Using the new R package for TL dating

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Abstract

Since the development of the SAR protocol (Murray and Wintle, 2000), most luminescence dating applications use OSL rather than TL. When it comes to dating sediments, as often in Geoscience, using OSL is clearly the best choice. However, for burnt material, e.g., in archaeological context, using TL is still relevant. Moreover, the SAR protocol was shown to be easily adaptable to TL dating (Schmidt, 2013).
R is a programming language and environment for statistical computing and graphics. It provides a wide variety of statistical and graphical techniques and is highly extensible (R core team, 2015). A package specifically designed for luminescence dating is available (Kreutzer *et al.*, 2012). However, it mainly includes functions for the analysis of OSL data.

We developed a new **R** package specifically designed for TL dating. The structure of this package is based on the existing *Luminescence package*. However, it treats the uncertainties completely differently. Analysis of TL data needs pre-treatment before any estimation of the equivalent dose. The background signal has to be subtracted and, very often, the peaks have to be aligned. These operations affect the uncertainties. Therefore, an *uncertainty matrix*, which contains an estimation of the random uncertainty for each data point, was added to the existing *signal matrix*, which contains the signal intensity/time information. Rather than estimating the uncertainties *at posteriori*, the new package functions update the *uncertainty matrix* each time the *signal matrix* is modified.

The *TLdating package* is designed to be as easy to use as possible. It includes two functions called *script_TL.MAAD* and *script_TL.SAR*, depending on the protocol applied. These functions only need the name of the *.binx* file, the uncertainty, and the temperature boundary for the integration, in order to provide De estimations. Complementary parameters, like the dose interval used for the growth curve, the fitting method (linear, exponential; weighted or unweighted) or the rejection criteria, help to improve the De estimation. However, if these are not specified, default values are provided. After using the *readBIN2R* function, from the *luminescence package*, these *script_** functions successively call a series of other functions from the *TLdating package*, including: (i) *Risoe.BINfileData2TLum.FileData*, which convert the data in the proper format and create the *uncertainty matrix*; (ii) *mod_extract.TL* and *mod_remove.preheat* which only keep the TL curves and removing those identified as preheat curves; (iii) *mod_substract.background* which subtracts the background signal from the luminescence signal; (iv) *mod_align.peaks* which aligns the peaks; and (v*) analyse_TL.MAAD* or *analyse_TL.SAR* which provides the equivalent dose estimation using the MAAD or the SAR protocol, respectively. For the SAR protocol, the final result can easily be plotted using plot_AbanicoPlot from the *Luminescence package*. On the other hand,

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TLum.fileData2Risoe.BINfileData converts your data backwards, allowing to use all the functions from the *luminescence package* including *writeR2BIN*. It is therefore possible to analyse the modified data with, e.g, *Risø Analyst*. Finally, it has to be noted that the *analyse_** functions provide not only a De estimation for the *growth curve* approach but also for the *De plateau* approach, allowing a better estimation of the temperature boundary that are used for the integration.

This project was realized in the context of the CRC 806 "Our way to Europe" funded by the German Research Foundation (DFG).

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