be applied to reduce the systematic differences. If any adjustments are applied, they are applied to sub-sample 1. The two sub-samples are combined into one data set and standardised using one-curve signal-free RCS. The signal-free "measurements" (see SM1) are then averaged into the two sub-sample groups (1: blue, 2: red) and shown as the mean growth plotted by age for the original values (top panel); and the values after the adjustment process described in Section PC2 has been applied (second panel). The chronology indices by calendar year and shown for the two sub-samples for the original values (third panel); and the values after adjustment (bottom panel). The sample replication against age (top panel) and against calendar year (third panel) is shown as grey shading for sub-sample 1 and for sub-sample 2 in the second and bottom panels.

Figure PC02 The data are TRW from "poluroot.raw" (sub-sample 1) and "polustem.raw" (sub-sample 2), and the adjusted data are saved as "polurootadj.raw". The "poluroot.raw" data have much larger growth (and index values) than the "polustem.raw" data. The adjustment (a 28% decrease of the mean of root measurements) is large, but this adjustment does not produce "matching" chronologies (i.e. there are still differences in the shape and position of curves from each sub-sample) illustrating the variable (non-homogeneous) nature of the root collar material. As these differences cannot be 'corrected' by simple scaling, we decided not to use the "poluroot.raw" data.

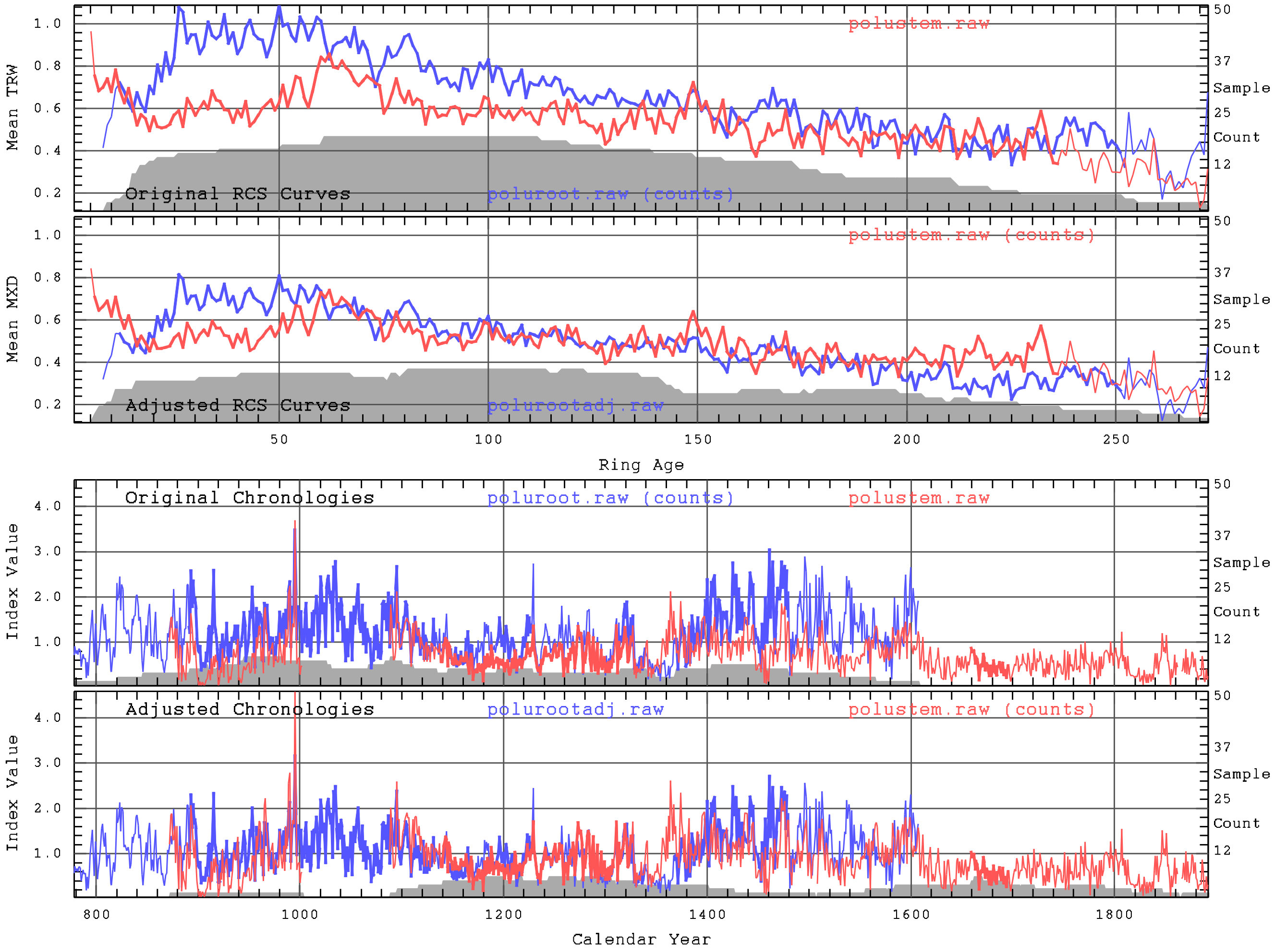


Figure PC03 The data are MXD from "poluroot.mxd" (sub-sample 1) and "polustem.mxd" (sub-sample 2), and the adjusted data are saved as "poluroot.mxd". The adjustment corrects the difference between the signal-free site RCS curves and the differences in the chronologies, both of which fit reasonably well despite relatively low sample counts. The adjustment of 6% was relatively large compared to the standard deviation of 10% and we decided to create the combined adjusted data set "polurulax" (32 trees) to evaluate the adjustment.

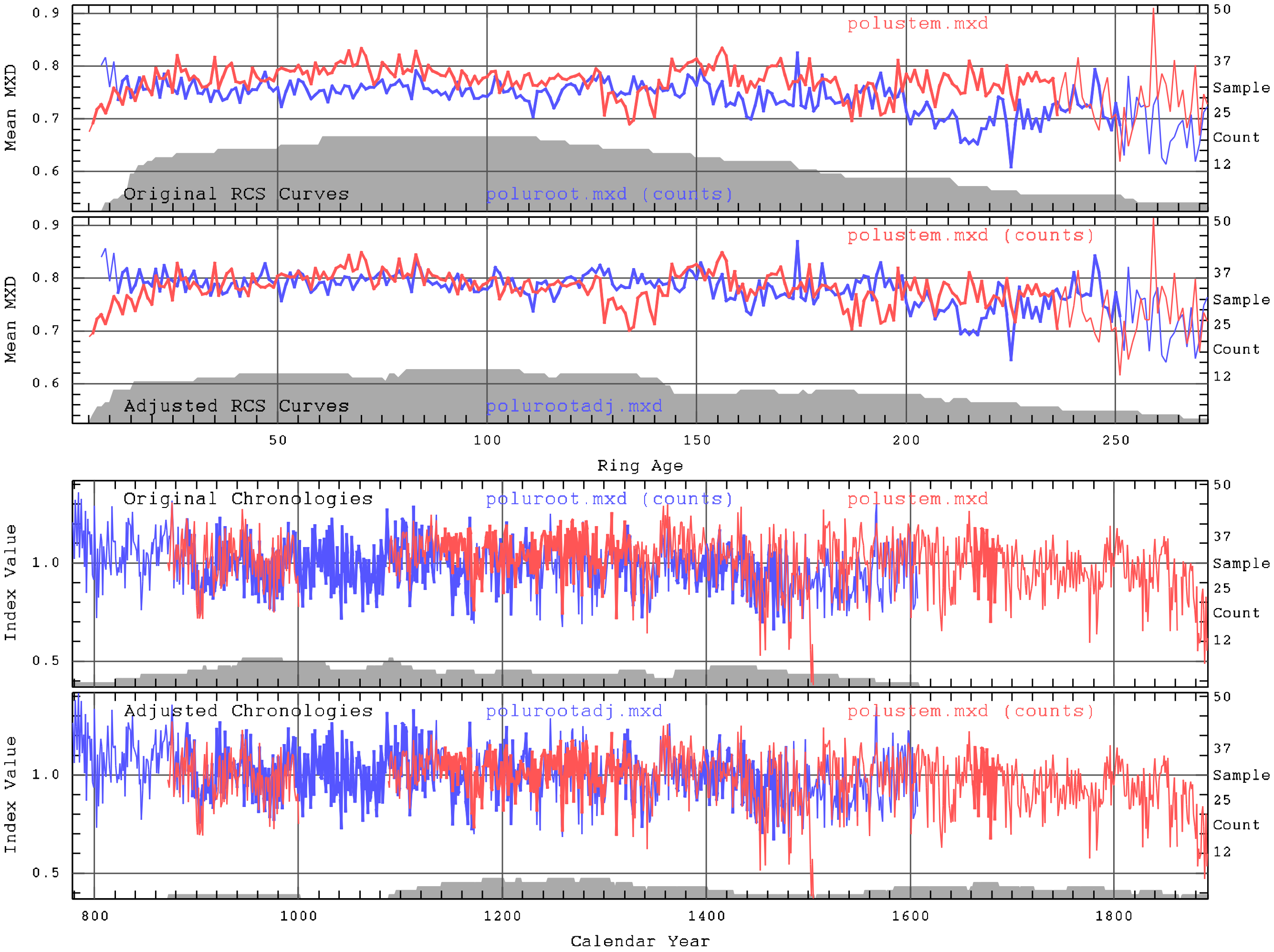


Figure PC04 The data are TRW from “pou_la_mod.raw” (sub-sample 1) and “pou_la_stem.raw” (sub-sample 2), and the adjusted data are saved as “poluroot.mxd”. The indicated adjustment (a 2% increase) is negligible.

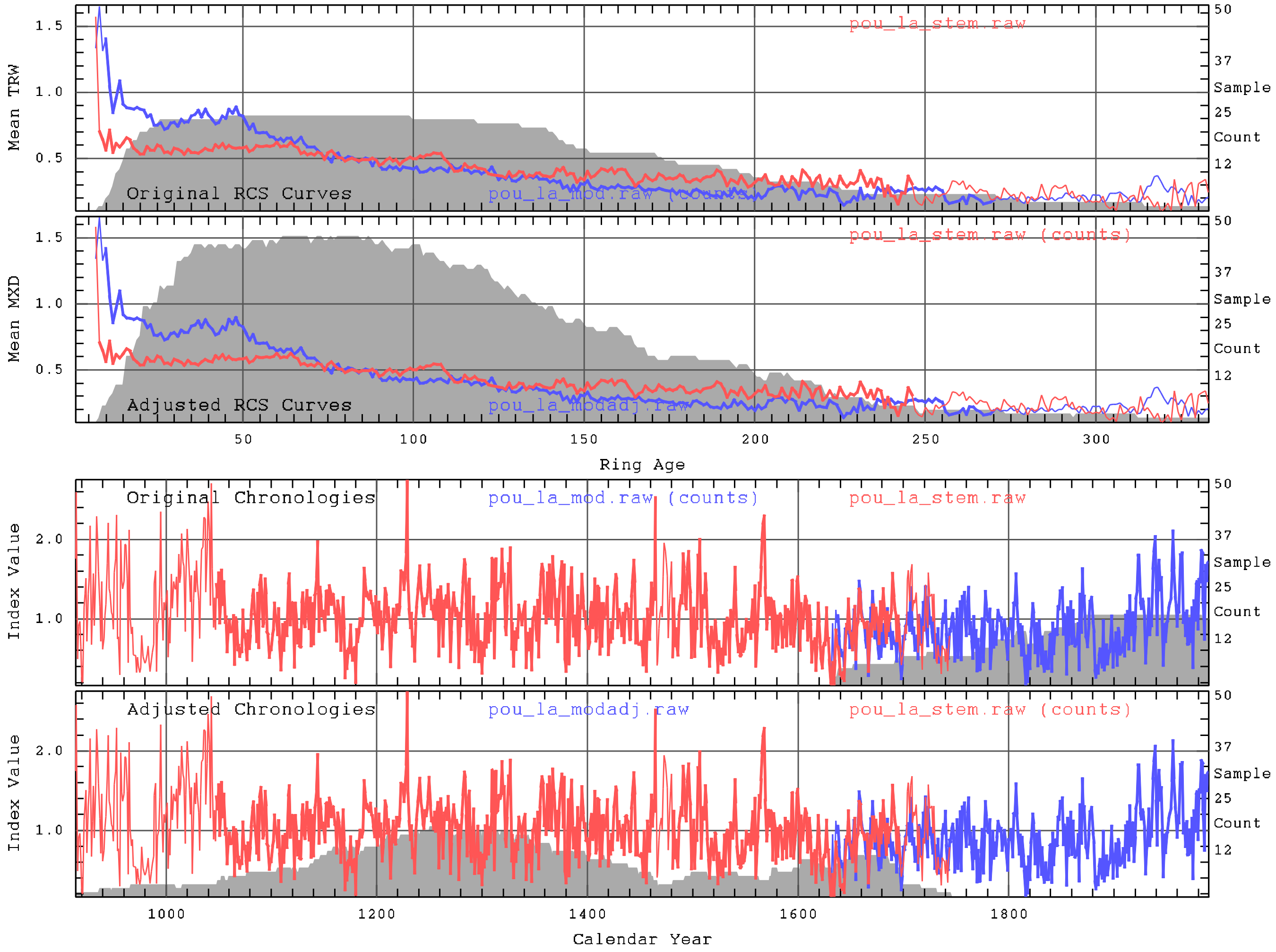


Figure PC05 The data are MXD from “pou_la_mod.mxd” (sub-sample 1) and “pou_la_stem.mxd” (sub-sample 2), and the adjusted data are saved as “pou_la_modadj.mxd”. The data sets have similar densities and index values with some difference during the 30 to 70 ring-age period. The adjustment (a 3% decrease) is small and the “pou_la_modadj.mxd” data were not used.

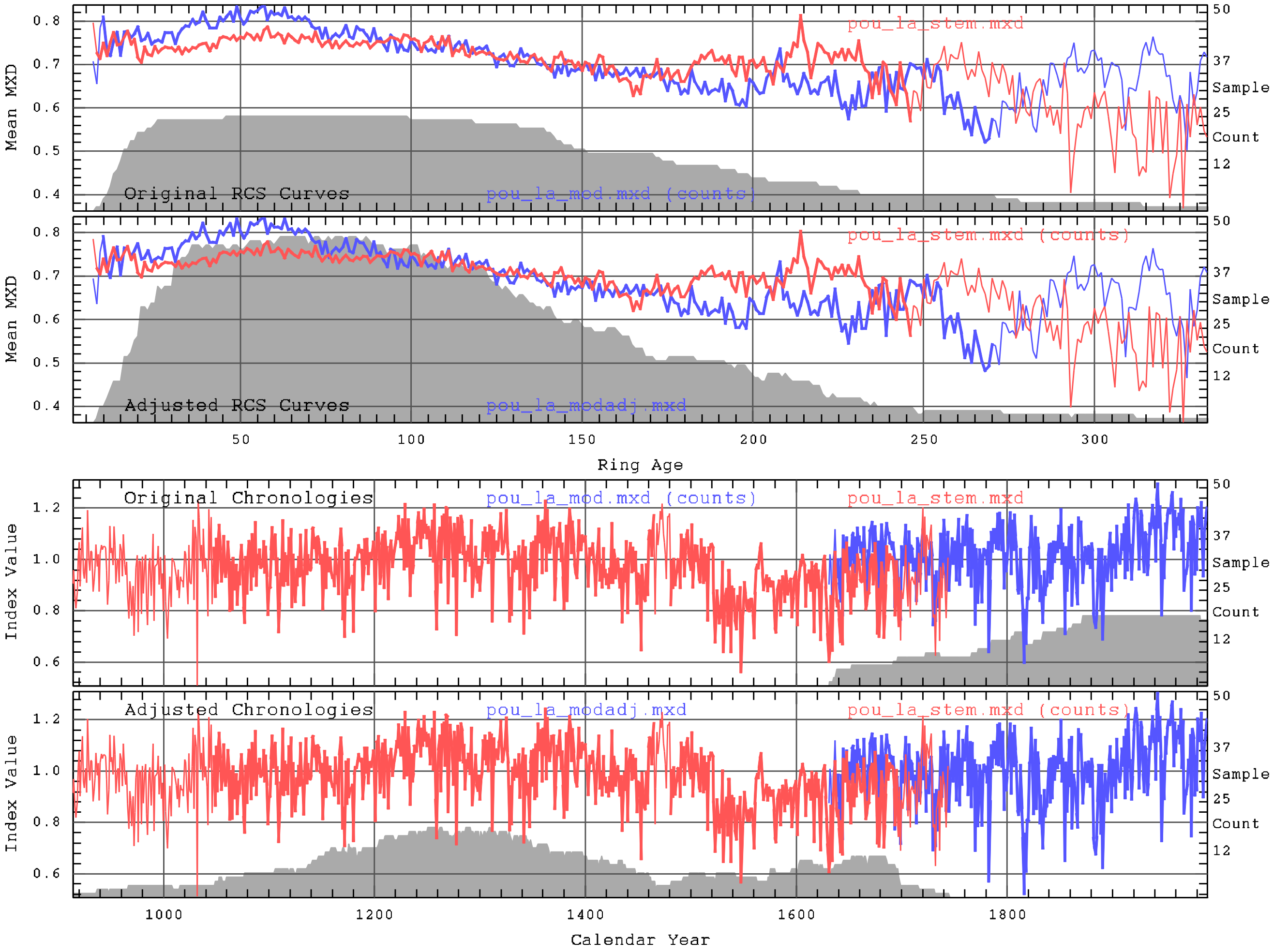


Figure PC06 The data are TRW from “polustem.raw” (sub-sample 1) and “pou_la_stem.raw” (sub-sample 2), and the adjusted data are saved as “polustemadj.raw”. The data sets have similar growth rates and index values. The adjustment (a 2% increase) is negligible.

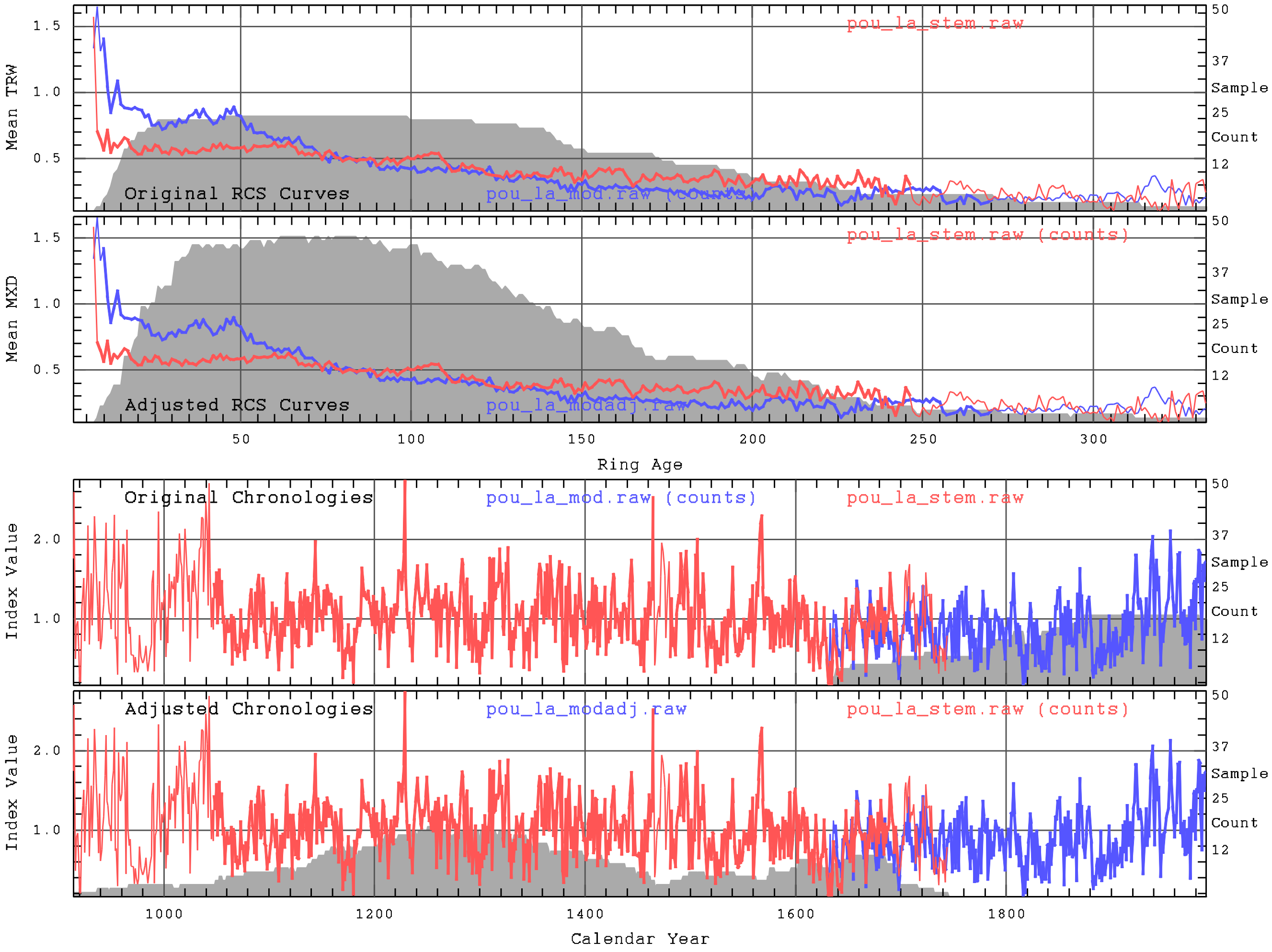


Figure PC07 The data are MXD from "polustem.mxd" (sub-sample 1) and "pou_la_stem.mxd" (sub-sample 2), and the adjusted data are saved as "polustemadj.mxd". The "polustem.mxd" data have much larger MXD values and larger index values than the "pou_la_stem.mxd" data. The adjustment (a 9% decrease relative to standard deviation of 13%) is large and likely due to the data sets being measured on different machine settings. It was decided to use the "polustemadj.mxd" data when creating a Polar Urals MXD chronology.

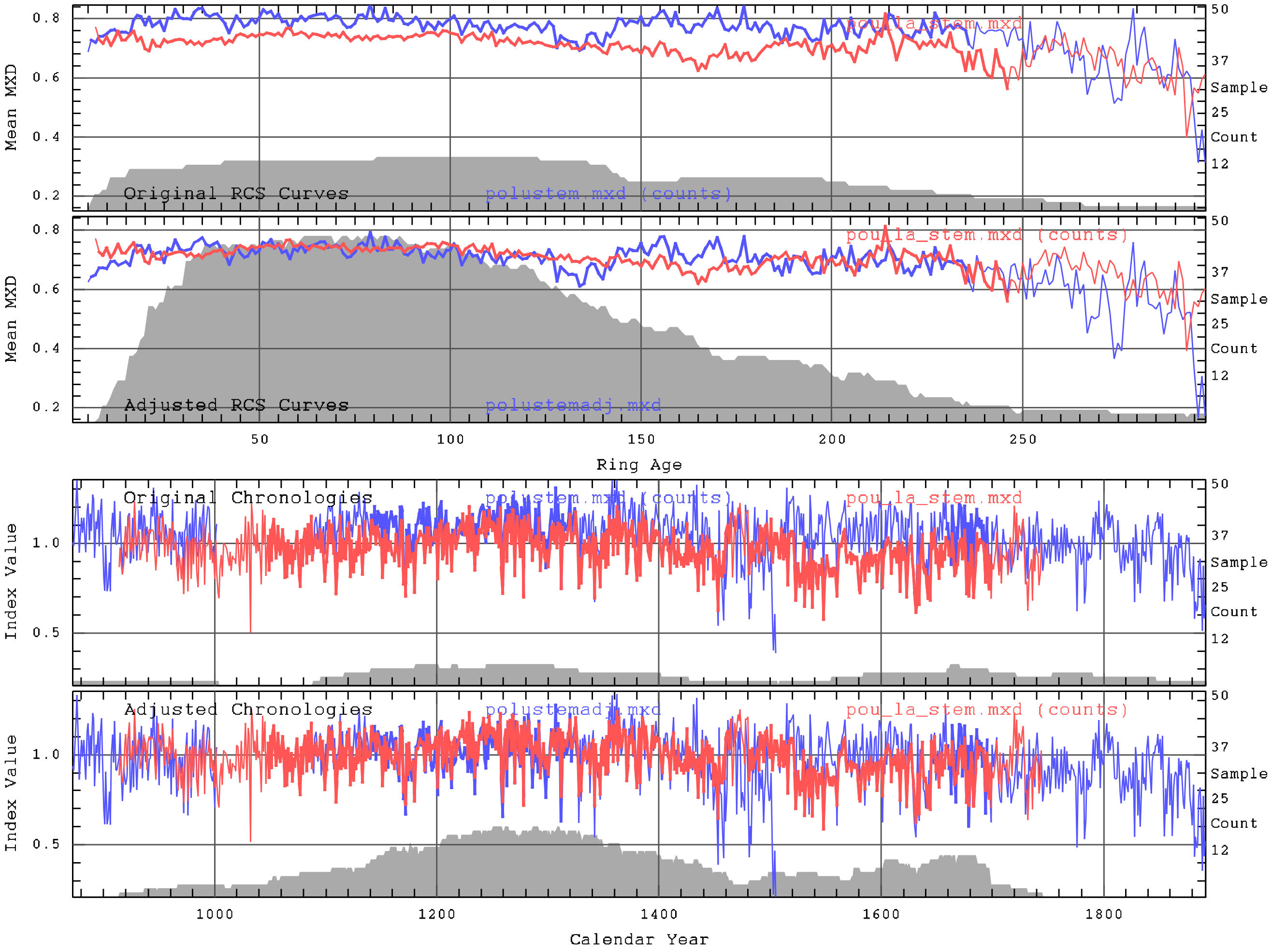


Figure PC08 The data are TRW from "purlax.raw" (sub-sample 1) and "poupolux.raw" (sub-sample 2), and the adjusted data are saved as "porlaxadj.raw". The data sets have similar growth rates and index values. The adjustment (a 3% increase) is negligible.

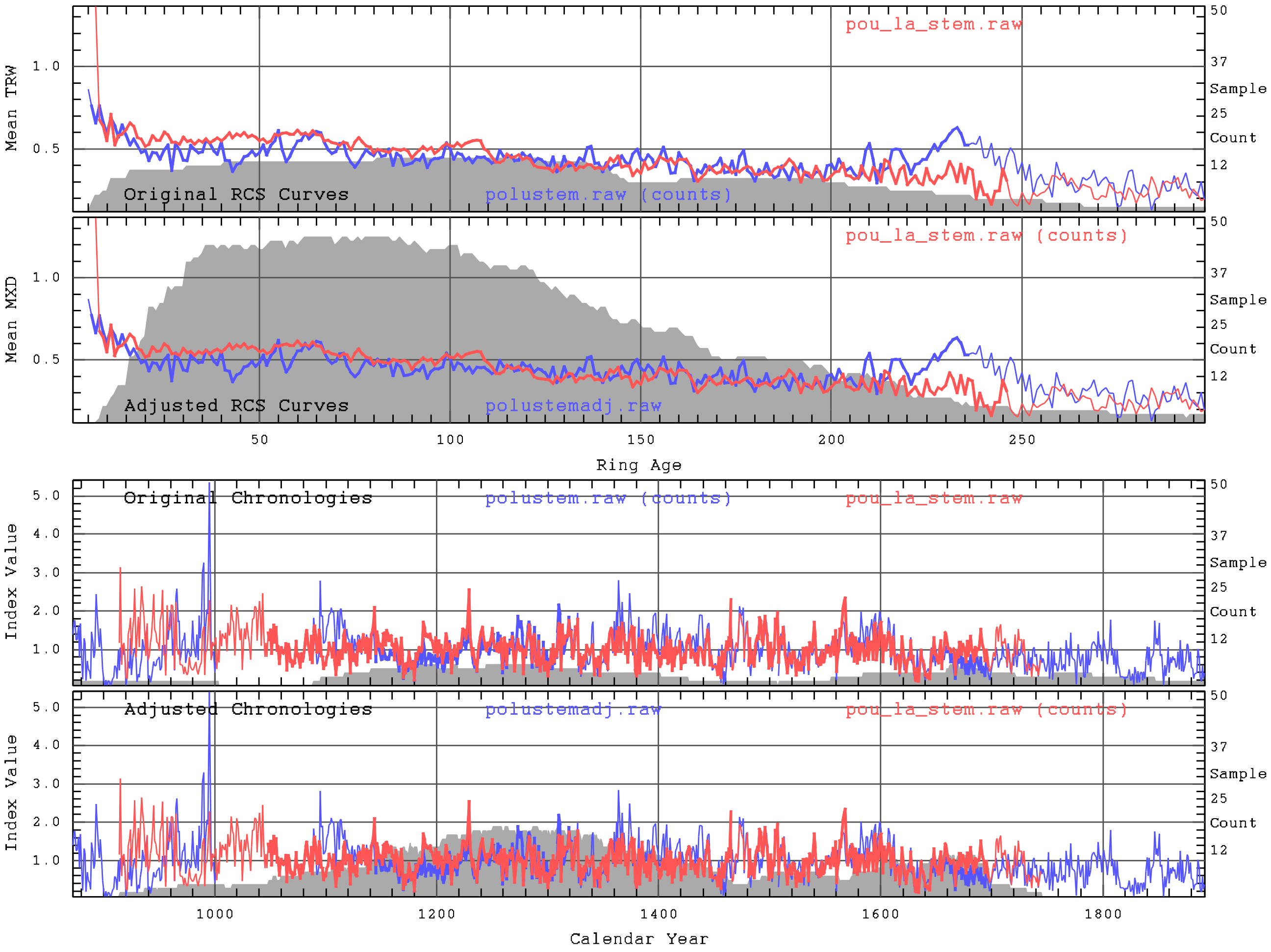


Figure PC09 The data are MXD from “purlax.mxd” (sub-sample 1) and “poupolux.mxd” (sub-sample 2), and the adjusted data are saved as “porlaxadj.mxd”. The “purlax.mxd” data have denser growth and index values. The adjustment corrects the difference between the signal-free site RCS curves and the differences in the chronologies, both of which fit well after adjustment. The adjustment of 13% was large (compared to the standard deviation of 25%) and it was considered necessary to use the adjusted data set “purlaxadj.mxd” in the creation of a combined data set.

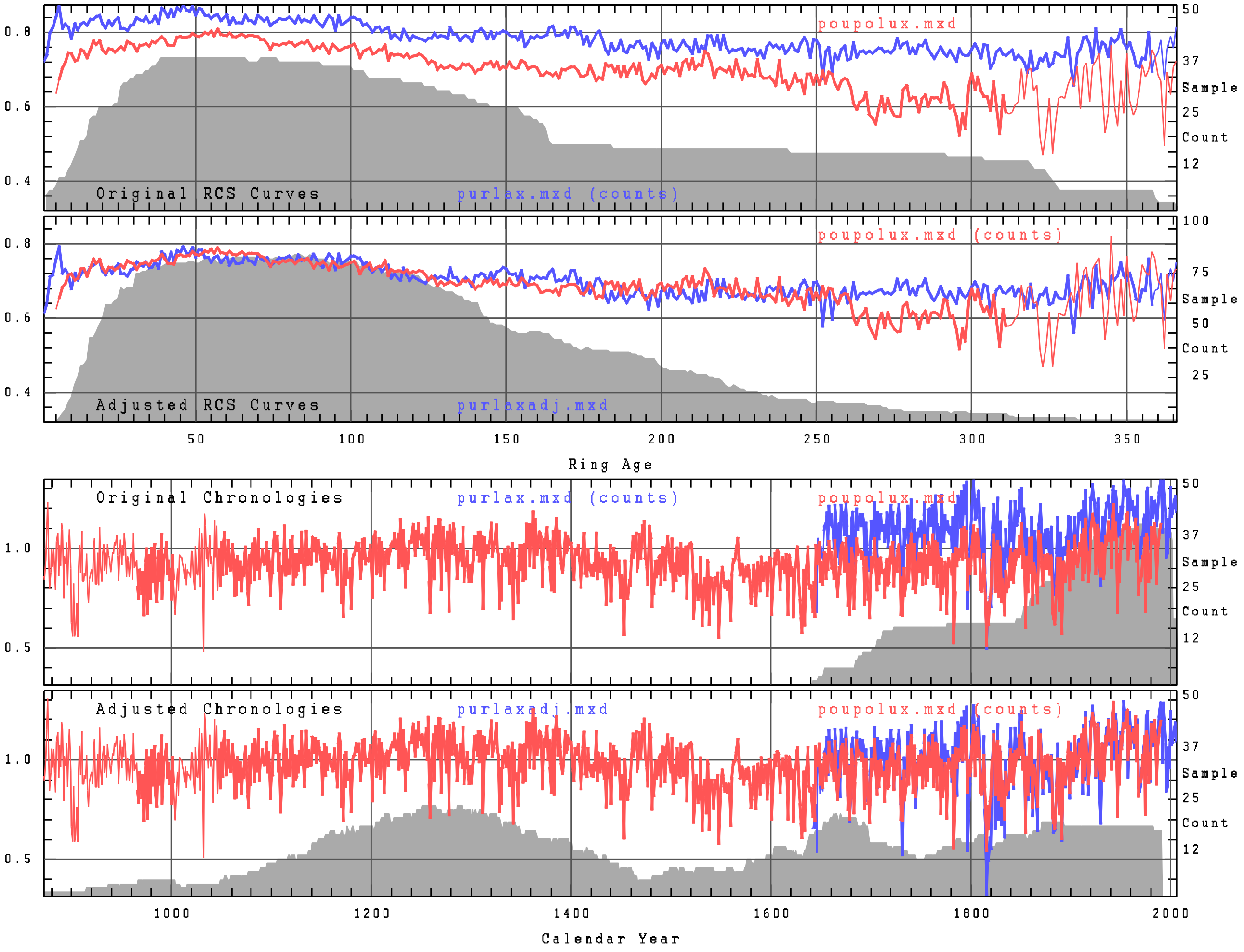


Figure PC10 The data are TRW from “polarulax.raw” (sub-sample 1) and “pou_la_stem.raw” (sub-sample 2), and the adjusted data are saved as “polurulaxadj.raw”. The data sets have similar growth rates and index values. The adjustment (a 7% decrease relative to standard deviation of 49%) is small.

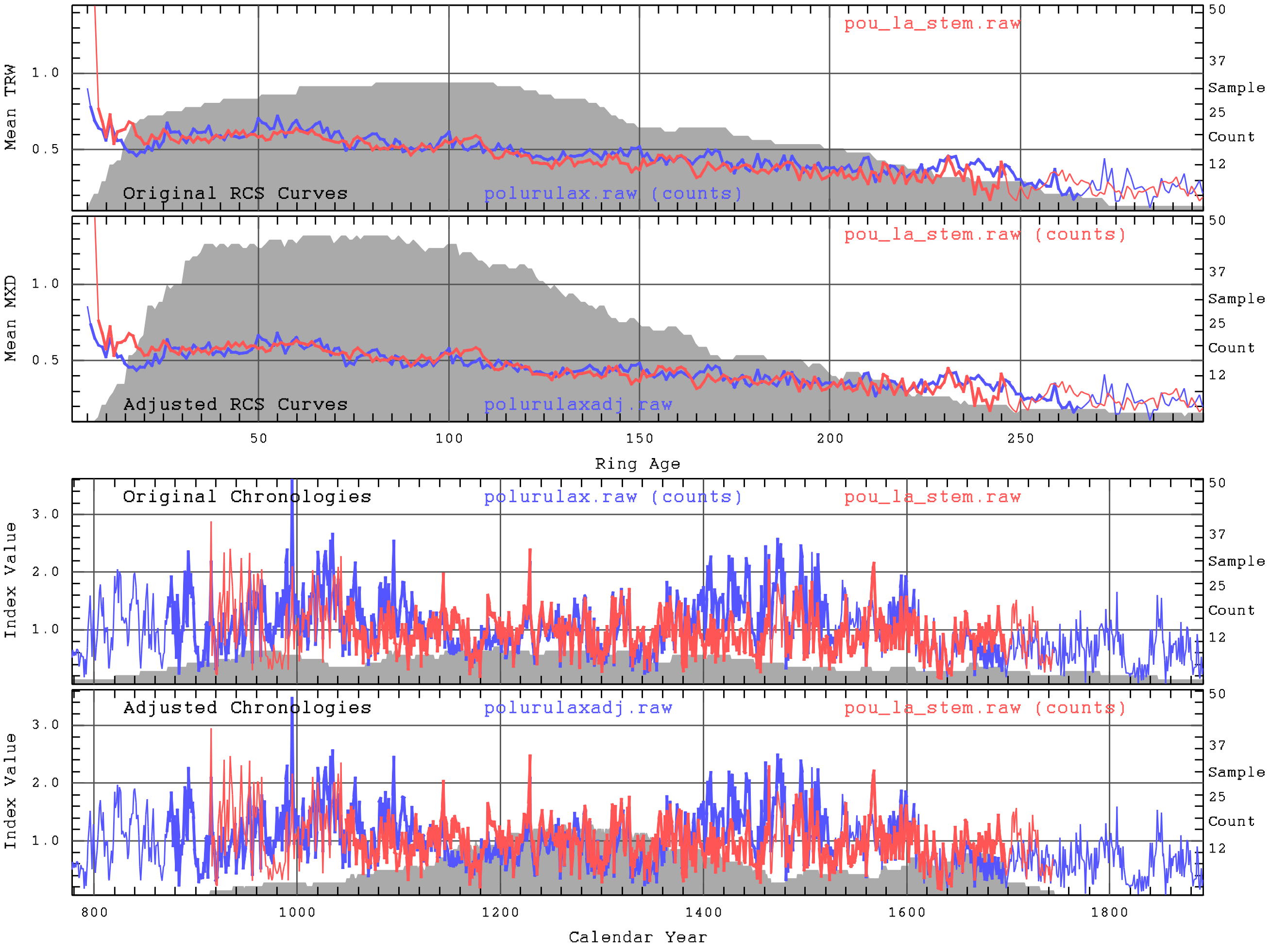


Figure PC11 The data are MXD from “polarulax.mxd” (sub-sample 1) and “pou_la_stem.mxd” (sub-sample 2), and the adjusted data are saved as “polurulaxadj.mxd”. The “polurulax.mxd” data have larger growth rate and index values. The adjustment corrects the difference between the signal-free site RCS curves and the differences in the chronologies, both of which fit well after adjustment. The adjustment of 9% was relatively large (compared to the standard deviation of 14%) and it was decided to use the adjusted data set “polurulaxadj.mxd” in the creation of a combined data set.

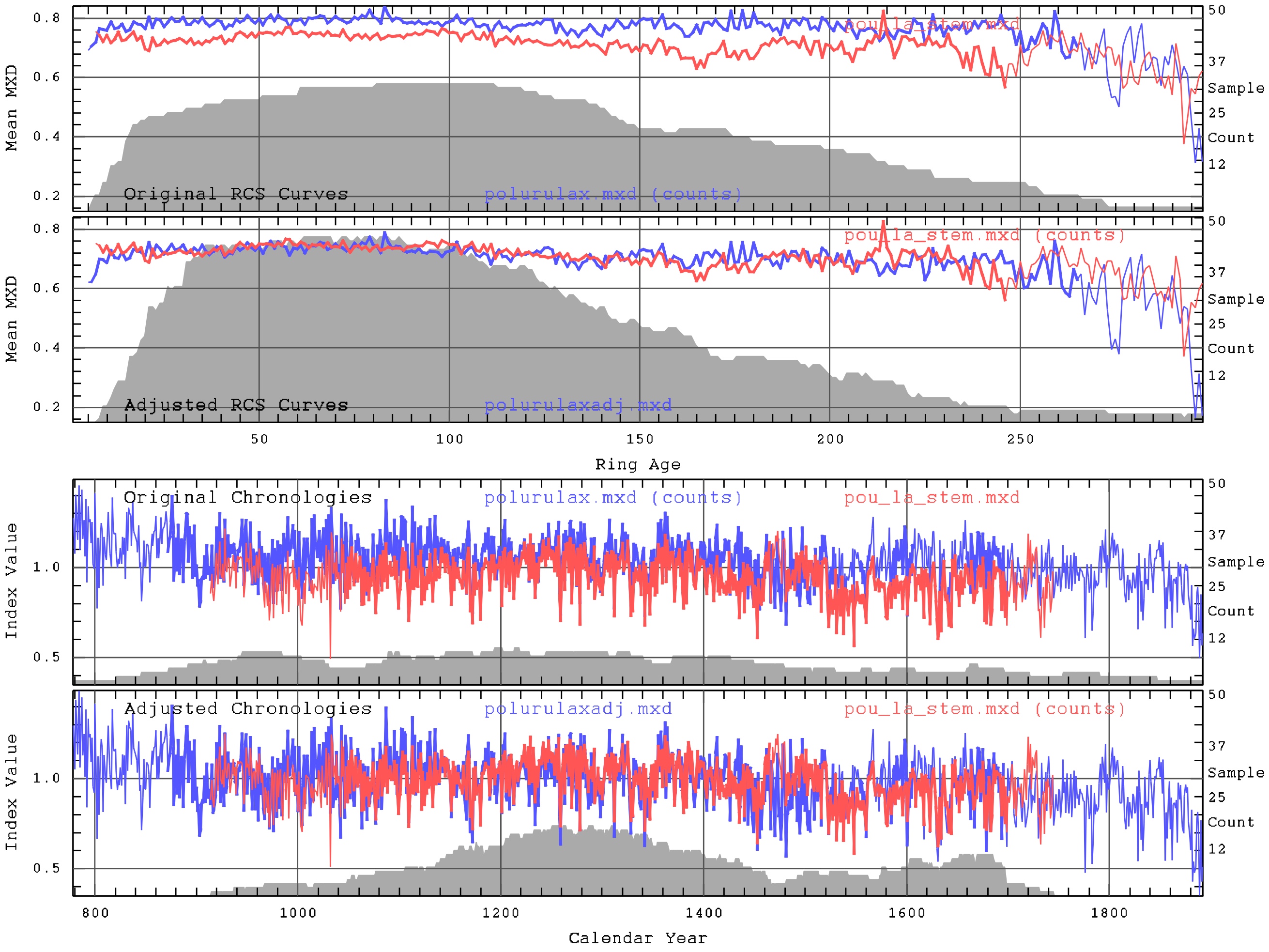


Figure PC12 The data are TRW from “purlasi_scm.raw” (sub-sample 1) and “purlasim.raw” (sub-sample 2), and the adjusted data are saved as “purlasi_scmadj.raw”. The purlasi_scm.raw data have higher growth values and higher index values than the purlasim.raw data. This is likely due to modern sample bias; the selection from younger trees which tend to be faster growing because the slower growing younger trees tend to be too small to sample. The adjustment corrects the difference between the signal-free site RCS curves and the difference in the means of the chronologies, both of which fit well after adjustment (using signal-free indices removes the need to compare over a common period). It would be possible to correct modern sample bias using multiple RCS curves but there are insufficient trees for this procedure to be applied to only these two sub-samples. The adjustment of 21% was relatively large (compared to the standard deviation of 39%). This demonstrates the need to correct for modern sample bias. Because the final chronologies are created using two-curve RCS, which corrects modern sample bias, it was not necessary to use the adjusted data to achieve the needed correction.

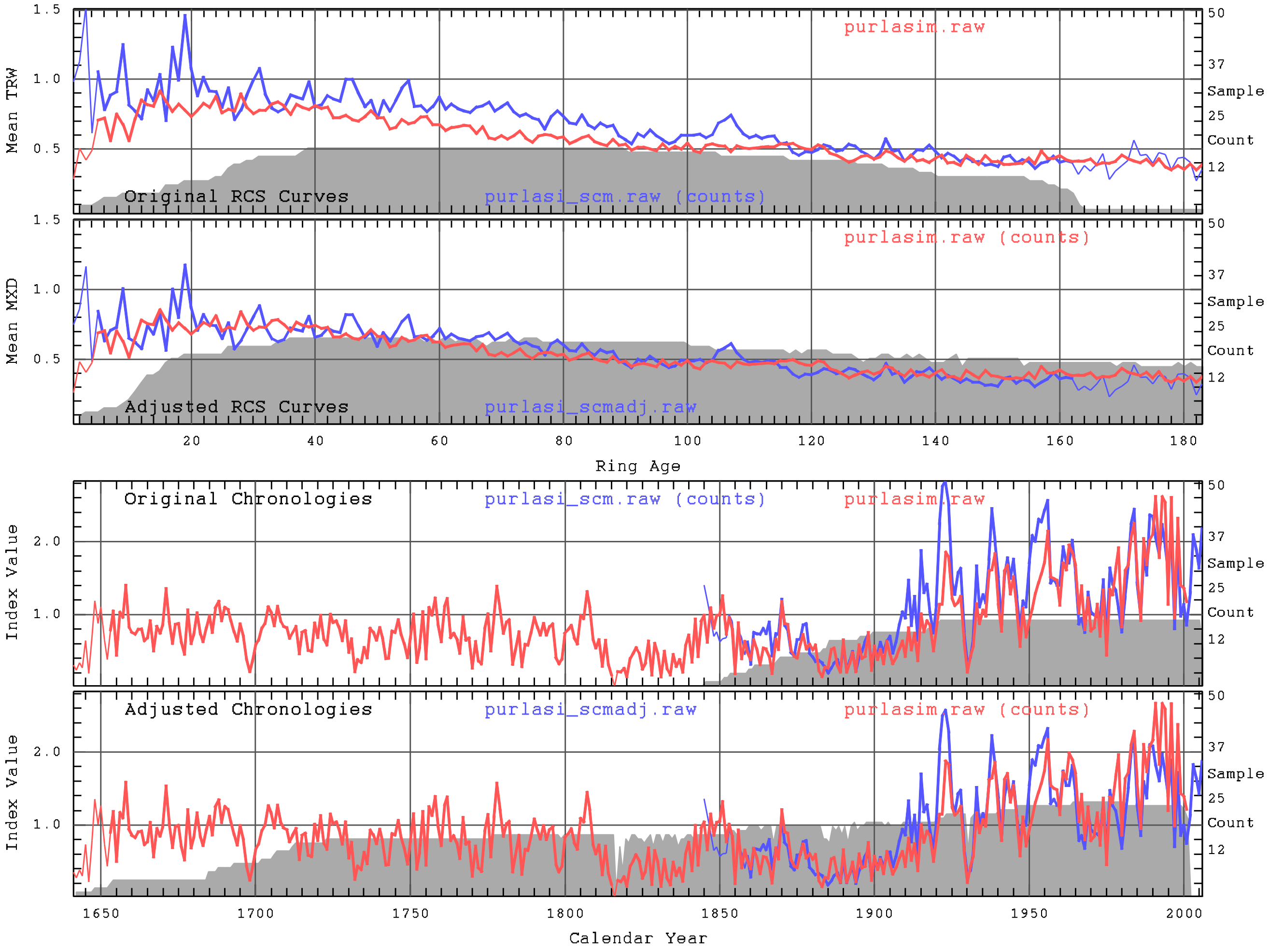


Figure PC13 The data are MXD from “purlasi_scm.mxd” (sub-sample 1) and “purlasim.mxd” (sub-sample 2), and the adjusted data are saved as “purlasi_scmadj.mxd”. The “purlasi_scm.mxd” data have lower MXD values and lower index values than the “purlasim.mxd” data. This is likely to be a measurement problem as the data sets were measured at different times and the means and standard deviations of density measurements are dependent on machine settings. The adjustment corrects the difference between the signal-free site RCS curves and the differences in the chronologies, both of which fit well after adjustment. The adjustment of 10% was relatively large (compared to the standard deviation of 7%) and it was decided to use the adjusted data for further processing.

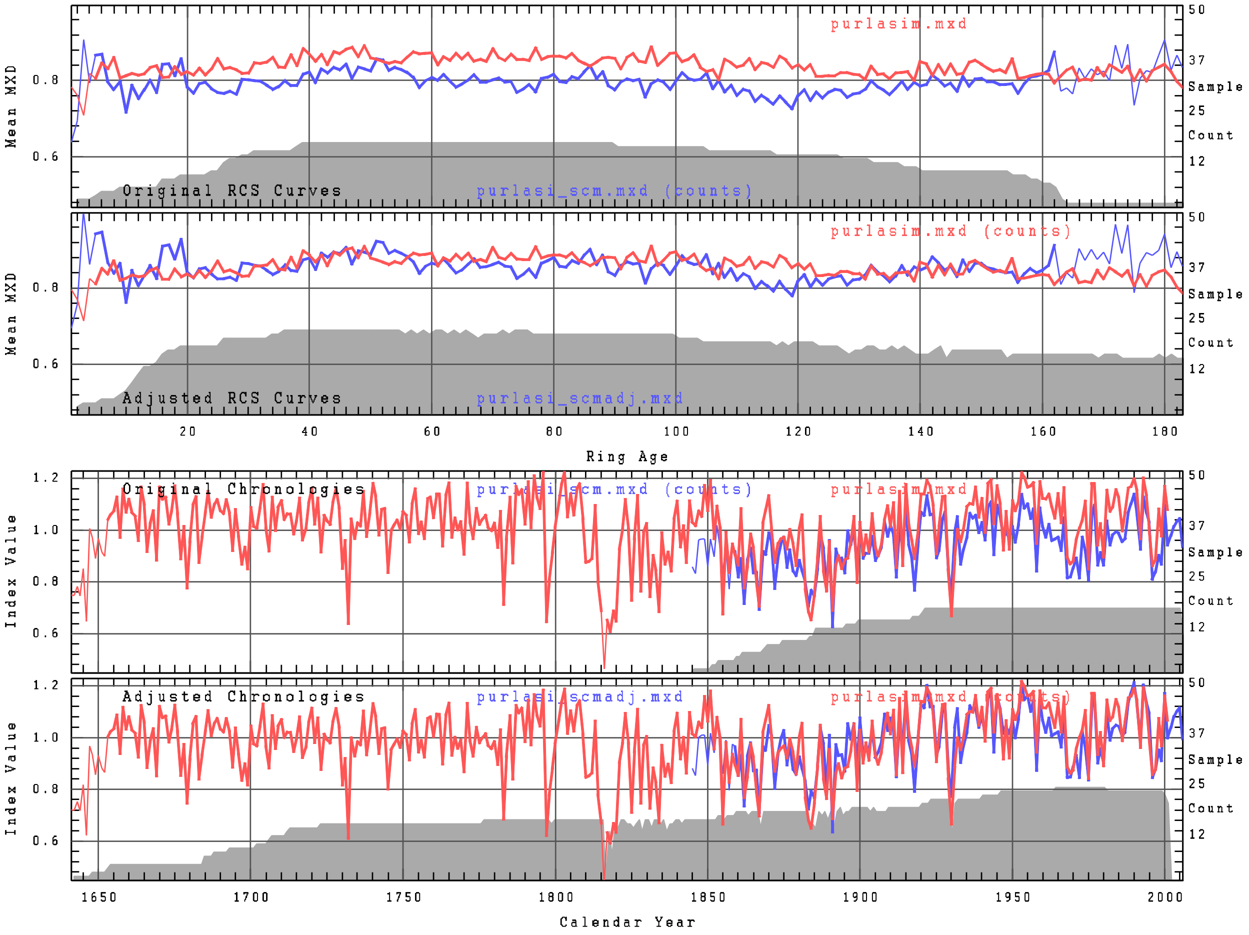


Figure PC14 The data are TRW from "polar.raw" (sub-sample 1) and "yml-all.raw" (sub-sample 2). The "polar.raw" data have lower ring width values during their first 50 years, showing a distinctly different juvenile growth phase than the Yamal trees. The adjustment does not correct the juvenile growth problem and this problem indicates that substantial bias might be present in a combined Yamal TRW and Polar Urals TRW chronology processed using the same set of RCS curves. This is the justification for using separate "site" specific processing (RCS curves) of data and not combining the data into a single, regional data set.