

Appendix D: Simple mortality calculations (m) to validate simple state-space models

To incorporate the mosaic of measurement intervals, random effects, and explanatory variables, we will ultimately create a state-space model for tree mortality. To validate the state space model, we also calculate a simple average annual mortality after Sheil et al. (1995). We compare this calculation with a simple version of our state-space model which uses a slightly different but equivalent model structure and a different inferential framework to estimate the same overall mortality parameter. Any subtle differences are due to the different estimation methods. Sheil et al. (1995) calculate an annual mortality rate in the following way: $N_1 = N_0(1 - m)^t$, where N_1 is the current number of stems, N_0 is the initial number of stems, m is the mortality per year, and t is the measurement interval. Solving for m : $m = 1 - (N_1/N_0)^{1/t}$.

This calculation is a kind of cohort analysis, assuming that no individuals have been added to N_1 which were not in N_0 . In our data, however, with every new census new individuals are included and therefore every unique measurement interval constitutes a different measurement cohort. In order to obtain a single estimate of m for each species, we maximize a binomial likelihood with N_0 , N_1 , and t for each cohort (defined as all trees sharing an inventory interval, aggregating over plots) as data and a single m for all intervals as the binomial probability parameter. Tables D1 and 1 (in the main paper) summarize the results of our m calculations. We obtain 95% confidence intervals using a profile likelihood; the details of the calculation, including code, are given in this Appendix. Calculations of m assume a constant mortality rate and have no easy way to include year-level variables (including time trends and climate and stand development variables). Note that the mortality rates from maximum likelihood m estimations agree with the Bayesian estimates for the simple state-space model (Table 1 in main paper). Therefore, any differences between the estimates of m and the survival rates in the more complex models are likely due to the hierarchical structure (plot effects) and covariates, not to the Bayesian vs. frequentist estimation methods (de Valpine 2009).

Simple visualization of m for each time interval for each species

Figures D1 and 1 (in the main paper) show m calculated for every interval in the inventory, pooled across plots sharing the same interval. The darker the line, the larger number of individuals used to calculate m .

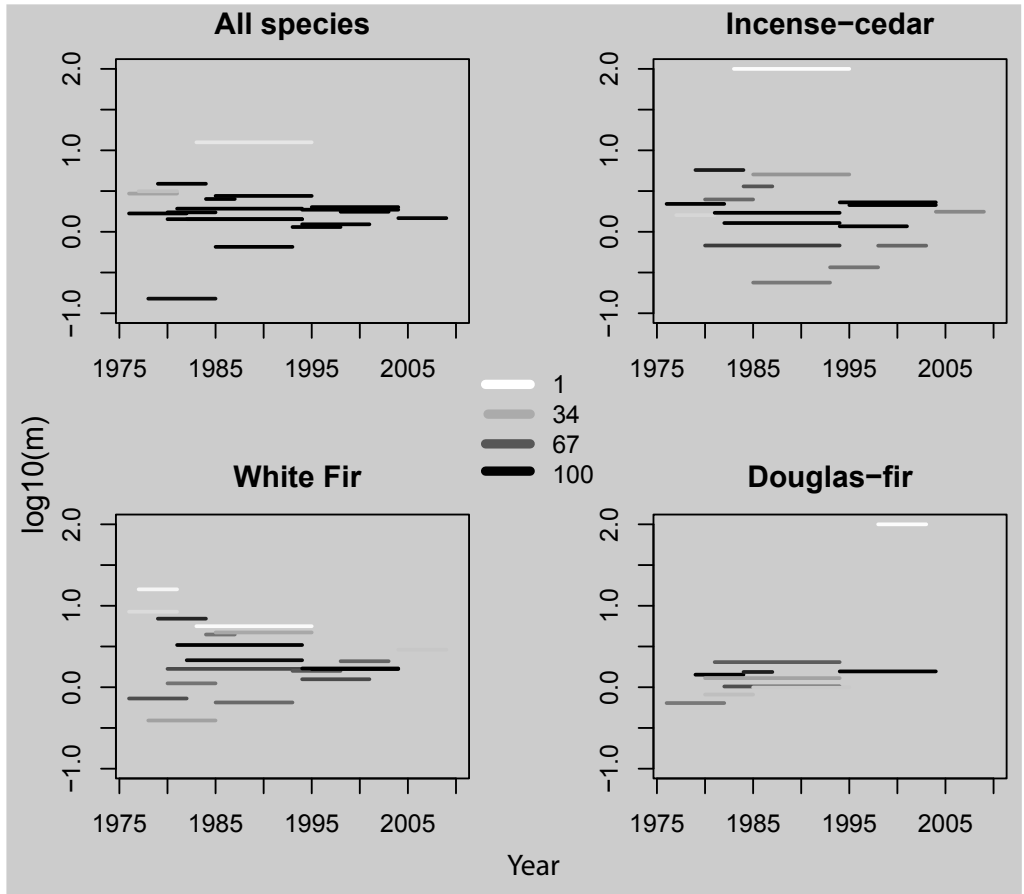


Figure D1: m for each interval in the inventory. Plots sharing the same interval are combined. Shown on the log scale for clarity. Grayscale indicates how many trees are used for the calculation; darker indicates more individuals.

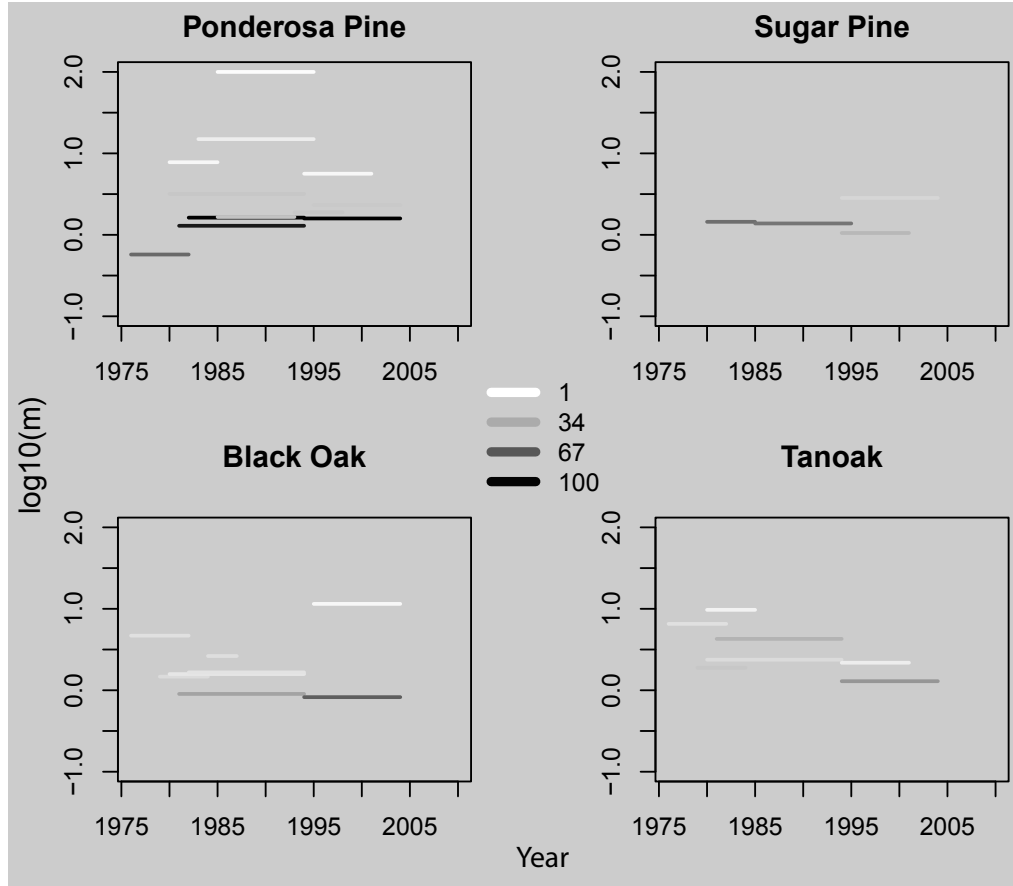


Figure D2: m for each interval in the inventory. Plots sharing the same interval are combined. Shown on the log scale for clarity. Grayscale indicates how many trees are used for the calculation; darker indicates more individuals.

Maximum likelihood calculations and code for obtaining single m estimates by species

We give the details and code for estimating a single m for a species using maximum likelihood. For each interval, we have N_0 , the initial number of stems, N_1 , the final number of stems, and t , the number of years in that measurement interval. We want to estimate the annual probability of death m based on these reductions in stems over these time periods. We write a likelihood $L(N_0, N_1, t|m) = \text{Bin}(N_1, N_0, P_s)$, with the number of successes, or survived trees, N_1 , out of the number of trials, or number of initial trees, N_0 , given a survival probability determined by the number of years a tree has successfully survived: $P_s = (1 - m)^t$. In the simple case, with one interval, \hat{P}_s is just N_1/N_0 . This is the same as Sheil et al. (1995)'s equation, which was derived based on discretized differential equations. We will maximize the likelihood of all the intervals together:

$$\sum_i^n \log(L(N_{0_i}, N_{1_i}, t_i|m)) = \sum_i^n \log(\text{Bin}(N_{1_i}, N_{0_i}, P_{s_i})) \quad (\text{D.1})$$

$$P_{s_i} = (1 - m)^{t_i}$$

This calculation will correctly weight plots with many or few trees, and those with no

deaths or complete mortality. Here is the R code for the likelihood function:

```
> mylogLik<-function(m, dat) {  
+   Psurv<-(1-m)^dat$t  
+   sum(dbinom(dat$Nfin, dat$Nini, Psurv, log=TRUE))  
+ }
```

And here is the code to maximize the likelihood using `optim` and get the profile likelihood for confidence intervals:

```
> get.profCI.m<-function(datf){  
+   res<-optimize(mylogLik,c(0,1),datf,maximum=TRUE)  
+   mgrid<-seq(0,.1, length.out=1000)  
+   proflik<-numeric()  
+   for(i in 1:length(mgrid))  
+     proflik[i]<-mylogLik(mgrid[i],datf)  
+   liklim<-res$objective-qchisq(p=.95,df=1)  
+   ms<-mgrid[which(proflik>=liklim)]  
+   return(c(m=res$maximum,LCI=min(ms), UCI=max(ms)))  
+ }  
>
```

Table D1 summarizes the results for m for all species with any deaths in our inventory.

Table D1: m results for all species (in percent) with profile-likelihood-based 95% confidence intervals.

Species	Deaths	Trees	(m)
All	833	3319	1.79 (1.62, 1.95)
IC	356	1378	1.81 (1.56, 2.08)
WF	231	846	2.14 (1.78, 2.54)
DF	78	395	1.39 (1.01, 1.87)
PP	90	332	1.62 (1.19, 2.12)
TO	17	110	1.28 (0.61, 2.32)
BO	20	104	1.21 (0.61, 2.1)
SP	31	101	2.3 (1.34, 3.61)
YW	3	18	1.27 (0.15, 4.44)
CH	6	16	2.75 (0.69, 7)
AL	1	7	0.64 (0.01, 4.23)

References

de Valpine, P. 2009. Shared challenges and common ground for Bayesian and classical analysis of hierarchical models. *Ecological Applications* **19**:584–588.

Sheil, D., D. F. Burslem, and D. Alder. 1995. The interpretation and misinterpretation of mortality rate measures. *Journal of Ecology* **83**:331–333.