

**Fig. S1.** Additional detail on sampling-based and process-based models. Dissimilarity in composition of intact and total (relic + intact) communities from sampling-based simulation models. We populated relic communities from a lognormal species abundance distribution (SAD) with different degrees of evenness ( $E$ ).

We calculated the parameters needed to obtain relic DNA proportions between 0.05 and 0.95 given the differential equations for our system:

$$\frac{dI}{dt} = rI - mI, \quad \frac{dR}{dt} = mI - dR$$

where  $I$  is the number of sequences in the intact DNA pool,  $R$  is the number of sequences in relic DNA pool,  $r$  is the per capita birth rate of populations in  $I$ ,  $m$  is the per capita mortality rate of bacterial populations in  $I$ , and  $d$  is the per capita degradation rate of sequences in  $R$ . The intact community is at steady state when  $r = m$ , and the relic community is at steady state when:

$$R = \frac{m \cdot I}{d}$$

Since the proportion of relic DNA ( $p$ ) is calculated as:

$$p = \frac{R}{I + R}$$

we can substitute  $R$ :

$$p = \frac{\frac{mI}{d}}{I + \frac{mI}{d}},$$

which simplifies to:

$$p = \frac{\frac{m}{d}}{1 + \frac{m}{d}}$$

Finally, we can solve for  $d$ :

$$d = \frac{m}{p} - m$$

Therefore, if given the mortality rate ( $m$ ), we can calculate the degradation rate ( $d$ ) needed to obtain any target proportion relic DNA ( $p$ ).

