Fig. 1
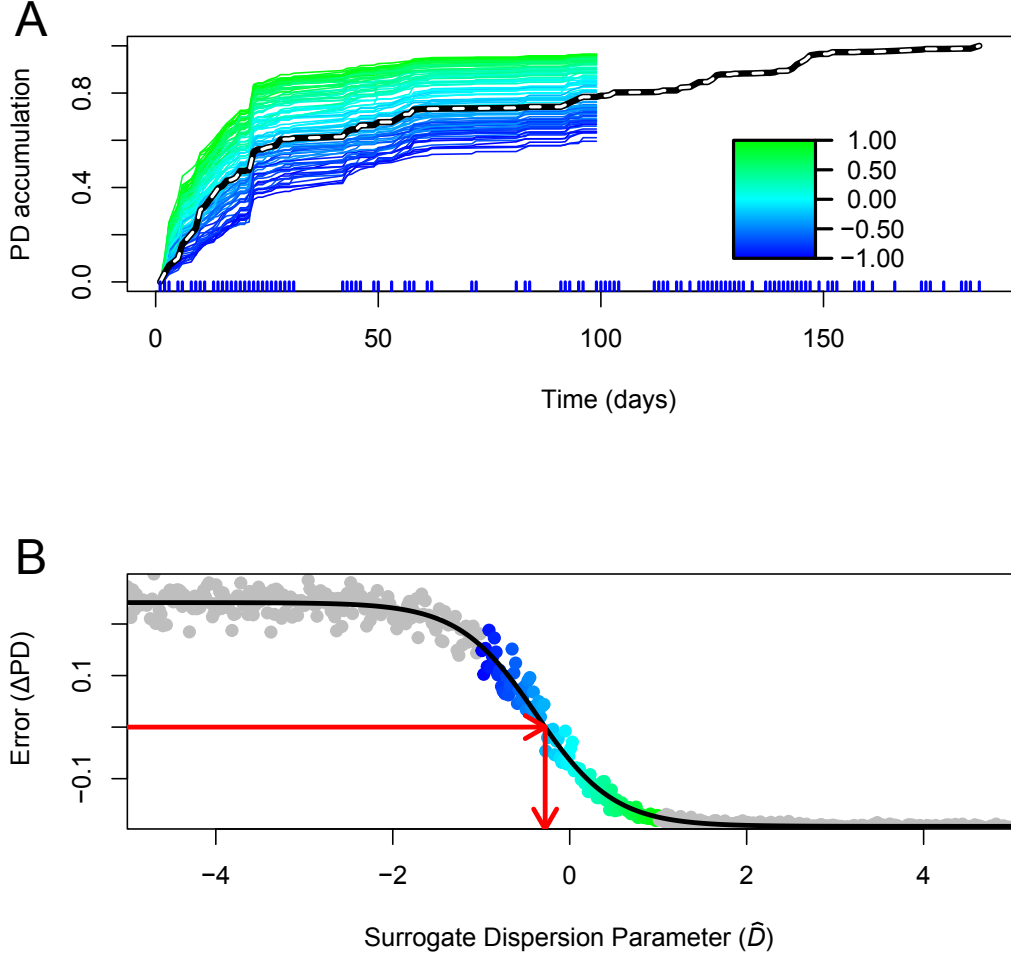

Phylodiversity accumulation and model fitting in the female feces dataset [13]. Plot A shows empirical (dashed) and surrogate phylodiversity accumulation curves. Surrogate curves are colored according to $\hat{D}$ value (Equation 1). New species that have a previously-detected close relative contribute little phylodiversity and cause slow phylodiversity accumulation (blue). New species that do not have a close relative contribute more phylodiversity and cause faster accumulation (green). The empirical model (dashed) is below the neutral model (teal), signifying underdispersion in the order of first-time species detections. The times of sampling points are shown as vertical blue lines below the X-axis. Curves are rescaled from 0 to 1 in this figure. Plot B shows how empirical and surrogate data are compared to generate an estimate for D. Differences between empirical and surrogate data at time m are shown on the Y-axis, and the $\hat{D}$ values used to generate surrogate datasets are shown on the X-axis. Color-coded points correspond to surrogate datasets shown in plot A. Values shown in gray result from using extreme values of $\hat{D}$, which help the logistic error model (black line) fit to the data, and are not shown in plot A. The red arrows show the process of error minimization, yielding a D estimate. A figure showing significance testing for these data is available as Fig. S1.