Swiss needle cast growth analysis, 2020

December 10, 2020

Doug Mainwaring
Gabriela Ritóková
Dave Shaw

Swiss needle cast growth analysis

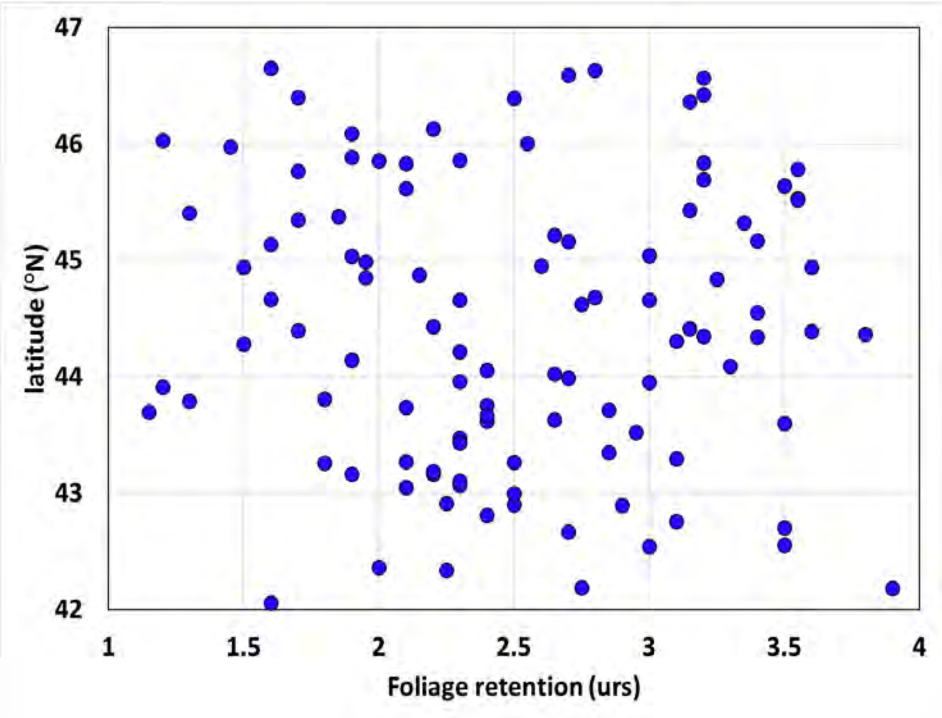
- Stand level growth analysis—How much growth loss?

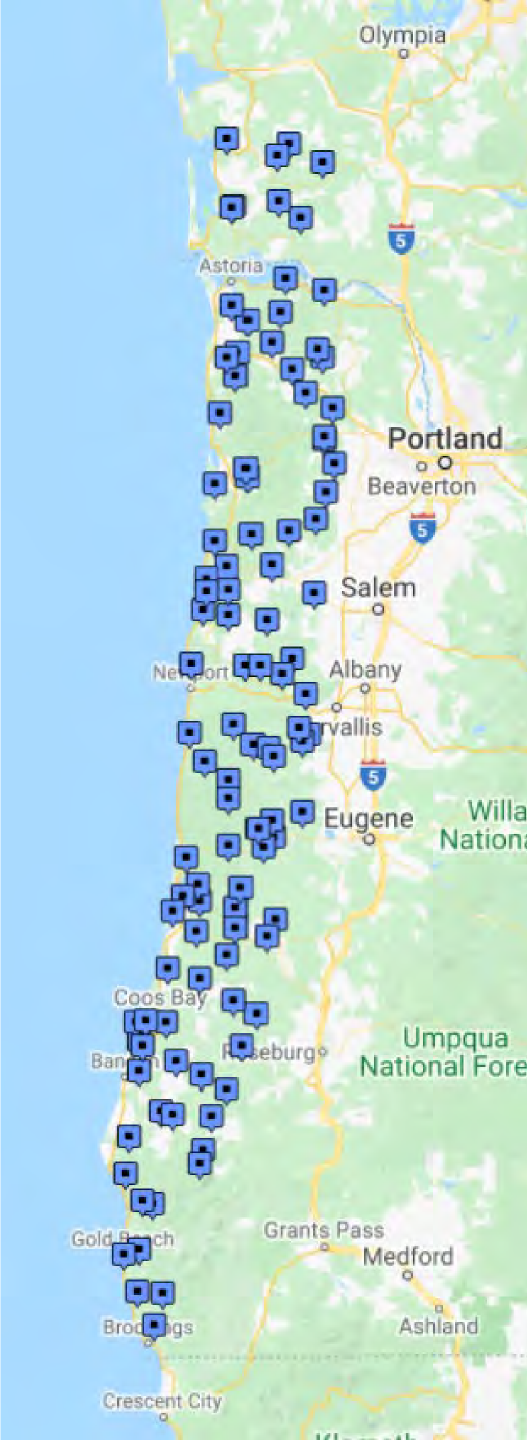
- Diameter and height growth modifiers for ORGANON

- Addition of SNC taper modifier to ORGANON

SNCC Research Plot Network

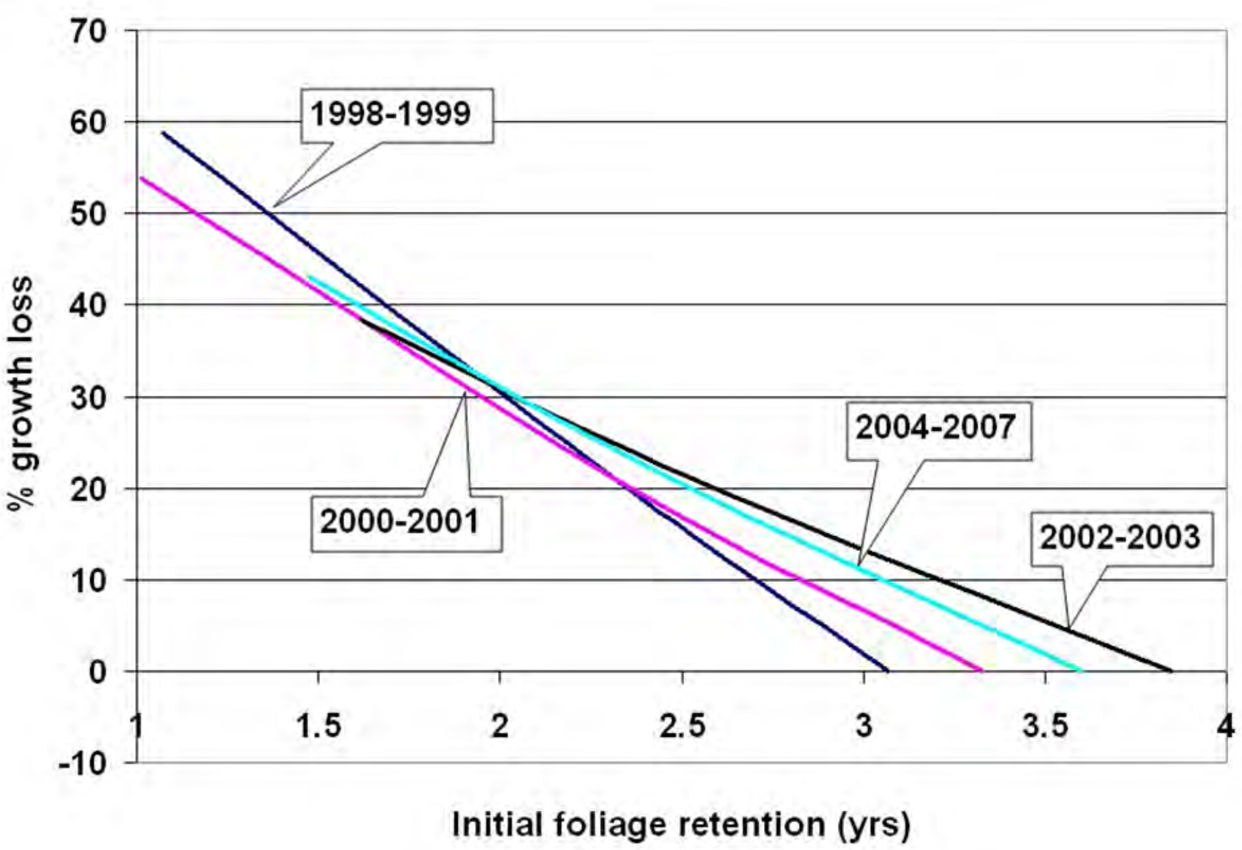
- New effort uses 102 plots from new SNCC plot network (2013-2018)
    - Has greater geographic range (than GIS)
    - Indicative of current stands
    - Doesn't include stunted stands that will never become merchantable



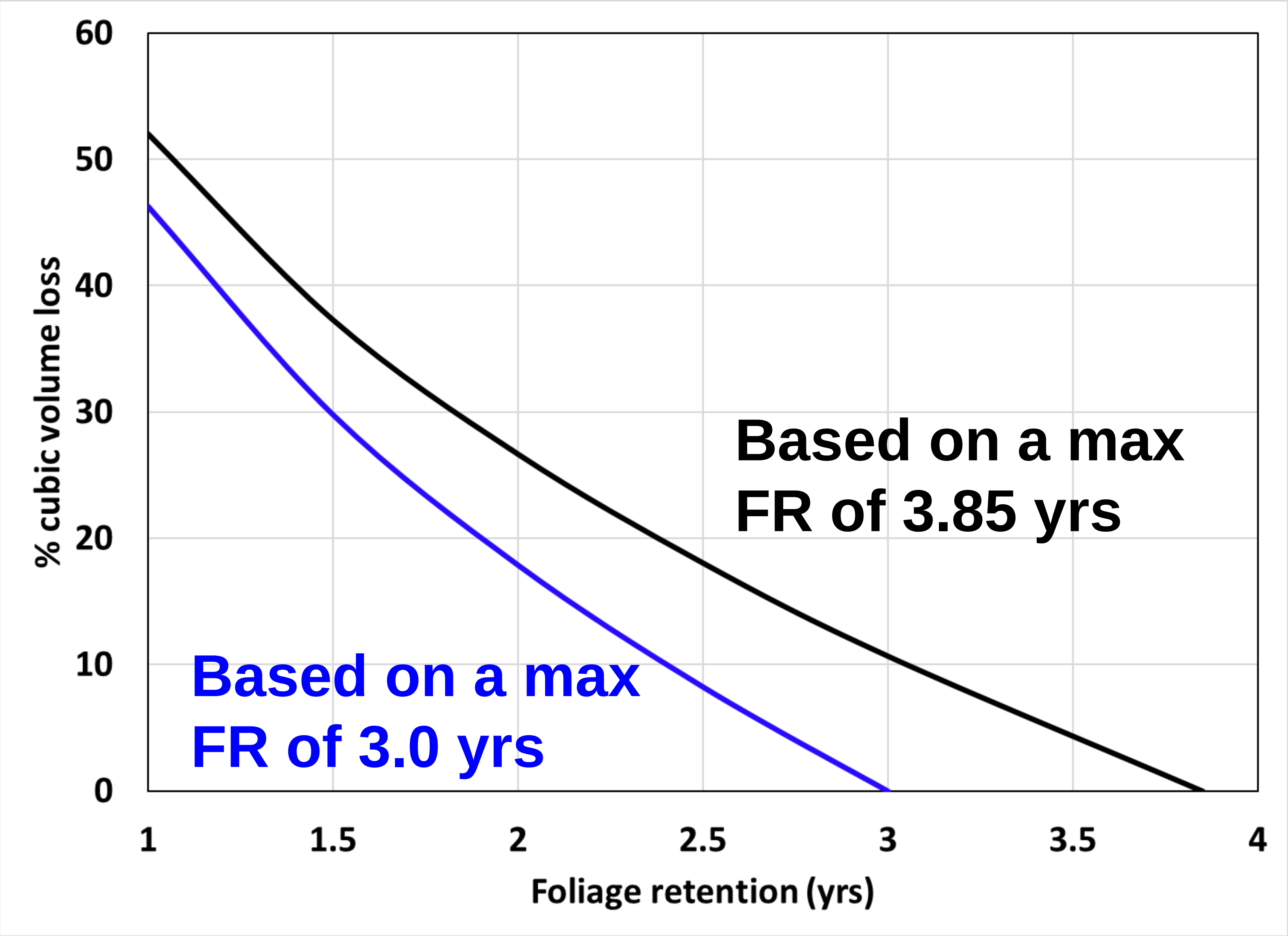


Stand level cubic volume growth loss, 1998-2008

- Growth loss is expressed relative to maximum foliage retention of plots within each growth period



Stand level cubic volume growth loss, 1998-2008 Combined, from 2011 publication



Based on a max FR of 3.85 yrs

Based on a max FR of 3.0 yrs

Stand level cubic volume growth, 2013-2019

$$CFV\_PAI = a \cdot (BA_{df}^{b}) \cdot \exp(c \cdot BA_{ndf}) \cdot Si_{adj}^{d} \cdot (1-\exp(e+f \cdot FR^{3}))$$

CFV estimated using Bruce and Demars vol eqn.
Doesn't account for taper differences

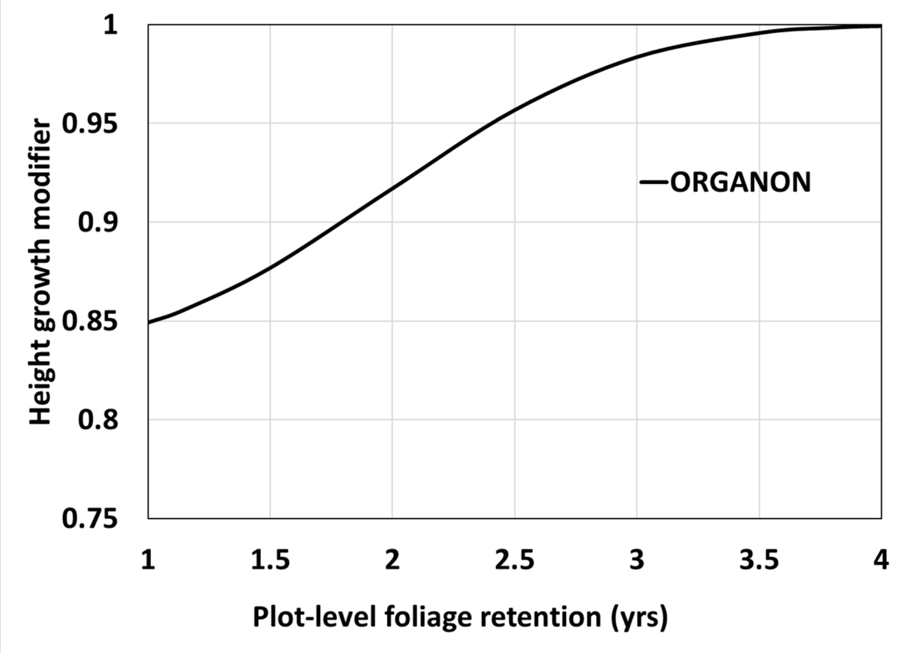
Periodic annual cubic volume growth dependent on:

- initial DF basal area (+)
- basal area in other species (-)
- Douglas-fir site index (+)
- Douglas-fir foliage retention (+)

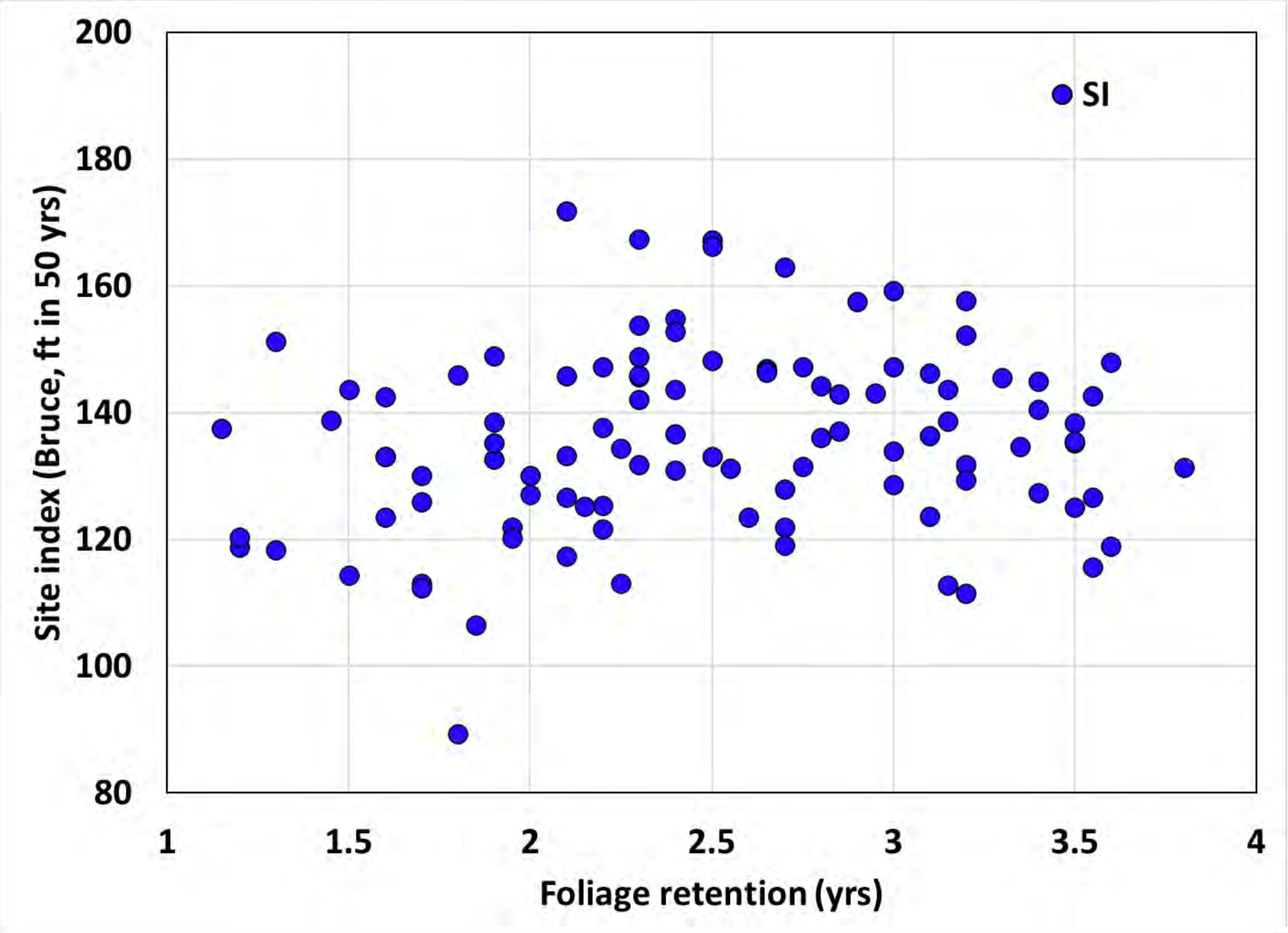
The site index problem

Dominant trees in infected stands have lost height increment due to SNC

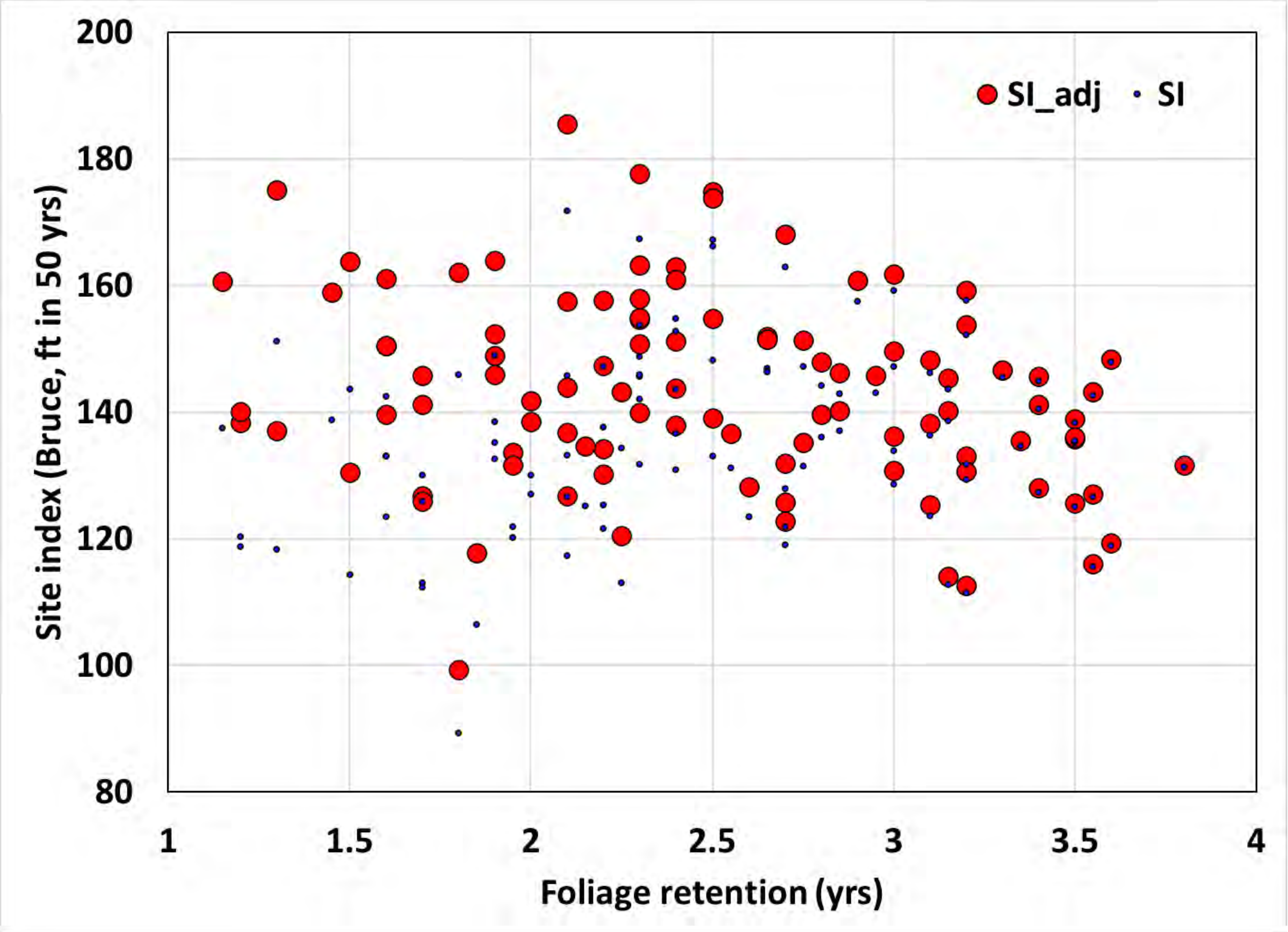
- Calculated the Bruce (1981) site index for each plot
  - SI= f(Ht_{40}, age)
- Adjusted the SI using the 2014 Hann SNC ORGANON height modifier
  - Adjusted SI =
  - SI_A= f(Ht_{40}/(SNC Htmod), age)
  - $SI_A = SI/(1\text{-}\exp(b_0+b_1 \cdot FR^3))$



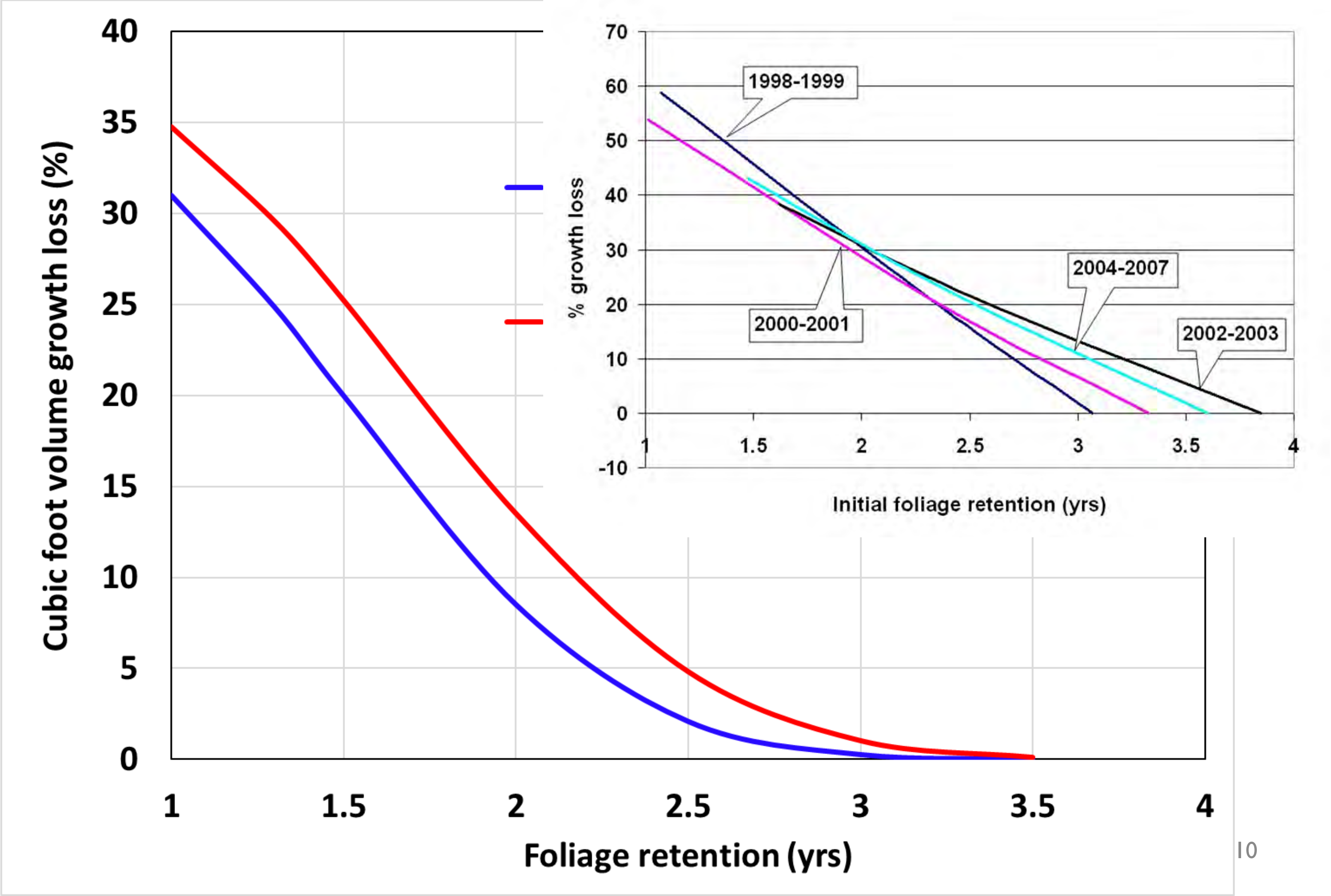
Site index (from height-age pairs) vs. Folret, new network



Site index (from height-age pairs) vs. Folret, new network, adjusted



Stand level cubic volume growth loss, 2013-2019



Why is the growth loss lower? The theory…

- GIS plot network represented the 1998 population.
- New plot network represents the current population
- Many of the worst stands that were sampled in 1998 are no longer present on the landscape. Those stands have been harvested and not replanted to Douglas-fir.
- Worst performing plots that resulted in high growth loss estimates are gone.
- If zones where those plots existed were replanted to DF, growth loss estimates would likely go back up.

Modifier equations for ORGANON

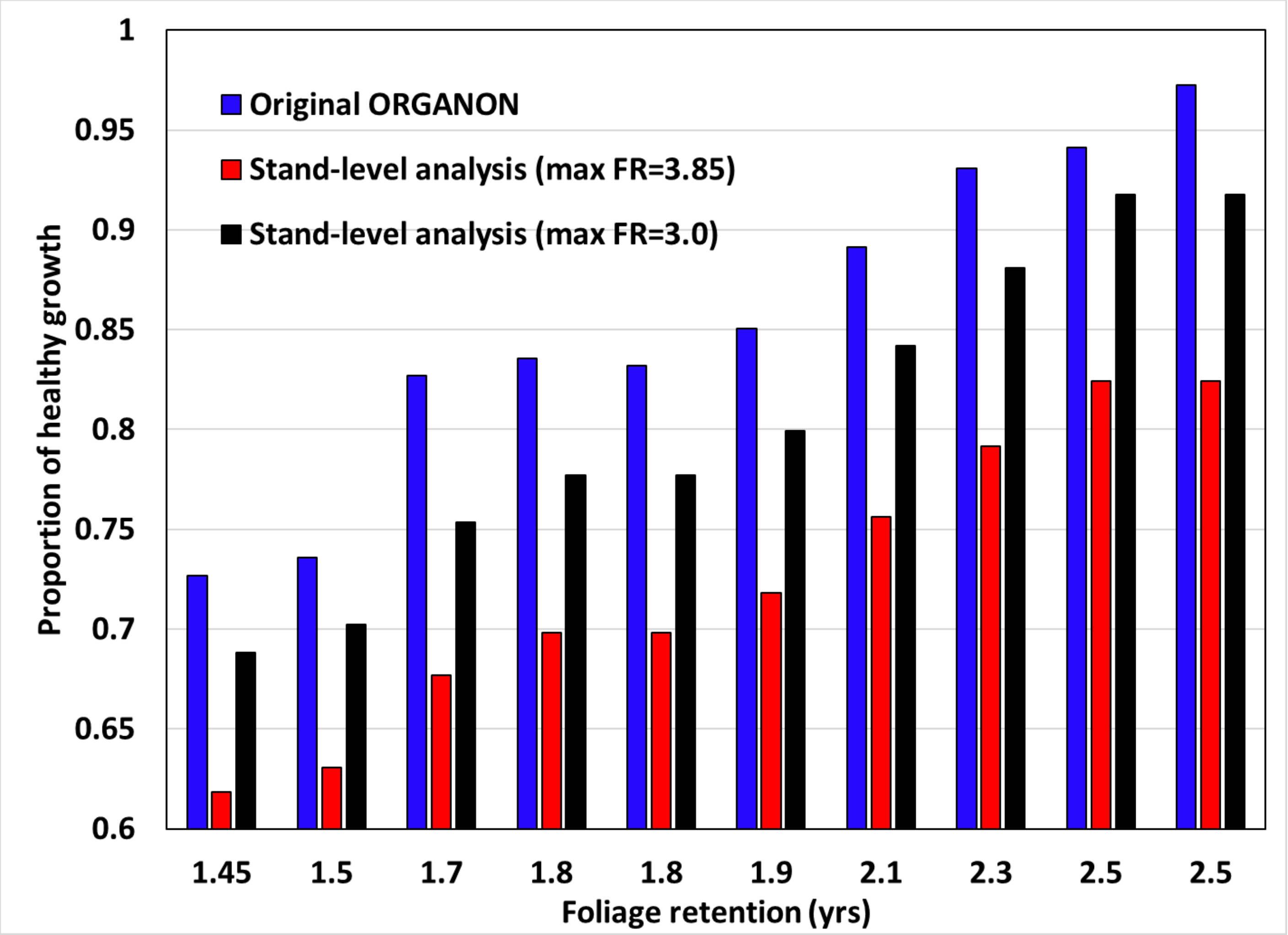
- Numerous efforts made to produce equations which would adjust ORGANON diameter and height growth for SNC infection

- There has been a continuing problem with a difference between stand level cubic volume loss and ORGANON predictions of loss from treelist projections

- ORGANON has predicted less volume growth loss than the stand level analysis does

Original modifier equations for ORGANON

- **Based on a 20-yr projection of 10-20 yr old stands**



Dbh and height increment: Modifier Equations

Estimate modifiers for both ΔD and ΔH:

$\Delta D_{\text{infected}} = \text{MOD} \cdot \Delta D_{\text{ORGANON}}$

$\Delta H_{\text{infected}} = \text{MOD} \cdot \Delta H_{\text{ORGANON}}$

where

MOD = Measured (infected) growth/Predicted growth

$= 1 - \exp(a_1 + a_2 \cdot FR^X)$

Calibration of Modifier equations

- For “healthy” plots with FR ≥ 3 yrs (n=30):

- Estimated calibration factor for each growth period (2013, 2014, 2015)

  $MG = cal \cdot OG$

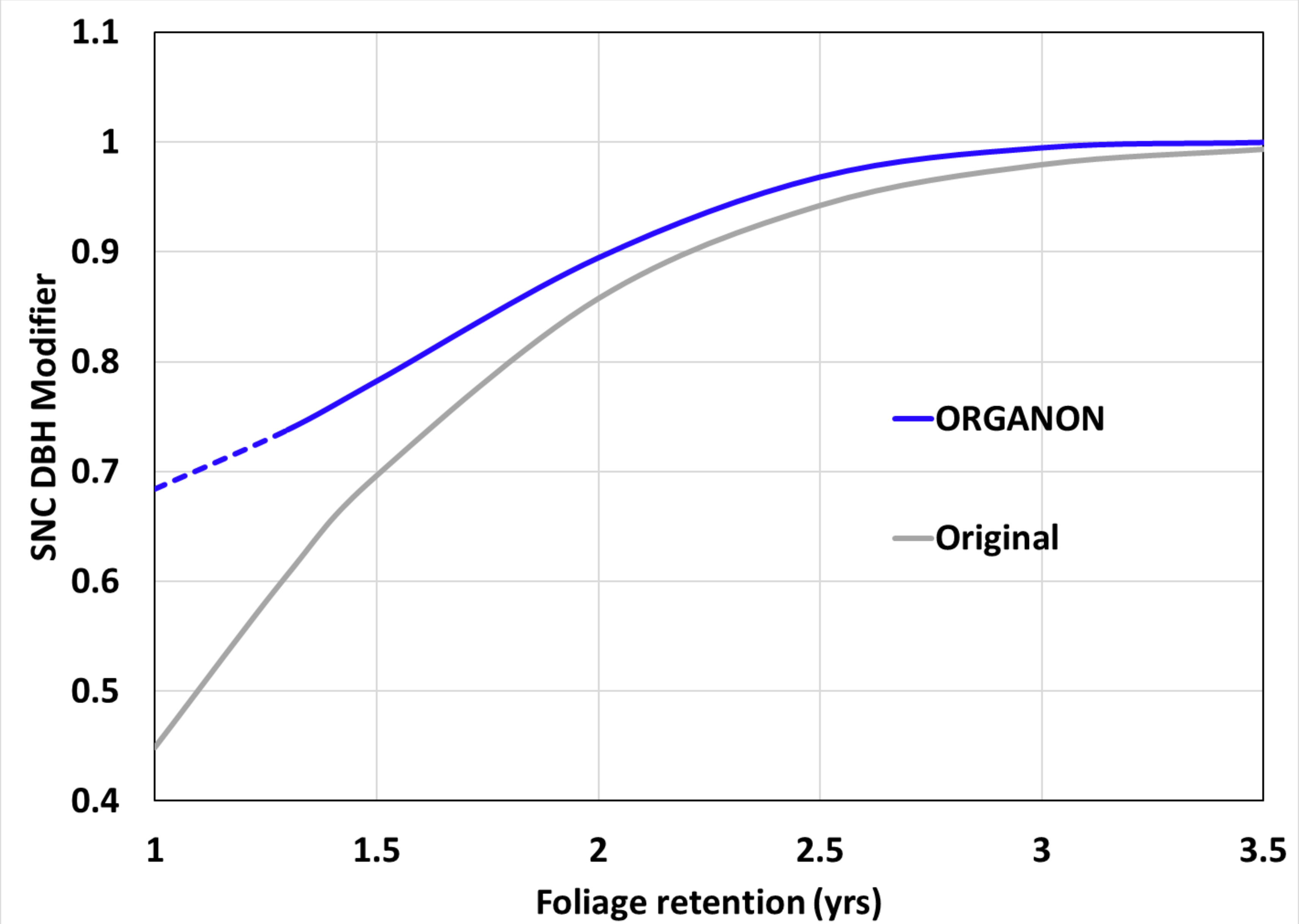
  where MG=measured dbh or ht. growth
  OG=ORGANON estimated dbh or ht. growth

- For “infected” plots with FR<3 yrs (n=72):

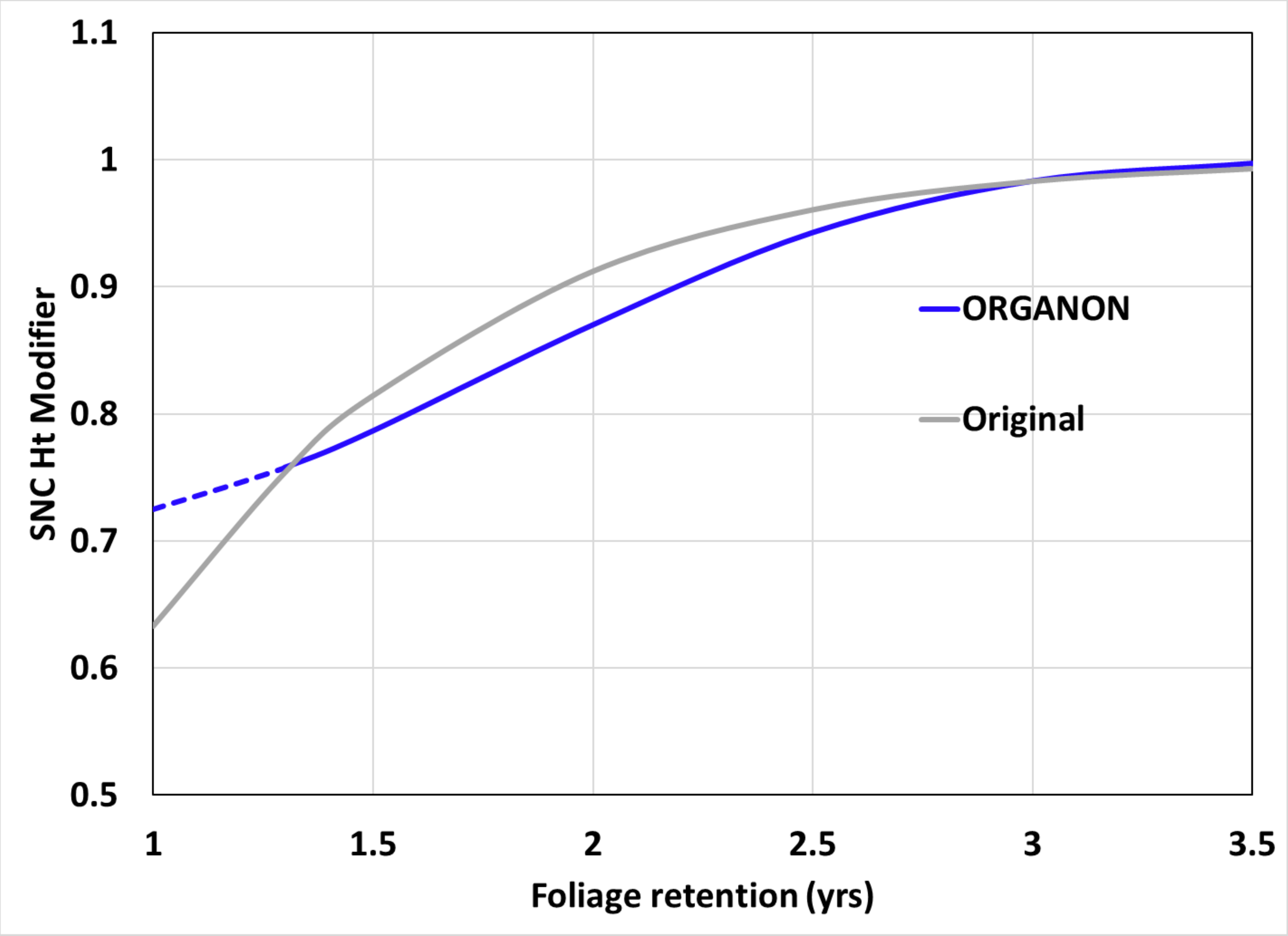
  Fit the following equation:

  $MG = cal \cdot OG \cdot (1 - \exp(a + b \cdot FR^3)$

Dbh growth modifier



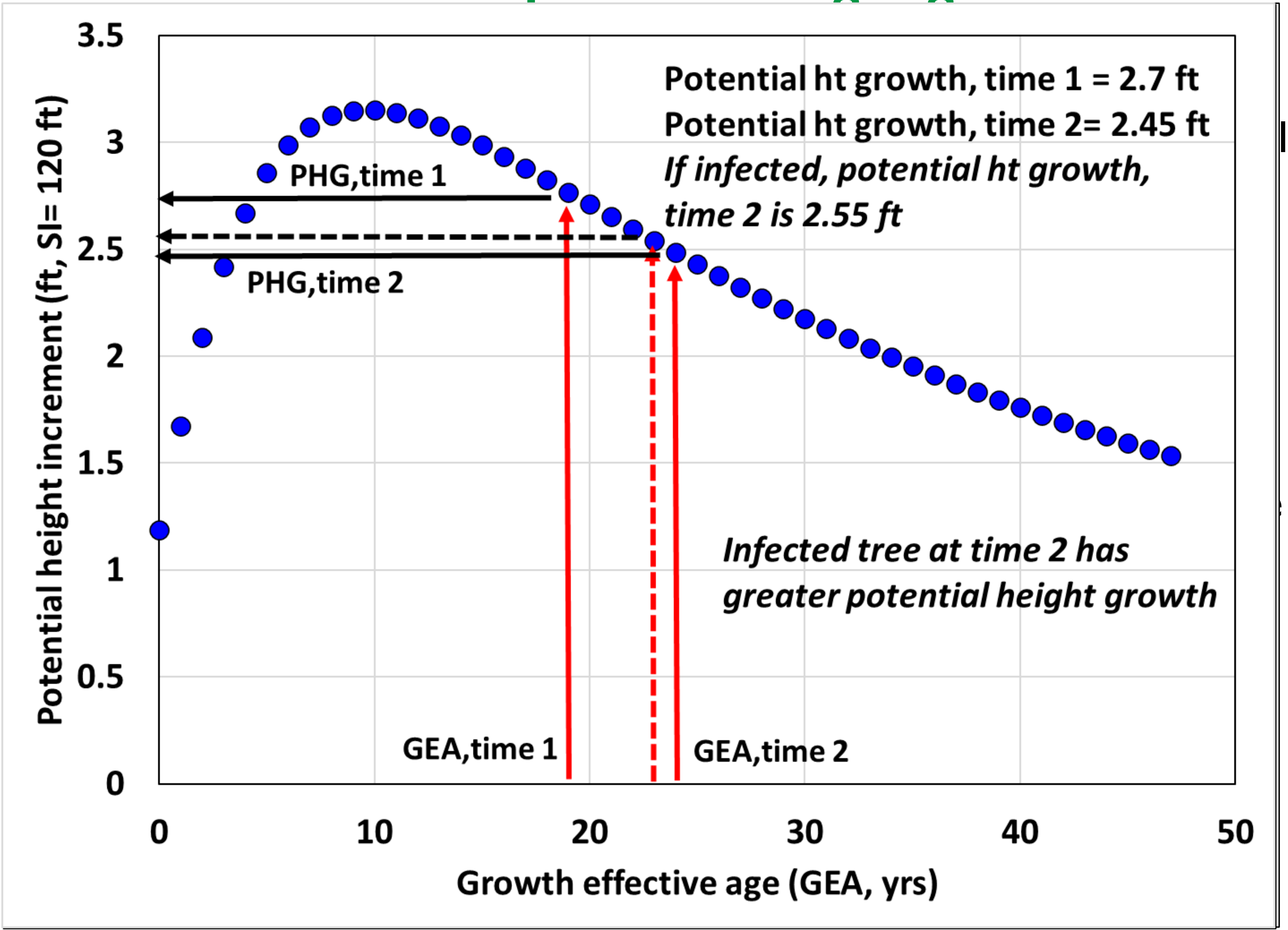
Height growth modifier



Calculation of potential height growth

- $HG_{ORGANON}=PHG_{Dom} \cdot f(CCH,CR)$
- In a simulation, height growth for each tree is based on it's potential height growth, which is based on it's growth effective age (GEA)
- For modeling data of a single period, GEA and potential height growth of a measured tree is the same whether infected or not.
- During multiple cycles of a simulation, GEA of an SNC-stunted tree falls further (and further) behind that of a healthy tree, and potential height growth for each cycle becomes larger and larger.
- When SNC modifier gets applied to a PHG that is becoming relatively larger with each cycle, the "growth loss" from SNC disappears

Calculation of potential height growth



Calculation of potential height growth

- $HG_{ORGANON} = PHG_{Dom} \cdot f(CCH, CR)$
- In a simulation, height growth for each tree is based on it's potential height growth, which is based on it's growth effective age (GEA)
- For modeling data of a single period, GEA and potential height growth of a measured tree is the same whether infected or not.
- During multiple cycles of a simulation, GEA of an SNC-stunted tree falls further (and further) behind that of a healthy tree, and potential height growth for each cycle becomes larger and larger.
- When SNC modifier gets applied to a PHG that is becoming relatively larger with each cycle, the "growth loss" from SNC disappears

Solution to calculation of PHG within ORGANON

- PHG of trees in an infected stand was assumed to be equal to PHG of the trees as if the stand wasn’t infected.
- ORGANON FORTRAN source code has been altered to maintain two separate height and height growth variables:
    - 1) Uninfected height and height growth for calculation of GEA and potential height growth
    - 2) Infected (modified) height and height growth for producing correct values for HT, HCB, HT40, CCH

Testing stand level output from ORGANON

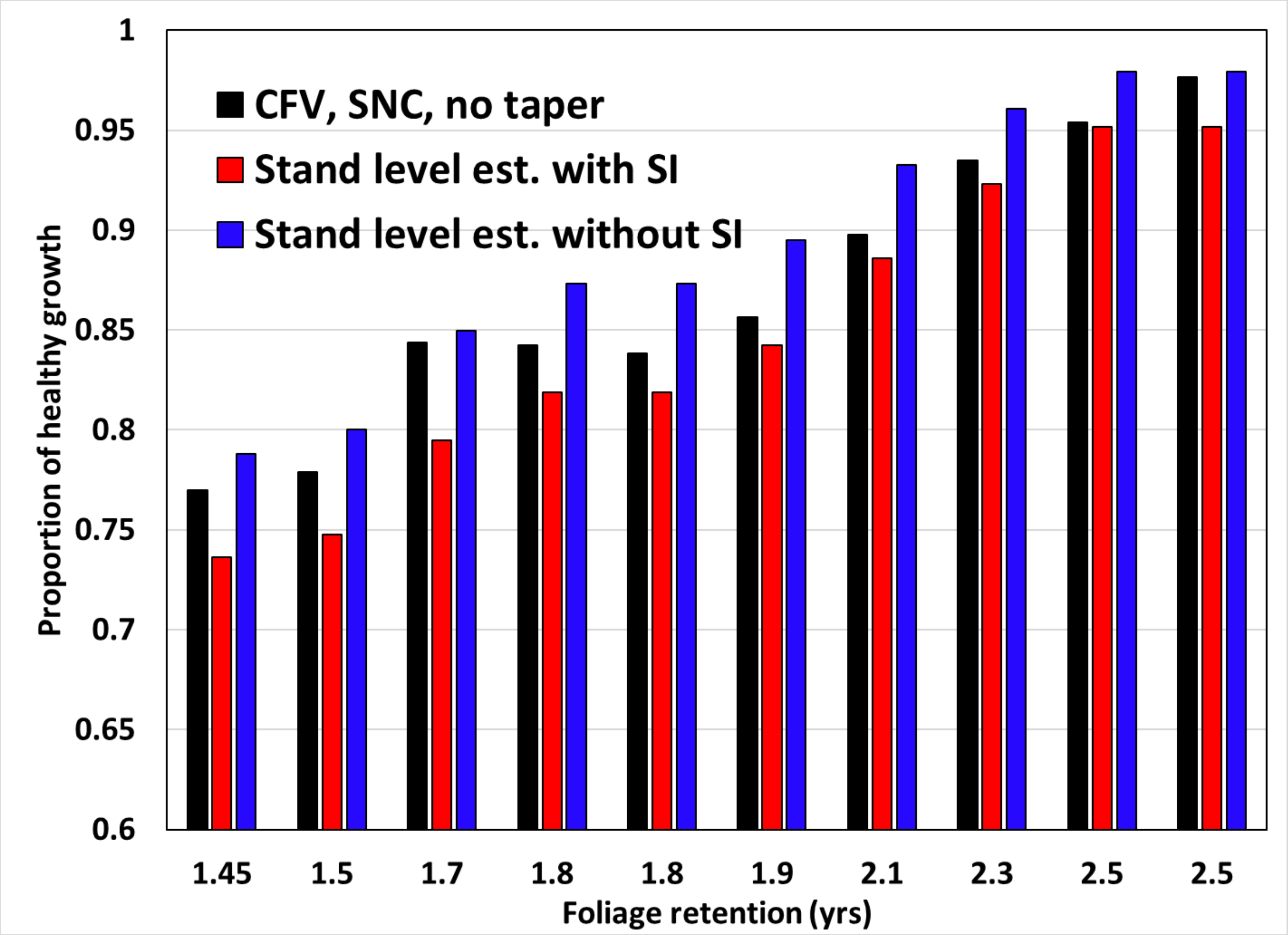
- Chose 10 stands from stand-level modeling database with the smallest residuals (initial ages 13-22 yrs;   FR 1.45-2.5 yrs)

- Projected initial measurement treelists for 20 yrs with 1) measured foliage retention; and 2) assumption of no SNC (SNC option turned off)

- Compared stand CFV PAI over 20 year period between options 1) and 2) using a) new dlls; and b) old dlls.

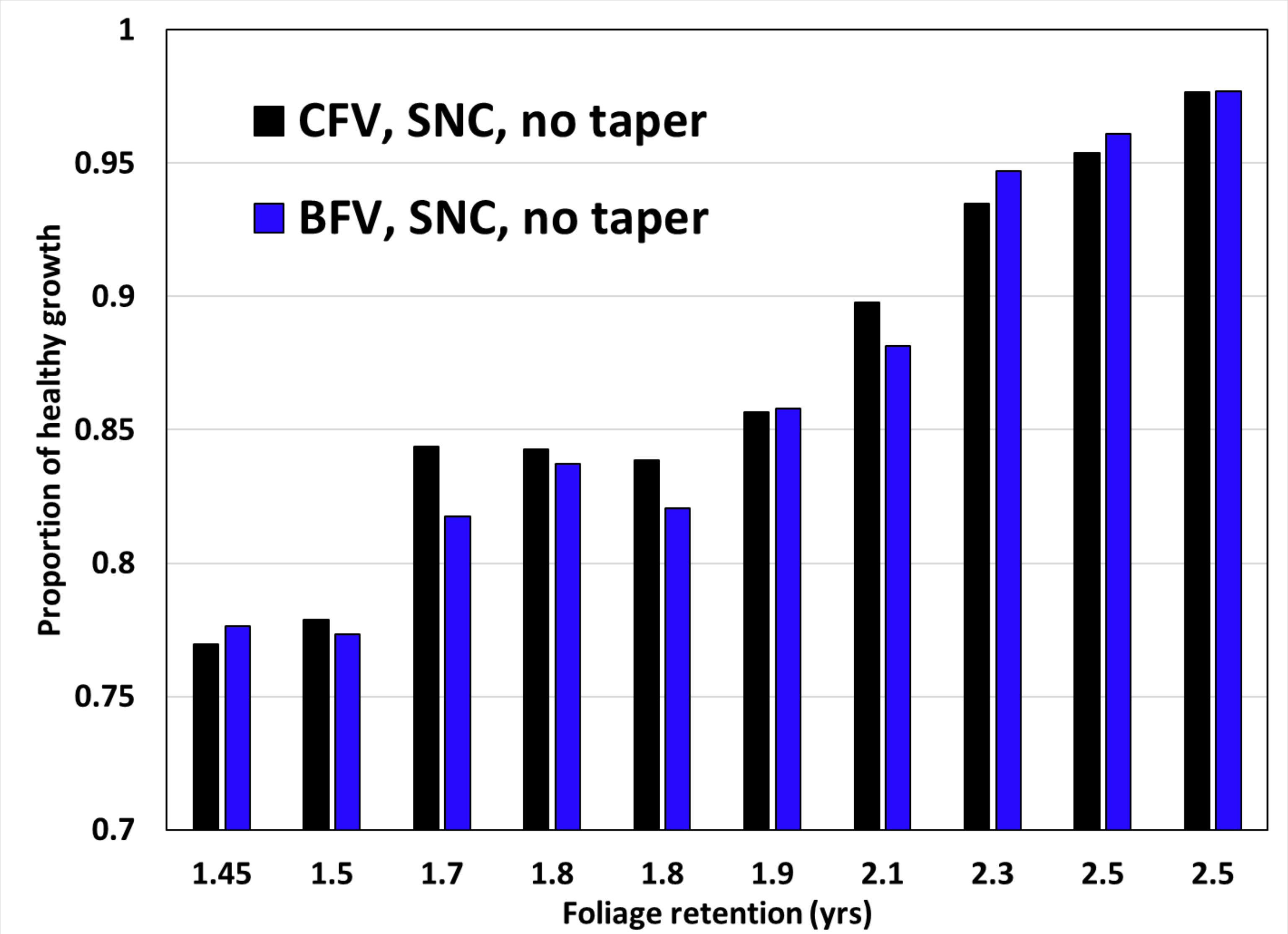
ORGANON, stand level output

- ORGANON CFV output (without applying taper differences) similar to average of stand level estimate with and without SI



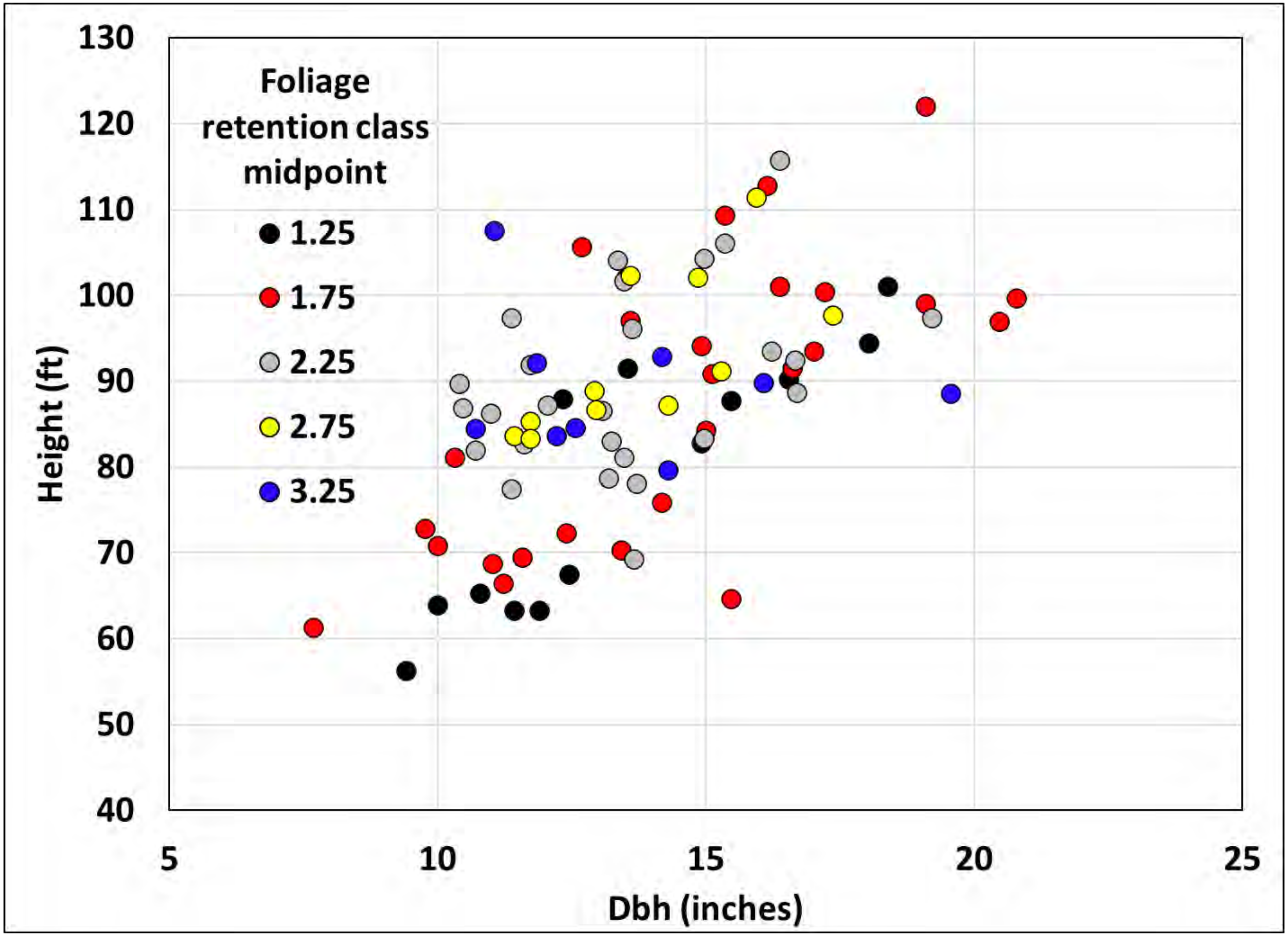
ORGANON, stand level output

- ORGANON CFV and BFV loss approximately equal



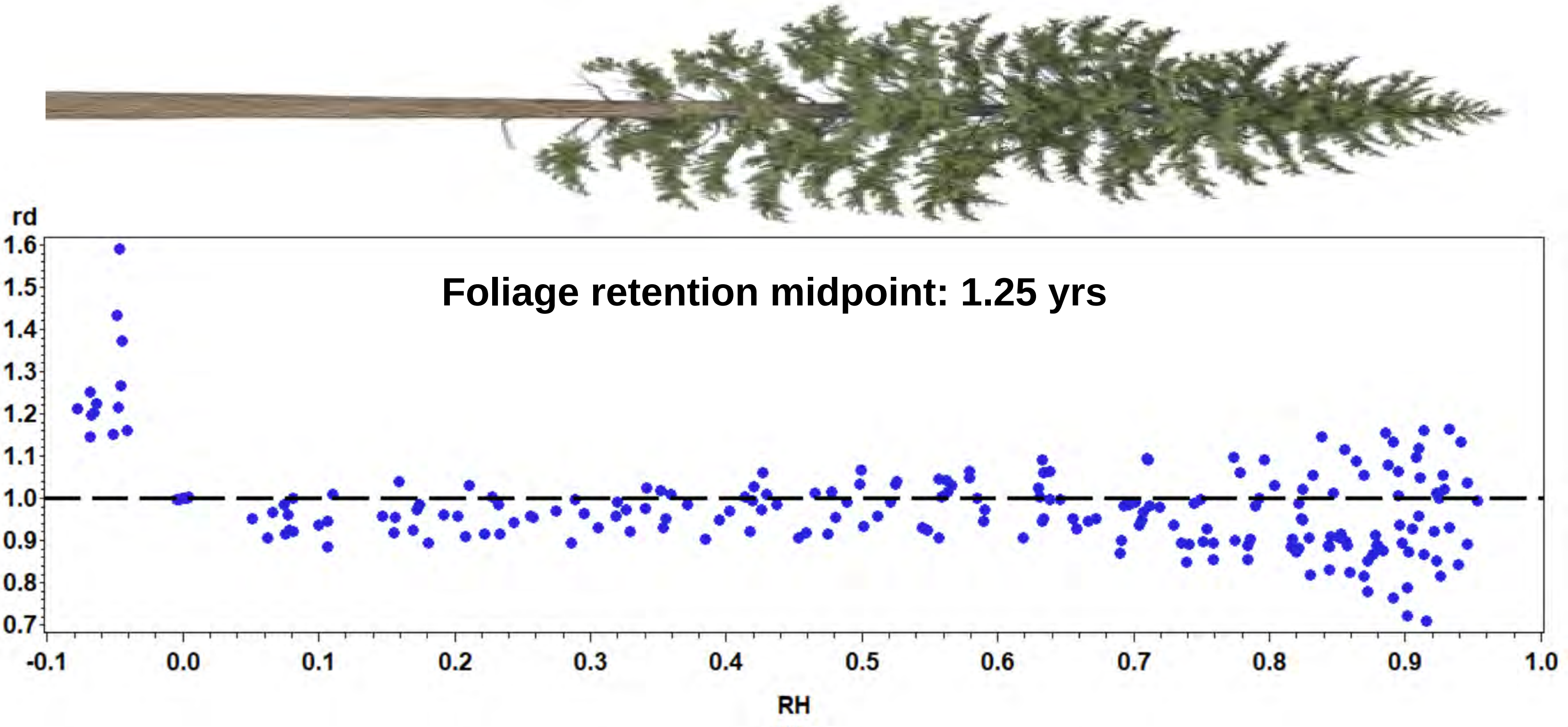
Effect of SNC on taper

- 86 trees from 18 GIS plots sampled for stem taper (disks = 1490)
- Sampled in 2015



SNC Taper results: incorporation into ORGANON

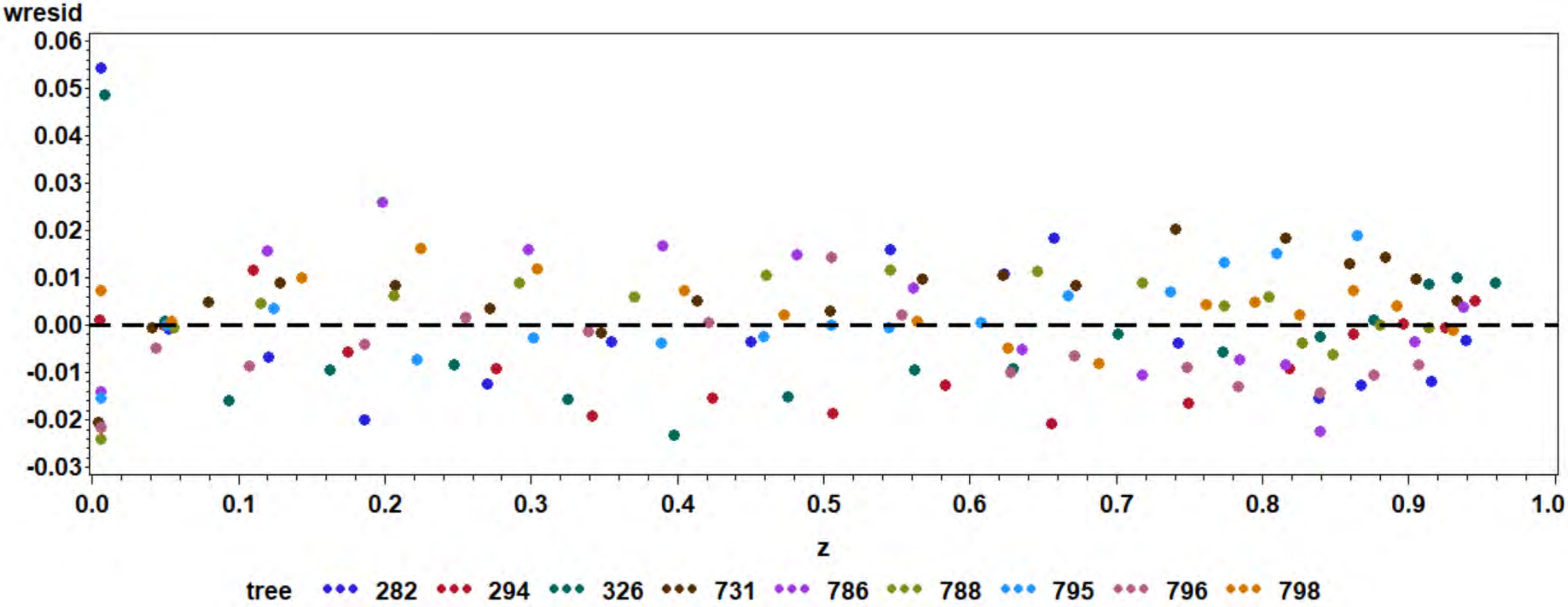
- ORGANON currently uses Walters and Hann segmented polynomial taper equation
- Walters/Hann doesn't fit the healthy trees of the SNC taper dataset well



SNC Taper results: incorporation into ORGANON

- Used Kozak model form to estimate taper of healthy trees within SNC taper dataset (ntrees = 9; ndisks=144)
- "healthy tree equation"

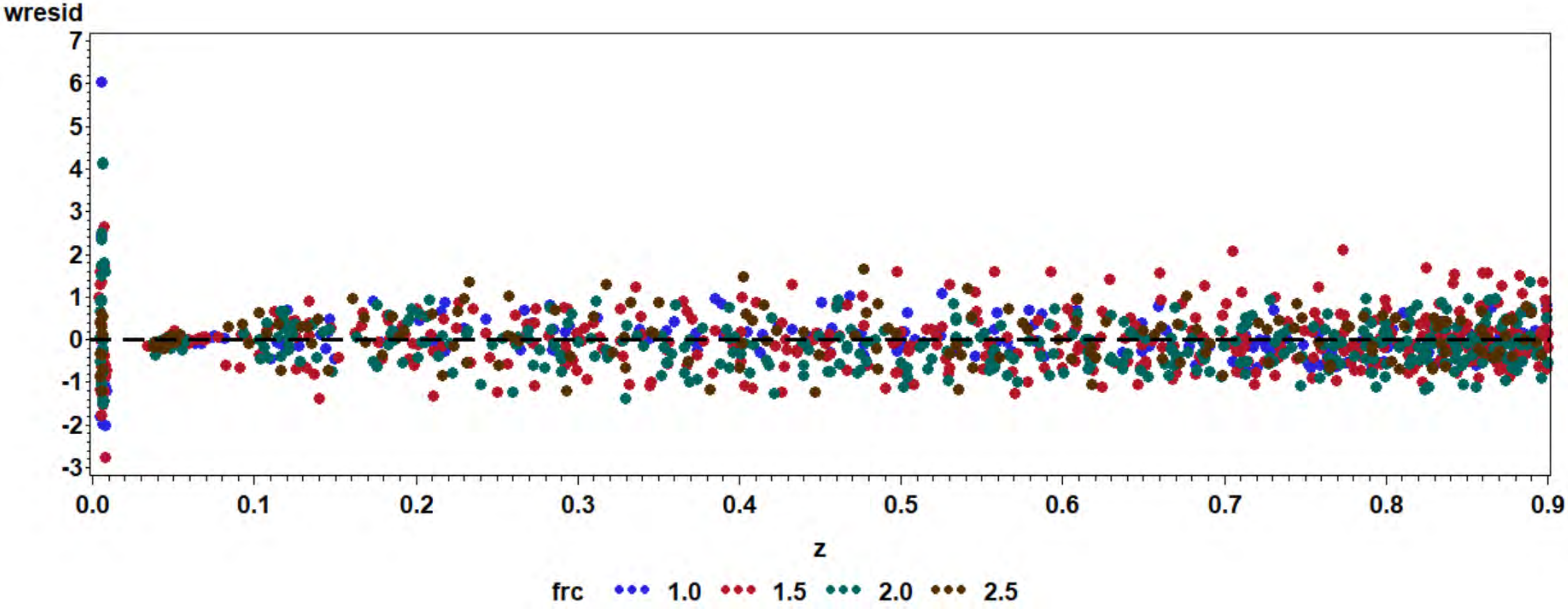
$$y=x^\wedge(b_0+b_1\cdot z^2+b_2\cdot z^{0.5}+b_3\cdot \exp(z)+b_4\cdot dbh/ht)$$

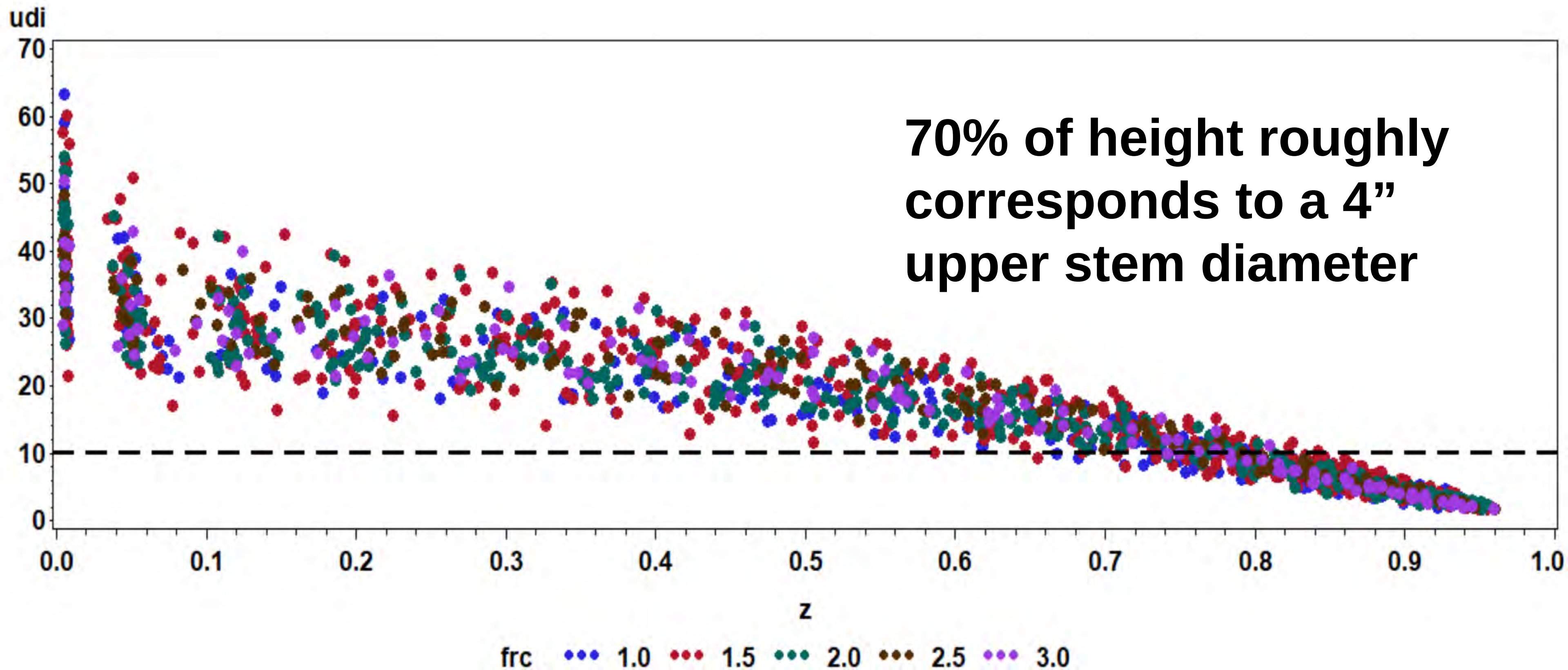


SNC Taper results: incorporation into ORGANON

- Used Kozak model form to estimate ratio of upper stem DIB of infected trees to that predicted using equation for healthy trees

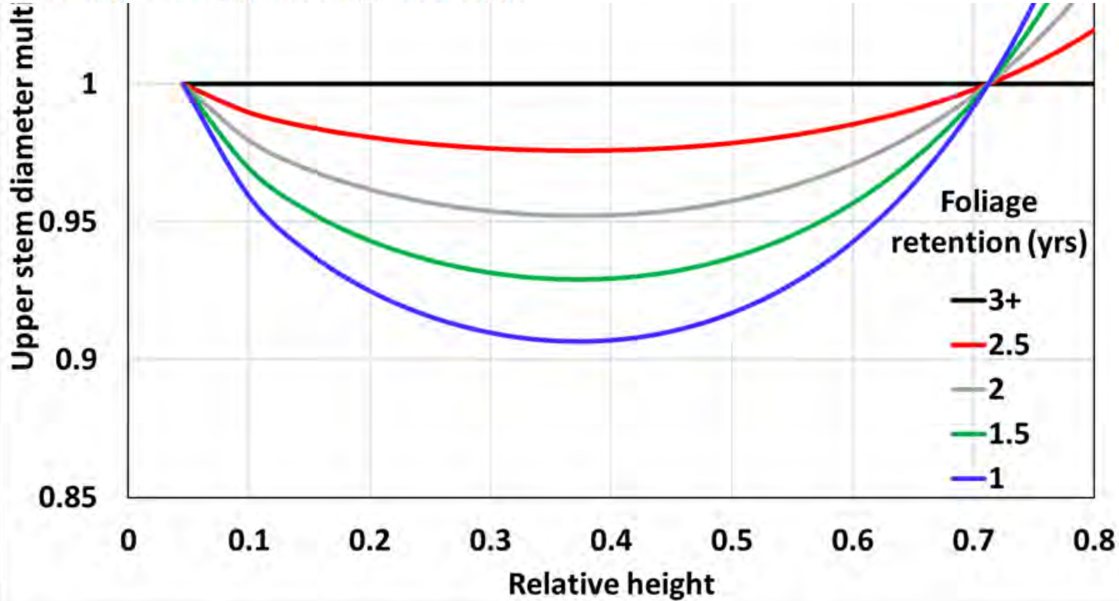
- $\text{SNC}_{\text{MOD}}=\text{DIB}_{\text{infected, measured}}/\text{DIB}_{\text{infected, estimated with healthy tree eq.}}$





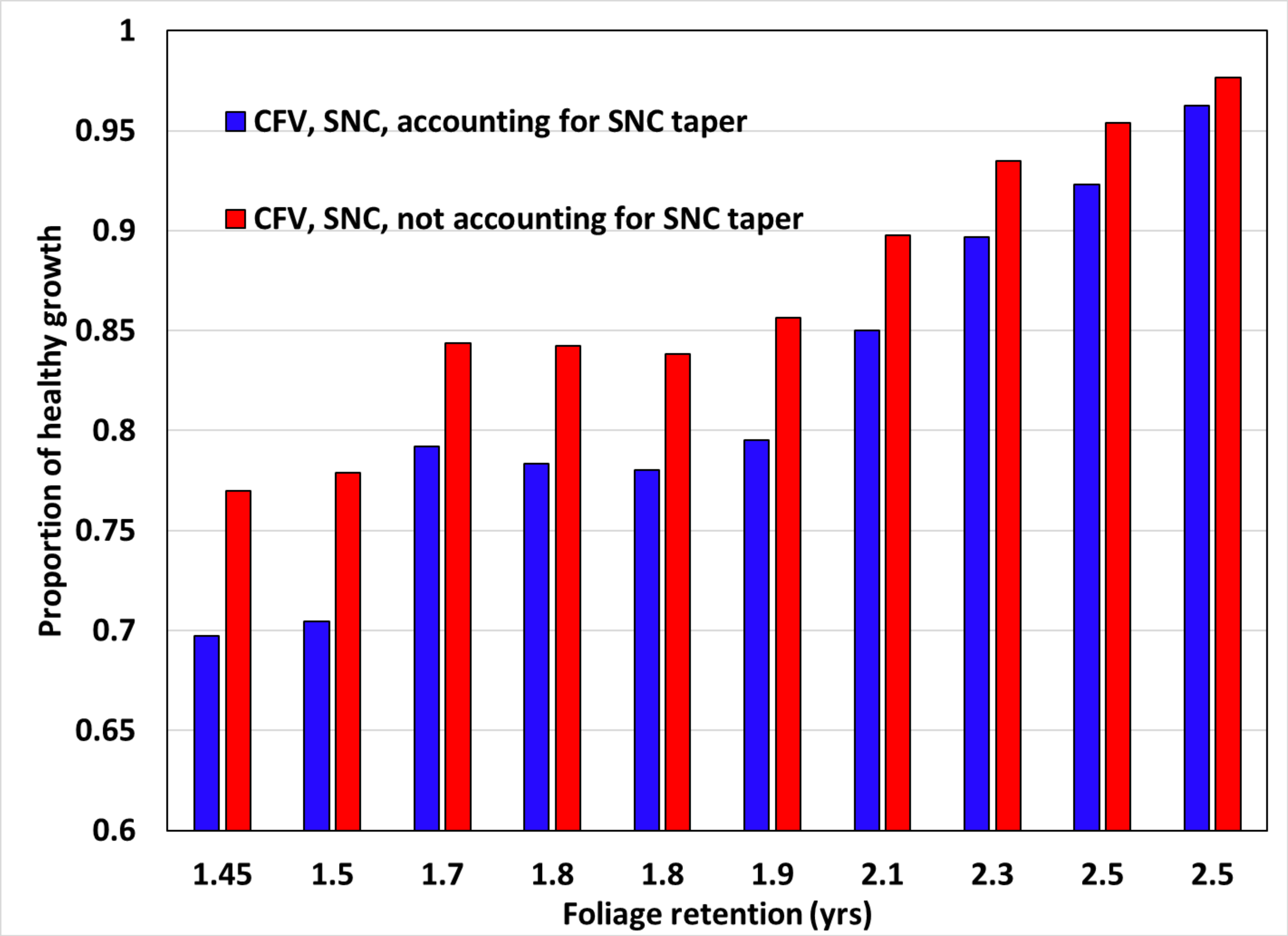
70% of height roughly corresponds to a 4” upper stem diameter

into ORGVOL and ORGLOG dlls



Vol. estimates with and without accounting for taper

- **Using same 10 test stands…**



Thanks