

Figure 3: Model fit and coefficients for GDM model of FEF community dissimilarity. The observed community dissimilarity (UniFrac distance) between pairwise samples exhibited a linear but noisy relationship with the community dissimilarity predicted by the GDM model (top), which roughly corresponded to a 1:1 line (dashed line). In the bottom plot, GDM i-splines are shown for statistically significant variables that explained over 2% of community dissimilarity. Spline height is the amount of cumulative community dissimilarity explained by its predictor variable, and the spline's slope corresponds to the rate of change in compositional dissimilarity over the range of pairwise dissimilarities within the variable (Ferrier et al., 2007; Landesman et al., 2014). NDVI and Evapotranspiration were the strongest predictor variables in our analysis (green and blue), although most of the explanatory power of evapotranspiration was at the lower 40% of its range. Elevation (red) significantly explained FEF community dissimilarity across the entire range of elevation (see Figure 2). Host plant phylogenetic distance (purple) was a significant driver of community dissimilarity across a deep phylogenetic breadth, and the significance of julian date (brown) indicates as small but important temporal trend that is strongest at short temporal scales (less than a year). Other significant variables in this analysis were cloud frequency, rainfall, relative humidity, solar radiation, and geographic distance, but they all explained very little community dissimilarity and overlapped to too large a degree to show in the figure.

