

1 Title: Evaluation of mixed-effects models for predicting Douglas-fir mortality

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ABSTRACT

We examined the performance of several generalized linear fixed- and mixed-effects individual-tree mortality models for Douglas-fir stands in the Pacific Northwest. The mixed-effects models accounted for sampling and study design overdispersion. Inclusion of a random intercept term reduced model bias by 88% relative to the fixed-effects model; however, model discrimination did not substantially differ. An uninformed version of the mixed model that used only its fixed effects parameters produced predicted mortality values that exceeded the fixed-effects model bias by 31%. Overall, we did not find compelling evidence to suggest that the mixed models fit our data better than the fixed-effects model. In particular, the mixed models produced fixed-effects parameter estimates that predicted unreasonably high mortality rates for trees approaching 1 m in diameter at breast height.

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INTRODUCTION

Tree mortality is a critical component of stand growth and yield models. It is also highly variable and difficult to predict (Lee, 1971; Dobbertin and Biging, 1998). The nature of data collected to model and quantify mortality, however, may challenge the assumptions inherent in statistical tools used to estimate mortality. In this study we examine a generalized linear mixed-effects method to account for data structure and lack of independence.

Lee (1971) and Staebler (1953) described tree mortality as either regular or irregular. Irregular mortality includes death occurring from insects, disease, fire, snow damage, and wind. This type of mortality typically is episodic, brief, and difficult to predict. Regular mortality is more predictable, and includes influences such as competition for light, moisture, and nutrients. As stands become more crowded, a degree of mortality usually occurs. Trees may die for several possibly co-occurring reasons: suppression where stands are differentiating, weakening due to insects and disease, and buckling where stems become tall and thin (Oliver and Larson, 1996). Trees in stands characterized by regular mortality exhibit a preponderance of mortality amongst smaller-diameter individuals that are over-topped by neighbors (Peet and Christensen, 1987). Mortality rates become low for established trees until larger diameters are reached and the mortality rate increases again (Buchman et al., 1983; Harcombe, 1987; Monserud and Sterba, 1999). Although both classes of mortality may affect stands, only single-tree regular mortality models are routinely incorporated in most growth and yield simulators such as FVS (Dixon, 2011) and ORGANON (Hann, 2011).

74 Single-tree mortality models have been developed using a variety of data and approaches.
75 Logistic models are common for data sets where revisit frequency consists of equal-length time
76 periods (Hamilton, 1986; Bigler and Bugmann, 2003; Jutras et al., 2003; Moore et al., 2004;
77 Adame et al., 2010). However, if the time periods differ, a common solution is to use the logistic
78 model but insert time as a power upon survival probabilities or use a complimentary log-log link
79 function (e.g., Monserud, 1976; Eid and Tuhus, 2001; Moore et al., 2004; Temesgen and
80 Mitchell, 2005; Fortin et al., 2008). For stands where remeasurement occurred multiple times,
81 researchers either avoid pseudoreplication at the level of the tree by omitting all but the last
82 remeasurement for each tree (Hamilton, 1986) or include the remeasurement information
83 (Temesgen and Mitchell, 2005; Fortin et al., 2008).

84

85 Data used in these analyses are from nested samples, with the highest level referred to as
86 installations. Each installation contains one or more plots; each plot contains many trees with
87 repeated measurements. Analyses performed on individual tree mortality data has recently
88 begun to account for the structured nature and non-independence by using generalized linear
89 mixed-effects models. Logistic models by Adame et al. (2010) and Jutras et al. (2003) include
90 random intercepts for study plots or stands. A complimentary log-log model by Fortin et al.
91 (2008) included an adjusted intercept with random effects for study plot and specific time
92 interval nested within plot.

93

94 Prediction performance for nonlinear mixed-effects models may be improved (less bias and
95 greater precision) when compared to corresponding fixed-effects models conditional on the
96 availability of previous information on the subject; however, in absence of random-effects

97 information, predictions using just the fixed portions of the parameterization from the nonlinear
 98 mixed-effects model exhibit greater bias and less precision than even the original fixed-effects
 99 model (Monleon, 2003; Temesgen et al., 2008; Garber et al., 2009). Setting the random effect to
 100 zero follows from prediction theory only for linear mixed models, but it has a different meaning
 101 for nonlinear models. Consider a linear mixed model where X is a $(n \times p)$ design matrix where n
 102 is the number of observations and p is the number of fixed-effects parameters, β is a vector of
 103 linear slope values, Z is a $(n \times r)$ design matrix where r is the number of random effects
 104 parameters, γ represents G-sided random effects parameterization, and ε is the random error:
 105 $y = X\beta + Z\gamma + \varepsilon$, where $E(\gamma) = E(\varepsilon) = 0$

106 Then, conditional on the random effect, and because the expectation is a linear operator,

107 $E(y | \gamma) = X\beta + Z\gamma$

108 Unconditionally,

109 $E(y) = E(X\beta + Z\gamma + \varepsilon) = X\beta + ZE(\gamma) = X\beta$

110 Thus, in a linear model, the unconditional expectation can be calculated from the conditional
 111 expectation by setting the random effect to zero:

112 $E(y) = E(y | \gamma = 0)$

113

114 For a nonlinear model, this is not the case. The nonlinear mixed model can be written as:

115 $y = f(X, \beta, Z, \gamma) + \varepsilon$, where $E(\gamma) = E(\varepsilon) = 0$.

116 Conditional on installation:

117 $E(y | \gamma) = f(X, \beta, Z, \gamma)$

118 Unconditionally:

119 $E(y) = E[E(y | \gamma)] = E[f(X, \beta, Z, \gamma)]$

120 Unlike linear models, for nonlinear models, the unconditional model is not the same as the
121 conditional model with the random effects set to zero:
122 $E(y) \neq E(y | \gamma = 0)$ because $E[f(X, \beta, Z, \gamma)] = \int f(X, \beta, Z, \gamma) d\mu(\gamma) \neq f(X, \beta, Z, \gamma = 0)$, where $\mu(\gamma)$ is
123 the distribution function of γ .
124
125 The model for $E(y)$ is known as the population-average model and the model for $E(y | \gamma)$ is
126 known as the subject-specific model. For nonlinear mixed models, those versions are different.
127 Choosing which type of model and inference is appropriate for each objective is fundamental
128 when dealing with nonlinear mixed models. For a tree from a completely new stand that does
129 not have information to estimate the random effects and, therefore, condition on the stand effect,
130 the proper model is a population average model. When using the subject-specific model with $\gamma =$
131 0 (i.e., the subject-specific model for the average stand), prediction performance is expected to
132 decline. Again, in linear mixed models this is not an issue, because setting $\gamma = 0$ yields the
133 population-average model.
134
135 Forest management requires models that are useful beyond their study areas. Generalized or
136 nonlinear mixed-effects models can increase bias when applied to novel data (e.g., Robinson and
137 Wykoff, 2004). Mixed models require estimated information about a hierarchical level that may
138 be unknown for novel data sets. One technique to extend generalized linear or nonlinear mixed-
139 effect model applicability is to utilize minimal data from new stands for estimating the random
140 effects parameters. This allows the application of nonlinear mixed effects models beyond their
141 original data frames (Monleon, 2003; Temesgen et al., 2008; Garber et al., 2009). However, this
142 technique may be limited by the response variable type. In those studies it worked for tree

143 height, a continuous static variable. Our study's response variable, individual tree mortality, is
144 rare, binomial, dynamic, and requires several years of data collection to observe. Thus,
145 incorporating subsample information from new plots to inform mixed-effects model predictions
146 is generally unfeasible.

147

148 The objectives of this study are to 1) determine whether a generalized linear mixed model fit to
149 repeatedly remeasured Douglas-fir (*Pseudotsuga menziesii* [Mirb.] trees can improve mortality
150 estimation over a previous nonlinear estimation approach (Hann et al., 2003; Hann et al., 2006),
151 and 2) compare the predictive abilities of mixed-effects models to nonlinear least squares
152 estimation in the presence and absence of random effects information. We expect biased
153 predictions from the mixed model that lacks random effects information, but examine the degree
154 by which those results are useful relative to the nonlinear least squares predictions. Taken
155 together, our goal is to examine how well models met our objectives and whether we produce a
156 model that is useful for current Douglas-fir growth and yield simulators.

157

158 METHODS

159 **Study Area and Data Acquisition**

160 Data used in this analysis were obtained from randomly located installations on nine land
161 ownerships and represent a subset of data described in Hann et al. (2003; 2006). One of the uses
162 of the overall data collection effort was to calibrate the ORGANON stand development model
163 (Hann, 2011) for intensively managed Douglas-fir in the Pacific Northwest region of the USA
164 and Canada. What follows is a description of the subsetted data. The data were from 304
165 permanent sample installations from Southwest British Columbia, Western Washington, and

166 Northwestern Oregon. The 820 plots within those installations contained 195,795 revisit data
167 collected from 70,720 Douglas-fir trees. Trees were revisited one to 18 times over the course of
168 data collection. Time between revisits was not equal among trees or plots, and varied from 3 to 7
169 years (median = 5 years). The fixed-area plots varied in size from 0.041 to 0.486 ha
170 (mean=0.069). The average breast height age was 27.8 years and ranged from 3 to 108 years.
171 Plots included in this study were not subject to thinning or fertilization experimental treatments.

172
173 We further reduced the data set according to two criteria. The first criterion only permitted data
174 from installations that had two or more plots. This criterion was necessary for creating mixed-
175 effects mortality predictions (described below), and it removed 12,616 trees, 38,314
176 observations, and 67 single-plot installations from the data set. The second criterion was that we
177 retained only trees with DBH < 101.6 cm. We removed larger-DBH trees to allay model
178 convergence issues likely arising from a paucity of mortality information leading to a lack of fit
179 at that extreme. This removed eight observations and five trees (<0.01% of data) and permitted
180 model convergence. The resulting data set included 157,473 revisits of 58,099 trees in 753 plots
181 located within 201 installations.

182 183 **Mortality estimation**

184 We based this analysis on a general equation of mortality given differing plot revisit schedules as
185 described by Hann et al. (2006):

186
187 [1]
$$PM = 1.0 - [1.0 + e^{-(X\beta)}]^{-PLEN} + \epsilon_{PM}$$

188

189 Where PLEN is the length of the growth period in 5-year increments (i.e., length of a growth
190 period in years divided by 5), PM is the 5-year mortality rate, and ε_{PM} is the random error on
191 PM. The response variable distribution is $y \sim \text{Bernoulli}(\pi)$ where the observed response was y
192 and π is the corresponding response probability. Several different parameterizations have been
193 examined for $X\beta$. Hann et al. (2006) modeled $X\beta$ as:

194

195 [2]
$$X\beta = \beta_0 + \beta_1 DBH + \beta_2 CR + \beta_3 BAL + \beta_4 DFSI$$

196

197 The variable DBH is diameter at breast height (cm) at 1.3 m, CR is tree crown ratio, BAL(m²/ha)
198 is basal area per ha in trees with diameters larger than that of the subject tree on the plot, and
199 DFSI is the Douglas-fir site index (Hann and Scrivani, 1987) in meters. We examined the
200 predictive ability of this model in three ways. We wished to investigate whether the mixed-
201 effects approach would provide a reasonable mortality prediction for older trees, so we included
202 the square of DBH (DBH²) as a predictor variable (e.g., Monserud and Sterba, 1999; Hann and
203 Hanus, 2001). CR was subsampled on many of the plots in the modeling data set and would
204 require the imputation of the missing values if used in a mortality equation. This would introduce
205 prediction error issues which we decided to avoid by removing CR from the analysis. We
206 retained BAL to represent competition experienced by an individual tree (Wykoff et al., 1982;
207 Wykoff, 1986; Temesgen and Mitchell, 2005). The parameterization we used in this analysis
208 was:

209

210 [3]
$$X\beta = \beta_0 + \beta_1 DBH + \beta_2 DBH^2 + \beta_3 BAL + \beta_4 DFSI$$

211

212 We present a generalized linear fit of this model, fit via a maximum likelihood estimator (PROC
 213 GLIMMIX, SAS Inc. 2008). This model produced results identical to those from the nonlinear
 214 approach employed by Hann et al. (2006) to estimate tree mortality. We refer to this model as
 215 NLS given its equality to the original procedure. We also examined two generalized linear
 216 models with the same parameterization as [3]. One corrected for model overdispersion by
 217 altering the model variance. The other corrected for overdispersion and included a random effect
 218 term for the model intercept grouped by installation. We selected installation as a grouping level
 219 instead of plot due to our desire to validate models using a leave-one-out approach (described
 220 below). We refer to these models as GXR and GXME respectively.

221

222 We constructed GXR and GXME using the generalized linear mixed-model procedure Proc
 223 GLIMMIX (SAS Institute Inc. 2008). The procedure made use of a pseudo-likelihood estimator
 224 instead of a maximum likelihood estimator due to the presence of R-sided mixed effects
 225 (Schabenberger, 2007). The advantages of GLIMMIX over other SAS procedures (e.g., Proc
 226 NLMIXED) included the ability to incorporate more than one random effect into the model (G-
 227 sided random effect) and to include a multiplicative overdispersion parameter (R-sided random
 228 effects). A disadvantage of GLIMMIX is that its pseudo-likelihood estimator may produce
 229 biased estimates in certain contexts (Breslow and Lin, 1995). The main structural difference
 230 between the marginal (fixed-effects or population-averaged; i.e., NLS, GXR) and the mixed-
 231 effects model GXME is the incorporation of the G-sided random effects terms $Z\gamma$ into the
 232 mixed-effects model structure:

233

234 [4]
$$PM = 1.0 - [1.0 + e^{-(X\beta + Z\gamma)}]^{-PLEN} + \varepsilon_{PM}$$

235

236 The $Z\gamma$ term alters the model linear predictors. We created a model with an installation grouped
237 random intercept by structuring the linear predictors of our model as:

238

239 [5]
$$\eta = X\beta + Z\gamma = \beta_0 + b_i + \beta_1 DBH_{ij} + \beta_2 DBH^2_{ij} + \beta_3 BAL_{ij} + \beta_4 DFSI_{ij}$$

240

241 The linear predictors included a population-level intercept β_0 , a deviation from that intercept of
242 amount b for installation i , and the remaining parameter estimates for observations j in
243 installations i . The modified logit function is:

244
$$\pi_{ij} = f(\eta) = 1 - \{1 + \exp(-[\eta])\}^{-PLEN}$$

245
$$b_i \sim N(0, \theta_b^2)$$

246 [6]
$$Var(y_{ij} | \pi_{ij}) = \pi_{ij}(1 - \pi_{ij})$$

247 In GLIMMIX, the variance of observations, conditional on the random effects, is:

248
$$var[Y|\gamma] = A^{1/2}RA^{1/2}$$

249 The diagonal matrix A contains the variance functions of the model (i.e., equation [6]) and
250 expresses the variance function for the i^{th} observation (Littell et al., 2006, p. 535). G -sided
251 random effects will therefore affect the values for A . The random effects matrix $R = \phi I$ where I
252 is an identity matrix and ϕ is a dispersion scale parameter. In binomial models where there is no
253 overdispersion, $\phi = 1$. However, if data are overdispersed, the variances can be accordingly
254 increased by changing this parameter. We tested for model overdispersion using the Pearson's
255 statistic (Littell et al., 2006). We additionally weighted our tree remeasurement data by their

256 respective plot sizes (Flewelling and Monserud, 2002). Model weighting is accomplished by
257 calculating ϕ/w_i , where w is the weight associated with observation i . To summarize, GXME
258 was constructed in PROC GLIMMIX with linear mixed- and fixed-effects predictors from [5]
259 used in the nonlinear equation [4]. A random intercept was estimated by installation and we
260 included an R-sided random effect to account for overdispersion. Observations for the model
261 were weighted by plot size.

262

263 A difficulty with using the estimates for GXME to predict mortality for trees that are not part of
264 a current installation is that no hierarchical parameter values for that installation would be
265 available. The random effects parameters remain uninformed. We explored the utility of
266 applying the uninformed mixed model by examining the predictive ability of an additional
267 model, GXFE. This model incorporates the fixed-effects parameter estimates from GXME but
268 discards its random effects parameterization.

269

270 We validated models NLS, GXME, and GXFE using a leave-one-out approach. GXR was
271 excluded as model validation relies on parameter point estimates and its parameter point
272 estimates (not error) should be identical to those for NLS. In this instance we repeatedly fit
273 models to subsets of the data. Each subset included all but one of the plots (model set). The
274 resulting model was used to predict the response of each of the excluded sites' observations
275 (prediction set). In order to facilitate inclusion of models that relied on random effects at the
276 level of installations, we reduced the data set to include only installations with two or more plots.
277 With one plot excluded, the model was still able to estimate a random effect for that installation.

278

279 We used model estimates from the model data set to produce residual values for the validation
280 set. We used the Hosmer-Lemeshow test to determine model goodness-of-fit (Hosmer and
281 Lemeshow, 2000) and compared model discrimination by using receiver operating characteristic
282 (ROC) curve analysis and examining the area under the ROC curves. We examined model and
283 bias for the overall validation data set and for different values of BAL, DFSI, and DBH. We
284 calculated mean bias using the following equation:

285 [8]
$$Bias = \frac{\sum(y_j - \hat{\pi}_{ij})}{n}$$

286 The symbol y_j is a single mortality observation (1 or 0), $\hat{\pi}_{ij}$ is the fitted value, and n is the
287 number of observations.

288

289 RESULTS

290 The data set included the mortality of 9982 trees (6.3% of total). Deaths appeared to be skewed
291 towards smaller DBH categories while mortality appeared to increase at higher BAL volumes,
292 indicating that trees may have been more likely to perish if the stand typically had more trees
293 with basal area greater than the tree in question (Figure 1).

294

295 Model coefficients for the three models were estimated from the full sample data set (Table 1).

296 The inclusion of R-sided random effects variables reduced overdispersion. The Pearson's
297 statistic for the condition distribution for the NLS model was 10.88, substantially different from
298 a value of 1. The Pearson's statistics for GXR and GXME were 1.00 indicating that the
299 inclusion of the R-sided or R- and G-sided random effects corrected for the overdispersion. As a
300 consequence, GXR fixed-effects parameter standard errors were greater than NLS standard

301 errors. A difference among models was the parameter values for DBH^2 , which increased by 60%
302 when comparing NLS to GXME.

303
304 Predicted values generated from the mixed-effects model with random variables improved bias
305 compared to the nonlinear model. However, the mixed model's bias suffered when only its fixed
306 effects were considered (Table 2). On average, GXME, with random effects and overdispersion
307 terms, exhibited a bias that was 22% the values of model NLS. Model GXFE's bias was 4 times
308 greater than the value of NLS.

309
310 The area under the ROC curve was 2.3% higher for GXME than for NLS or GXFE, indicating
311 that the mixed model exhibited a slightly greater degree of model discrimination. The values for
312 NLS and GXFE were nearly identical. The Hosmer-Lemeshow goodness-of-fit test statistics
313 were significant ($df = 8, p < 0.001$) for all models considered, indicating that no models fit data at
314 an acceptable level (e.g., $\chi^2 \leq 15.5$). Pearson's residuals increased with $DBH > 20$ cm and BAL
315 < 40 m²/ha; a pattern did not appear evident between residuals and DFSI. Among the models,
316 GXFE's score was substantially higher than either NLS or GXME, and NLS had the lowest score
317 of the three. Pearson's correlations among variables was highest between DBH and DBH^2
318 (0.935), the next highest was between DBH^2 and DFSI (0.191).

319
320 Bias was generally lowest for model GXME across all values of all predictor variables with a
321 few close exceptions (Figure 2). Values and patterns of bias were similar for NLS and GXFE
322 across variables, although the bias values for GXFE were generally but not always more
323 extreme. In particular, bias for GXFE was more than twice as great as other models at $DBH <$

324 20 cm. Comparisons of observed and predicted values of mortality (Figure 3) demonstrate the
325 generally closer fit of the mixed model predicted values to observed mortality. Relative to
326 GXFE, NLS better predicts tree mortality at DBH values < 20 cm and is fairly equivalent at other
327 DBH values. NLS mortality predictions were closer to observed values at all BAL categories
328 except 50-59 m. NLS also outperformed GXFE at four of the six DFSI categories (not including
329 30-34m and > 45m).

330

331 We compared predicted model performance to observed values to determine where model
332 shortcomings were (Figure 4). Of note, GXME appeared to best match observed mortality at
333 DBH values < 20 cm while the other models generally underpredicted tree mortality. However,
334 all models except for NLS predicted a dramatic increase in mortality beyond 90 cm DBH. The
335 20% observed mortality at 97 cm DBH represented one of five trees of that size class perishing.
336 We examined fixed-effects parameter values for GXME for trees with DBH < 90 cm to
337 determine if this mortality was exhibiting a strong influence on DBH^2 and found that results
338 were virtually unchanged.

339

340 DISCUSSION

341 We report partial success at meeting our study objectives. The mixed-effect models accounted
342 for overdispersion in the data and accordingly increased parameter standard errors. The mixed-
343 effects model GXME additionally reduced prediction bias relative to NLS. However, the
344 predicted fits at observed parameter values were of concern; the DBH^2 parameter of the mixed-
345 effects model GXME and its related models predicted an unreasonably high mortality rate for
346 trees with DBH > 90 cm. The larger-DBH predictions for NLS were more reasonable. The

347 GXME model appeared to best fit the data at DBH < 40 cm, a range that included the bulk of our
348 data.

349
350 The inclusion of R-sided random effects assisted in reducing model overdispersion. Although
351 unreported, the estimated standard errors of parameter estimates resulting from earlier analyses
352 such as Temesgen and Mitchell (2005) and Hann et al. (2003; 2006) would have been too small.
353 For those authors the models were used in validation trials so the means, not standard errors,
354 affected validation outcomes. The increase in error terms could indicate that previously-
355 supported parameters were not contributing to the model, although all of our parameters
356 remained supported in all models.

357
358 Once we included a random intercept in the model along with an R-sided random effect, the term
359 for DBH² increased markedly. Bias for the mixed-effects model was improved relative to the
360 marginal model. However, when we examined predicted fits for the mixed model's fixed-effects
361 parameters without taking into account the individual installation information (random intercept)
362 the bias increased to an amount four times greater than the marginal model. Clearly, it would be
363 difficult to justify this model's use. This finding is similar to results reported by several other
364 authors (Monleon 2003; Temesgen et al. 2008; Garber et al. 2009), and confirms our expectation
365 that this would be the case.

366
367 Other authors provide examples of studies in which mixed models produce an improvement in
368 predictive ability, and minimal data collection allowed for an application of the mixed models to
369 novel stands (Monleon, 2003; Temesgen et al., 2008; Garber et al., 2009). Obtaining ancillary

370 mortality data to estimate random effects is prohibitively difficult. Given the modest
371 improvements in prediction from the G-sided mixed model, the anticipated poor performance of
372 the uninformed mixed model, and our lack of ability to apply the mixed model to novel stands,
373 we find no advantage here with utilizing the generalized linear mixed-effects models for
374 predicting Douglas-fir mortality.

375
376 Our issues with model bias when fixed-effects parameter estimates were extracted from the
377 generalized mixed model indicate a problem with our application, not a problem with the model.
378 We wished to obtain a finding we could generalize between subjects when the mixed models
379 were best able to generalize results within subjects. We imagine that if we desired inference to
380 additional plots within installations, our mixed model would have proven more useful than the
381 marginal model.

382
383 All of our models examined failed the goodness-of-fit test; it appears this may be in part due to
384 results for larger-diameter trees that were among the largest trees in a stand. We interpret this to
385 indicate that our model did not fit mortality data well at these larger ranges where we had a
386 relative paucity of data. Other possible contributing issues include overfitting the model or
387 providing insufficient fixed-effects parameters. Among models, the goodness-of-fit scores were
388 lowest for GXME with GXFE a distant third.

389
390 Across models, bias was highest at low DBH and high BAL values (both well-represented in the
391 data set). With DFSI, bias was high for the smallest category which corresponded with few data
392 relative to other categories. Bias patterns differed across models as well. GXME tended to

393 exhibit a different and reduced pattern of bias across all three predictor variable categories. The
394 models that were not incorporating installation-specific effects into their estimates tended to
395 behave similarly with model GXFE frequently providing the most extreme bias per variable
396 category.

397

398 The intensity of the effect DBH^2 had on mortality prediction at greater DBH values surprised us.
399 Although our predicted U-shaped mortality curve is in spirit similar to that discussed by
400 Harcombe (1987) and found by Monserud and Sterba (1999) for Norway Spruce and Hann and
401 Hanus (2001) for Douglas-fir, grand fir, white fir, incense-cedar, ponderosa pine, and California
402 black oak, only the predicted mortality for large DBH values from the model NLS appeared
403 reasonable. The mixed-effects based models predicted mortality rates at 95 cm DBH that are
404 simply too extreme; if those estimates were real, old-growth (> 180 year) Douglas fir stands
405 would not exist. However, the models, particularly GXME, did appear to predict observed
406 mortality for trees <80 cm DBH. GXFE appeared most severely underpredict the 5-year
407 mortality rate.

408

409 CONCLUSION

410 Our generalized linear mixed model of Douglas-fir mortality did not outperform a similar model
411 lacking mixed effects. In particular, the incorporation of mixed effects resulted in alterations to
412 fixed effects that produced unreasonably high mortality rates for trees approaching 1 m in
413 diameter. The practical application of predicting mortality rates for novel stands did not improve
414 with the utilization of a mixed model. We believe this will generally be the case for tree
415 mortality estimation when random effects information is unavailable, a condition that should be

416 common. The correction for model overdispersion was appropriate and represented an
417 improvement in parameter variance estimation, but overall we cannot recommend the mixed
418 model as a suitable replacement for the original model form.

419

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542 Model. Gen. Tech. Rprt. INT-133. USDA For. Serv., Ogden, UT. 112 p.
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 546 Table 1. Fixed and random effects estimates and standard errors (SE) for the generalized linear
 548 least squares models NLS, GXR, and GXME. The overdispersion parameter (Residual) indicates
 549 the size of the underlying residual effect's variance and the standard error of that effect.

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	NLS		GXR		GXME	
	Estimate	StdError	Estimate	StdError	Estimate	StdError
<u>Fixed Effects</u>						
Intercept	-4.5118	0.02807	-4.5118	0.09267	-5.0958	0.2891
DBH	-0.2105	0.00251	-0.2105	0.00829	-0.2719	0.00677
DBHSQ	0.00168	7.8E-05	0.00168	0.00026	0.00279	0.00017
BAL	0.00421	1.8E-05	0.00421	6.1E-05	0.00495	8.3E-05
DFSI	0.04897	0.00068	0.04897	0.00224	0.05996	0.00804
Random Effects						
Residual (Subject = Tree)			10.884	0.03879	10.275	0.03665
Intercept (Subject = Installation)					0.6353	0.07953

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 557 Table 2: Comparisons of model performance at predicting the probability of tree mortality over a
 558 five-year period (PM_5). Comparisons include model bias, area under the ROC curve (AUC), a
 559 and the Hosmer-Lemeshow goodness-of-fit test statistic (H-L Test). Number of observations =
 560 157,473.

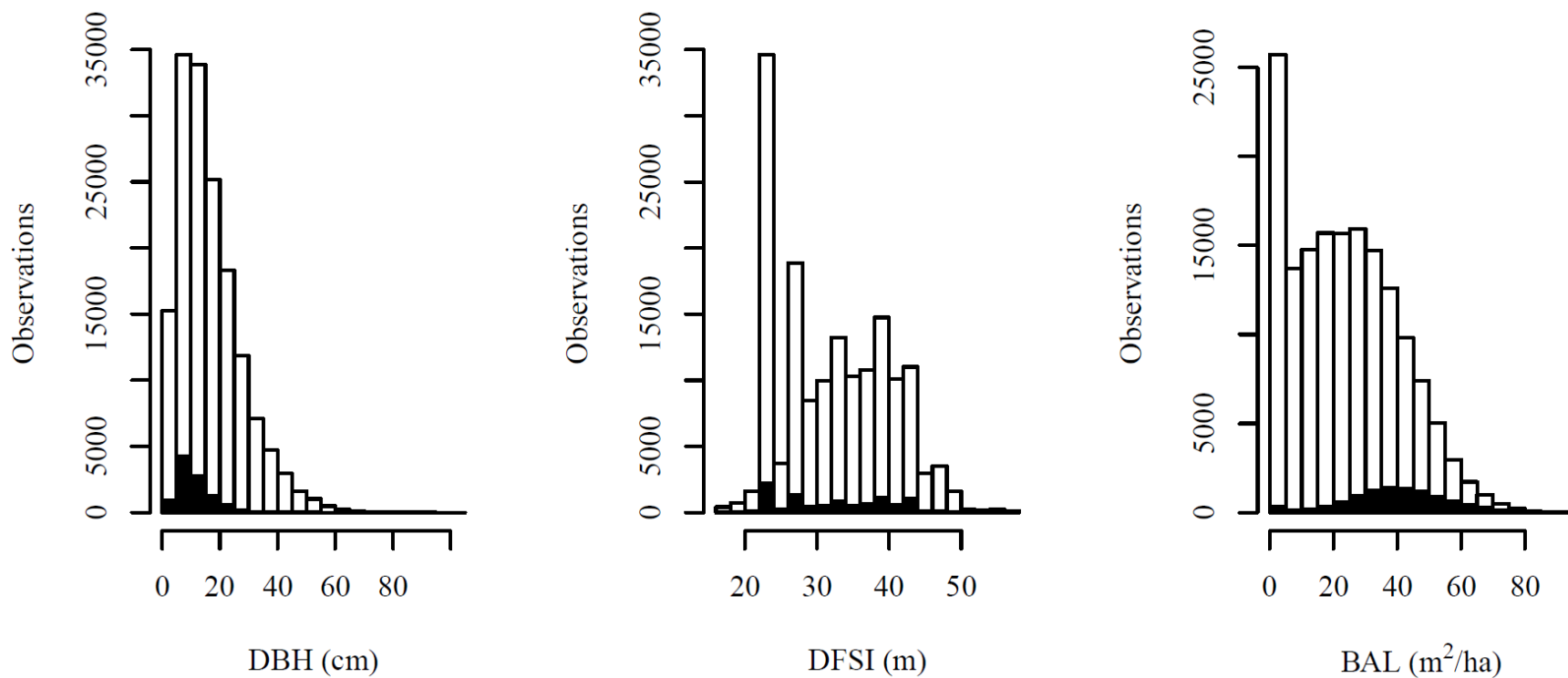
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Models	Bias ($P_{5\text{-year mort}}$)	AUC	H-L Test
NLS	0.002643908	0.845	366.8
GXME	-0.000604775	0.864	388.8
GXFE	0.0110345	0.844	1505.6

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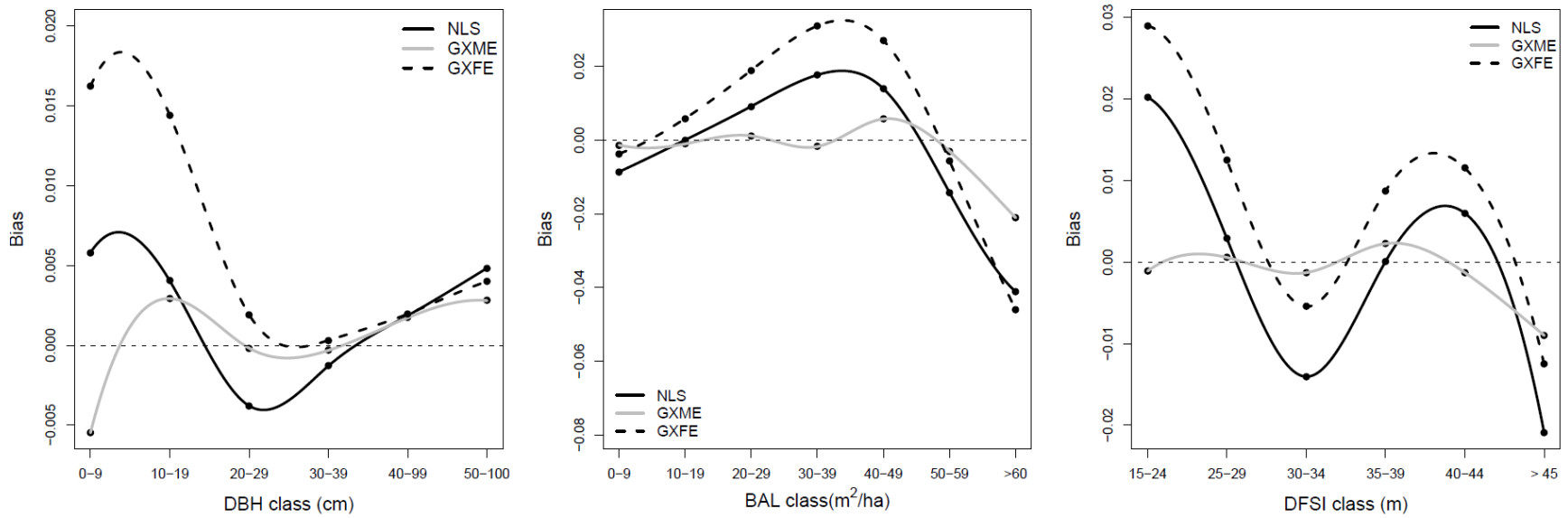
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568 Figure 1. Histograms of observations (live + dead) by variable name. The clear bars represent all data of a particular category; black
569 bars represent the number of dead observations.

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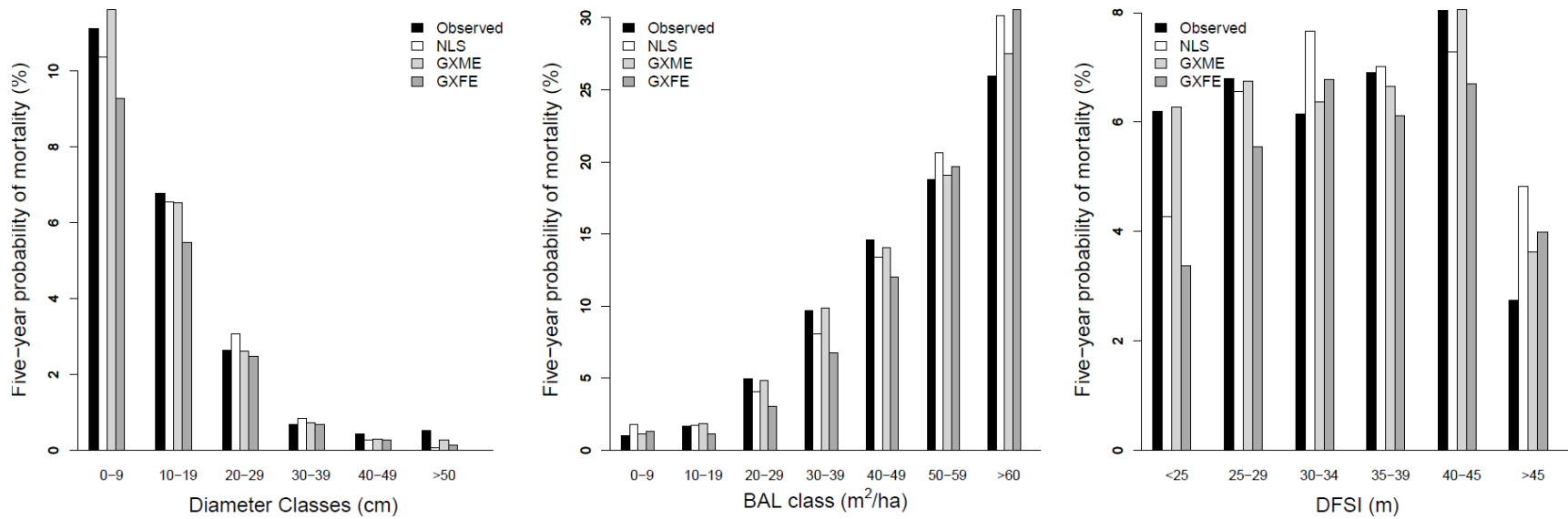
573 Figure 2. Prediction bias associated with models NLS, GXME, and GXFE across the range of data values for DBH, BAL, and DFSI.

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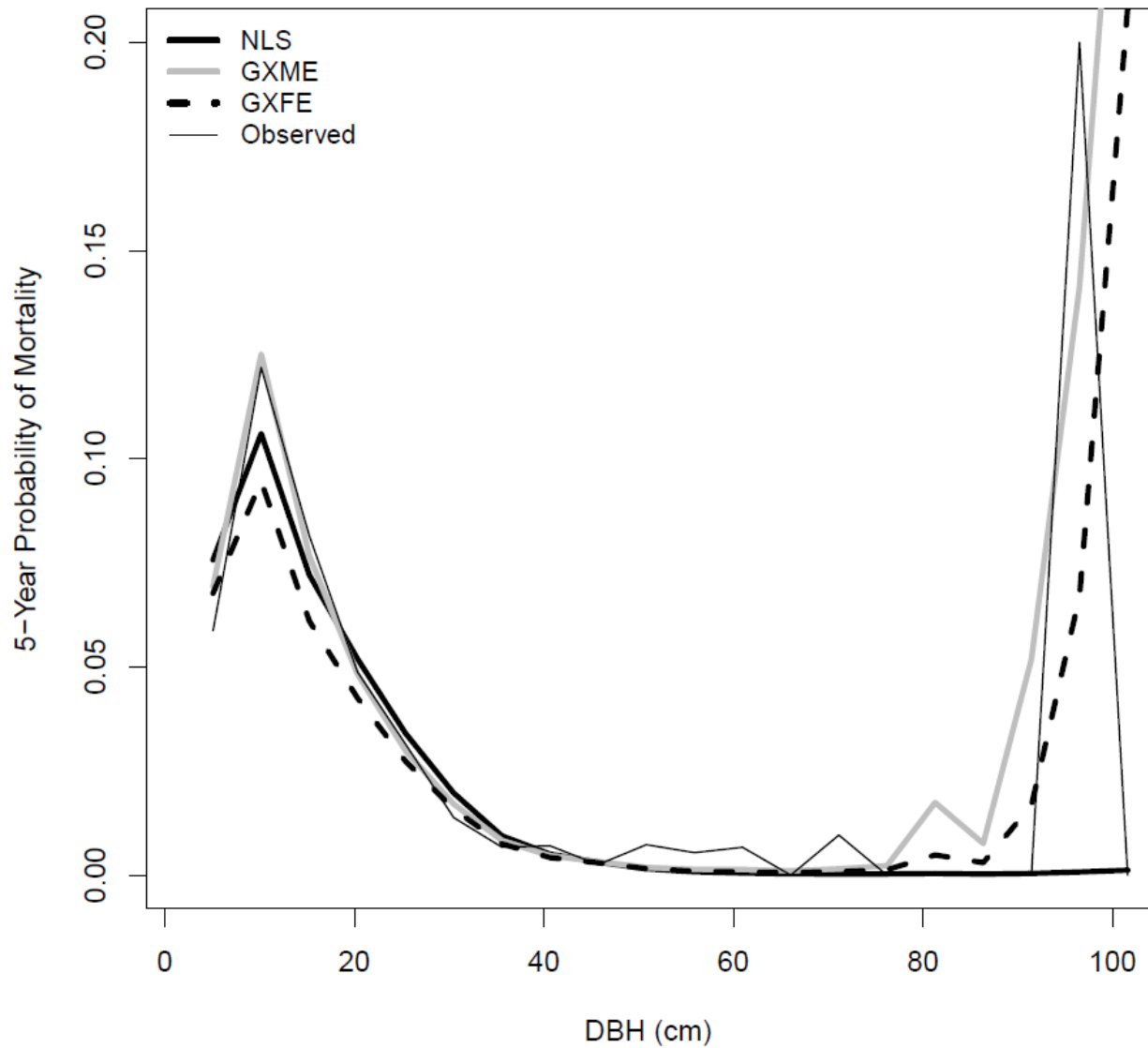
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579 Figure 3. Five-year predicted and observed probability of mortality. Mortality probabilities are presented by diameter, BAL, and

580 DFSI classes.

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585 Figure 4. Predicted mortality rates by DBH and average parameter values at specific DBH
 586 values.

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