Dear authors,

thanks for your responses. I’m looking forward to the revised version and to see another application to a paleorecord.

Among the "minor issues" I’m specifically interested how Characeae were treated, which appear in the underlying datatables on GitHub. Did those macroalgae actually go into the "algae"-cluster, or were they treated as macrophytes (which they rather resemble in terms of their n-alkane patterns)?

I have one other question:

This whole approach might appear complicated to researchers which are less into modelling and statistics. I.e. who prefer -for example- to use simple compound ratios as proxies. Is there anything which can be done to "lower the hurdle", i.e. to make the approach more accessible and easy to apply to a broad range of researchers?

This aspect includes, how gaussian endmember distributions should be treated and calculated for local applications. Does each application require an own calculation of prior distributions (according to the authors who use regional plant data for their two examples); or should it run towards using a global average (e.g. for C3 and C4 plants).

The authors discuss this a bit in section 4.3.1 (e.g. mention the benefits that would come from a global plant lipid database), but it would be interesting to hear a bit more how this should be handled.