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SHORT BRANCH SINGULARITIES IN PHYLOGENETIC COMPARATIVE METHODS

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ABSTRACT

It is often observed that estimation for phylogenetically structured datasets can seemingly unexpectedly fail or silently produce improbable parameter estimates. We explain here that this can be due to very short branch lengths in the phylogeny, causing a nearly singular covariance. We show ways of rectifying the situation either through appropriate data preprocessing or using possibilities of estimation software. We illustrate the situation with an analysis of morphometric measurements of the zygomatic arch in Caninae.

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