

# “Growing Trees Backwards”: Description of a Stand Reconstruction Model

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**Abstract**—We describe an individual-tree model that uses contemporary measurements to “grow trees backward” and reconstruct past tree diameters and stand structure in ponderosa pine dominated stands of the Southwest. Model inputs are contemporary structural measurements of all snags, logs, stumps, and living trees, and radial growth measurements, if available. Key steps include the application of inverse decay functions to estimate snag and log death dates, and the estimation of tree size in the reconstruction year via radial growth data or accrued basal area increment. The model is provided as a function for R, and can be modified for other species and regions.

## Introduction

Understanding stand development is an important line of evidence about reference conditions that can guide current restoration activities. Furthermore, biometric measurements such as diameter at breast height (DBH) can be related to tree biomass, nutrient storage, and other aspects of ecosystem structure and function (Jenkins and others 2004). We often lack empirical information about stand development and are therefore required to use models to estimate how stands developed. Stand reconstruction models are one means to obtain information on past forest structure such as tree density and diameter classes (Everett and others 2007, Groven and others 2002, Harrod and others 1999).

Fulé and others (1997) and Huffman and others (2001) outlined a method of reconstructing past forest structure in southwestern ponderosa pine forests on the basis of contemporary measurements. Their model, which is built upon in this paper, overestimated tree size and forest density by ~ 7% (Huffman and others 2001). Model accuracy was assessed by comparing reconstructed forest structure with actual data from the Woolsey plots, a unique set of historical stem-mapped plots on the Fort Valley Experimental Forest (FVEF) and throughout Arizona and New Mexico (Moore and others 2004). However, the model utility is limited by

how it was parameterized. First, the allometric equations used in the model were compiled from a variety of sources rather than being locally parameterized, and therefore did not fit the data as good as possible. For example, DBH and diameter at stump height (DSH) were regressed, but the published regression was based on a stump height of 30 cm (12”; Hann 1976) while the data used to validate the model were obtained at 40 cm stump height. Second, the model was written using a software language that is no longer commonly used, and thus its utility was greatly diminished. We have ported the model to R, an open-source statistical language (R Development Core Team 2007), and have published the code as a script (Appendix 1) that can be updated for other species and forest types.

Here, we summarize the model structure, including the improvements we have made to it. We also note some of the limitations of the model as it is currently formulated.

## Model Requirements

The model operates on an individual-tree basis. It requires data on all trees in the stand, both live and dead. A number of field-collected variables are recorded for each tree (Table 1, Table 3). If available, radial growth data from increment cores can also be incorporated to provide accurate information about individual trees. Although the original model

**Table 1.** Variables to be measured, and allowed values for each.

Variable	Values / Comments
Species	Required.
Condition	Required. See Table 3 for details.
Field-called Age Class	Required. 0 (post-plot; ~100 years old), 1 (pre-plot; >100 years old), or 2 (pre-settlement; >130 years old). See Moore et al. (2004) for details.
DBH	Outside bark, in cm. Either DBH or DSH is required.
DSH	Outside bark, in cm. Either DBH or DSH is required.
Increment Core	Optional. If a core is taken, the following variables should be measured on it: i) center date; ii) radial increment from inventory year back to Year X, in cm; iii) radial increment from inventory year back to pith, in cm.

included more species, the revised model presented here is parameterized for ponderosa pine (*Pinus ponderosa* Laws. var. *scopulorum* Engelm.) and Gambel oak (*Quercus gambelii* Nutt.). All variables must be in metric units.

## Model Structure

### Step 1: Parameter Specification

Parameters to be specified include the inventory year (year when measurements were obtained; can differ among trees), reconstruction year (Year X, a constant; all trees will be reconstructed back to this year), and death dates of stumps, if known.

### Step 2: Populate Required Inventory Year Variables

It is often not practical to measure all required variables for all trees. For example, we generally measure DBH on live trees but DSH on dead trees, snags, and logs. Therefore, we used DBH-DSH regressions to estimate missing data values. The regressions (Table 2) were developed from trees on the Woolsey plots, a series of permanent plots on the Fort Valley Experimental Forest and throughout Arizona and New Mexico (Moore and others 2004). For each species, multiple regression analysis indicated that this relationship did not differ between trees of different field-called age classes.

Second, all trees were assigned in the field to one of three field-called age classes, but our model is based on two age classes. In ponderosa pine, these age classes

**Table 2.** Regressions between outside-bark diameter at breast height (DBH, in cm) and diameter at a stump height of 40 cm (DSH, in cm) and between DSH and annual basal area increment (Annual.BAI, in cm<sup>2</sup>) for ponderosa pine (PIPO) and Gambel oak (QUGA) trees. Data are from Woolsey plots throughout Arizona and New Mexico.

Species	Equation	N	R <sup>2</sup>	SEE <sup>a</sup>	Range of independent variable	Range of dependent variable
<b>DBH-DSH Regressions</b>						
PIPO	DSH = 1.664 + 1.063 DBH	8375	0.9935	1.511	0.25 to 99.06	1.02 to 103.63
QUGA	DSH = 1.093 + 1.034 DBH	1400	0.9884	1.268	0.25 to 77.98	0.25 to 72.14
<b>DSH-Annual.BAI Regressions</b>						
PIPO <sup>b</sup>	ln(Annual.BAI) = -3.718 + 1.736 ln(DSH)	3008	0.9612	0.227	1.5 to 64.0	0.05 to 35.58
PIPO <sup>c</sup>	ln(Annual.BAI) = -3.216 + 1.541 ln(DSH)	2014	0.6772	0.314	7.6 to 92.0	0.62 to 72.97
QUGA <sup>b</sup>	ln(Annual.BAI) = -3.161 + 1.370 ln(DSH)	206	0.8777	0.284	1.8 to 25.7	0.07 to 6.04
QUGA <sup>c</sup>	ln(Annual.BAI) = -3.090 + 1.384 ln(DSH)	143	0.5828	0.263	9.7 to 64.5	0.93 to 19.21

<sup>a</sup> Standard error of the estimate.

<sup>b</sup> "Post-plot" field-called age class.

<sup>c</sup> "Pre-plot" and "Presettlement" field-called age classes.

roughly correspond to black jack (trees <150 years old) and yellow pine (trees >150 years old, Moore and others 2004). Calculated age classes are adjusted based on age data, where available, or on the field-called age class and size of the tree.

### Step 3: Estimating Snag and Log Death Dates

Dead trees, snags, and logs are ‘undecomposed’ to estimate their death dates (Table 3). Decay rates are based on Rogers and others (1984) and assumed the 50<sup>th</sup> decomposition rate percentile as this percentile has been shown to work well (Huffman and others 2001).

### Step 4: Back-Growth of Trees

Trees are back-grown from their inventory or death date (whichever is earlier) to Year X. Three methods are used, depending on the availability of increment data. If a complete increment core (i.e., containing radial increments from Year X to present and from pith to present) is available, diameter in Year X is reconstructed using the proportional reconstruction method (Bakker 2005). If only the radial increment from Year X to present is available, diameter in Year X is reconstructed by subtracting twice the radial increment from the inside bark diameter. Inside bark diameters were calculated using published equations for ponderosa pine (Myers 1963) and assuming that bark thickness equaled 5% of stem diameter for

Gambel oak. Finally, if no increment data are available, diameter in Year X is reconstructed by calculating the expected basal area increment for the interval between Year X and the inventory year and subtracting that increment from the basal area in the inventory year. Diameter-BAI regressions were calculated from trees on Woolsey plots through Arizona and New Mexico (Table 2). Advantages of these regressions are that they are on a log-log scale, are based on large sample sizes from a wide geographic range, and span a much larger DBH range than previous regressions. All back-growth calculations are conducted at DSH since that is the height at which increment cores and BAI data were obtained.

## Discussion

The accuracy with which individual trees are modeled directly affects the accuracy of stand-level attributes such as tree density and basal area. There are three main elements that affect model accuracy. First, reconstructions presume that all tree structures in the stand, including highly decomposed snags, logs, and stumps, were identified. This is feasible in arid environments like the Southwest; during sampling in 1997-1999, Moore and others (2004) missed only 9% of the trees present at plot establishment (1909-1913). In environments with more mesic climates or faster decomposition rates, this model may not be applicable over as long of time periods. Similarly, stand disturbances such as fires that

**Table 3.** Condition classes and decay rates applied to trees on the Woolsey plots. The example shows the estimated death date for a 50 cm DBH tree measured in 2008. For instance, a 50 cm DBH condition 3 tree is estimated to have died in 2008 while a condition 7 log of the same size is estimated to have died in 1943.

Condition	Description	Annual transition rate	Example
1	Live	-	
2	Fading	-	
3	Recently dead snag	0 (assumed to have died in inventory year)	2008
4	Loose bark snag	20%	2004
5	Clean bark snag	Condition 4 + 15%	1999
6	Snag broken above breast height (BH)	Condition 5 + Diameter dependent snag fall rate	1971
7	Log (snag broken below BH)	Condition 5 + 2(Diameter dependent snag fall rate)	1943
8	Windthrow (dead and down; log with root ball present)	Diameter dependent snag fall rate	1980
9	Cut stump	Death date = Cut date, if known, else default date assigned to all stumps	
10	Stump hole	Same as Condition 7	1943
11	Tree missing	Same as Condition 7	1943

Note: Transition rates are for ponderosa pine and are derived from Rogers and others (1984).

consume woody debris will reduce the number of detectable tree structures.

Second, there are a number of known issues related to estimates of snag and log death dates. First, these rates were derived for ponderosa pine but are applied to all species since we lack specific rates for other species. Second, tree condition 6 (snags broken below BH) is poorly linked to age (Waskiewicz and others 2007). Third, death dates of condition 8 (logs with root balls) trees appear to be underestimated since they are calculated to be of an age intermediate between conditions 5 and 6 (Table 3). Fourth, conditions 10 (stump hole) and 11 (missing) were not included in Rogers and others (1984); we have assumed that trees of these conditions are at least as old as condition 7 (log; snag broken below BH) trees. Finally, the decay functions are linear and deterministic, and do not capture the range of variability observed (Waskiewicz and others 2007).

Third, the three back-growth methods yield different estimates of historical DBH. To assess this, we identified 389 live ponderosa pine trees on the Woolsey plots that have complete increment cores and for which we knew their actual DBH at plot establishment. These particular trees are located on the Coconino and Prescott National Forests (Sánchez Meador and Moore, this proceedings; De Blois and others, this proceedings). Plots on the Coconino were established in 1909-1913 while those on the Prescott were established in 1925-1930. We estimated the DBH of each tree at plot establishment using all three reconstruction methods, and calculated the precision of each estimate as the deviation between the estimated and actual DBH divided by the actual DBH. On average, the proportional reconstruction method underestimated the actual DBH by 3.3% ( $s = 16.8\%$ ) while the radial increment method underestimated DBH by 15.2% ( $s = 16.0\%$ ). Using the BAI method, 6.4% of trees were estimated to have been too small to be present at plot establishment (i.e., their estimated diameters were negative). For those trees large enough to be present, DBH was underestimated by 12.7% ( $s = 29.1\%$ ).

Future research should address the model limitations identified here and explore the effect of time interval on reconstruction accuracy. Future enhancements could include the incorporation of variable stump heights and spatial information such as distance-dependent competition from neighbors. In addition, although the model is currently parameterized for only two species in the Southwest, the code (Appendix 1) can be edited to parameterize it for other species or regions. In spite of these limitations, stand reconstructions permit us to visualize stand development, estimate reference conditions that guide current restoration activities, and quantify the effects of stand development on ecosystem function.

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The content of this paper reflects the views of the author(s), who are responsible for the facts and accuracy of the information presented herein.

Appendix 1. R function. Text following a '#' on a line are comments, not executable code.

```
# R code to calculate prior forest structure in northern Arizona ponderosa
# pine forests
# based on contemporary Data.
# J.D. Bakker, May 30, 2008
# Based on R code from A.J. Sanchez Meador and a R-Base macro from
# P.Z. Fule, A. Waltz, J. Crouse, D. Huffman, and A.J. Sanchez Meador.

# Formatting Notes:
# 1.All Data must be in metric units.
# 2.Data must be comma delimited (csv), with headers on the first line.
# 3.No spaces in column headings (use '.' instead)

# Model Arguments (variables):
# tree.num - Unique tree number. Required.
# orig.tree.num - number assigned at plot establishment or remeasurement.
# Optional.
# spp - Species code. Valid codes: PIPO, QUGA. All other species omitted at
# present. Required.
# cond - tree condition. Valid numbers range from 1 to 11. Required.
# age - Field call of age class. Valid codes are 0 (post-plot), 1 (pre-plot),
# or 2 (pre-settlement). Required.
# dbh - DBH, outside bark, in cm. Optional, but either dbh or dsh is
# required.
# dsh - DSH, in cm. Usually outside bark. Optional, but either dbh or dsh is
# required.
# core - 0 (no core) or 1 (cored). Optional.
# center.date - Center date. Optional.
# inc.x.yr - Increment from inventory year to desired reconstruction year
# (Year X), in cm. Optional.
# inc.excl.yr - Increment from inventory year to fire exclusion year, in cm.
# Optional.
# inc.pith - Increment from inventory year to pith of stem, in cm. Optional.
# cut.date - Cut date of stump or death date of tree. Optional.
# inv.yr - Inventory year. Required.
# dbh.inv - Calculated DBH (outside bark) in inventory year for use in model.
# Returned by model.
# dsh.inv - Calculated DSH (outside bark) in inventory year for use in model.
# Returned by model.
# age.inv - Calculated age class in inventory year for use in model. Returned
# by model.
# death.yr - Calculated; last year in which tree was alive (inventory year
# for live trees) Returned by model..
# dsh.x - Calculated DSH (outside bark) in Year X. Returned by model.
# dbh.x - Calculated DBH (outside bark) in Year X. Returned by model.

# Future Enhancements:
# -parameterize for other species
# -incorporate stump height

##### RECON.MODEL FUNCTION #####
recon.model<-function(Data, xyr, exclyr) {
```

```

for(i in 1:nrow(Data)) {
  if(Data$cond[i] <= 2) {
    if(!is.na(Data$center.date[i]) && Data$center.date[i] <= excl.yr) ||
!is.na(Data$inc.excl.yr[i])) {
      Data$age.inv[i]=1 }
  }
  if(Data$cond[i] >= 3 && Data$age[i] > 0) Data$age.inv[i]=1
}

cat("Determine Presettlement age class for dead trees/stumps with/without
field calls", "\n")
for(i in 1:nrow(Data)) {
  if(Data$spp[i] == 'PIPO' && Data$cond[i] == 9 && Data$age[i] < 1) { if
(Data$dsh.inv[i] >= 31.8) Data$age.inv[i]=1 }
  if(Data$spp[i] == 'QUGA' && Data$dbh.inv[i] >= 17) Data$age.inv[i]=1
}

cat("Final check for age inconsistencies", "\n")
for(i in 1:nrow(Data)) {
  if(!is.na(Data$center.date[i]) && Data$center.date[i] <= excl.yr)
Data$age.inv[i]=1
  if(Data$age[i] > 0 && Data$cond[i] <= 2 && (is.na(Data$center.date[i]) ||
Data$center.date[i] >= Data$inv.yr[i]) && (is.na(Data$inc.x.yr[i]) ||
Data$inc.x.yr[i] == 0)) Data$age.inv[i]=1
  if(!is.na(Data$center.date[i]) && Data$center.date[i] > excl.yr &&
Data$center.date[i] < Data$inv.yr[i]) Data$age.inv[i]=0
}
cat("Age/Size Class determination complete", "\n")

### "UN-DECOMPOSE" DEAD TREES TO DETERMINE DEATH DATES ###
cat("Step 4. Estimate Death Dates of Dead Trees", "\n")
cat("Initialize death date at inventory year for all trees", "\n")
Data$death.yr <- Data$inv.yr
pctile = 0.5 # Set decomposition percentile
cat("Decomposition percentile =", pctile, "\n")

for(i in 1:nrow(Data)) {
# Condition 3 assumed to have died in inventory year
  if(Data$cond[i] == 4) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1.2)) }
  if(Data$cond[i] == 5) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1.2)) + ((log(pctile)-log(1))/log(1.15)) }
  if(Data$cond[i] == 6) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1.2)) + ((log(pctile)-log(1))/log(1.15)) + ((log(pctile)-
log(1))/log(1+(1/(2*(Data$dbh.inv[i]/2.54)))))) }
  if(Data$cond[i] == 7) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1.2)) + ((log(pctile)-log(1))/log(1.15)) + 2*((log(pctile)-
log(1))/log(1+(1/(2*(Data$dbh.inv[i]/2.54)))))) }
  if(Data$cond[i] == 8) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1+(1/(2*(Data$dbh.inv[i]/2.54)))))) }
  if(Data$cond[i] == 9) {
    if(!is.na(Data$cut.date[i])) { Data$death.yr[i] = Data$cut.date[i] }
    else {
      if(!is.na(Data$orig.tree.num[i])) { Data$death.yr[i] = 1940 }
      else { Data$death.yr[i] = 1980 } } }
  if(Data$cond[i] == 10) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-

```

```

for(i in 1:nrow(Data)) {
  if(Data$cond[i] <= 2) {
    if(!is.na(Data$center.date[i]) && Data$center.date[i] <= excl.yr) ||
!is.na(Data$inc.excl.yr[i])) {
      Data$age.inv[i]=1 }
  }
  if(Data$cond[i] >= 3 && Data$age[i] > 0) Data$age.inv[i]=1
}

cat("Determine Presettlement age class for dead trees/stumps with/without
field calls", "\n")
for(i in 1:nrow(Data)) {
  if(Data$spp[i] == 'PIPO' && Data$cond[i] == 9 && Data$age[i] < 1) { if
(Data$dsh.inv[i] >= 31.8) Data$age.inv[i]=1 }
  if(Data$spp[i] == 'QUGA' && Data$dbh.inv[i] >= 17) Data$age.inv[i]=1
}

cat("Final check for age inconsistencies", "\n")
for(i in 1:nrow(Data)) {
  if(!is.na(Data$center.date[i]) && Data$center.date[i] <= excl.yr)
Data$age.inv[i]=1
  if(Data$age[i] > 0 && Data$cond[i] <= 2 && (is.na(Data$center.date[i]) ||
Data$center.date[i] >= Data$inv.yr[i]) && (is.na(Data$inc.x.yr[i]) ||
Data$inc.x.yr[i] == 0)) Data$age.inv[i]=1
  if(!is.na(Data$center.date[i]) && Data$center.date[i] > excl.yr &&
Data$center.date[i] < Data$inv.yr[i]) Data$age.inv[i]=0
}
cat("Age/Size Class determination complete", "\n")

### "UN-DECOMPOSE" DEAD TREES TO DETERMINE DEATH DATES ###
cat("Step 4. Estimate Death Dates of Dead Trees", "\n")
cat("Initialize death date at inventory year for all trees", "\n")
Data$death.yr <- Data$inv.yr
pctile = 0.5 # Set decomposition percentile
cat("Decomposition percentile =", pctile, "\n")

for(i in 1:nrow(Data)) {
# Condition 3 assumed to have died in inventory year
  if(Data$cond[i] == 4) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1.2)) }
  if(Data$cond[i] == 5) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1.2)) + ((log(pctile)-log(1))/log(1.15)) }
  if(Data$cond[i] == 6) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1.2)) + ((log(pctile)-log(1))/log(1.15)) + ((log(pctile)-
log(1))/log(1+(1/(2*(Data$dbh.inv[i]/2.54)))))) }
  if(Data$cond[i] == 7) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1.2)) + ((log(pctile)-log(1))/log(1.15)) + 2*((log(pctile)-
log(1))/log(1+(1/(2*(Data$dbh.inv[i]/2.54)))))) }
  if(Data$cond[i] == 8) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1+(1/(2*(Data$dbh.inv[i]/2.54)))))) }
  if(Data$cond[i] == 9) {
    if(!is.na(Data$cut.date[i])) { Data$death.yr[i] = Data$cut.date[i] }
    else {
      if(!is.na(Data$orig.tree.num[i])) { Data$death.yr[i] = 1940 }
      else { Data$death.yr[i] = 1980 } } }
  if(Data$cond[i] == 10) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-

```



```

log(1)/log(1.2)) + ((log(pctile)-log(1))/log(1.15)) + 2*((log(pctile)-
log(1))/log(1+(1/(2*(Data$dbh.inv[i]/2.54)))))) }
  if(Data$cond[i] == 11) { Data$death.yr[i] = Data$inv.yr[i] + ((log(pctile)-
log(1))/log(1.2)) + ((log(pctile)-log(1))/log(1.15)) + 2*((log(pctile)-
log(1))/log(1+(1/(2*(Data$dbh.inv[i]/2.54)))))) }
}

Data$death.yr <- as.integer(Data$death.yr)
cat("Determination of Death Dates Complete", "\n")

### UN-GROW ALL TREES TO YEAR X ###
cat("Step 5. Un-Grow Trees to Year X", "\n")

for(i in 1:nrow(Data)) {
  if(!is.na(Data$center.date[i]) & Data$center.date[i] > x.yr) |
(Data$death.yr[i] < x.yr)) {
    Data$dbh.x[i] = 0
  } # Trees obviously not present in Year X
  if(Data$spp[i] == 'PIPO') {
    if(!is.na(Data$inc.x.yr[i])) {
      if(!is.na(Data$inc.pith[i])) { # Proportional reconstruction method if
increment to pith measured
        prop = (Data$inc.pith[i] - Data$inc.x.yr[i]) / Data$inc.pith[i]
        Data$dsh.x[i] = Data$dsh.inv[i] * prop
      }
    } else { # For trees without increment to pith measured
      if(Data$age.inv[i] == 1) { # Yellow pine bark thickness equations
(Myers 1963)
        Data$dsh.x[i] = 1.0524 * (((0.9498 * Data$dsh.inv[i]) - 2.8491) -
(2 * Data$inc.x.yr[i])) - 3.0272
      }
      else { # Blackjack bark thickness equations (Myers 1963)
        Data$dsh.x[i] = 1.0698 * (((0.9344 * Data$dsh.inv[i]) - 3.0284) -
(2 * Data$inc.x.yr[i])) - 3.2614
      }
    }
    Data$dbh.x[i] = (Data$dsh.x[i] - 1.6643787) / 1.0632921
    # Formula from Woolsey plots; r^2 = 0.994; N = 8375
    if(Data$dbh.x[i] < 0) { Data$dbh.x[i] == 0 }
  }
  else { # For trees without increment data
    if(Data$age.inv[i] == 1) { # Yellow pine equation from Woolsey plots;
r^2 = 0.6772; N = 2014
      Data$dbh.x[i] = sqrt(Data$dbh.inv[i]^2 - (4/pi * exp(-3.21600 +
1.54140 * log(Data$dbh.inv[i])) * (Data$death.yr[i] - x.yr)))
      if(is.nan(Data$dbh.x[i])) { Data$dbh.x[i] = 0 }
    }
    else { # Blackjack equation from Woolsey plots; r^2 = 0.9612; N = 3008
      Data$dbh.x[i] = sqrt(Data$dbh.inv[i]^2 - (4/pi * exp(-3.718047 +
1.735790 * log(Data$dbh.inv[i])) * (Data$death.yr[i] - x.yr)))
      if(is.nan(Data$dbh.x[i])) { Data$dbh.x[i] = 0 }
    }
  }
}
  if(Data$spp[i] == 'QUGA') {
    if(!is.na(Data$inc.x.yr[i])) { # For trees with increment data
# NOTE - All formulas here assume 5% bark thickness for QUGA (no literature)

```

```

# TODO - Develop QUGA bark thickness equations
  if(!is.na(Data$inc.pith[i])) { # Proportional reconstruction method if
increment to pith measured
    prop = (Data$inc.pith[i] - Data$inc.x.yr[i]) / Data$inc.pith[i]
    Data$dsh.x[i] = Data$dsh.inv[i] * prop
  }
  else { # For trees without increment to pith measured
    Data$dsh.x[i] = ((0.95 * Data$dsh.inv[i]) - (2 * Data$inc.x.yr[i])) /
0.95
  }
  Data$dbh.x[i] = (Data$dsh.x[i] - 1.092945) / 1.033582
  # Formula from Woolsey plots; r^2 = 0.988; N = 1400
  if(Data$dbh.x[i] < 0) { Data$dbh.x[i] = 0 }
}
  else { # For trees without increment data
    if(Data$age.inv[i] == 1) { # Large/old tree equation from Woolsey
plots; r^2 = 0.5828; N = 143
      Data$dbh.x[i] = sqrt(Data$dbh.inv[i]^2 - (4/pi * exp(-3.09044 +
1.38412 * log(Data$dbh.inv[i])) * (Data$death.yr[i] - x.yr)))
      if(is.nan(Data$dbh.x[i])) { Data$dbh.x[i] = 0 }
    }
    else { # Small tree equation from Woolsey plots; r^2 = 0.8777; N = 206
      Data$dbh.x[i] = sqrt(Data$dbh.inv[i]^2 - (4/pi * exp(-3.16137 +
1.37009 * log(Data$dbh.inv[i])) * (Data$death.yr[i] - x.yr)))
      if(is.nan(Data$dbh.x[i])) { Data$dbh.x[i] = 0 }
    }
  }
}
}
# Other species omitted at present
cat("Un-Growth of Trees to Year X Complete", "\n")

### SUMMARIZE DATA ###
cat("Step 6. Summarize Data", "\n")

cat("Comparison of field Age Class calls with model age/size classes", "\n")
table(Data[c("age", "age.inv", "spp")]) # Creates a contingency table, by
species

hist(Data$dbh.x[Data$dbh.x > 0])

write.csv(Data, file = file.choose())
#NOTE - Remember to specify a ".csv" ending to file name, otherwise R will
specify no file extension!
cat("Data Saved to CSV file", "\n")

#detach(Data)
}
##### END OF RECON.MODEL FUNCTION #####

### CODE TO RUN RECON.MODEL FUNCTION ###
Data <- read.csv(file.choose(), header = TRUE, sep = ",", quote="\"",
dec=".", fill = TRUE, na.strings = "NA")
recon.model(Data, xyr=1909, exclyr=1876)

```