

2021.8.25.6741

1 APSIM Description

The Agricultural Production Systems sIMulator (APSIM) is a farming systems modelling framework that is being actively developed by the APSIM Initiative.

It is comprised of

1. a set of biophysical models that capture the science and management of the system being modelled,
2. a software framework that allows these models to be coupled together to facilitate data exchange between the models,
3. a set of input models that capture soil characteristics, climate variables, genotype information, field management etc,
4. a community of developers and users who work together, to share ideas, data and source code,
5. a data platform to enable this sharing and
6. a user interface to make it accessible to a broad range of users.

The literature contains numerous papers outlining the many uses of APSIM applied to diverse problem domains. In particular, [Holzworth et al., 2014](#); [Keating et al., 2003](#); [McCown et al., 1996](#); [McCown et al., 1995](#) have described earlier versions of APSIM in detail, outlining the key APSIM crop and soil process models and presented some examples of the capabilities of APSIM.

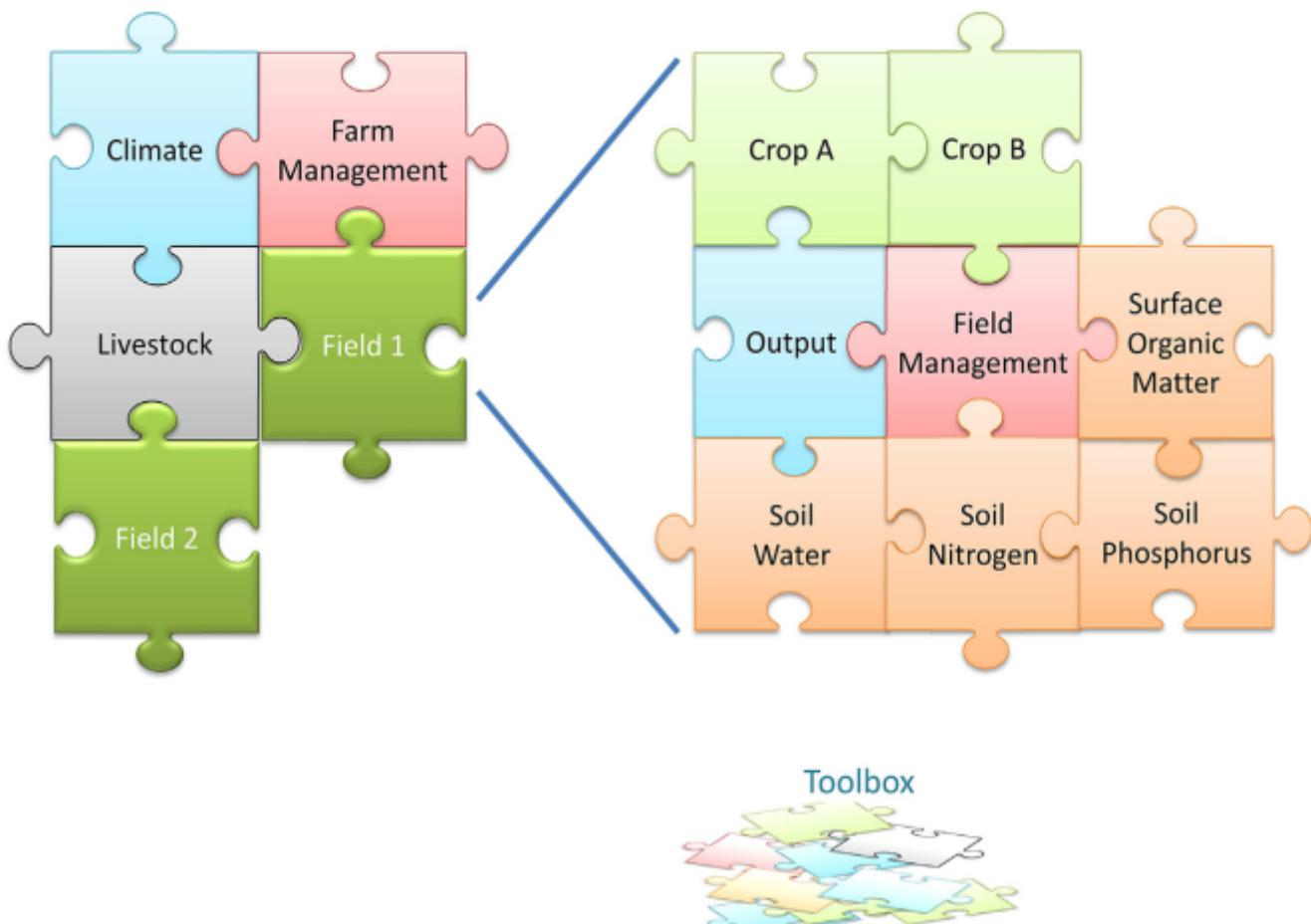


Figure 2: This conceptual representation of an APSIM simulation shows a “top level” farm (with climate, farm management and livestock) and two fields. The farm and each field are built from a combination of models found in the toolbox. The APSIM infrastructure connects all selected model pieces together to form a coherent simulation.*

The APSIM Initiative has begun developing a next generation of APSIM (APSIM Next Generation) that is written from scratch and designed to run natively on Windows, LINUX and MAC OSX. The new framework incorporates the best of the APSIM 7.x framework with an improved supporting framework. The Plant Modelling Framework (a generic collection of plant building blocks) was ported from the existing APSIM to bring a rapid development pathway for plant models. The user interface paradigm has been kept the same as the existing APSIM version, but completely rewritten to support new application domains and the newer Plant Modelling Framework. The ability to describe experiments has been added which can also be used for rapidly building factorials of simulations. The ability to write C# scripts to control farm and paddock management has been retained. Finally, all simulation outputs are written to an SQLite database to make it easier and quicker to query, filter and graph outputs.

The model described in this documentation is for APSIM Next Generation.

APSIM is freely available for non-commercial purposes. Non-commercial use of APSIM means public-good research & development and educational activities. It includes the support of policy development and/or implementation by, or on behalf of, government bodies and industry-good work where the research outcomes are to be made publicly available. For more information visit the [licensing page on the APSIM web site](#)

2 Model description

The Pinus model is constructed from the following list of software components. Details of the implementation and model parameterisation are provided in the following sections.

List of Plant Model Components.

Component Name	Component Type
Age	Models.Functions.AccumulateFunction
MortalityRate	Models.Functions.Constant
Phenology	Models.PMF.Phen.Phenology

Component Name	Component Type
Arbitrator	Models.PMF.OrganArbitrator
IndividualTreeLiveWt	Models.Functions.DivideFunction
IndividualTreeStemWt	Models.Functions.DivideFunction
Cone	Models.PMF.Organs.GenericOrgan
Leaf	Models.PMF.Organs.PerennialLeaf
Branch	Models.PMF.Organs.GenericOrgan
Stem	Models.PMF.Organs.GenericOrgan
CoarseRoot	Models.PMF.Organs.GenericOrgan
FineRoot	Models.PMF.Organs.Root
RootShootRatio	Models.Functions.DivideFunction

Although Pinus trees have needles as their foliage, they are the Leaf component of the model to conform to PMF needs. Although the reproductive component of the model (called Cone here) is of minor interest for wood production, it can make up several percent of tree weight and for which we found some data to guide calibration. Phenology is simple in this model and could become a focus for future model development, e.g. for tree breeding or pollen production. Allometric relationships for height (Ht, m), stem diameter (DBH, cm, over bark at 1.3 m height), and their derivatives (stem volume Vol m³/ha, and mean annual increment MAI m³/ha/year) were developed as a function of above-ground biomass based on observations. Root:shoot ratio is an emergent property of the model based on separate calibrations for root and shoot mass. Wood density remains poorly calibrated as few observations of whole tree wood density are available and based on stem analysis. So here wood density is an emergent property of the model, and observed versus predicted graphs of it are included only as a general check that both wood volume and wood weight are correctly simulated.

2.1 Age

Accumulates day between [Start] and [End]

day = 0.00273972602739726 ()

This converts days of growth to age in years.

MortalityRate = 0 ()

Mortality, and therefore its effect on population density (stocking), is set by the user of the model as a thinning operation.

2.2 Phenology

Pinus's phenological development is simulated as the progression through a series of developmental phases, each bound by distinct growth stages.

Phenology is currently very simplistic in the Pinus model.

2.2.1 ThermalTime

ThermalTime = 1 ()

2.3 Phases

List of stages and phases used in the simulation of crop phenological development

Phase Number	Phase Name	Initial Stage	Final Stage
1	Germinating	Sowing	Germination
2	Emerging	Germination	Emergence

Phase Number	Phase Name	Initial Stage	Final Stage
3	Juvenile	Emergence	EndJuvenile
4	Mature	EndJuvenile	Maturity
5	Declining	Maturity	Old
6	Old	Old	Unused

2.3.1 Germinating Phase

The Germinating phase goes from Sowing stage to Germination stage and assumes germination will be reached on the day after sowing or the first day thereafter when the extractable soil water at sowing depth is greater than zero."

We make no distinction between sowing and transplanting in this model, but all sites used transplants not sown seeds. Initial weights are specified for Leaf (1 g/plant) and fine root (0.2 g/plant), which implies these are transplants. Germinating and emerging phenology phases are included in case they are needed by later users. No planting shock is included, but this could be considered in future versions, e.g. delay in commencement of root downward growth.

2.3.2 Emerging Phase

The Emerging phase goes from Germination stage to Emergence stage and simulates time to emergence as a function of sowing depth. The *ThermalTime Target* for this phase is given by

$$\text{Target} = \text{SowingDepth} \times \text{ShootRate} + \text{ShootLag}$$
Where: ShootRate = + ShootRate + ShootLag
SowingDepth (mm) is sent from the manager with the sowing event; Progress toward emergence is driven by Thermal time accumulation from Phenology.Thermaltime

ThermalTime = [Phenology].ThermalTime

2.3.3 Juvenile Phase

The *Juvenile* phase goes from the *Emergence* stage to the *EndJuvenile* stage.

The *Target* for completion is calculated as

Target = 365 (oD)

Progression through the *Juvenile* phase is calculated daily and accumulated until the *Target* is reached.

Progression = 1 ()

2.3.4 Mature Phase

The *Mature* phase goes from the *EndJuvenile* stage to the *Maturity* stage.

The *Target* for completion is calculated as

Target = 1825 (oD)

Progression through the *Mature* phase is calculated daily and accumulated until the *Target* is reached.

Progression = 1 ()

2.3.5 Declining Phase

The *Declining* phase goes from the *Maturity* stage to the *Old* stage.

The *Target* for completion is calculated as

Target = 27010 (oD)

Progression through the *Declining* phase is calculated daily and accumulated until the *Target* is reached.

Progression = 1 ()

It is the end phase in phenology and the crop will sit, unchanging, in this phase until it is harvested or removed by other method

ThermalTime = 1 ()

2.3.6 StageCode

A value is linearly interpolated between phenological growth stages

2.4 Arbitrator

The Arbitrator class determines the allocation of dry matter (DM) and Nitrogen between each of the organs in the crop model. Each organ can have up to three different pools of biomass:

- **Structural biomass** which is essential for growth and remains within the organ once it is allocated there.
- **Metabolic biomass** which generally remains within an organ but is able to be re-allocated when the organ senesces and may be retranslocated when demand is high relative to supply.
- **Storage biomass** which is partitioned to organs when supply is high relative to demand and is available for retranslocation to other organs whenever supply from uptake, fixation, or re-allocation is lower than demand.

The process followed for biomass arbitration is shown in Figure 3. Arbitration calculations are triggered by a series of events (shown below) that are raised every day. For these calculations, at each step the Arbitrator exchange information with each organ, so the basic computations of demand and supply are done at the organ level, using their specific parameters.

1. **doPotentialPlantGrowth.** When this event occurs, each organ class executes code to determine their potential growth, biomass supplies and demands. In addition to demands for structural, non-structural and metabolic biomass (DM and N) each organ may have the following biomass supplies:
 - **Fixation supply.** From photosynthesis (DM) or symbiotic fixation (N)
 - **Uptake supply.** Typically uptake of N from the soil by the roots but could also be uptake by other organs (eg foliage application of N).
 - **Retranslocation supply.** Storage biomass that may be moved from organs to meet demands of other organs.
 - **Reallocation supply.** Biomass that can be moved from senescing organs to meet the demands of other organs.
1. **doPotentialPlantPartitioning.** On this event the Arbitrator first executes the DoDMSetup() method to gather the DM supplies and demands from each organ, these values are computed at the organ level. It then executes the DoPotentialDMAAllocation() method which works out how much biomass each organ would be allocated assuming N supply is not limiting and sends these allocations to the organs. Each organ then uses their potential DM allocation to determine their N demand (how much N is needed to produce that much DM) and the arbitrator calls DoNSetup() to gather the N supplies and demands from each organ and begin N arbitration. Firstly DoNReallocation() is called to redistribute N that the plant has available from senescing organs. After this step any unmet N demand is considered as plant demand for N uptake from the soil (N Uptake Demand).
2. **doNutrientArbitration.** When this event occurs, the soil arbitrator gets the N uptake demands from each plant (where multiple plants are growing in competition) and their potential uptake from the soil and determines how much of their demand that the soil is able to provide. This value is then passed back to each plant instance as their Nuptake and doNUptakeAllocation() is called to distribute this N between organs.
3. **doActualPlantPartitioning.** On this event the arbitrator call DoNRetranslocation() and DoNFixation() to satisfy any unmet N demands from these sources. Finally, DoActualDMAAllocation is called where DM allocations to each organ are reduced if the N allocation is insufficient to achieve the organs minimum N concentration and final allocations are sent to organs.

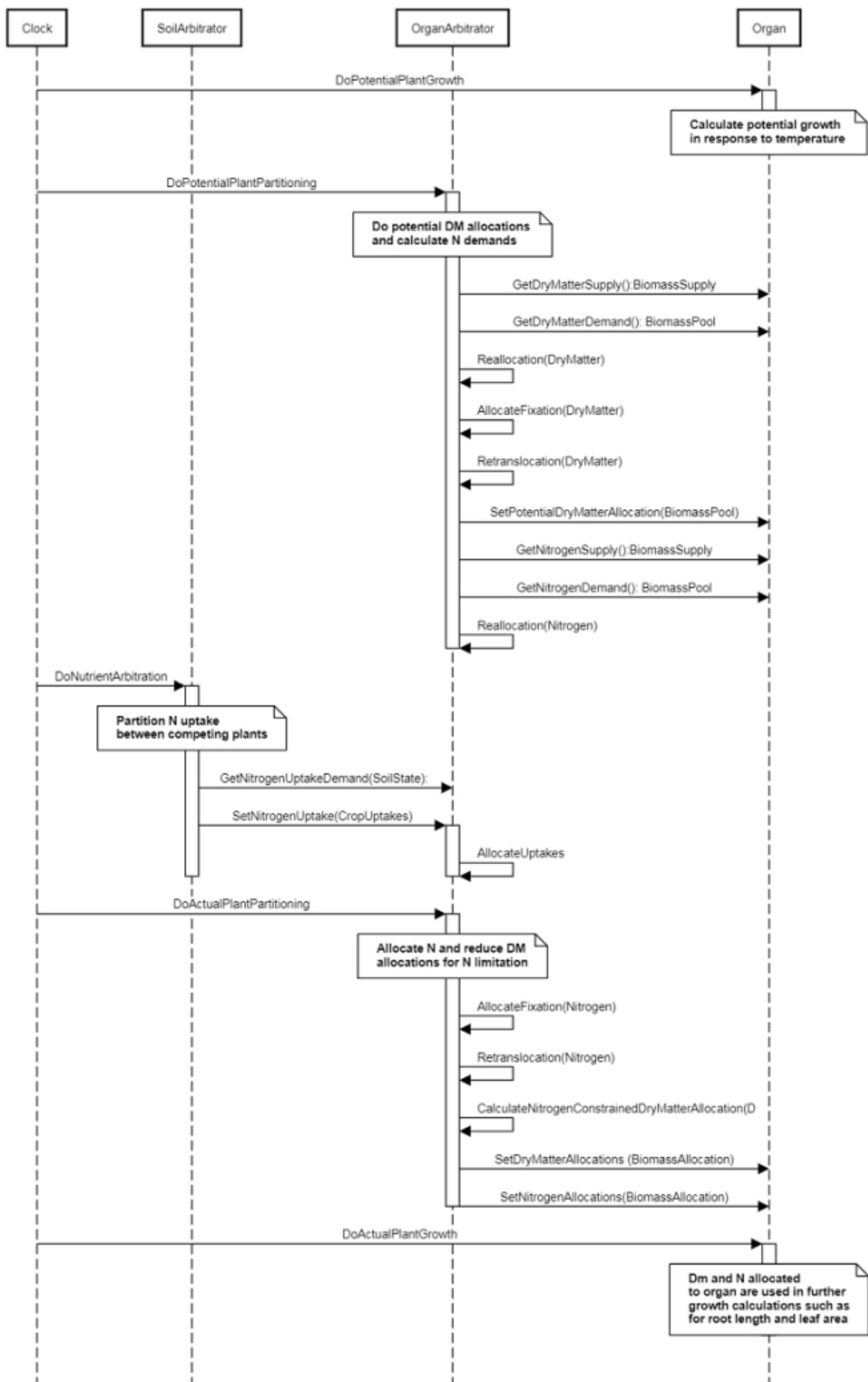


Figure 3: Schematic showing the procedure for arbitration of biomass partitioning. Pink boxes represent events that occur every day and their numbering shows the order of calculations. Blue boxes represent the methods that are called when these events occur. Orange boxes contain properties that make up the organ/arbitrator interface. Green boxes are organ specific properties.

2.5 AboveGround Biomass

This is a composite biomass class, representing the sum of 1 or more biomass objects.

AboveGround summarises the following biomass objects:

- [Branch].Live
- [Branch].Dead
- [Leaf].Live
- [Leaf].Dead
- [Stem].Live
- [Stem].Dead
- [Cone].Live
- [Cone].Dead

2.6 BelowGround Biomass

This is a composite biomass class, representing the sum of 1 or more biomass objects.

BelowGround summarises the following biomass objects:

- [FineRoot].Live
- [FineRoot].Dead
- [CoarseRoot].Live
- [CoarseRoot].Dead

2.7 TotalWoodBark Biomass

This is a composite biomass class, representing the sum of 1 or more biomass objects.

TotalWoodBark summarises the following biomass objects:

- [Stem].Live
- [Stem].Dead
- [Branch].Live
- [Branch].Dead

2.8 Total Biomass

This is a composite biomass class, representing the sum of 1 or more biomass objects.

Total summarises the following biomass objects:

- [Leaf].Live
- [Leaf].Dead
- [Stem].Live
- [Stem].Dead
- [Branch].Live
- [Branch].Dead
- [FineRoot].Live
- [FineRoot].Dead
- [CoarseRoot].Live
- [CoarseRoot].Dead

2.9 TotalLive Biomass

This is a composite biomass class, representing the sum of 1 or more biomass objects.

TotalLive summarises the following biomass objects:

- [Leaf].Live
- [Branch].Live

- [Stem].Live
- [FineRoot].Live
- [CoarseRoot].Live
- [Cone].Live

2.10 TotalDead Biomass

This is a composite biomass class, representing the sum of 1 or more biomass objects.

TotalDead summarises the following biomass objects:

- [Leaf].Dead
- [Branch].Dead
- [Stem].Dead
- [FineRoot].Dead
- [CoarseRoot].Dead
- [Cone].Dead

IndividualTreeLiveWt = [Pinus].Aboveground.Wt / [Pinus].Population

ABGWt = [Pinus].Aboveground.Wt

Population = [Pinus].Population

IndividualTreeStemWt = [Pinus].Stem.Wt / [Pinus].Population

StemWt = [Pinus].Stem.Wt

Population = [Pinus].Population

2.11 Cone

This organ is simulated using a GenericOrgan type. It is parameterised to calculate the growth, senescence, and detachment of any organ that does not have specific functions.

2.11.1 Dry Matter Demand

The dry matter demand for the organ is calculated as defined in DMDemands, based on the DMDemandFunction and partition fractions for each biomass pool.

2.11.1.1 DMDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

Structural = DMDemandFunction x StructuralFraction

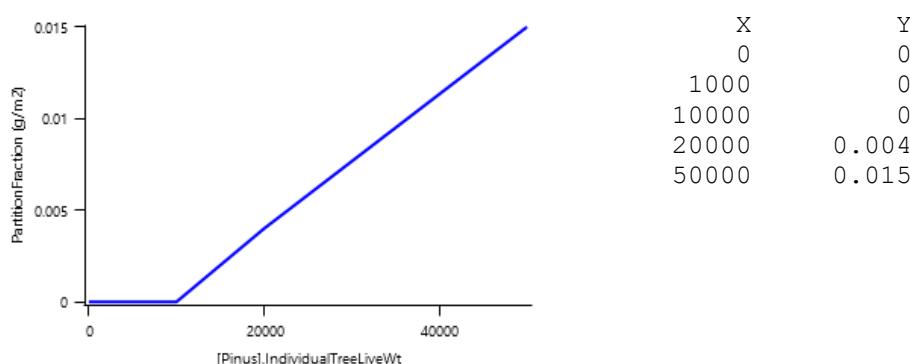
Where:

2.11.1.1.1 DMDemandFunction

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

Where:

PartitionFraction is calculated using linear interpolation.



StructuralFraction = 0.99 (g/m²)

Metabolic = 0 (g/m²)

2.11.1.2 Storage

The partitioning of daily growth to storage biomass is based on a storage fraction.

StorageFraction = 1 - [Cone].DMDemands.Structural.StructuralFraction

One = 1 (g/m²)

StructuralFraction = [Cone].DMDemands.Structural.StructuralFraction

QStructuralPriority = 1 (g/m²)

QMetabolicPriority = 1 (g/m²)

QStoragePriority = 1 (g/m²)

2.11.2 Nitrogen Demand

The N demand is calculated as defined in NDemand, based on DM demand the N concentration of each biomass pool.

2.11.2.1 NDemand

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

Structural = [Cone].minimumNconc x [Cone].potentialDMAAllocation.Structural

MinNconc = [Cone].minimumNconc

PotentialDMAAllocation = [Cone].potentialDMAAllocation.Structural

Metabolic = MetabolicNconc x [Cone].potentialDMAAllocation.Structural

Where:

MetabolicNconc = [Cone].criticalNConc - [Cone].minimumNconc

CritNconc = [Cone].criticalNConc

MinNconc = [Cone].minimumNconc

PotentialDMAAllocation = [Cone].potentialDMAAllocation.Structural

2.11.2.1.1 Storage

The partitioning of daily N supply to storage N attempts to bring the organ's N content to the maximum concentration.

Storage = [Cone].maximumNconc × ([Cone].Live.Wt + potentialAllocationWt) - [Cone].Live.N

The demand for storage N is further reduced by a factor specified by the [Cone].NitrogenDemandSwitch.

QStructuralPriority = 1 (g/m²)

QMetabolicPriority = 1 (g/m²)

QStoragePriority = 1 (g/m²)

MinimumNConc = 0.0014 (g/g)

CriticalNConc = [Cone].MinimumNConc

MaximumNConc = 0.01 (g/g)

The demand for N is reduced by a factor specified by the NitrogenDemandSwitch.

NitrogenDemandSwitch has a value between Emergence and Old calculated as:

Constant = 1 ()

2.11.3 Dry Matter Supply

Cone does not reallocate DM when senescence of the organ occurs.

Cone does not retranslocate non-structural DM.

2.11.4 Nitrogen Supply

Cone does not reallocate N when senescence of the organ occurs.

Cone can retranslocate up to 5% of non-structural N each day if required by the plant arbitrator to meet N demands.

2.11.5 Senescence and Detachment

Cone has senescence parameterised to zero so all biomass in this organ will remain alive.

Cone detaches 5% of its live biomass each day, passing it to the surface organic matter model for decomposition.

2.11.6 BiomassRemovalDefaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	100	100
Cut	100	0	0	0
Prune	0	0	60	0
Thin	0	0	5	5

2.12 Leaf

This organ is parameterised using a simple leaf organ type which provides the core functions of intercepting radiation, providing a photosynthesis supply and a transpiration demand. It also calculates the growth, senescence and detachment of leaves.

2.12.1 CO2internal

Concentrations of CO2 change enough over two or more decades to noticeably affect simulated Pinus growth within even one plantation cycle, as the rotation length for most Pinus plantations is commonly more than one decade. For such simulations we recommend specification in the met file of either the average CO2 during the simulation (if more 1-3 decades) or daily values for longer simulations.

Standard PMF use of CO2 concentration data is provided here.

$$\text{CO2internal} = (163 - [\text{IWeather}].\text{MeanT}) / (5 - 0.1x[\text{IWeather}].\text{MeanT})$$

$$\text{StomatalConductanceCO2Modifier} = [\text{Leaf}].\text{Photosynthesis.FCO2} / \text{RelativeCO2Gradient}$$

Where:

2.12.1.1 RelativeCO2Gradient

$$\text{RelativeCO2Gradient} = ([\text{IWeather}].\text{CO2} - [\text{Leaf}].\text{CO2internal}) / (350 - [\text{Leaf}].\text{CO2internal})$$

$$\text{FCO2} = [\text{Leaf}].\text{Photosynthesis.FCO2}$$

InitialWtFunction = InitialPlantWt x [Plant].Population

Where:

InitialPlantWt = 1 (g/m²)

This value is nominally low to reflect the dry weight of leaves on a transplanted seedling.

Population = [Plant].Population

LaiDeadFunction = 0 ()

2.12.2 FRGRFunction

FRGRFunction is calculated as the minimum of *FT*, *FN* and *FVPD*

Where:

The FRGRFunction, as used to calculate water uptake, is sensitive to stresses of temperature, N status and vpd.

FT = [Leaf].Photosynthesis.FT.FTDaytime

FN = [Leaf].Photosynthesis.FN

FVPD = [Leaf].Photosynthesis.FVPD

2.12.3 ExtinctionCoefficient

Typical extinction coefficients for other plant types are provided here.

ExtinctionCoefficient = ([ExtinctionCoefficient].KMatureTrees+([ExtinctionCoefficient].KYoungTrees-[ExtinctionCoefficient].KMatureTrees)xExp((0-2)x([Pinus].Leaf.LAI/[ExtinctionCoefficient].LAIIntermediateK)^[ExtinctionCoefficient].ShapeCurve))

KYoungTrees = 0.5 ()

KMatureTrees = 0.5 ()

LAIIntermediateK = 0.7 ()

ShapeCurve = 2 ()

ExtinctionCoefficientDead = 0.5 ()

MaximumNConc = 0.02 (g/g)

Maximum and minimum N concentration data were guided by those available in some datasets.

MinimumNConc = 0.012 (g/g)

NReallocationFactor = 0.5 (/d)

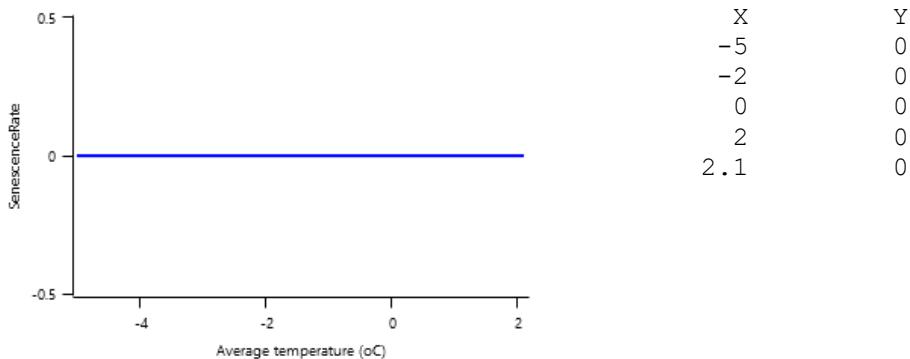
A value of zero assumes there is no N reallocation. The value of 0.5 used here ensures rapid reallocation.

2.12.4 SenescenceRate

SenescenceRate is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0

A zero senescence rate is not assumed here.



2.12.5 Biomass Removal Defaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Values in this table reflect the live and dead fractions that are either removed from the system or transferred to the residue pool. Harvest, Cut and Prune methods will affect these values, but default values assume for Harvest assume dellimbing at the stump.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	99	99
Cut	80	0	0	0
Prune	0	0	60	0
Thin	0	0	5	5

DMConversionEfficiency = 1 ()

LeafDetachmentTime = 14 ()

A value here is the number of days between senescence and detachment. A value of 14 days is assumed.

DetachmentRateFunction = 0 ()

A value for DetachmentRateFunction is required in Leaf, Branch, Stem and CoarseRoot components of the model, but a zero value means that immediate detachment has been triggered. A non-zero option might be useful in the future for defining some genotypes.

DMRetranslocationFactor = 0 (/d)

A value of zero assumes there is no dry matter retranslocation.

NRetranslocationFactor = 0.05 (/d)

A value of zero assumes there is no N retranslocation. The value of 0.05 used here leads to slow retranslocation.

2.12.6 Photosynthesis

Biomass fixation is modelled as the product of intercepted radiation and its conversion efficiency, the radiation use efficiency (RUE) (Monteith et al., 1977). This approach simulates net photosynthesis rather than providing separate estimates of growth and respiration. The potential photosynthesis calculated using RUE is then adjusted according to stress factors, these account for plant nutrition (FN), air temperature (FT), vapour pressure deficit (FVPD), water supply (FW) and atmospheric CO₂ concentration (FCO₂). NOTE: RUE in this model is expressed as g/MJ for a whole plant basis, including both above and below ground growth.

The value of RUE for tree crops is generally in the range 1.3-1.7. Here a value of 1.3 is used, and modified by stresses for temperature, vpd, nitrogen, water and CO₂.

$$\text{RUE} = 1.3 \text{ (g/MJ)}$$

Aboveground RUE for Gliricidia was measured as 1.06 g/MJ by [Harrington et al., 1995](#). Adding c. 0.3 for belowground allocation provides a value of 1.4 g/MJ.

2.12.6.1 FT

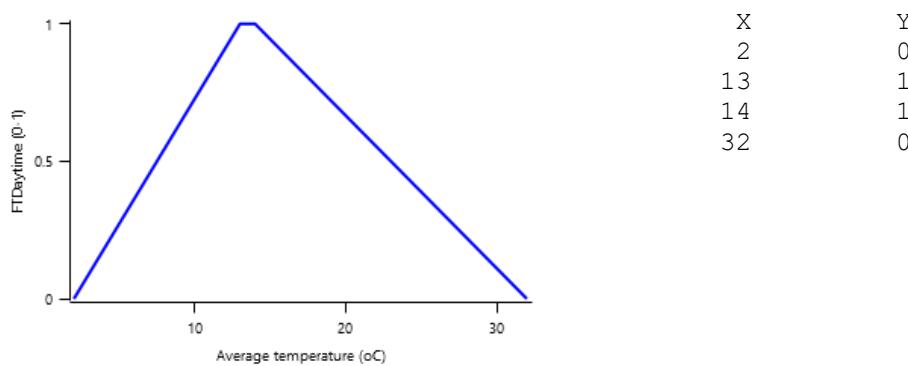
FT is calculated as the minimum of *FTDaytime* and *FTFrost*

Where:

2.12.6.1.1 FTDaytime

FTDaytime is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

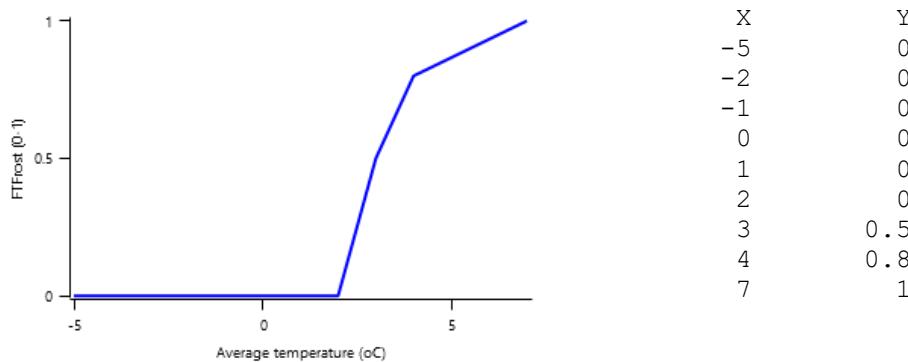
$$\text{MaximumTemperatureWeighting} = 0.75$$



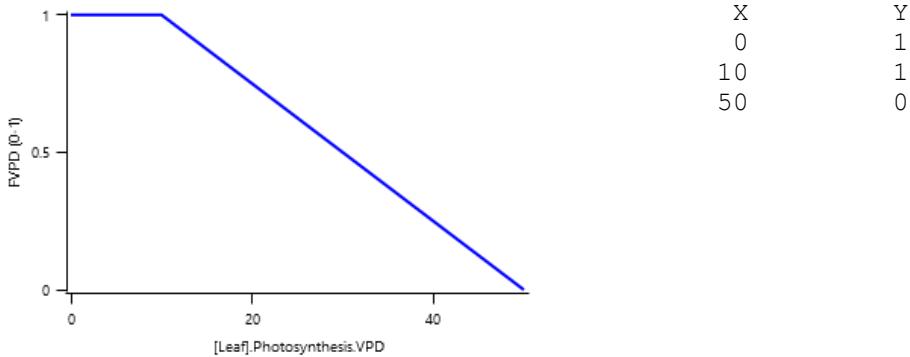
2.12.6.1.2 FTFrost

FTFrost is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

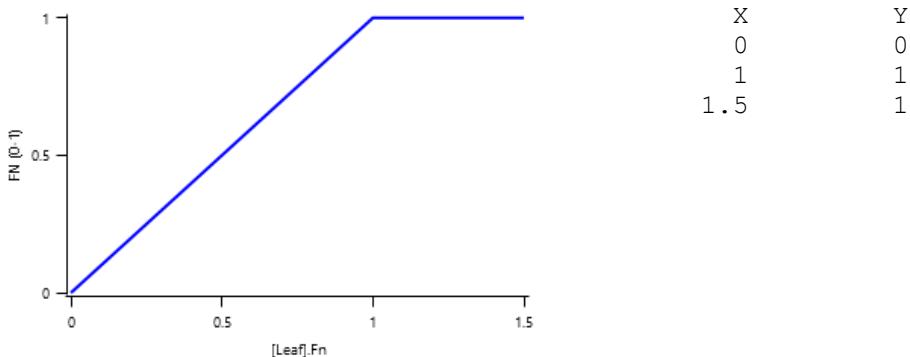
$$\text{MaximumTemperatureWeighting} = 0$$



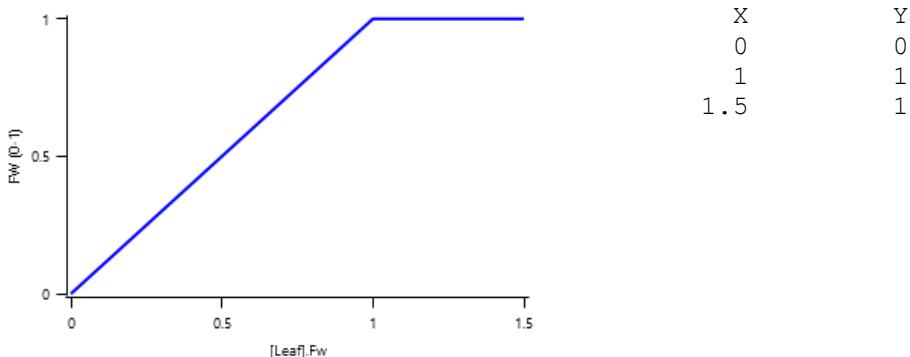
FVPD is calculated using linear interpolation.



FN is calculated using linear interpolation.



FW is calculated using linear interpolation.



2.12.6.2 FCO₂

This model calculates the CO₂ impact on RUE using the approach of Reyenga et al., 1999.

For C3 plants,

$$F_{CO_2} = (CO_2 - CP) \times (350 + 2 \times CP) / (CO_2 + 2 \times CP) \times (350 - CP)$$

where CP, is the compensation point calculated from daily average temperature (T) as

$$CP = (163.0 - T) / (5.0 - 0.1 * T)$$

For C4 plants,

$$F_{CO_2} = 0.000143 * CO_2 + 0.95$$

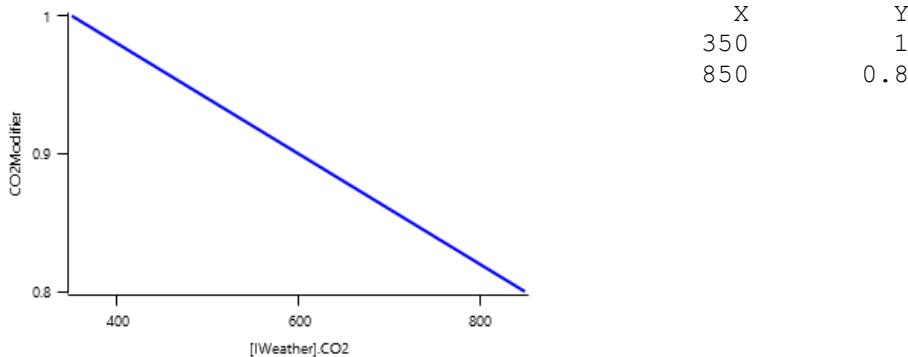
$$RadnInt = [Leaf].RadiationIntercepted$$

$$\text{MinimumLAI} = 0.01 ()$$

$$\text{SpecificLeafAreaFunction} = CO2Modifier \times SLAPotential$$

Where:

CO2Modifier is calculated using linear interpolation.

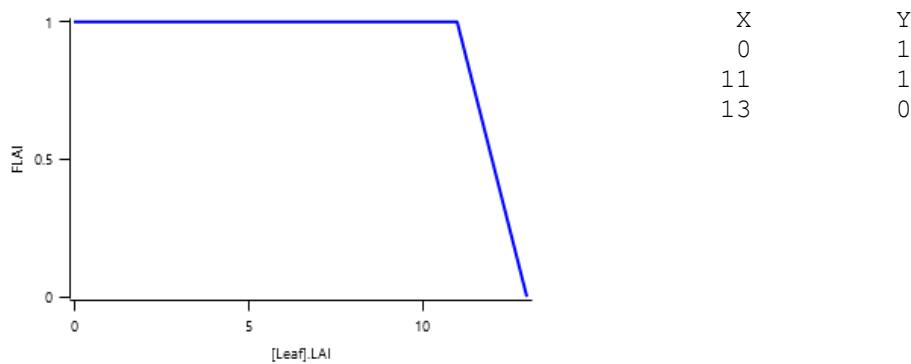


2.12.6.3 SLAPotential

$$\text{SLAPotential} = 0.06 - [\text{Pinus}].\text{Leaf.Wtx} \cdot 0.0000003$$

Some SLA data were for some of the datasets included in this validation, but rarely accurately enough to estimate average canopy SLA. So high model skill for this attribute cannot be expected.

FLAI is calculated using linear interpolation.



2.12.7 LeafKillFractionFactor

LeafKillFractionFactor is calculated as the minimum of *FLAI*

Where:

$$\text{FLAI} = [\text{Leaf}].\text{FLAI}$$

2.12.8 LeafKillFraction

$$\text{LeafKillFraction} = 0.0 + 0.0x(1 - [\text{Leaf}].\text{LeafKillFractionFactor})$$

$$\text{LeafDevelopmentRate} = \text{LDR} \times \text{FT}$$

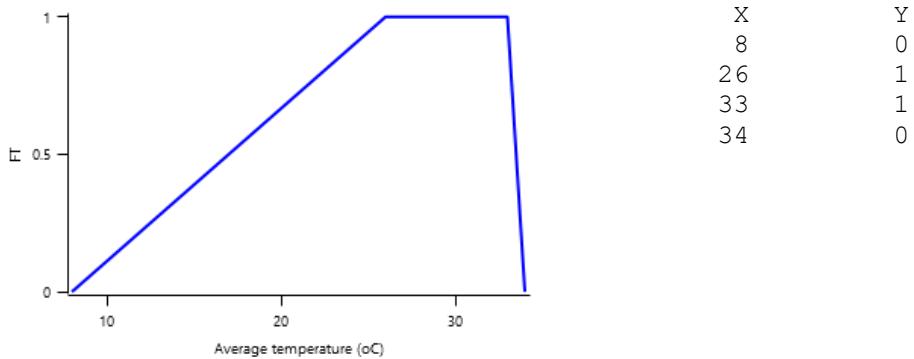
Where:

$$\text{LDR} = 1 ()$$

2.12.8.1 FT

FT is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified *MaximumTemperatureWeighting* factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

$$\text{MaximumTemperatureWeighting} = 1$$



CarbonConcentration = 0.52 ()

This value is within the range of 0.50-0.53 reported by [Beets et al., 2018](#) for *P. radiata* foliage.

2.12.9 HeightFunction

This converts stem height in m to mm for use elsewhere in the model, particularly in relation to competing vegetation.

HeightFunction = [Stem].Htx1000

2.12.10 DMDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

DM demands are set in a similar ways for each organ, but with different values: structural (default specified), metabolic (value = 0), and storage functions (1 - structural). Values measured range from about 5 to 50% for Pinus leaves ([Quentin et al., 2015](#)), which also covers the range of 1-20% for other species and plant parts ([Hoch et al., 2003](#)). Metabolic demand is set to zero, because RUE is a value for net growth for which a respiration calculation is not needed. These values may become an important focus if one attempts to use the model for coppicing, as is already the case in several other APSIM models, e.g. lucerne and gliricidia.

Structural = *DMDemandFunction* × *StructuralFraction*

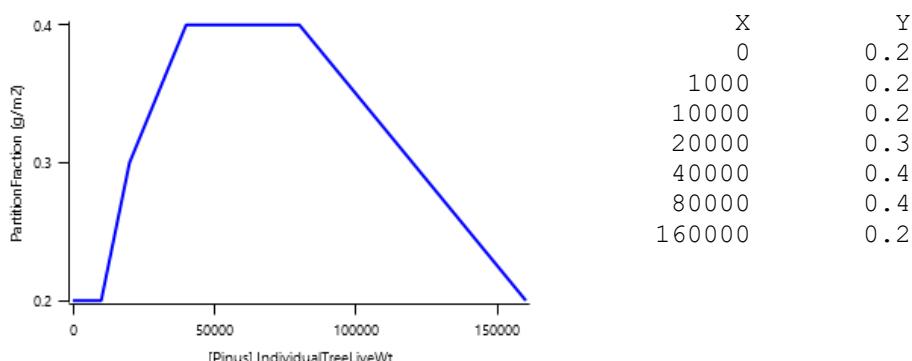
Where:

2.12.10.1 DMDemandFunction

DMDemandFunction = *PartitionFraction* × [*Arbitrator*].*DM.TotalFixationSupply*

Where:

PartitionFraction is calculated using linear interpolation.



StructuralFraction = 0.99 (g/m²)

Metabolic = 0 (g/m²)

Storage = 0 (g/m²)

2.12.11 NDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

N demands are set in a similar ways to DM demands, which are described above.

$$\text{Structural} = [\text{Leaf}].\text{minimumNconc} \times [\text{Leaf}].\text{potentialDMAlocation.Structural}$$

$$\text{MinNconc} = [\text{Leaf}].\text{minimumNconc}$$

$$\text{PotentialDMAlocation} = [\text{Leaf}].\text{potentialDMAlocation.Structural}$$

$$\text{Metabolic} = 0 \text{ (g/m2)}$$

2.12.11.1 Storage

The partitioning of daily N supply to storage N attempts to bring the organ's N content to the maximum concentration.

$$\text{Storage} = [\text{Leaf}].\text{maximumNconc} \times ([\text{Leaf}].\text{Live.Wt} + \text{potentialAllocationWt}) - [\text{Leaf}].\text{Live.N}$$

The demand for storage N is further reduced by a factor specified by the [Leaf].NitrogenDemandSwitch.

2.13 Branch

This organ is simulated using a GenericOrgan type. It is parameterised to calculate the growth, senescence, and detachment of any organ that does not have specific functions.

2.13.1 Dry Matter Demand

The dry matter demand for the organ is calculated as defined in DMDemands, based on the DMDemandFunction and partition fractions for each biomass pool.

2.13.1.1 DMDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

$$\text{Structural} = \text{DMDemandFunction} \times \text{StructuralFraction}$$

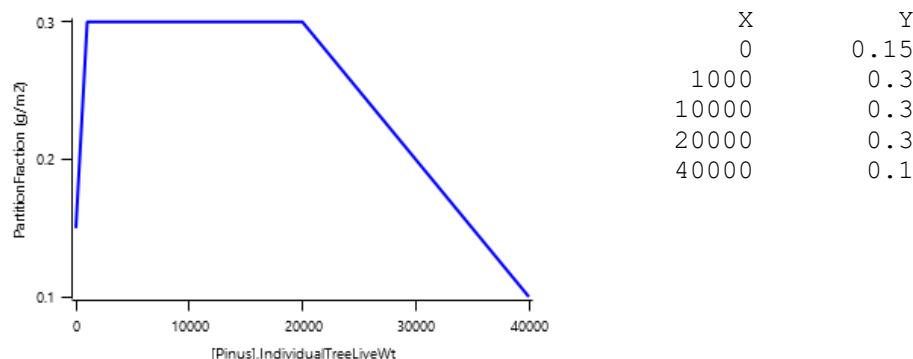
Where:

2.13.1.1.1 DMDemandFunction

$$\text{DMDemandFunction} = \text{PartitionFraction} \times [\text{Arbitrator}].\text{DM.TotalFixationSupply}$$

Where:

PartitionFraction is calculated using linear interpolation.



$$\text{StructuralFraction} = 0.99 \text{ (g/m2)}$$

$$\text{Metabolic} = 0 \text{ (g/m2)}$$

2.13.1.1.2 Storage

The partitioning of daily growth to storage biomass is based on a storage fraction.

$$\text{StorageFraction} = 1 - [\text{Branch}].\text{DMDemands}.Structural.\text{StructuralFraction}$$

One = 1 (g/m²)

$$\text{StructuralFraction} = [\text{Branch}].\text{DMDemands}.Structural.\text{StructuralFraction}$$

QStructuralPriority = 1 (g/m²)

QMetabolicPriority = 1 (g/m²)

QStoragePriority = 1 (g/m²)

2.13.2 Nitrogen Demand

The N demand is calculated as defined in NDemands, based on DM demand the N concentration of each biomass pool.

2.13.2.1 NDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

DM or N demands here are set in a similar way to those described above for the Leaf organ.

$$\text{Structural} = [\text{Branch}].\text{minimumNconc} \times [\text{Branch}].\text{potentialDMAlocation}.Structural$$

MinNconc = [Branch].minimumNconc

$$\text{PotentialDMAlocation} = [\text{Branch}].\text{potentialDMAlocation}.Structural$$

$$\text{Metabolic} = \text{MetabolicNconc} \times [\text{Branch}].\text{potentialDMAlocation}.Structural$$

Where:

$$\text{MetabolicNconc} = [\text{Branch}].\text{criticalNConc} - [\text{Branch}].\text{minimumNconc}$$

$$\text{CritNconc} = [\text{Branch}].\text{criticalNConc}$$

$$\text{MinNconc} = [\text{Branch}].\text{minimumNconc}$$

$$\text{PotentialDMAlocation} = [\text{Branch}].\text{potentialDMAlocation}.Structural$$

2.13.2.1.1 Storage

The partitioning of daily N supply to storage N attempts to bring the organ's N content to the maximum concentration.

$$\text{Storage} = [\text{Branch}].\text{maximumNconc} \times ([\text{Branch}].\text{Live.Wt} + \text{potentialAllocationWt}) - [\text{Branch}].\text{Live.N}$$

The demand for storage N is further reduced by a factor specified by the [Branch].NitrogenDemandSwitch.

QStructuralPriority = 1 (g/m²)

QMetabolicPriority = 1 (g/m²)

QStoragePriority = 1 (g/m²)

MinimumNConc = 0.003 (g/g)

CriticalNConc = [Branch].MinimumNConc

MaximumNConc = 0.006 (g/g)

The demand for N is reduced by a factor specified by the NitrogenDemandSwitch.

NitrogenDemandSwitch has a value between Emergence and Old calculated as:

Constant = 1 ()

2.13.3 Dry Matter Supply

Branch does not reallocate DM when senescence of the organ occurs.

Branch does not retranslocate non-structural DM.

2.13.4 Nitrogen Supply

Branch does not reallocate N when senescence of the organ occurs.

Branch can retranslocate up to 5% of non-structural N each day if required by the plant arbitrator to meet N demands.

2.13.5 Senescence and Detachment

Branch has senescence parameterised to zero so all biomass in this organ will remain alive.

Branch has detachment parameterised to zero so all biomass in this organ will remain with the plant until a defoliation or harvest event occurs.

2.13.6 BiomassRemovalDefaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	100	100
Cut	80	0	0	0
Prune	0	0	60	0
Thin	0	0	5	5

2.14 Stem

This organ is simulated using a GenericOrgan type. It is parameterised to calculate the growth, senescence, and detachment of any organ that does not have specific functions.

Stem metrics useful for plantation forestry are derived here from stem weight using an allometric relationship with stem diameter at breast height (DBH over bark). Basal area (BA, sum of areas of stems in m² per ha) and stem height (Ht) depends on DBH, and volume (Vol over bark) is provided (g per ha) as a function of both Ht and BA. However, underbark metrics were also required, which necessitated the division of stem weight and volume into wood and bark components using the volume component, which depends on bark thickness. All these functions are empirical and calibrated to provide adequate model skill. Finally, wood and bark densities are calculated. Tree stems are not exactly conical, and bark thickness and wood and bark densities vary radially and with height up the stem, with age, and between trees due to inter-tree competition and growth rate. All parameters, and even functions, can be redefined within genotype (cultivar) settings.

2.14.1 Dry Matter Demand

The dry matter demand for the organ is calculated as defined in DMDemands, based on the DMDemandFunction and partition fractions for each biomass pool.

2.14.1.1 DMDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

Structural = DMDemandFunction x StructuralFraction

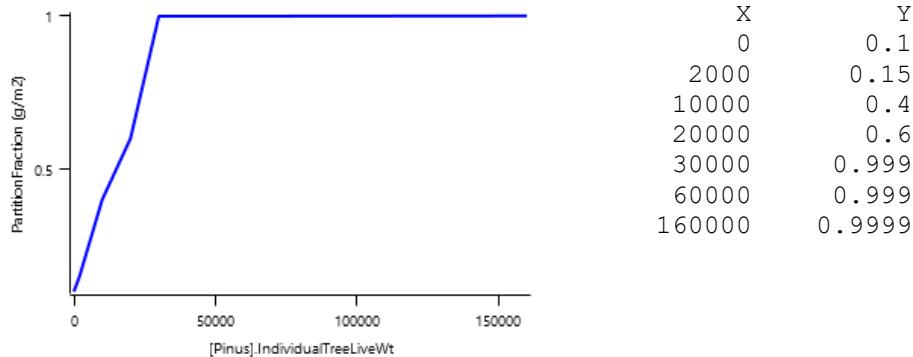
Where:

2.14.1.1.1 DMDemandFunction

$$DMDemandFunction = PartitionFraction \times [Arbitrator].DM.TotalFixationSupply$$

Where:

PartitionFraction is calculated using linear interpolation.



$$\text{StructuralFraction} = 0.99 \text{ (g/m}^2\text{)}$$

$$\text{Metabolic} = 0 \text{ (g/m}^2\text{)}$$

2.14.1.1.2 Storage

The partitioning of daily growth to storage biomass is based on a storage fraction.

$$\text{StorageFraction} = 1 - [\text{Stem}].\text{DMDemands.Structural.StructuralFraction}$$

$$\text{One} = 1 \text{ (g/m}^2\text{)}$$

$$\text{StructuralFraction} = [\text{Stem}].\text{DMDemands.Structural.StructuralFraction}$$

$$\text{QStructuralPriority} = 1 \text{ (g/m}^2\text{)}$$

$$\text{QMetabolicPriority} = 1 \text{ (g/m}^2\text{)}$$

$$\text{QStoragePriority} = 1 \text{ (g/m}^2\text{)}$$

2.14.2 Nitrogen Demand

The N demand is calculated as defined in NDemand, based on DM demand the N concentration of each biomass pool.

2.14.2.1 NDemand

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

$$\text{Structural} = [\text{Stem}].\text{minimumNconc} \times [\text{Stem}].\text{potentialDMAAllocation.Structural}$$

$$\text{MinNconc} = [\text{Stem}].\text{minimumNconc}$$

$$\text{PotentialDMAAllocation} = [\text{Stem}].\text{potentialDMAAllocation.Structural}$$

$$\text{Metabolic} = \text{MetabolicNconc} \times [\text{Stem}].\text{potentialDMAAllocation.Structural}$$

Where:

$$\text{MetabolicNconc} = [\text{Stem}].\text{criticalNConc} - [\text{Stem}].\text{minimumNconc}$$

$$\text{CritNconc} = [\text{Stem}].\text{criticalNConc}$$

$$\text{MinNconc} = [\text{Stem}].\text{minimumNconc}$$

$$\text{PotentialDMAAllocation} = [\text{Stem}].\text{potentialDMAAllocation.Structural}$$

2.14.2.1.1 Storage

The partitioning of daily N supply to storage N attempts to bring the organ's N content to the maximum concentration.

$$\text{Storage} = [\text{Stem}].\text{maximumNconc} \times ([\text{Stem}].\text{Live.Wt} + \text{potentialAllocationWt}) - [\text{Stem}].\text{Live.N}$$

The demand for storage N is further reduced by a factor specified by the [Stem].NitrogenDemandSwitch.

$$\text{QStructuralPriority} = 1 \text{ (g/m}^2\text{)}$$

$$\text{QMetabolicPriority} = 1 \text{ (g/m}^2\text{)}$$

$$\text{QStoragePriority} = 1 \text{ (g/m}^2\text{)}$$

$$\text{MinimumNConc} = 0.002 \text{ (g/g)}$$

$$\text{CriticalNConc} = [\text{Stem}].\text{MinimumNConc}$$

$$\text{MaximumNConc} = 0.004 \text{ (g/g)}$$

Branch, stem and coarse root minimum N concentrations are based on [Raymond et al., 2000](#).

The demand for N is reduced by a factor specified by the NitrogenDemandSwitch.

NitrogenDemandSwitch has a value between Emergence and Old calculated as:

$$\text{Constant} = 1 ()$$

2.14.3 Dry Matter Supply

Stem does not reallocate DM when senescence of the organ occurs.

Stem does not retranslocate non-structural DM.

2.14.4 Nitrogen Supply

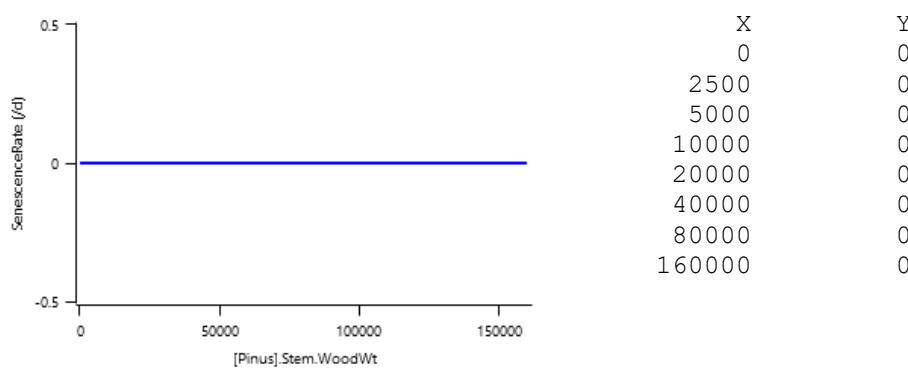
Stem does not reallocate N when senescence of the organ occurs.

Stem can retranslocate up to 5% of non-structural N each day if required by the plant arbitrator to meet N demands.

2.14.5 Senescence and Detachment

The proportion of live biomass that senesces and moves into the dead pool each day is quantified by the SenescenceRate.

SenescenceRate is calculated using linear interpolation.



Stem detaches 1% of its live biomass each day, passing it to the surface organic matter model for decomposition.

2.14.6 BiomassRemovalDefaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil

surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	100	100	0	0
Cut	80	0	0	0
Prune	0	0	60	0
Thin	0	0	5	5

2.15 CoarseRoot

This organ is simulated using a GenericOrgan type. It is parameterised to calculate the growth, senescence, and detachment of any organ that does not have specific functions.

2.15.1 Dry Matter Demand

The dry matter demand for the organ is calculated as defined in DMDemands, based on the DMDemandFunction and partition fractions for each biomass pool.

2.15.1.1 DMDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

$$\text{Structural} = \text{DMDemandFunction} \times \text{StructuralFraction}$$

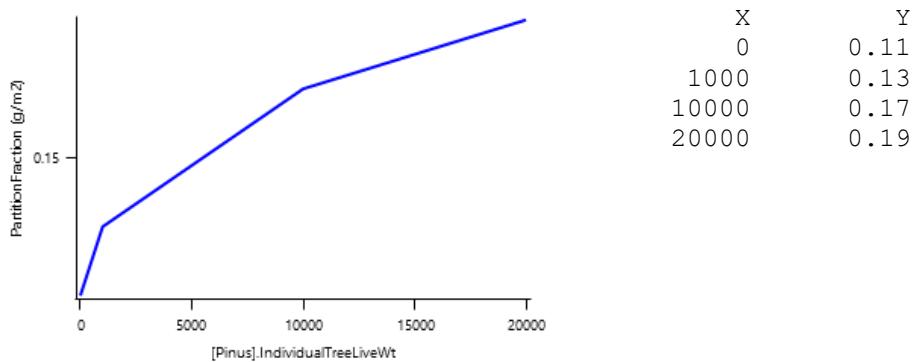
Where:

2.15.1.1.1 DMDemandFunction

$$\text{DMDemandFunction} = \text{PartitionFraction} \times [\text{Arbitrator}].\text{DM}. \text{TotalFixationSupply}$$

Where:

PartitionFraction is calculated using linear interpolation.



$$\text{StructuralFraction} = 0.99 \text{ (g/m}^2\text{)}$$

$$\text{Metabolic} = 0 \text{ (g/m}^2\text{)}$$

2.15.1.1.2 Storage

The partitioning of daily growth to storage biomass is based on a storage fraction.

$$\text{StorageFraction} = 1 - [\text{CoarseRoot}].\text{DMDemands}. \text{Structural}. \text{StructuralFraction}$$

$$\text{One} = 1 \text{ (g/m}^2\text{)}$$

$$\text{StructuralFraction} = [\text{CoarseRoot}].\text{DMDemands}. \text{Structural}. \text{StructuralFraction}$$

QStructuralPriority = 1 (g/m²)

QMetabolicPriority = 1 (g/m²)

QStoragePriority = 1 (g/m²)

2.15.2 Nitrogen Demand

The N demand is calculated as defined in NDemands, based on DM demand the N concentration of each biomass pool.

2.15.2.1 NDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

Structural = [CoarseRoot].minimumNconc x [CoarseRoot].potentialDMAAllocation.Structural

MinNconc = [CoarseRoot].minimumNconc

PotentialDMAAllocation = [CoarseRoot].potentialDMAAllocation.Structural

Metabolic = MetabolicNconc x [CoarseRoot].potentialDMAAllocation.Structural

Where:

MetabolicNconc = [CoarseRoot].criticalNConc - [CoarseRoot].minimumNconc

CritNconc = [CoarseRoot].criticalNConc

MinNconc = [CoarseRoot].minimumNconc

PotentialDMAAllocation = [CoarseRoot].potentialDMAAllocation.Structural

2.15.2.1.1 Storage

The partitioning of daily N supply to storage N attempts to bring the organ's N content to the maximum concentration.

Storage = [CoarseRoot].maximumNconc × ([CoarseRoot].Live.Wt + potentialAllocationWt) - [CoarseRoot].Live.N

The demand for storage N is further reduced by a factor specified by the [CoarseRoot].NitrogenDemandSwitch.

QStructuralPriority = 1 (g/m²)

QMetabolicPriority = 1 (g/m²)

QStoragePriority = 1 (g/m²)

MinimumNConc = 0.0012 (g/g)

CriticalNConc = [Stem].MinimumNConc

MaximumNConc = 0.008 (g/g)

The demand for N is reduced by a factor specified by the NitrogenDemandSwitch.

NitrogenDemandSwitch has a value between Emergence and Old calculated as:

Constant = 1 ()

2.15.3 Dry Matter Supply

CoarseRoot does not reallocate DM when senescence of the organ occurs.

CoarseRoot does not retranslocate non-structural DM.

2.15.4 Nitrogen Supply

CoarseRoot does not reallocate N when senescence of the organ occurs.

CoarseRoot can retranslocate up to 5% of non-structural N each day if required by the plant arbitrator to meet N demands.

2.15.5 Senescence and Detachment

CoarseRoot has senescence parameterised to zero so all biomass in this organ will remain alive.

CoarseRoot has detachment parameterised to zero so all biomass in this organ will remain with the plant until a defoliation or harvest event occurs.

2.15.6 Biomass Removal Defaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	100	100
Cut	80	0	0	0
Prune	0	0	60	0
Thin	0	0	5	5

2.16 FineRoot

The generic root model calculates root growth in terms of rooting depth, biomass accumulation and subsequent root length density in each soil layer.

Root Growth

Roots grow downwards through the soil profile, with initial depth determined by sowing depth and the growth rate determined by RootFrontVelocity. The RootFrontVelocity is modified by multiplying it by the soil's XF value, which represents any resistance posed by the soil to root extension.

$$\text{Root Depth Increase} = \text{RootFrontVelocity} \times \text{XF}_i \times \text{RootDepthStressFactor}$$

where i is the index of the soil layer at the rooting front.

Root depth is also constrained by a maximum root depth.

Root length growth is calculated using the daily DM partitioned to roots and a specific root length. Root proliferation in layers is calculated using an approach similar to the generalised equimarginal criterion used in economics. The uptake of water and N per unit root length is used to partition new root material into layers of higher 'return on investment'. For example, the Root Activity for water is calculated as

$$RAw_i = -\text{WaterUptake}_i / \text{LiveRootWt}_i \times \text{LayerThickness}_i \times \text{ProportionThroughLayer}$$

The amount of root mass partitioned to a layer is then proportional to root activity

$$DMAAllocated_i = \text{TotalDMAAllocated} \times RAw_i / \text{TotalRAw}$$

Dry Matter Demands

A daily DM demand is provided to the organ arbitrator and a DM supply returned. By default, 100% of the dry matter (DM) demanded from the root is structural. The daily loss of roots is calculated using a SenescenceRate function. All senesced material is automatically detached and added to the soil FOM.

Nitrogen Demands

The daily structural N demand from root is the product of total DM demand and the minimum N concentration. Any N above this is considered Storage and can be used for retranslocation and/or reallocation as the respective factors are set to values other than zero.

Nitrogen Uptake

Potential N uptake by the root system is calculated for each soil layer (*i*) that the roots have extended into. In each layer potential uptake is calculated as the product of the mineral nitrogen in the layer, a factor controlling the rate of extraction (kNO₃ or kNH₄), the concentration of N form (ppm), and a soil moisture factor (NUptakeSWFactor) which typically decreases as the soil dries.

$$NO_3 \text{ uptake} = NO_{3,i} \times kNO_3 \times NO_{3,ppm,i} \times NUptakeSWFactor$$

$$NH_4 \text{ uptake} = NH_{4,i} \times kNH_4 \times NH_{4,ppm,i} \times NUptakeSWFactor$$

As can be seen from the above equations, the values of kNO₃ and kNH₄ equate to the potential fraction of each mineral N pool which can be taken up per day for wet soil when that pool has a concentration of 1 ppm.

Nitrogen uptake demand is limited to the maximum daily potential uptake (MaxDailyNUptake) and the plant's N demand. The former provides a means to constrain N uptake to a maximum value observed in the field for the crop as a whole. The demand for soil N is then passed to the soil arbitrator which determines how much of the N uptake demand each plant instance will be allowed to take up.

Water Uptake

Potential water uptake by the root system is calculated for each soil layer that the roots have extended into. In each layer potential uptake is calculated as the product of the available water in the layer (water above LL limit) and a factor controlling the rate of extraction (KL). The values of both LL and KL are set in the soil interface and KL may be further modified by the crop via the KLModifier function.

$$SW \text{ uptake} = (SW_i - LL_i) \times KL_i \times KLModifier$$

2.16.1 RootShape

NitrogenDemandSwitch has a value between Emergence and Old calculated as:

$$\text{Constant} = 1 ()$$

$$\text{RootFrontVelocity} = 10 (\text{mm/d})$$

[Huth et al., 2008](#) measured a constant root front velocity of 24.3 mm/d down to 1.4 m depth under favourable growing conditions, which was similar to wheat. [de Moraes Goncalves et al., 2013](#) report eucalypt root front velocities averaging 19 mm/day for the first 1.5 years to 12 mm/day by 3.5 years in conditions of little impedance to root growth. The value of 10 mm/d used here is lower to reflect more common limiting conditions.

$$\text{SenescenceRate} = 0.001 (/d)$$

$$\text{MaxDailyNUptake} = 6 (\text{kg N/ha/d})$$

$$\text{MaximumNConc} = 0.01 (\text{g/g})$$

Fine root N concentrations are based on Misra et al (1998).

$$\text{MinimumNConc} = 0.003 (\text{g/g})$$

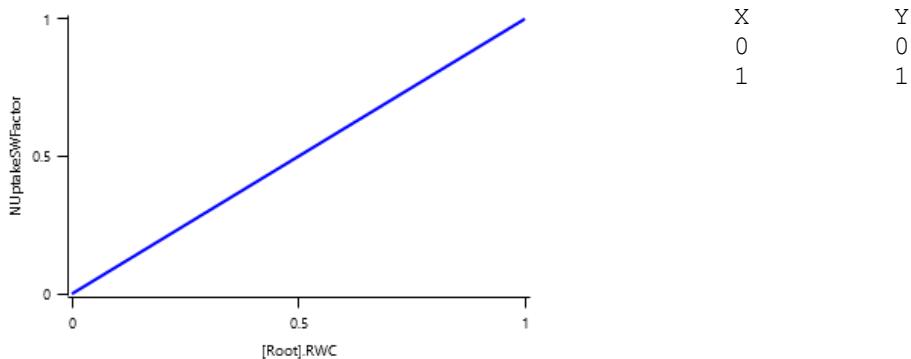
$$\text{MaximumRootDepth} = 10000 (\text{mm})$$

$$\text{KLModifier} = 1 (0-1)$$

$$KNO_3 = 0.03 (/d/ppm)$$

$$KNH_4 = 3E-06 (/d/ppm)$$

NUptakeSWFactor is calculated using linear interpolation.



SpecificRootLength = 40 (m/g)

Specific root length was based on [Jourdan et al., 2008](#).

2.16.2 BiomassRemovalDefaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	100	100
Cut	80	0	0	0
Prune	0	0	60	0
Thin	0	0	5	5

DMConversionEfficiency = 1 (g/g)

MaintenanceRespirationFunction = 0 (/d)

RemobilisationCost = 0 ()

CarbonConcentration = 0.5 (g/g)

2.16.3 DMDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

Structural = DMDemandFunction x StructuralFraction

Where:

2.16.3.1 DMDemandFunction

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

Where:

PartitionFraction = 0.11 (g/m²)

StructuralFraction = 1 (g/m²)

Metabolic = 0 (g/m²)

2.16.3.2 Storage

The partitioning of daily growth to storage biomass is based on a storage fraction.

StorageFraction = 1 - [FineRoot].DMDemands.Structural.StructuralFraction

One = 1 (g/m²)

StructuralFraction = [FineRoot].DMDemands.Structural.StructuralFraction

QStructuralPriority = 1 (g/m²)

QMetabolicPriority = 1 (g/m²)

QStoragePriority = 1 (g/m²)

2.16.4 NDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

Structural = [FineRoot].minimumNconc x [FineRoot].potentialDMAAllocation.Structural

MinNconc = [FineRoot].minimumNconc

PotentialDMAAllocation = [FineRoot].potentialDMAAllocation.Structural

Metabolic = MetabolicNconc x [FineRoot].potentialDMAAllocation.Structural

Where:

MetabolicNconc = [FineRoot].criticalNConc - [FineRoot].minimumNconc

CritNconc = [FineRoot].criticalNConc

MinNconc = [FineRoot].minimumNconc

PotentialDMAAllocation = [FineRoot].potentialDMAAllocation.Structural

2.16.4.1 Storage

The partitioning of daily N supply to storage N attempts to bring the organ's N content to the maximum concentration.

Storage = [FineRoot].maximumNconc × ([FineRoot].Live.Wt + potentialAllocationWt) - [FineRoot].Live.N

The demand for storage N is further reduced by a factor specified by the [FineRoot].NitrogenDemandSwitch.

QStructuralPriority = 1 (g/m²)

QMetabolicPriority = 1 (g/m²)

QStoragePriority = 1 (g/m²)

CriticalNConc = [Root].MinimumNConc

2.16.5 InitialWt

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

Structural = 0.2 (g/m²)

Metabolic = 0 (g/m²)

Storage = 0 (g/m²)

RootDepthStressFactor = 1 (0-1)

RootShootRatio = [Pinus].BelowGround.Wt / [Pinus].AboveGround.Wt

Numerator = [Pinus].BelowGround.Wt

Denominator = [Pinus].AboveGround.Wt

2.17 caribaea

caribaea

2.17.1 caribaea

caribaea overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=1.3

[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.X=4, 20, 30, 38

[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.Y=0, 1, 1, 0

[Cone].MaximumNConc.FixedValue = 0.0024

[Cone].MinimumNConc.FixedValue = 0.0014

[Leaf].MaximumNConc.FixedValue = 0.011

[Leaf].MinimumNConc.FixedValue = 0.005

[Branch].MaximumNConc.FixedValue = 0.0024

[Branch].MinimumNConc.FixedValue = 0.0014

[Stem].MaximumNConc.FixedValue = 0.00075

[Stem].MinimumNConc.FixedValue = 0.00035

[CoarseRoot].MaximumNConc.FixedValue = 0.00075

[CoarseRoot].MinimumNConc.FixedValue = 0.00035

[FineRoot].MaximumNConc.FixedValue = 0.011

[FineRoot].MinimumNConc.FixedValue = 0.005

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.000, 0.000, 0.000, 0.025, 0.045, 0.044, 0.042, 0.04, 0.035

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.31, 0.1, 0.10, 0.10, 0.1, 0.1, 0.1, 0.1, 0.1

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.07, 0.08, 0.09, 0.065, 0.05, 0.05, 0.05, 0.04, 0.04

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0,

1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.15, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.8, 0.8

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.45, 0.55, 0.65, 0.67, 0.7, 0.73, 0.75

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
 10000, 25000, 50000, 100000, 200000, 400000, 800000
 [CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.008, 0.020, 0.060,
 0.08, 0.100, 0.120, 0.140, 0.16, 0.18
 [FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.15
 [Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.006-[Pinus].Leaf.Wt*0.00000025
 [Leaf].LeafResidenceTime.XYPairs.X=0,1,2,3,6,9
 [Leaf].LeafResidenceTime.XYPairs.Y=550, 580, 630, 700, 850, 850
 [Stem].DBH.DBHEquation.Expression=-3.24+(0.82*[Pinus].IndividualTreeStemWt^0.29)
 [Stem].Ht.HeightFunction.Expression=0.304375+(0.245023*[Pinus].Stem.DBH^1.2668)+(0.211611*([Pinus].Population*10000)^0.161)+0.317
 [Stem].Vol.VolumeEquation.Expression=[Pinus].Stem.Ht*[Pinus].Stem.BA*(0.942*(([Pinus].Stem.Ht-1.4)^-1.161)+0.317)
 [Stem].BarkThickness.BarkThickness.XYPairs.X=0, 8, 12, 16, 20, 24, 28, 40, 80
 [Stem].BarkThickness.BarkThickness.XYPairs.Y=0, .6, 0.8, 1, 1.3, 1.6, 1.9, 2.05, 2.1

This cultivar was initially developed for the IMPAC site.

2.18 *elliottii*

elliottii, *elliottiiIMPAC*, *elliottiiQLD*, PEE

2.18.1 *elliottii*

elliottii overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=1.3
 [Leaf].Photosynthesis.FT.FTDaytime.XYPairs.X=4, 20, 30, 38
 [Leaf].Photosynthesis.FT.FTDaytime.XYPairs.Y=0, 1, 1, 0
 [Cone].MaximumNConc.FixedValue = 0.0024
 [Cone].MinimumNConc.FixedValue = 0.0014
 [Leaf].MaximumNConc.FixedValue = 0.011
 [Leaf].MinimumNConc.FixedValue = 0.005
 [Branch].MaximumNConc.FixedValue = 0.0024
 [Branch].MinimumNConc.FixedValue = 0.0014
 [Stem].MaximumNConc.FixedValue = 0.00075
 [Stem].MinimumNConc.FixedValue = 0.00035
 [CoarseRoot].MaximumNConc.FixedValue = 0.00075
 [CoarseRoot].MinimumNConc.FixedValue = 0.00035
 [FineRoot].MaximumNConc.FixedValue = 0.011
 [FineRoot].MinimumNConc.FixedValue = 0.005
 [Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
 10000, 25000, 50000, 100000, 200000, 400000, 800000

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.000, 0.000, 0.000, 0.025, 0.045, 0.044, 0.042, 0.04, 0.035

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.31, 0.1, 0.10, 0.10, 0.1, 0.1, 0.1, 0.1, 0.1

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.07, 0.08, 0.09, 0.065, 0.05, 0.05, 0.05, 0.04, 0.04

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0,

1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.15, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.8, 0.8

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.008, 0.020, 0.060, 0.08, 0.100, 0.120, 0.140, 0.16, 0.18

[FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.15

[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.006-[Pinus].Leaf.Wt*0.00000025

[Leaf].LeafResidenceTime.XYPairs.X=0,1,2,3,6,9

[Leaf].LeafResidenceTime.XYPairs.Y=550, 580, 630, 700, 850, 850

[Stem].DBH.DBHEquation.Expression=-3.24+(0.82*[Pinus].IndividualTreeStemWt^0.29)

[Stem].Ht.HeightFunction.Expression=0.304375+(0.245023*[Pinus].Stem.DBH^1.2668)+(0.211611*([Pinus].Population*10000)^0.25)

[Stem].BarkThickness.BarkThickness.XYPairs.X=0, 8, 12, 16, 20, 24, 28, 40, 80

[Stem].BarkThickness.BarkThickness.XYPairs.Y=0, .6, 0.8, 1, 1.3, 1.4, 1.5, 1.6, 1.7

This cultivar was initially developed for the IMPAC site.

2.18.2 PEE

PEE overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=1.3

[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.X=4, 20, 30, 38

[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.Y=0, 1, 1, 0

[Cone].MaximumNConc.FixedValue = 0.0024

[Cone].MinimumNConc.FixedValue = 0.0014

[Leaf].MaximumNConc.FixedValue = 0.011

[Leaf].MinimumNConc.FixedValue = 0.005

[Branch].MaximumNConc.FixedValue = 0.0024

[Branch].MinimumNConc.FixedValue = 0.0014

[Stem].MaximumNConc.FixedValue = 0.00075

[Stem].MinimumNConc.FixedValue = 0.00035

[CoarseRoot].MaximumNConc.FixedValue = 0.00075

[CoarseRoot].MinimumNConc.FixedValue = 0.00035

[FineRoot].MaximumNConc.FixedValue = 0.011

[FineRoot].MinimumNConc.FixedValue = 0.005

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.000, 0.000, 0.000, 0.025,
0.045, 0.044, 0.042, 0.04, 0.035

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.31, 0.1, 0.10, 0.10,
0.1, 0.1, 0.1, 0.1, 0.1

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.07, 0.08, 0.09, 0.065,
0.05, 0.05, 0.05, 0.04, 0.04

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0,
1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.15, 0.3, 0.4, 0.5, 0.6, 0.7,
0.8, 0.8, 0.8

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.45, 0.55, 0.65, 0.67, 0.7, 0.73, 0.75

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.008, 0.020, 0.060,
0.08, 0.100, 0.120, 0.140, 0.16, 0.18

[FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.15

[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.006-[Pinus].Leaf.Wt*0.00000025

[Leaf].LeafResidenceTime.XYPairs.X=0,1,2,3,6,9

[Leaf].LeafResidenceTime.XYPairs.Y=550, 580, 630, 700, 850, 850

[Stem].DBH.DBHEquation.Expression=-3.24+(0.82*[Pinus].IndividualTreeStemWt^0.29)

[Stem].Ht.HeightFunction.Expression=0.304375+(0.245023*[Pinus].Stem.DBH^1.2668)+(0.211611*([Pinus].Population*10000)^0.00000025)

[Stem].Vol.VolumeEquation.Expression=[Pinus].Stem.Ht*[Pinus].Stem.BA*(0.942*(([Pinus].Stem.Ht-1.4)^-1.161)+0.317)

[Stem].BarkThickness.BarkThickness.XYPairs.X=0, 8, 12, 16, 20, 24, 28, 40, 80

[Stem].BarkThickness.BarkThickness.XYPairs.Y=.1, .3, 0.5, 6, .7, .8, 1, 1.1,
1.1

This cultivar was initially developed for the a south-east Queensland site.

2.18.3 *elliottiiIMPAC*

elliottiiIMPAC overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=1.4

[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.X=4, 24, 33, 38

[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.Y=0, 1, 1, 0

[Cone].MaximumNConc.FixedValue = 0.0024

[Cone].MinimumNConc.FixedValue = 0.0014

[Leaf].MaximumNConc.FixedValue = 0.017

[Leaf].MinimumNConc.FixedValue = 0.007

[Branch].MaximumNConc.FixedValue = 0.0024

[Branch].MinimumNConc.FixedValue = 0.0014

[Stem].MaximumNConc.FixedValue = 0.001

[Stem].MinimumNConc.FixedValue = 0.0005

[CoarseRoot].MaximumNConc.FixedValue = 0.001

[CoarseRoot].MinimumNConc.FixedValue = 0.0005

[FineRoot].MaximumNConc.FixedValue = 0.017

[FineRoot].MinimumNConc.FixedValue = 0.007

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0, 0, 0, 0.045, 0.065

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000, 100000, 200000

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.2, 0.3, 0.4, 0.3, 0.18, .1, .0

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 40000, 80000, 160000, 200000

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.4, 0.4, 0.4, 0.39, 0.35, 0.2, 0.16, .15

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 50000, 100000, 200000, 300000

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.5, 0.9, 0.9, 0.9, 0.9, 0.1, 0.0

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.7, 0.9, 0.95, 0.95, 0.985, 0.995, 0.99

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000, 100000, 200000, 500000

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.15, 0.15, 0.15, 0.16, 0.16, 0.16, 0.15, 0.15

[FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.12

[FineRoot].SenescenceRate.FixedValue=0.001

[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.0063-[Pinus].Leaf.Wt*0.000004

[Stem].DBH.DBHEquation.Expression=-1.8+(0.815*[Pinus].IndividualTreeStemWt^0.29)

[Stem].Ht.HeightFunction.Expression=0.304375+(0.9*[Pinus].Stem.DBH^0.9)+(0*([Pinus].Population*10000)^0.218209)

This cultivar was initially developed for the IMPAC site.

2.18.4 *elliottiiQLD*

elliottiiQLD overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=1.3

[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.X=4, 20, 30, 38

[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.Y=0, 1, 1, 0

[Cone].MaximumNConc.FixedValue = 0.0024

[Cone].MinimumNConc.FixedValue = 0.0014

[Leaf].MaximumNConc.FixedValue = 0.011

[Leaf].MinimumNConc.FixedValue = 0.005

[Branch].MaximumNConc.FixedValue = 0.0024

[Branch].MinimumNConc.FixedValue = 0.0014

[Stem].MaximumNConc.FixedValue = 0.00075

[Stem].MinimumNConc.FixedValue = 0.00035

[CoarseRoot].MaximumNConc.FixedValue = 0.00075

[CoarseRoot].MinimumNConc.FixedValue = 0.00035

[FineRoot].MaximumNConc.FixedValue = 0.011

[FineRoot].MinimumNConc.FixedValue = 0.005

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.000, 0.000, 0.000, 0.025, 0.045, 0.044, 0.042, 0.04, 0.035

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.31, 0.1, 0.10, 0.10, 0.1, 0.1, 0.1, 0.1, 0.1

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.07, 0.08, 0.09, 0.065, 0.05, 0.05, 0.05, 0.04, 0.04

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0,

1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.15, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.8, 0.8

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000
[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.45, 0.55, 0.65, 0.67, 0.7, 0.73, 0.75
[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000
[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.008, 0.020, 0.060,
0.08, 0.100, 0.120, 0.140, 0.16, 0.18
[FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.15
[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.006-[Pinus].Leaf.Wt*0.00000025
[Leaf].LeafResidenceTime.XYPairs.X=0,1,2,3,6,9
[Leaf].LeafResidenceTime.XYPairs.Y=550, 580, 630, 700, 850, 850
[Stem].DBH.DBHEquation.Expression=-3.24+(0.82*[Pinus].IndividualTreeStemWt^0.29)
[Stem].Ht.HeightFunction.Expression=0.304375+(0.245023*[Pinus].Stem.DBH^1.2668)+(0.211611*([Pinus].Population*10000)^0.161)+0.317)
[Stem].BarkThickness.BarkThickness.XYPairs.X=0, 8, 12, 16, 20, 24, 28, 40, 80
[Stem].BarkThickness.BarkThickness.XYPairs.Y=.1, .3, 0.5, .6, .7, 1.1, 1.46, 1.5, 1.5

This cultivar was initially developed for the a south-east Queensland site.

2.19 ellottiiXcaribaeaF1

ellottiiXcaribaeaF1

2.19.1 ellottiiXcaribaeaF1

ellottiiXcaribaeaF1 overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=1.3
[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.X=4, 20, 30, 38
[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.Y=0, 1, 1, 0
[Cone].MaximumNConc.FixedValue = 0.0024
[Cone].MinimumNConc.FixedValue = 0.0014
[Leaf].MaximumNConc.FixedValue = 0.011
[Leaf].MinimumNConc.FixedValue = 0.005
[Branch].MaximumNConc.FixedValue = 0.0024
[Branch].MinimumNConc.FixedValue = 0.0014
[Stem].MaximumNConc.FixedValue = 0.00075
[Stem].MinimumNConc.FixedValue = 0.00035
[CoarseRoot].MaximumNConc.FixedValue = 0.00075
[CoarseRoot].MinimumNConc.FixedValue = 0.00035
[FineRoot].MaximumNConc.FixedValue = 0.011
[FineRoot].MinimumNConc.FixedValue = 0.005

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.000, 0.000, 0.000, 0.025, 0.045, 0.044, 0.042, 0.04, 0.035

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.31, 0.1, 0.10, 0.10, 0.1, 0.1, 0.1, 0.1, 0.1

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.07, 0.08, 0.09, 0.065, 0.05, 0.05, 0.05, 0.04, 0.04

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0,

1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.15, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.8, 0.8

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.45, 0.55, 0.65, 0.67, 0.7, 0.73, 0.75

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,

10000, 25000, 50000, 100000, 200000, 400000, 800000

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.008, 0.020, 0.060, 0.08, 0.100, 0.120, 0.140, 0.16, 0.18

[FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.15

[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.006-[Pinus].Leaf.Wt*0.00000025

[Leaf].LeafResidenceTime.XYPairs.X=0,1,2,3,6,9

[Leaf].LeafResidenceTime.XYPairs.Y=550, 580, 630, 700, 850, 850

[Stem].DBH.DBHEquation.Expression=-3.24+(0.82*[Pinus].IndividualTreeStemWt^0.29)

[Stem].Ht.HeightFunction.Expression=0.304375+(0.245023*[Pinus].Stem.DBH^1.2668)+(0.211611*([Pinus].Population*10000)^0.0001)

[Stem].Vol.VolumeEquation.Expression=[Pinus].Stem.Ht*[Pinus].Stem.BA*(0.942*(([Pinus].Stem.Ht-1.4)^-1.161)+0.317)

[Stem].BarkThickness.BarkThickness.XYPairs.X=0, 8, 12, 16, 20, 24, 28, 40, 80

[Stem].BarkThickness.BarkThickness.XYPairs.Y=0, .6, 0.8, 1, 1.3, 1.4, 1.6, 1.9, 1.9

This cultivar was initially developed for the a south-east Queensland site.

2.20 ellottiiXcaribaeaF2

ellottiiXcaribaeaF2

2.20.1 ellottiiXcaribaeaF2

ellottiiXcaribaeaF2 overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=1.3
[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.X=4, 20, 30, 38
[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.Y=0, 1, 1, 0
[Cone].MaximumNConc.FixedValue = 0.0024
[Cone].MinimumNConc.FixedValue = 0.0014
[Leaf].MaximumNConc.FixedValue = 0.011
[Leaf].MinimumNConc.FixedValue = 0.005
[Branch].MaximumNConc.FixedValue = 0.0024
[Branch].MinimumNConc.FixedValue = 0.0014
[Stem].MaximumNConc.FixedValue = 0.00075
[Stem].MinimumNConc.FixedValue = 0.00035
[CoarseRoot].MaximumNConc.FixedValue = 0.00075
[CoarseRoot].MinimumNConc.FixedValue = 0.00035
[FineRoot].MaximumNConc.FixedValue = 0.011
[FineRoot].MinimumNConc.FixedValue = 0.005
[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000
[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.000, 0.000, 0.000, 0.025,
0.045, 0.044, 0.042, 0.04, 0.035
[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000
[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.31, 0.1, 0.10, 0.10,
0.1, 0.1, 0.1, 0.1, 0.1
[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000
[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y= 0.07, 0.08, 0.09, 0.065,
0.05, 0.05, 0.05, 0.04, 0.04
[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0,
1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000
[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.15, 0.3, 0.4, 0.5, 0.6, 0.7,
0.8, 0.8, 0.8
[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000
[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.45, 0.55, 0.65, 0.67, 0.7, 0.73, 0.75
[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000,
10000, 25000, 50000, 100000, 200000, 400000, 800000
[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.008, 0.020, 0.060,
0.08, 0.100, 0.120, 0.140, 0.16, 0.18

[FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.15
[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.006-[Pinus].Leaf.Wt*0.00000025
[Leaf].LeafResidenceTime.XYPairs.X=0,1,2,3,6,9
[Leaf].LeafResidenceTime.XYPairs.Y=550, 580, 630, 700, 850, 850
[Stem].DBH.DBHEquation.Expression=-3.24+(0.82*[Pinus].IndividualTreeStemWt^0.29)
[Stem].Ht.HeightFunction.Expression=0.304375+(0.245023*[Pinus].Stem.DBH^1.2668)+(0.211611*([Pinus].Population*10000)^0.161)+0.317
[Stem].Vol.VolumeEquation.Expression=[Pinus].Stem.Ht*[Pinus].Stem.BA*(0.942*(([Pinus].Stem.Ht-1.4)^-1.161)+0.317)
[Stem].BarkThickness.BarkThickness.XYPairs.X=0, 8, 12, 16, 20, 24, 28, 40, 80
[Stem].BarkThickness.BarkThickness.XYPairs.Y=0, .6, 0.8, 1, 1.3, 1.4, 1.6, 1.8, 1.8

This cultivar was initially developed for the a south-east Queensland site.

2.21 radiata

BFG, GF7, TowerHill

2.21.1 BFG

BFG overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=0.95
[Leaf].Photosynthesis.FN.XYPairs.X=0,1,1.5
[Leaf].Photosynthesis.FN.XYPairs.Y=0,1,1
[Leaf].Photosynthesis.FW.XYPairs.X=0,1,1.5
[Leaf].Photosynthesis.FW.XYPairs.Y=0.8,1,1
[Cone].MaximumNConc.FixedValue = 0.0024
[Cone].MinimumNConc.FixedValue = 0.0014
[Leaf].MaximumNConc.FixedValue = 0.011
[Leaf].MinimumNConc.FixedValue = 0.005
[Branch].MaximumNConc.FixedValue = 0.0024
[Branch].MinimumNConc.FixedValue = 0.0014
[Stem].MaximumNConc.FixedValue = 0.00075
[Stem].MinimumNConc.FixedValue = 0.00035
[CoarseRoot].MaximumNConc.FixedValue = 0.00075
[CoarseRoot].MinimumNConc.FixedValue = 0.00035
[FineRoot].MaximumNConc.FixedValue = 0.011
[FineRoot].MinimumNConc.FixedValue = 0.005
[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000
[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0, 0, 0, 0.045, 0.065
[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000
[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.1, 0.13, 0.16, 0.2, 0.22

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 40000, 80000, 160000, 200000

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.13, 0.13, 0.13, 0.13, 0.14, 0.22, 0.3, .15

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 50000, 100000, 200000, 300000

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.1, 0.2, 0.3, 0.6, 0.8, 0.85, 0.99

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.6, 0.85, 0.9, 0.93, 0.975, 0.985, 0.99

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000, 100000, 200000, 500000

[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.3, 0.3, 0.28, 0.23, 0.19, 0.19, 0.14, 0.12

[FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.215

[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.0067-[Pinus].Leaf.Wt*0.0000002

[Stem].DBH.DBHEquation.Expression=-1.5+(0.76*[Pinus].IndividualTreeStemWt^0.3)

This cultivar was initially developed for the BFG site.

2.21.2 GF7

GF7 overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=1.3

[Leaf].Photosynthesis.FN.XYPairs.X=0,1,1.5

[Leaf].Photosynthesis.FN.XYPairs.Y=0,1,1

[Leaf].Photosynthesis.FW.XYPairs.X=0,1,1.5

[Leaf].Photosynthesis.FW.XYPairs.Y=0,1,1

[Cone].MaximumNConc.FixedValue = 0.001

[Cone].MinimumNConc.FixedValue = 0.006

[Leaf].MaximumNConc.FixedValue = 0.017

[Leaf].MinimumNConc.FixedValue = 0.007

[Branch].MaximumNConc.FixedValue = 0.0065

[Branch].MinimumNConc.FixedValue = 0.002

[Stem].MaximumNConc.FixedValue = 0.002

[Stem].MinimumNConc.FixedValue = 0.0003

[CoarseRoot].MaximumNConc.FixedValue = 0.002

[CoarseRoot].MinimumNConc.FixedValue = 0.0003

[FineRoot].MaximumNConc.FixedValue = 0.017

[FineRoot].MinimumNConc.FixedValue = 0.007

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 40000, 80000, 160000, 200000

[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.2, 0.2, 0.2, 0.2, 0.2, 0.28, 0.3, .15

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000, 100000, 200000

[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.12, 0.15, 0.2, 0.3, 0.4, .35, .3

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 50000, 100000, 200000, 300000

[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.08, 0.12, 0.3, 0.8, 0.9, 0.95, 0.99

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000

[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.9, 0.95, 0.99, 0.99, 0.99, 0.999, 0.9999

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000

[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0, 0, 0, 0, 0.01

[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.0053+[Pinus].Leaf.Wt*0.0000001

[Pinus].Stem.DBH.DBHEquation.Expression=-15+(3.748*[Pinus].IndividualTreeStemWt^0.21)

[Pinus].Stem.Ht.HeightFunction.Expression=-6+(1.0*[Pinus].Stem.DBH^(1.001-(2200-[Pinus].Population*10000)*0.00004))

[Stem].Vol.VolumeEquation.Expression=[Pinus].Stem.Ht*[Pinus].Stem.BA*(0.942*(([Pinus].Stem.Ht-1.4)^-1.161)+0.317)

[Stem].BarkThickness.BarkThickness.XYPairs.X=0, 8, 12, 16, 20, 24, 28, 40, 80

[Stem].BarkThickness.BarkThickness.XYPairs.Y=0.4, .9, 0.93, 0.95, 0.97, 1.3, 1.4, 1.5, 1.5

[Stem].Volub.Expression=[Pinus].Stem.Vol-[Pinus].Stem.VolBark*0.3

This cultivar was initially developed for the Puruki site.

2.21.3 TowerHill

TowerHill overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=0.85

[Leaf].Photosynthesis.FN.XYPairs.X=0,1,1.5

[Leaf].Photosynthesis.FN.XYPairs.Y=0,1,1

[Leaf].Photosynthesis.FW.XYPairs.X=0,1,1.5

[Leaf].Photosynthesis.FW.XYPairs.Y=0.7,1,1

[Cone].MaximumNConc.FixedValue = 0.0024

[Cone].MinimumNConc.FixedValue = 0.0014

[Leaf].MaximumNConc.FixedValue = 0.011

[Leaf].MinimumNConc.FixedValue = 0.005

[Branch].MaximumNConc.FixedValue = 0.0024

[Branch].MinimumNConc.FixedValue = 0.0014

[Stem].MaximumNConc.FixedValue = 0.00075

[Stem].MinimumNConc.FixedValue = 0.00035

[CoarseRoot].MaximumNConc.FixedValue = 0.00075
[CoarseRoot].MinimumNConc.FixedValue = 0.00035
[FineRoot].MaximumNConc.FixedValue = 0.011
[FineRoot].MinimumNConc.FixedValue = 0.005
[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000
[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0, 0, 0, 0.03, 0.05
[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000
[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.04, 0.06, 0.08, 0.1, 0.1
[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 40000, 80000, 160000, 200000
[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.13, 0.13, 0.13, 0.13, 0.14, 0.22, 0.3, .15
[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 50000, 100000, 200000, 300000
[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.1, 0.2, 0.3, 0.6, 0.8, 0.85, 0.99
[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000, 800000
[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.5, 0.82, 0.84, 0.87, 0.86, 0.87, 0.88, 0.92
[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000, 100000, 200000, 500000
[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.3, 0.3, 0.29, 0.25, 0.24, 0.23, 0.2, 0.16
[FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.23
[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.0067-[Pinus].Leaf.Wt*0.0000002
[Stem].DBH.DBHEquation.Expression=-1.5+(0.76*[Pinus].IndividualTreeStemWt^0.298)

This cultivar was initially developed for the TowerHill site.

2.22 taeda

taeda, taedalMPAC

2.22.1 taeda

taeda overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=0.9
[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.X=4, 24, 33, 38
[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.Y=0, 1, 1, 0
[Cone].MaximumNConc.FixedValue = 0.0024
[Cone].MinimumNConc.FixedValue = 0.0014
[Leaf].MaximumNConc.FixedValue = 0.015
[Leaf].MinimumNConc.FixedValue = 0.007
[Branch].MaximumNConc.FixedValue = 0.0024
[Branch].MinimumNConc.FixedValue = 0.0014

[Stem].MaximumNConc.FixedValue = 0.00075
[Stem].MinimumNConc.FixedValue = 0.00035
[CoarseRoot].MaximumNConc.FixedValue = 0.00075
[CoarseRoot].MinimumNConc.FixedValue = 0.00035
[FineRoot].MaximumNConc.FixedValue = 0.015
[FineRoot].MinimumNConc.FixedValue = 0.007
[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000
[Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0, 0, 0, 0.045, 0.065
[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000, 100000, 200000
[Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.1, 0.13, 0.16, 0.2, 0.22, .19, .16
[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 40000, 80000, 160000, 200000
[Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.18, 0.16, 0.15, 0.14, 0.14, 0.14, 0.14, .14
[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 50000, 100000, 200000, 300000
[Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.1, 0.2, 0.3, 0.6, 0.8, 0.85, 0.99
[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000
[Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.6, 0.85, 0.9, 0.93, 0.975, 0.985, 0.99
[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000, 100000, 200000, 500000
[CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.12, 0.13, 0.14, 0.15, 0.16, 0.17, 0.17, 0.17
[FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.13
[FineRoot].SenescenceRate.FixedValue=0.003
[Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.006-[Pinus].Leaf.Wt*0.00000025
[Stem].DBH.DBHEquation.Expression=-3.24+(0.82*[Pinus].IndividualTreeStemWt^0.3)
[Stem].Ht.HeightFunction.Expression=0.304375+(0.245023*[Pinus].Stem.DBH^1.2668)+(0.211611*([Pinus].Population*10000)^0.00000025

This cultivar was initially developed for the SETRES sites.

2.22.2 taedalMPAC

taedalMPAC overrides the following properties:

[Leaf].Photosynthesis.RUE.FixedValue=1.1
[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.X=4, 24, 33, 38
[Leaf].Photosynthesis.FT.FTDaytime.XYPairs.Y=0, 1, 1, 0
[Cone].MaximumNConc.FixedValue = 0.0024
[Cone].MinimumNConc.FixedValue = 0.0014
[Leaf].MaximumNConc.FixedValue = 0.017

[Leaf].MinimumNConc.FixedValue = 0.007
 [Branch].MaximumNConc.FixedValue = 0.0024
 [Branch].MinimumNConc.FixedValue = 0.0014
 [Stem].MaximumNConc.FixedValue = 0.001
 [Stem].MinimumNConc.FixedValue = 0.0005
 [CoarseRoot].MaximumNConc.FixedValue = 0.001
 [CoarseRoot].MinimumNConc.FixedValue = 0.0005
 [FineRoot].MaximumNConc.FixedValue = 0.017
 [FineRoot].MinimumNConc.FixedValue = 0.007
 [Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 50000
 [Cone].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0, 0, 0, 0.045, 0.065
 [Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000,
 50000, 100000, 200000
 [Branch].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.3, 0.4, 0.3, 0.25, 0.18, .03,
 .0
 [Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000, 40000,
 80000, 160000, 200000
 [Leaf].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.4, 0.39, 0.38, 0.37, 0.3, 0.17,
 0.16, .15
 [Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 50000,
 100000, 200000, 300000
 [Stem].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.4, 0.9, 0.9, 0.8, 0.7, 0.1, 0.0
 [Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.X=0, 2000, 10000, 20000, 100000, 200000, 400000
 [Stem].WoodWt.WoodWt.WoodWtFactor.XYPairs.Y=0.6, 0.8, 0.9, 0.93, 0.975, 0.985, 0.99
 [CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.X=0, 1000, 10000, 20000,
 50000, 100000, 200000, 500000
 [CoarseRoot].DMDemands.Structural.DMDemandFunction.PartitionFraction.XYPairs.Y=0.1, 0.15, 0.15, 0.15,
 0.15, 0.15, 0.15
 [FineRoot].DMDemands.Structural.StructuralFraction.FixedValue=0.15
 [FineRoot].SenescenceRate.FixedValue=0.002
 [Leaf].SpecificLeafAreaFunction.SLAPotential.Expression=0.0063-[Pinus].Leaf.Wt*0.0000025
 [Stem].DBH.DBHEquation.Expression=-1.3+(0.82*[Pinus].IndividualTreeStemWt^0.28)
 [Stem].Ht.HeightFunction.Expression=0.304375+(0.8*[Pinus].Stem.DBH^1.1)+(0*([Pinus].Population*10000)^0.218209)

This cultivar was initially developed for the IMPAC site.

3 Pinus Model Notes

3.1 Plant Modelling Framework

The APSIM Pinus model has been developed using the Plant Modelling Framework (PMF) of [Brown et al., 2014](#) within APSIM Next Generation [Holzworth et al., 2014](#). This new framework provides a library of plant organ and process submodels that can be coupled, at runtime, to construct a model in much the same way that models can be coupled to construct a simulation. This means that dynamic composition of lower level processes and organ classes (e.g. photosynthesis, Leaf) into larger constructions (e.g. maize, wheat, Pinus) can be achieved by the model developer without additional coding.

3.2 Peculiarities of Pinus and This Model

The Pinus model consists of:

- a phenology model to simulate development through sequential growth phases
- a collection of organs to simulate the various plant parts
- an arbitrator to allocate resources (N, biomass) to the various plant organs

This work builds upon earlier APSIM forest models such as described by [Huth et al., 2002](#), [Huth et al., 2001](#), [Huth et al., 2008](#), and [Smethurst et al., 2020](#).

Pinus is a reasonably straight forward perennial crop to model. This model has been set up for simulation of even-aged plantations (transplanted seedlings) or native forests (also assumed to start the simulation as a transplanted seedling, but in practice it would be sown from naturally distributed seed). Plants grow in accordance with available resources and conditions, which in this version of the model are temperature, radiation, available soil water, and available soil nitrogen. Leaf, branch and roots senesce, remain attached for some time, then detach to produce litter. Above-ground biomass is the main target of production, which is made up of organs that develop from default partitioning targets that are modified daily due to organ demand. Forest managers also deal with tree size, which are set in the model as a function of aboveground biomass. During model development, we found that Pinus model performance (plant or stand development) was particularly sensitive to Leaf lifespan/longevity, specific Leaf area, dead Leaf detachment, partitioning to roots and shoots, mortality and thinning, and weeds (if present).

There are many Pinus genotypes (species, closely related genera, provenances, families, clones, and hybrids) that can behave differently in response to their growing environment. This build of the Pinus model was calibrated on datasets of three species (*P. radiata*, *P. caribaea*, *P. elliottii*) and F1 and F2 hybrids of (*P. caribaea*, *P. elliottii*). Many of the genotype are poorly described, but some are probably from early-stage domestication, while others are the result of several generations of tree breeding. Early genetic material was mostly selected, for example, for states in Australia from provenance that performed adequately in state of interest, and tree breeding programmes for several decades were state-run. During more recent decades, company and collaborative breeding programs have provided the genetic material for planting. A summary of domestication and genetic material of planted *P. radiata* in Australia and New Zealand is provided in [Burdon et al., 2008](#), [Wu et al., 2007](#), and [Johnson et al., 2008](#). The implications are that genotypic control of physiological traits is poorly defined, requiring the model to be calibrated for assumed rather than measured differences.

3.3 Including a Pinus crop in an APSIM simulation

There will be a Pinus and/or PinusRotation example simulation available by clicking the "Open an Example" icon available on the second tab displayed when APSIM Next Gen is opened. This provides a useful demonstration of how to simulate a Pinus crop and provides some useful graphs for viewing model behaviour and performance.

To include a Pinus crop in a simulation the "Pinus" model needs to be added to the paddock, field or zone in which it is to be grown. This can be done by (a) right clicking on the "Paddock", selecting "Add" from the drop down menu and then selecting "Pinus" from the list that comes up, or (b) dragging or copying and pasting the model up from the standard toolbox or an example. A TreeSowing rule or TreeManagement rule needs to be set up to start the crop off.

This document provides a description of the model, describes the validation and test datasets, and model performance.

Major Eucalyptus model developments:

2020-2021

- Copied the Eucalyptus model and modified it to fit the observed Pinus datasets. The Eucalyptus and Pinus models were expanded (beyond the original Eucalyptus model in APSIM Next Generation) to include an expansion of stem metrics beyond just diameter at breast height (DBH, cm), height (m), and overbark stem volume (Vol, m³/ha). New stem metrics include underbark parameters of stem volume (Volub) and wood density, and basal area (BA, m²/ha) the mean annual increment of overbark and underbark volumes (m³/ha/year). This required partitioning of stem biomass into bark and wood, calculation of bark thickness, and an estimation of volumes overbark and underbark. All stem metrics are empirically calculated rather than process-based. These metrics are known to be highly effected by stem taper, bark thickness and wood density, which in-turn are highly influenced by site, genetics and management. Few data are available on wood density (underbark, whole tree), so it is included here only as a check that underlying calculations are sensible. Validations of these metrics are included.

Suggested future developments:

1. Make SLA a function of stress level
2. Create a set of functional weeds specifically for use with these forestry models, e.g. N-fixing/non-N-fixing
X herbaceous/shrub/tree X tropical/sub-tropical/temperate
3. Self-thinning rule or process-based mortality
4. Improve effects of stocking, if necessary. Leaf allocation as a function of aboveground.wt (g/m²) rather than individual tree weight (g/tree) has been included, but further checking of this is required to see if that is all that is needed for a wide range of stockings. Allocation patterns might need to be explicitly related to population.
5. Waterlogging – I (Philip) would have thought it was important, particularly for some euc and pine genotypes, but so far I haven't run into a really need for it amongst our current observed datasets.
6. Soil P (and K) and fertiliser responses
7. Pruning, thinning and various other effects on knot-free wood and other wood quality measures
8. Geo-locate and interact adjacent plots for predicting area-based metrics like run-on (above- and below-ground), stream flow and wood production
9. Tree and log size class distributions
10. Development of outputs for greenhouse accounting (water use, C sequestration, greenhouse gases, biodiversity indexes)

4 Validation

Validation datasets have been included to assist with validation during model development. Validation datasets cover a range of environmental (soil and climate) conditions, management options (populations, nitrogen rates, irrigation) and genetic backgrounds (different regions, provenance, clones). These datasets have been grouped and ordered alphabetically by climatic zone, country and site. Currently, all temperate data are for *P. radiata*, but a range of tropical and sub-tropical genotypes are included. Graphs of model performance are provided for stocking, canopy development, biomass production, stem metrics, and soil water.

Observed data are shown compared to predictions, with statistics for model skill.

The following map shows the location of sites used in this validation.

4.1 Map



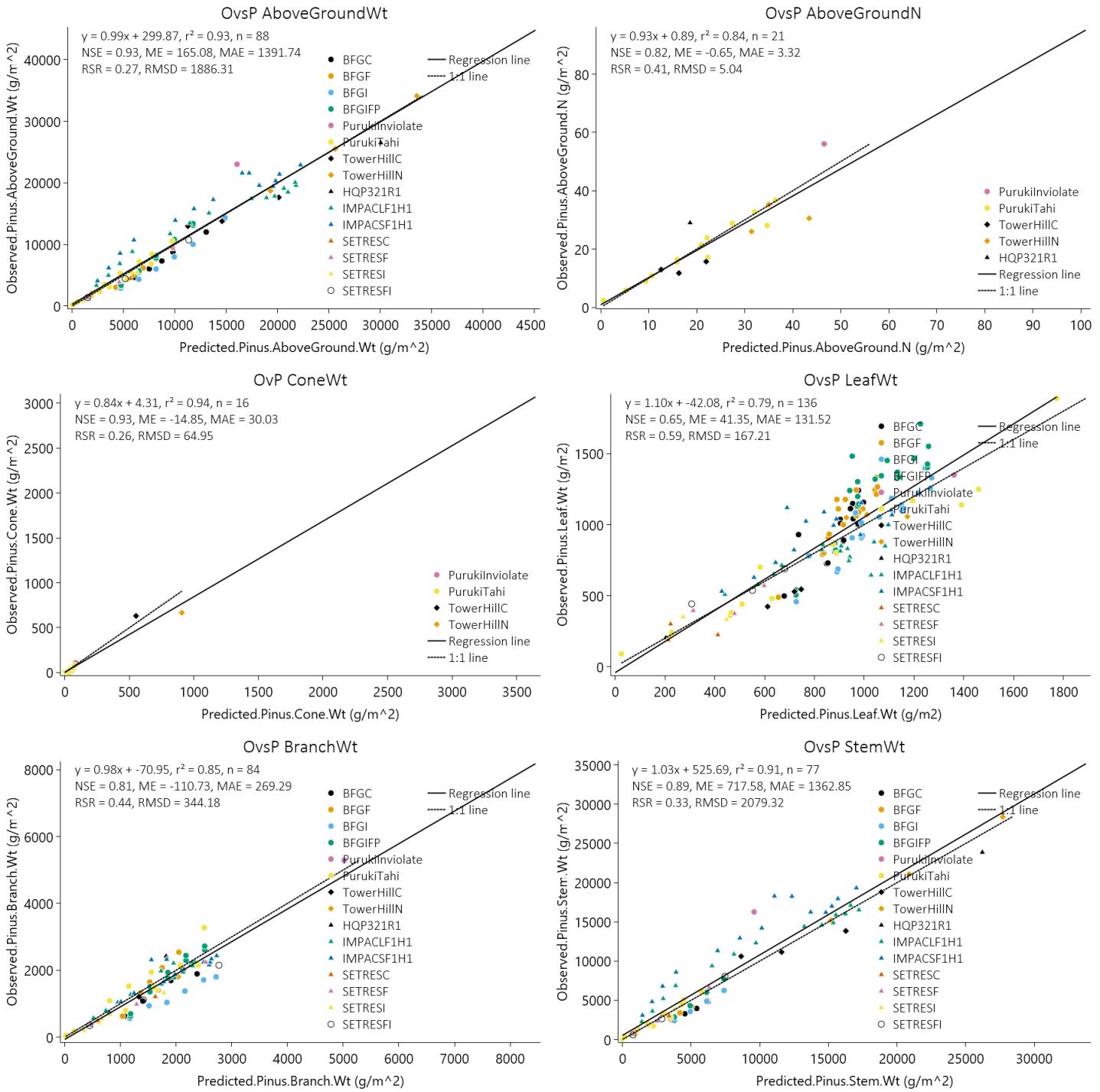
4.2 Combined Validation

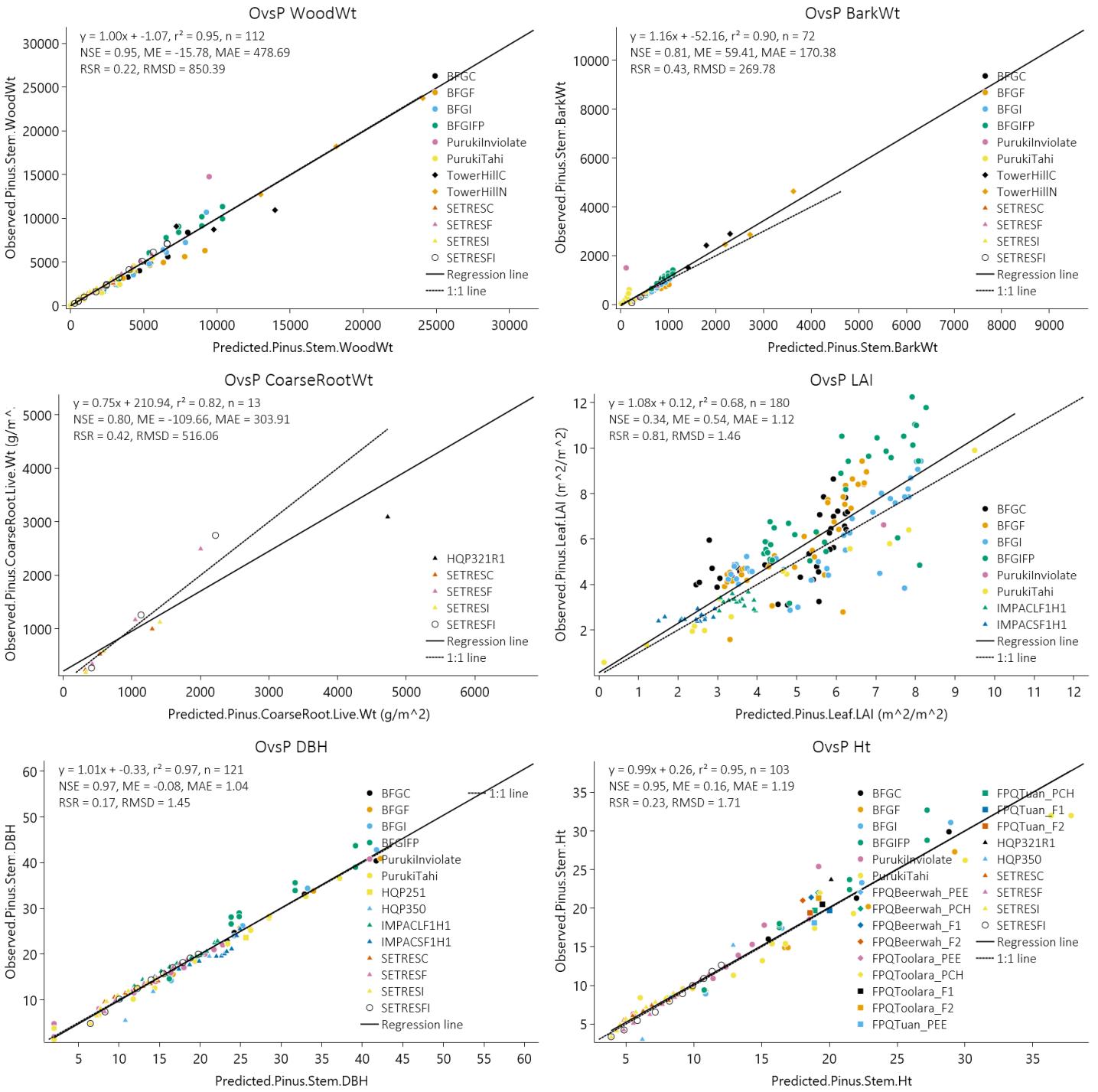
These graphs are for the combined datasets of *Temperate* and *Tropical and SubTropical* climatic zones.

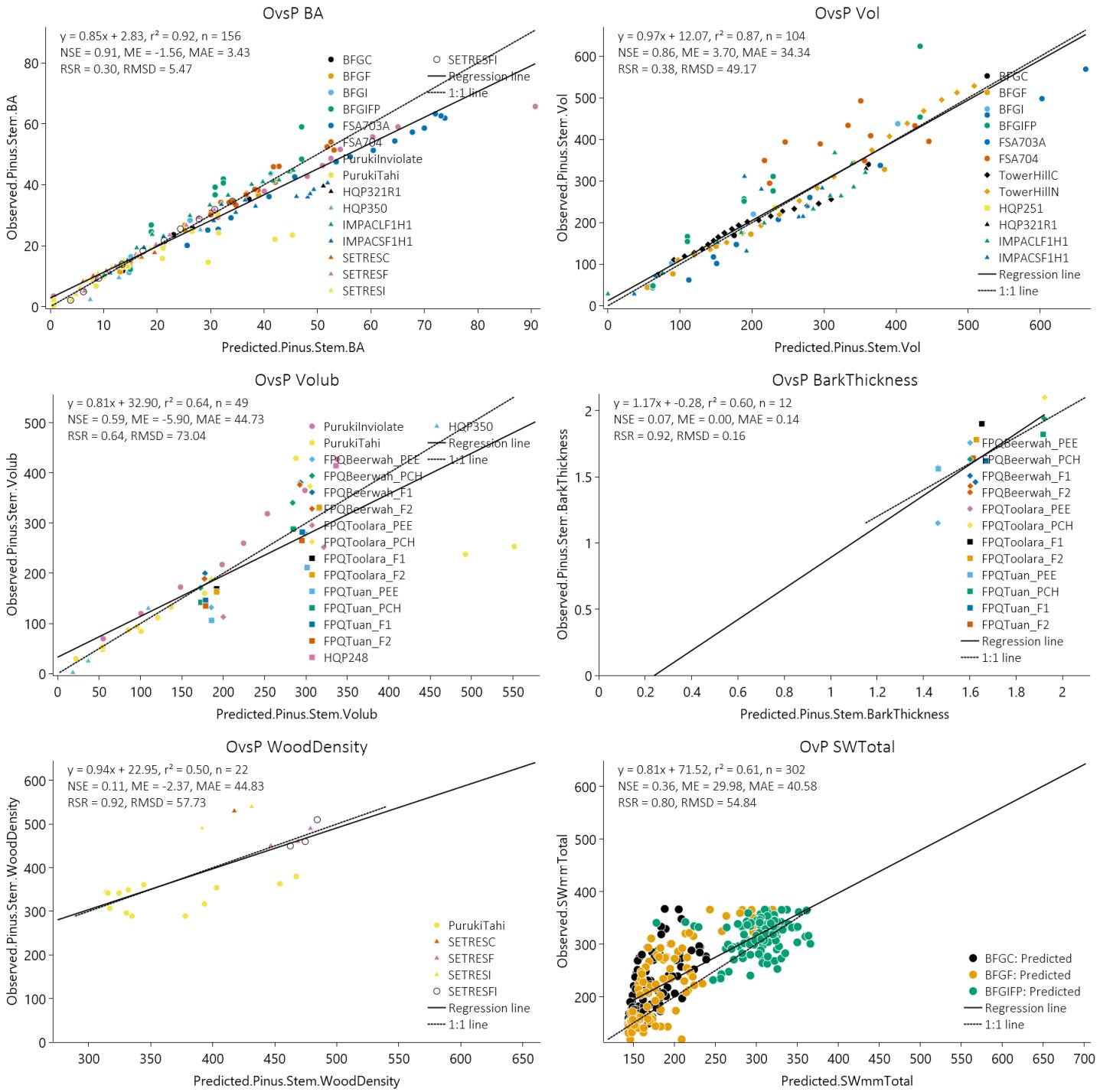
Graphs from individual sites, particularly temporal trends of observed and predicted values, are available but currently disabled. If you wish to view these graphs, please download the validation from GitHub, run it, and enable those graphs and/or add others.

Two sites are simulated to ages beyond when there was a reasonable expectation of satisfactory model skill, due to very low stocking being reached where allocation patterns would probably not have been simulated correctly (Puruki site) or due to not correctly predicting disease-induced loss of tree vigor (IMPAC site). However, all data have been included in these OvP graphs.

Many of these simulations for stem metrics could be further improved by better specifying allometric relations between biomass and tree size, which we know are highly environment-by-genotype specific, but what is provided here is a minimal range of genotypes that were needed to achieve the level of model skill currently shown.







4.3 Temperate

These are the Temperate datasets.

4.3.1 BFG

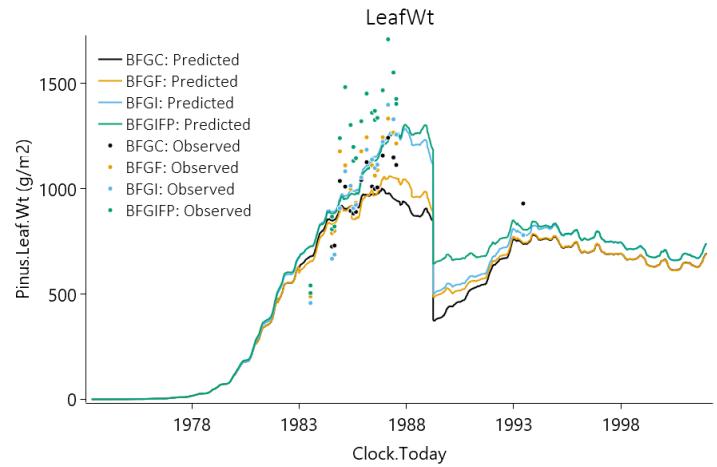
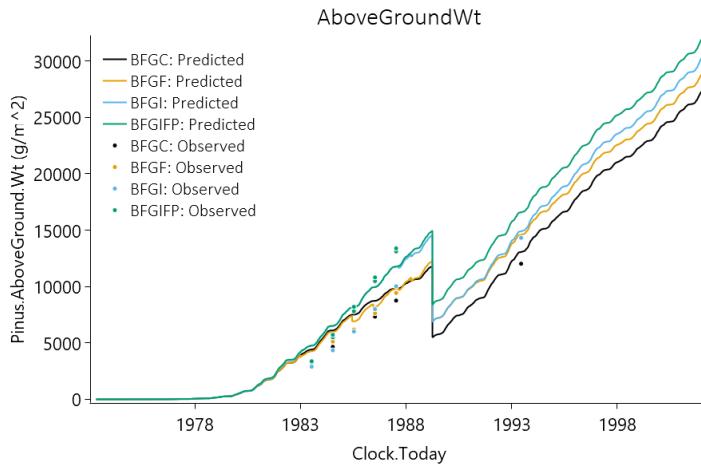
These data are for an experiment with fertilizer, irrigation and fertigation treatments established in a 10-year-old *P. radiata* plantation near Canberra, Australia. The experiment was officially entitled Biology of Forest Growth (BFG) as it focused on improving the physiological understanding of growth of this species in a somewhat common Australian environment.

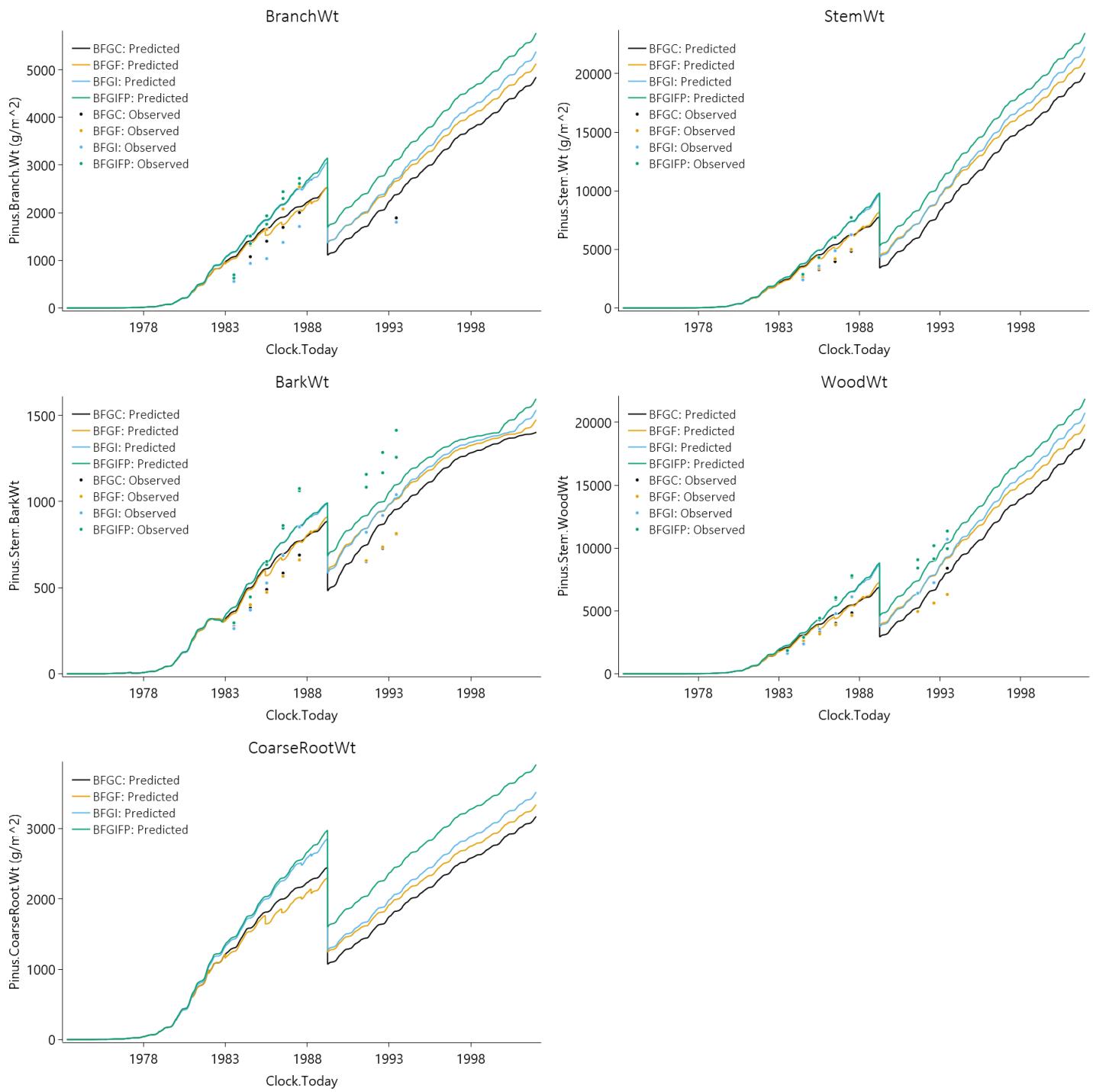
Numerous publications about this experiment reported on its management, tree growth, biomass components, phenology, climate, and soils. Many of these publications were produced in a special issue of *Forest Ecology and Management* (Volume 52, Issues 1–4, September 1992) several from which data have been sourced for developing the APSIM Pimus model: Benson et al., 1992, Benson et al., 1992, Crane et al., 1992, Cremer, 1992, Khanna et al., 1992, Kirschbaum, 1999, McMurtie et al., 1992, Myers et al., 1992, Raison et al., 1992, Raison et al., 1992, Raison et al., 1992, Raison et al., 1990, and Snowdon et al., 1992. A later thesis Pongracic, 2001 and paper Waterworth et al., 2007 also provided data. Many of these data and additional data were also provided by Keryn Paul (CSIRO), which we greatly appreciated.

List of experiments.

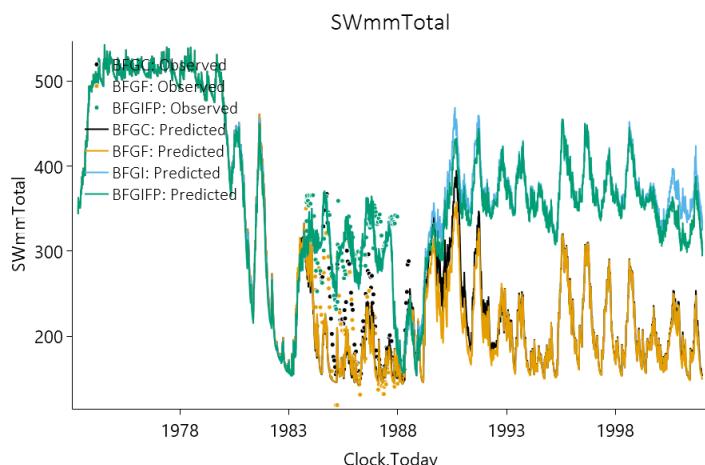
Experiment Name	Design (Number of Treatments)
BF	G (4)

4.3.1.1 GraphsWeights

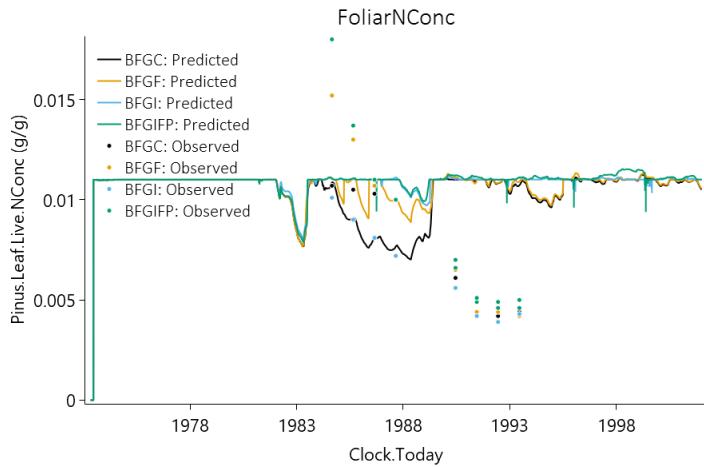




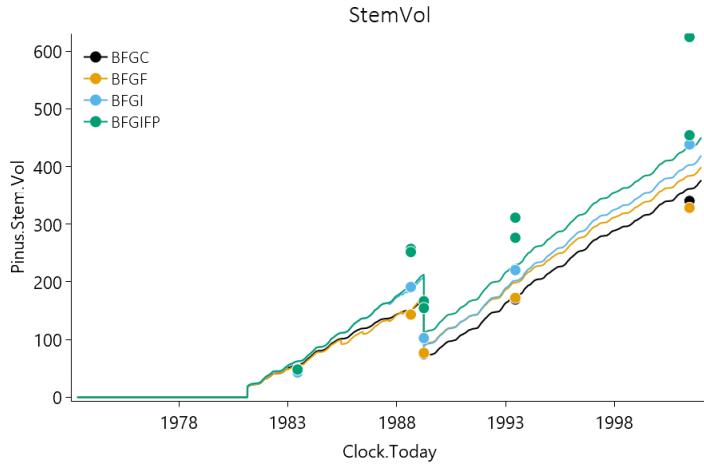
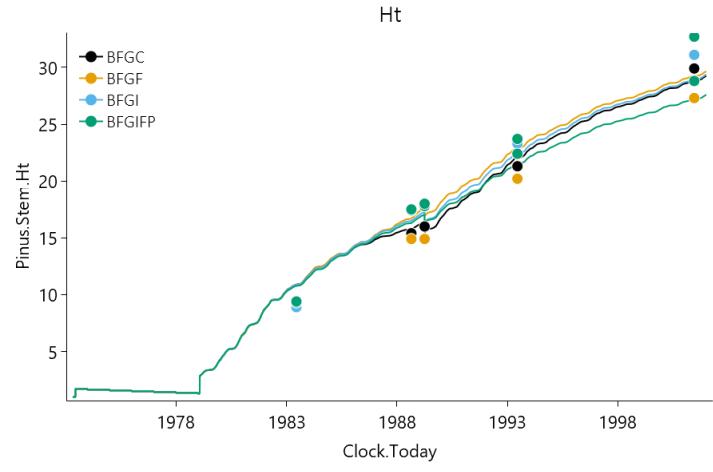
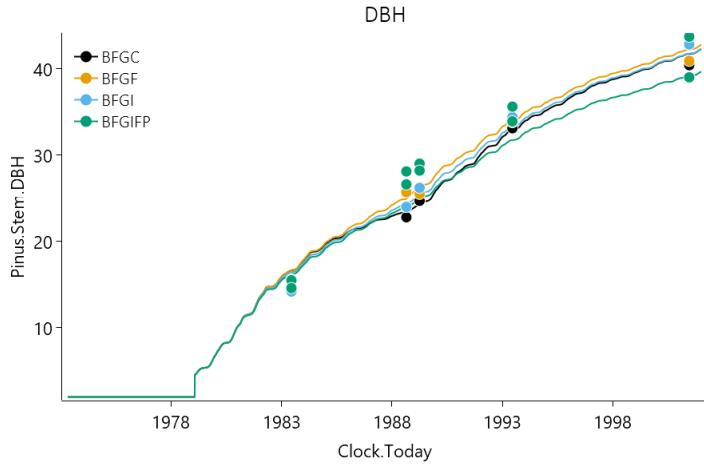
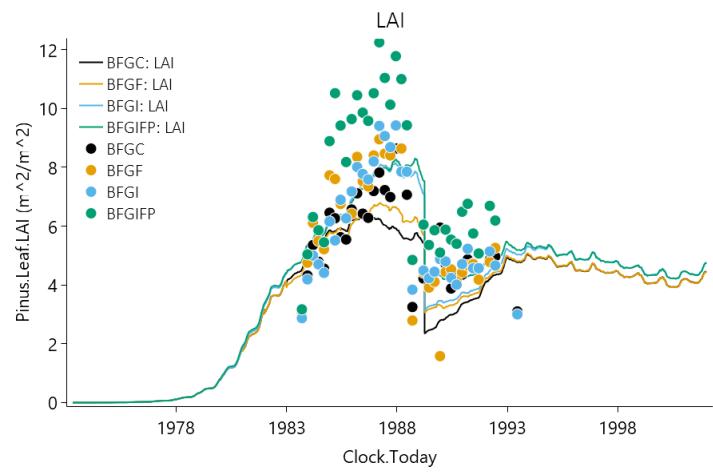
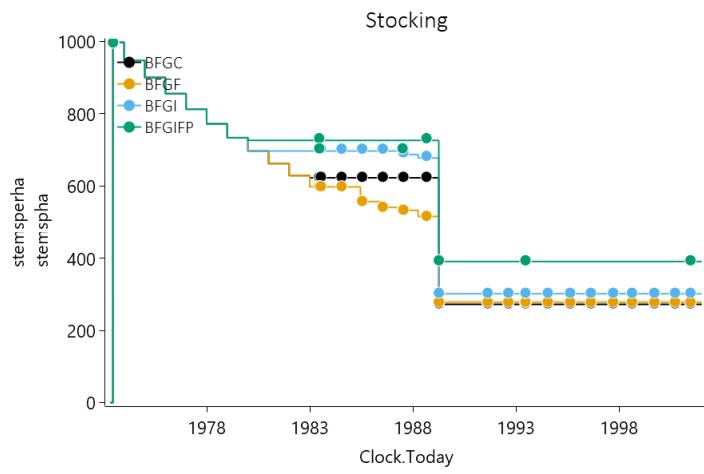
4.3.1.2 GraphsWater



4.3.1.3 GraphsN



4.3.1.4 GraphsMetrics

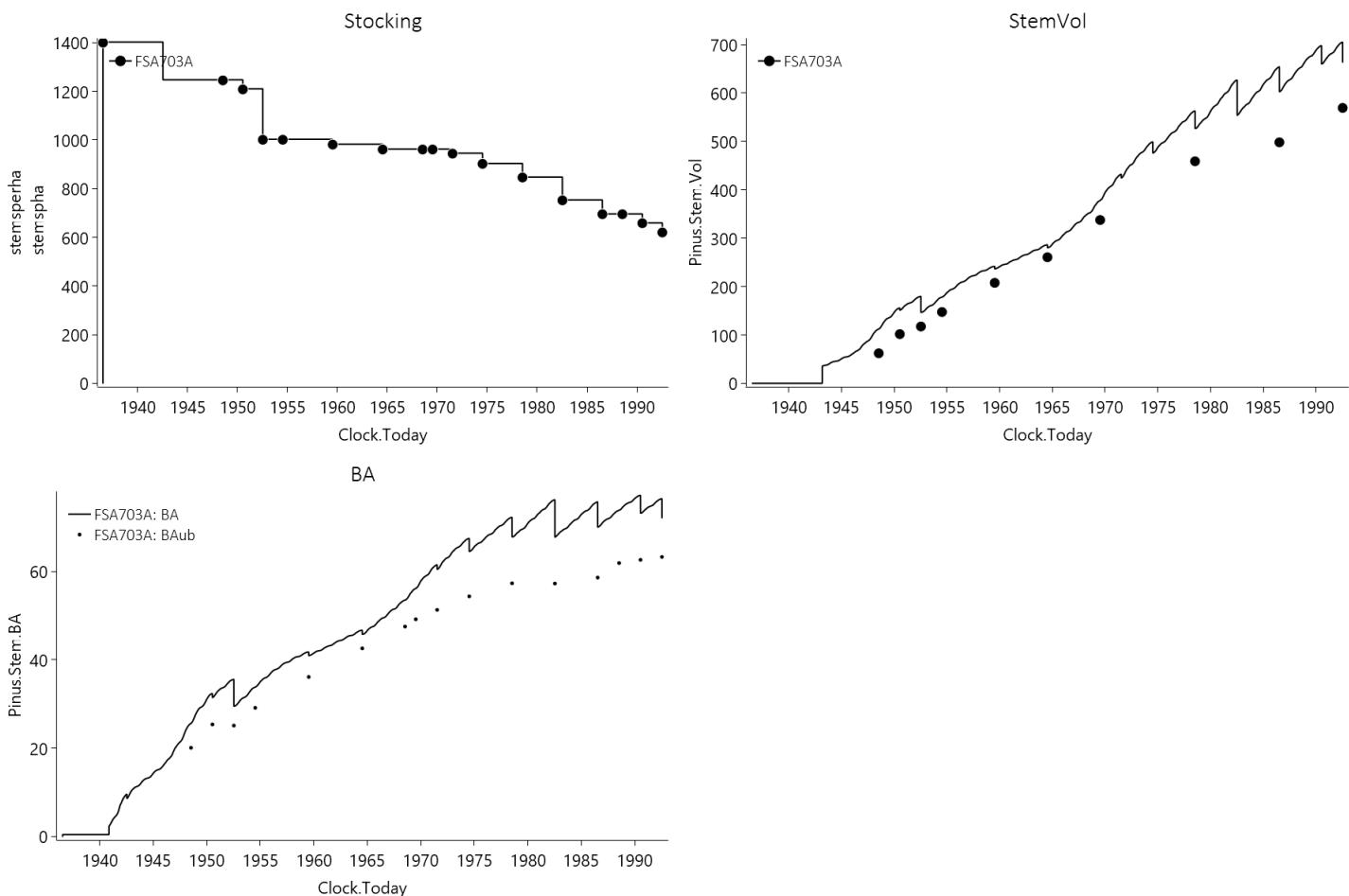


4.3.2 FSA703A

These data are a plot in operational plantations that were previously managed by Forestry South Australia (FSA). We appreciate the provision of data by Jim O'Hehir. This plot reached an old age relative to many other *P. radiata* plantations in the world.

4.3.2.1 Graphs

4.3.2.1.1 GraphsMetrics

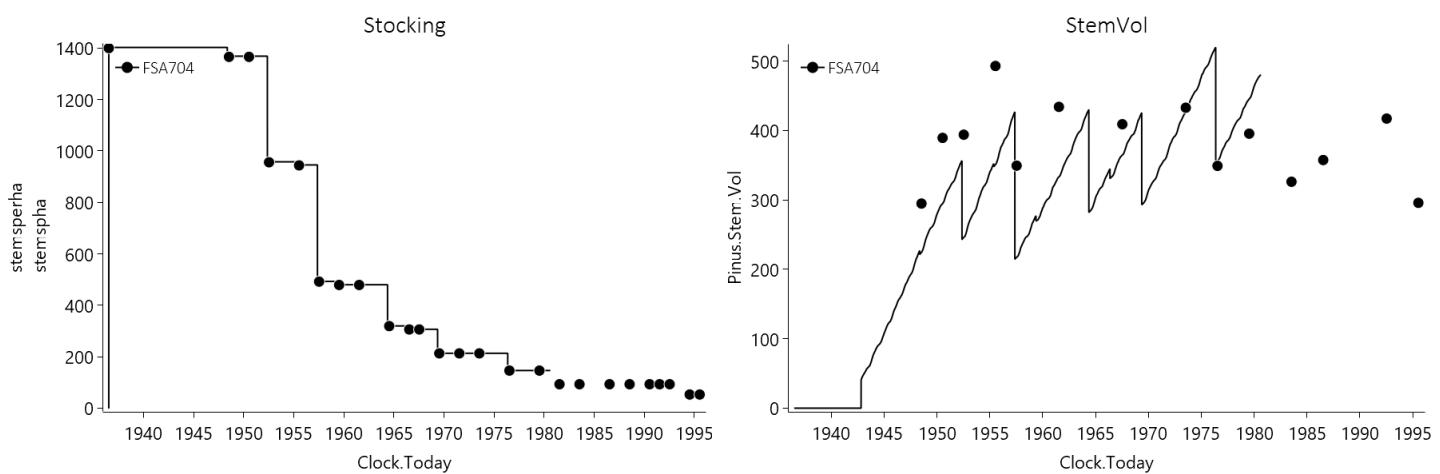


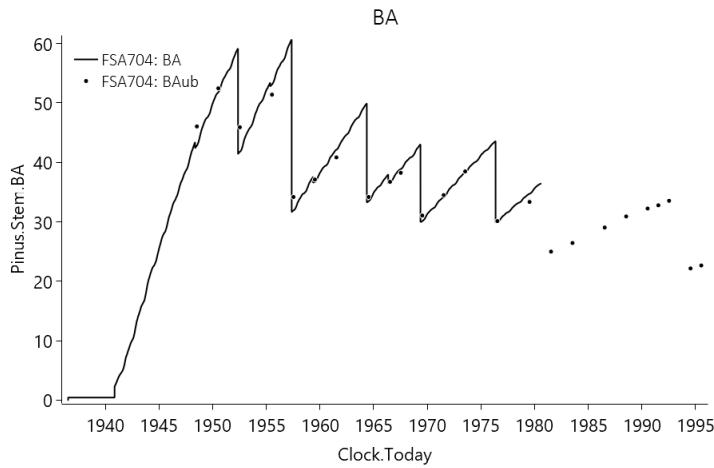
4.3.3 FSA704

These data are a plot in operational plantations that were previously managed by Forestry South Australia (FSA). We appreciate the provision of data by Jim O'Hehir. This plot reached an old age relative to many other *P. radiata* plantations in the world.

4.3.3.1 Graphs

4.3.3.1.1 GraphsMetrics





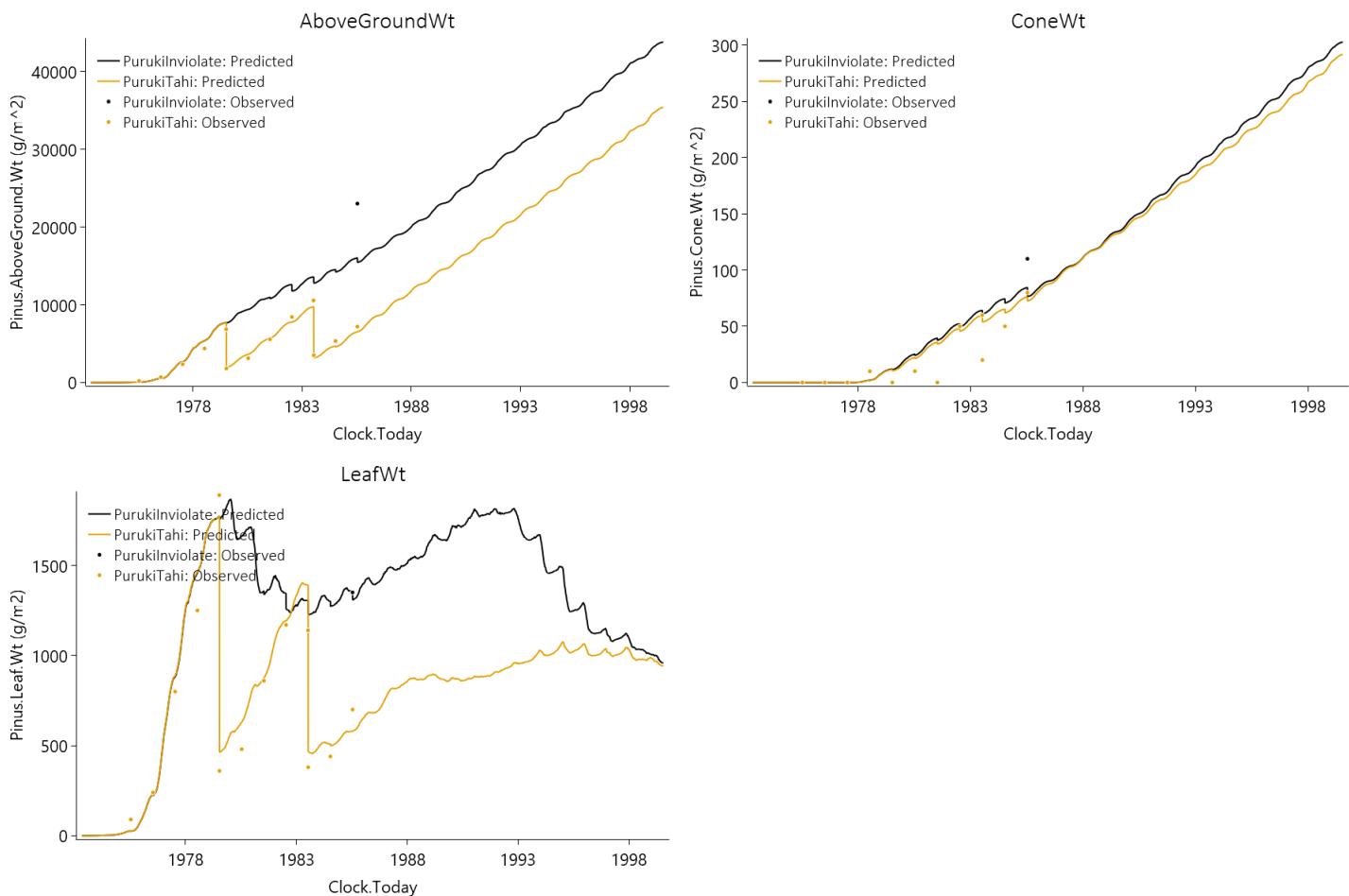
4.3.4 Puruki

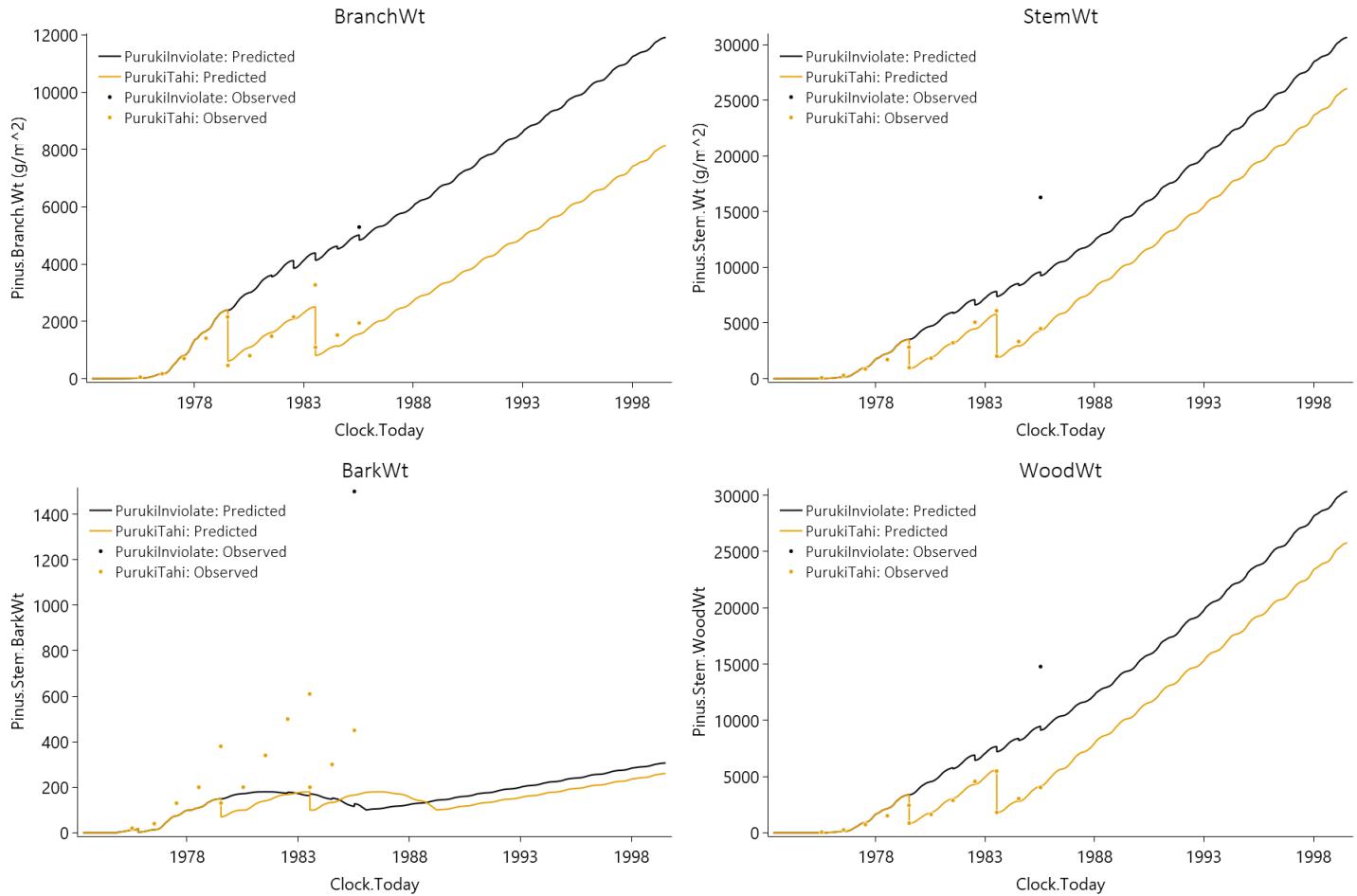
These data are from one plot at a highly productive site in New Zealand. Studies at the site included physiology and growth, nutrition, soils and hydrology, which were published. This site was of particular interest for this validation because it had high nutrient availability and high rainfall, and it was well-published. Publications drawn on were [Rijkse et al., 1974](#), [Beets et al., 1987](#), [Dyck et al., 1987](#), [Beets et al., 1996](#), [Parfitt et al., 2006](#), [Kimberley et al., 2007](#), [Oliver et al., 2004](#), [Beets et al., 2007](#), [Beets et al., 2011](#), [Beets et al., 2018](#), Beets et al (2018 Puruki field trip - a productive ex-pasture site DOI:10.13140/RG.2.2.16726.50243), [Garrett et al., 2019](#), and [Beets et al., 2020](#).

List of experiments.

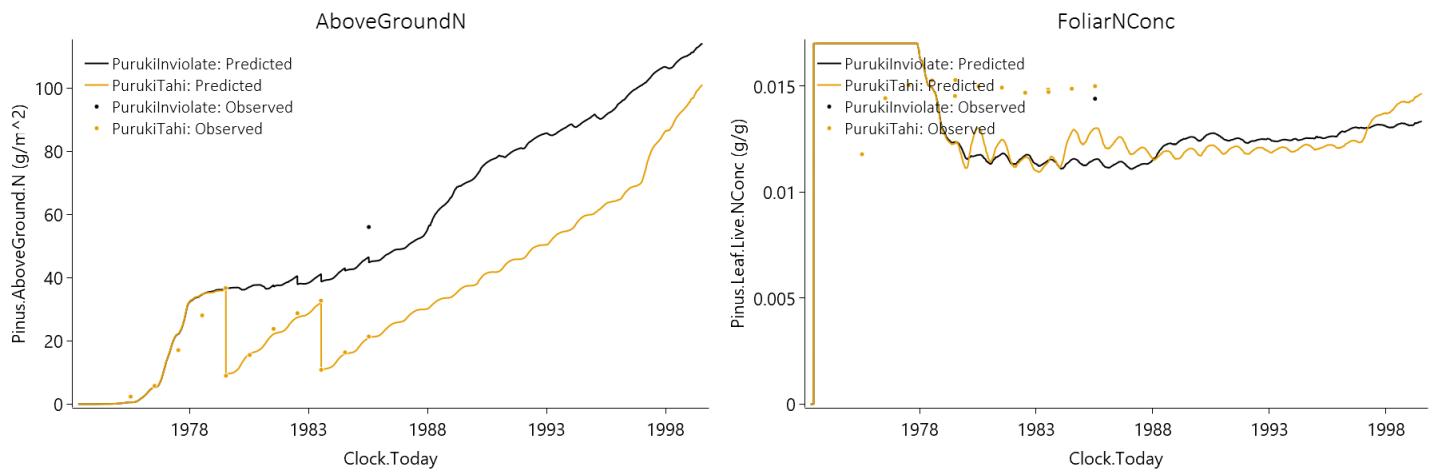
Experiment Name	Design (Number of Treatments)
Puruk	i (2)

4.3.4.1 GraphsWeights

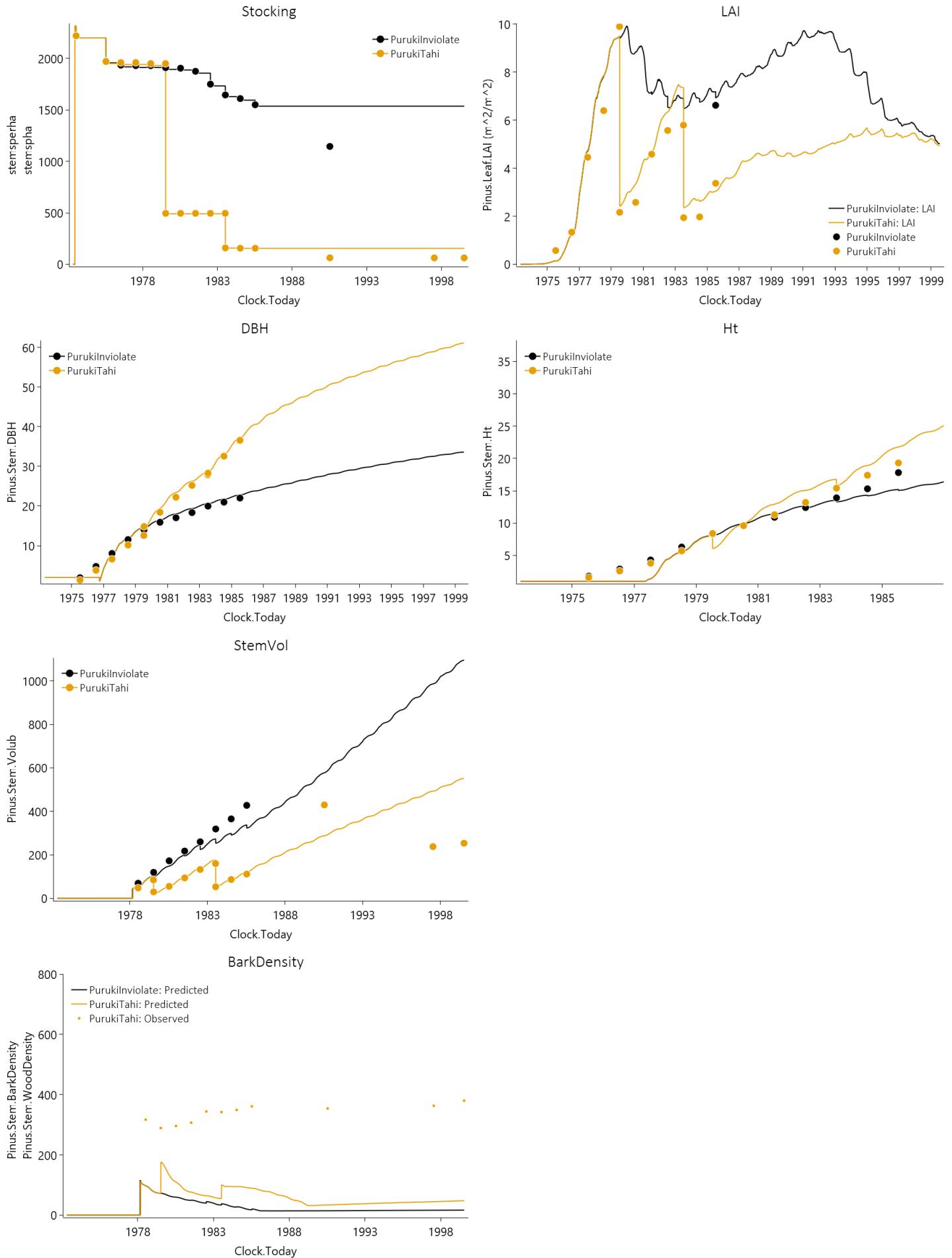


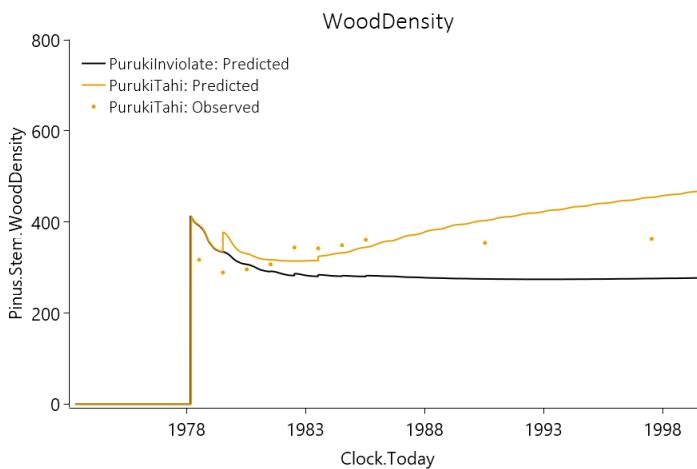


4.3.4.2 GraphsN



4.3.4.3 GraphsMetrics





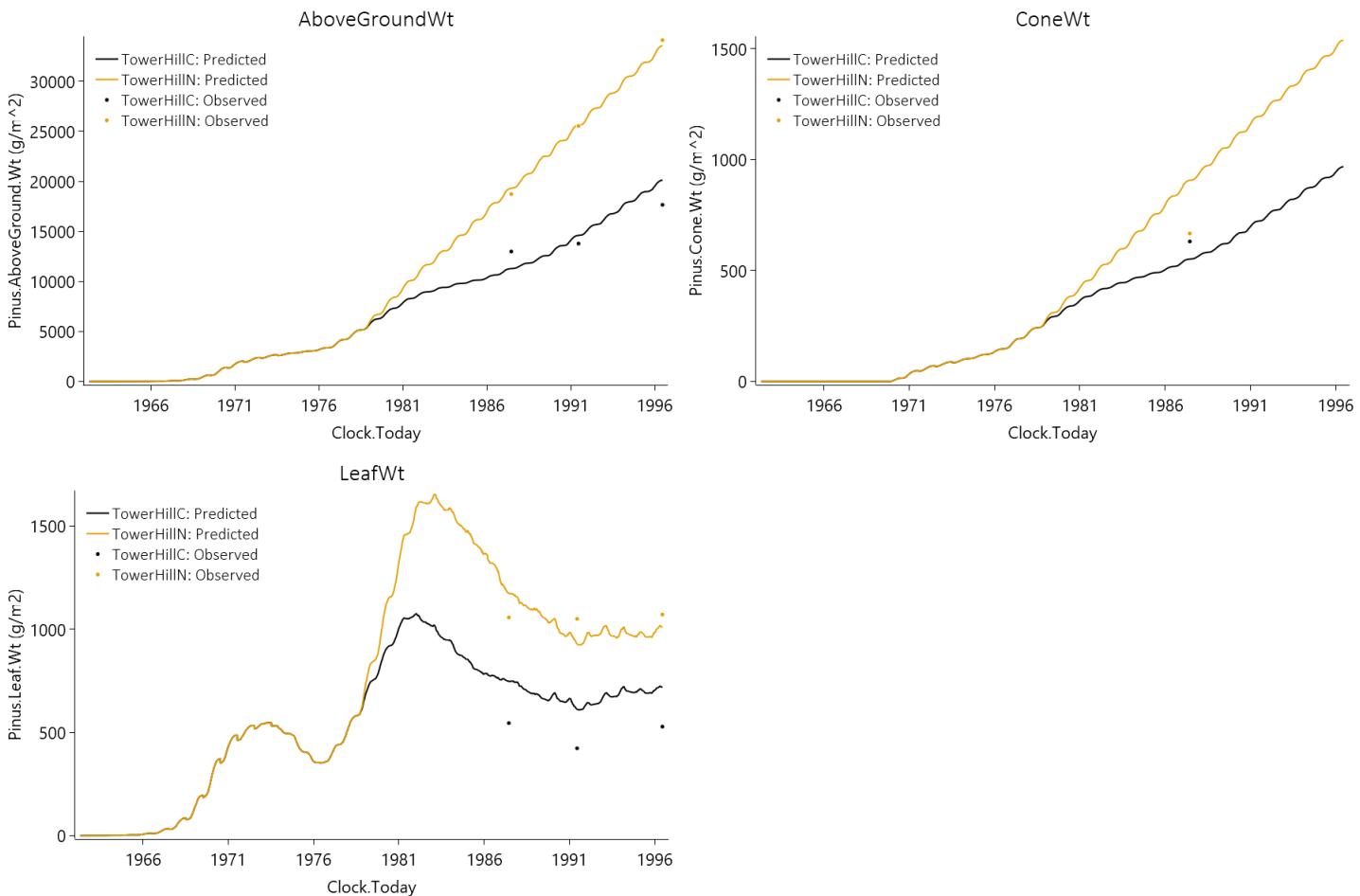
4.3.5 TowerHill

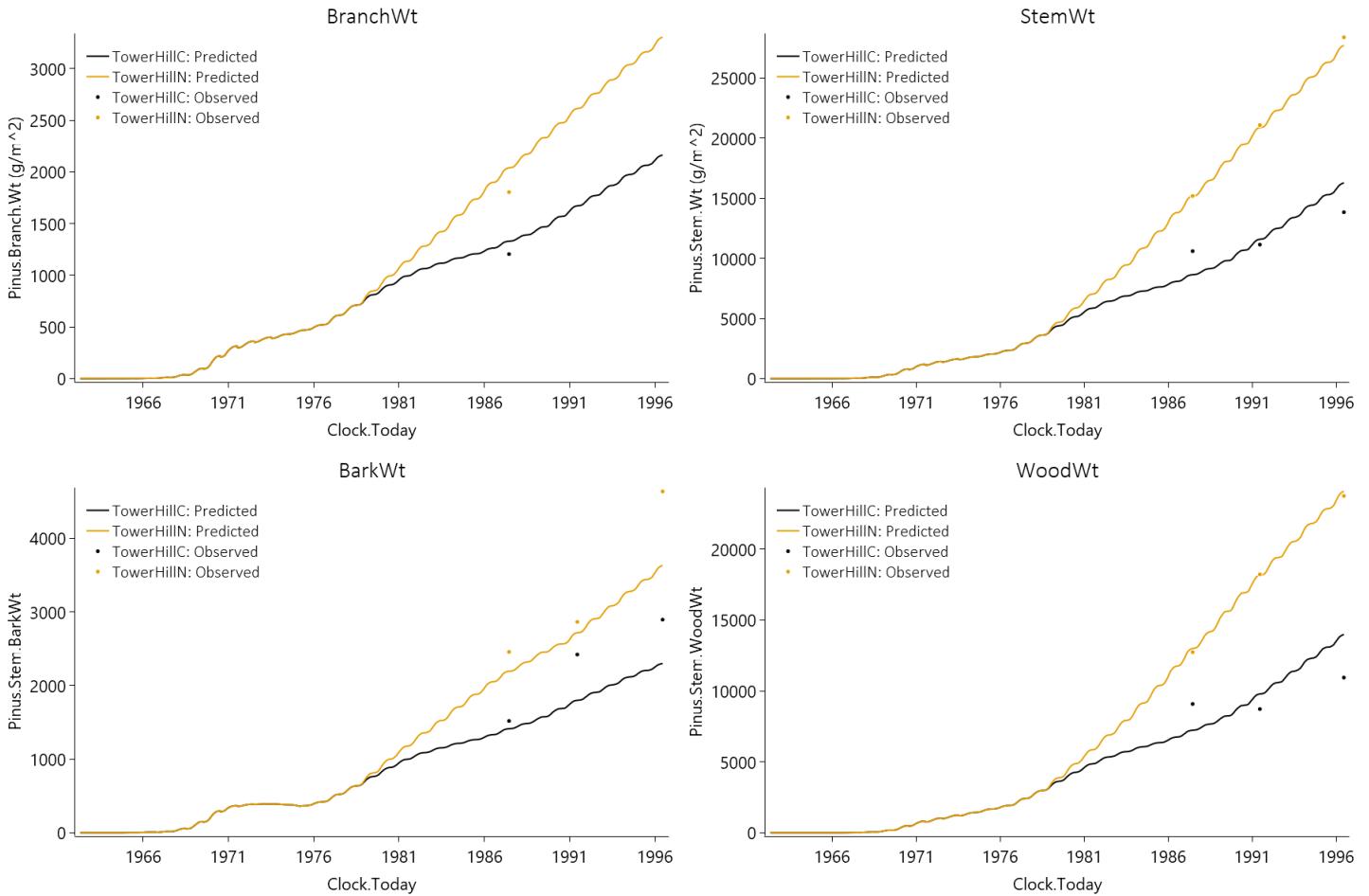
These data are from an experiment with fertilizer on very shallow soils with moderate rainfall. Substantial rates of accumulated N applications changed the C-N dynamics of the site and stand growth. Data were reported in [Neilsen et al., 1992](#) and [Neilsen et al., 1998](#), and some details were checked in the original files with permission of the current manager of the site (Sustainable Timber Tasmania).

List of experiments.

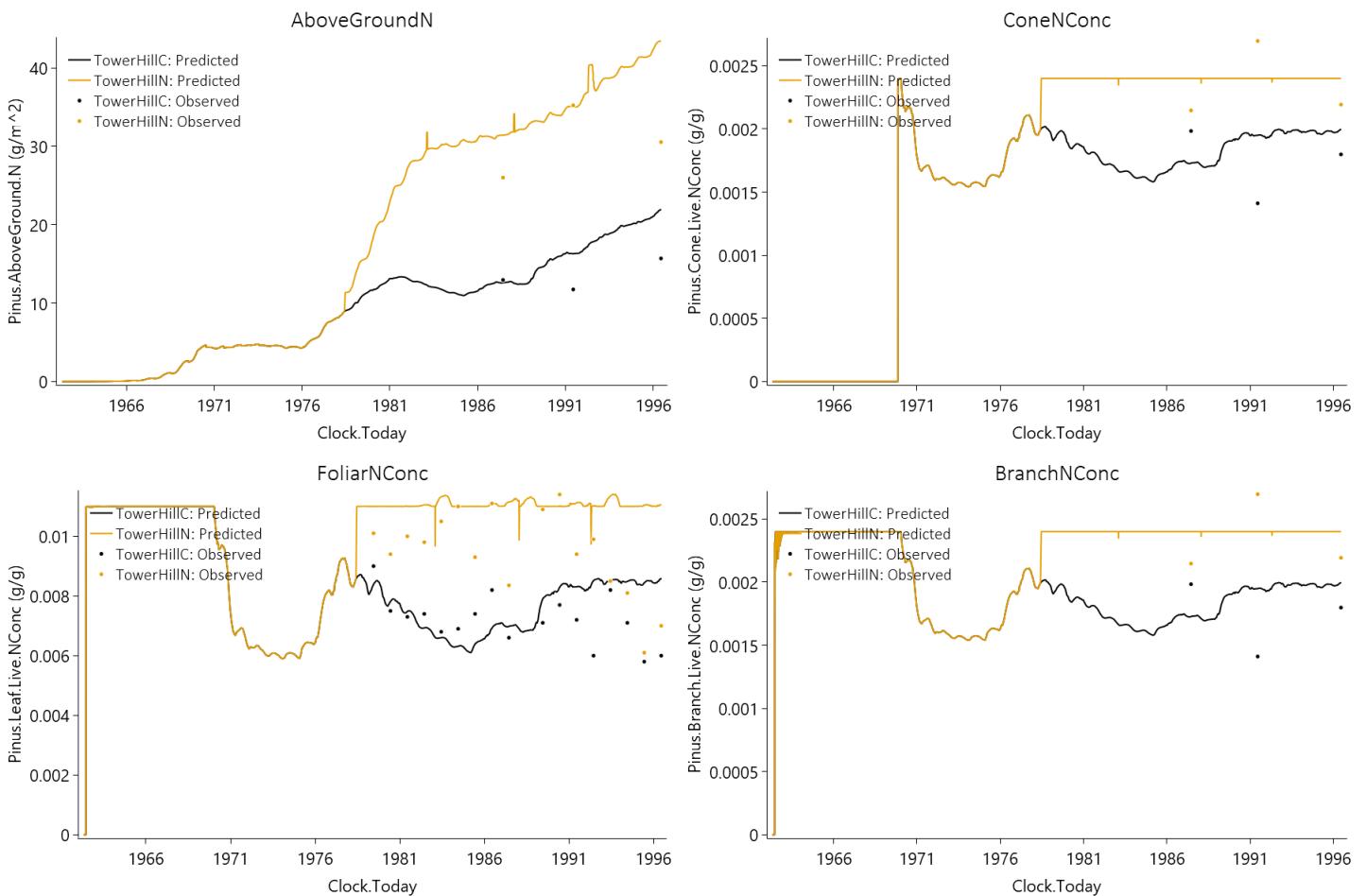
Experiment Name	Design (Number of Treatments)
TowerHil	I (2)

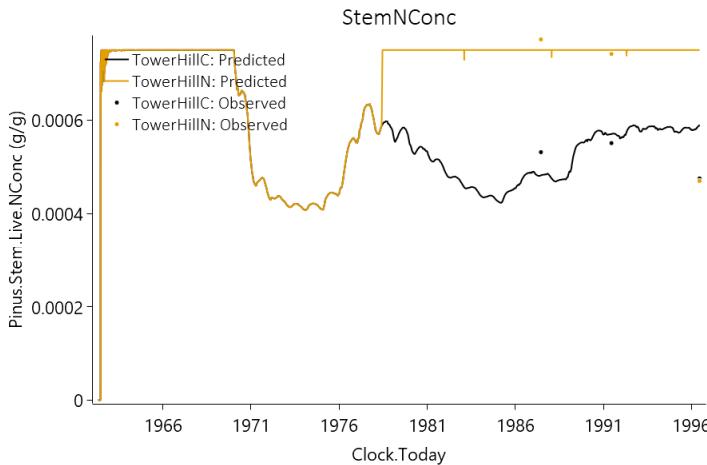
4.3.5.1 GraphsWeights



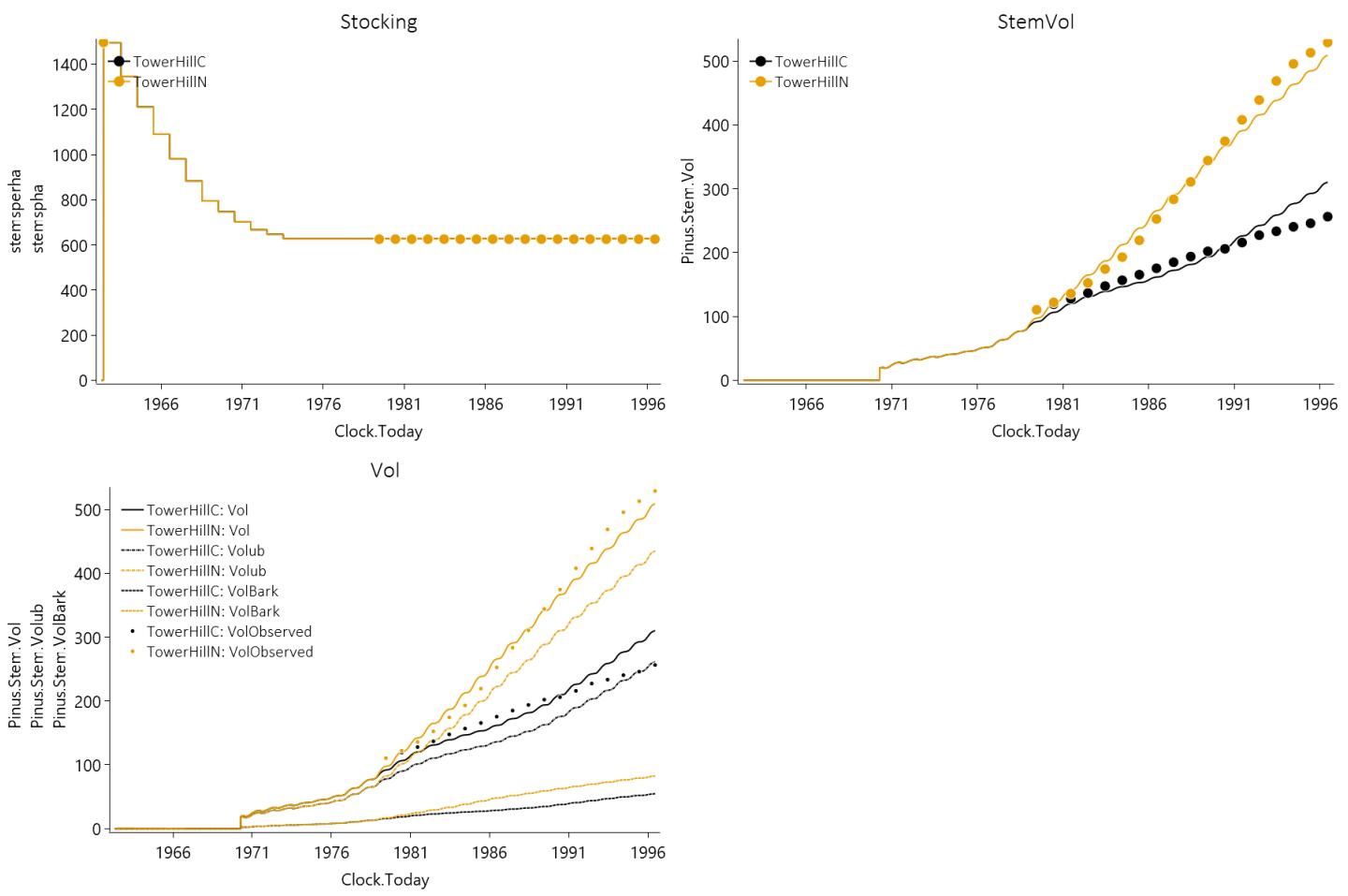


4.3.5.2 GraphsN





4.3.5.3 GraphsMetrics



4.4 Tropical and SubTropical

These are the Tropical and SubTropical datasets.

4.4.1 Australia

These are the Australian sites of the Tropical and SubTropical datasets.

Data come from sites of Forestry Plantations Queensland (FPQ; [Dieters et al., 2007](#)) and Hancocks Queensland Plantations (HQP).

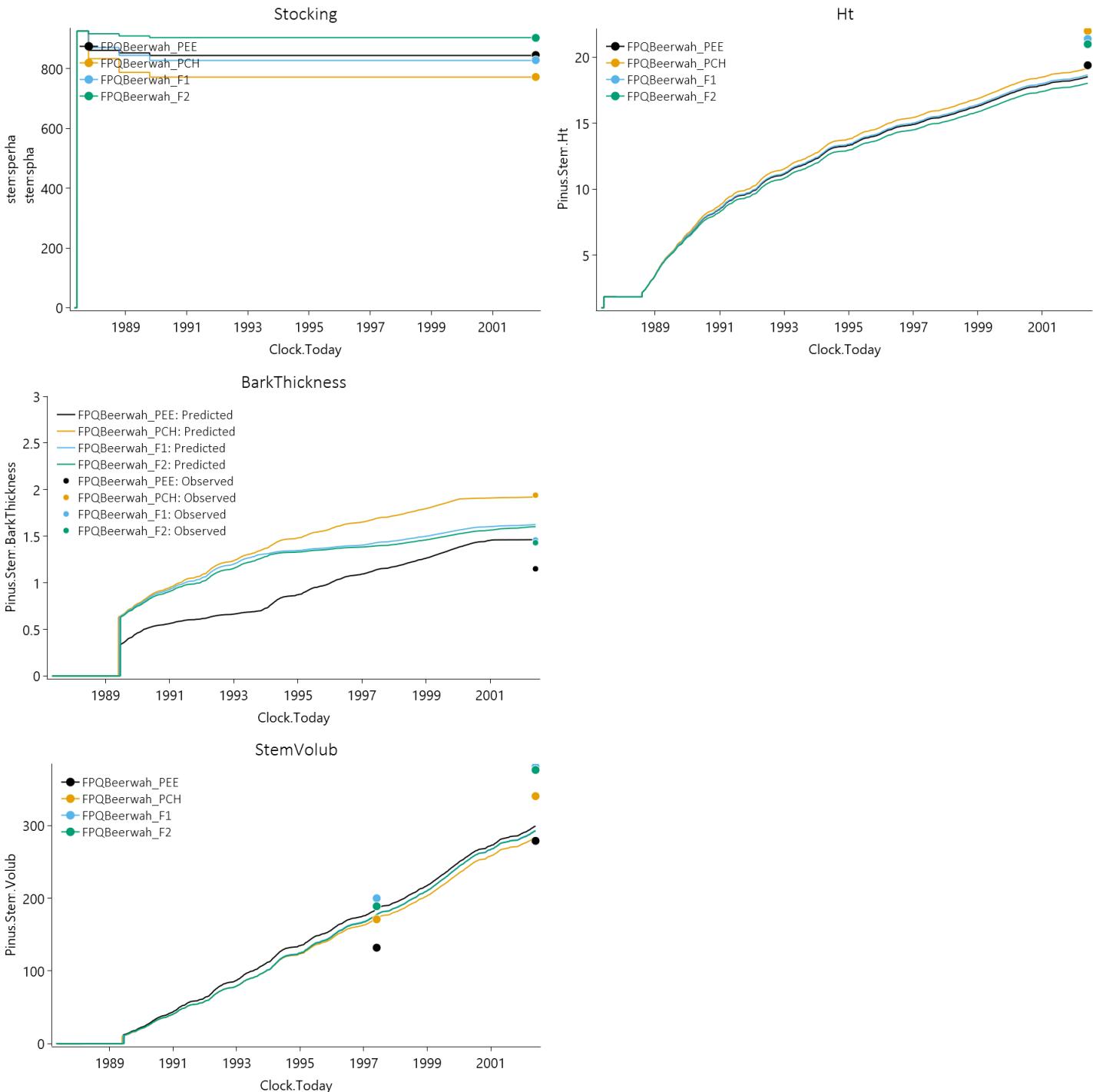
4.4.1.1 FPQBeerwah

These data are from a genetics experiment in south-east Queensland described by [Dieters et al., 2007](#). Four genotypes are compared: *P. elliottii* var. *elliottii* (PEE), *P. caribaea* var. *hondurensis* (PCH), the F1 hybrid, and the F2 hybrid. As only stem metrics were provided in the paper, genotypes were not calibrated for biomass components and other physiological attributes.

List of experiments.

Experiment Name	Design (Number of Treatments)
FPQBeerwah	_ (4)

4.4.1.1.1 GraphsMetrics



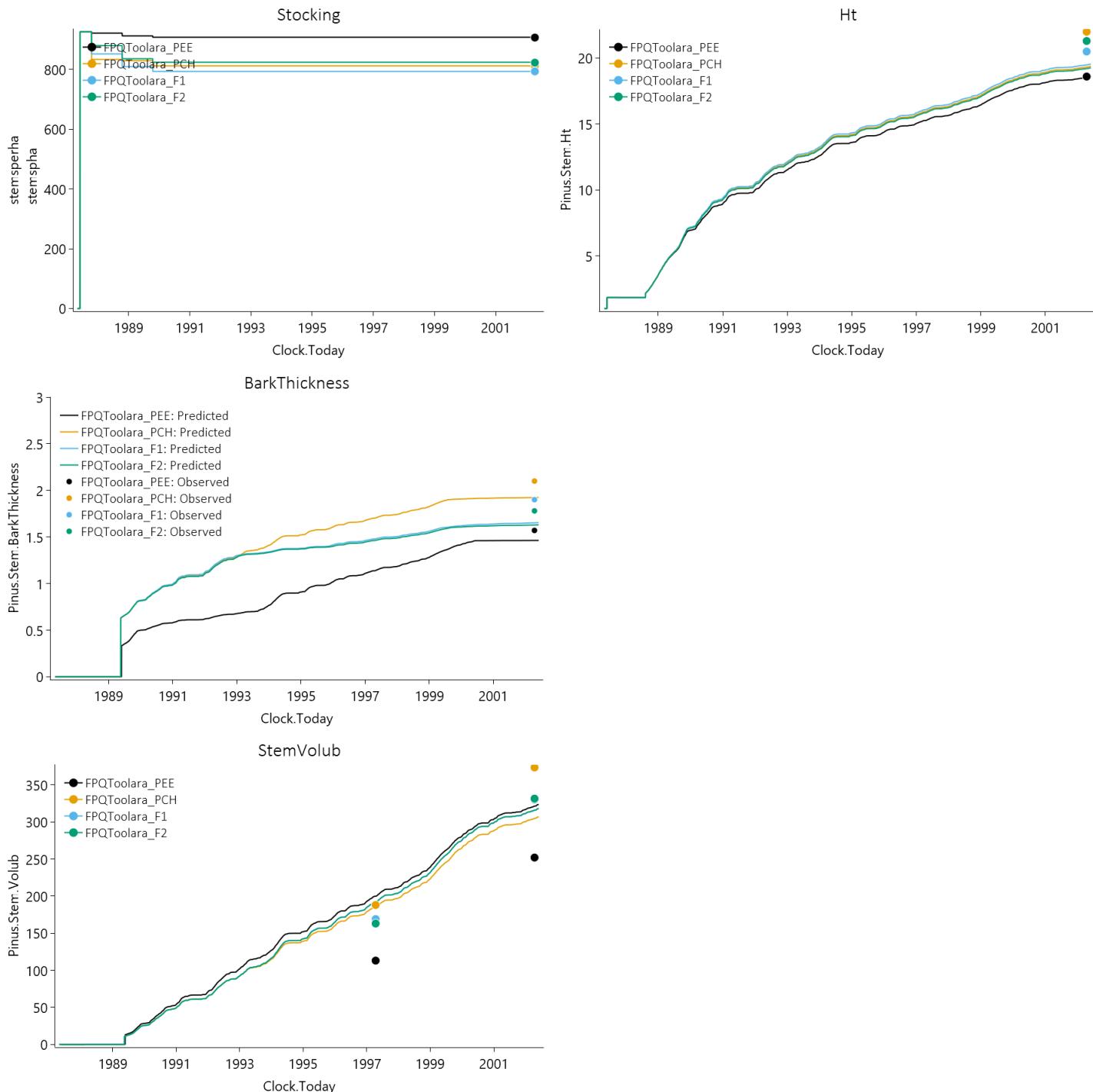
4.4.1.2 FPQToolara

These data are from a genetics experiment in south-east Queensland described by [Dieters et al., 2007](#). Four genotypes are compared: *P. elliottii* var. *elliottii* (PEE), *P. caribaea* var. *hondurensis* (PCH), the F1 hybrid, and the F2 hybrid. As only stem metrics were provided in the paper, genotypes were not calibrated for biomass components and other physiological attributes.

List of experiments.

Experiment Name	Design (Number of Treatments)
FPQToolara	_ (4)

4.4.1.2.1 GraphsMetrics



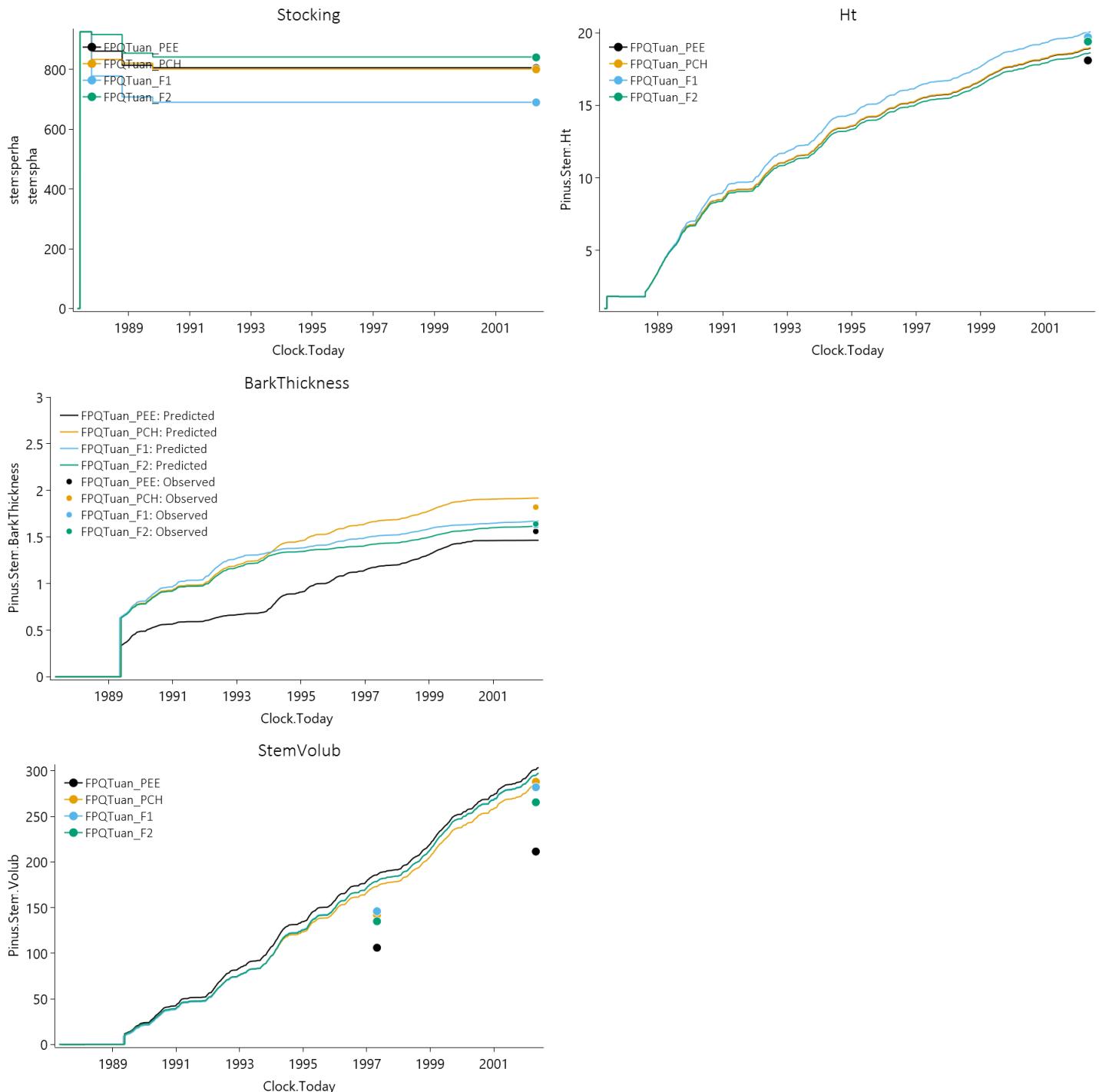
4.4.1.3 FPQTuan

These data are from a genetics experiment in south-east Queensland described by [Dieters et al., 2007](#). Four genotypes are compared: *P. elliottii* var. *elliottii* (PEE), *P. caribaea* var. *hondurensis* (PCH), the F1 hybrid, and the F2 hybrid. As only stem metrics were provided in the paper, genotypes were not calibrated for biomass components and other physiological attributes.

List of experiments.

Experiment Name	Design (Number of Treatments)
FPQTuan	_ (4)

4.4.1.3.1 GraphsMetrics

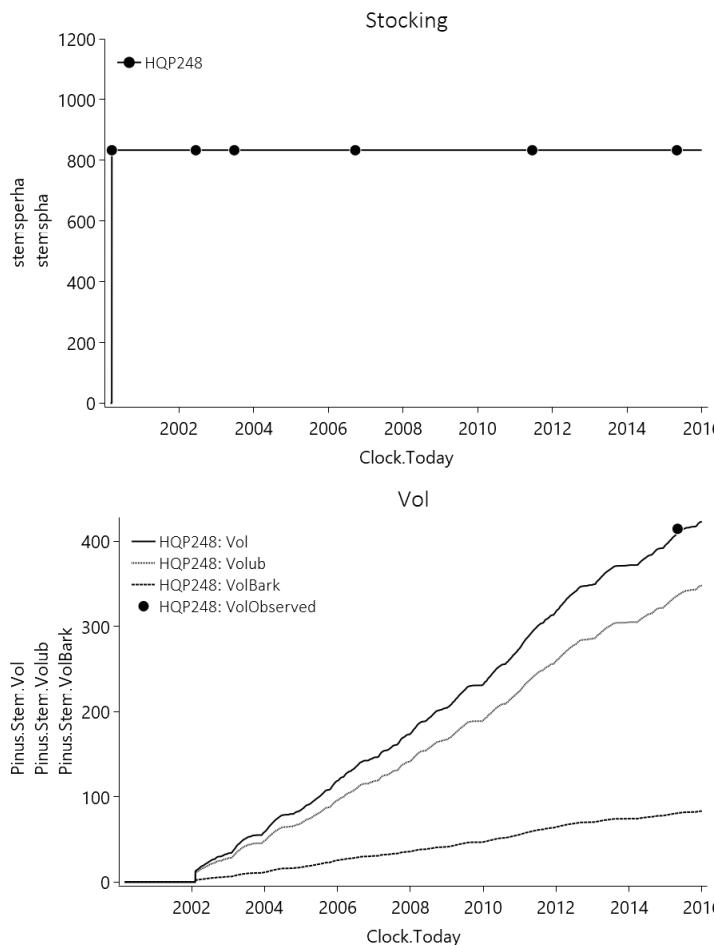


4.4.1.4 HQP248

These data were kindly provided by Hancock Queensland Plantations (HQPlantations, HQP) from Experiment 248 MBR, which was established to determine the most appropriate taxa (including stock production systems) and site preparation prescription(s) for use on wet sites in south-east Queensland. As the model was not designed to simulate various details of each treatment, only one of the best performing treatment was simulated (Experiment 248MBR, Treatment F1-Container-LargeMound).

4.4.1.4.1 Graphs

4.4.1.4.1.1 GraphsMetrics

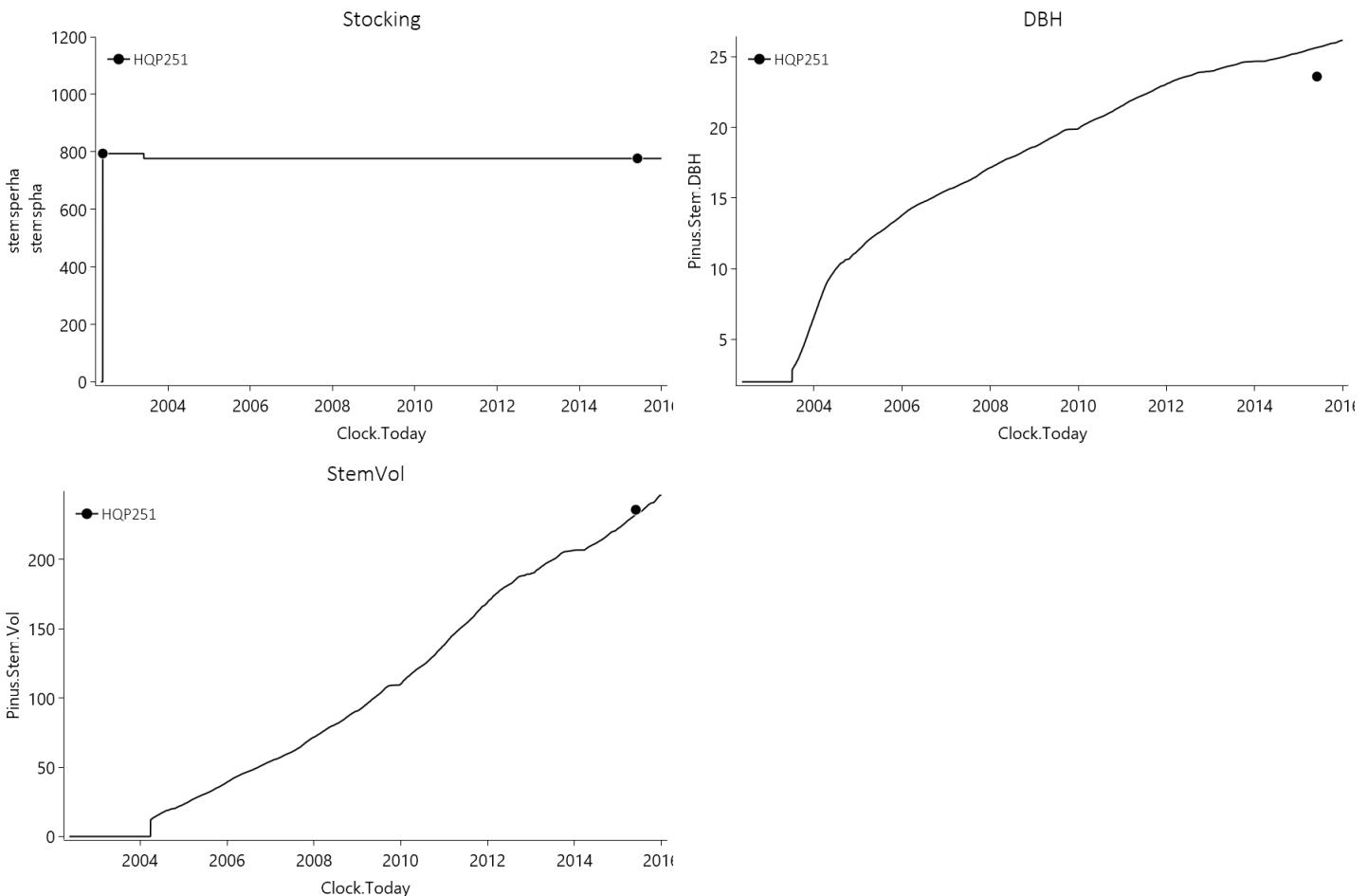


4.4.1.5 HQP251

These data were kindly provided by Hancock Queensland Plantations (HQPlantations) from Experiment 251 MBR, which was established to investigate the impact of various 2R site preparation methods at a high-mounded first rotation (1R) site with hard-setting soil in south-east Queensland. As the model was not designed to simulate various details of each treatment, only one of the best performing treatments was simulated (Experiment 251MBR, Treatment F1-MB6).

4.4.1.5.1 Graphs

4.4.1.5.1.1 GraphsMetrics

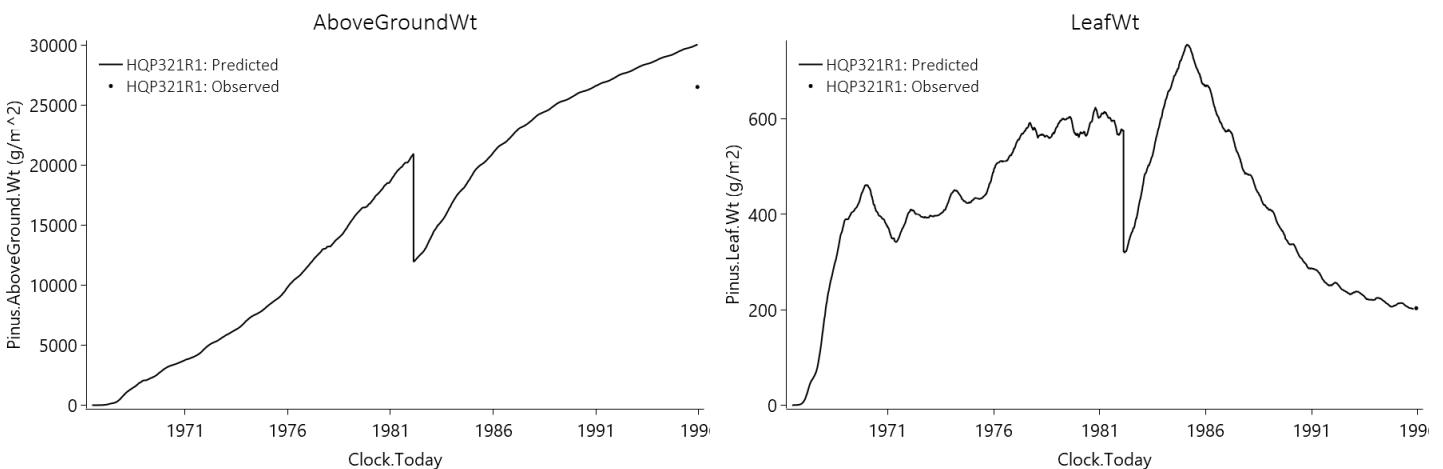


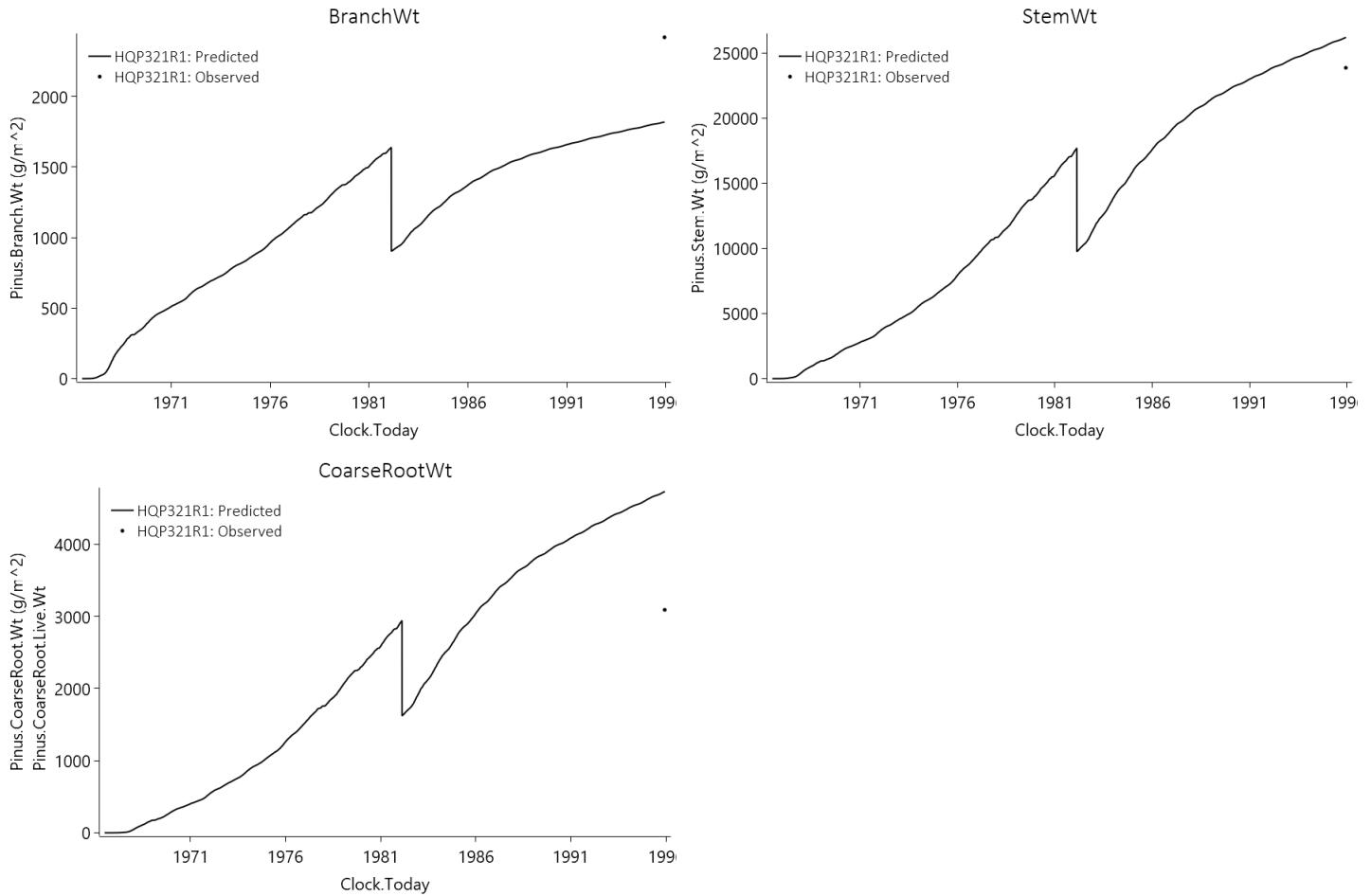
4.4.1.6 HQP321R1

These data were kindly provided by Hancock Queensland Plantations (HQPlantations) from Experiment 321GYM, which was established to:(1) examine the impacts of slash management, fertilization and cover crops on tree growth and nutrient status; (2) quantify the effects on soil properties; and (3) contribute to the CIFOR international network of long term experiments designed to identify and develop sustainable inter-rotation management practices. Early results were reported in [Simpson et al., 2000](#). Data here are reported only for the first rotation (1R) to age 29.4 years.

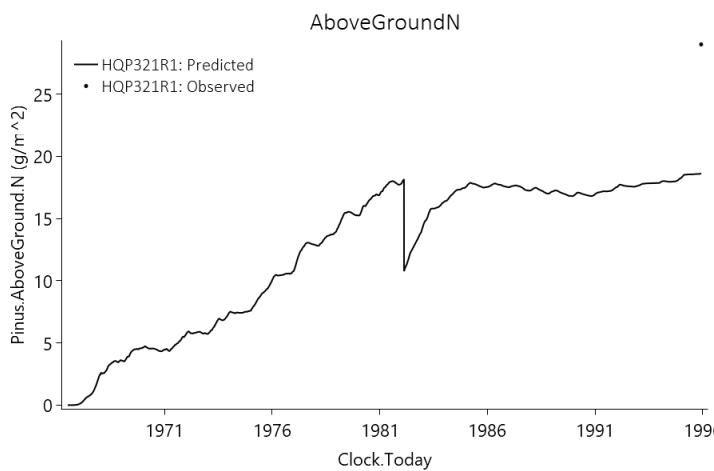
4.4.1.6.1 Graphs

4.4.1.6.1.1 GraphsWeights

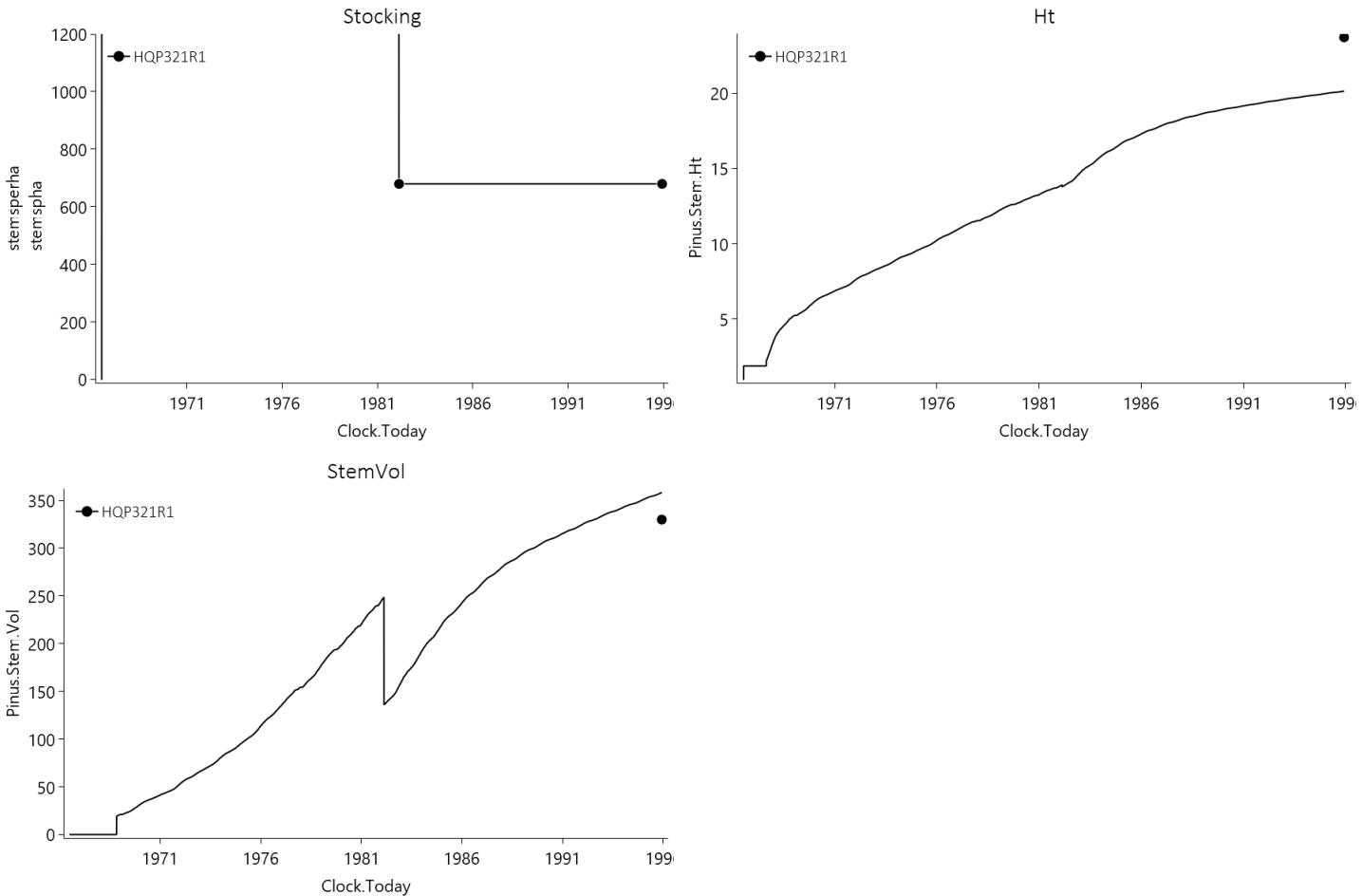




4.4.1.6.1.2 GraphsN



4.4.1.6.1.3 GraphsMetrics

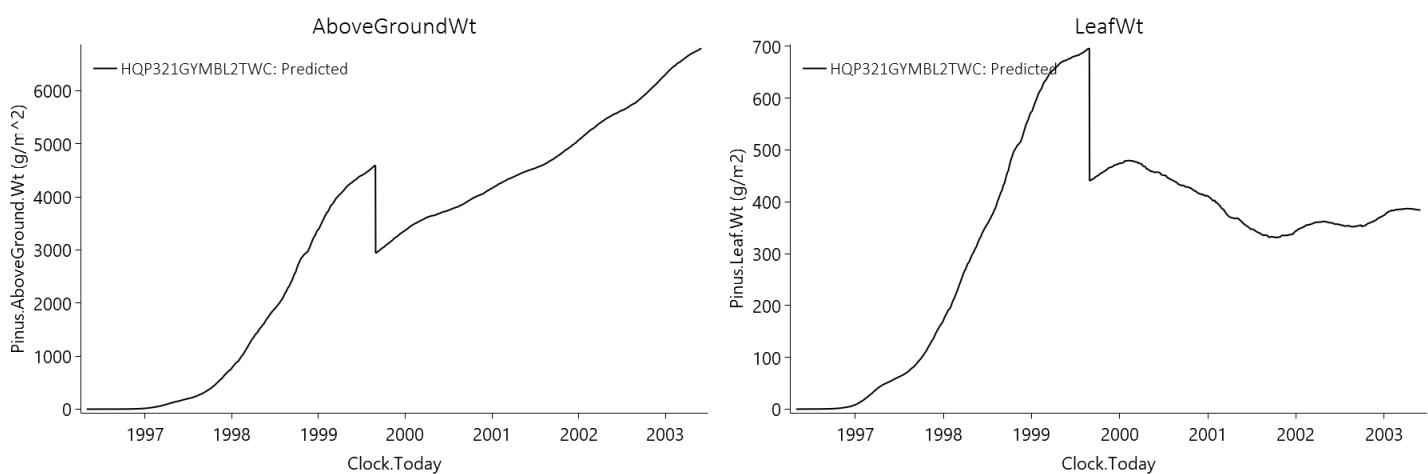


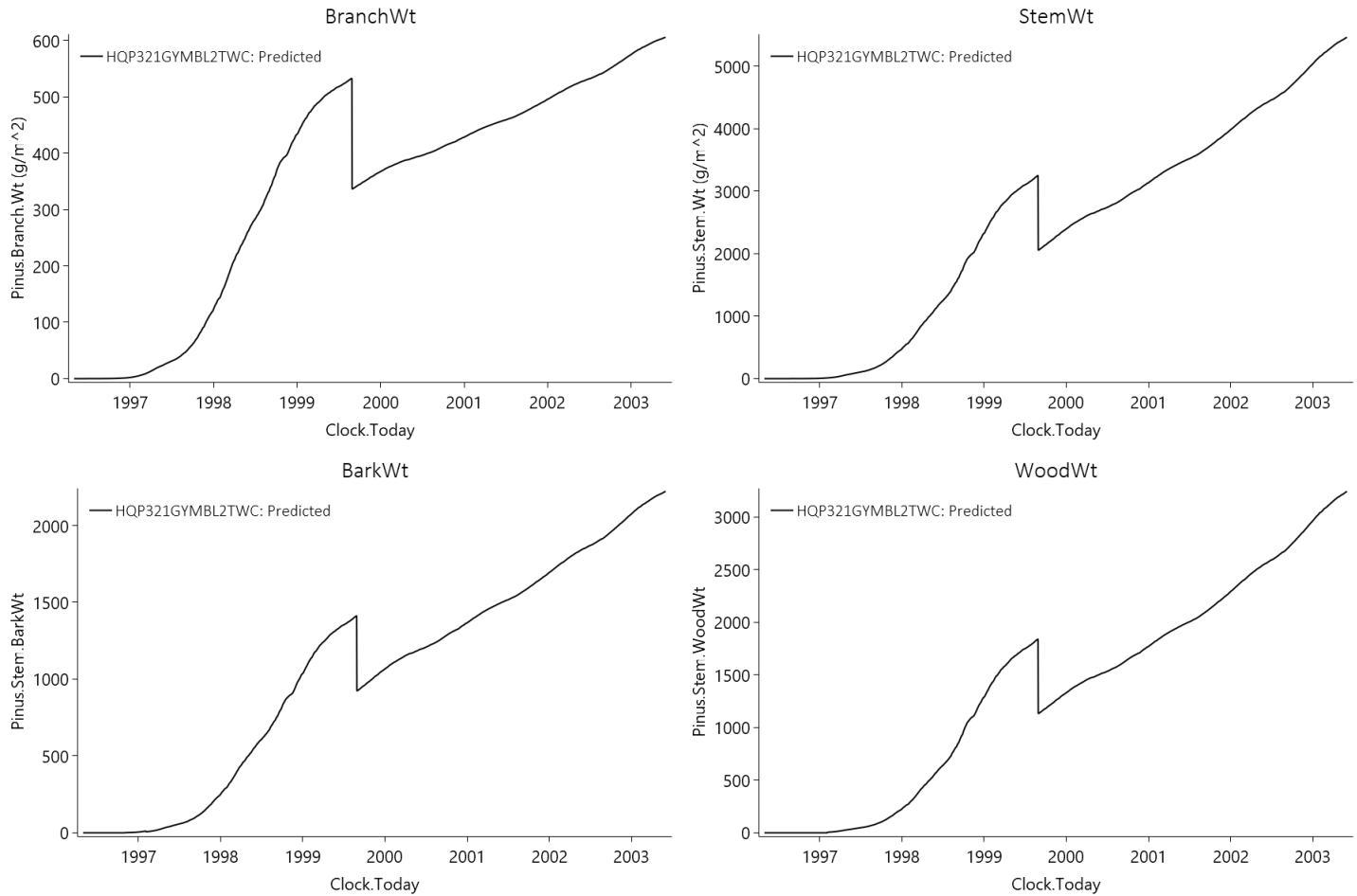
4.4.1.7 HQP321R2

These data were kindly provided by Hancock Queensland Plantations (HQPlantations) from Experiment 321GYM, which was established to:(1) examine the impacts of slash management, fertilization and cover crops on tree growth and nutrient status; (2) quantify the effects on soil properties; and (3) contribute to the CIFOR international network of long term experiments designed to identify and develop sustainable inter-rotation management practices. Early results were reported in [Simpson et al., 2000](#). Data here are reported only for one of the best performing treatments of the second rotation (2R) to age 8 years (Experiment 321GYM, Treatment BL2-TWC).

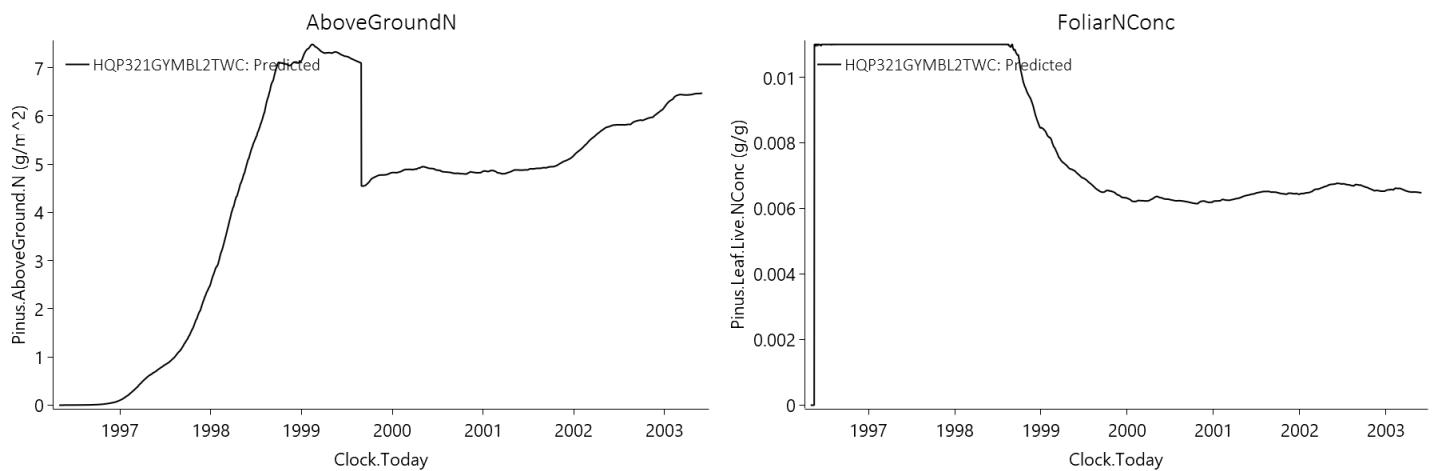
4.4.1.7.1 Graphs

4.4.1.7.1.1 GraphsWeights

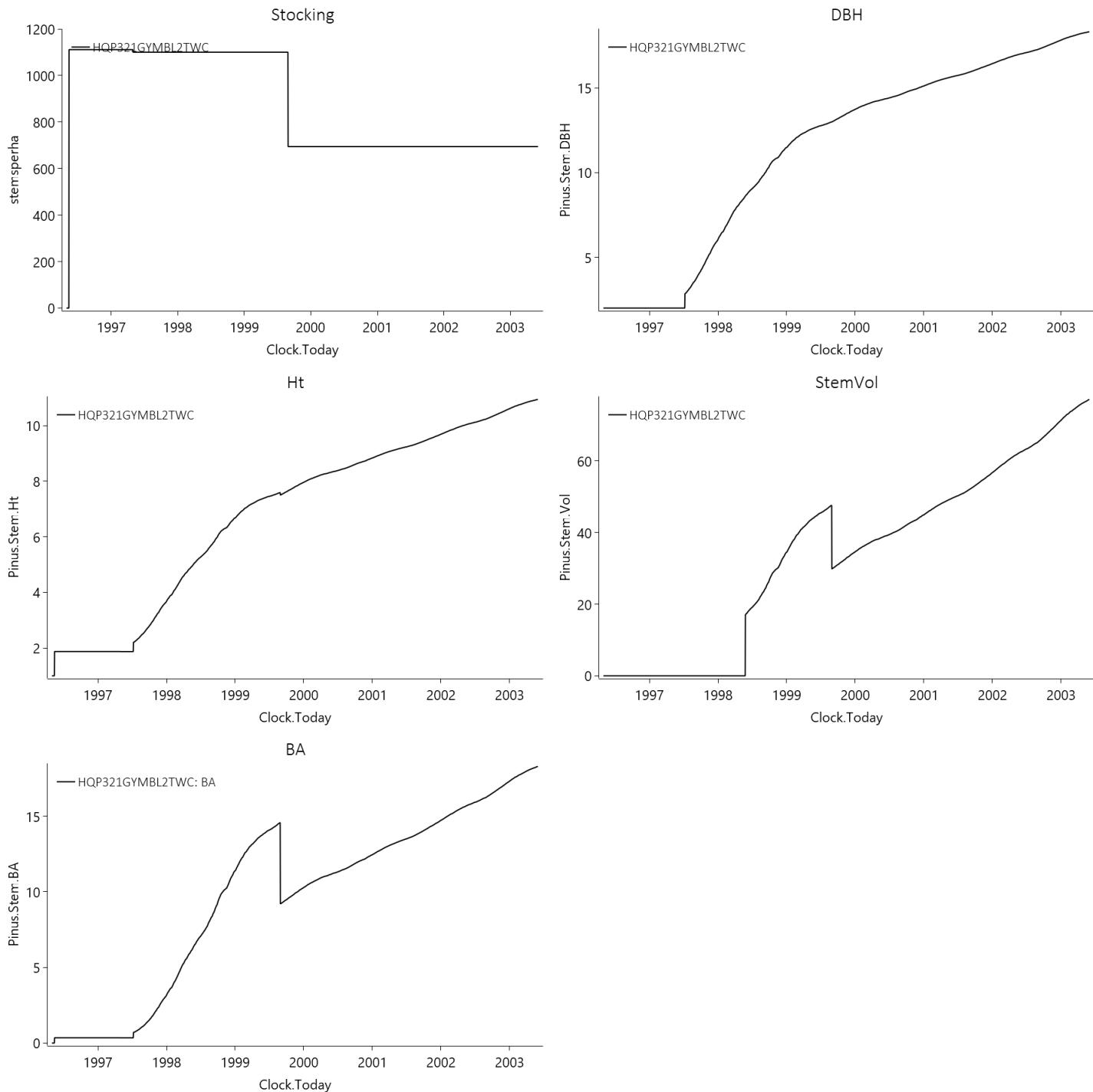




4.4.1.7.1.2 GraphsN



4.4.1.7.1.3 GraphsMetrics

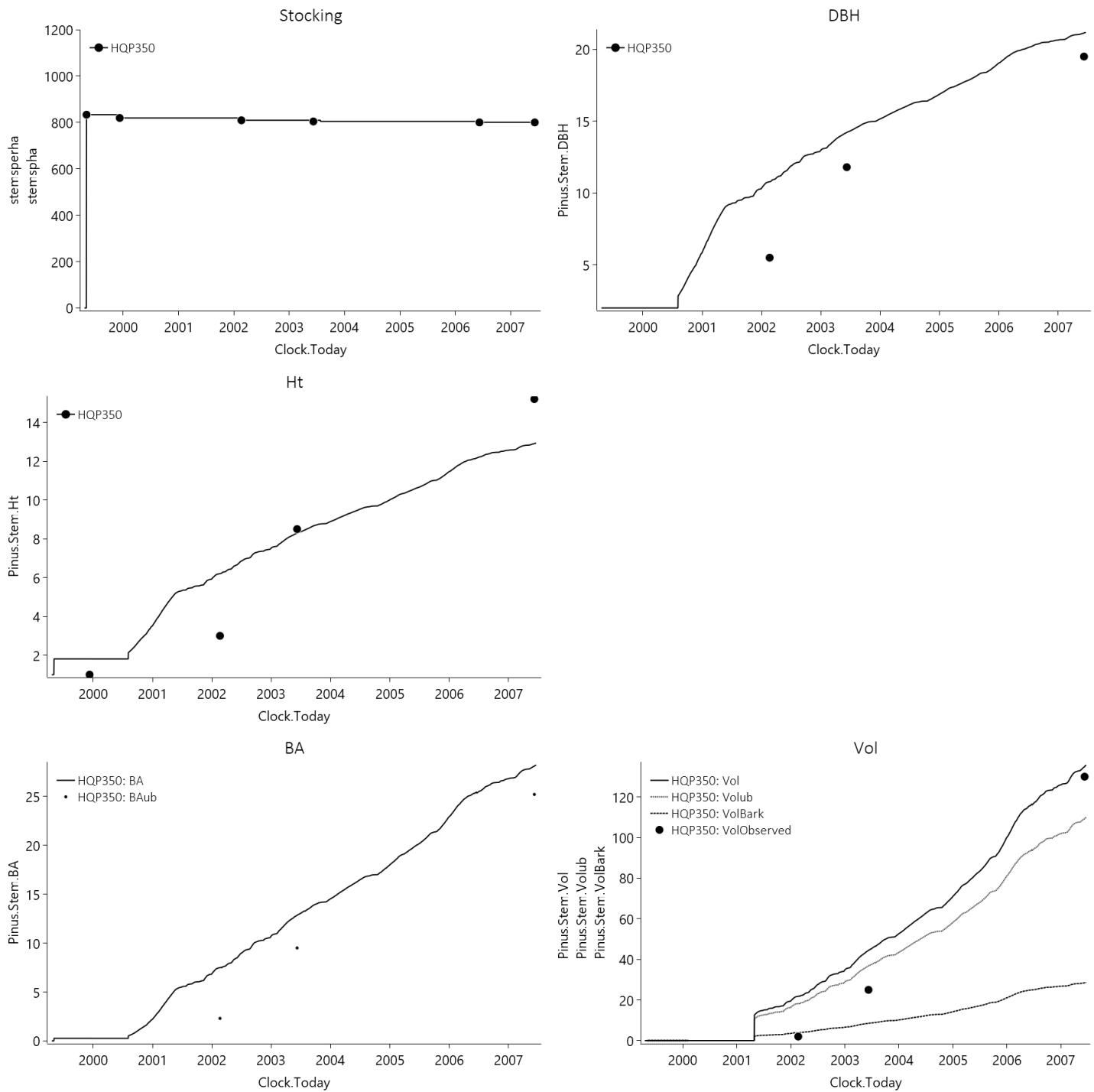


4.4.1.8 HQP350

These data were kindly provided by Hancock Queensland Plantations (HQPlantations) from Experiment 350GYM, which was established to assess the relative benefits, both short-term and long-term, of major factors and their interactions on PEE x PCH hybrid plantations when grown on an average site in the Maryborough district. Data here are reported only for one of the best performing treatments (Experiment 350GYM, Treatment High-FWC).

4.4.1.8.1 Graphs

4.4.1.8.1.1 GraphsMetrics



4.4.2 USA

These are the USA sites of the Tropical and SubTropical datasets.

4.4.2.1 IMPAC

These data are from an experiment with fertilizer and herbicide treatments and both *P. taeda* and *P. elliottii* near Gainesville, north-central Florida, USA. As nutrients other than N were probably limiting in some treatments, which the model could not be expected to simulate, only the high input treatment was simulated.

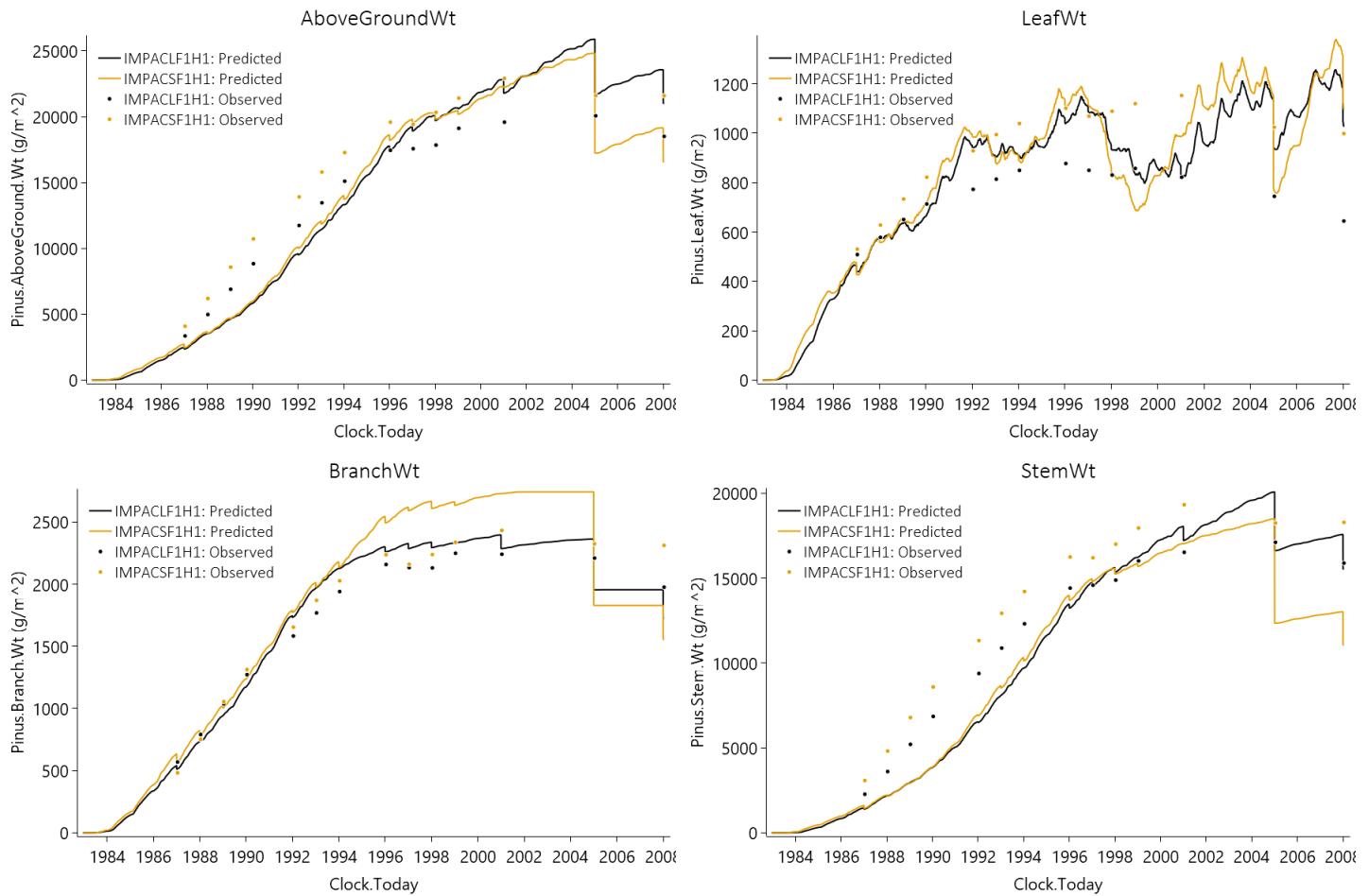
Numerous publications report on this experiment: [Jokela et al., 2000](#), [Vogel et al., 2011](#), [Martin et al., 2004](#), [Gonzalez-Benecke et al., 2012](#), [Jokela et al., 2010](#), [Subedi et al., 2019](#), [Jokela et al., 2004](#), and [Gonzalez-Benecke et al., 2016](#). A consolidated dataset was kindly provided by Eric Jokela and Jason Vogel, University of Florida.

List of experiments.

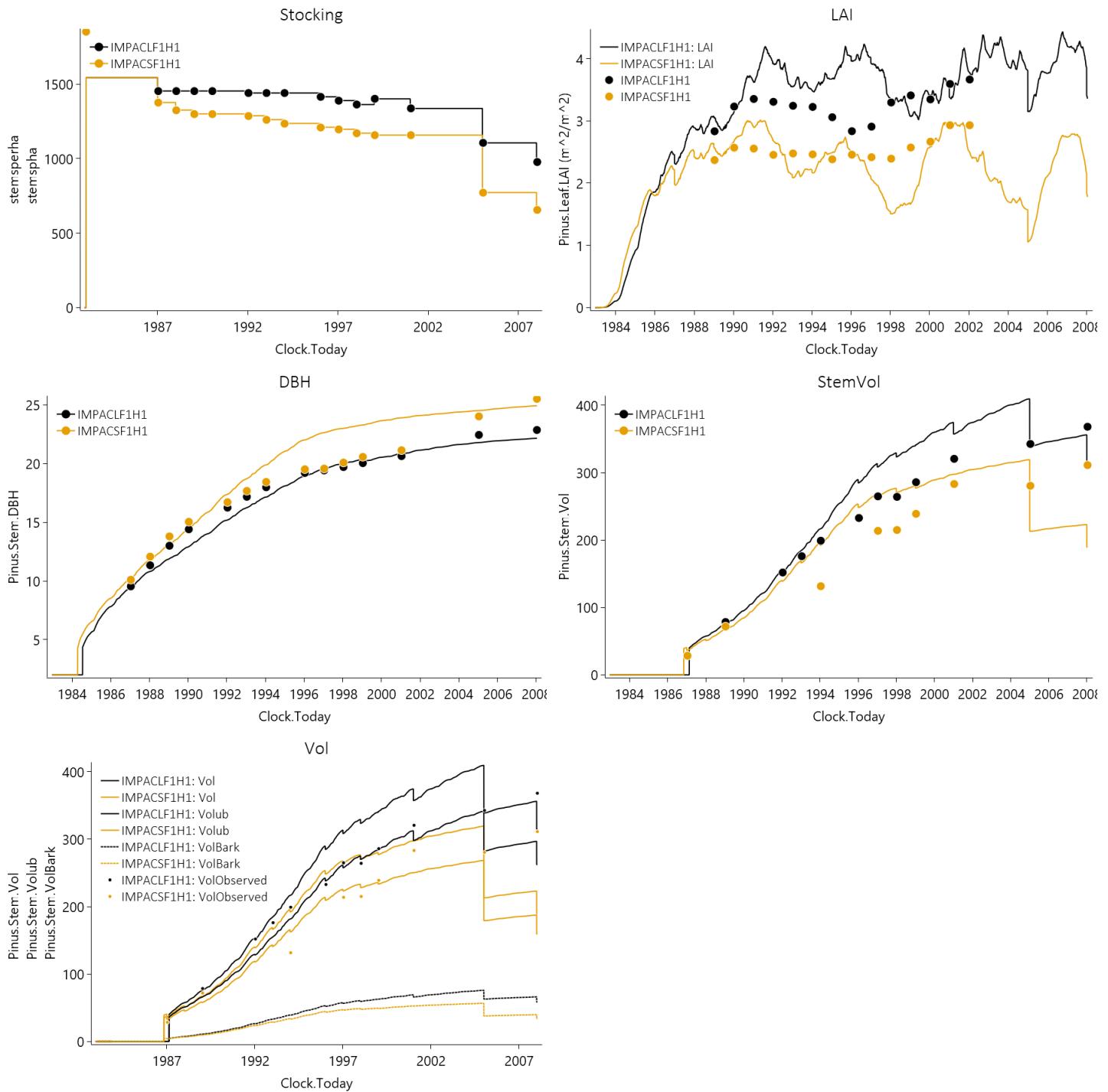
Experiment Name	Design (Number of Treatments)
IMPAC	L x S (2)

4.4.2.1.1 Graphs

4.4.2.1.1.1 GraphsWeights



4.4.2.1.1.2 GraphsMetrics



4.4.2.2 SETRES

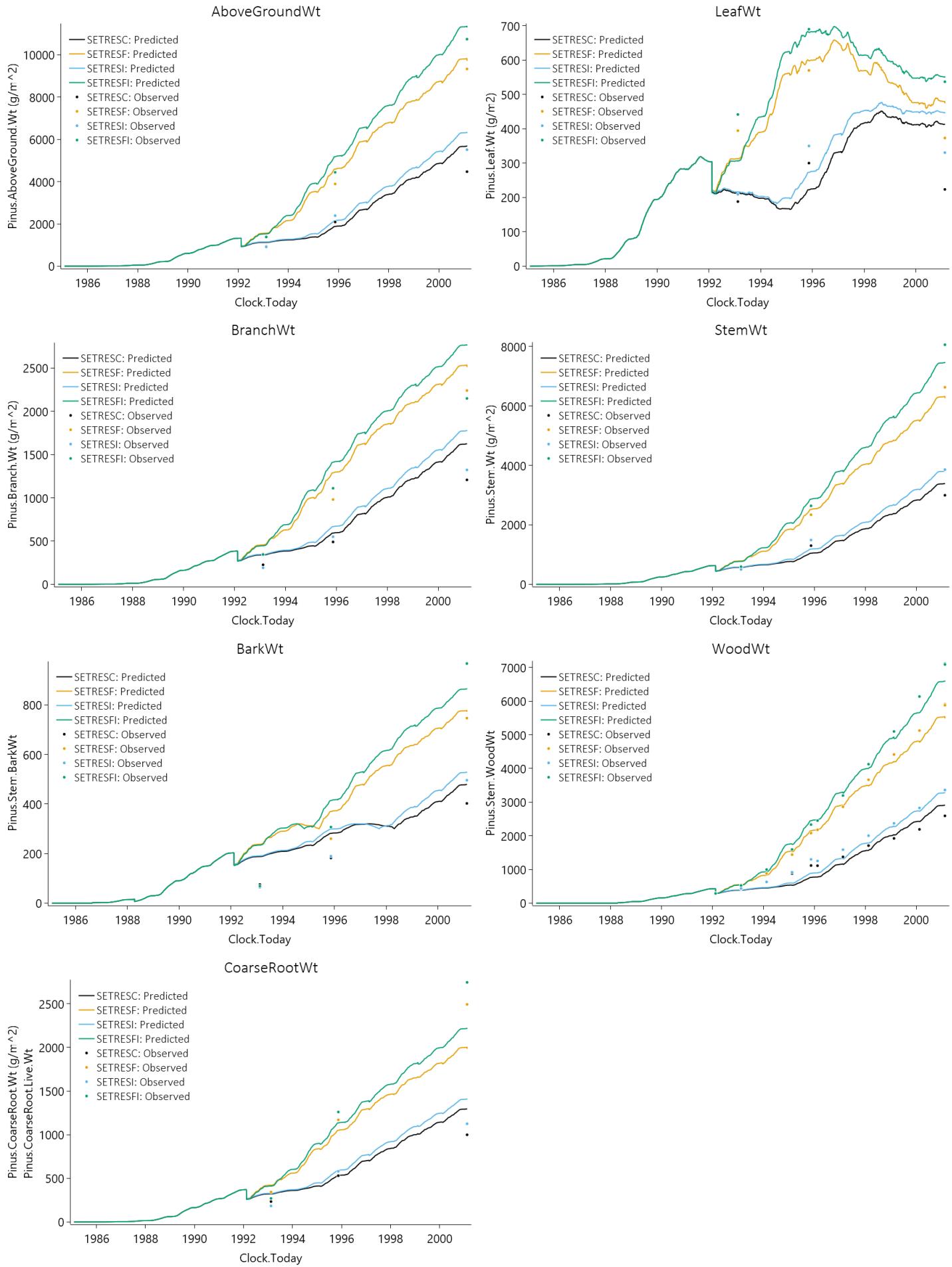
These data are from an experiment of 2x nutrient and water treatments in *P. taeda* near Sandhills, North Carolina, USA. As nutrients other than N were probably limiting in some treatments, which the the model could not be expected to simulate, only the high input treatment was simulated.

Numerous publications report on this experiment, of which we drew on [Zhao et al., 2016](#), [Landsberg et al., 2001](#), [Albaugh et al., 2009](#), [Albaugh et al., 2004](#), and [Albaugh et al., 1998](#).

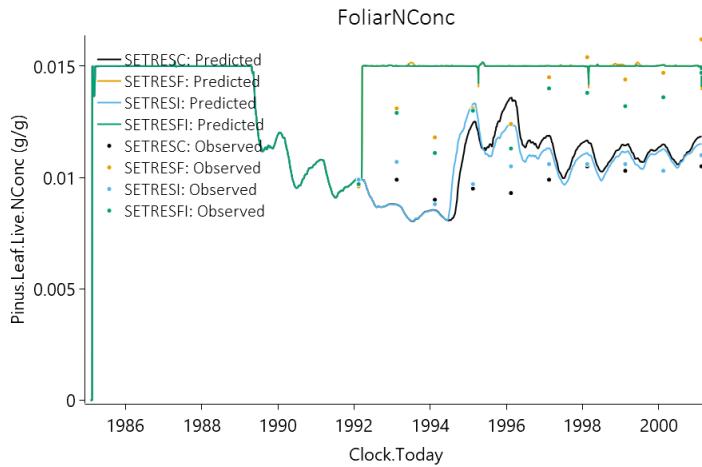
List of experiments.

Experiment Name	Design (Number of Treatments)
SETRE	S (4)

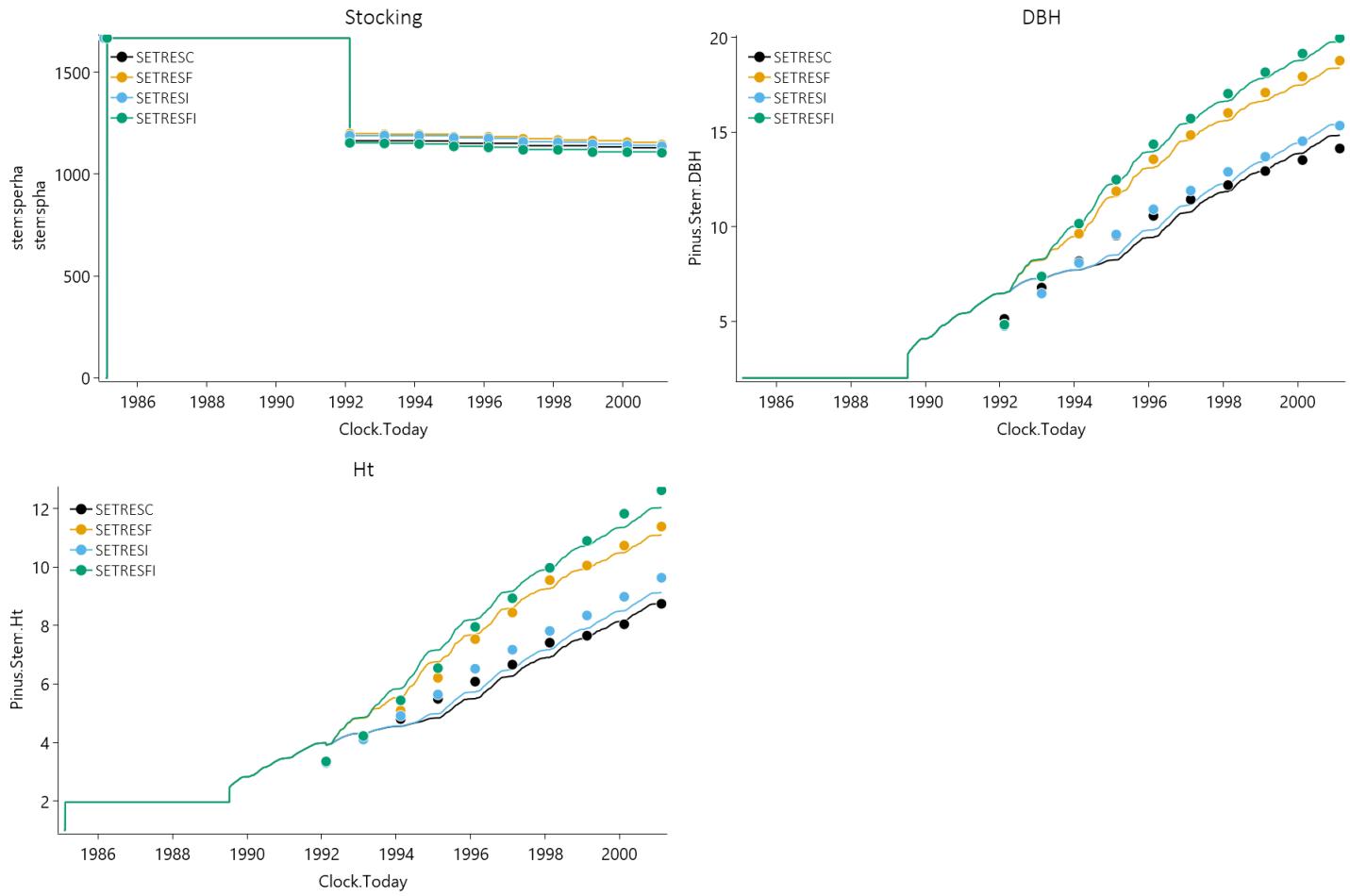
4.4.2.2.1 GraphsWeights



4.4.2.2.2 GraphsN



4.4.2.2.3 GraphsMetrics

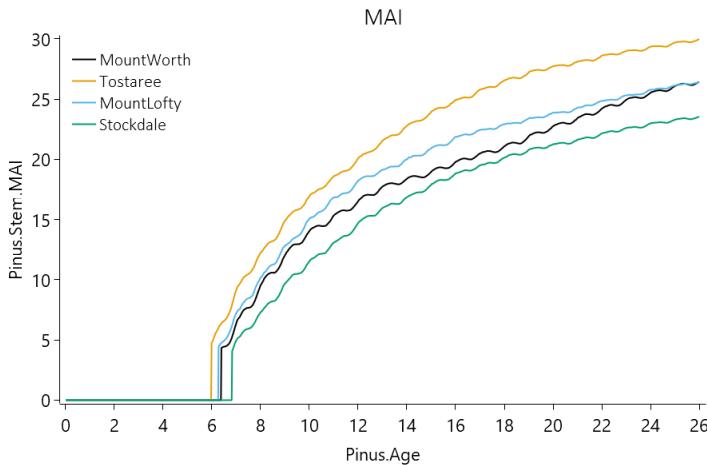


5 Sensibility

A series of sensibility tests have been employed to test the behaviour of the model in regions not explicitly included in the previous test set. Furthermore, these tests explore the emergent behaviour of the model under a range of changing climate, fertility and management scenarios to ensure that simulated patterns agree with expected behaviours.

5.1 MAI in SE Australia

Representative growth rates (MAI) for *P. radiata* in temperate Australia are up to 30 m³/ha/year of stem wood volume overbark, or more where accessing an aquifer or receiving irrigation. Simulations for 4 sites are presented here to capture a range of environmental conditions. Climate data has been taken from nearby towns and common soil properties have been used for all sites, with soil properties reflecting a relatively high state of fertility. The peak MAI values for these simulations are 13-29 m³/ha/year at 26 years, i.e. within the range of expectations [Turvey, 1983](#), and the relativities in relation to rainfall and temperature are also as expected. Rainfall is explored explicitly for the Mount Worth site in the next sensibility test.

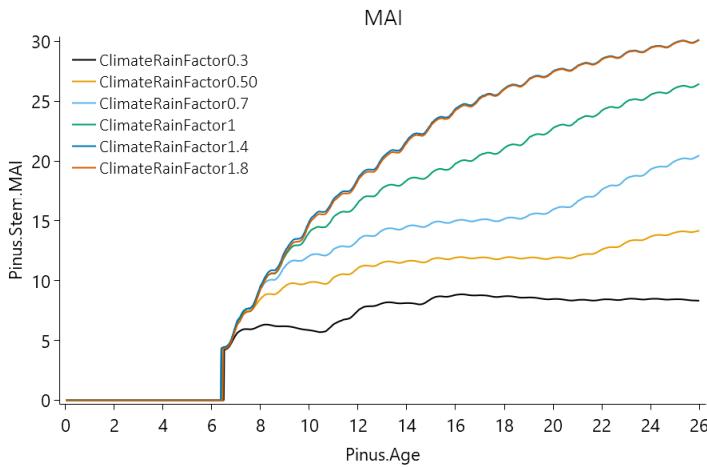
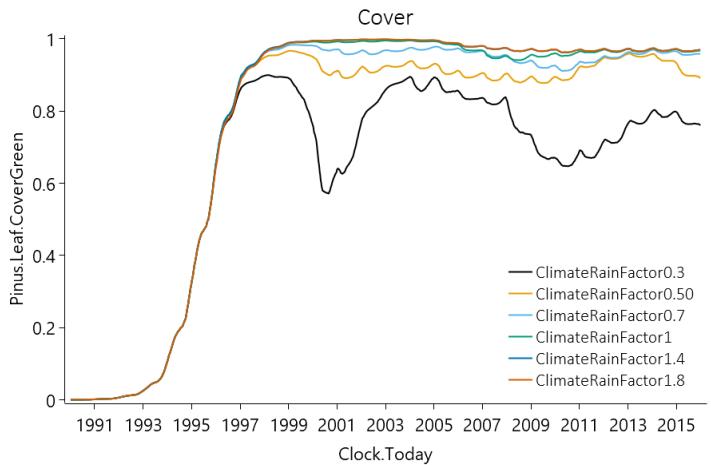
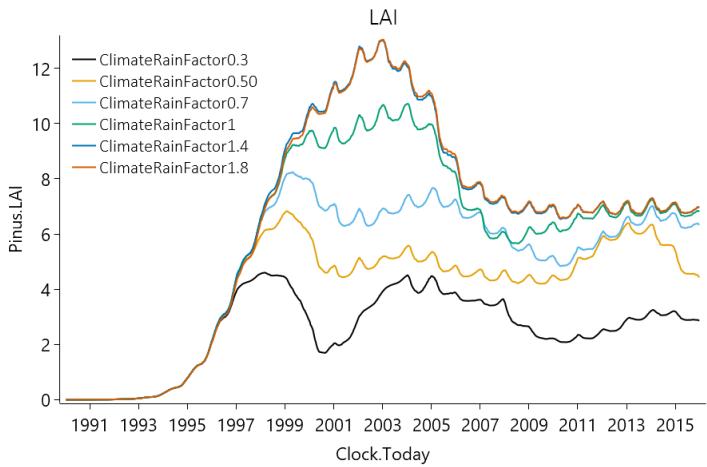


5.2 Response to Rainfall

LAI and MAI of *P. radiata* should increase with rainfall. This simulation experiment explores the changes in LAI and MAI with a hypothetical rainfall gradient created for the Mount Worth site (fertile soil and mean annual rainfall 1131 mm) above by multiplying daily rainfall by factors in the range 0.3-1.8, i.e. annual rainfall of 339-2036 mm. Data from [Specht, 1972](#) show that canopy cover should be almost complete for the wetter sites in this study, and decrease to approximately 50% at the drier sites, which is approxiamtely simulated here.

List of experiments.

Experiment Name	Design (Number of Treatments)
Climate	RainFactor (6)



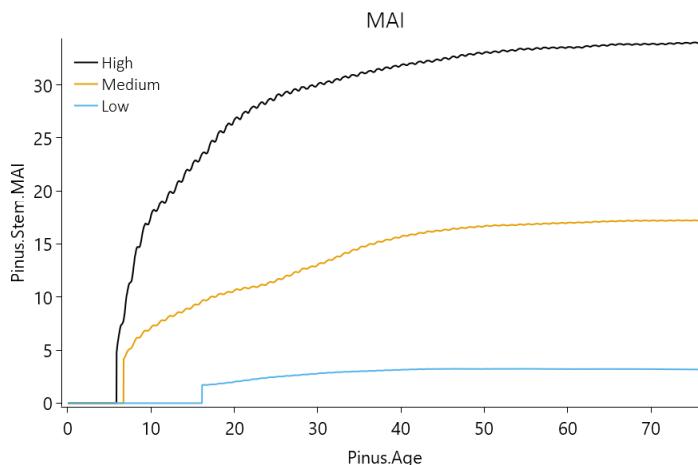
5.3 Response to Soil Fertility

Site fertility is an important driver of the pattern of tree growth rates. As site fertility declines, the long term growth rate (e.g. MAI) should also decrease, and the time to obtaining peak MAI can remain the similar or decrease. This sensibility test uses the Mount Worth location in Victoria, with soil fertility hypothetically altered to

three levels. As expected, simulated MAI decreased with soil fertility, and there was a decrease in time to peak MAI.

List of experiments.

Experiment Name	Design (Number of Treatments)
Fertility	Level (3)



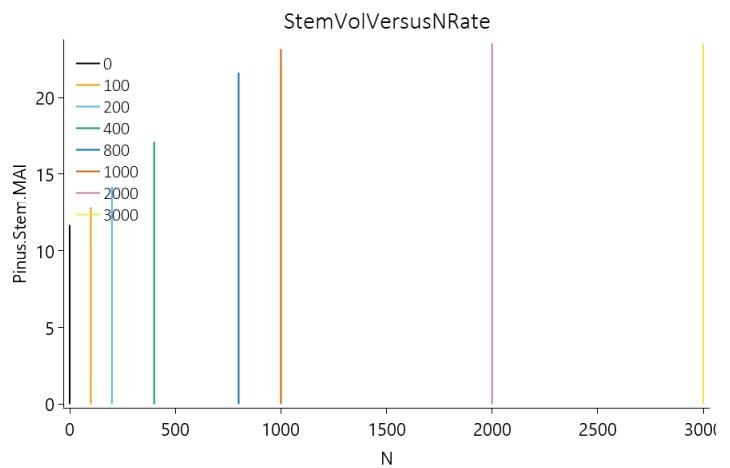
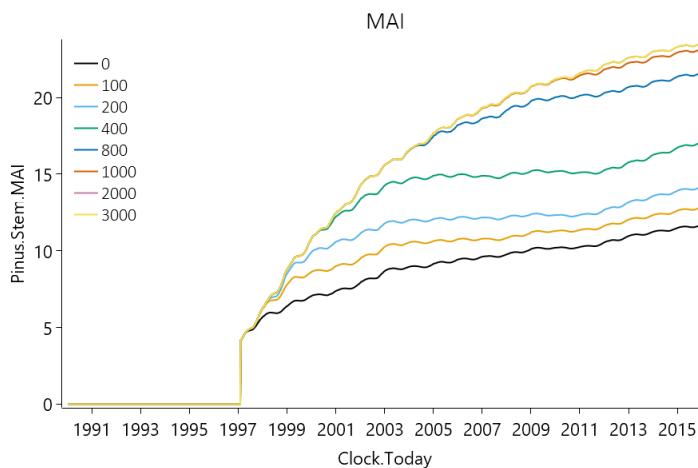
5.4 Reponse to N Fertilizer

Pinus response to rate of N fertiliser are often asymptotic, the plateau of which is determined by other limiting factors. In the sensibility test presented here, an infertile soil at Stockdale, Victoria, Australia, was used as the basis for the simulations *P. radiata* was fertilised at 3 years of age and stem volume assessed at 26 years of age.

Operationally, *P. radiata* plantations in Australia receive several hundred kg N/ha during a rotation. The approximate optimum rate simulated (90% of maximum) was 900 kg N/ha, which is therefore within the range of expectation.

List of experiments.

Experiment Name	Design (Number of Treatments)
Stockdale	N (8)



5.5 GxE

These graphs show the simulated yields (MAI) of all genotypes in the model grown for 26 years at northern and southern contrasting sites in Australia (Toolara and TowerHill). There is a tendency for Australian genotypes of *P. radiata* (TowerHill and BFG) to grow best in southern Australia, as expected, and conversely Australian tropical and sub-tropical genotypes (e.g. elliotiiXcaribaeaF1) to grow best in northern Australia. The New Zealand genotype (GF7) was simulated to grow best in the long-term at both locations, and the USA genotypes were worst. A wide range of yield potentials and patterns are therefore available.

Although the MAI values are generally as expected for all genotypes of *P. radiata* Turvey, 1983 and others, this analysis raises some questions that could help focus further model improvements.

Calibration of the model focussed on Australian datasets.

The elliotiiIMPAC and taedalIMPAC genotypes simulate noticeably reduced performance at later ages. This is probably a consequence of simulations at the IMPAC site in Florida only going to 18 years of age for calibration, as thereafter stocking (and probably vigour of survivors) decreased considerably due to disease, which could not be simulated.

Calibration of the GF7 genotype of *P. radiata* for the Puruki site in New Zealand went only 12 years of age as stocking thereafter went to very low values which was not a focus of the calibrations needed for Australia. If such low stocking values need to be calibrated for in future, one might need to explore biomass allocation a function stocking (population) to attain better model skill in these circumstances.

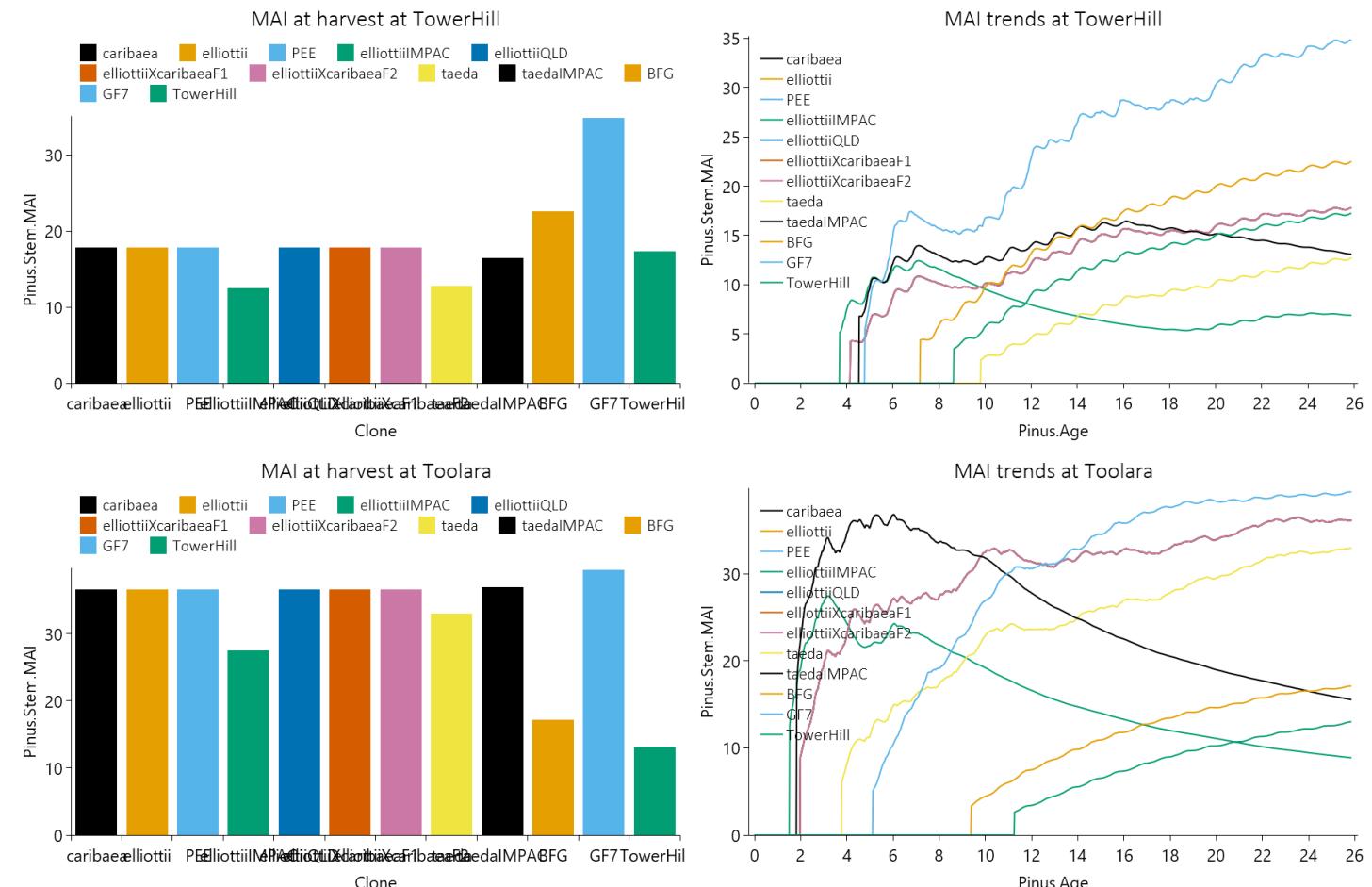
Several Australian genotypes performed similarly during simulations, indicating little practical difference in their calibration and therefore scope for merging, e.g. the elliotiiXcaribaeaF1 and elliotiiXcaribaeaF2 genotypes.

One would expect more discrimination than simulated between temperate and other genotypes when simulating growth at these northern and southern extremes of commercial plantations in Australia. To achieve that though model capability might be needed for disease occurrence and impacts on survival and growth, which beyond the current scope of validation.

Note that due to the long-term nature of plantation forestry, observed datasets are necessarily old and probably using out-dated genotypes. Therefore, using the genotypes currently available in the model might not be appropriate for simulating the performance of current or future plantations.

List of experiments.

Experiment Name	Design (Number of Treatments)
GxE	Site x Clone (24)



6 References

- Albaugh, Timothy J, Allen, H Lee, Dougherty, Phillip M, Kress, Lance W, King, John S, 1998. Leaf area and above-and belowground growth responses of loblolly pine to nutrient and water additions. *Forest Science* 44 (2), 317-328.
- Albaugh, Timothy J, Allen, H Lee, Dougherty, Phillip M, Johnsen, Kurt H, 2004. Long term growth responses of loblolly pine to optimal nutrient and water resource availability. *Forest ecology and management* 192 (1), 3-19.
- Albaugh, Timothy, Allen, H Lee, Fox, Thomas R, Carlson, Colleen A, Rubilar, Rafael A, 2009. Opportunities for fertilization of loblolly pine in the sandhills of the southeastern United States. *Southern Journal of Applied Forestry* 33 (3), 129-136.
- Beets, PN, Pollock, DS, 1987. Accumulation and partitioning of dry matter in *Pinus radiata* as related to stand age and thinning.. *New Zealand Journal of Forestry Science* 17 (2), 246-271.
- Beets, PN, Lane, PM, 1987. Specific leaf area of *Pinus radiata* as influenced by stand age, leaf age, and thinning.. *New Zealand Journal of Forestry Science* 17 (2), 283-291.
- Beets, PN, Brownlie, RK, 1987. Puruki experimental catchment: site, climate, forest management, and research. *New Zealand Journal of Forestry Science* 17 (2/3), 137-160.
- Beets, PN, Pollock, DS, 1987. Uptake and accumulation of nitrogen in *Pinus radiata* stands as related to age and thinning.. *New Zealand Journal of Forestry Science* 17 (2), 353-371.
- Beets, Peter N, Whitehead, David, 1996. Carbon partitioning in *Pinus radiata* stands in relation to foliage nitrogen status. *Tree physiology* 16 (1-2), 131-138.
- Beets, PN, Pearce, SH, Oliver, GR, Clinton, PW, 2007. Root/shoot ratios for deriving below-ground biomass of *Pinus radiata* stands. *New Zealand Journal of Forestry Science* 37 (2), 267.
- Beets, Peter N, Kimberley, Mark O, Paul, Thomas SH, Garrett, Loretta G, 2011. Planted Forest Carbon Monitoring System-forest carbon model validation study for *Pinus radiata*.. *New Zealand Journal of Forestry Science* (New Zealand Forest Research Institute Ltd (trading as Scion)) 41.
- Beets, Peter N, Garrett, Loretta G, 2018. Carbon fraction of *Pinus radiata* biomass components within New Zealand. *New Zealand Journal of Forestry Science* 48 (1), 1-8.
- Beets, PN, Beets, JM, 2020. Soil water storage changes in a small headwater catchment in the central North Island of New Zealand following afforestation with *Pinus radiata*. *Forest Ecology and Management* 462, 117967.
- Benson, ML, Myers, BJ, Raison, RJ, 1992. Dynamics of stem growth of *Pinus radiata* as affected by water and nitrogen supply. *Forest Ecology and Management* 52 (1-4), 117-137.
- Benson, ML, Landsberg, JJ, Borough, CJ, 1992. The Biology of Forest Growth experiment: an introduction. *Forest Ecology and Management* 52 (1-4), 1-16.
- [Brown, Hamish E., Huth, Neil I., Holzworth, Dean P., Teixeira, Edmar I., Zyskowski, Rob F., Hargreaves, John N. G., Moot, Derrick J., 2014. Plant Modelling Framework: Software for building and running crop models on the APSIM platform. Environmental Modelling and Software](#) 62, 385-398.
- Burdon, RD, Carson, MJ, Shelbourne, CJA, 2008. Achievements in forest tree genetic improvement in Australia and New Zealand 10: *Pinus radiata* in New Zealand. *Australian Forestry* 71 (4), 263-279.
- Crane, WJB, Banks, JCG, 1992. Accumulation and retranslocation of foliar nitrogen in fertilised and irrigated *Pinus radiata*. *Forest Ecology and Management* 52 (1-4), 201-223.
- Cremer, KW, 1992. Relations between reproductive growth and vegetative growth of *Pinus radiata*. *Forest Ecology and Management* 52 (1-4), 179-199.
- de Moraes Goncalves, Jose Leonardo, Alvares, Clayton Alcarde, Higa, Antonio Rioyei, Silva, Luciana Duque, Alfenas, Acelino Couto, Stahl, James, de Barros Ferraz, Silvio Frosini, de Paula Lima, Walter, Brancalion, Pedro Henrique Santin, Hubner, Ayeska, others, 2013. Integrating genetic and silvicultural strategies to minimize abiotic and biotic constraints in Brazilian eucalypt plantations. *Forest Ecology and Management* 301, 6-27.
- Dieters, Mark, Brawner, Jeremy, 2007. Productivity of *Pinus elliottii*, *P. caribaea* and their F 1 and F 2 hybrids to 15 years in Queensland, Australia. *Annals of forest science* 64 (7), 691-698.

- Dyck, WJ, Mees, CA, Hodgkiss, PD, 1987. Nitrogen availability and comparison to uptake in two New Zealand Pinus radiata forests.. *New Zealand journal of forestry science* 17 (2), 338-352.
- Garrett, LG, Beets, PN, Clinton, PW, Smaill, SJ, 2019. National series of long-term intensive harvesting trials in Pinus radiata stands in New Zealand: Initial biomass, carbon and nutrient pool data. *Data in brief* 27, 104757.
- Gonzalez-Benecke, Carlos A, Jokela, Eric J, Martin, Timothy A, 2012. Modeling the effects of stand development, site quality, and silviculture on leaf area index, litterfall, and forest floor accumulations in loblolly and slash pine plantations. *Forest Science* 58 (5), 457-471.
- Gonzalez-Benecke, Carlos A, Teskey, Robert O, Martin, Timothy A, Jokela, Eric J, Fox, Thomas R, Kane, Michael B, Noormets, Asko, 2016. Regional validation and improved parameterization of the 3-PG model for Pinus taeda stands. *Forest Ecology and Management* 361, 237-256.
- Harrington, Robin A, Fownes, James H, 1995. Radiation interception and growth of planted and coppice stands of four fast-growing tropical trees. *Journal of Applied Ecology*, 1-8.
- Hoch, Gunter, Richter, Andreas, Körner, Ch, 2003. Non-structural carbon compounds in temperate forest trees. *Plant, Cell and Environment* 26 (7), 1067-1081.
- Holzworth, Dean P., Huth, Neil I., deVoil, Peter G., Zurcher, Eric J., Herrmann, Neville I., McLean, Greg, Chenu, Karine, van Oosterom, Erik J., Snow, Val, Murphy, Chris, Moore, Andrew D., Brown, Hamish, Whish, Jeremy P. M., Verrall, Shaun, Fainges, Justin, Bell, Lindsay W., Peake, Allan S., Poulton, Perry L., Hochman, Zvi, Thorburn, Peter J., Gaydon, Donald S., Dalgliesh, Neal P., Rodriguez, Daniel, Cox, Howard, Chapman, Scott, Doherty, Alastair, Teixeira, Edmar, Sharp, Joanna, Cichota, Rogerio, Vogeler, Iris, Li, Frank Y., Wang, Enli, Hammer, Graeme L., Robertson, Michael J., Dimes, John P., Whitbread, Anthony M., Hunt, James, van Rees, Harm, McClelland, Tim, Carberry, Peter S., Hargreaves, John N. G., MacLeod, Neil, McDonald, Cam, Harsdorf, Justin, Wedgwood, Sara, Keating, Brian A., 2014. APSIM – Evolution towards a new generation of agricultural systems simulation. *Environmental Modelling and Software* 62, 327-350.
- Huth, N. I., Snow, V. O., Keating, B. A., 2001. Integrating a forest modelling capability into an agricultural production systems modelling environment-current applications and future possibilities.., Eds: Zerger, A. and Argent, R.M., 1895-1900.
- Huth, Neil Ian, Carberry, P.S., Poulton, P.L., Brennan, L.E., Keating, Brian A., 2002. A framework for simulating agroforestry options for the low rainfall areas of Australia using APSIM. *European Journal of Agronomy* 18, 171-185.
- Huth, N. I., Carberry, P. S., Cocks, B., Graham, S., McGinness, H. M., O'Connell, D. A., 2008. Managing drought risk in eucalypt seedling establishment: An analysis using experiment and model. *Forest Ecology and Management* 255 (8-9), 3307-3317.
- Johnson, IG, Cotterill, IM, Raymond, Carolyn A, Henson, M, others, 2008. Half a century of Pinus radiata tree improvement in New South Wales. *New Zealand Journal of Forestry* 52 (4), 7.
- Jokela, Eric J, Martin, Timothy A, 2000. Effects of ontogeny and soil nutrient supply on production, allocation, and leaf area efficiency in loblolly and slash pine stands. *Canadian Journal of Forest Research* 30 (10), 1511-1524.
- Jokela, Eric J, Dougherty, Philip M, Martin, Timothy A, 2004. Production dynamics of intensively managed loblolly pine stands in the southern United States: a synthesis of seven long-term experiments. *Forest ecology and management* 192 (1), 117-130.
- Jokela, Eric J, Martin, Timothy A, Vogel, Jason G, 2010. Twenty-five years of intensive forest management with southern pines: Important lessons learned. *Journal of Forestry* 108 (7), 338-347.
- Jourdan, C, Silva, EV, Goncalves, JLM, Ranger, J, Moreira, RM, Laclau, J-P, 2008. Fine root production and turnover in Brazilian Eucalyptus plantations under contrasting nitrogen fertilization regimes. *Forest ecology and management* 256 (3), 396-404.
- Keating, B. A., Carberry, P. S., Hammer, G. L., Probert, M. E., Robertson, M. J., Holzworth, D., Huth, N. I., Hargreaves, J. N. G., Meinke, H., Hochman, Z., McLean, G., Verburg, K., Snow, V., Dimes, J. P., Silburn, M., Wang, E., Brown, S., Bristow, K. L., Asseng, S., Chapman, S., McCown, R. L., Freebairn, D. M., Smith, C. J., 2003. An overview of APSIM, a model designed for farming systems simulation. *European Journal of Agronomy* 18 (3-4), 267-288.
- Khanna, PK, Raison, RJ, Falkiner, RA, Willett, IR, Connell, MJ, 1992. Effects of NPK fertilisation on the chemistry of a yellow podzolic soil under Pinus radiata. *Forest ecology and management* 52 (1-4), 65-85.

- Kimberley, MO, Beets, PN, 2007. National volume function for estimating total stem volume of *Pinus radiata* stands in New Zealand. *New Zealand Journal of Forestry Science* 37 (3), 355.
- Kirschbaum, Miko UF, 1999. CenW, a forest growth model with linked carbon, energy, nutrient and water cycles. *Ecological Modelling* 118 (1), 17-59.
- Landsberg, Joe J, Johnsen, Kurt H, Albaugh, Timothy J, Allen, H Lee, McKeand, Steven E, 2001. Applying 3-PG, a simple process-based model designed to produce practical results, to data from loblolly pine experiments. *Forest Science* 47 (1), 43-51.
- Martin, TA, Jokela, EJ, 2004. Developmental patterns and nutrition impact radiation use efficiency components in southern pine stands. *Ecological Applications* 14 (6), 1839-1854.
- McCown, R. L., Hammer, G. L., Hargreaves, J. N. G., Holzworth, D., Huth, N. I., 1995. APSIM: an agricultural production system simulation model for operational research. *Mathematics and Computers in Simulation* 39 (3-4), 225-231.
- McCown, R. L., Hammer, G. L., Hargreaves, J. N. G., Holzworth, D. P., Freebairn, D. M., 1996. APSIM: a Novel Software System for Model Development, Model Testing and Simulation in Agricultural Systems Research. *Agricultural Systems* 50 (3), 255-271.
- McMurtrie, RE, Landsberg, JJ, 1992. Using a simulation model to evaluate the effects of water and nutrients on the growth and carbon partitioning of *Pinus radiata*. *Forest Ecology and Management* 52 (1-4), 243-260.
- Monteith, J. L., Moss, C. J., 1977. Climate and the Efficiency of Crop Production in Britain [and Discussion]. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences* 281 (980), 277-294.
- Myers, BJ, Talsma, T, 1992. Site water balance and tree water status in irrigated and fertilised stands of *Pinus radiata*. *Forest Ecology and Management* 52 (1-4), 17-42.
- Neilsen, WA, Pataczek, W, Lynch, T, Pyrke, R, 1992. Growth response of *Pinus radiata* to multiple applications of nitrogen fertilizer and evaluation of the quantity of added nitrogen remaining in the forest system. *Plant and Soil* 144 (2), 207-217.
- Neilsen, WA, Lynch, T, 1998. Implications of pre-and post-fertilizing changes in growth and nitrogen pools following multiple applications of nitrogen fertilizer to a *Pinus radiata* stand over 12 years. *Plant and soil* 202 (2), 295-307.
- Oliver, GR, Beets, PN, Garrett, LG, Pearce, SH, Kimberly, MO, Ford-Robertson, JB, Robertson, KA, 2004. Variation in soil carbon in pine plantations and implications for monitoring soil carbon stocks in relation to land-use change and forest site management in New Zealand. *Forest Ecology and Management* 203 (1-3), 283-295.
- Parfitt, R. L., Schipper, L. A., Baisden, W. T., Elliott, A. H., 2006. Nitrogen inputs and outputs for New Zealand in 2001 at national and regional scales. *Biogeochemistry* 80 (1), 71-88.
- Pongracic, Silvia, 2001. Influence of irrigation and fertilization on the belowground carbon allocation in a pine plantation.
- Quentin, AG, Pinkard, EA, Ryan, MG, Tissue, DT, Baggett, LS, Adams, HD, Maillard, P, Marchand, J, Landhausser, SM, Lacointe, A, others, 2015. Non-structural carbohydrates in woody plants compared among laboratories. *Tree physiology* 35 (11), 1146-1165.
- Raison, RJ, Khanna, PK, Connell, MJ, Falkiner, RA, 1990. Effects of water availability and fertilization on nitrogen cycling in a stand of *Pinus radiata*. *Forest Ecology and Management* 30 (1-4), 31-43.
- Raison, RJ, Khanna, PK, Benson, ML, Myers, BJ, McMurtrie, RE, Lang, ARG, 1992. Dynamics of *Pinus radiata* foliage in relation to water and nitrogen stress: II. Needle loss and temporal changes in total foliage mass. *Forest ecology and management* 52 (1-4), 159-178.
- Raison, RJ, Myers, BJ, Benson, ML, 1992. Dynamics of *Pinus radiata* foliage in relation to water and nitrogen stress: I. Needle production and properties. *Forest Ecology and Management* 52 (1-4), 139-158.
- Raison, RJ, Myers, BJ, 1992. The biology of forest growth experiment: linking water and nitrogen availability to the growth of *Pinus radiata*. *Forest Ecology and Management* 52 (1-4), 279-308.
- Raymond, Carolyn A, Muneri, Allie, 2000. Effect of fertilizer on wood properties of *Eucalyptus globulus*. *Canadian Journal of Forest Research* 30 (1), 136-144.

Reyenga, P.J., Howden, S. M., Meinke, H., McKeon, G.M., 1999. Modelling global change impacts on wheat cropping in south-east Queensland, Australia. Environmental Modelling & Software 14, 297-306.

Rijkse, Willem Cornelis, Bell, JL, 1974. Soils of Purukohukohu IHD Experimental Basin, Rotorua County, North Island, New Zealand. NZ soil survey report.

Simpson, JA, Xu, ZH, Smith, T, Keay, P, Osborne, DO, Podberscek, M, others, 2000. Effects of site management in pine plantations on the coastal lowlands of subtropical Queensland, Australia.. Site management and productivity in tropical plantation forests: a progress report. Workshop Proceedings, Kerala, India, 7-11 December 1999, 73-81.

Smethurst, Philip J, Valadares, Rafael V, Huth, Neil I, Almeida, Auro C, Elli, Elvis F, Neves, J'ulio CL, 2020. Generalized model for plantation production of *Eucalyptus grandis* and hybrids for genotype-site-management applications. Forest Ecology and Management 469, 118164.

Snowdon, P, Benson, ML, 1992. Effects of combinations of irrigation and fertilisation on the growth and above-ground biomass production of *Pinus radiata*. Forest Ecology and Management 52 (1-4), 87-116.

Specht, RL, 1972. Water use by perennial evergreen plant communities in Australia and Papua New Guinea. Australian Journal of Botany 20 (3), 273-299.

Subedi, Praveen, Jokela, Eric J, Vogel, Jason G, Martin, Timothy A, 2019. Sustained productivity of intensively managed loblolly pine plantations: Persistence of fertilization and weed control effects across rotations. Forest Ecology and Management 446, 38-53.

Turvey, Nigel D, 1983. Soil-type yield curves for *Pinus radiata* in Gippsland, Victoria. Australian Forestry 46 (2), 118-125.

Vogel, Jason G, Suau, Luis J, Martin, Timothy A, Jokela, Eric J, 2011. Long-term effects of weed control and fertilization on the carbon and nitrogen pools of a slash and loblolly pine forest in north-central Florida. Canadian Journal of Forest Research 41 (3), 552-567.

Waterworth, Robert, Raison, R John, Brack, Cris, Benson, Martin, Khanna, Partap, Paul, Keryn, 2007. Effects of irrigation and N fertilization on growth and structure of *Pinus radiata* stands between 10 and 29 years of age. Forest ecology and management 239 (1-3), 169-181.

Wu, Harry X, Eldridge, Ken G, Matheson, A Colin, Powell, Mike P, McRae, Tony A, 2007. Successful introduction and breeding of radiata pine to Australia. Growing Forest Values, Proceedings of ANZIF 2007 Conference, Coffs Harbour, NSW, Australia, 3-7.

Zhao, Dehai, Kane, Michael, Teskey, Robert, Fox, Thomas R, Albaugh, Timothy J, Allen, H Lee, Rubilar, Rafael, 2016. Maximum response of loblolly pine plantations to silvicultural management in the southern United States. Forest Ecology and Management 375, 105-111.