

## QUANTITATIVE MAMMALIAN BIOCHRONOLOGY AND BIOGEOGRAPHY OF THE LATE EOCENE THROUGH EARLY PLEISTOCENE

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Multivariate analysis of paleobiological species lists is made difficult by taphonomic, monographic, collection, and sample-size bias. These problems can be partially surmounted by determining which pairs of taxa have overlapping (conjunct) or non-overlapping (disjunct) distributions. Two taxa are conjunct if they are found together in at least one species list. The conjunction data type has two important properties that strongly contrast with other measures of taxonomic association: 1) the set of known and actual conjunctions converge on each other as more and more conjunctions are demonstrated by new species lists; and 2) the fact of conjunction between two species is independent of particular sampling regimes.

While an apparent conjunction is necessarily real, apparent disjunctions can result from sampling bias. Methods that use conjunction data should therefore attempt to "explain" a pattern of disjunction. One approach is to order taxonomic "first" and "last" appearance events to form a hypothetical age-range zonation. Disjunction is accounted for when age-ranges do not overlap, and the most parsimonious zonation minimizes implied conjunction. An appropriate algorithm is as follows: 1) compute a conjunction matrix; 2) perform a correspondence analysis on this matrix; 3) multiply the resulting taxonomic scores by the original taxon-by-species list matrix to produce a set of species list scores; 4) arrange the lists in the order of their scores; and 5) deduce an appearance event sequence from the species list sequence. In some cases a "zonation" can best be interpreted as a biogeographic or paleoecological gradient.

A conjunction analysis of 1030 mammalian species lists from the late Eocene - Pleistocene of North America was performed. Radiometric dates are correlated strongly with the positions of species lists in the sequence. Because they are independently derived, the radiometric and event time scales are truly cross-confirmatory. Calibration of the event sequence using 54 independent dates was carried out, and separate diversity curves for species and lineages were computed directly from the event sequence. The major features of the curves are 1) a moderate Chadronian-Orellan (Eocene-Oligocene) boundary extinction; 2) middle Miocene diversity peak; and 3) a major Mio-Pliocene boundary mass extinction. Finally, the North American Land-Mammal "Ages" (NALMAs) were redefined on the basis of the event sequence. Boundaries within the sequence were optimized to prevent apparently disjunct taxa from ranging into the same time unit. The most important result is that the "Arikareean" consists of two easily distinguished and lengthy NALMAs separated at the Oligo-Miocene boundary. The two new NALMAs will be named and defined in a later paper. Additionally, the "early Hemingfordian" is placed in the "late Arikareean"; the "early Barstovian" is transferred to the Hemingfordian; and the "late late Barstovian" is unquestionably early Clarendonian. Most of the quantitatively defined NALMA and "subage" boundaries coincide with small extinction episodes.

A similar, more preliminary analysis of the European Miocene generated biochrons that match most of Mein's MN zones. Most of the revised Mein zone boundaries coincide precisely with the NALMA boundaries. This could indicate that global factors (climate change, asteroid impacts, etc.) are responsible for the majority of the minor mammalian extinction events that are spaced at 1 - 2 m.y. intervals, and, therefore, for a significant fraction of species-level mammalian extinctions.