Supporting document S1
Supplementary figures

A guide to the application of Hill numbers to DNA based diversity analyses

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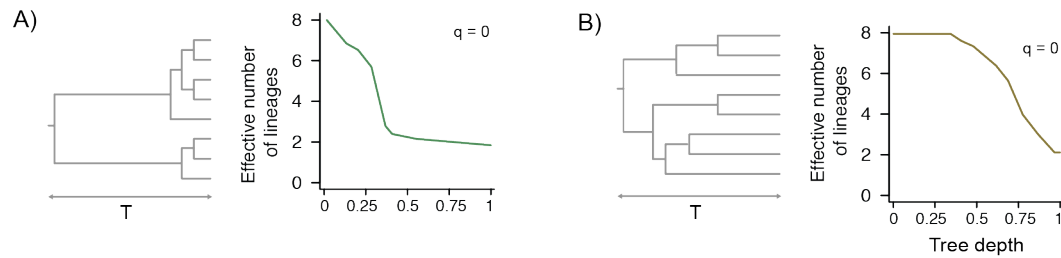
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Figure S1. **Examples of T-profiles of OTU phylogenetic trees with different branching patterns**. In example A, as the OTU phylogenetic tree exhibits a very recent radiation, the T-profile drops rapidly. In contrast, in example B the diversification occurs close to the root of the OTU phylogenetic tree, and thus the diversity values in the T-profile remain high until getting closer to the root.
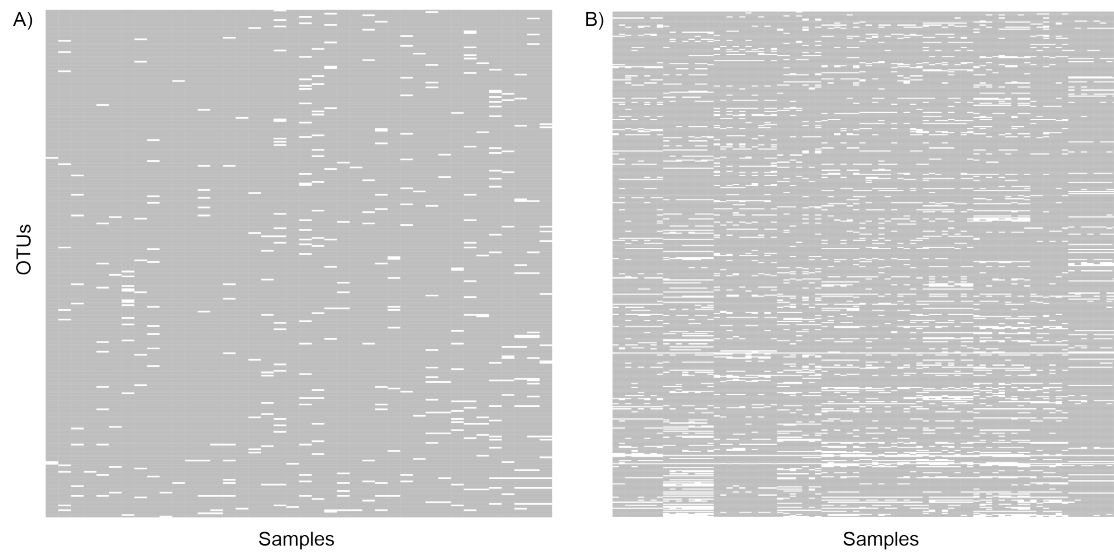
A)
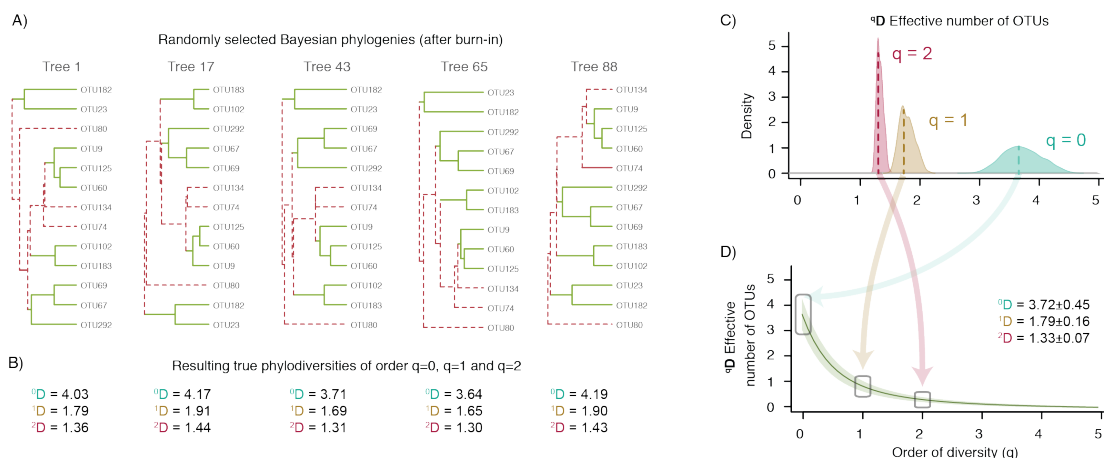
B)

OTUs

Samples

Samples

Figure S2. **Heatmaps of binary OTU tables.** A) OTU table corresponding to the diet of 40 bats belonging eight bat species. B) OTU table corresponding to the diet of 80 animals belonging to eleven cervid species. White cells correspond to presences and grey cells to absences.

Figure S3. Accounting for phylogenetic uncertainty in phylodiversity measurements. (A) Five randomly selected Bayesian phylogenetic trees from the stationary phase (after 95% burn-in) of the MCMC chain (Figure S2). Note that there are differences in the topology and branch lengths of the trees. Consistent branches across the five trees are indicated with solid green lines, while varying branches are shown in dashed red lines. (B) True diversity values of order q=0, q=1 and q=2 derived from each of the five phylogenetic trees. (C) Density curves (softened histograms) of the true diversity values of orders q=0, q=1 and q=2 derived from 100 trees (including the 5 trees shown in Fig. S1A) randomly selected from the stationary phase of the MCMC chain. (D) Diversity profile with confidence area indicating standard deviation. The arrows and grey squares establish the connection between the density curves for the three specific q values shown in Fig. S1C and the diversity profile. The data corresponds to the sample Mem3 shown in Fig. 3. Hence, the average line of the diversity profile is identical to the red dashed line shown in Fig. 4B2.
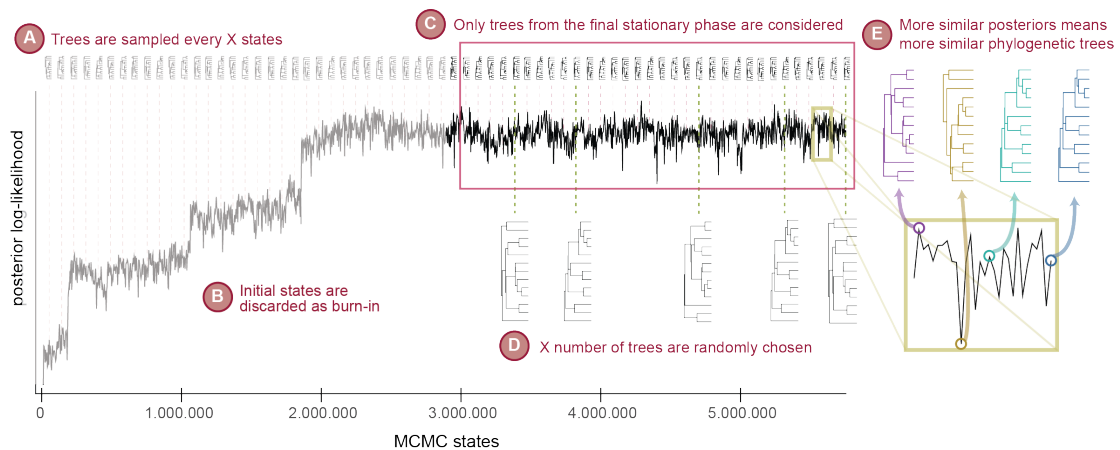
Figure S4. **Sampling trees for phylodiversity analyses from a MCMC chain of a Bayesian phylogenetic analysis.** A) During the MCMC chain of a Bayesian phylogenetic analysis trees are sampled every X states, usually 1000. The posterior probabilities vary drastically until the chain reaches a stationary stage. Hence, (B) the initial states are discarded as burn-in, and (C) only the trees from the final stationary phase are considered. D) X (e.g. 100) number of trees are randomly chosen and phylodiversity measurements are performed with each of these trees. E) Trees with similar posteriors are usually more alike, thus the phylodiversity values will also be more similar.