



New Tools and the Road to Quantitative Models in Sedimentary Provenance Analysis

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Sedimentary provenance analysis is one of the major techniques to link source area geology, climate evolution, and basin dynamics to the compositional characteristics of the clastic basin fill. The high potential of sediments for precise chronostratigraphic calibration in combination with state-of-the-art provenance analysis allows for detailed reconstruction of source area evolution in space and time. A wealth of new and/or refined analytical techniques has been developed in the last decade, especially regarding high-precision single-grain geochemical and geochronological techniques. Accordingly, ultrastable heavy minerals such as rutile or zircon provide inert mineral tracers in sedimentary systems and their analysis yield precise information on source rock petrology and chronology. In terms of quantitative provenance analysis there is, however, a strong need for connecting these detailed information on specific source rocks to the bulk mass transfer and sediment modification from source to sink.

Such quantitative provenance models are still in their infancy for a number of reasons, among them (1) the overall complexity of the processes involved including multiple feedback mechanisms, (2) the heterogeneity of data bases with respect to large-scale basin-wide studies, and (3) the lack of tailor-made and user-friendly statistical-numerical models allowing for both forward and inverse modelling that consider the compositional nature of most bulk sediment data. First steps towards fully quantitative models include (i) development of algorithms relating petrographic-mineralogical and geochemical data to sediment grain size, (ii) quantifying chemical, physical, and biological processes and their impact on sediment production and modification, (iii) compositional mixture models, and (iv) verifying these analytical modules in large-scale modern systems, followed by (v) similar ancient systems that are even more complicated due to diagenetic processes.