Computer-assisted stemmatology

Statistical methods have been used in textual criticism at least since the beginning of the 20th century (Quentin 1926, Greg 1927), and attempts at using computers for the classification of manuscripts appeared as early as the 1960's (Dearing 1968, Froger 1968, Griffith 1968, Zarri 1971, Irigoin and Zarri 1979). Recently, the field of bioinformatics seemed to offer many opportunities in that respect. Indeed stemmatology and the study of evolution in e.g. biology have much in common: the former studies the evolution of texts and the latter that of organisms. The use of computerised approaches developed in the field of phylogenetics have proved to be very useful for stemmatology as well.

Possibly the greatest advantages of computer-assisted methods are their speed, calculation power, the possibility of using different methods on the same data, of assessing the results and of easily redoing the calculation whenever necessary (after having added a new witness, for example). The algorithms underlying the methods used are often black boxes, however, and one should also keep in mind that the quality of the input is of primary importance for the reliability of the results. Data used by computer programs must be encoded in some way by philologists, and not only the data format is important, but also the preparation of the data (based on manual collation or on computer-assisted collations, themselves based on transcriptions).

Computer assisted methods and tools used in stemmatology treated in this lexicon are: bootstrapping, chi-squared test, distance-based methods, Juxta, maximum parsimony method, Method, Leitfehler-based, NeighborNet, Neighbour joining, PAUP, PHYLIP, RHM, SplitsTree, Semstem, Stemmaweb, UPGMA.

See Trovato 2014, 179–227 for a partial survey of computer-assisted stemmatology, and Reeve 2000 for a critical evaluation of the results.

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In other languages

DE: computergestützte Stemmatologie
FR: stemmatologie assistée par ordinateur
IT: stemmatologia digitale

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