

## ***Interactive comment on “Relative roles of local disturbance, current climate and palaeoclimate in determining phylogenetic and functional diversity in Chinese forests” by G. Feng et al.***

**Anonymous Referee #1**

Received and published: 29 October 2013

### General comments

This manuscript aims to determine the relative effects of regional and local drivers on phylogenetic and functional diversity in woody plants on the example of Chinese trees and shrubs. The authors derive functional diversity from maximum canopy height (Hmax) for 958 species as collated from a regional flora and phylogenetic diversity from 1102 species from 11 plots across a range of ecosystems. Local drivers are calculated using the fraction of light-demanding species as surrogates for disturbance. Regional drivers are mean annual temperature (MAT), mean annual precipitation as well as velocity and anomaly of MAT (calculated as the ratio of temporal MAT gradient to spatial MAT gradient and present day MAT – LGM MAT respectively). Feng et al. conclude

C6217

that local disturbance was the best predictor for functional diversity whilst temperature anomaly was the best predictor of phylogenetic diversity. They interpret this as evidence for two fundamentally different drivers acting on functional vs. phylogenetic diversity.

The authors present the analysis of an impressive dataset. Statistical approaches are generally well explained. With some changes to improve clarity, testing for overdispersion and the inclusion of results mentioned but not elaborated on, this manuscript will be a valuable contribution to BG.

### Specific comments

The authors put emphasis on distinguishing between trees and shrubs but do not present many results (e.g. a functional dendrogram for trees vs. shrubs). Hmax has been shown to differ significantly between trees and shrubs on a global scale (e.g. Kattge et al. 2011) and some results shown here (Table 4) support this notion. It would thus be extremely interesting to present results in this manuscript, also distinguishing between different growth forms in more detail.

It is not clear how many species Hmax could be found for. In 2.1.3, the authors state that data was assembled for a total of 958 species but the values given in brackets for trees and shrubs respectively add up to only 720!

Figure 2 is not clear. Results are only mentioned once but not explained. The second line, first plot should be NRIPHY\_ang\_pr vs. MAT, not Anomaly. It would be good to show which plots the points correspond to.

NRI has been shown to be sensitive to overdispersion due to the branching structure of the phylogenies. This might induce considerable bias and should be tested. The Pylocom package offers several ways of doing this (see Webb et al. 2008).

Discuss why relationships between MAT and NRIPHY\_ang\_pr and NRIPHY\_ang\_ab are reversed comparing the Spearman correlations and the Pseudo R<sup>2</sup> for the GLMs.

C6218

Explain which Pseudo-R2 you applied.

Technical corrections

The line numbering is not continuous: I thus mention the page as well as line numbers in the following comments. Also, there are a few spelling errors, of which I only mention some here. Please check the manuscript carefully again.

14660

L 21 Space between a and broad

L 24 connectivity

14661

L 2 delete "been" or "remained"; "but is" should be "but are"

L 10 organisms or groups

L11 functional

14662

L 4 from the Chinese

14664

L23 numbers

L26 Gaussian error were

Table 3 Should Hmax\_pr be NRIFUN\_pr?

Table A2 "indicates" instead of "means" and "within" instead of "with"

The phylogenetic trees presented in Fig.A1 and A2 are illegible in the printed version. Please improve.

---

C6219

Interactive comment on Biogeosciences Discuss., 10, 14657, 2013.

C6220