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A substantially complete and well preserved skull of a small crocodyliform was recently found on the foreshore near the village of Yaverland on the south-east coast of the Isle of Wight, southern England. The specimen comprises two parts found by different collectors and in a remarkable stroke of serendipity the gracile rostral section, which has suffered little post-exhumation abrasion, was recovered some three months after the posterior part. Both are now in the collections of the Isle of Wight County Museum Service. The locality, mode of preservation and associated matrix confirm that the skull is derived from one of the plant debris beds of the Lower Cretaceous Wessex Formation (Barremian, Wealden Group) exposed in low cliffs and occasionally on the foreshore in the immediate vicinity. The dentition, unique among crocodyliforms, serves to confirm that the specimen is referable to the, until now, monotypic family Bernissartidae Dollo, 1883. Autapomorphies, including the disposition of cranial sutures demonstrate that the Isle of Wight skull cannot be referred to *Bernissartia fagesii* Dollo, 1883, known from contemporaneous strata at the type locality, Bernissart, Belgium, and possibly Galve, Spain. Furthermore, placement of the secondary choana suggests that the specimen should be referred to a new genus and species rather than a new species of *Bernissartia*. Uniquely among neosuchian crocodyliforms, the secondary choana is bounded entirely by the pterygoids, although occupying an extreme anterior position within them.

Re-evaluating "*Apatosaurus*" *minimus*, a bizarre Morrison Formation sauropod with diplodocoid and macronarian features

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American Museum of Natural History 675 is a sauropod specimen consisting of a sacrum with fused ilia, two ischia and a partial pubis. It was initially described as belonging to *Apatosaurus*, and subsequently given its own species, *Apatosaurus minimus*. However, it is universally recognised that this assignment was incorrect: the specimen differs from *Apatosaurus* in many respects including proportional width of the sacrum, relative lowness of the neural spines, apparent absence of pneumatic foramina in the sacral centra, low and broadly flared ilia, and less expanded distal ends of ischium and pubis. Numerous other details preclude referral to other well-known Morrison sauropods.

The specimen shows a strange mix of diplodocoid characters (the tall and elaborately laminated neural spines), macronarian characters (the breadth of sacrum and flaring ilia), and characters unique to it (e.g. the ilium remains vertical as it projects laterally, and has a distinctive horizontal ridge above the pubic articulation).

We attempted to determine its affinities by phylogenetic analysis. In a diplodocoid-focussed analysis, "*Apatosaurus*" *minimus* was scored for 22 of 189 characters (12%), yielding 3 most parsimonious trees differing only in the arrangement of diplodocines. In all trees, "*Apatosaurus*" *minimus* was the most basal diplodocoid. However, in a more general sauropod analysis, scoring for 37 of 331 characters (11%) yielded 86 most parsimonious trees, of which 74 placed "*Apatosaurus*" *minimus* as a very derived titanosaur, sister to *Saltasaurus*. These conflicting results underline the paradoxical nature of the specimen. Whether it belongs to Diplodocoidea or Macronaria, it has features convergent with the other clade.

Justifications for combining data partitions in phylogenetics

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In phylogenetics, researchers aim to reconstruct evolutionary trees using all relevant forms of data. This may simply involve the combination of cranial and postcranial characters in a purely palaeontological analysis or, as is becoming increasingly common, the combination of large numbers of genetic loci with a morphological dataset. This data combination is often performed despite apparent disagreement between the topologies produced by each data partition in isolation. In such analyses the underlying assumption is that signal common to the majority of partitions should dominate the combined topology at the expense of any signal idiosyncratic to an isolated partition, theoretically resulting in a topology that more closely reflects the true course of evolution. A number of metrics, including hidden branch support (HBS), have been used to demonstrate unexpectedly high levels of support for such combined topologies. Here, we use artificial and real datasets to assess when HBS reflects synergy across data partitions, as opposed to data set conflict. We have found that high levels of hidden support do not necessarily justify data combination, but they do provide a valuable tool for exploring the interactions of such disparate datasets. Through careful application and interpretation of such metrics, morphologists can gain a better insight into the contribution of their characters to a phylogenetic hypothesis based on as large a dataset as possible. Ultimately