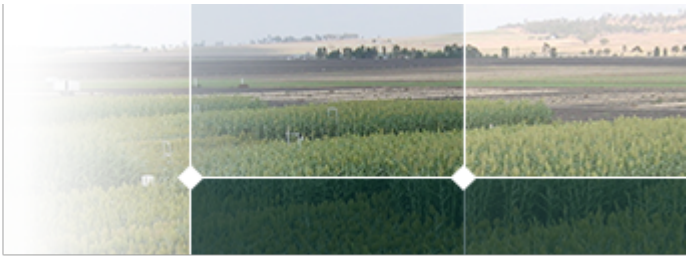


1 The APSIM Pinus Model

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 wieght and for which we found some data to guide calibration. Phenology is simple in this model and could become a focus for future model develompent, 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 pooly calibrated as few observations of whole tree wood density are available and based on stem analysis. So here wood density is an emergent proporty 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.

The model has been developed using the Plant Modelling Framework (PMF) of Brown 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 process and organ classes(e.g.photosynthesis, leaf) into larger constructions(e.g.maize, wheat, sorghum) can be achieved by the model developer without additional coding.

The 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
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

1.1 Age

Age = Accumulated *day* between emergence and old

This converts days of growth to age in years.

day = 0.0027397260273972603 (years)

1.2 MortalityRate

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

MortalityRate = 0

1.3 Phenology

The phenological development is simulated as the progression through a series of developmental phases, each bound by distinct growth stage.

Phenology is currently very simplistic in the Pinus model.

1.3.1 ThermalTime

ThermalTime = 1 (^od)

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
3	Juvenile	Emergence	EndJuvenile
4	Mature	EndJuvenile	Maturity
5	Declining	Maturity	Old
6	Old	Old	Unused

1.3.2 Germinating

The phase goes from sowing to germination 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.

1.3.3 Emerging

This phase goes from germination to emergence and simulates time to emergence as a function of sowing depth. The *ThermalTime Target* for ending this phase is given by:

Target = *SowingDepth* x *ShootRate* + *ShootLag*

Where:

ShootRate = 0 (deg day/mm),

ShootLag = 1 (deg day),

SowingDepth (mm) is sent from the manager with the sowing event.

Progress toward emergence is driven by thermal time accumulation, where thermal time is calculated as:

ThermalTime = [Phenology].ThermalTime

1.3.4 Juvenile

This phase goes from emergence to endjuvenile.

The *Target* for completion is calculated as:

Target = 365 (^o)

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

Progression = 1 (^od)

1.3.5 Mature

This phase goes from endjuvenile to maturity.

The *Target* for completion is calculated as:

Target = 1825 (^o)

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

Progression = 1 (^od)

1.3.6 Declining

This phase goes from maturity to old.

The *Target* for completion is calculated as:

Target = 27010 (^o)

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

Progression = 1 (^od)

1.3.7 Old

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

1.3.8 Constants

ThermalTime = 1 (^od)

1.3.9 StageCode

1.3.9.1 StageCode

A value is linearly interpolated between phenological growth stages

1.4 Arbitrator

1.4.1 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 the figure below. 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

DoPotentialDMAllocation() 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, DoActualDMAllocation 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.

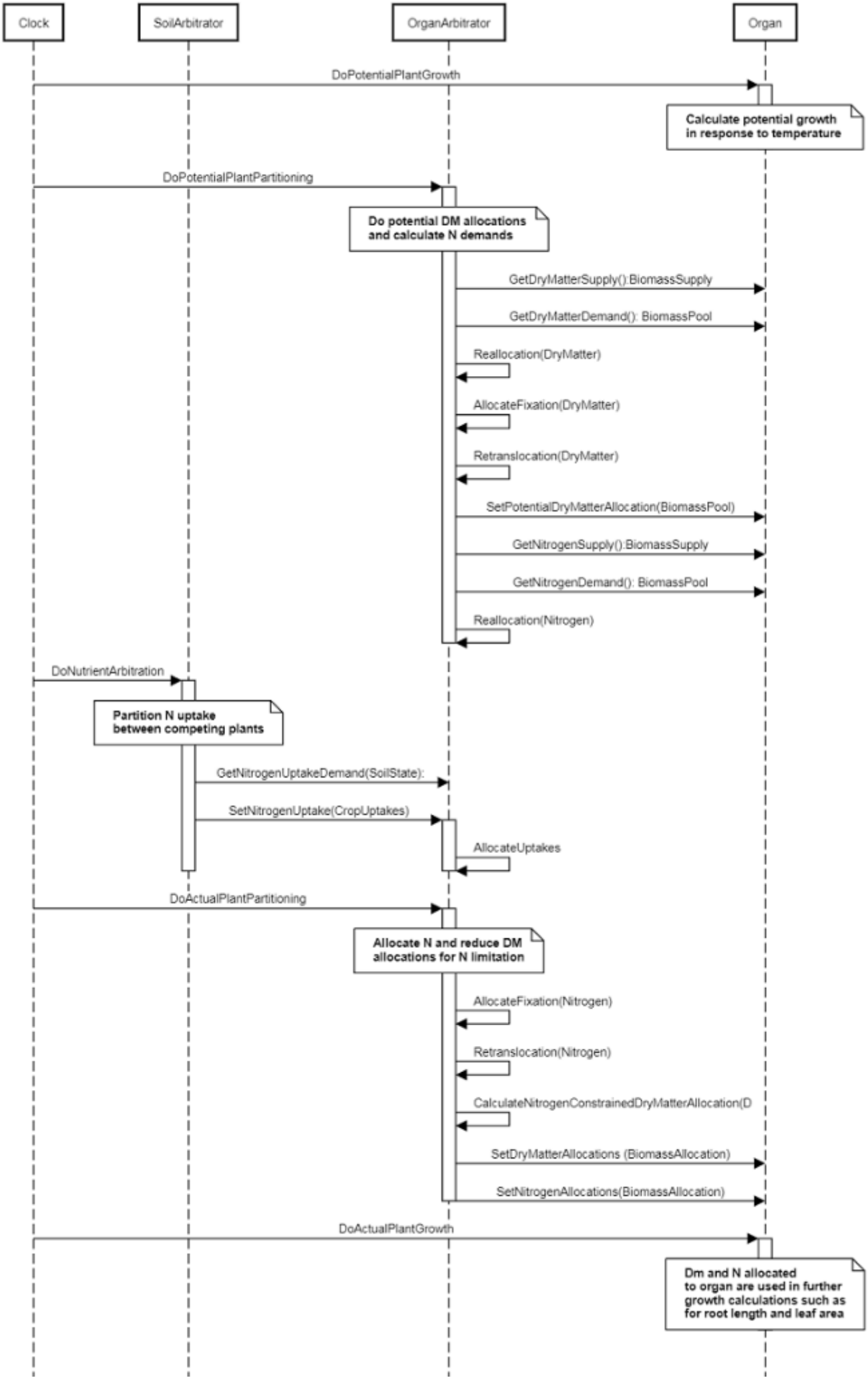

Clock
SoilArbitrator
OrganArbitrator
Organ
DoPotentialPlantGrowth
Calculate potential growth in response to temperature
DoPotentialPlantPartitioning
Do potential DM allocations and calculate N demands
GetDryMatterSupply():BiomassSupply
GetDryMatterDemand(): BiomassPool
Reallocation(DryMatter)
AllocateFixation(DryMatter)
Retranslocation(DryMatter)
SetPotentialDryMatterAllocation(BiomassPool)
GetNitrogenSupply():BiomassSupply
GetNitrogenDemand(): BiomassPool
Reallocation(Nitrogen)
DoNutrientArbitration
Partition N uptake between competing plants
GetNitrogenUptakeDemand(SoilState):
SetNitrogenUptake(CropUptakes)
AllocateUptakes
DoActualPlantPartitioning
Allocate N and reduce DM allocations for N limitation
AllocateFixation(Nitrogen)
Retranslocation(Nitrogen)
CalculateNitrogenConstrainedDryMatterAllocation(D
SetDryMatterAllocations (BiomassAllocation)
SetNitrogenAllocations(BiomassAllocation)
DoActualPlantGrowth
Dm and N allocated to organ are used in further growth calculations such as for root length and leaf area

Figure 1: 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.

1.5 AboveGround

1.5.1 AboveGround

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

AboveGround summarises the following biomass objects:

* Branch
* Leaf
* Stem
* Cone

1.6 BelowGround

1.6.1 BelowGround

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

BelowGround summarises the following biomass objects:

* FineRoot
* CoarseRoot

1.7 TotalWoodBark

1.7.1 TotalWoodBark

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

TotalWoodBark summarises the following biomass objects:

* Stem
* Branch

1.8 Total

1.8.1 Total

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

Total summarises the following biomass objects:

* Leaf
* Stem
* Branch
* FineRoot
* CoarseRoot

1.9 TotalLive

1.9.1 TotalLive

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

TotalLive summarises the following biomass objects:

* Leaf
* Branch
* Stem
* FineRoot
* CoarseRoot
* Cone

1.10 TotalDead

1.10.1 TotalDead

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

TotalDead summarises the following biomass objects:

* Leaf
* Branch
* Stem
* FineRoot
* CoarseRoot
* Cone

1.11 IndividualTreeLiveWt

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

1.12 IndividualTreeStemWt

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

1.13 Cone

1.13.1 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.

1.13.2 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.

1.13.2.1 DMDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

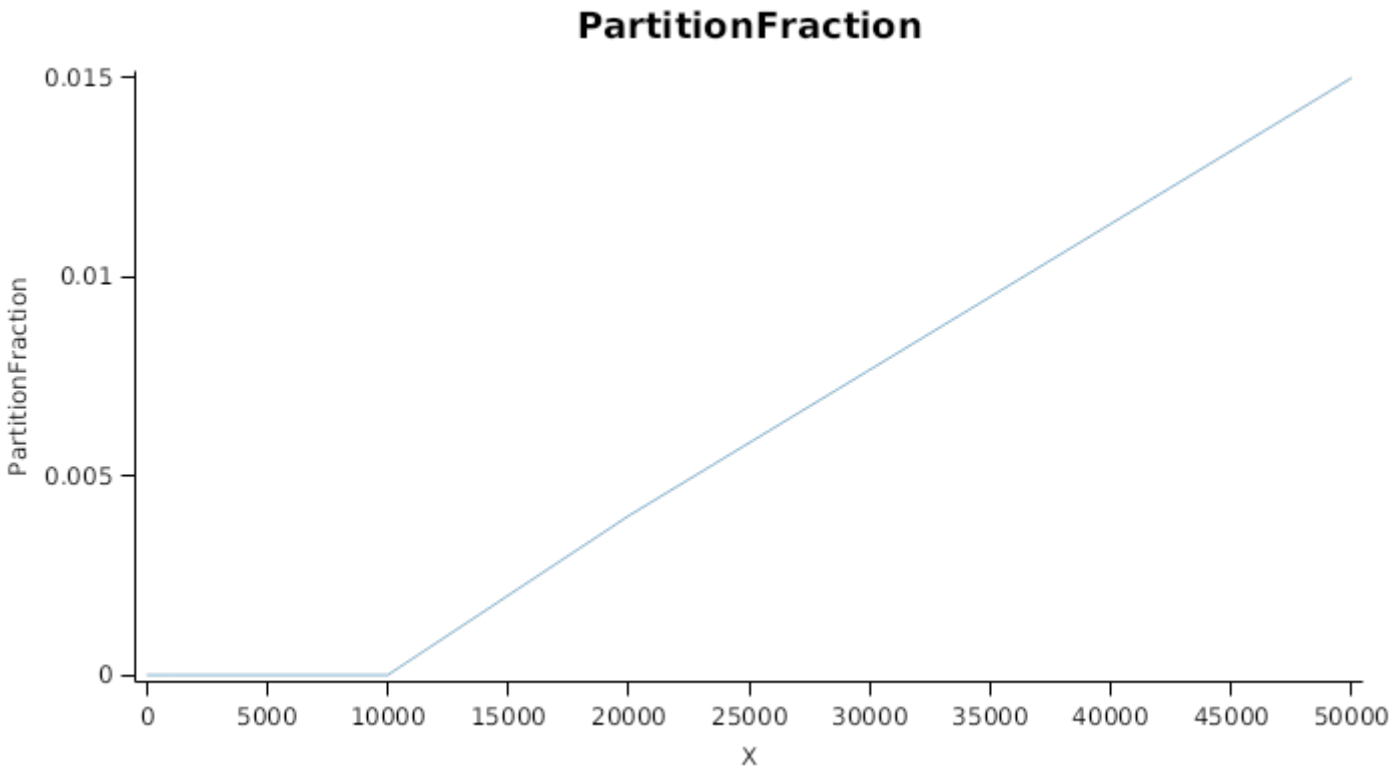
Structural = *DMDemandFunction* x *StructuralFraction*

Returns the product of its PartitionFraction and the total DM supplied to the arbitrator by all organs.

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

PartitionFraction is calculated using linear interpolation

X	PartitionFraction
0.0	0.0
1000.0	0.0
10000.0	0.0
20000.0	0.0
50000.0	0.0



StructuralFraction = 0.99 (0-1)

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.13.3 Nitrogen Demand

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

1.13.3.1 NDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

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

Metabolic = *MetabolicNconc* x [Cone].potentialDMAllocation.Structural

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

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.

NitrogenDemandSwitch = [Cone].nitrogenDemandSwitch

MaxNconc = [Cone].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.13.4 N Concentration Thresholds

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

1.13.5 Dry Matter Supply

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

Cone does not retranslocate non-structural DM.

1.13.6 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.

1.13.7 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.

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

1.14 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.

1.14.1 Constants

LaiDeadFunction = 0 ($m^{2/m}2$)

ExtinctionCoefficientDead = 0.5

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

MaximumNConc = 0.02 (g/g)

MinimumNConc = 0.012 (g/g)

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

NReallocationFactor = 0.5 (/d)

DMConversionEfficiency = 1 (g/g)

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

LeafDetachmentTime = 14 (d)

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.

DetachmentRateFunction = 0 (/d)

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

DMRetranslocationFactor = 0 (/d)

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

NRetranslocationFactor = 0.05 (/d)

MinimumLAI = 0.01 ($m^{2/m}2$)

This value is wtihin the range of 0.50-0.53 reported by Beets et al., 2018 for *P. radiata* foliage.

CarbonConcentration = 0.52 (g/g)

1.14.2 CO2internal

CO2internal = (163 - [IWeather].MeanT)/(5 - 0.1x[IWeather].MeanT)

1.14.3 StomatalConductanceCO2Modifier

StomatalConductanceCO2Modifier = [Leaf].Photosynthesis.FCO2 / *RelativeCO2Gradient*

RelativeCO2Gradient = ([IWeather].CO2 - [Leaf].CO2internal)/(350 - [Leaf].CO2internal)

1.14.4 InitialWtFunction

InitialWtFunction = *InitialPlantWt* x [Plant].Population

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

InitialPlantWt = 1 (g/plant)

1.14.5 FRGRFunction

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

FRGRFunction = Min(*FT*, *FN*, *FVPD*)

Where:

FT = [Leaf].Photosynthesis.FT.FTDaytime

FN = [Leaf].Photosynthesis.FN

FVPD = [Leaf].Photosynthesis.FVPD

1.14.6 ExtinctionCoefficient

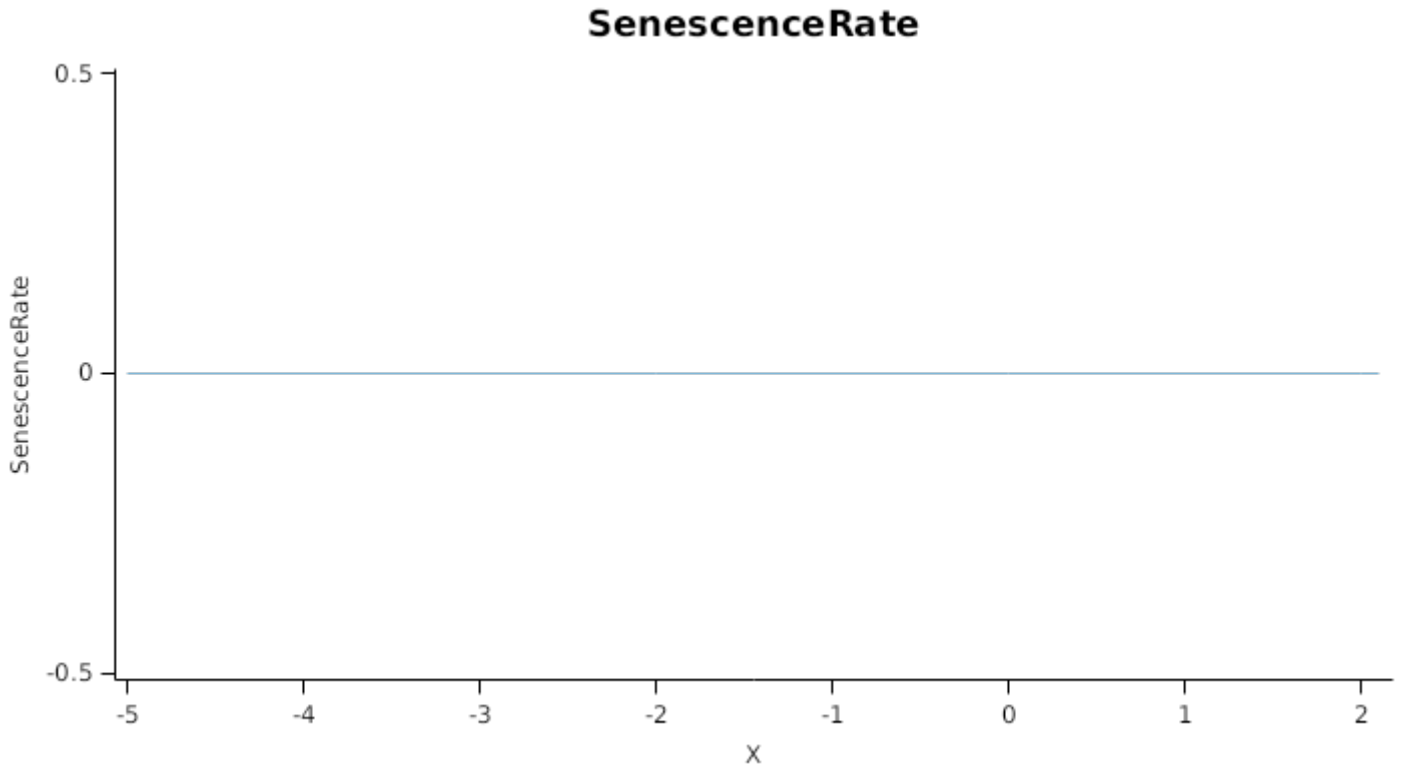
ExtinctionCoefficient = ([ExtinctionCoefficient].KMatureTrees+([ExtinctionCoefficient].KYoungTrees-[ExtinctionCoefficient].KMatureTrees)xExp((0-2)x([Pinus].Leaf.LAI/[ExtinctionCoefficient].LAIIntermediateK)^[ExtinctionCoefficient].ShapeCurve))

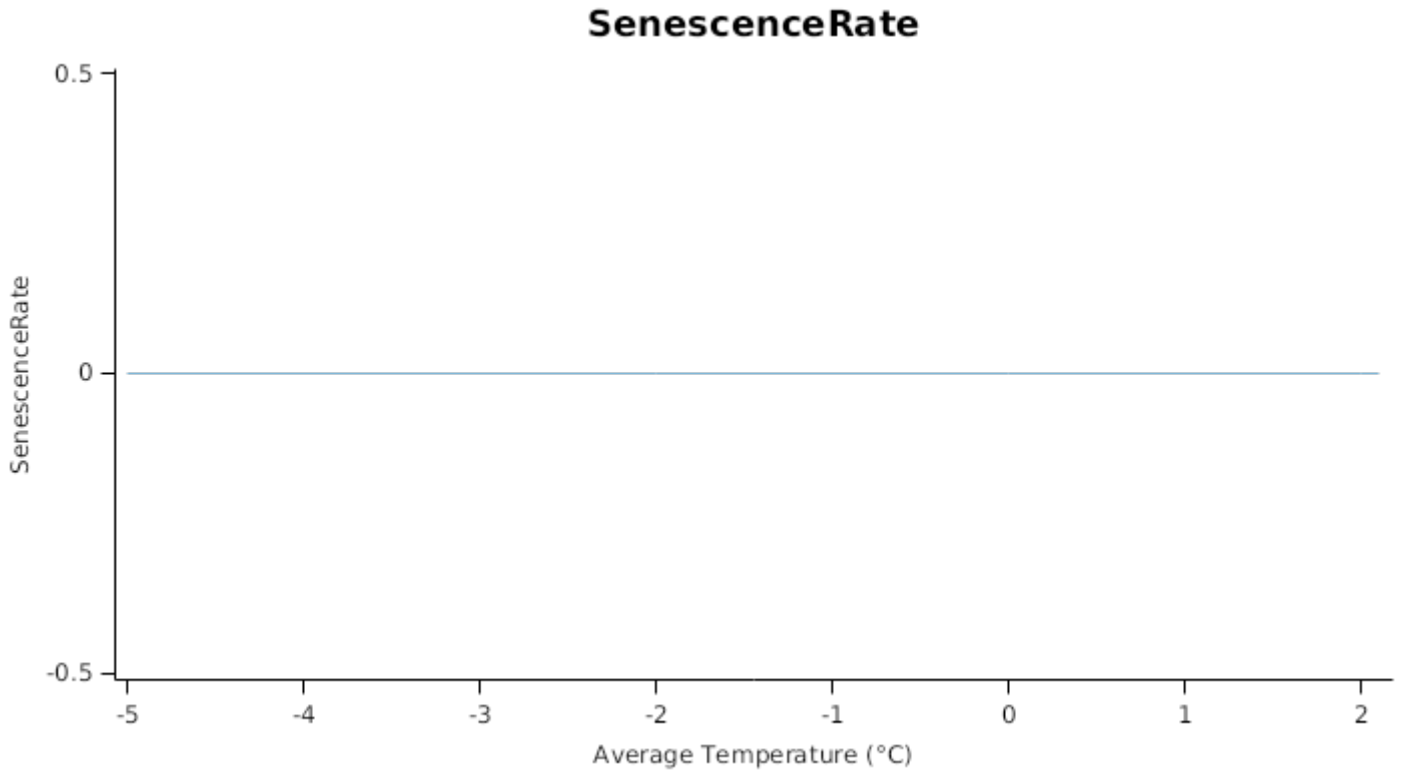
1.14.7 SenescenceRate

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

X	SenescenceRate
-5.0	0.0
-2.0	0.0
0.0	0.0
2.0	0.0
2.1	0.0





1.14.8 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	99	99
Cut	80	0	0	0
Prune	0	0	60	0
Thin	0	0	5	5

1.14.9 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 CO_2 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.

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.

RUE = 1.3 (g/MJ)

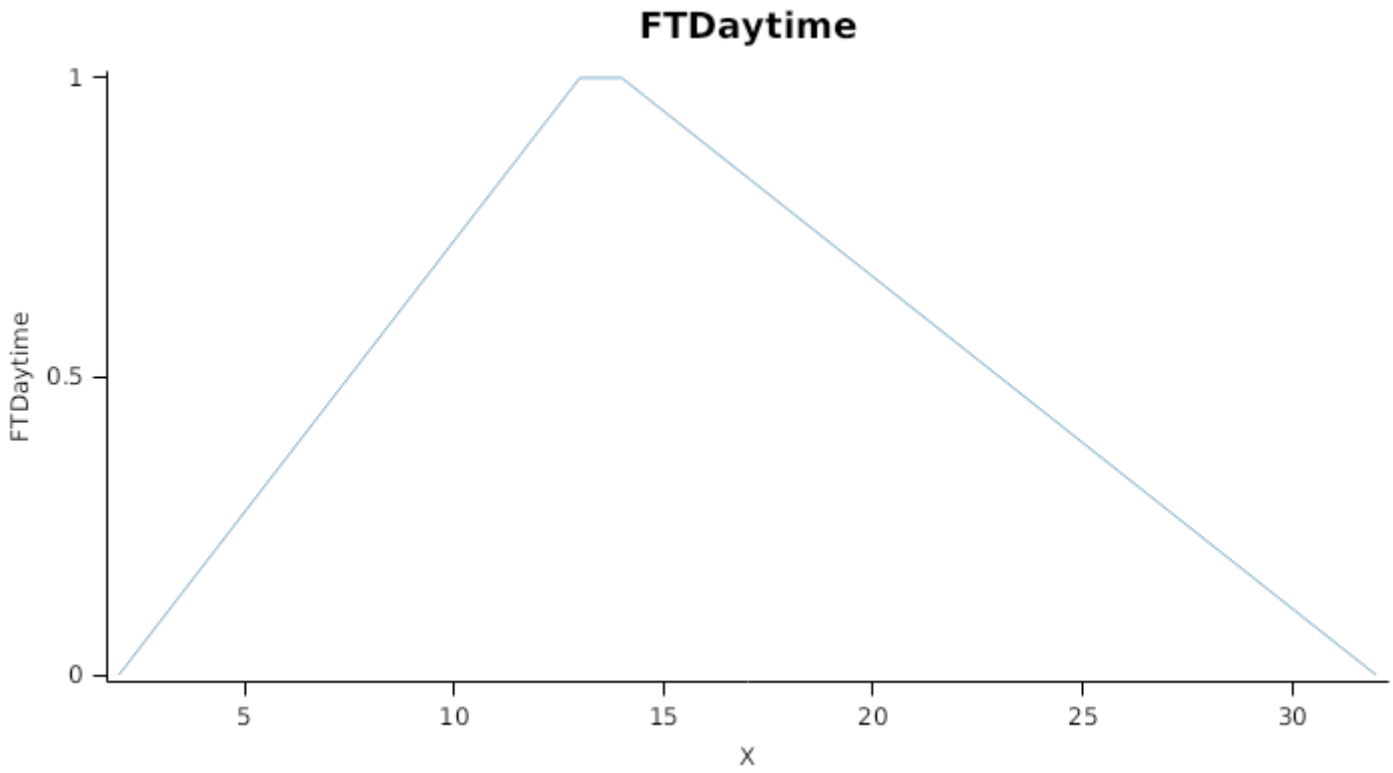
FT = Min(*FTDaytime*, *FTFrost*)

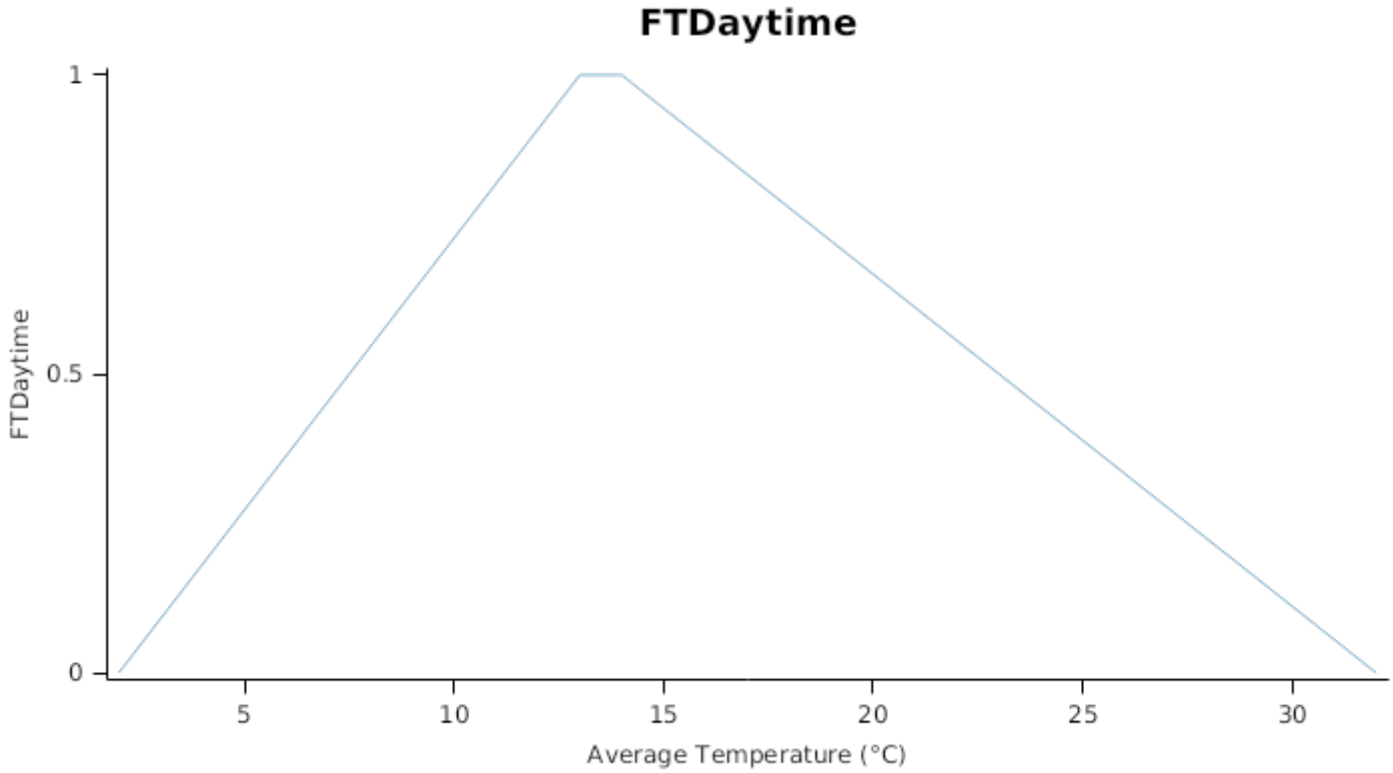
Where:

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.

MaximumTemperatureWeighting = 0.75

X	FTDaytime
2.0	0.0
13.0	1.0
14.0	1.0
32.0	0.0



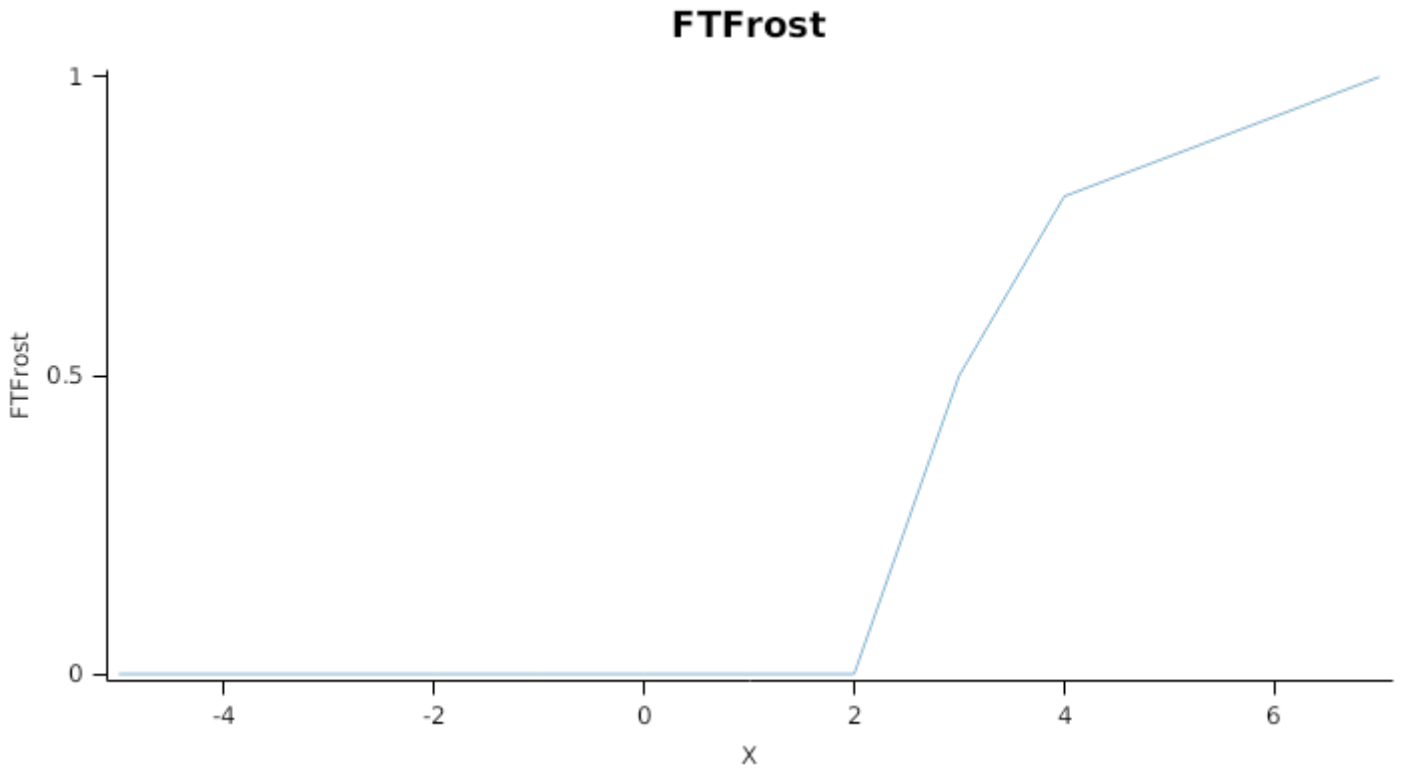


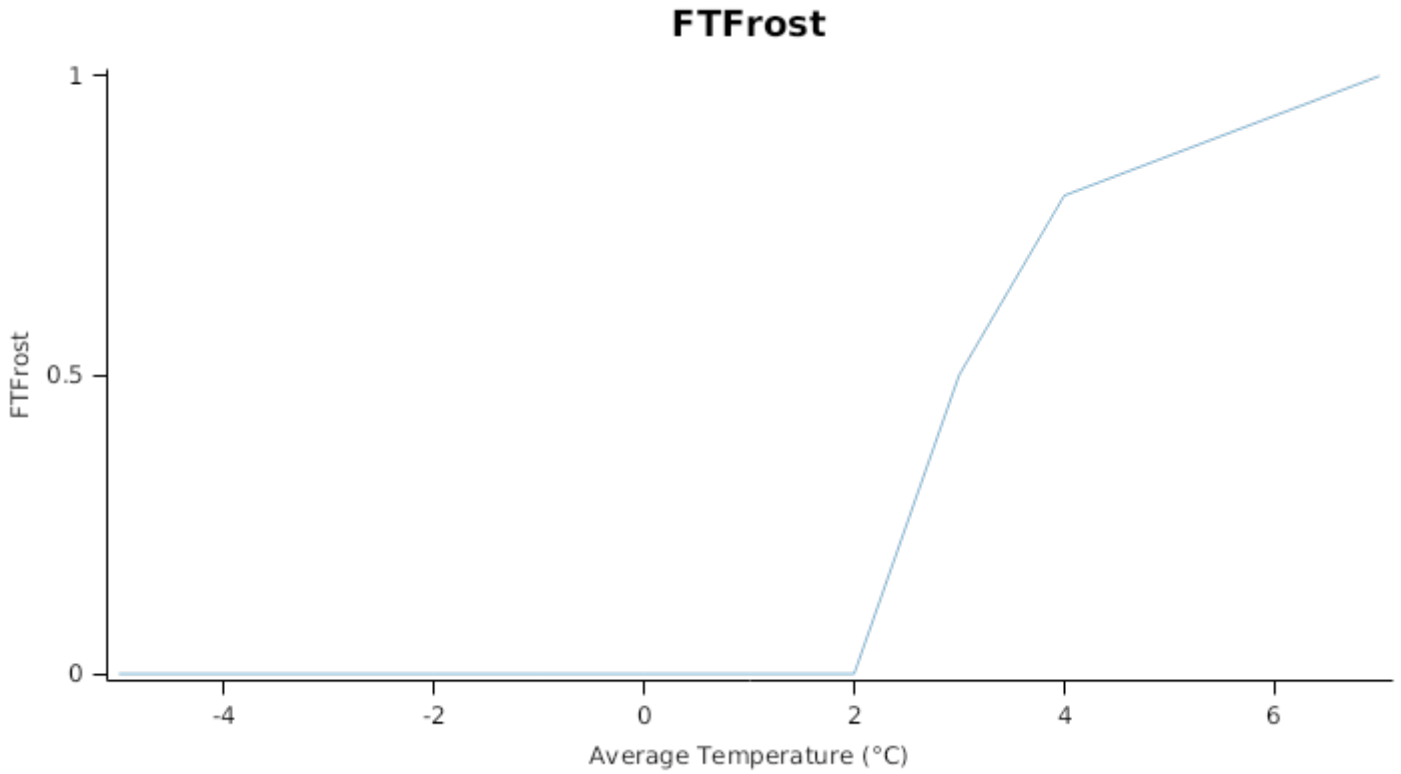
FTFrost is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0

X	FTFrost
-5.0	0.0
-2.0	0.0
-1.0	0.0

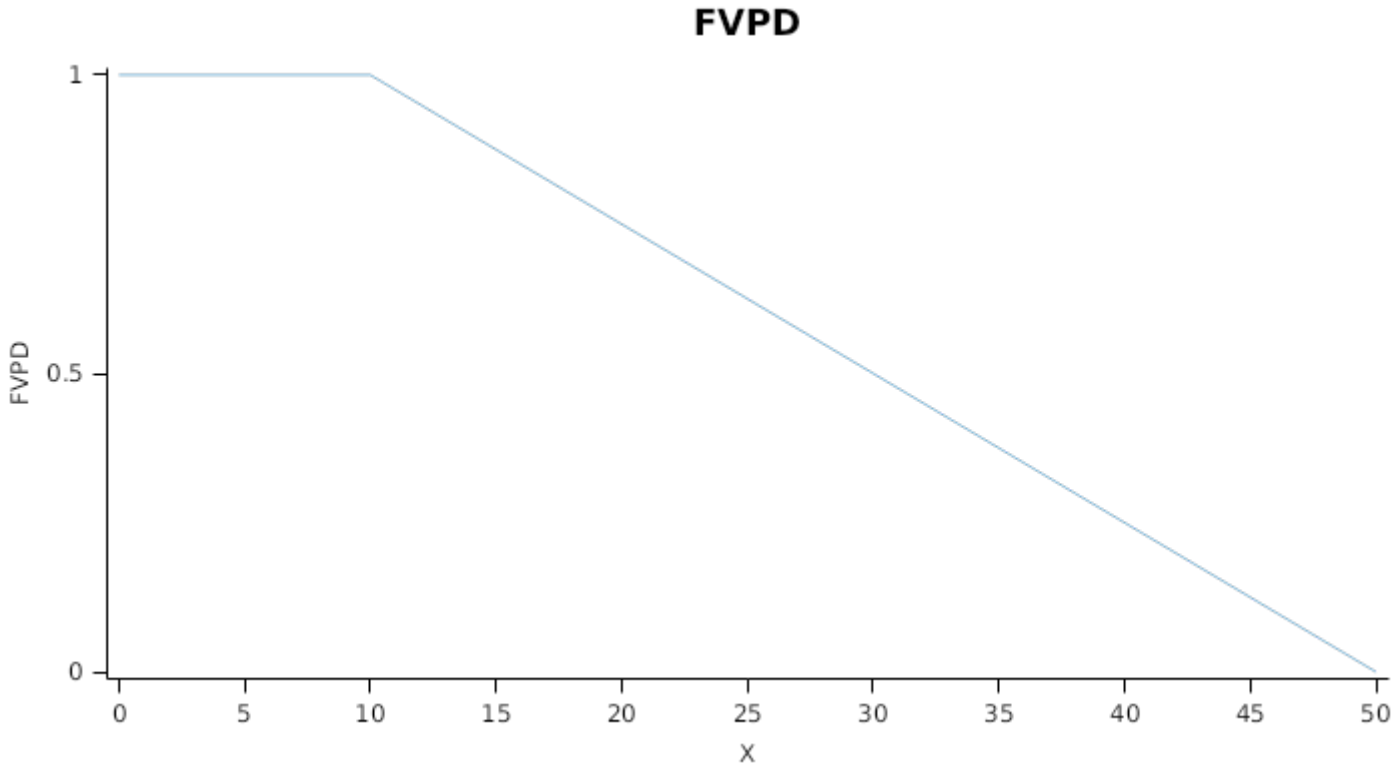
X	FTFrost
0.0	0.0
1.0	0.0
2.0	0.0
3.0	0.5
4.0	0.8
7.0	1.0





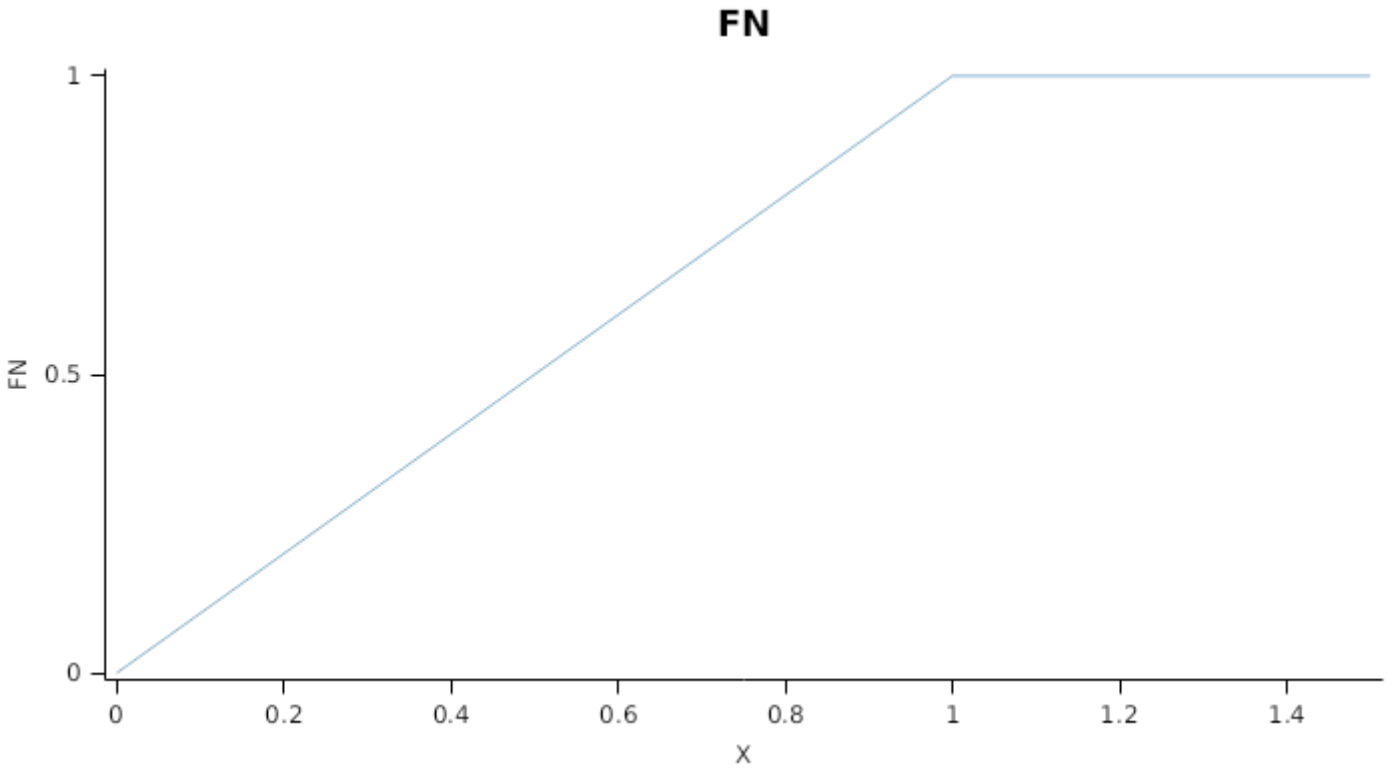
FVPD is calculated using linear interpolation

X	FVPD
0.0	1.0
10.0	1.0
50.0	0.0



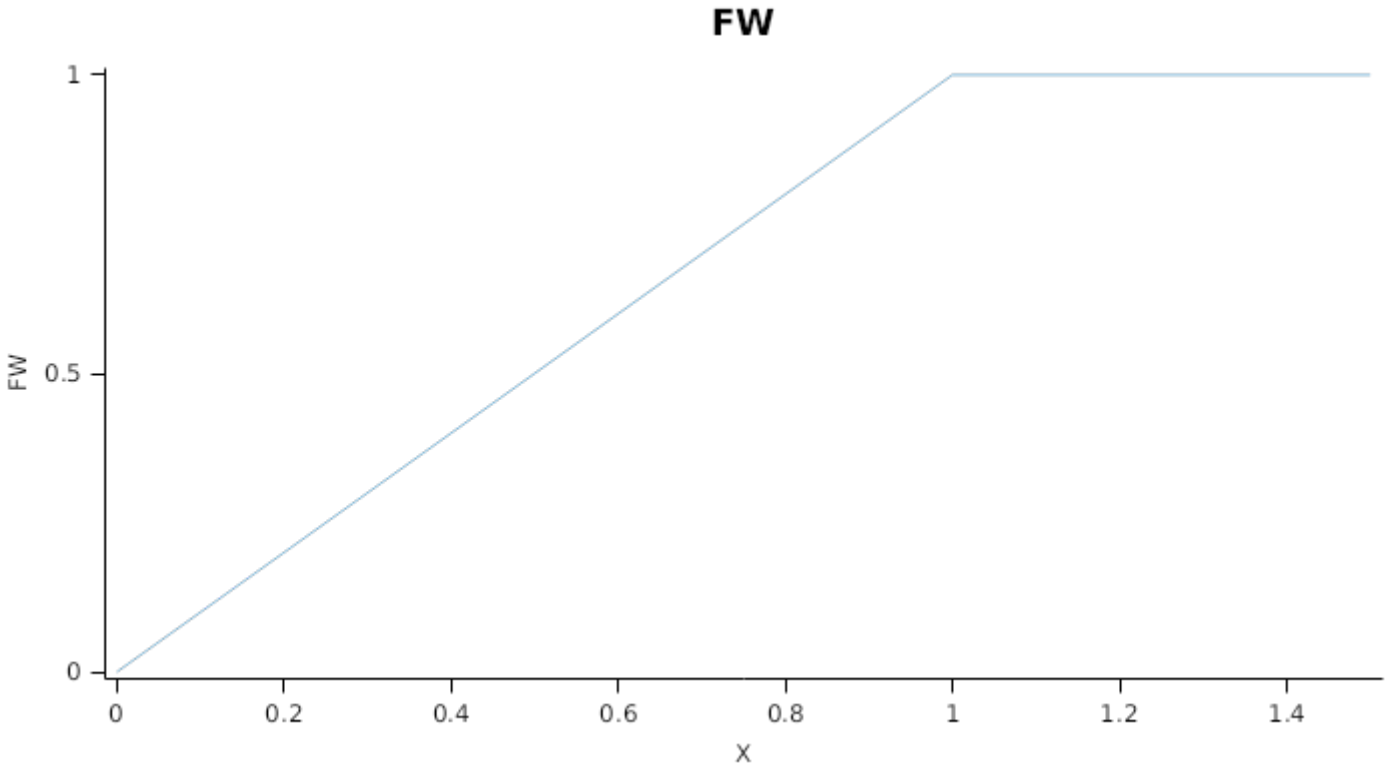
FN is calculated using linear interpolation

X	FN
0.0	0.0
1.0	1.0
1.5	1.0



FW is calculated using linear interpolation

X	FW
0.0	0.0
1.0	1.0
1.5	1.0



This model calculates the CO_2 impact on RUE using the approach of Reyenga et al., 1999.

For C3 plants,

$F_{CO2} = (CO_2 - CP) \times (350 + 2 \times CP)/(CO_2 + 2 \times CP) \times (350 - CP)$

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,

$F_{CO2} = 0.000143 * CO_2 + 0.95$

RadnInt = [Leaf].RadiationIntercepted

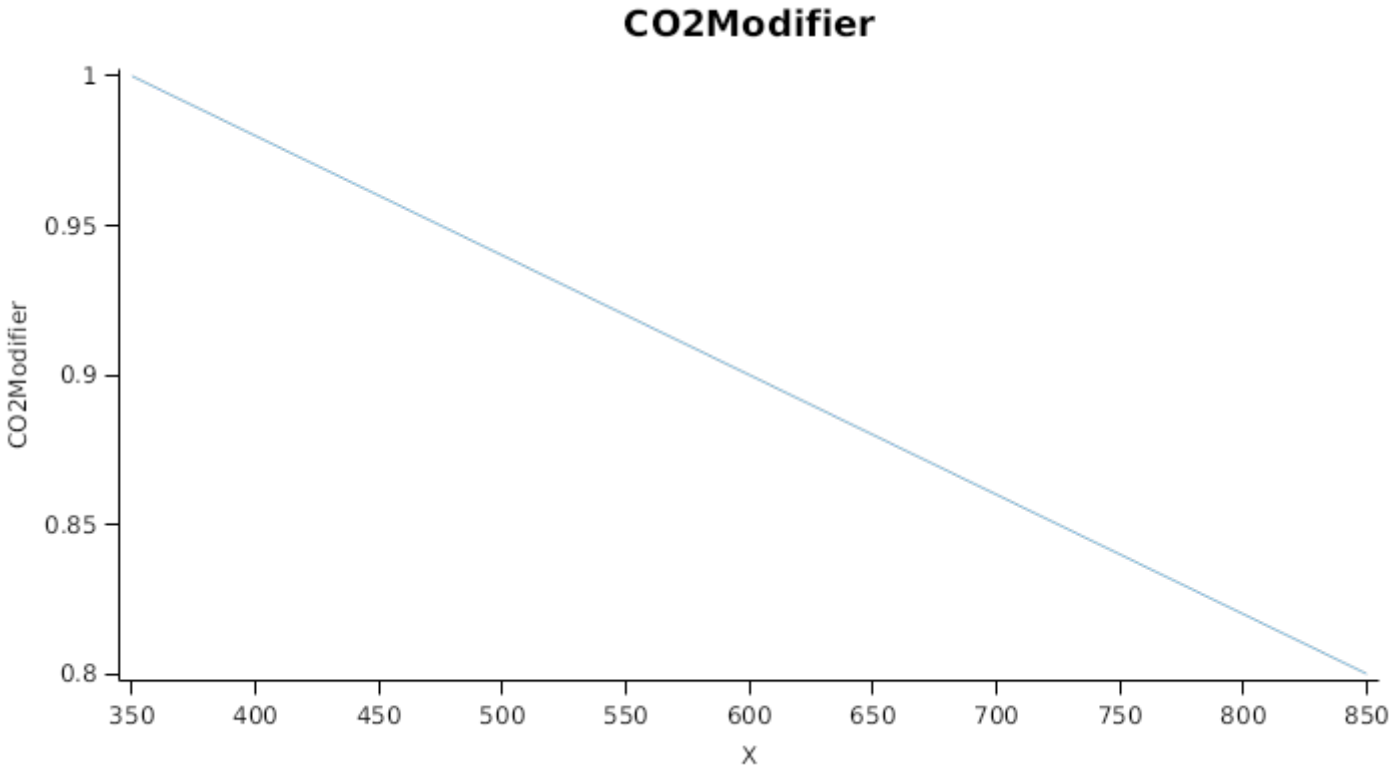
1.14.10 SpecificLeafAreaFunction

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

SpecificLeafAreaFunction = *CO2Modifier* x *SLAPotential*

CO2Modifier is calculated using linear interpolation

X	CO2Modifier
350.0	1.0
850.0	0.8



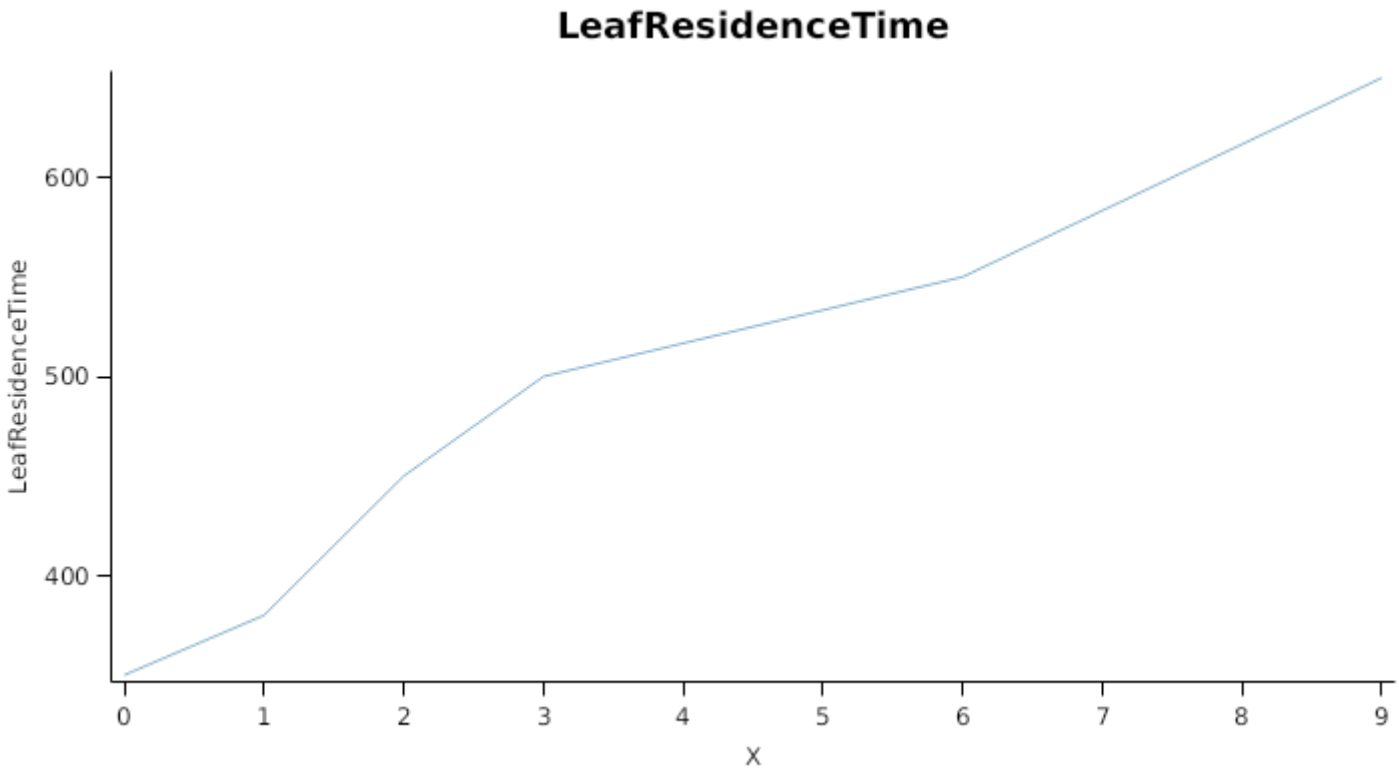
SLAPotential = 0.06-[Pinus].Leaf.Wtx0.0000003

1.14.11 LeafResidenceTime

LeafResidenceTime is calculated using linear interpolation

X	LeafResidenceTime
0.0	350.0
1.0	380.0
2.0	450.0
3.0	500.0

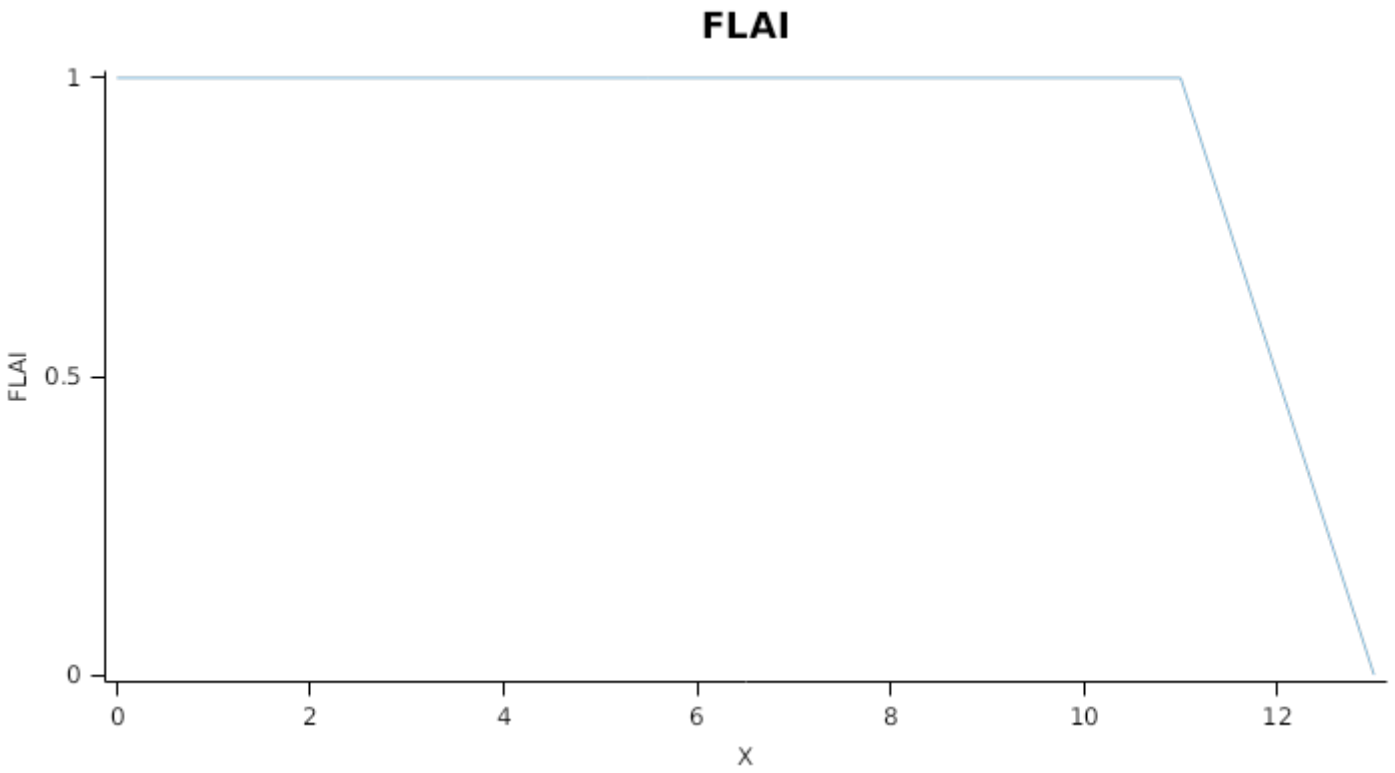
X	LeafResidenceTime
6.0	550.0
9.0	650.0



1.14.12 FLAI

FLAI is calculated using linear interpolation

X	FLAI
0.0	1.0
11.0	1.0
13.0	0.0



1.14.13 LeafKillFractionFactor

LeafKillFractionFactor = Min(*FLAI*)

Where:

FLAI = [Leaf].FLAI

1.14.14 LeafKillFraction

LeafKillFraction = 0.0+0.0x(1-[Leaf].LeafKillFractionFactor)

1.14.15 LeafDevelopmentRate

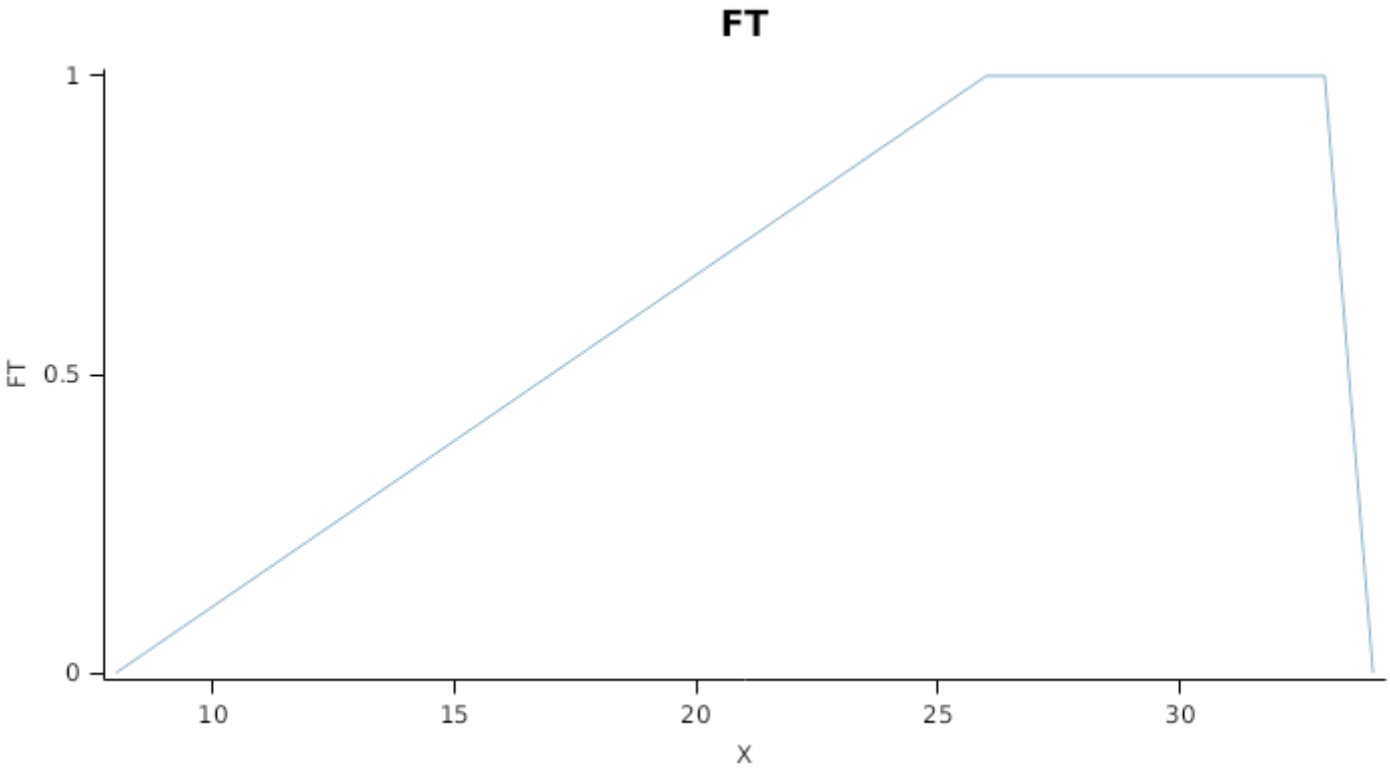
LeafDevelopmentRate = *LDR* x *FT*

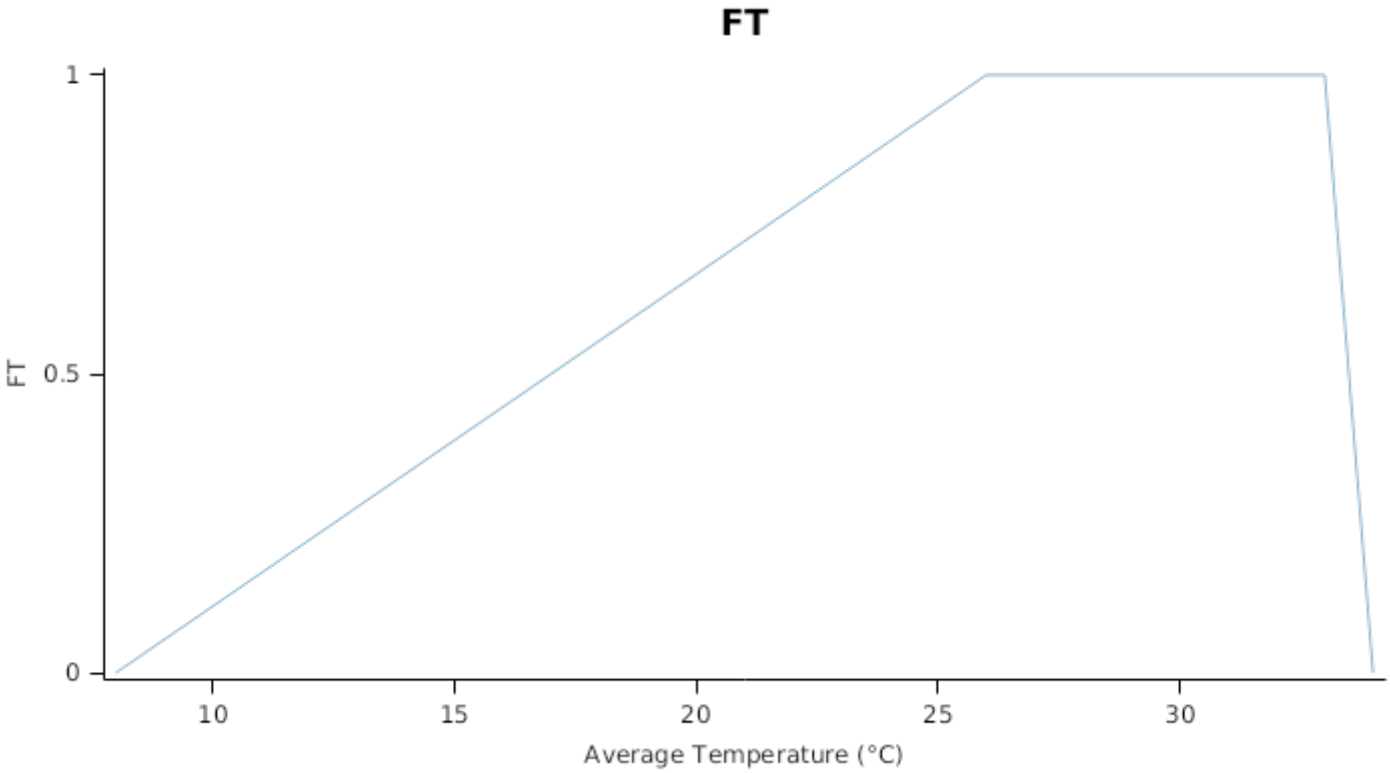
LDR = 1 (0-1)

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.

MaximumTemperatureWeighting = 1

X	FT
8.0	0.0
26.0	1.0
33.0	1.0
34.0	0.0





1.14.16 HeightFunction

HeightFunction = [Stem].Htx1000

1.14.17 DMDemands

This class holds the functions for calculating the absolute demands for each biomass fraction.

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.

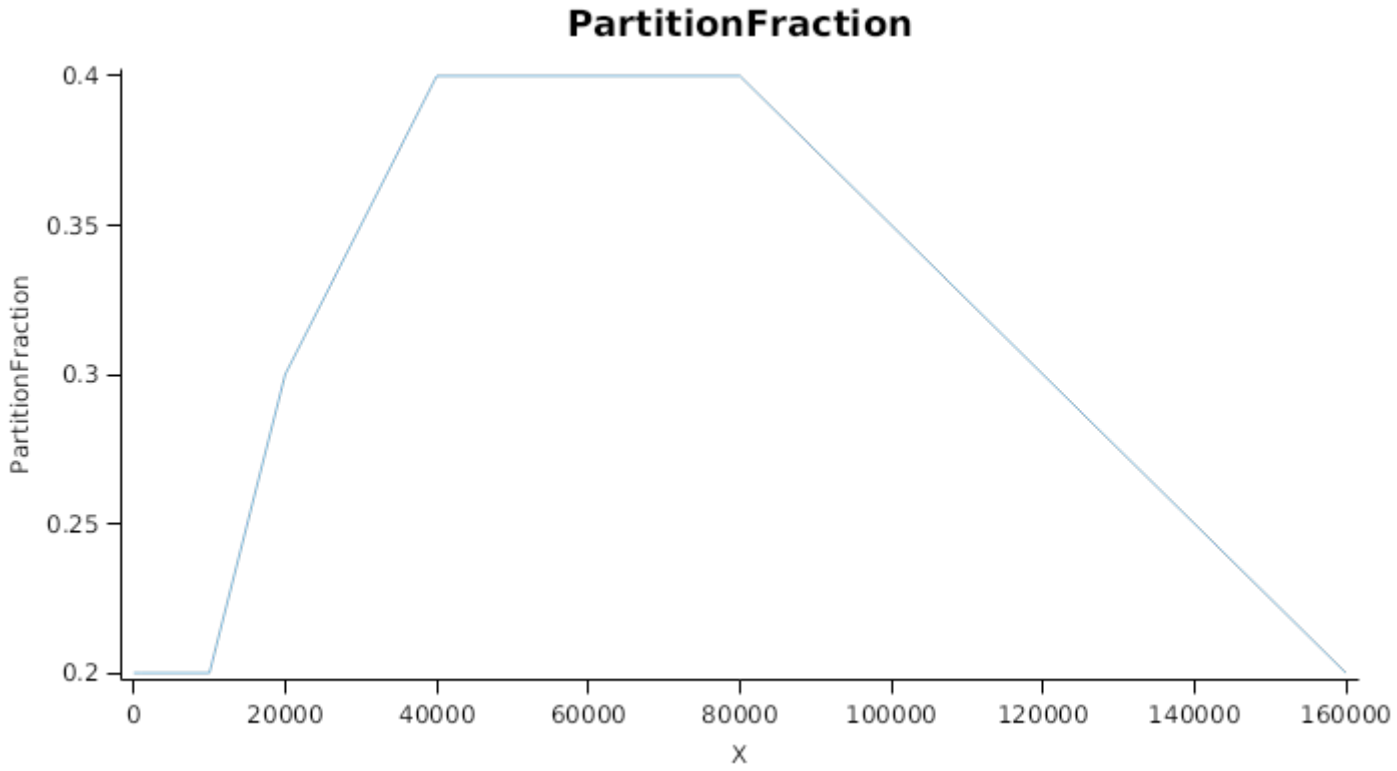
Structural = *DMDemandFunction* x *StructuralFraction*

Returns the product of its PartitionFraction and the total DM supplied to the arbitrator by all organs.

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction is calculated using linear interpolation

X	PartitionFraction
0.0	0.2
1000.0	0.2
10000.0	0.2
20000.0	0.3
40000.0	0.4
80000.0	0.4
160000.0	0.2



StructuralFraction = 0.99 (0-1)

Metabolic = 0

Storage = 0

1.14.18 NDemands

This class holds the functions for calculating the absolute demands for each biomass fraction.

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

Structural = [Leaf].minimumNconc x [Leaf].potentialDMAllocation.Structural

Metabolic = 0

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

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

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

MaxNconc = [Leaf].MaximumNconc

NitrogenDemandSwitch = 1

1.15 Branch

1.15.1 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.

1.15.2 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.

1.15.2.1 DMDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

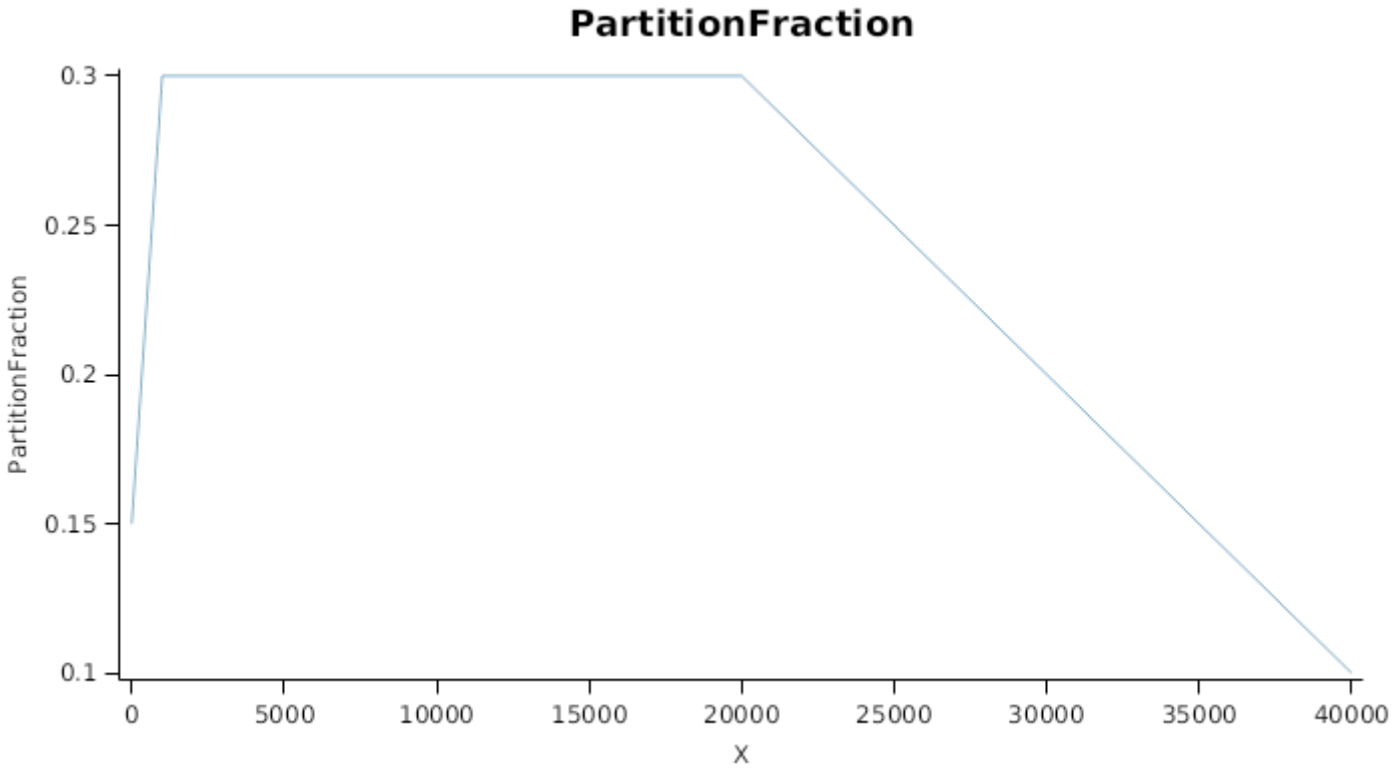
Structural = DMDemandFunction x *StructuralFraction*

Returns the product of its PartitionFraction and the total DM supplied to the arbitrator by all organs.

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction is calculated using linear interpolation

X	PartitionFraction
0.0	0.1
1000.0	0.3
10000.0	0.3
20000.0	0.3
40000.0	0.1



StructuralFraction = 0.99 (0-1)

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.15.3 Nitrogen Demand

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

1.15.3.1 NDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

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

Structural = [Branch].minimumNconc x [Branch].potentialDMAllocation.Structural

Metabolic = *MetabolicNconc* x [Branch].potentialDMAllocation.Structural

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

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

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

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

NitrogenDemandSwitch = [Branch].nitrogenDemandSwitch

MaxNconc = [Branch].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.15.4 N Concentration Thresholds

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

1.15.5 Dry Matter Supply

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

Branch does not retranslocate non-structural DM.

1.15.6 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.

1.15.7 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.

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

1.16 Stem

1.16.1 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.

1.16.2 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.

1.16.2.1 DMDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

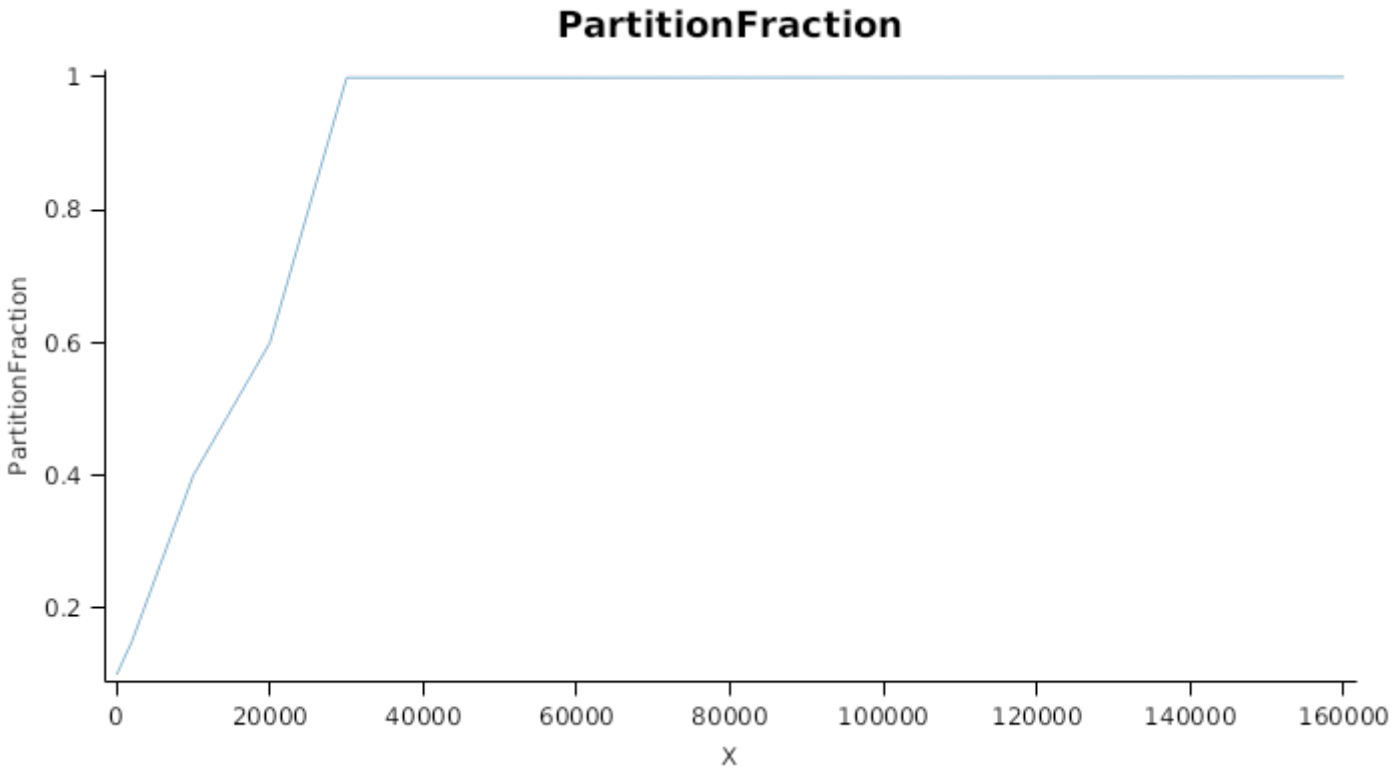
Structural = DMDemandFunction x *StructuralFraction*

Returns the product of its PartitionFraction and the total DM supplied to the arbitrator by all organs.

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction is calculated using linear interpolation

X	PartitionFraction
0.0	0.1
2000.0	0.1
10000.0	0.4
20000.0	0.6
30000.0	1.0
60000.0	1.0
160000.0	1.0



StructuralFraction = 0.99 (0-1)

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.16.3 Nitrogen Demand

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

1.16.3.1 NDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

Structural = [Stem].minimumNconc x [Stem].potentialDMAllocation.Structural

Metabolic = *MetabolicNconc* x [Stem].potentialDMAllocation.Structural

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

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

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

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

NitrogenDemandSwitch = [Stem].nitrogenDemandSwitch

MaxNconc = [Stem].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.16.4 N Concentration Thresholds

MinimumNConc = 0.002 (g/g)

CriticalNConc = [Stem].MinimumNConc

Branch, stem and coarse root minimum N concentrations are based on Raymond et al., 2000.

MaximumNConc = 0.004 (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

1.16.5 Dry Matter Supply

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

Stem does not retranslocate non-structural DM.

1.16.6 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.

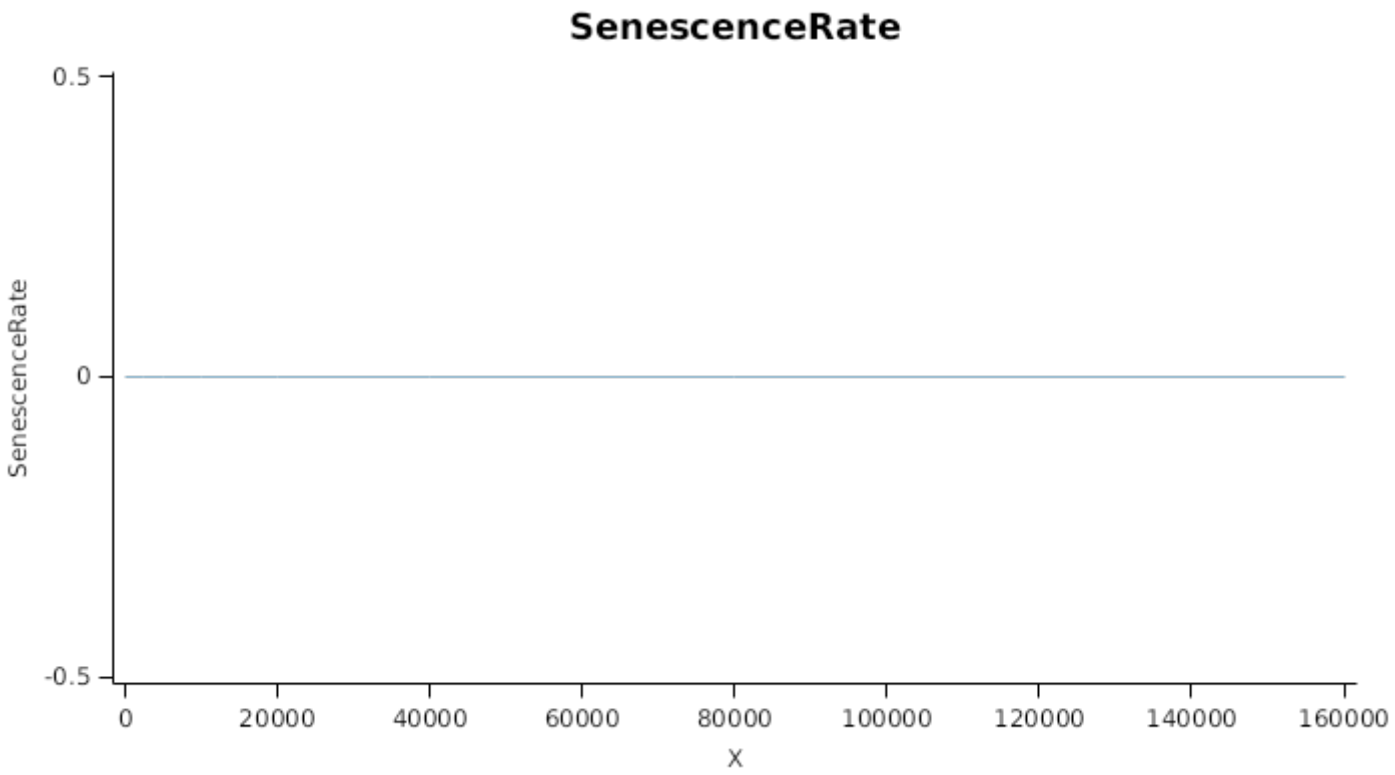
1.16.7 Senescence and Detachment

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

X	SenescenceRate
0.0	0.0
2500.0	0.0
5000.0	0.0
10000.0	0.0
20000.0	0.0
40000.0	0.0
80000.0	0.0

X	SenescenceRate
160000.0	0.0



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

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

1.17 CoarseRoot

1.17.1 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.

1.17.2 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.

1.17.2.1 DMDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

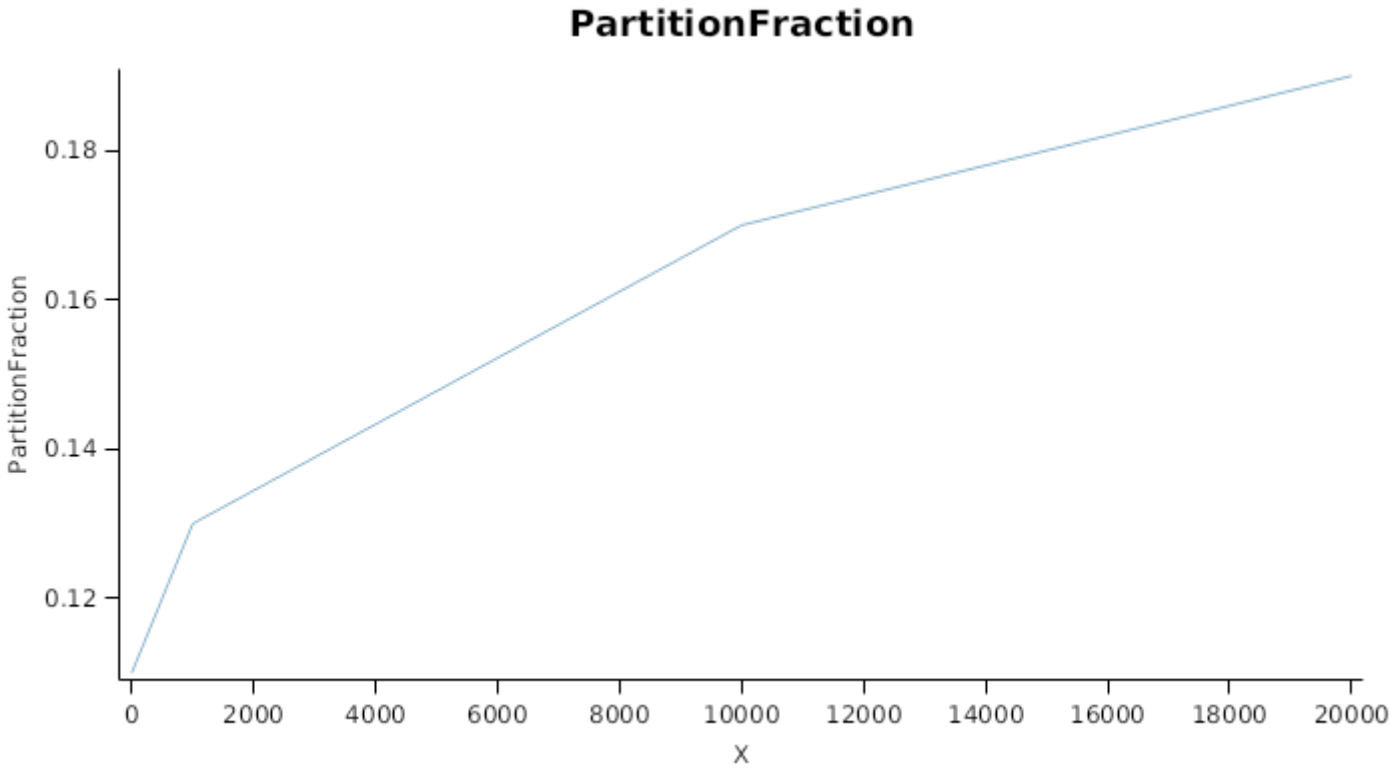
Structural = *DMDemandFunction* x *StructuralFraction*

Returns the product of its PartitionFraction and the total DM supplied to the arbitrator by all organs.

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction is calculated using linear interpolation

X	PartitionFraction
0.0	0.1
1000.0	0.1
10000.0	0.2
20000.0	0.2



StructuralFraction = 0.99 (0-1)

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.17.3 Nitrogen Demand

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

1.17.3.1 NDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

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

Metabolic = *MetabolicNconc* x [CoarseRoot].potentialDMAllocation.Structural

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

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.

NitrogenDemandSwitch = [CoarseRoot].nitrogenDemandSwitch

MaxNconc = [CoarseRoot].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.17.4 N Concentration Thresholds

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

1.17.5 Dry Matter Supply

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

CoarseRoot does not retranslocate non-structural DM.

1.17.6 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.

1.17.7 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.

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

1.18 FineRoot

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

1.18.1 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.

Root Depth Increase = RootFrontVelocity x XF_i x 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 = -$WaterUptake_i$ / $LiveRootWt_i$ x $LayerThickness_i$ x ProportionThroughLayer

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

$DMAllocated_i$ = TotalDMAllocated x RAw_i / TotalRAw

1.18.2 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.

1.18.3 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 then zero.

1.18.4 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. *$NO3\ uptake = NO3_i$ x kNO3 x $NO3_{ppm,\ i}$ x NUptakeSWFactor* _NH4 uptake = $NH4_i$ x kNH4 x $NH4_{ppm,\ i}$ x 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 demandeach plant instance will be allowed to take up.

1.18.5 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 uptake = (SW_i - LL_i) x KL_i x KLModifier*

1.18.6 Constants

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 impedence to root growth. The value of 10 mm/d used here is lower to reflect more common limiting conditions.

RootFrontVelocity = 10 (mm/d)

SenescenceRate = 0.001 (/d)

MaxDailyNUptake = 6 (kg/ha/d)

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

MaximumNConc = 0.01 (g/g)

MinimumNConc = 0.003 (g/g)

MaximumRootDepth = 10000 (mm)

KLModifier = 1

KNO3 = 0.03

KNH4 = 3E-06

Specific root length was based on Jourdan et al., 2008.

SpecificRootLength = 40 (m/g)

DMConversionEfficiency = 1 (0-1)

MaintenanceRespirationFunction = 0 (0-1)

RemobilisationCost = 0

CarbonConcentration = 0.5 (g/g)

RootDepthStressFactor = 1

1.18.7 RootShape

This model calculates the proportion of each soil layer occupied by roots.

1.18.8 NitrogenDemandSwitch

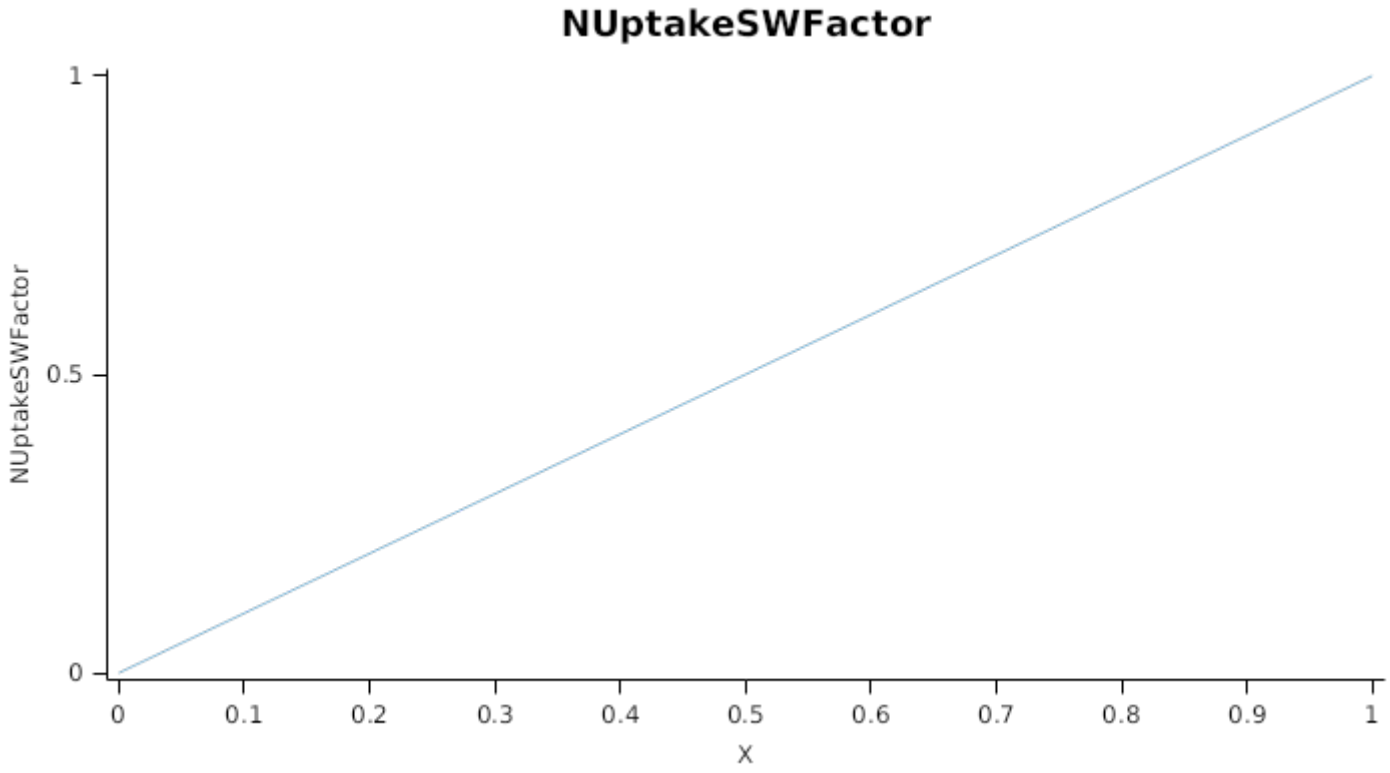
NitrogenDemandSwitch has a value between Emergence and Old calculated as:

Constant = 1

1.18.9 NUptakeSWFactor

NUptakeSWFactor is calculated using linear interpolation

X	NUptakeSWFactor
0.0	0.0
1.0	1.0



1.18.10 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

1.18.11 DMDemands

1.18.11.1 DMDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

Structural = *DMDemandFunction* x *StructuralFraction*

Returns the product of its PartitionFraction and the total DM supplied to the arbitrator by all organs.

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction = 0.11

StructuralFraction = 1

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.18.12 NDemands

1.18.12.1 NDemands

This class holds the functions for calculating the absolute demands and priorities for each biomass fraction.

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

Metabolic = *MetabolicNconc* x [FineRoot].potentialDMAllocation.Structural

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

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.

NitrogenDemandSwitch = [FineRoot].nitrogenDemandSwitch

MaxNconc = [FineRoot].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.18.13 CriticalNConc

CriticalNConc = *[FineRoot].MinimumNConc*

1.18.14 InitialWt

This class holds the functions for calculating the absolute demands for each biomass fraction.

Structural = 0.2 (g/plant)

Metabolic = 0

Storage = 0

1.19 RootShootRatio

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

1.20 caribaea

1.20.1 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, 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)^0.218209)

[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

1.21 elliottii

1.21.1 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)^0.218209)

[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

1.21.2 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)^0.218209)

[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

1.21.3 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)

1.21.4 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)^0.218209)

[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, 1.1, 1.46, 1.5, 1.5

1.22 elliottiiXcaribaeaF1

1.22.1 elliottiiXcaribaeaF1

elliottiiXcaribaeaF1 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)^0.218209)

[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

1.23 elliottiiXcaribaeaF2

1.23.1 elliottiiXcaribaeaF2

elliottiiXcaribaeaF2 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)^0.218209)

[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

1.24 radiata

1.24.1 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)

1.24.2 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

1.24.3 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)

1.25 taeda

1.25.1 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)^0.218209)

1.25.2 taedaIMPAC

taedaIMPAC 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, 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)

2 The APSIM Pinus Model

3 Pinus Model Notes

4 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.

##Pecularities 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 partitioniing targets that is 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 calbirated 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, whiole others are the result of several generations of tree breeding. Early genetic material was mostly selected, for example, for states in Australian from provenance that performed adequately in state of interest, and tree breeding programes 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.

##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 Eucaluptus 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 empricially 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:

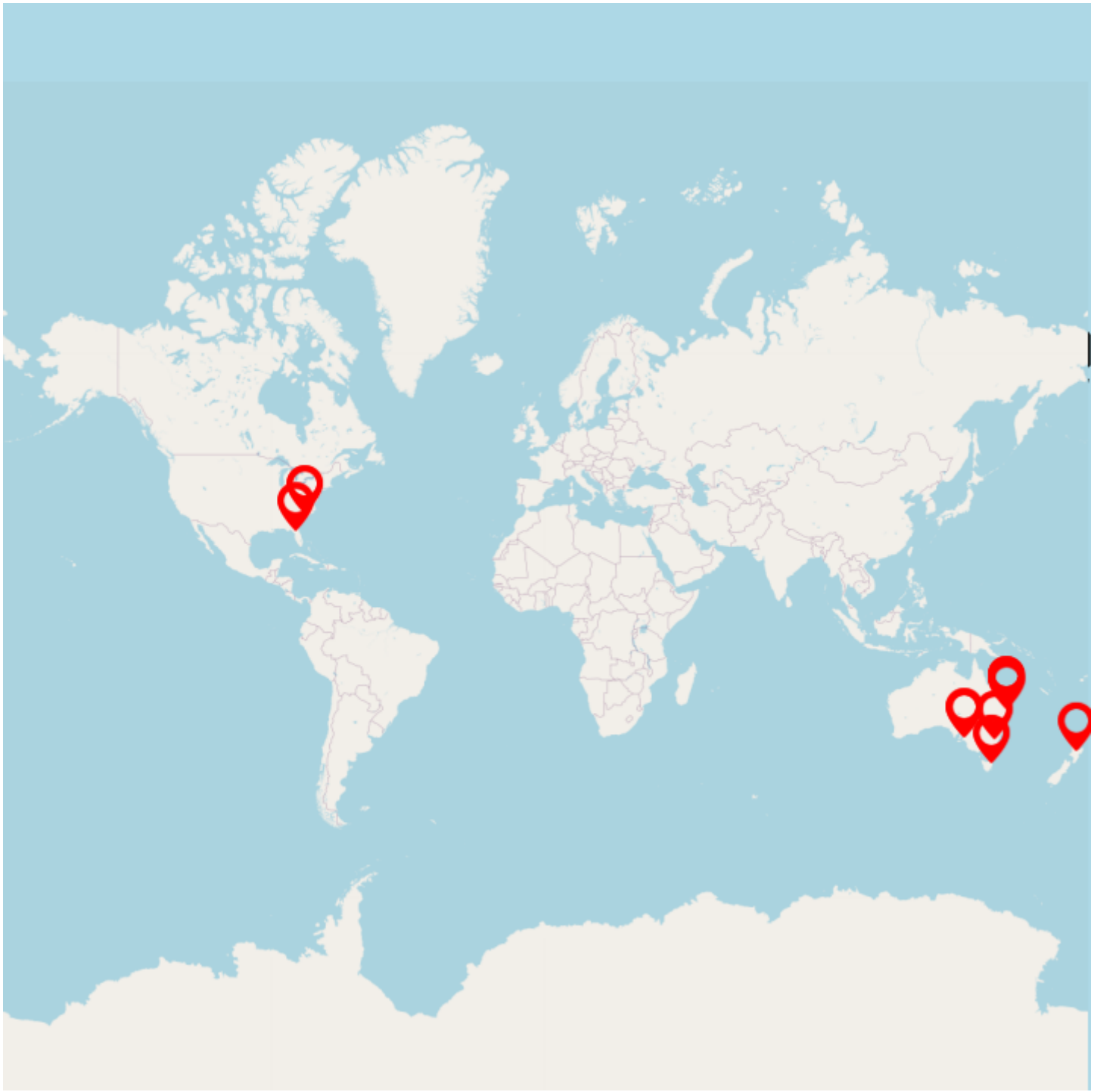
1. Make SLA a function of stress level
2. Create a set of functional weeds specifically for use with these forestry models, e.g. N-fixing/non-N-fixing X herbaceous/shrub/tree X tropical/sub-tropical/temperate
3. Self-thinning rule or process-based mortality
4. Improve effects of stocking, if necessary. 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 otehr 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 idiexes)

5 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, provenence, clones). These datasets have been grouped and ordered alphebetically by climatic zone, country and site. Currently, all temperate data are for *P. radiata*, but a range of tropical and sub-tropical genpotypes 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.



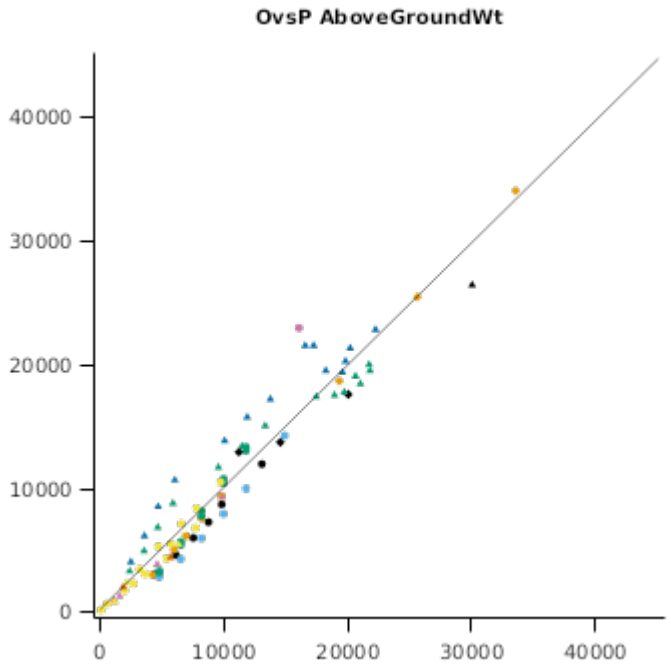
5.1 Combined Validation

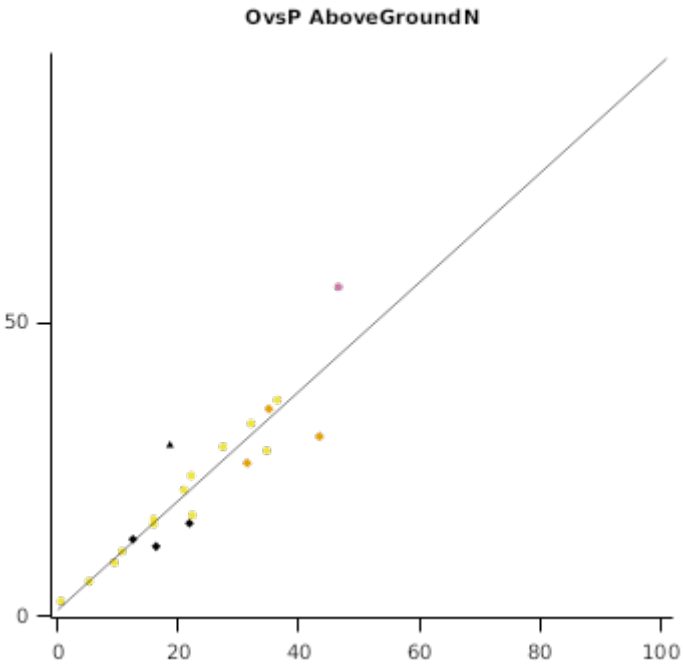
These graphs are for the combined datasets of *Temperate* and *Tropical and SubTropical* climatic zones.

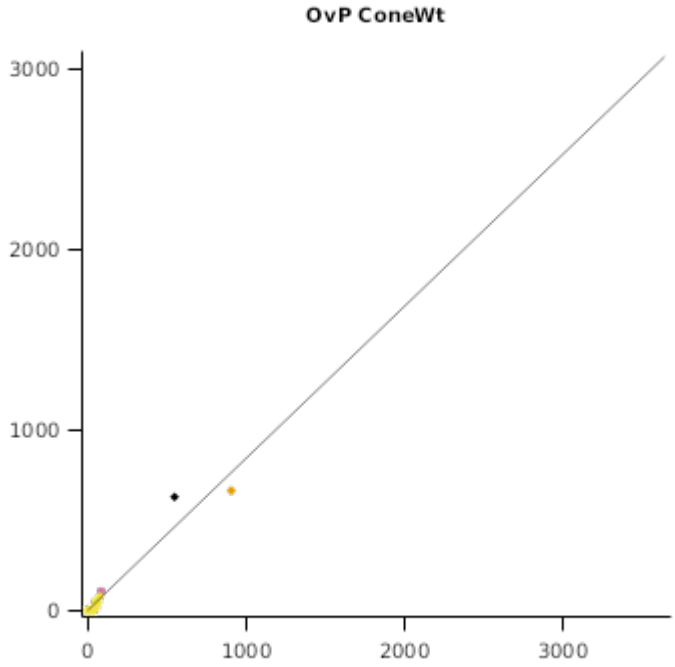
Graphs from individual sites, particularly temporal trends of observed and predicted values, are available but currently disabled. If you wish to view these graphs, please download the validation from GitHub, run it, and enable those graphs and-or add others.

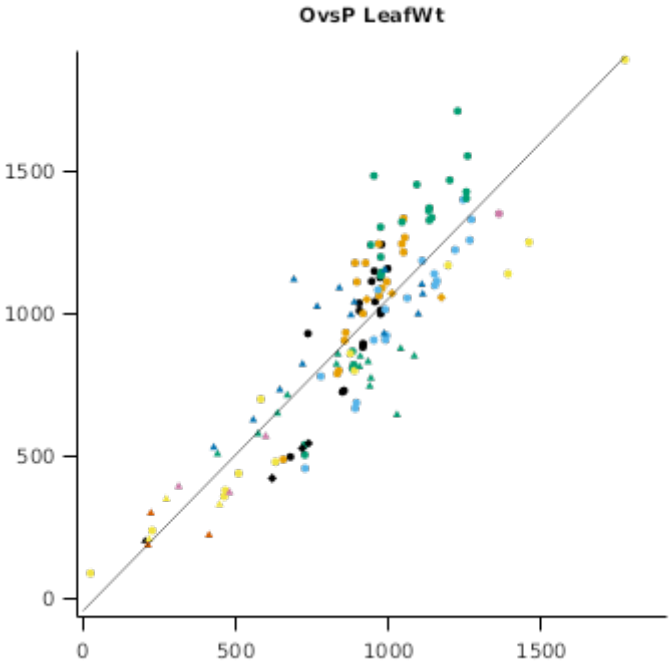
Two sites are simulated to ages beyond when there was a reasonable expectation of satisfactory model skill, due to very low stocking being reached where allocation patterns would probably not have been simulated correctly (Puruki site) or due to not correctly predicting disease-induced loss of tree vigor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

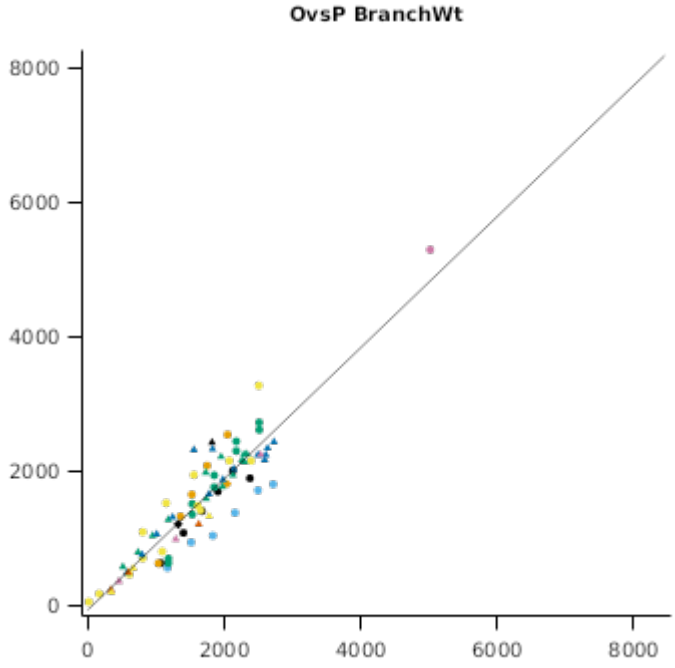
Many of these simualtions for stem metrics could be further improved by better specifying allometric relations between biomass and tree size, which we know are highly environment-by-genotype specific, but what is provided here is a minimal range of genotypes that were needed to achieve the level of model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

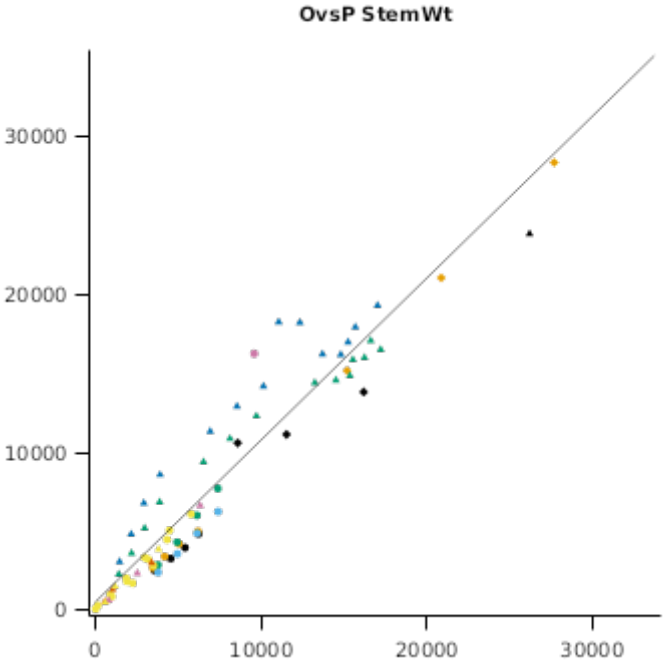

OvsP AboveGroundWt
40000
30000
20000
10000
0
0
10000
20000
30000
40000

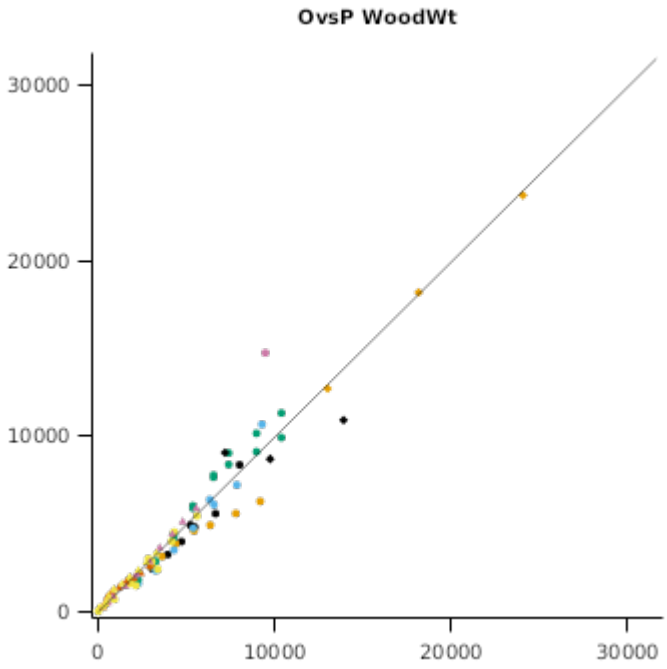

OvsP AboveGroundN
50
0
0
20
40
60
80
100

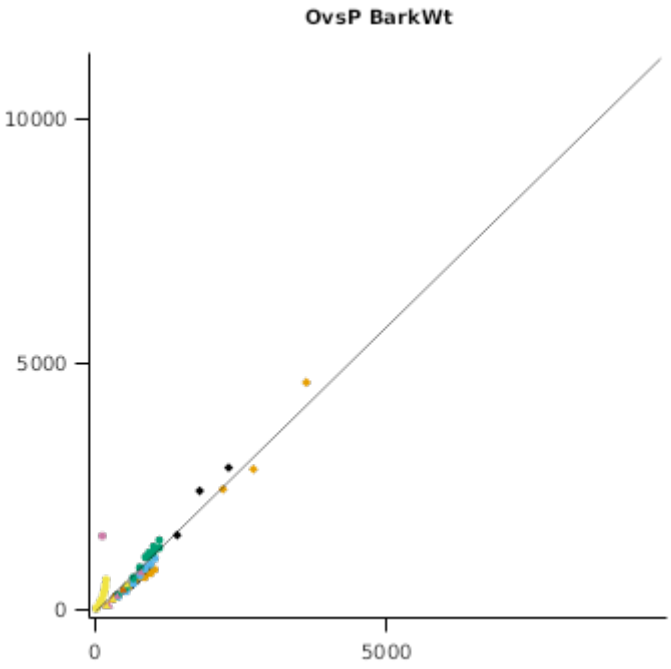

OvP ConeWt
3000
2000
1000
0
0
1000
2000
3000

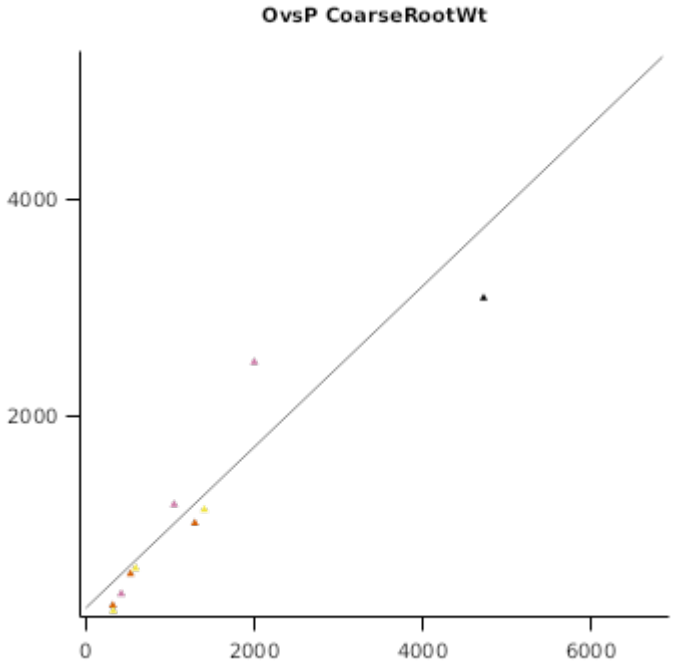

OvsP LeafWt
1500
1000
500
0
0
500
1000
1500

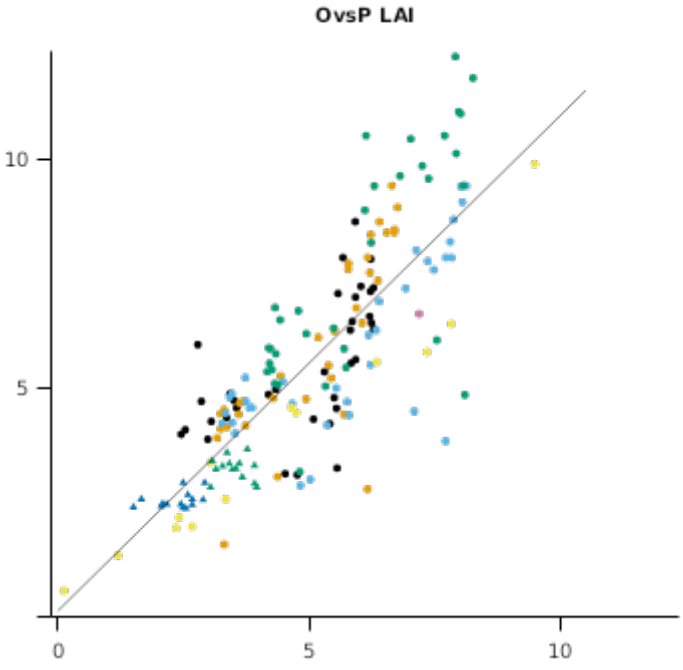

OvsP BranchWt
8000
6000
4000
2000
0
0
2000
4000
6000
8000

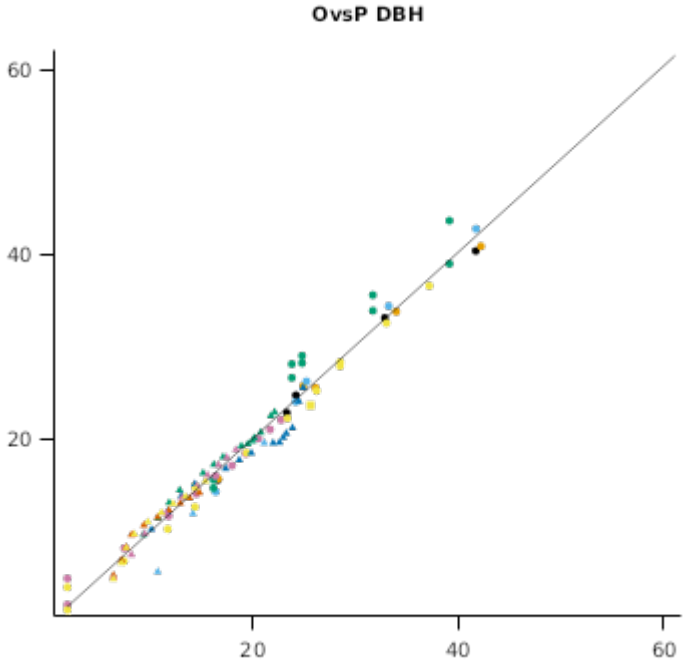

OvsP StemWt
30000
20000
10000
0
0
10000
20000
30000

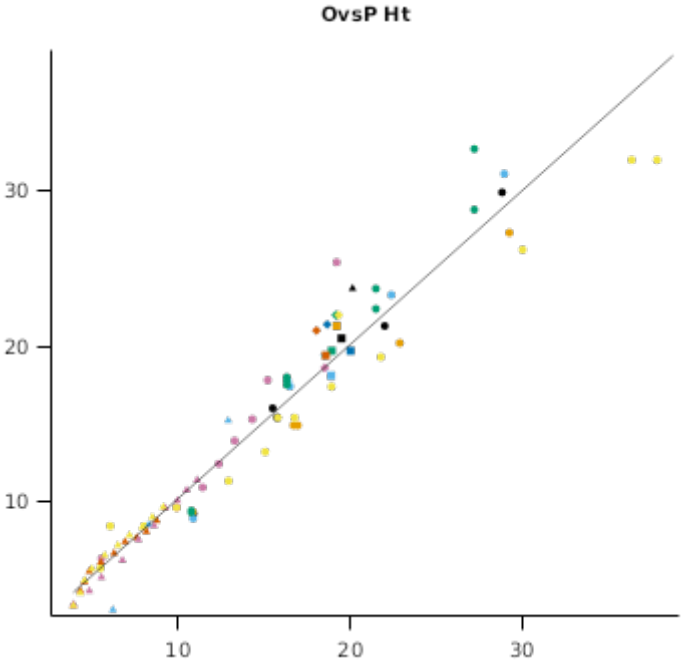

OvsP WoodWt
30000
20000
10000
0
0
10000
20000
30000

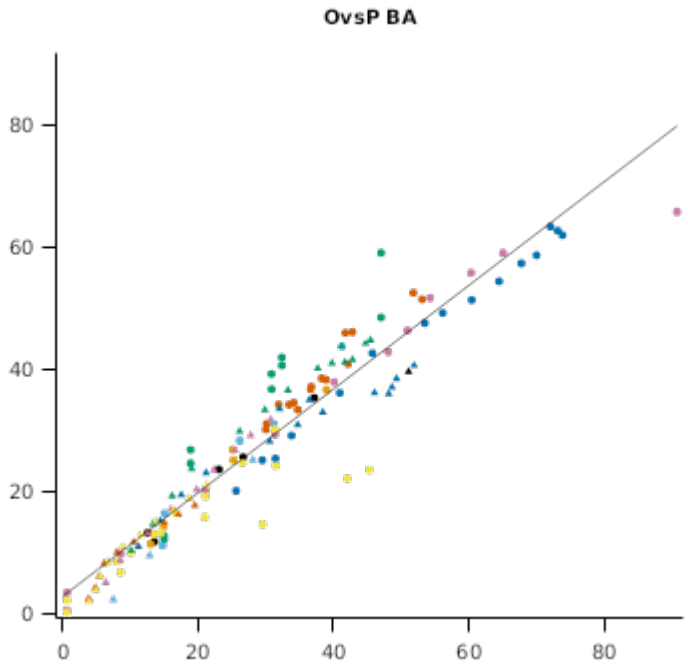

OvsP BarkWt
10000
5000
0
0
5000

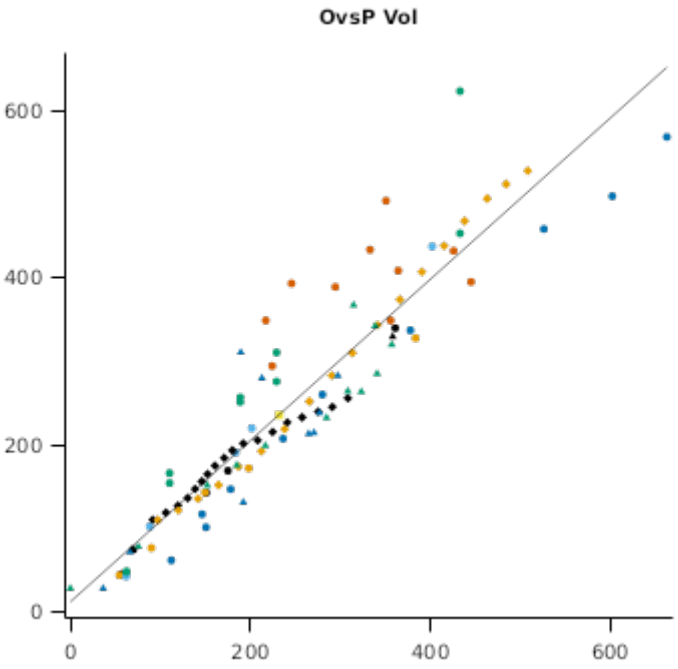

OvsP CoarseRootWt
4000
2000
0
2000
4000
6000

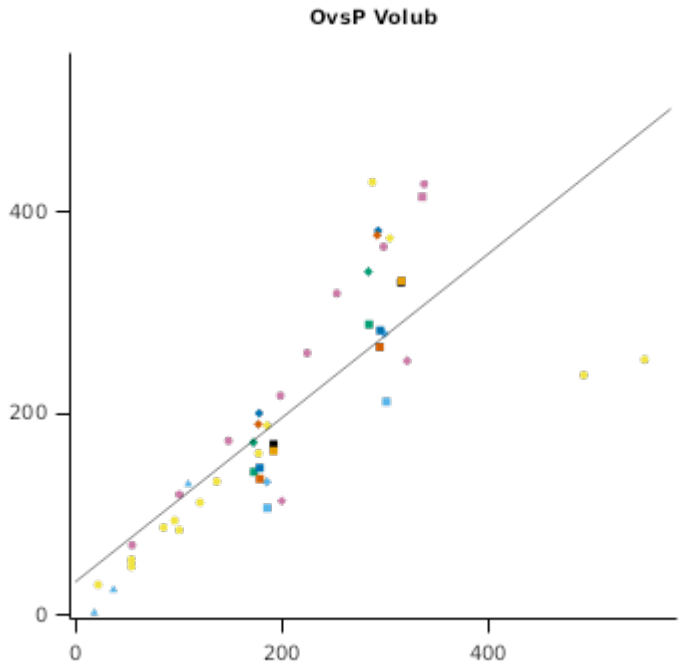

OvsP LAI
10
5
0
5
10

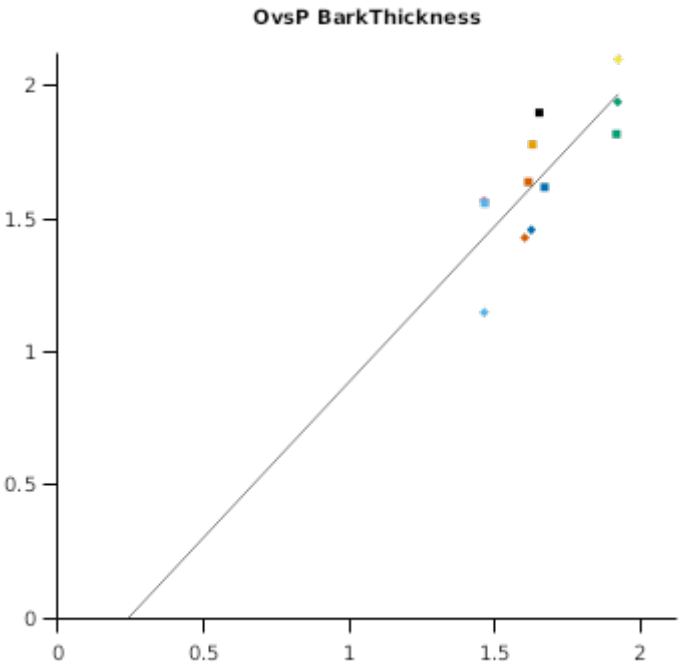

OvsP DBH
60
40
20
20
40
60

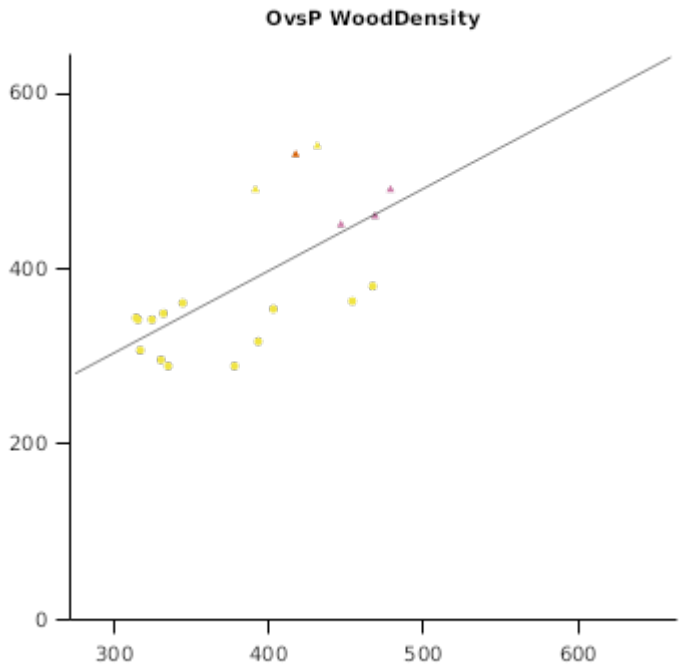

OvsP Ht
30
20
10
10
20
30

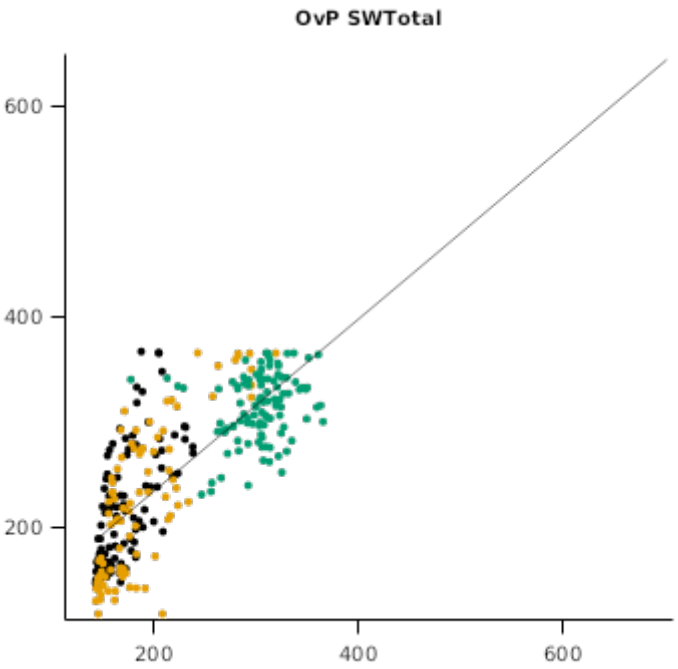

OvsP BA
0
20
40
60
80


OvsP Vol
0
200
400
600


OvsP Volub
0
200
400


OvsP BarkThickness
0
0.5
1
1.5
2


OvsP WoodDensity
0
200
400
600
300
400
500
600


OvP SWTotal
200
400
600

5.2 Temperate

These are the Temperate datasets.

5.2.1 BFG

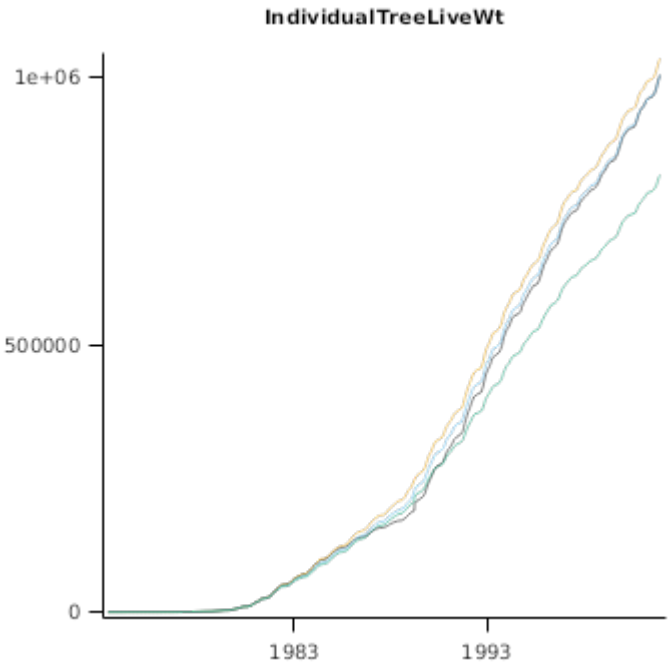
These data are for an experiment with fertilizer, irrigation and fertigation treatments established in a 10-year-old *P. radiata* plantation near Canberra, Australia. The experiment was officially entitled Biology of Forest Growth (BFG) as if focused on improving the physiogical understanding of growth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

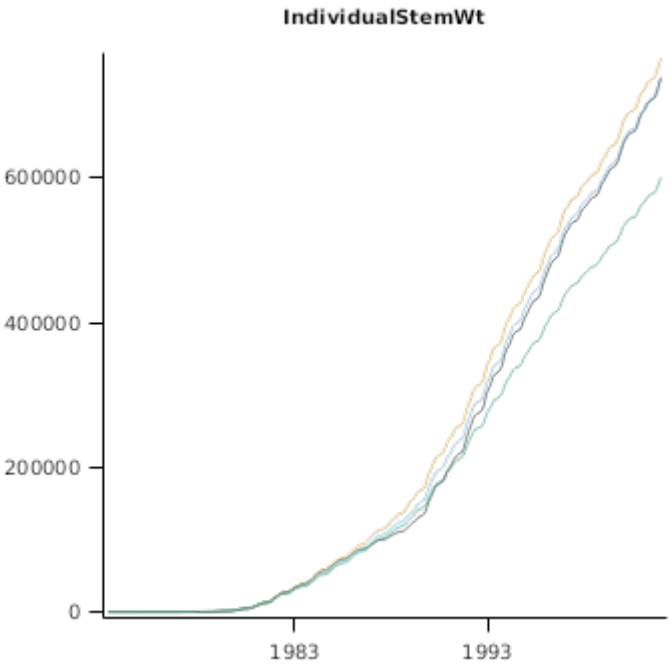
Numerous publications about this experiment reported on its management, tree growth, biomass components, phenology, climate, and soils. Many of these publications were produced in a special issue of Forest Ecology and Management (Volume 52, Issues 1–4, September 1992) several from which data have been 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, McMurtrie 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 addition data were also provided by Keryn Paul (CSIRO), which we greatly apprecaited.

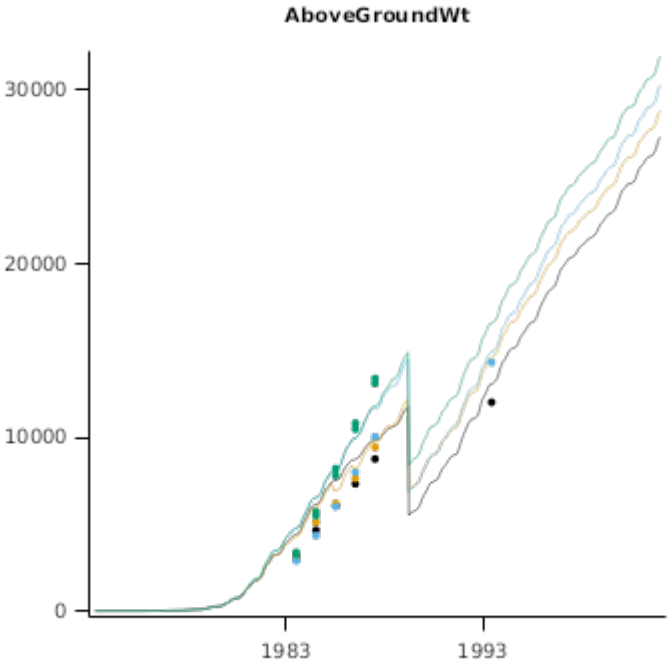
List of experiments.

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

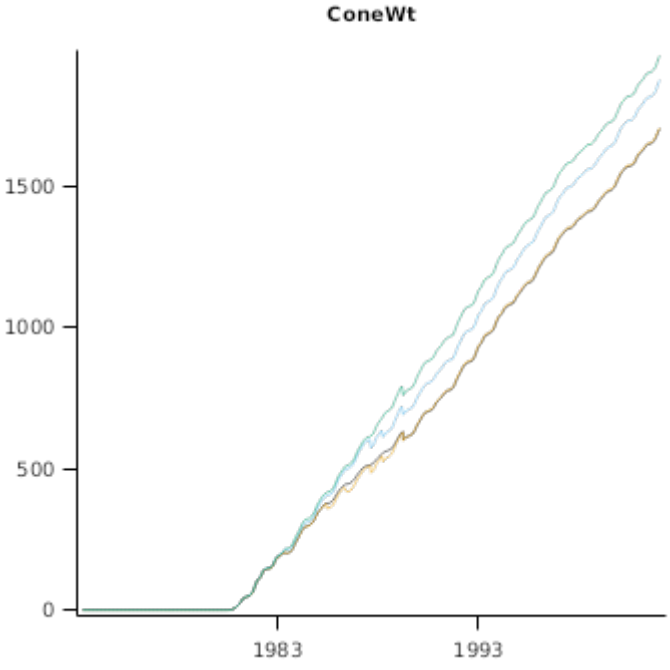
5.2.1.1 GraphsWeights

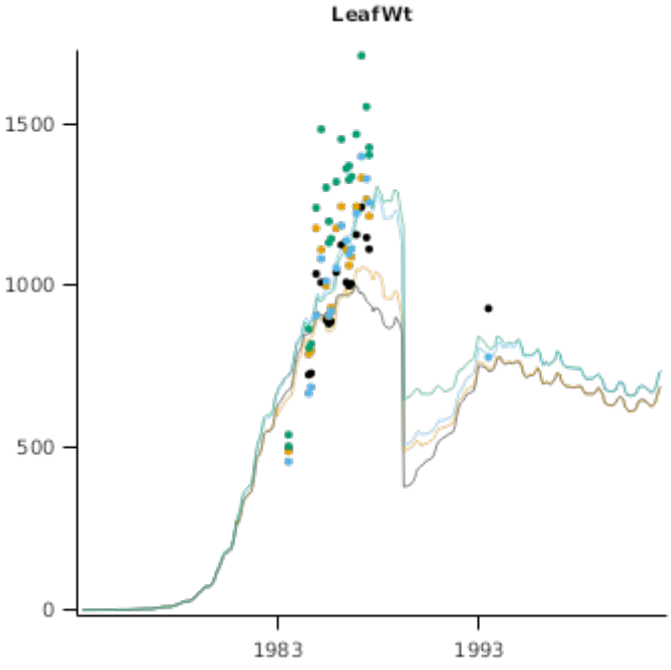


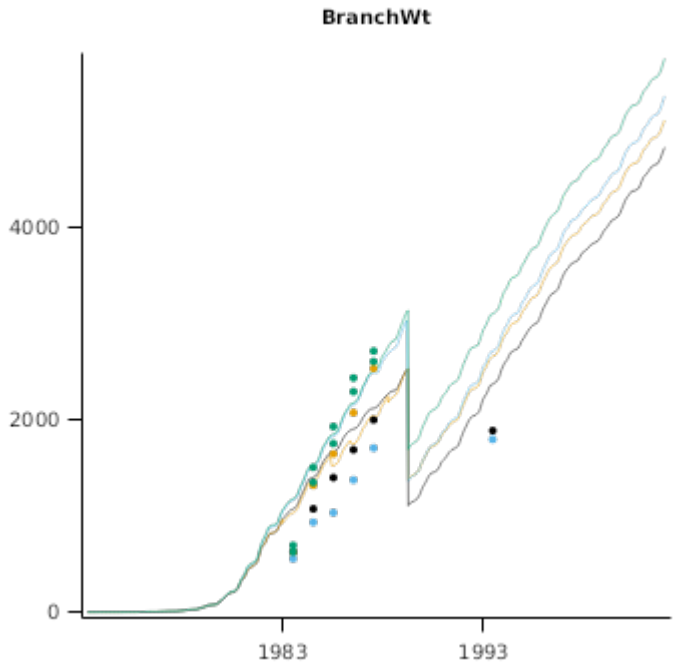


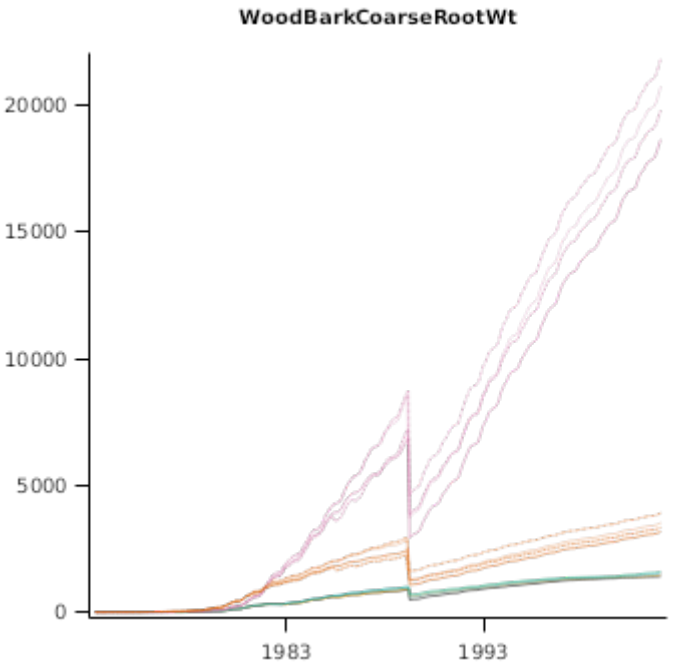


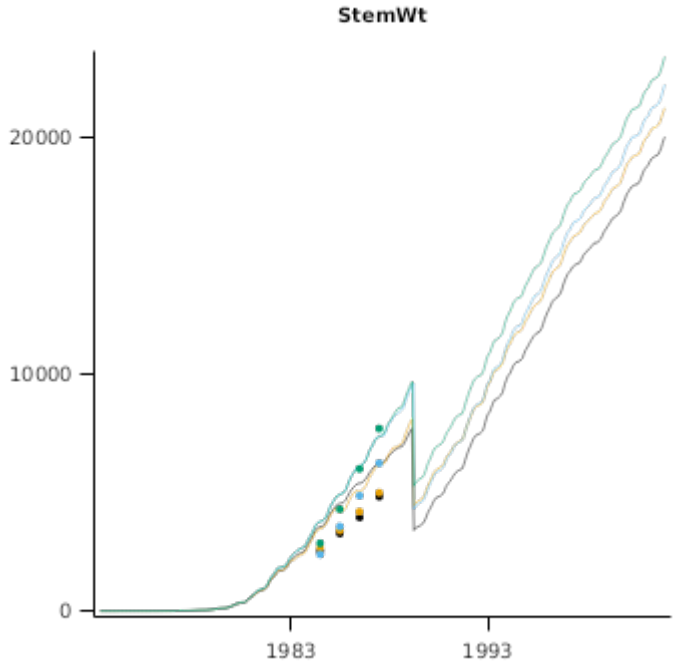
ComponentWts

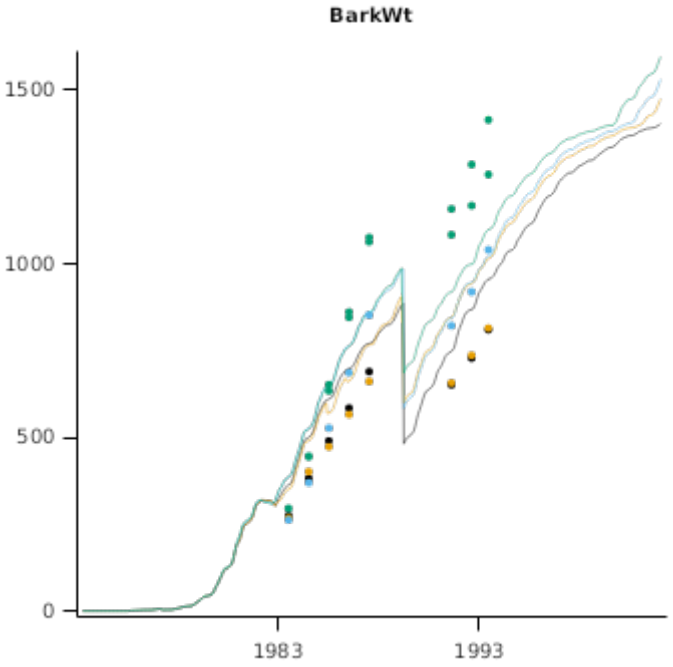


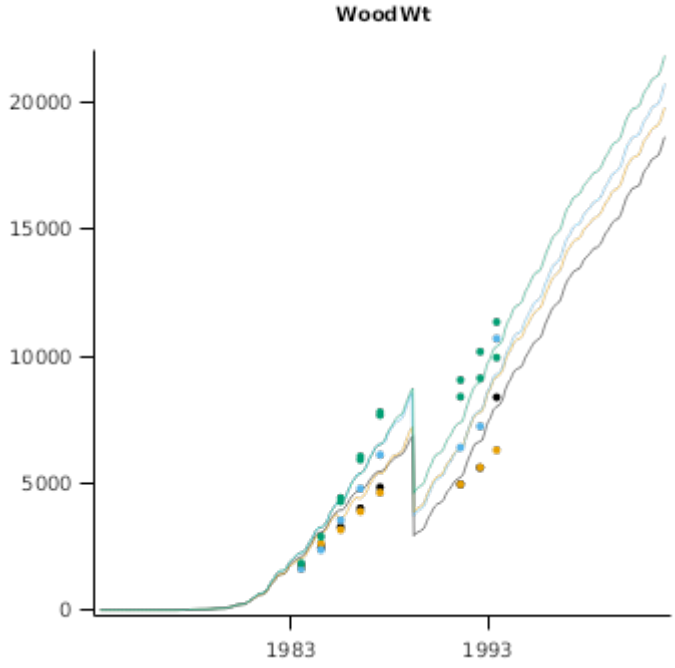


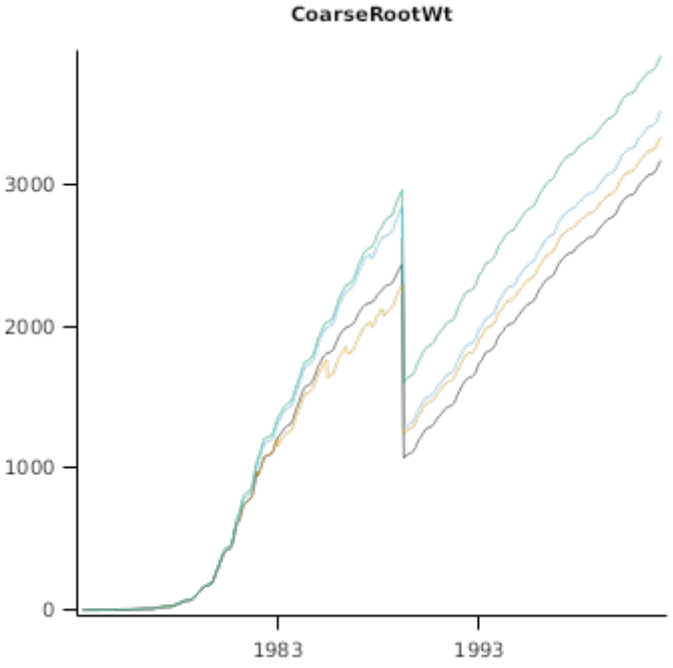

BranchWt
4000
2000
0
1983
1993

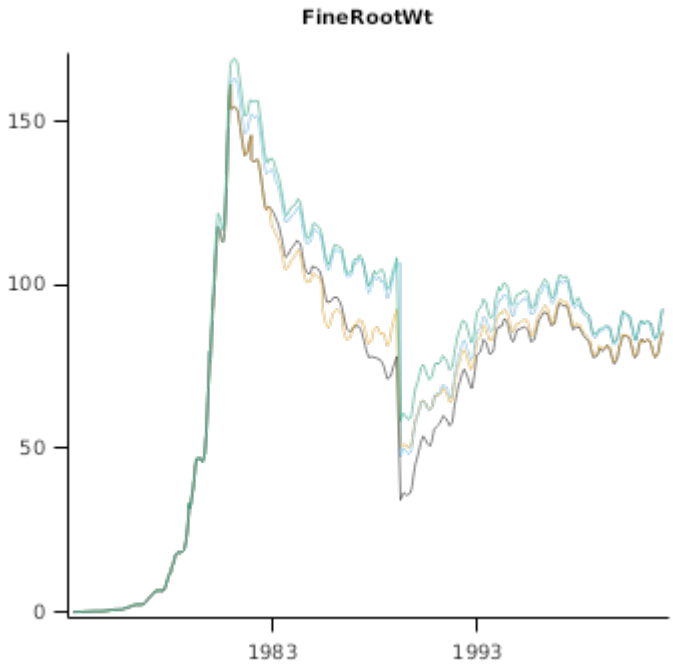

WoodBarkCoarseRootWt
20000
15000
10000
5000
0
1983
1993

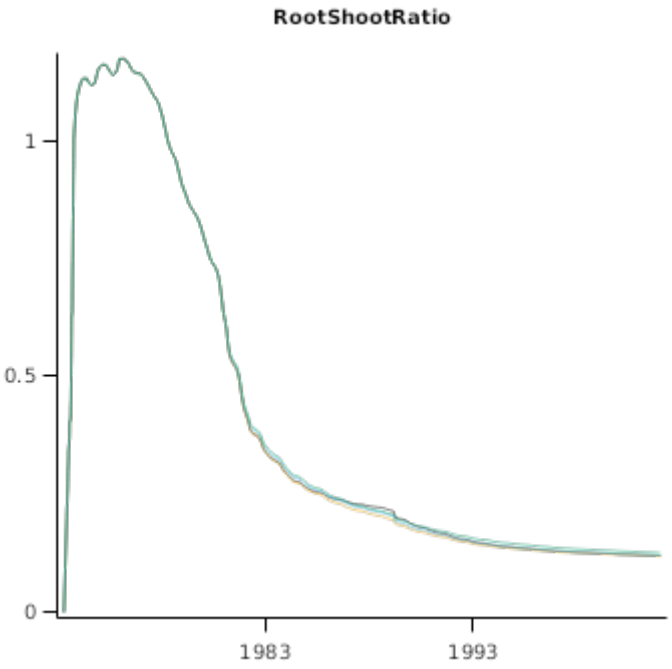

StemWt
20000
10000
0
1983
1993


BarkWt
1500
1000
500
0
1983
1993

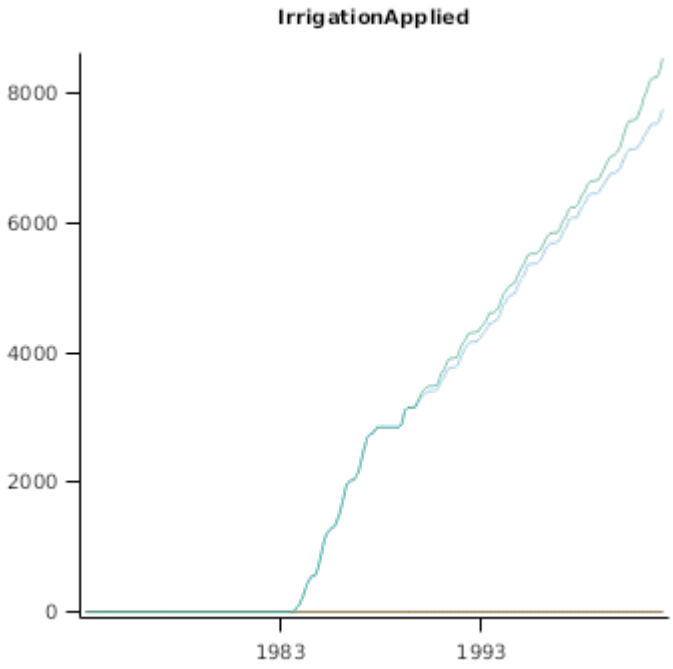

WoodWt
20000
15000
10000
5000
0
1983
1993

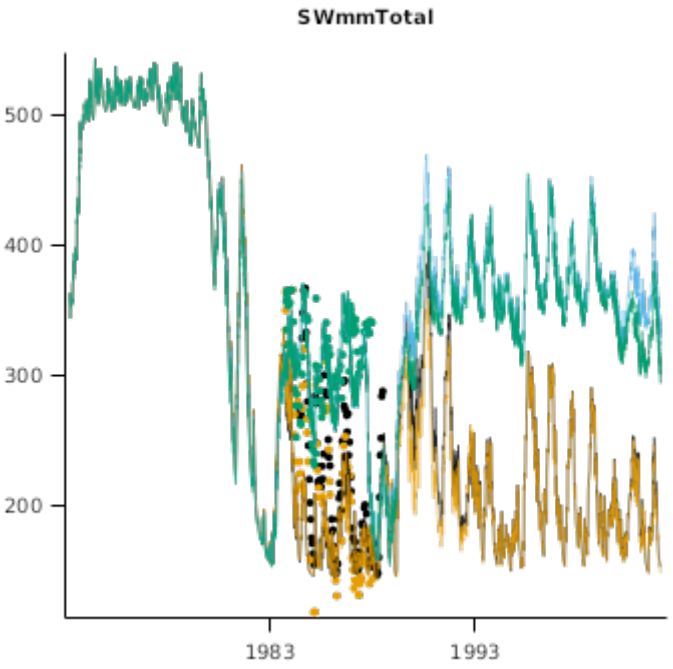

CoarseRootWt
3000
2000
1000
0
1983
1993

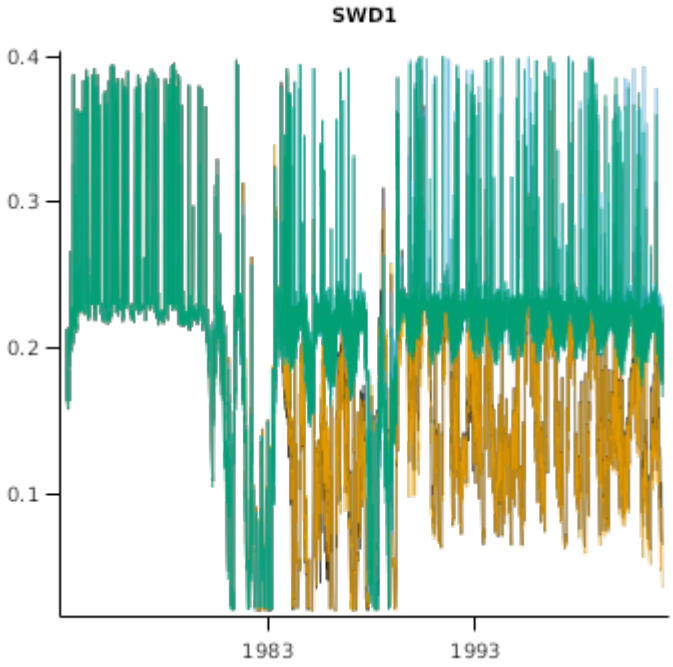




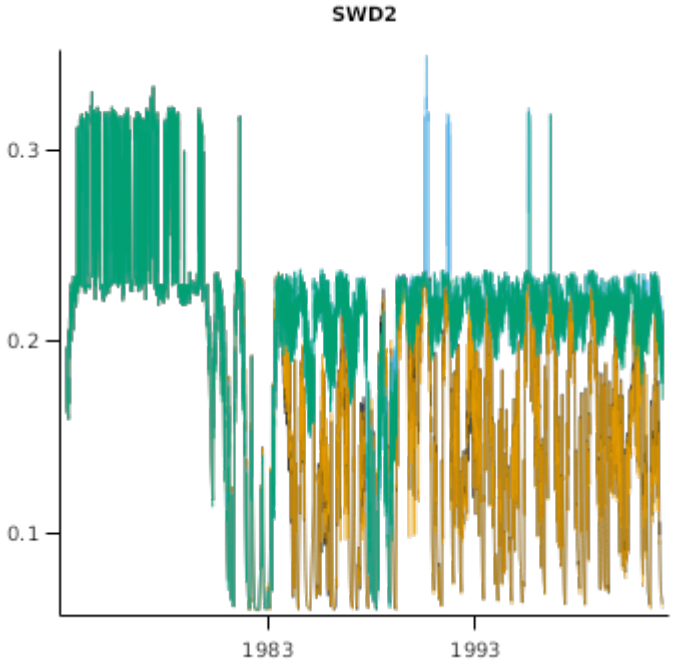
5.2.1.2 GraphsWater

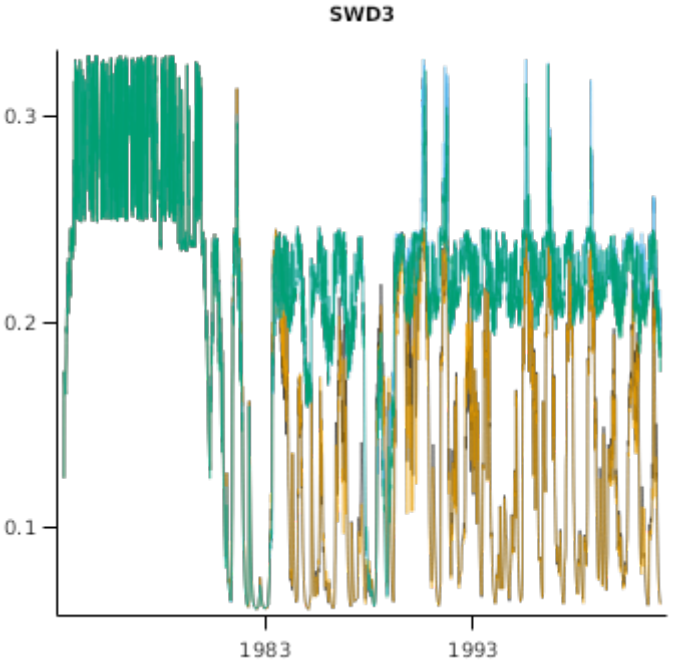

IrrigationApplied
8000
6000
4000
2000
0
1983
1993

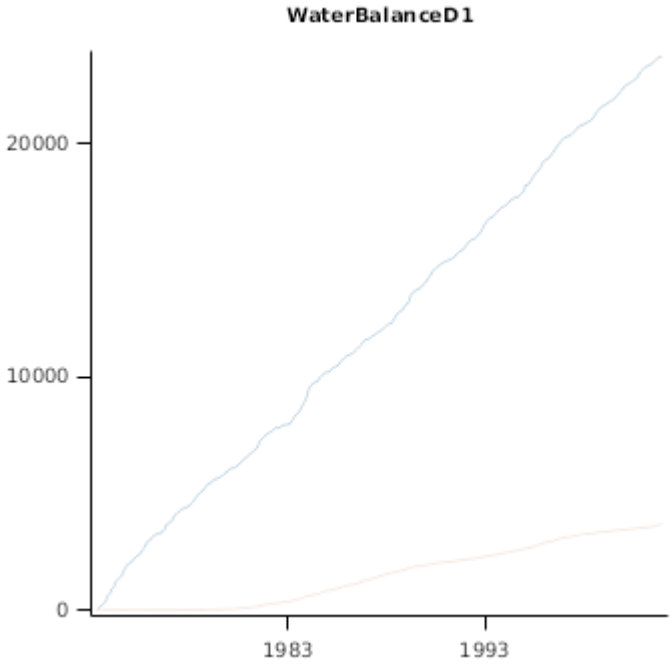

SWmmTotal
500
400
300
200
1983
1993


SWD1
0.4
0.3
0.2
0.1
1983
1993

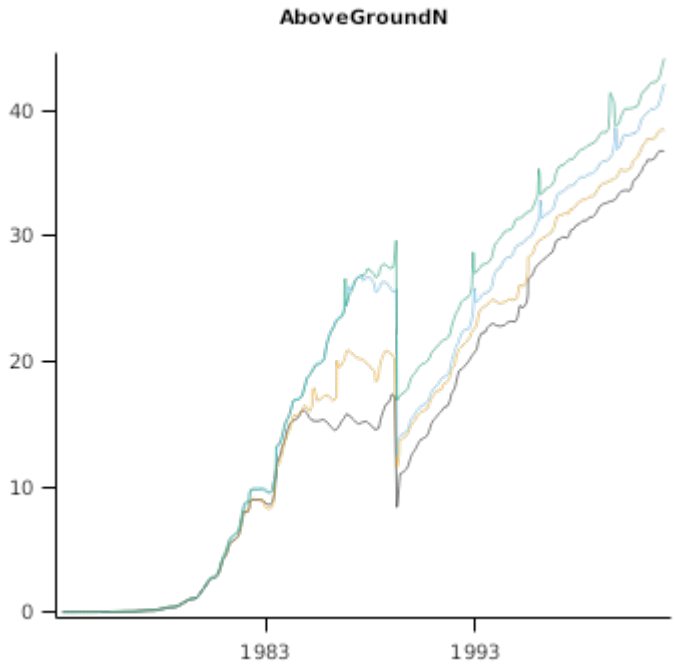
SWmmD1

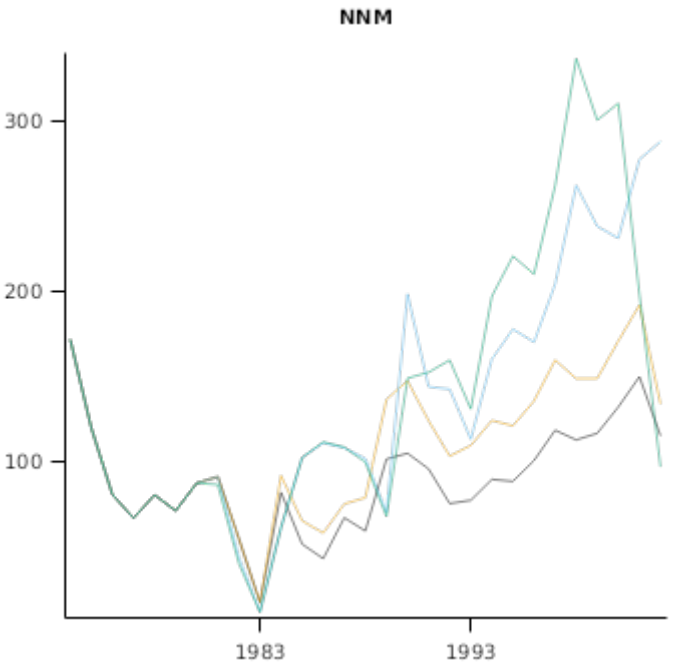

SWD2
0.3
0.2
0.1
1983
1993

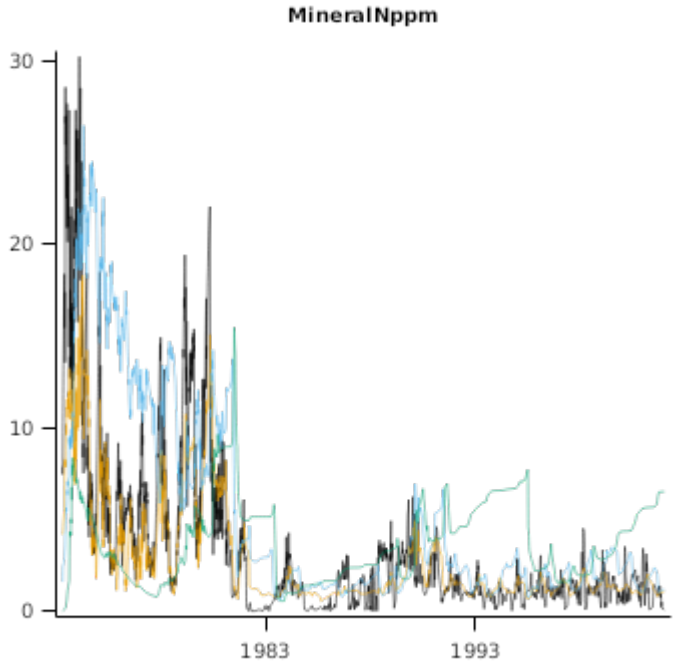

SWD3
0.3
0.2
0.1
1983
1993

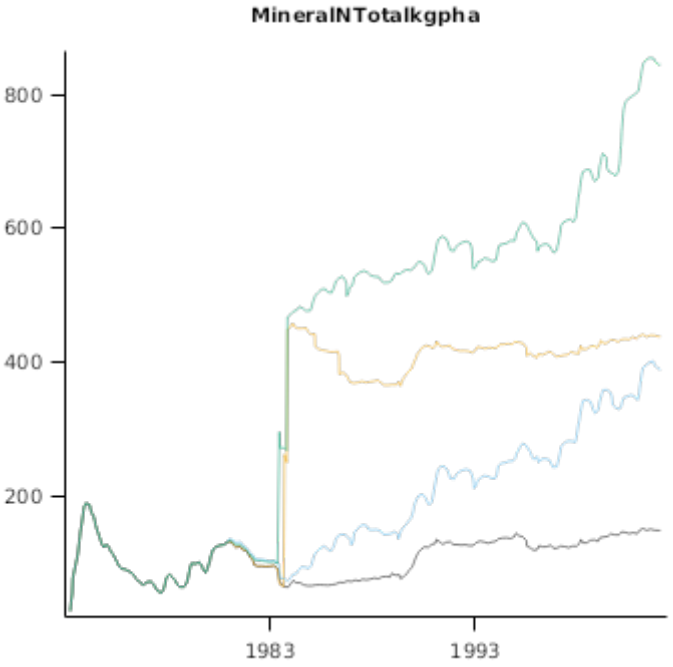


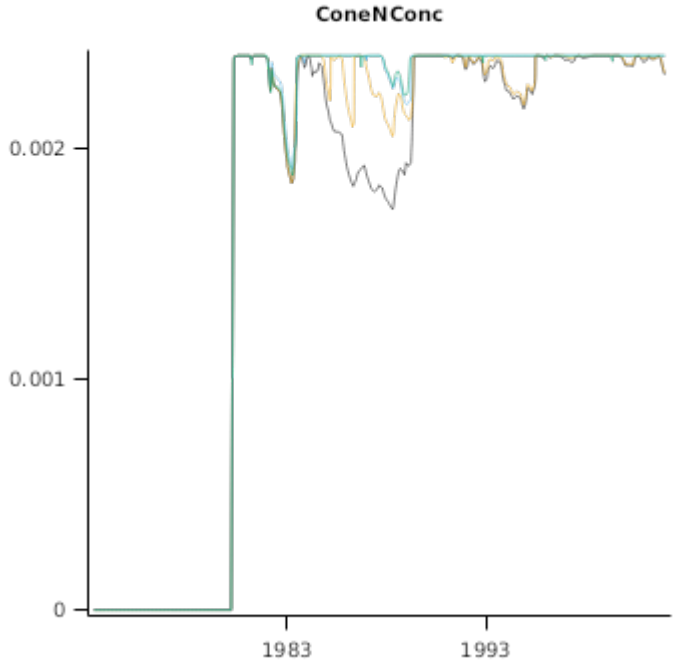
5.2.1.3 GraphsN

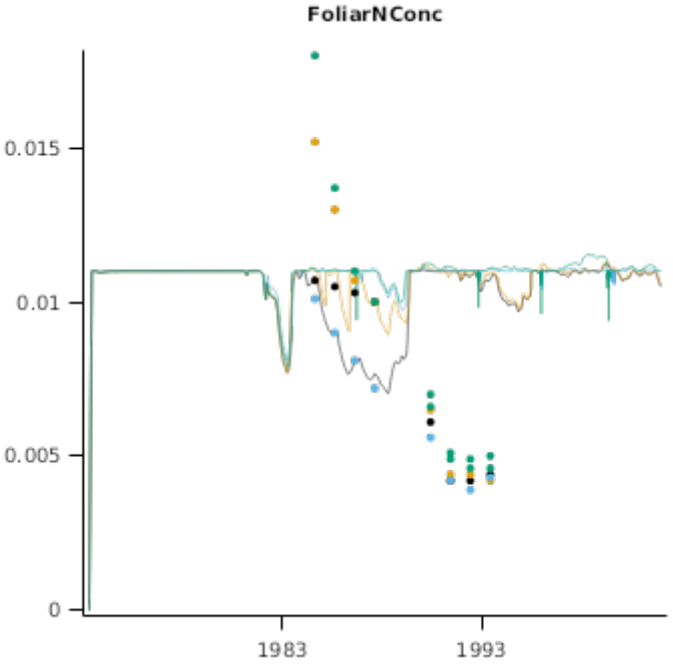

AboveGroundN
40
30
20
10
0
1983
1993

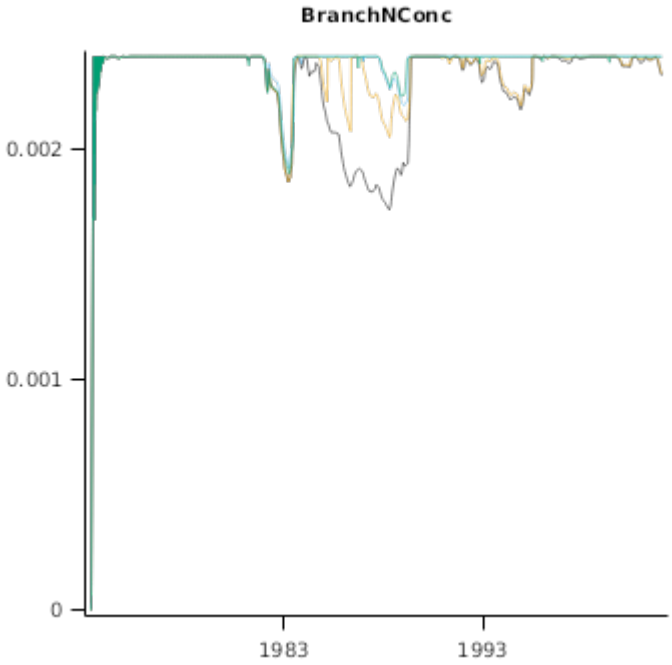

NNM
300
200
100
1983
1993

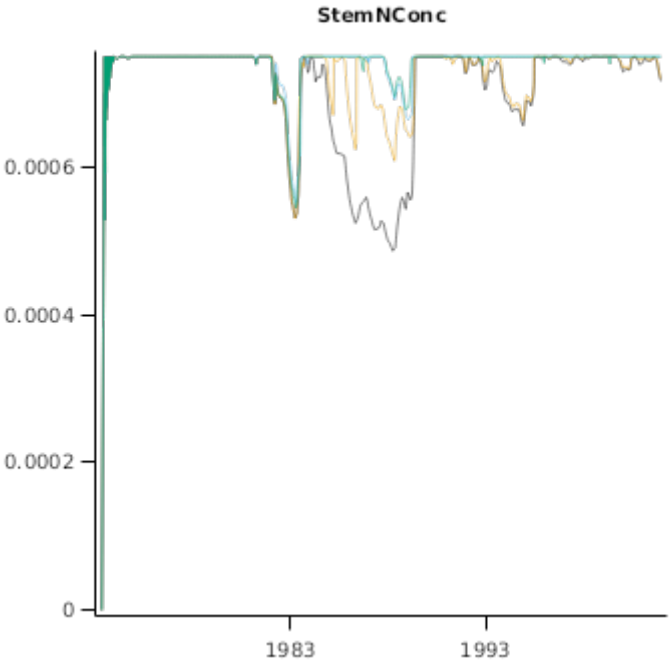

MineralNppm
30
20
10
0
1983
1993

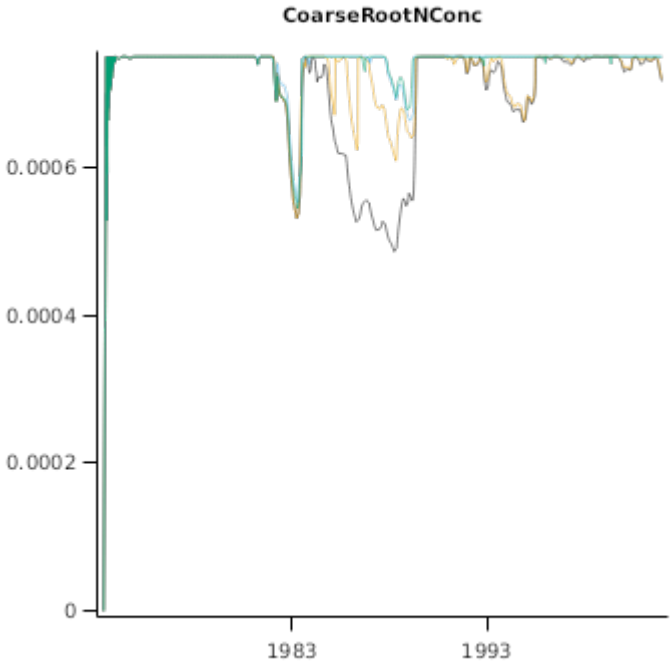

MineralNTotalkgpha
800
600
400
200
1983
1993

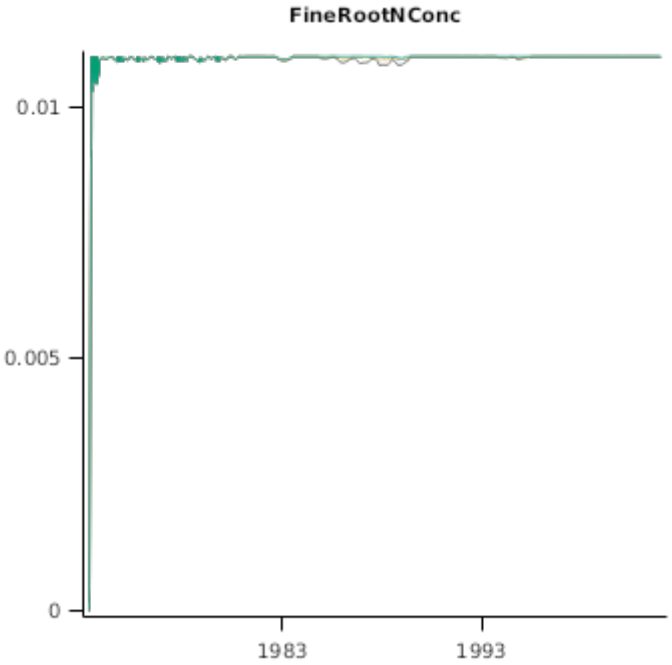

ConeNConc
0.002
0.001
0
1983
1993


FoliarNConc
0.015
0.01
0.005
0
1983
1993

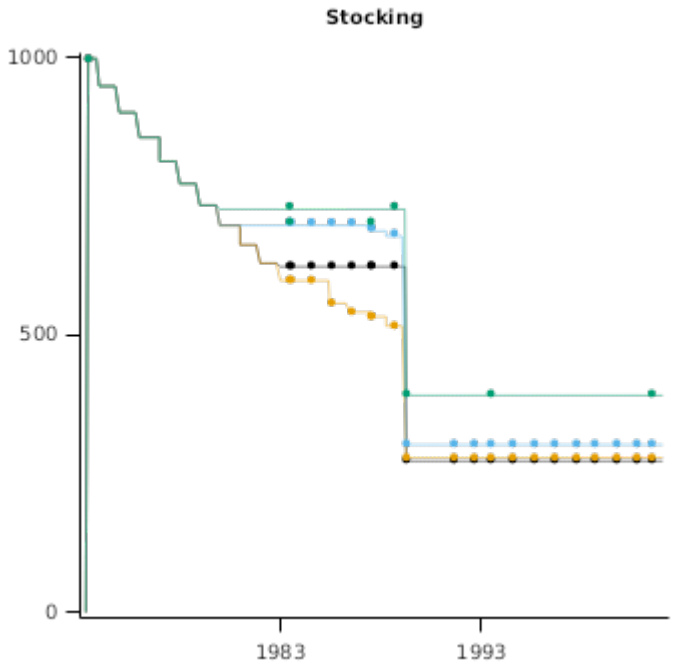


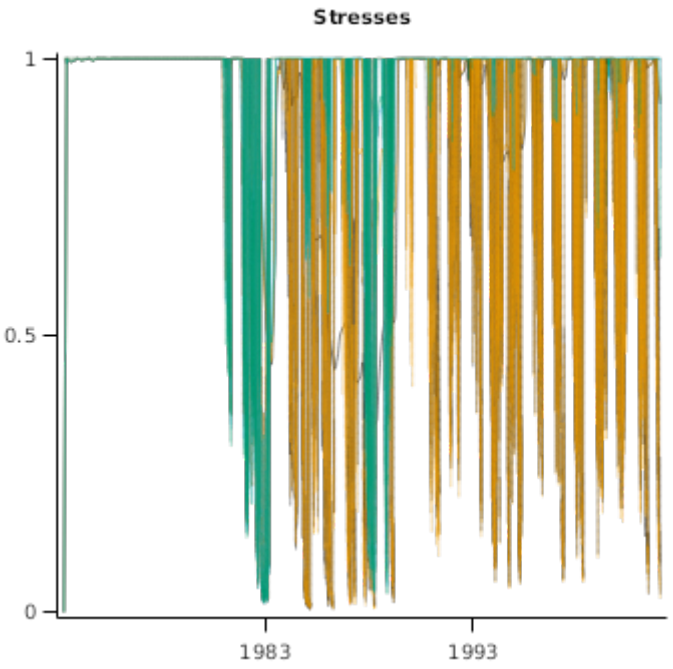


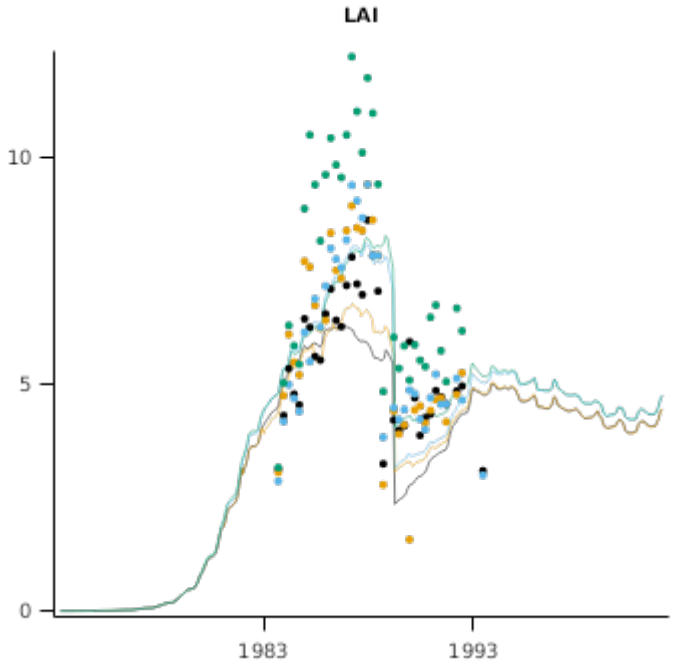


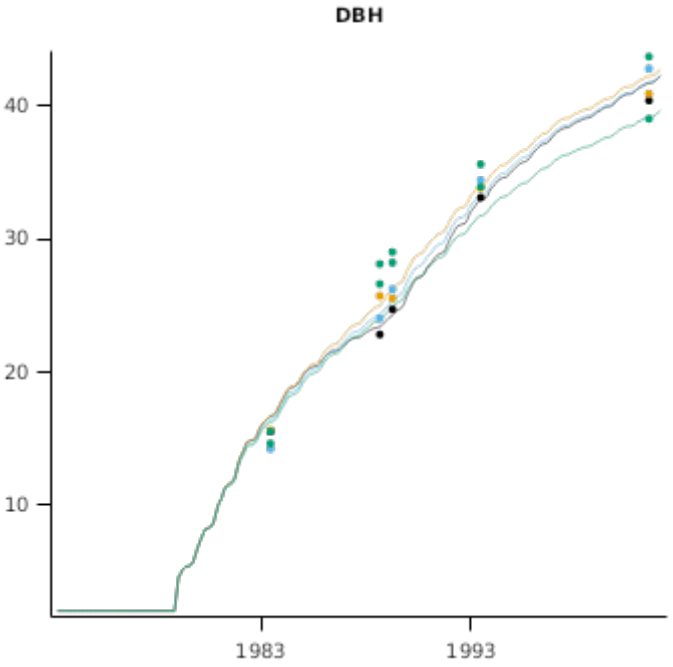


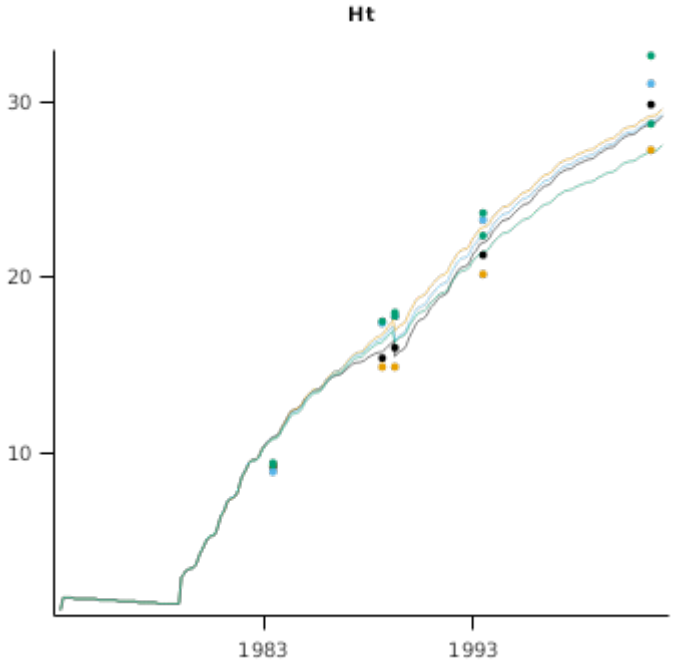
5.2.1.4 GraphsMetrics

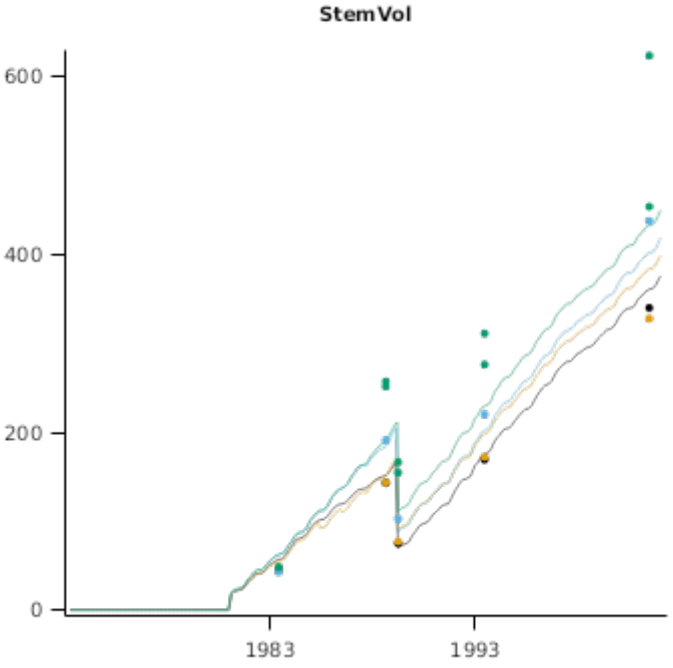

Stocking
1000
500
0
1983
1993

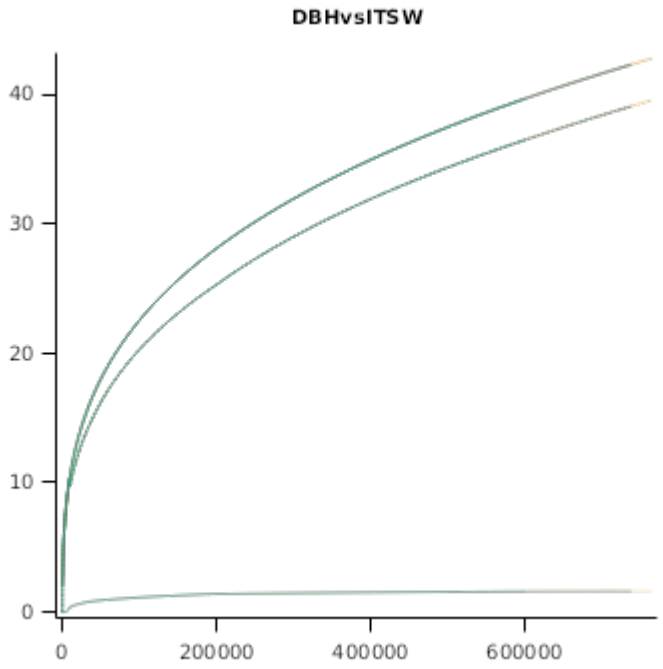

Stresses
1
0.5
0
1983
1993

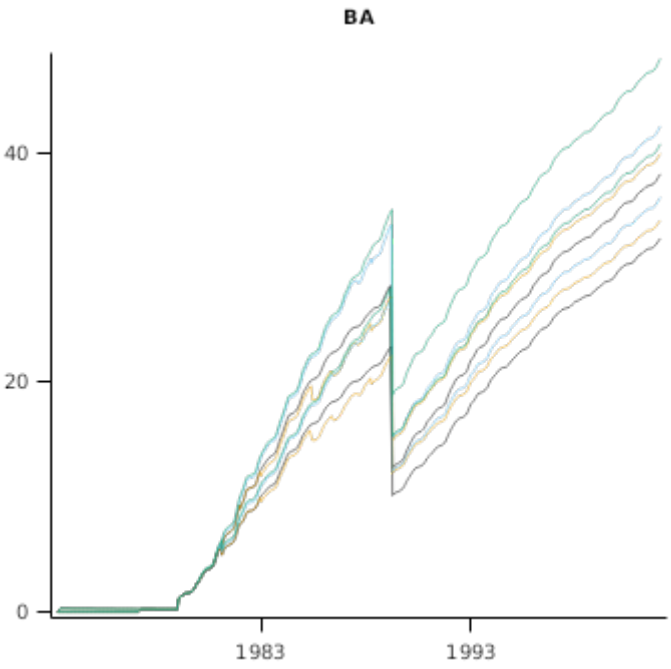

LAI
10
5
0
1983
1993

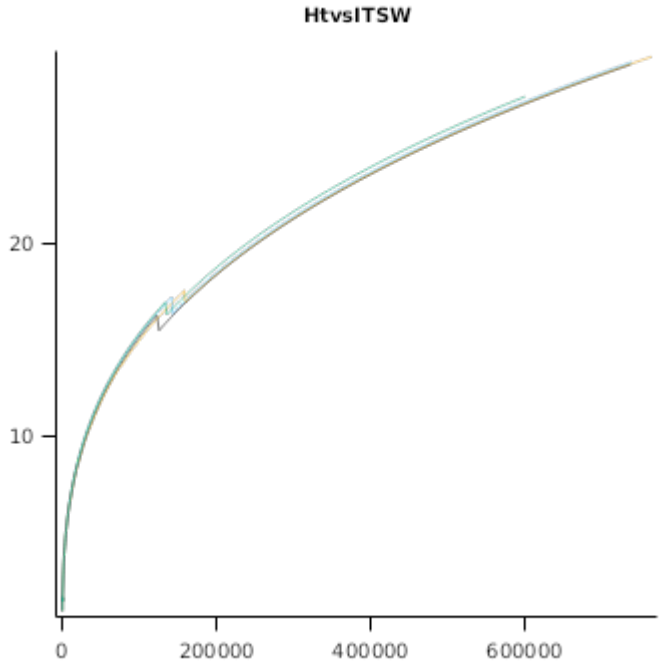

DBH
40
30
20
10
1983
1993

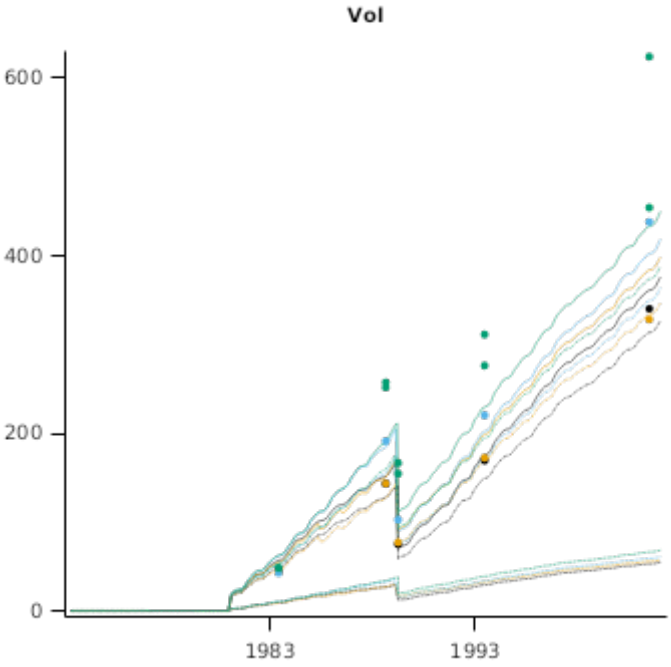

Ht
30
20
10
1983
1993

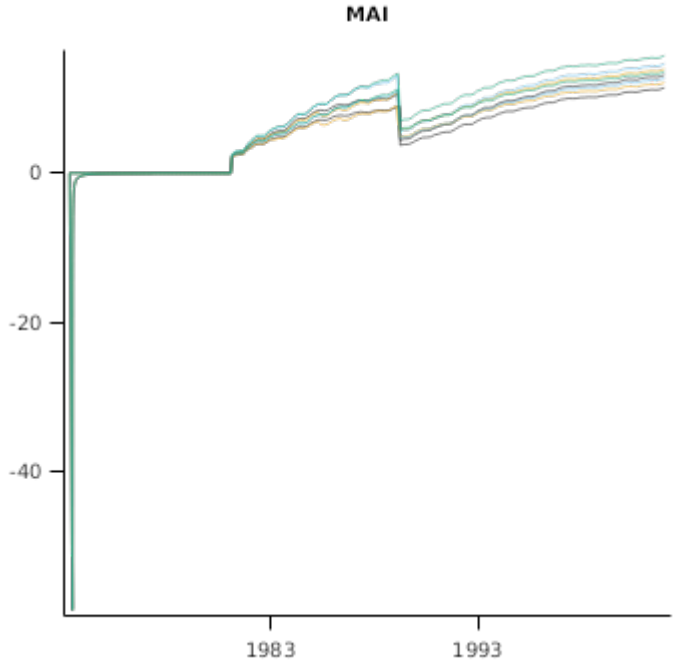

StemVol
600
400
200
0
1983
1993

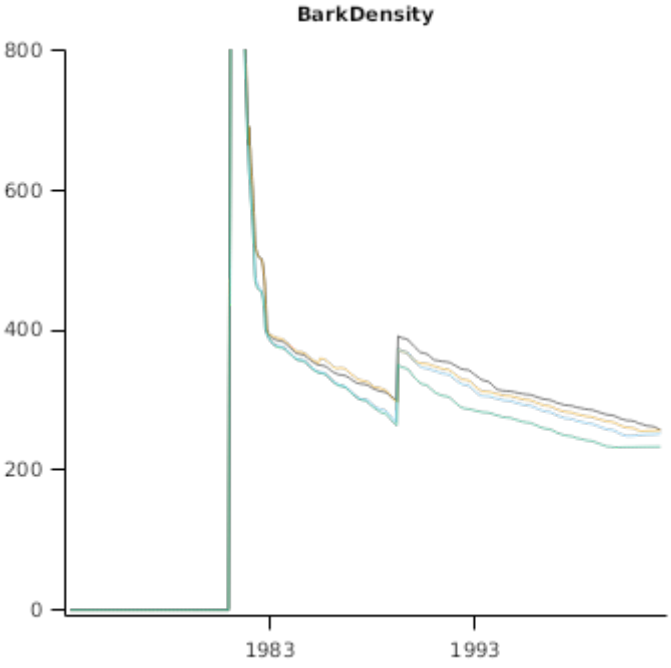

DBHvsITSW
40
30
20
10
0
0
200000
400000
600000

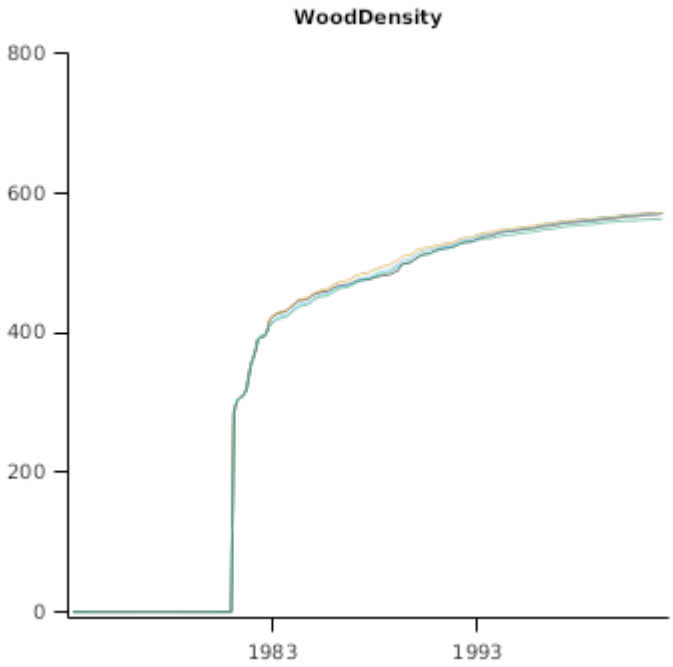

BA
40
20
0
1983
1993

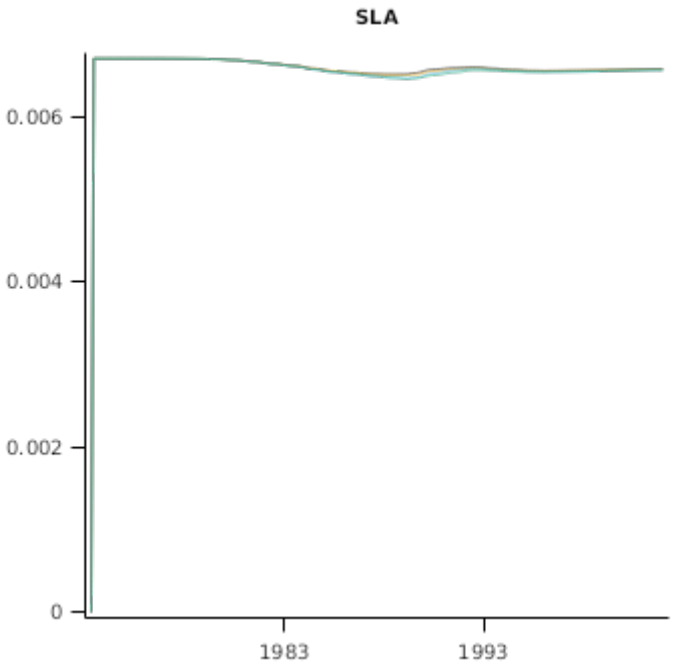

HtvsITSW
20
10
0
200000
400000
600000


Vol
600
400
200
0
1983
1993


MAI
0
-20
-40
1983
1993


BarkDensity
800
600
400
200
0
1983
1993



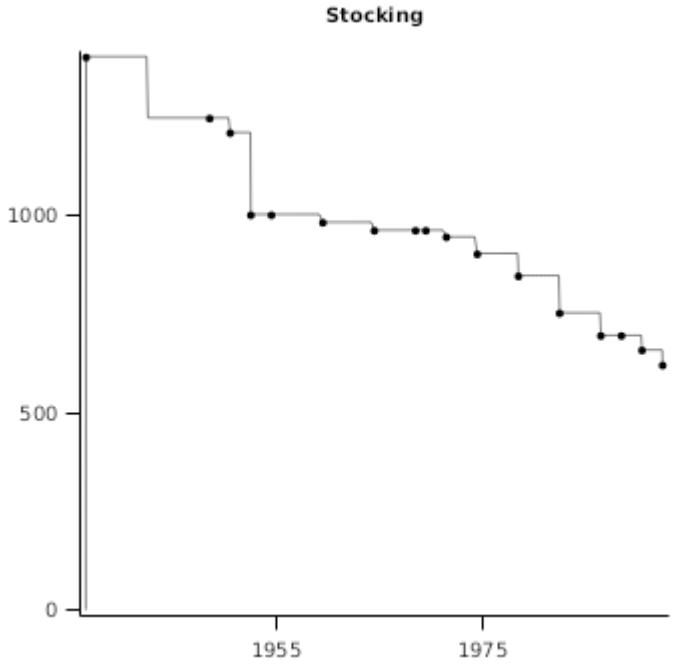


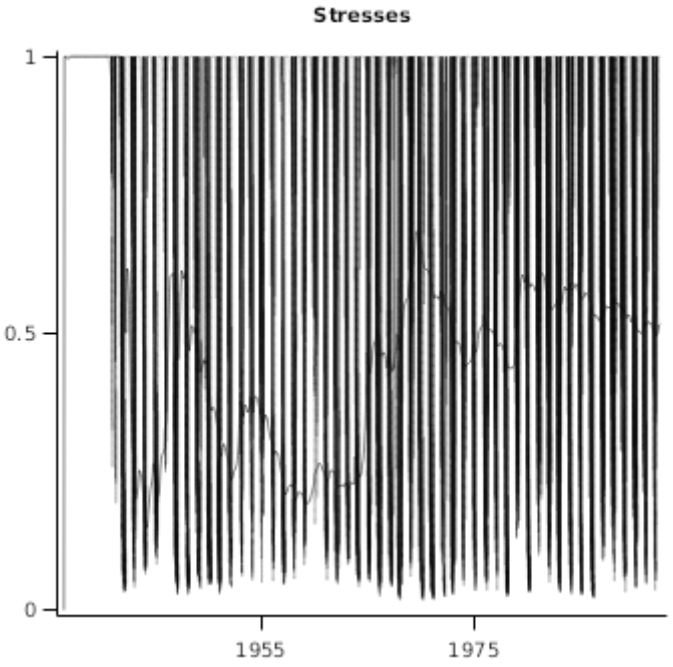
5.2.2 FSA703A

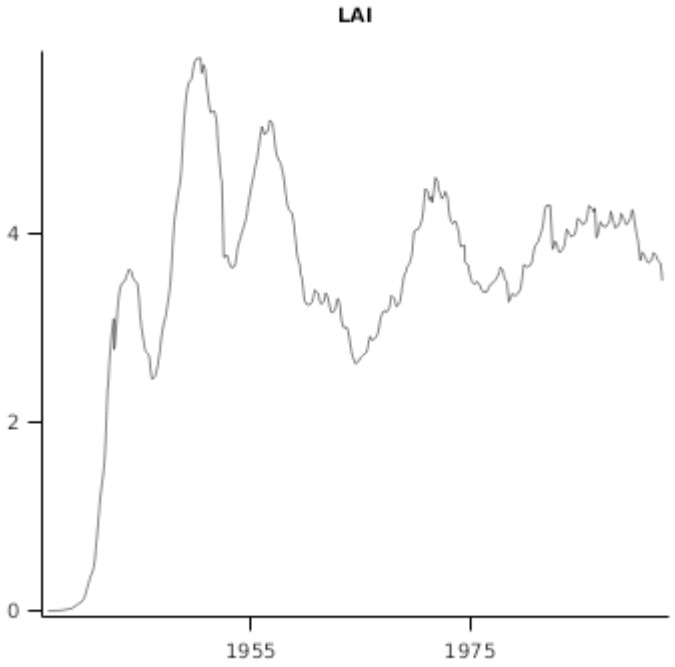
These data are a plot in operational plantations that were previously managed by Forestry South Australia (FSA). We appreciate the provision of data by Jim O'Hehir. This plot reached an old age relative to many other *P. radiata* plantations in the world.

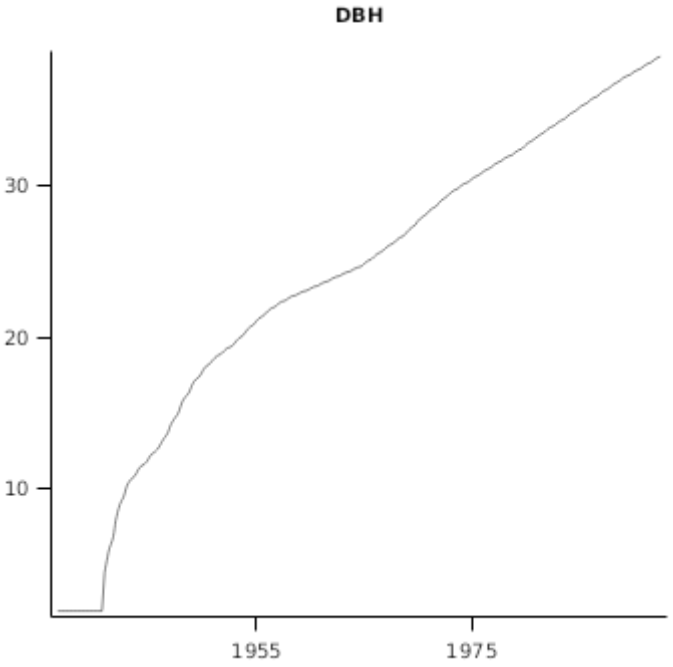
5.2.2.1 Graphs

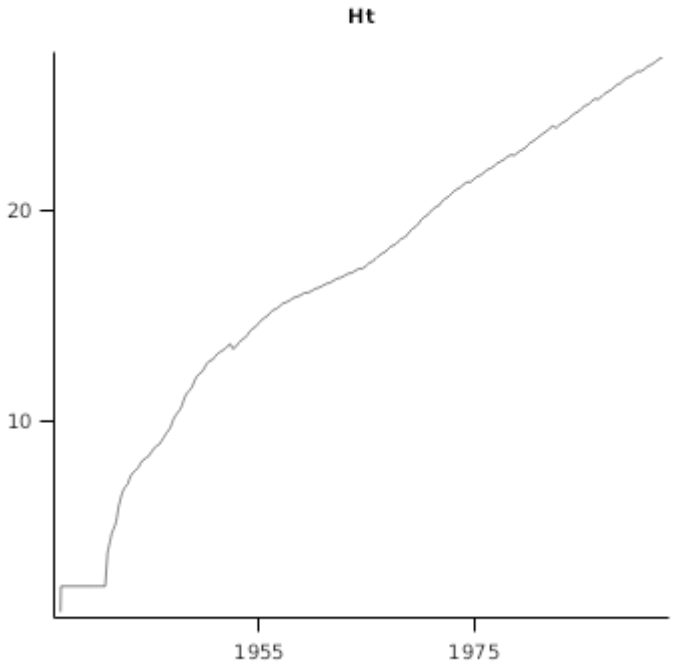
5.2.2.1.1 GraphsMetrics

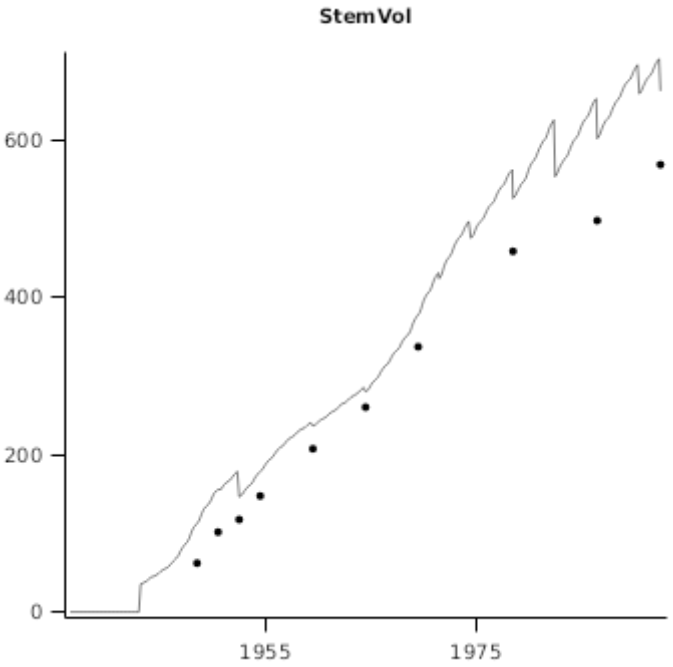

Stocking
1000
500
0
1955
1975

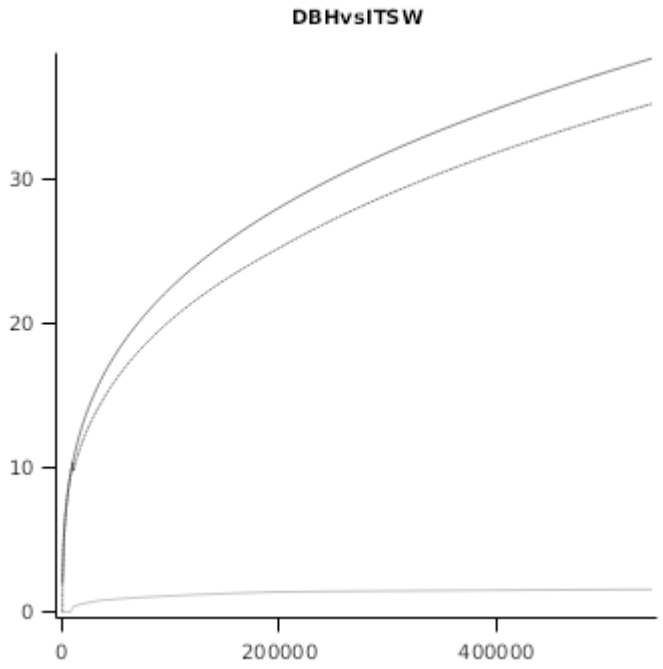

Stresses
1
0.5
0
1955
1975

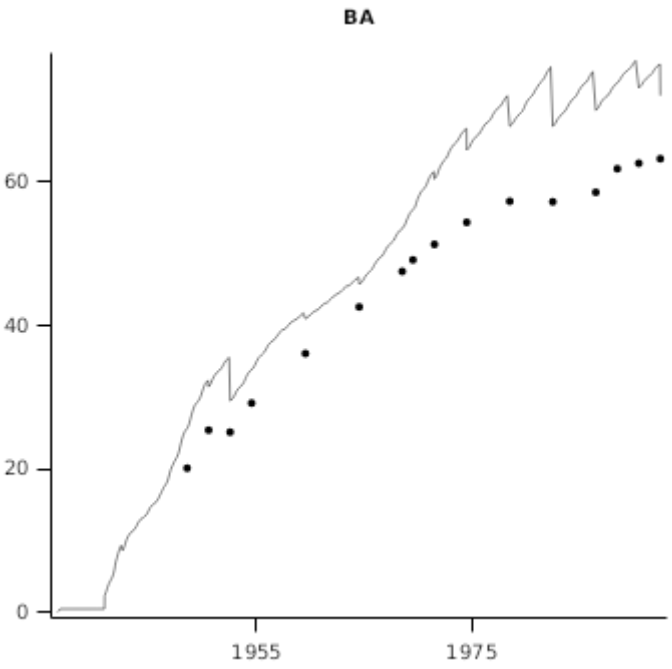

LAI
4
2
0
1955
1975

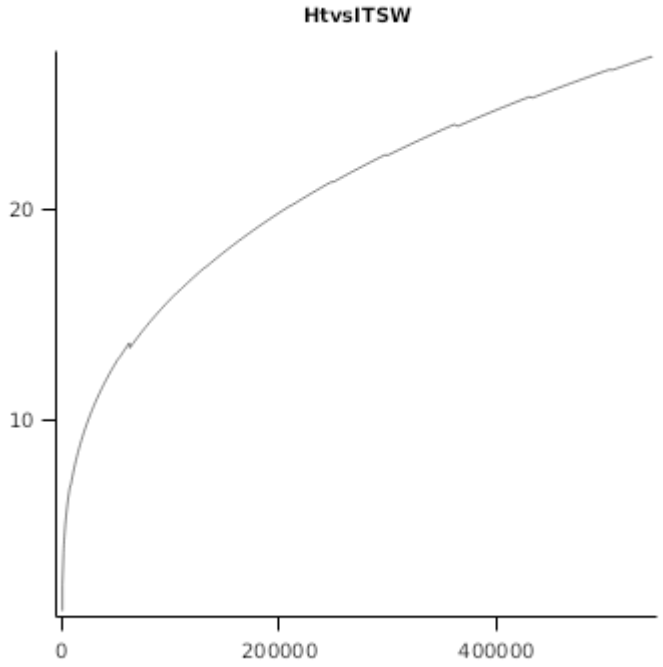

DBH
30
20
10
1955
1975

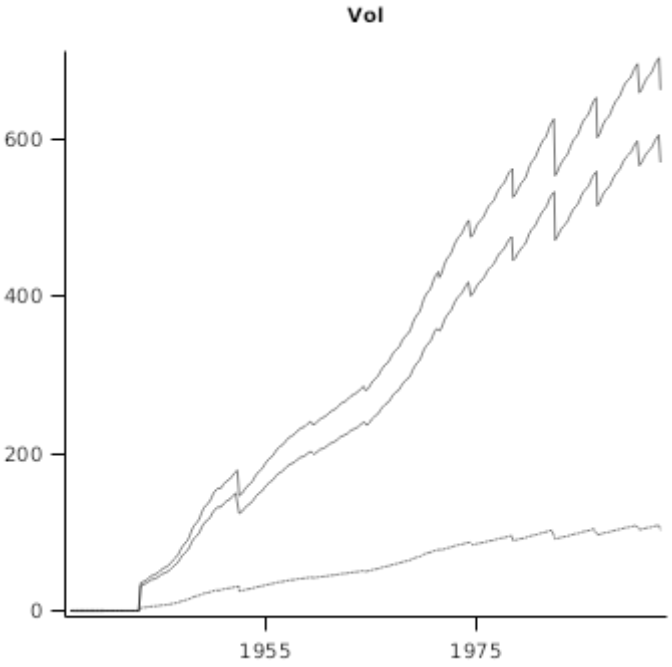

Ht
20
10
1955
1975

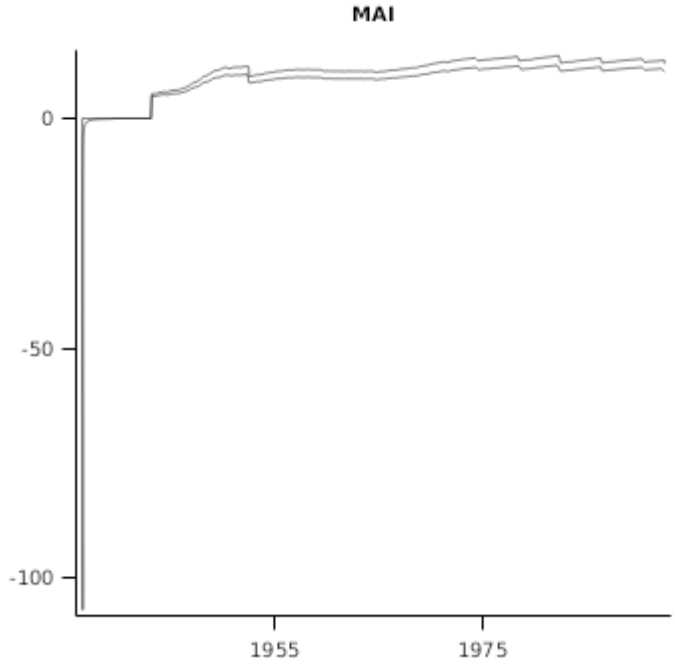

StemVol
600
400
200
0
1955
1975

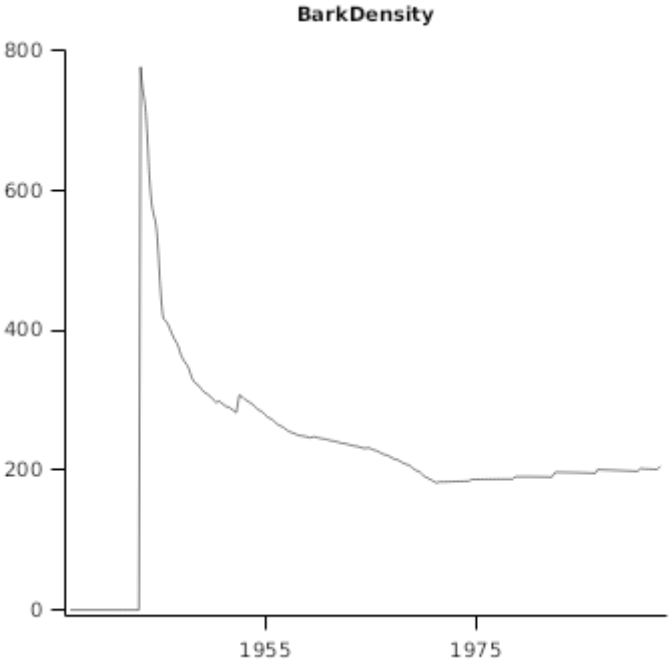

DBHvsITSW
30
20
10
0
0
200000
400000


BA
60
40
20
0
1955
1975


HtvsITSW
20
10
0
200000
400000


Vol
600
400
200
0
1955
1975


MAI
0
-50
-100
1955
1975

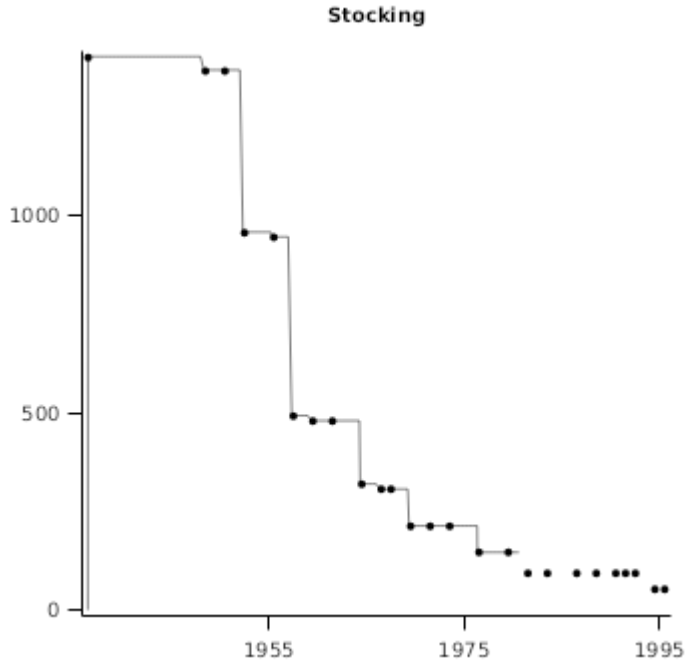

BarkDensity
800
600
400
200
0
1955
1975

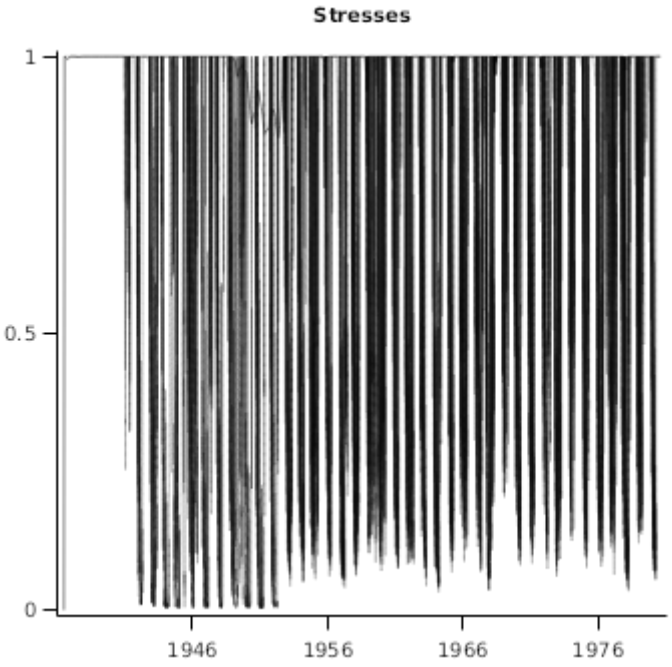
5.2.3 FSA704

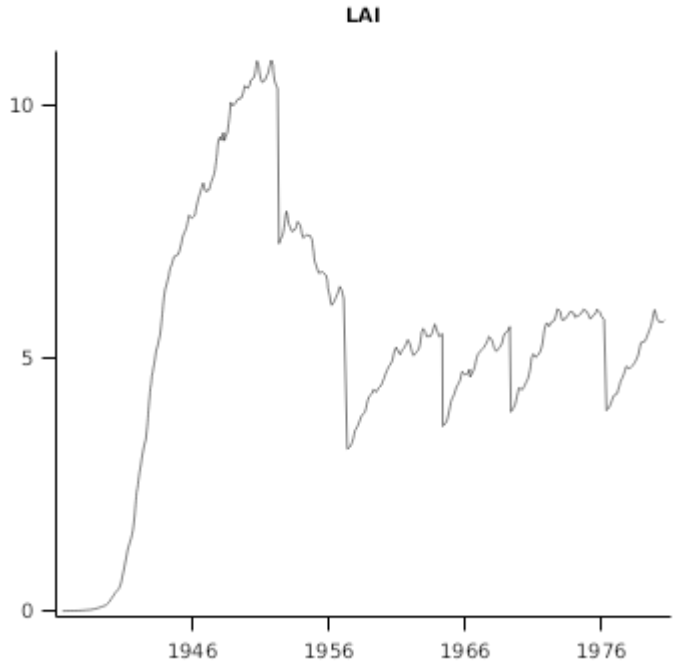
These data are a plot in operational plantations that were previously managed by Forestry South Australia (FSA). We appreciate the provision of data by Jim O'Hehir. This plot reached an old age relative to many other *P. radiata* plantations in the world.

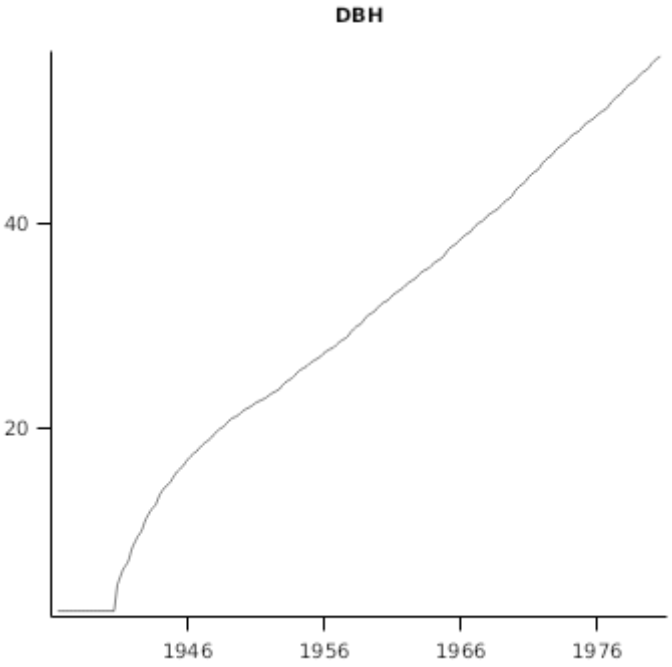
5.2.3.1 Graphs

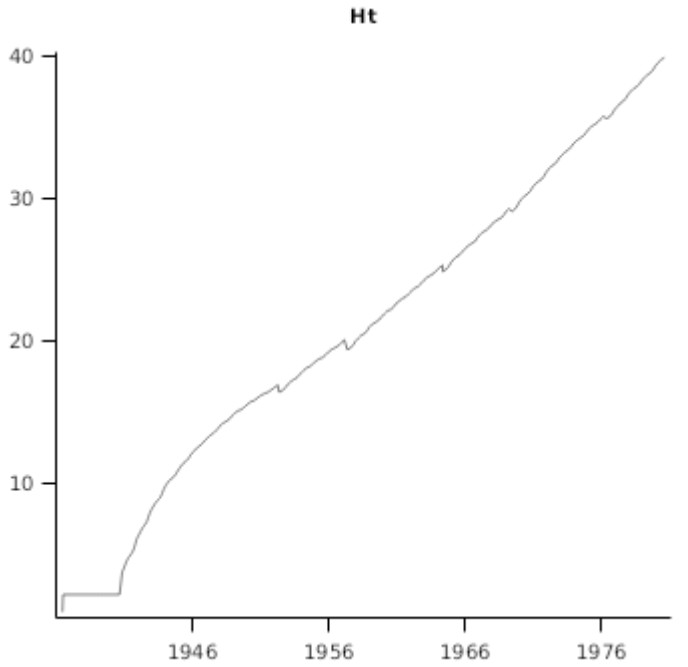
5.2.3.1.1 GraphsMetrics

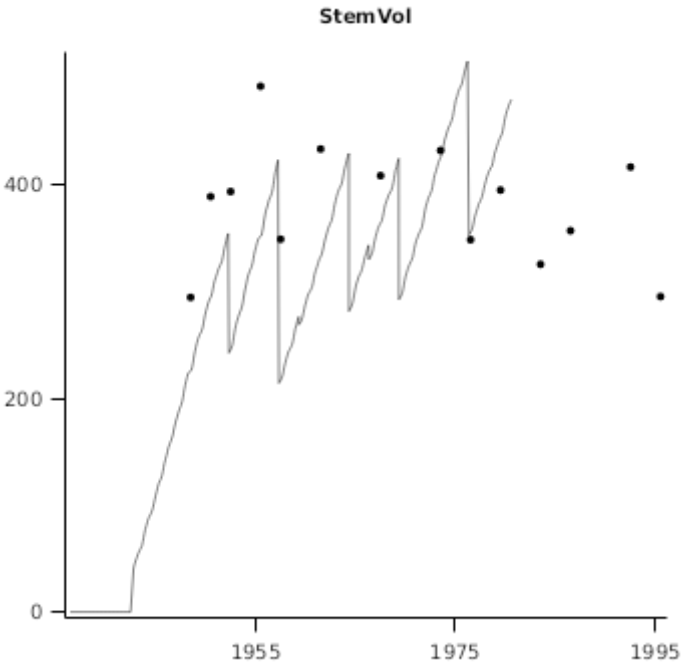

Stocking
1000
500
0
1955
1975
1995

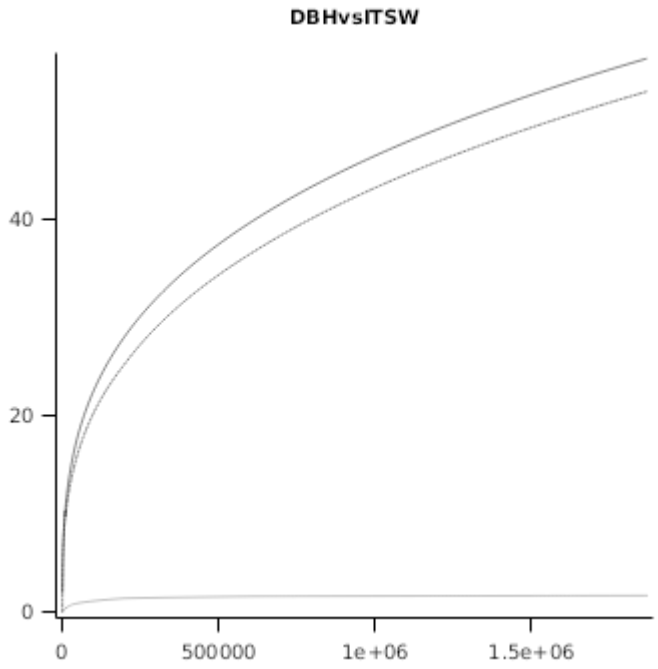

Stresses
1
0.5
0
1946
1956
1966
1976

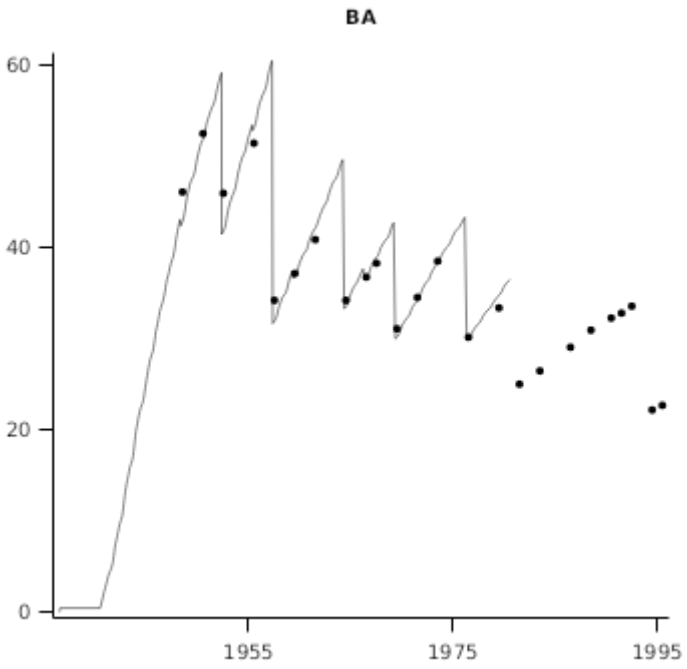

LAI
10
5
0
1946
1956
1966
1976

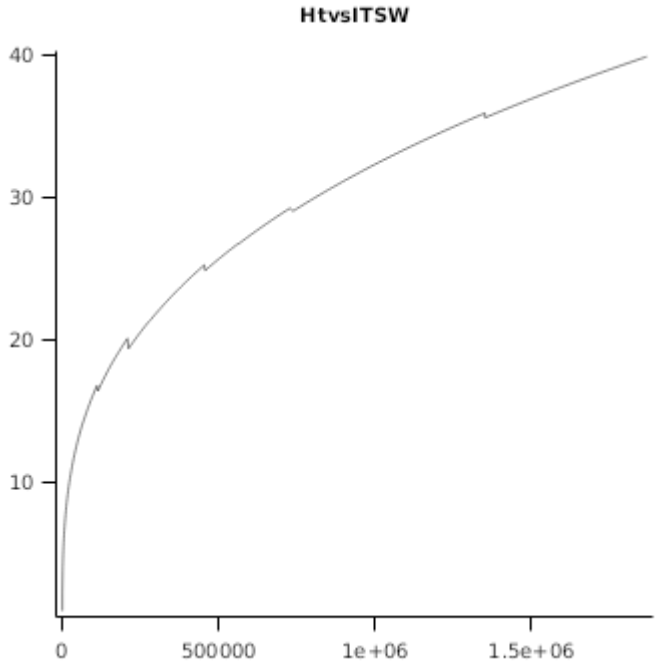

DBH
40
20
1946
1956
1966
1976

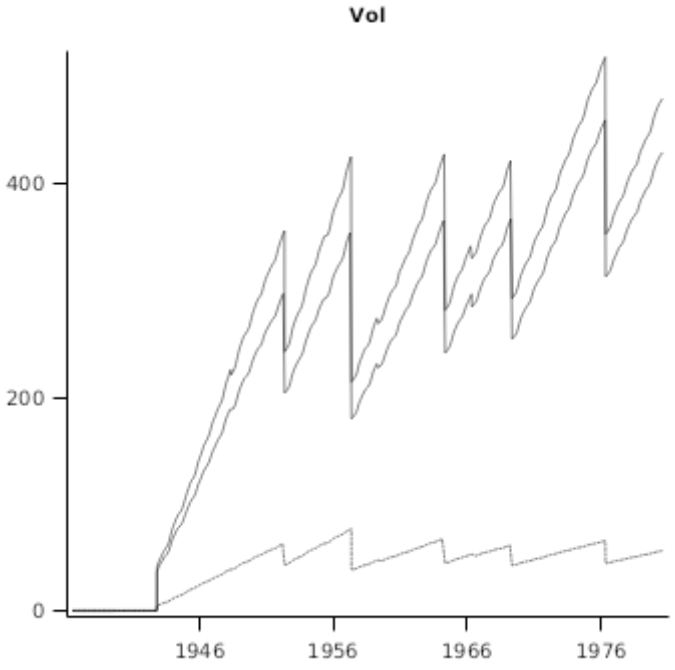

Ht
40
30
20
10
1946
1956
1966
1976

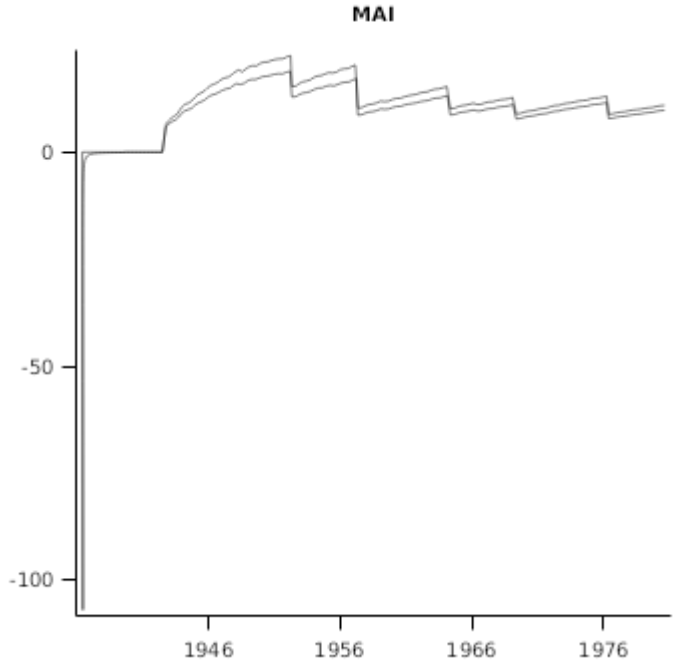

StemVol
400
200
0
1955
1975
1995


DBHvsITSW
40
20
0
0
500000
1e+06
1.5e+06


BA
60
40
20
0
1955
1975
1995


HtvsITSW
40
30
20
10
0
500000
1e+06
1.5e+06


Vol
400
200
0
1946
1956
1966
1976


MAI
0
-50
-100
1946
1956
1966
1976

BarkDensity
800
600
400
200
0
1946
1956
1966
1976

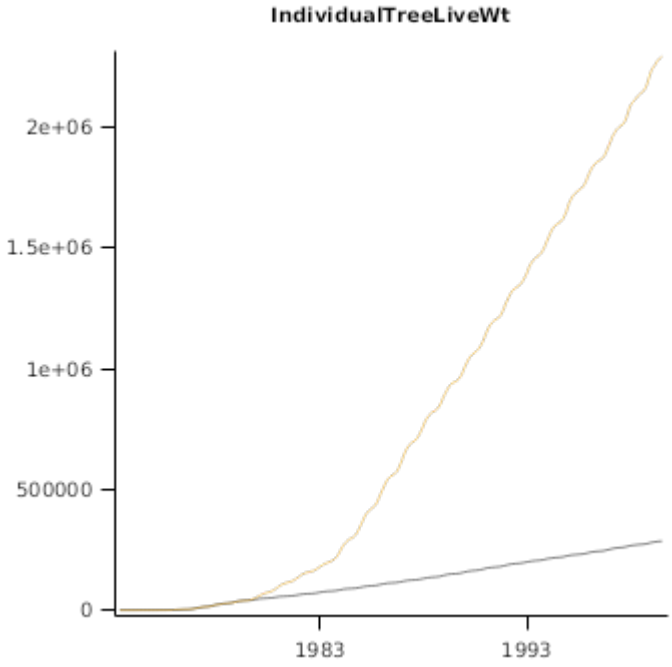
5.2.4 Puruki

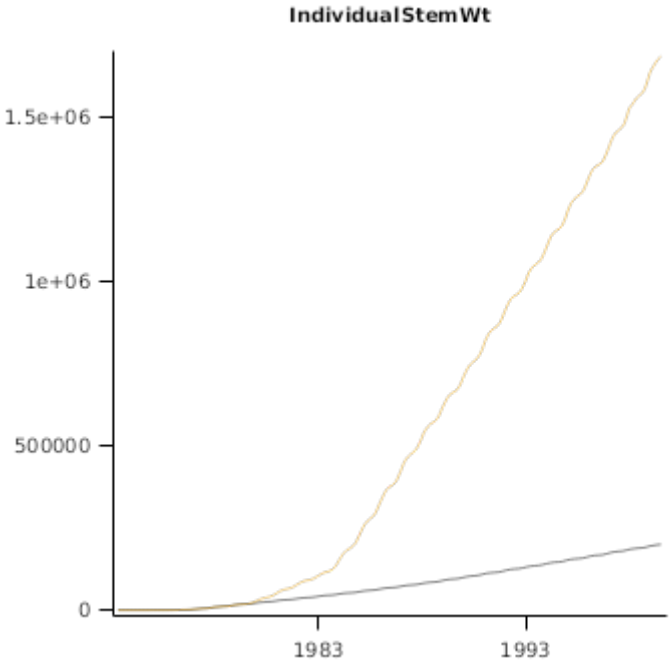
These data are from one plot at a highly productive site in New Zealand. Studies at the site included physiology and growth, nutrition, soils and hydrology, which were published. This site was of particular interest for this validation because it had high nutrient availability and high rainfall, and it was well-published. Publications drawn on were Rijkse et al., 1974, Beets et al., 1987, Beets et al., 1987, Beets et al., 1987, 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.

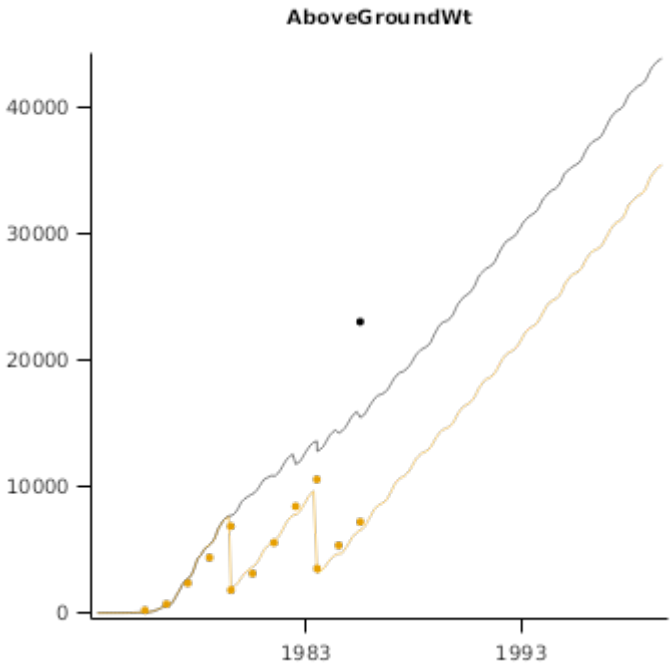
List of experiments.

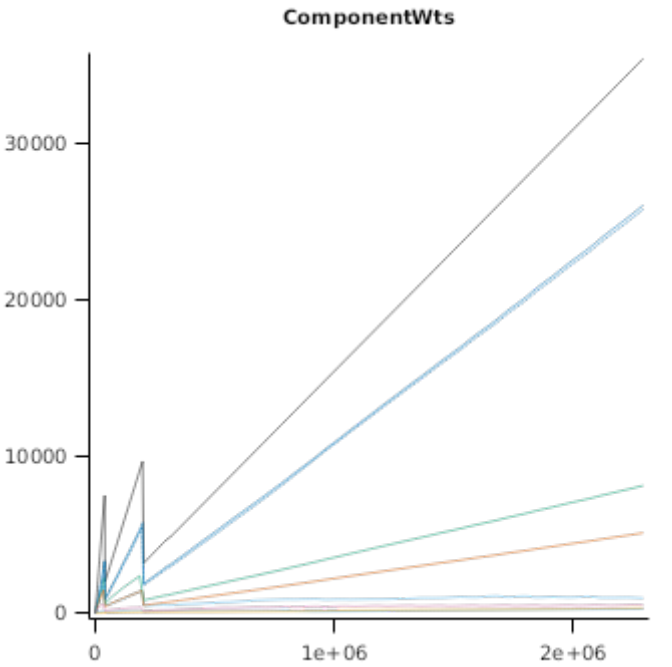
Experiment Name	Design (Number of Treatments)
Puruk	i (2)

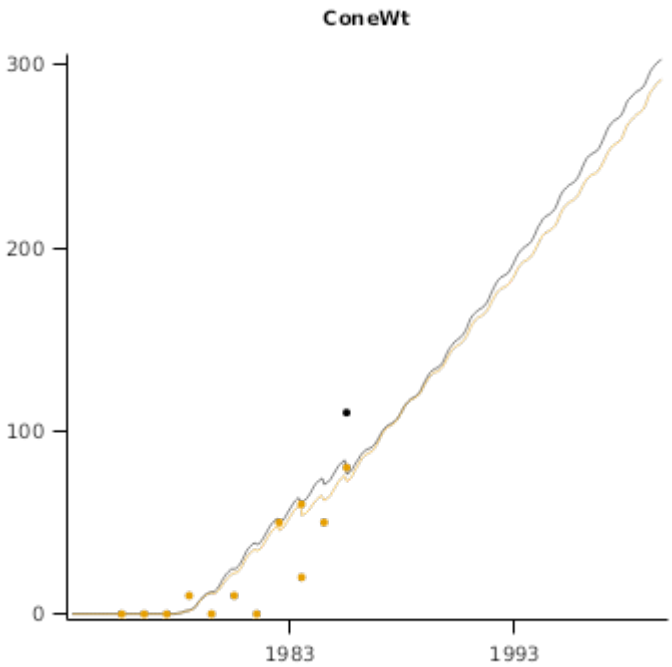
5.2.4.1 GraphsWeights

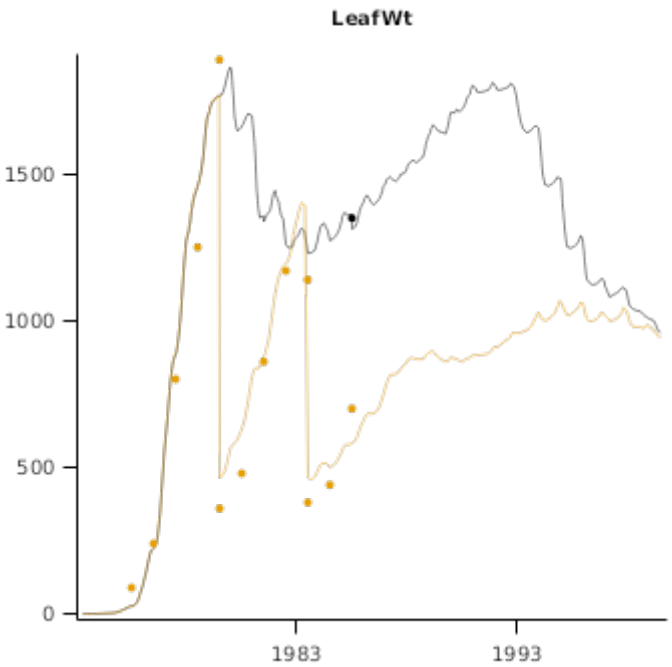

IndividualTreeLiveWt
2e+06
1.5e+06
1e+06
500000
0
1983
1993

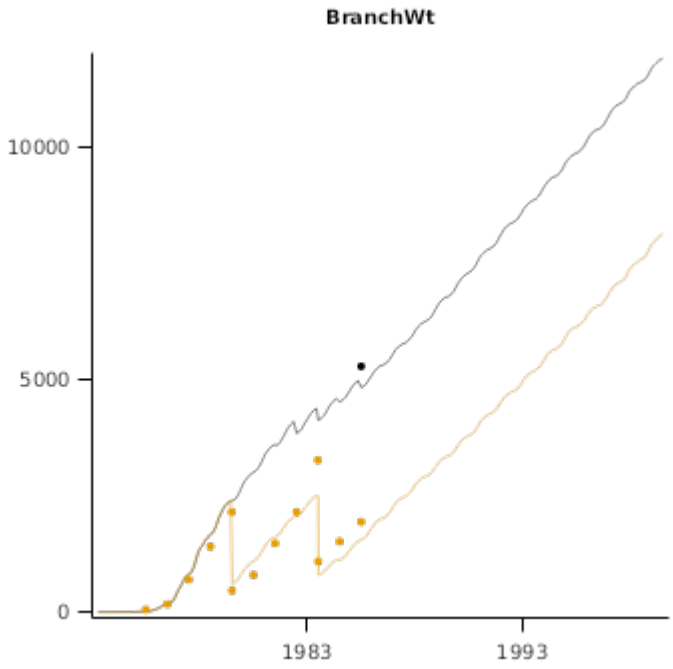

IndividualStemWt
1.5e+06
1e+06
500000
0
1983
1993

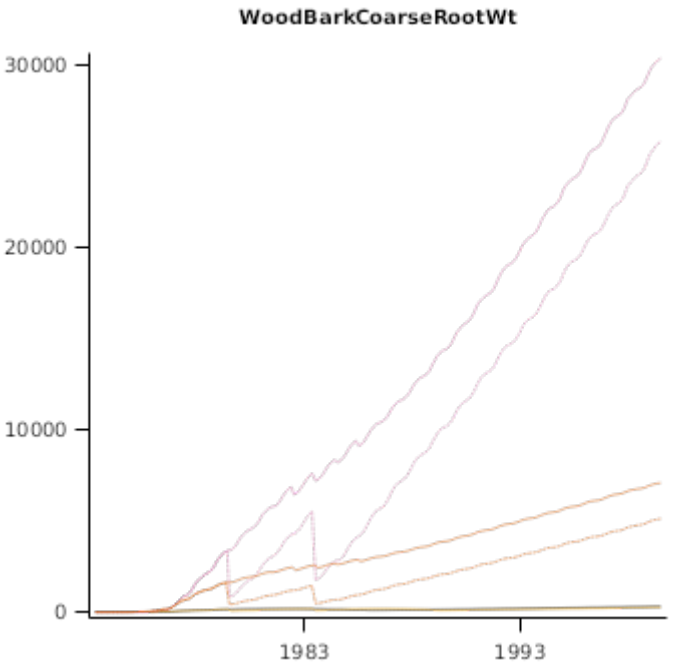

AboveGroundWt
40000
30000
20000
10000
0
1983
1993

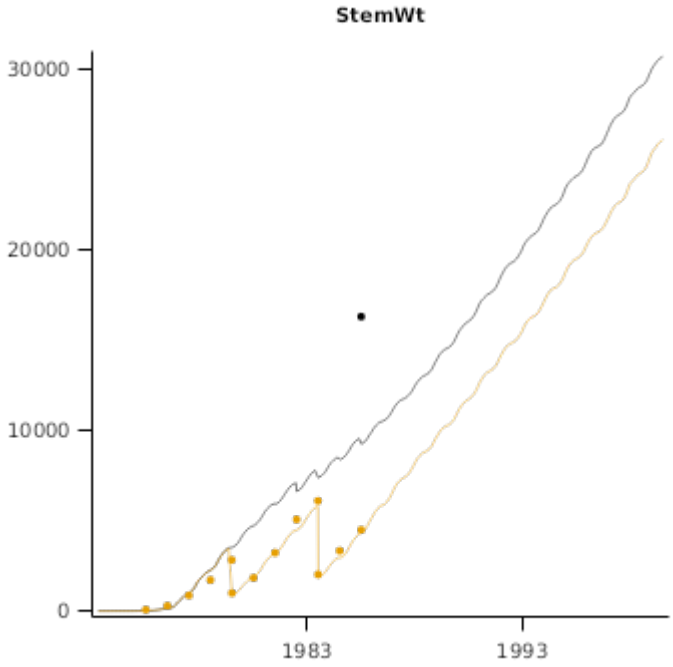

ComponentWts
30000
20000
10000
0
0
1e+06
2e+06

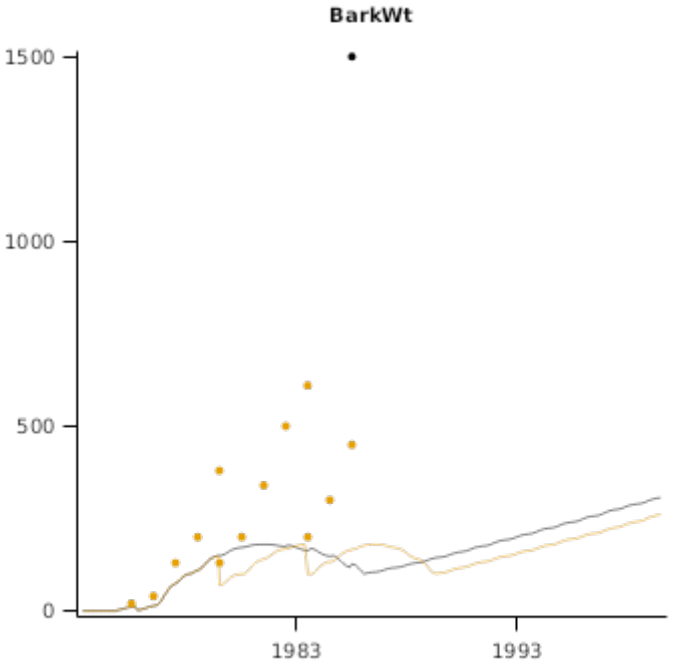

ConeWt
300
200
100
0
1983
1993

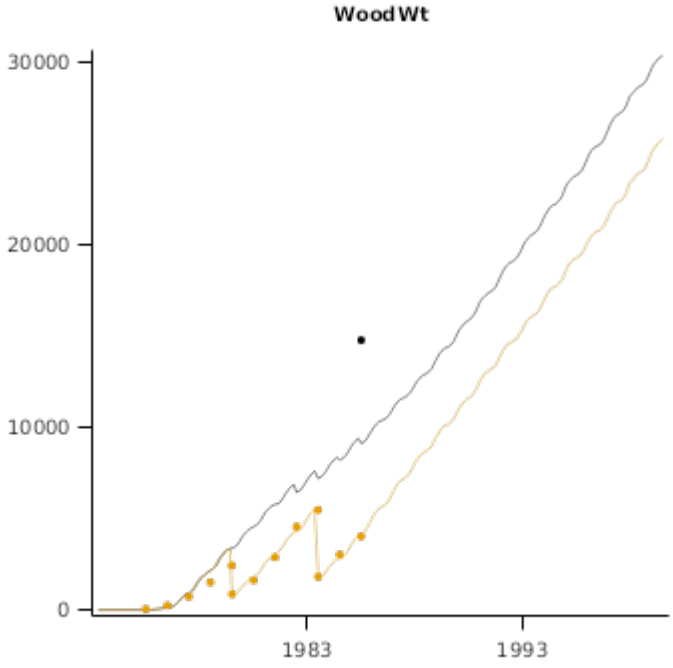

LeafWt
1500
1000
500
0
1983
1993

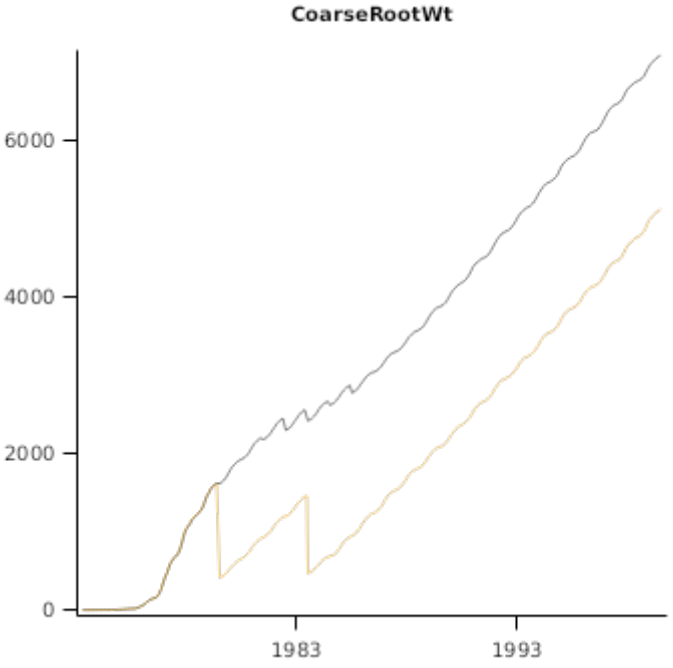

BranchWt
10000
5000
0
1983
1993

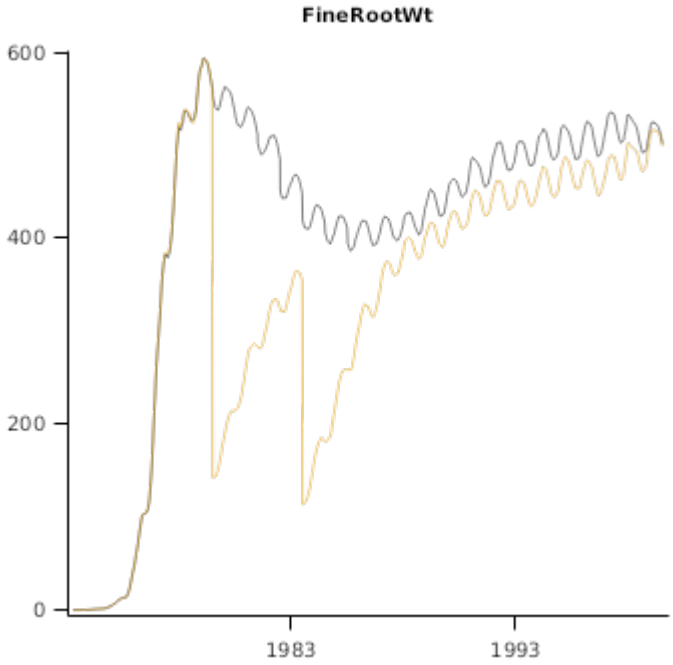

WoodBarkCoarseRootWt
30000
20000
10000
0
1983
1993

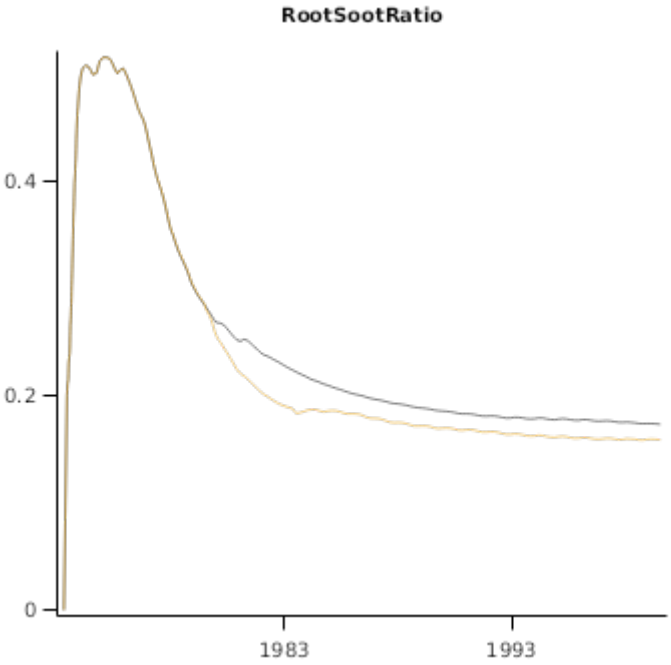

StemWt
30000
20000
10000
0
1983
1993


BarkWt
1500
1000
500
0
1983
1993

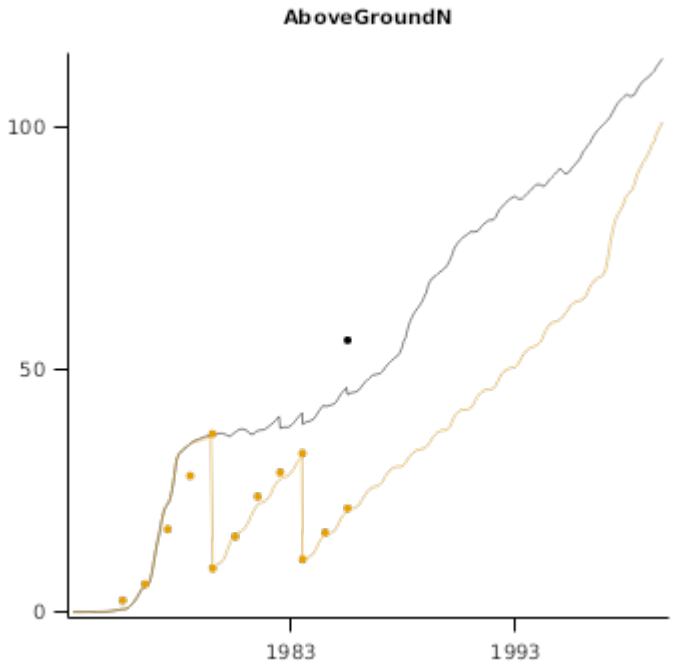

WoodWt
30000
20000
10000
0
1983
1993

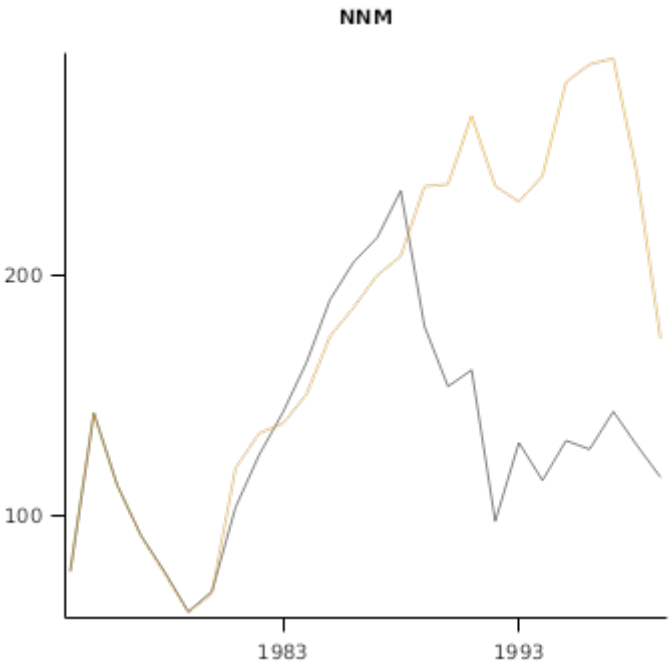

CoarseRootWt
6000
4000
2000
0
1983
1993



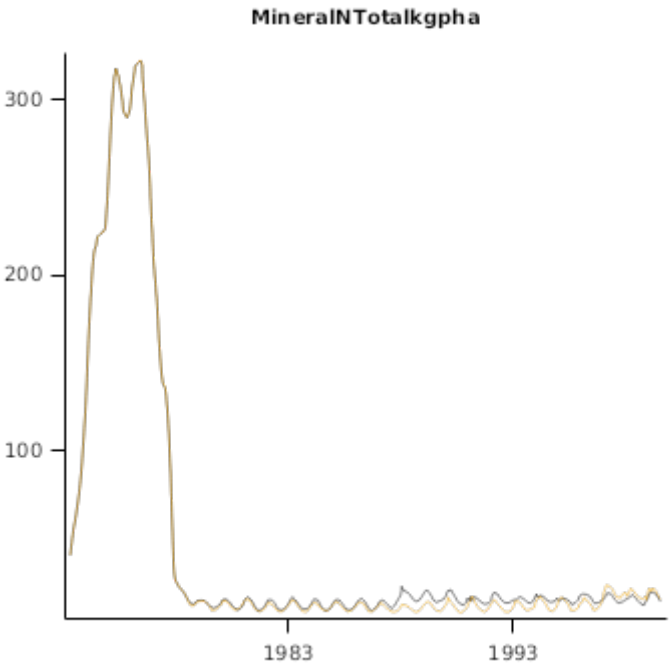


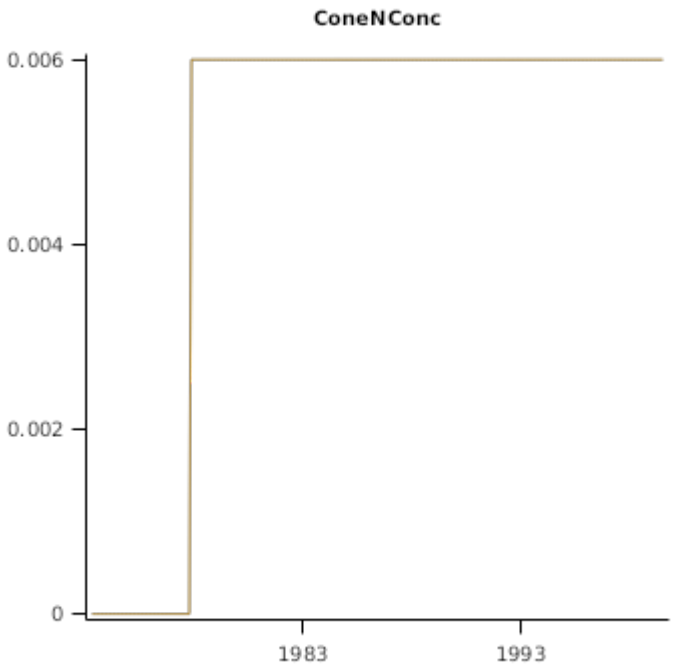
5.2.4.2 GraphsN

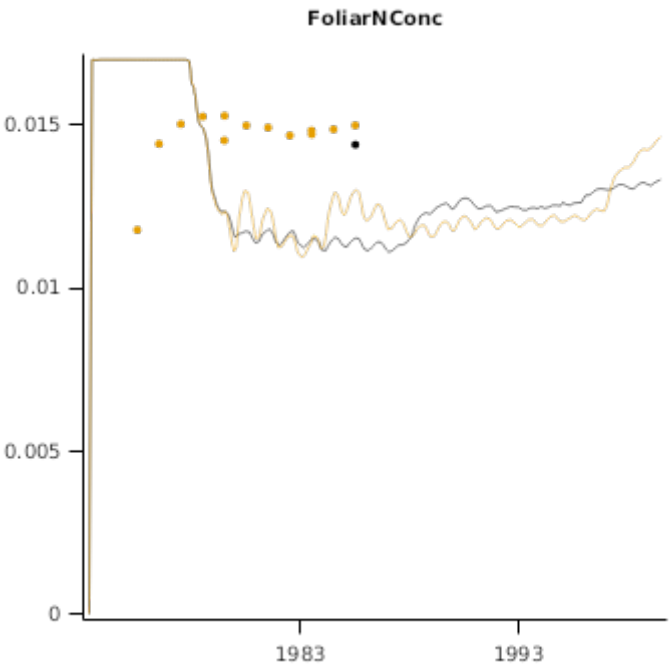

AboveGroundN
100
50
0
1983
1993

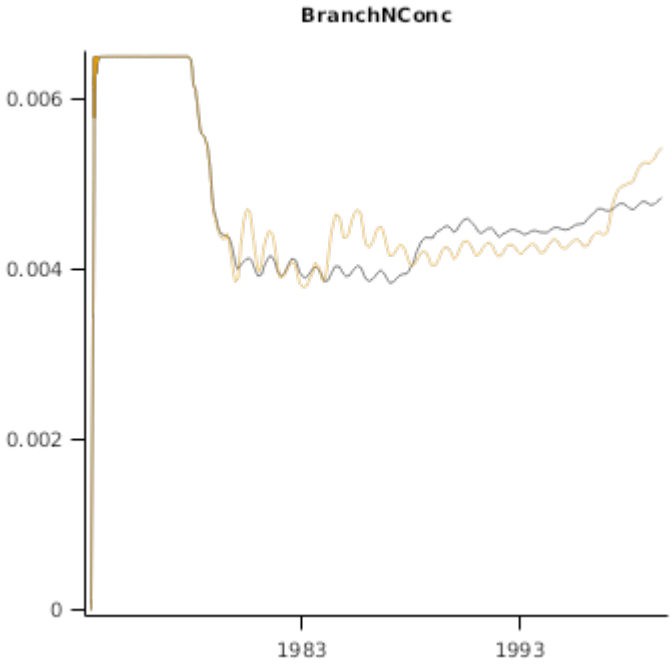

NNM
200
100
1983
1993

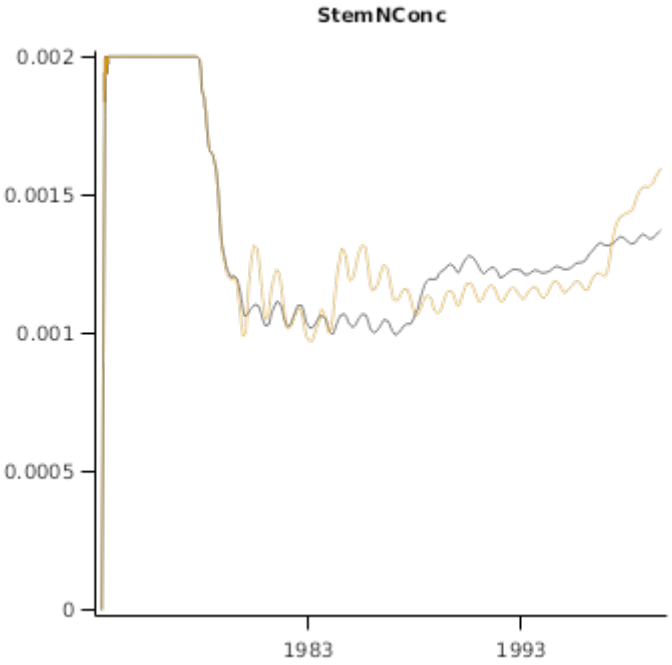
MineralNppm

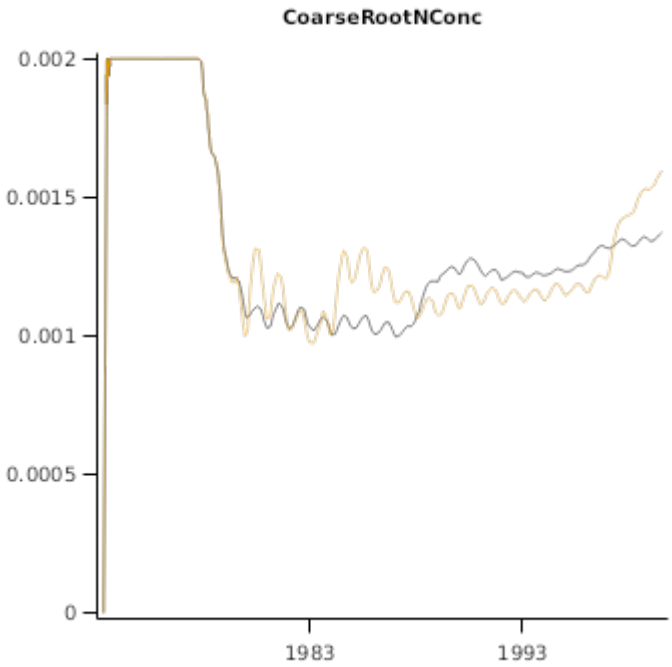

MineralNTotalkgpha
300
200
100
1983
1993

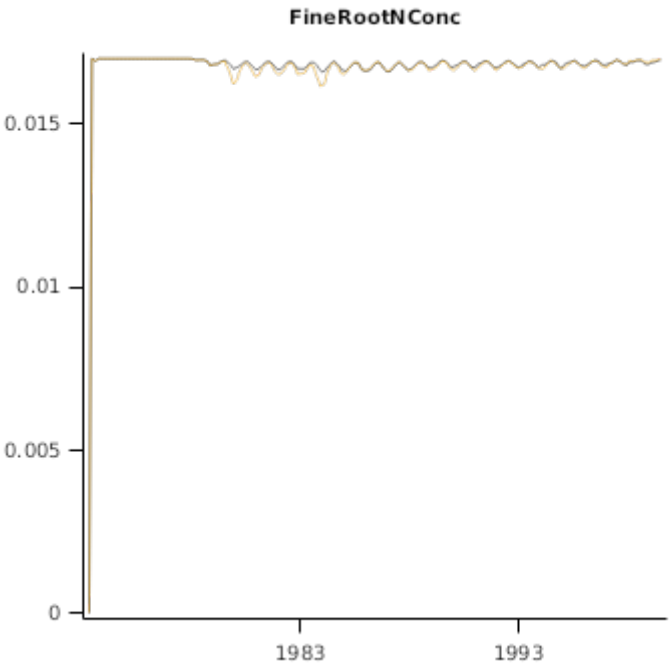

ConeNConc
0.006
0.004
0.002
0
1983
1993


FoliarNConc
0.015
0.01
0.005
0
1983
1993

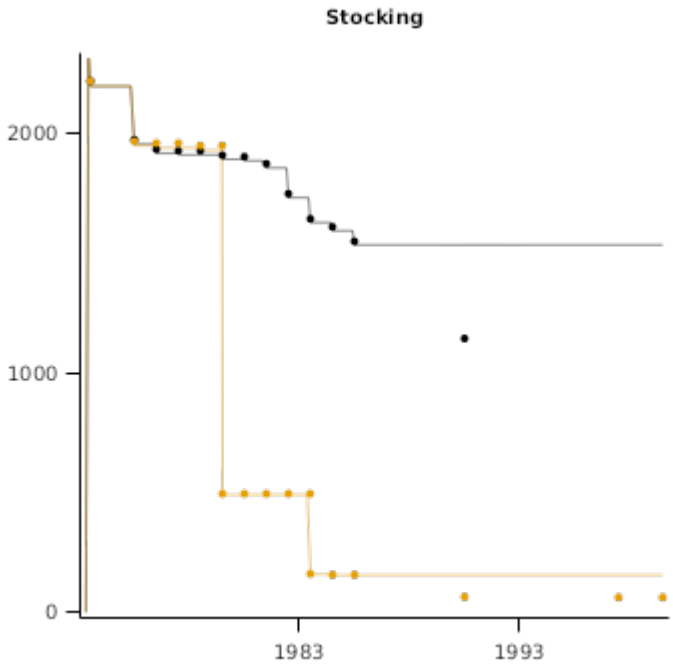


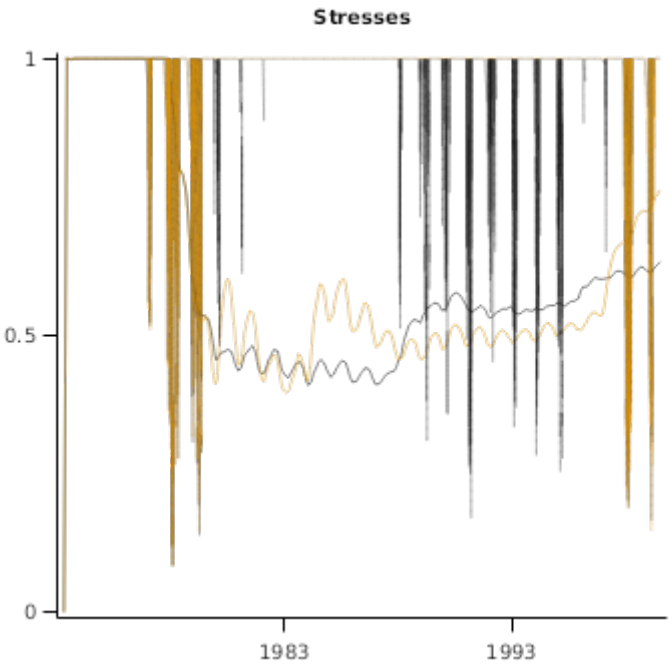


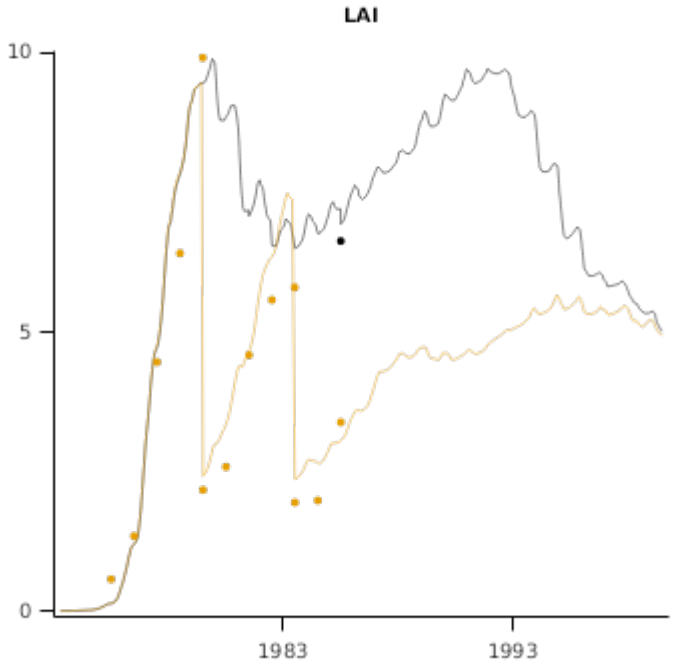


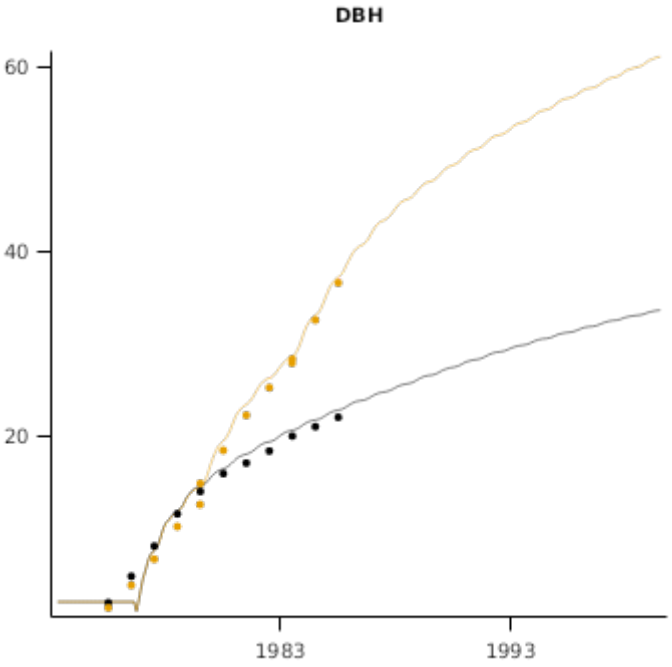


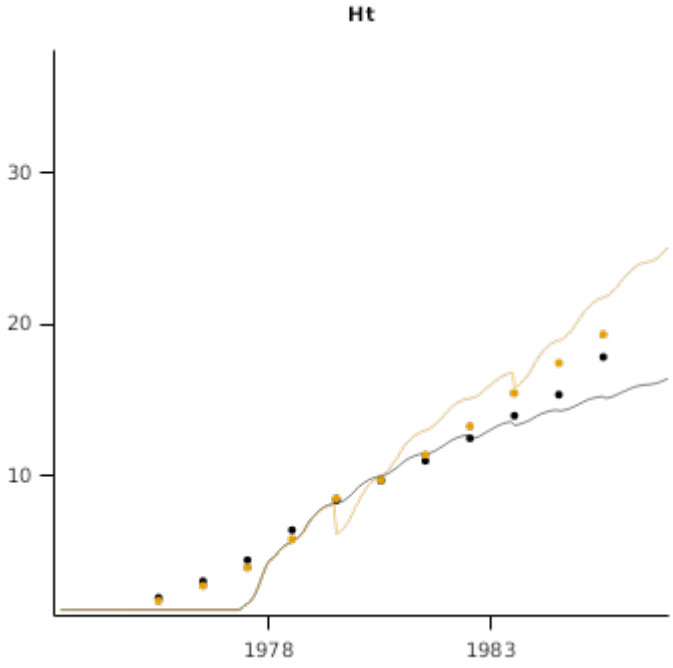
5.2.4.3 GraphsMetrics

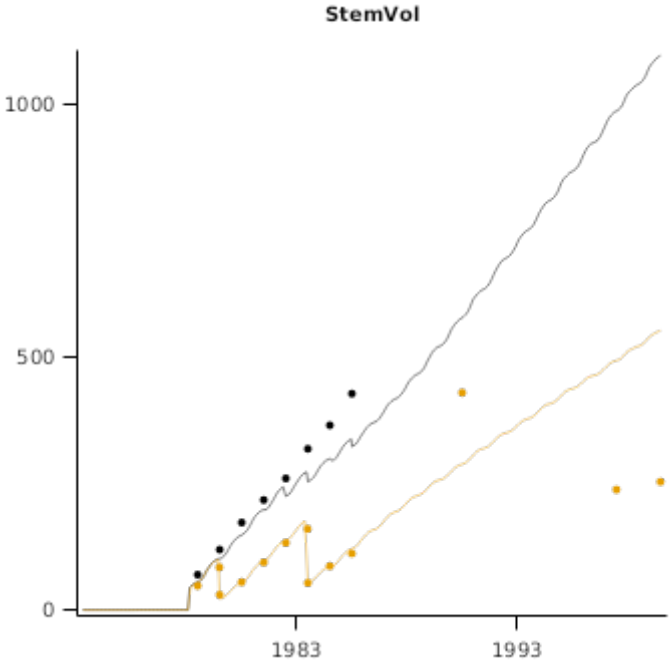

Stocking
2000
1000
0
1983
1993

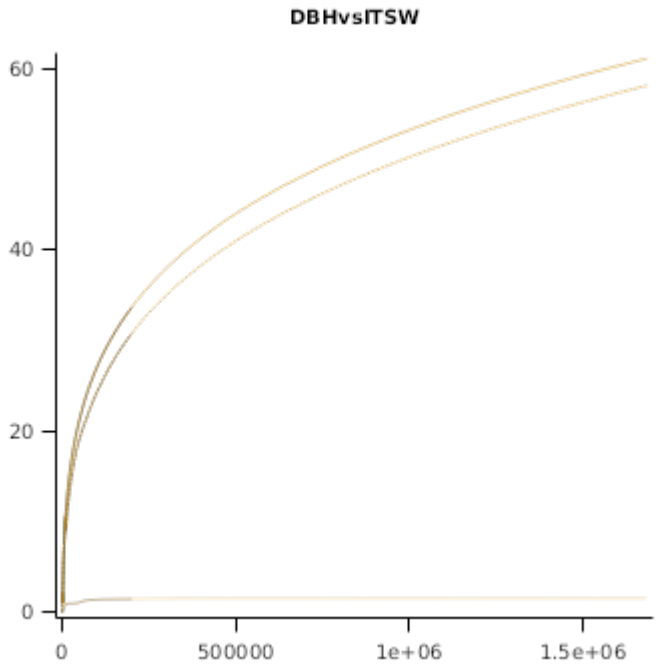

Stresses
1
0.5
0
1983
1993

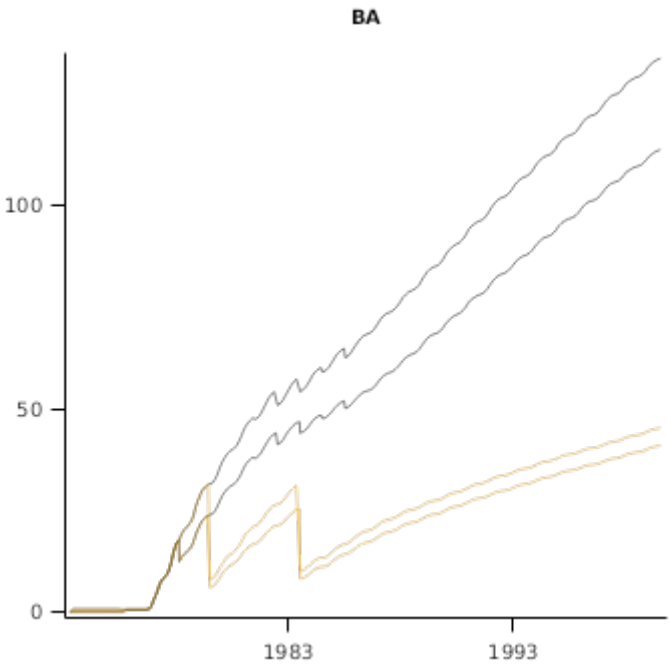

LAI
10
5
0
1983
1993

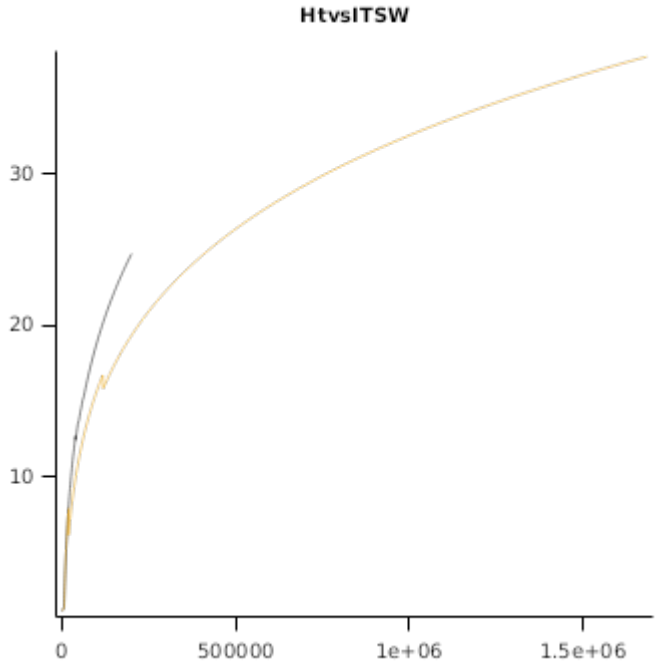

DBH
60
40
20
1983
1993

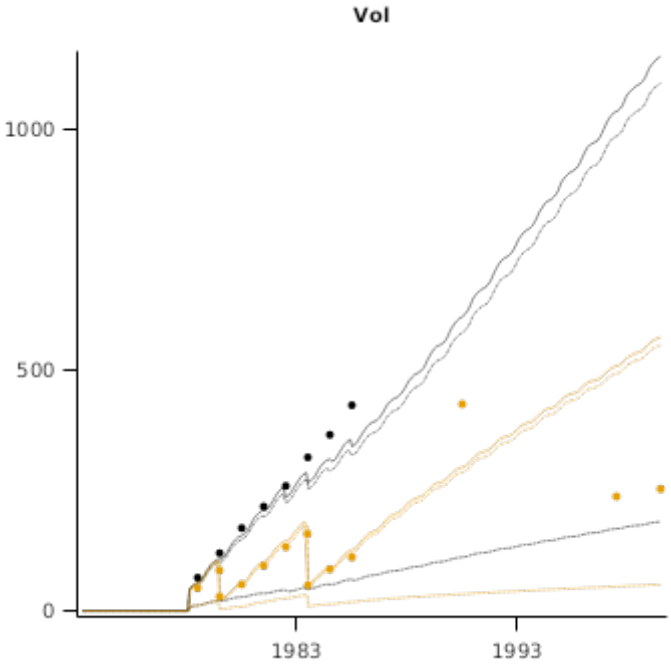

Ht
30
20
10
1978
1983

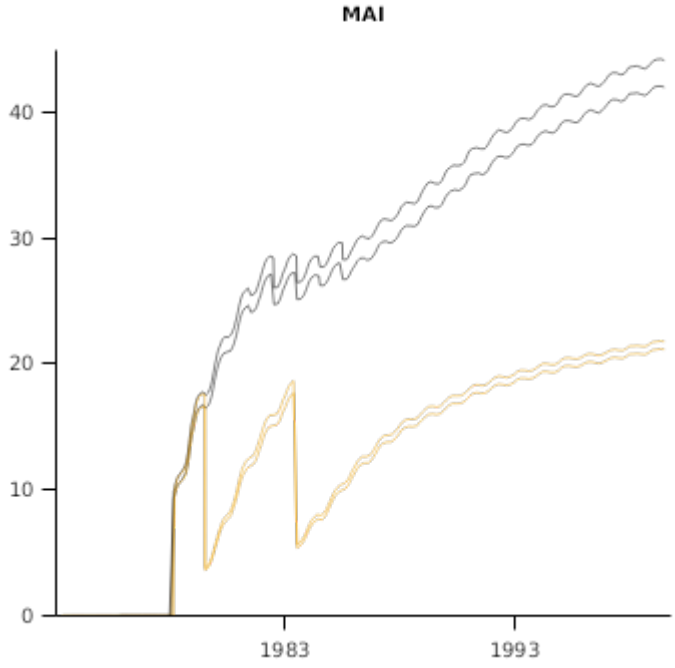

StemVol
1000
500
0
1983
1993

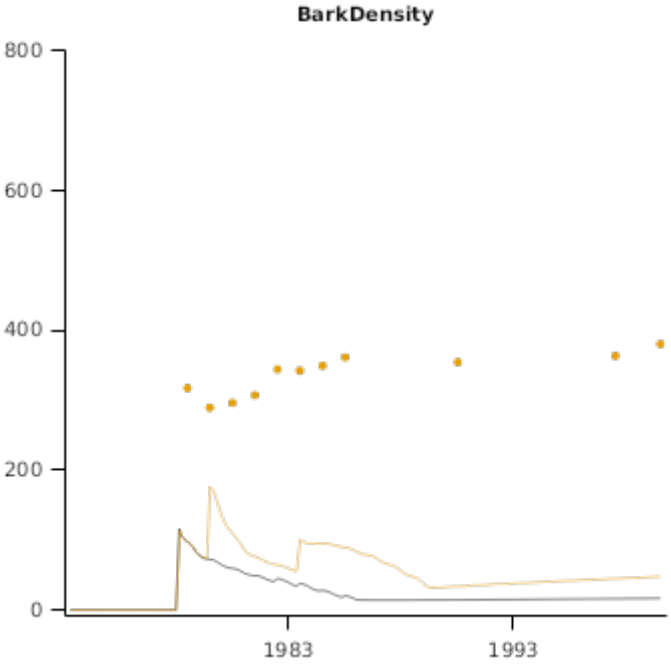

DBHvsITSW
60
40
20
0
0
500000
1e+06
1.5e+06

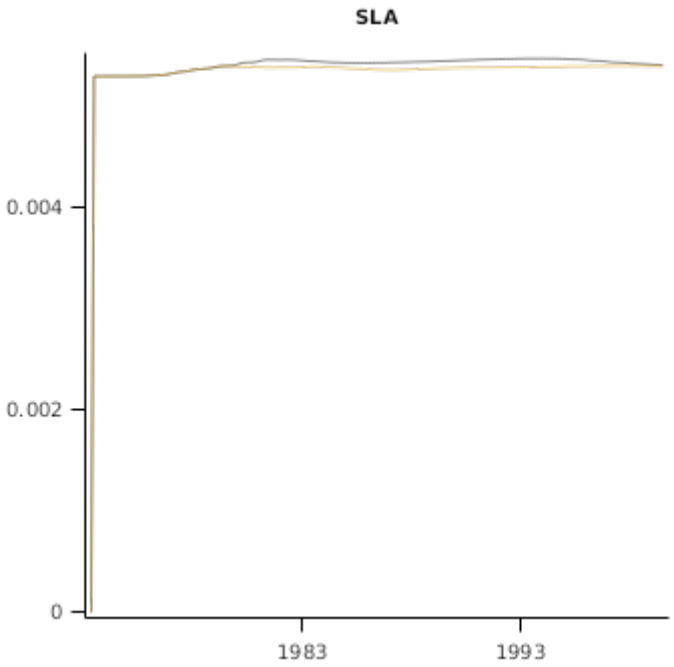

BA
100
50
0
1983
1993

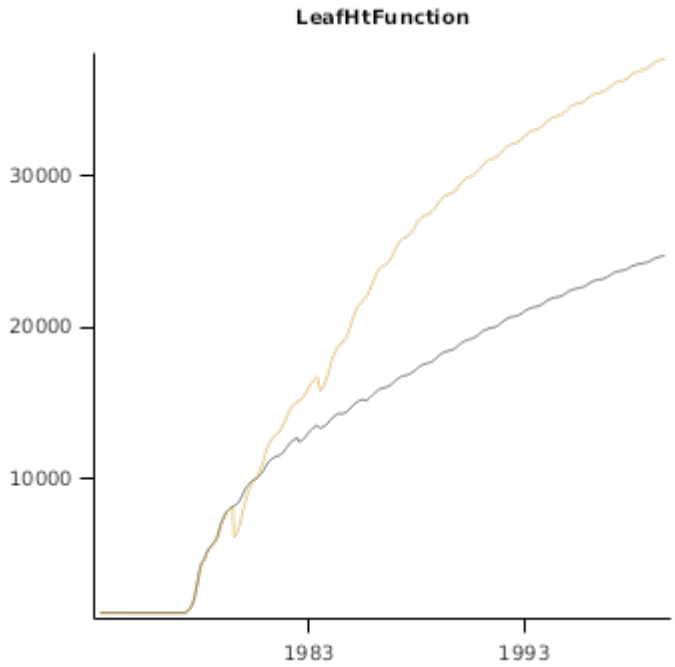

HtvsITSW
30
20
10
0
500000
1e+06
1.5e+06


Vol
1000
500
0
1983
1993


MAI
40
30
20
10
0
1983
1993


BarkDensity
800
600
400
200
0
1983
1993





5.2.5 TowerHill

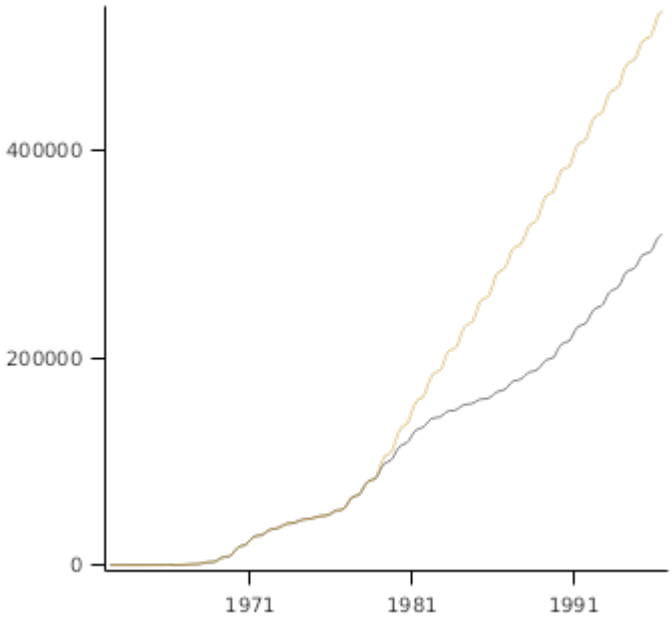
These data are from an experiment with ferilizer on very shallow soils with moderate rainfall. Substantial rates of accumulated N applications changed the C-N dynamics of the site and stand growth. Data were reported in Neilsen et al., 1992 and Neilsen et al., 1998, and some details were checked in the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

List of experiments.

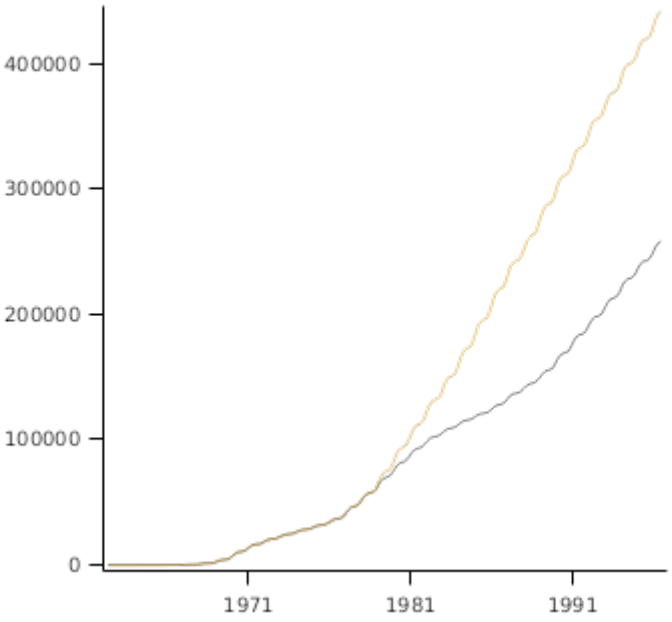
Experiment Name	Design (Number of Treatments)
TowerHil	I (2)

5.2.5.1 GraphsWeights

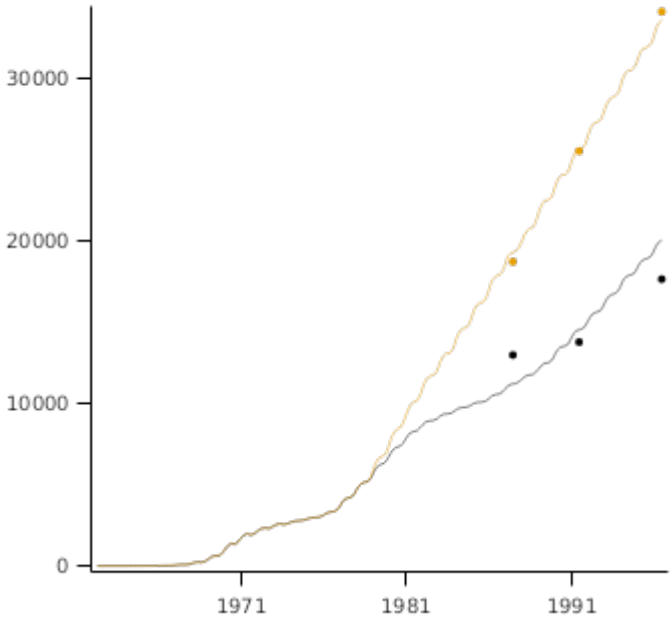
IndividualTreeLiveWt



IndividualStemWt

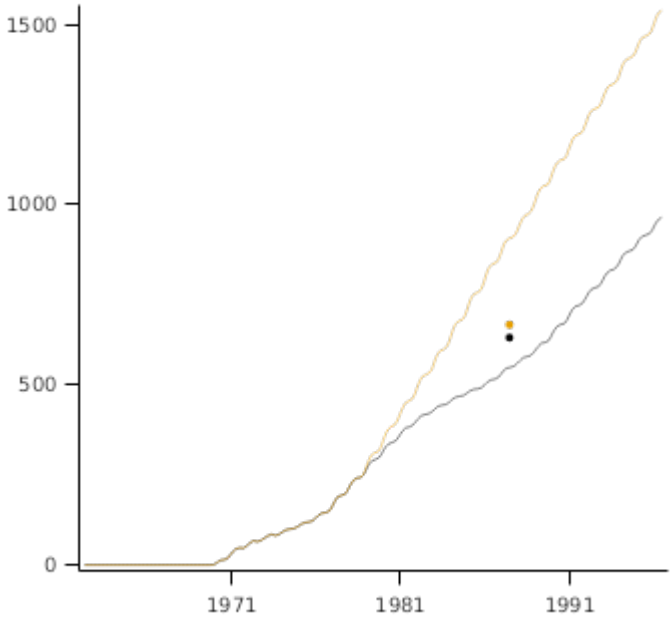


AboveGroundWt

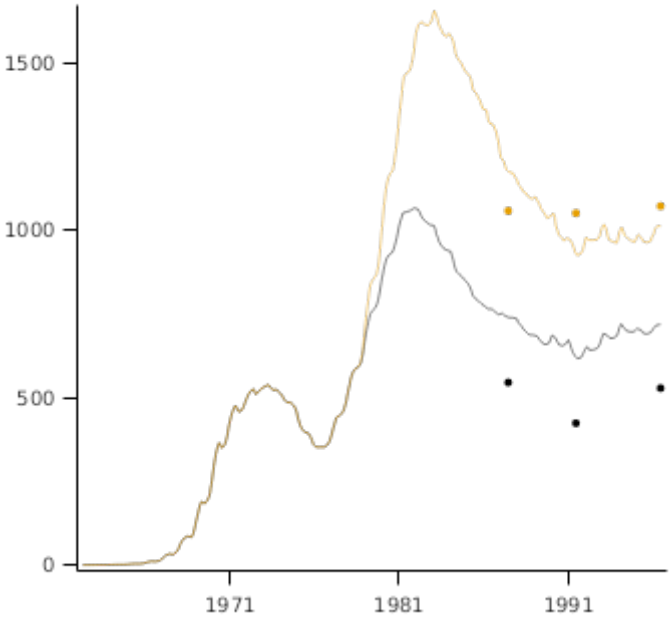


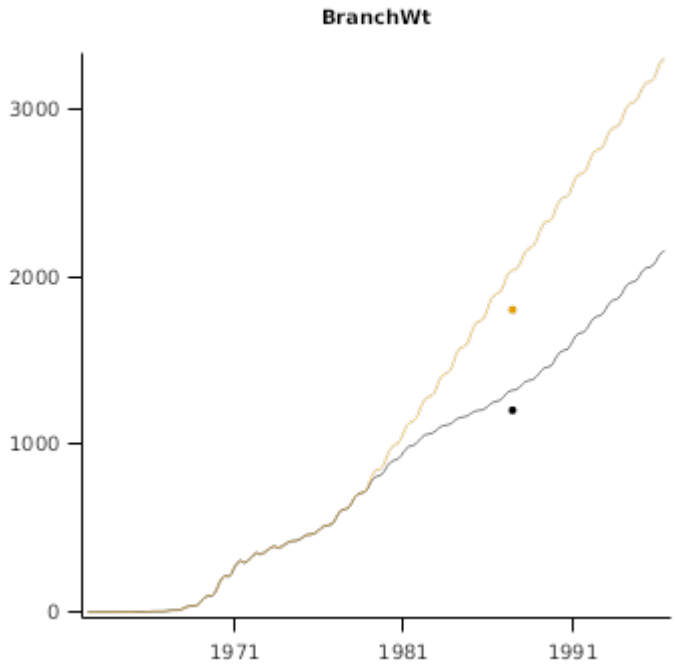
ComponentWts

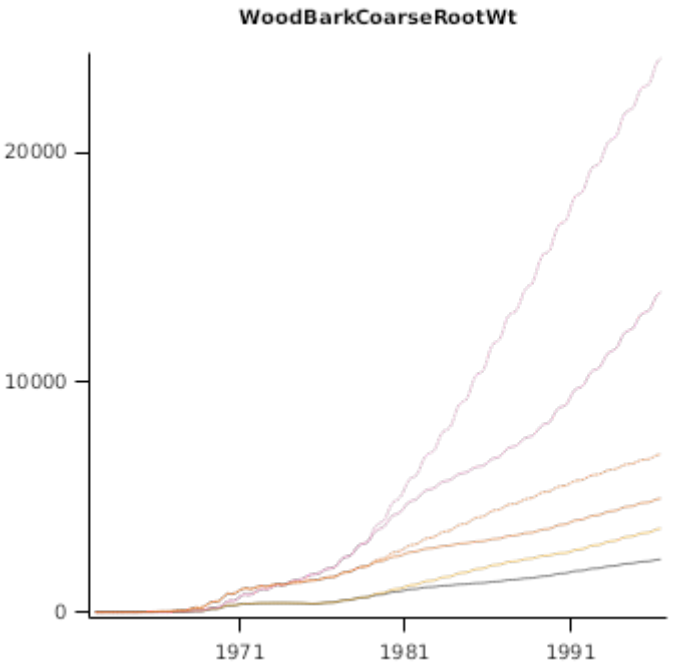
ConeWt

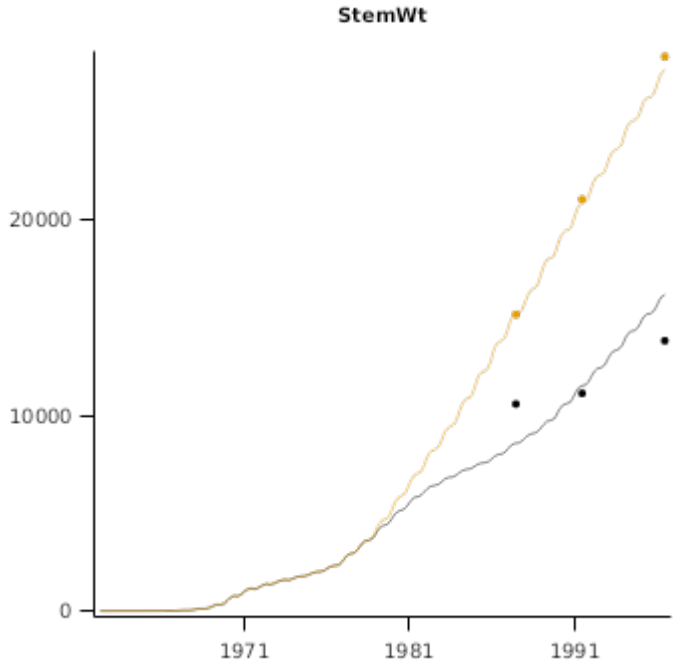


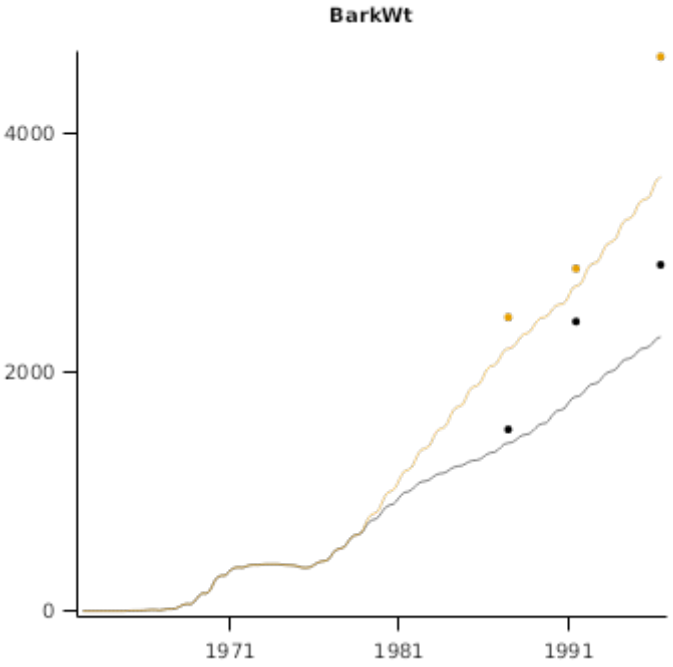
LeafWt

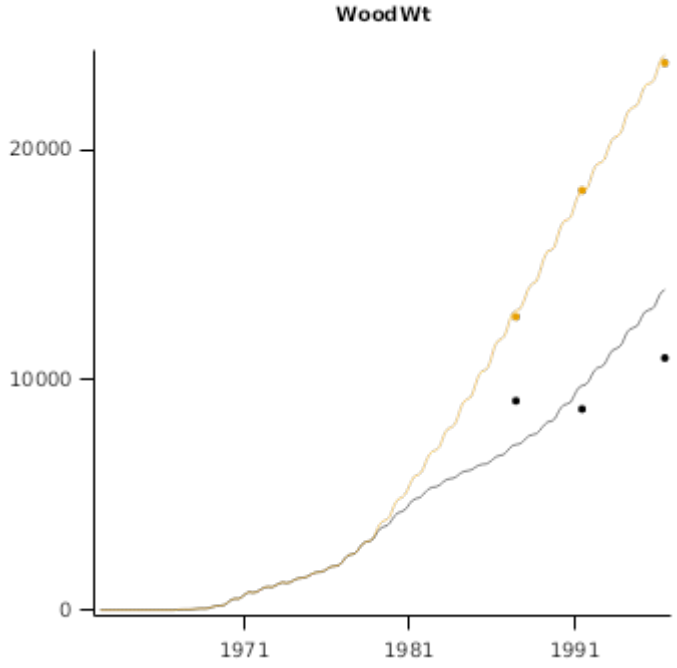


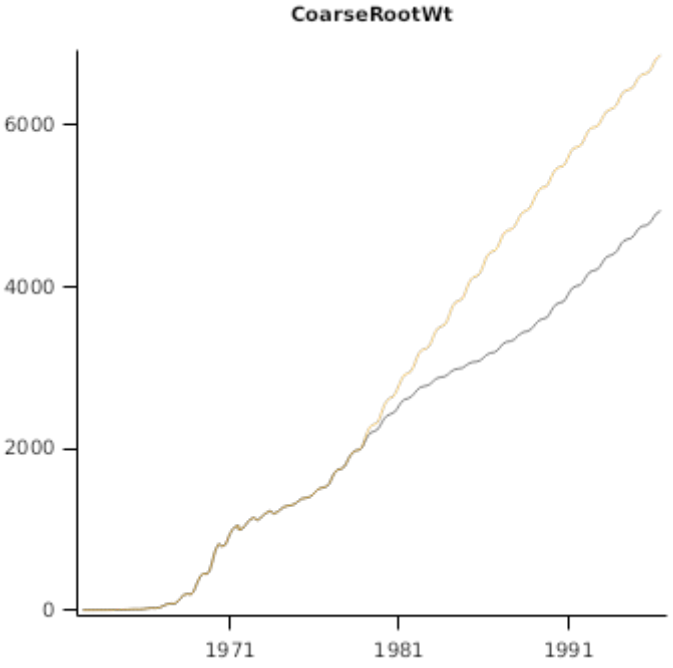

BranchWt
3000
2000
1000
0
1971
1981
1991

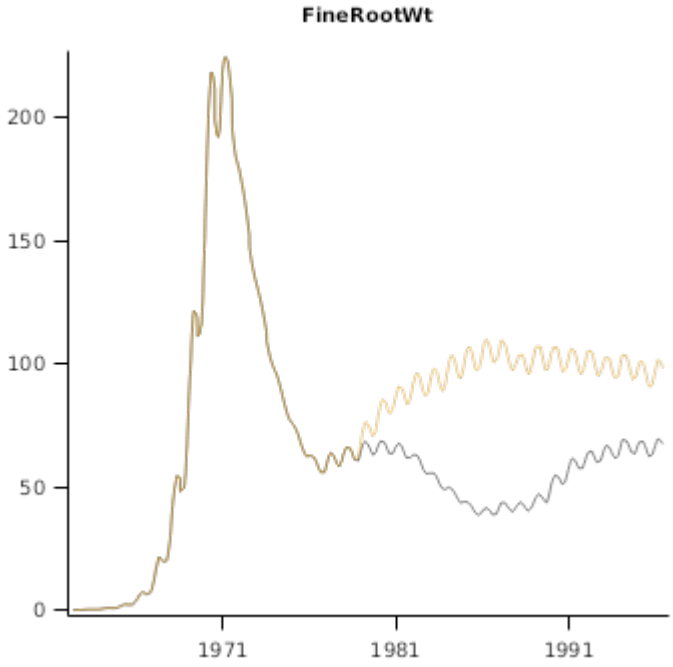

WoodBarkCoarseRootWt
20000
10000
0
1971
1981
1991

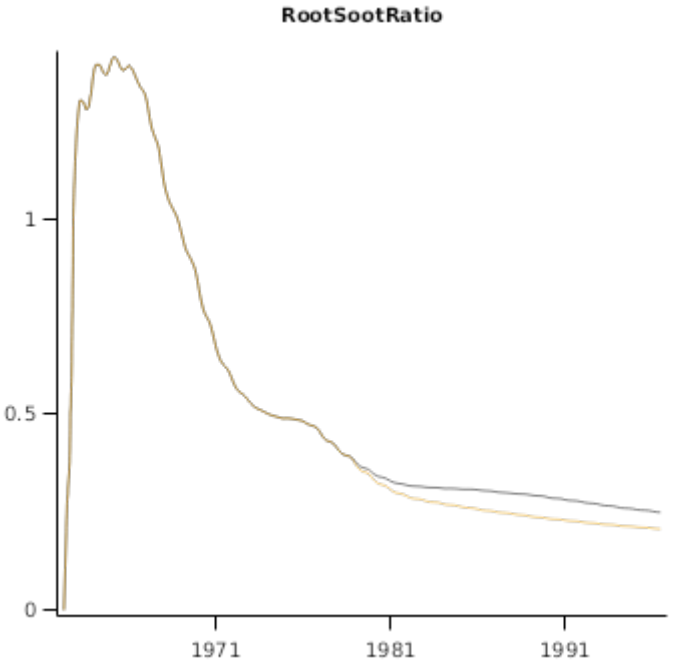

StemWt
20000
10000
0
1971
1981
1991


BarkWt
4000
2000
0
1971
1981
1991

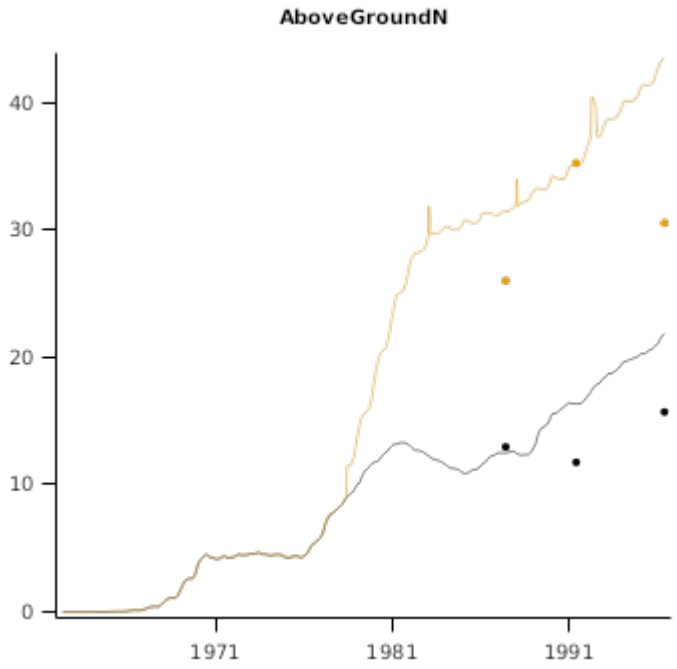

WoodWt
20000
10000
0
1971
1981
1991

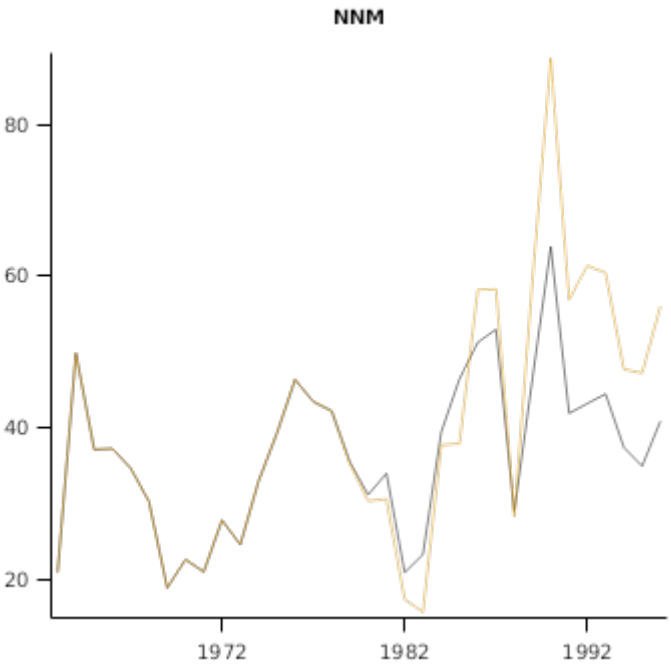

CoarseRootWt
6000
4000
2000
0
1971
1981
1991

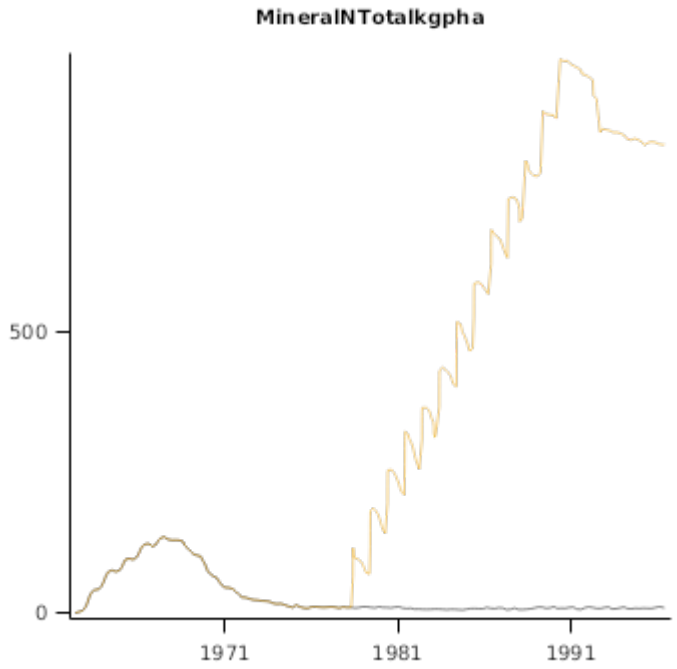


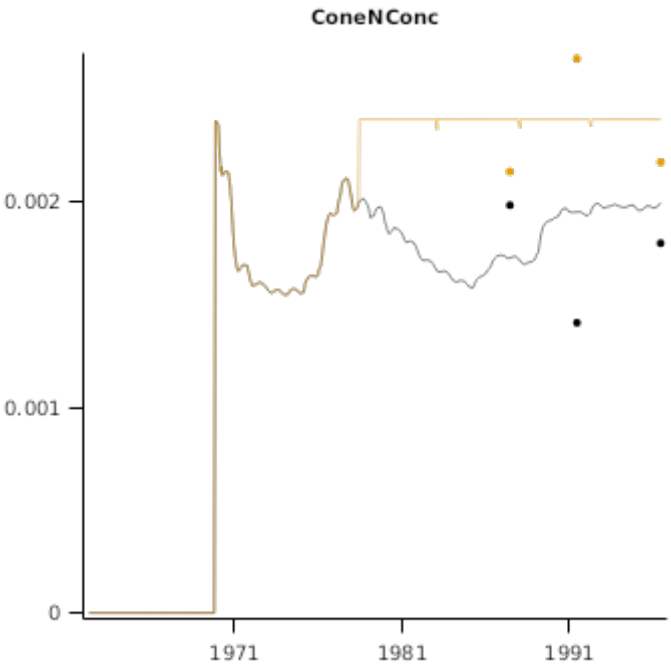


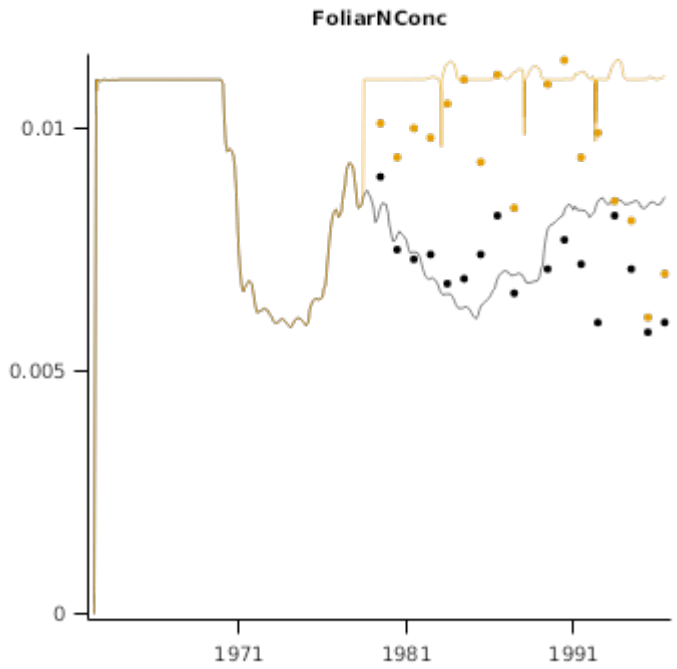
5.2.5.2 GraphsN

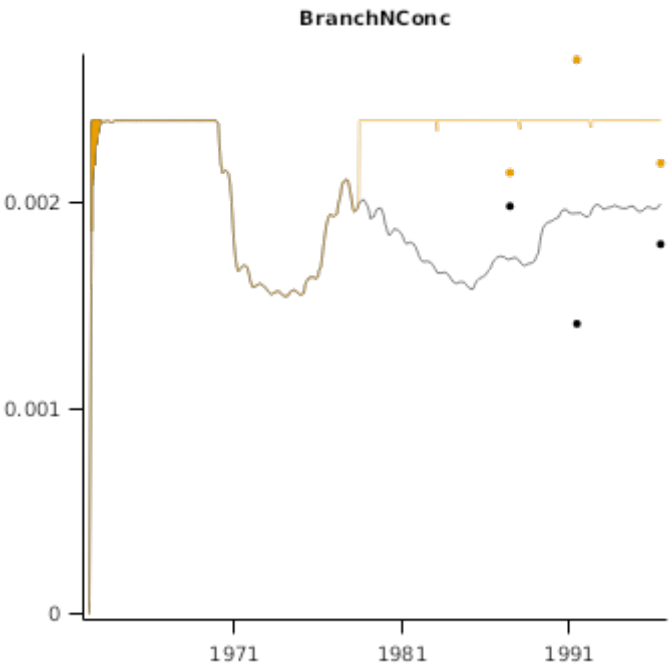

AboveGroundN
40
30
20
10
0
1971
1981
1991

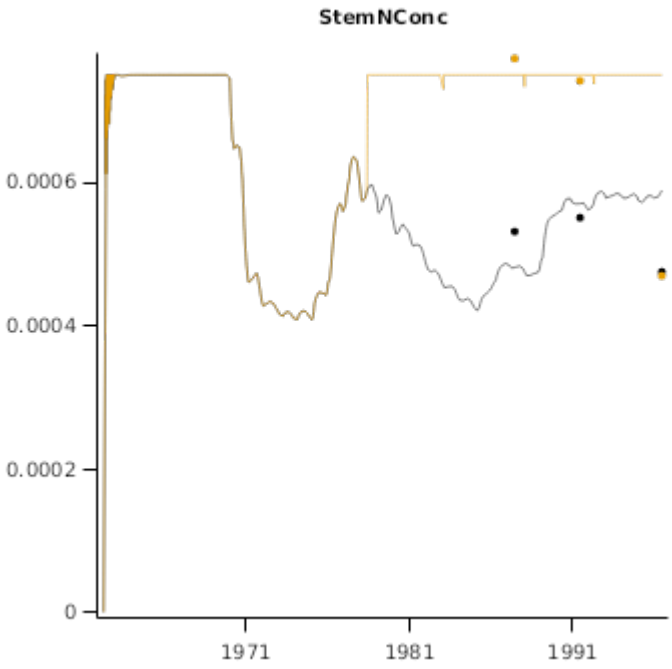

NNM
80
60
40
20
1972
1982
1992

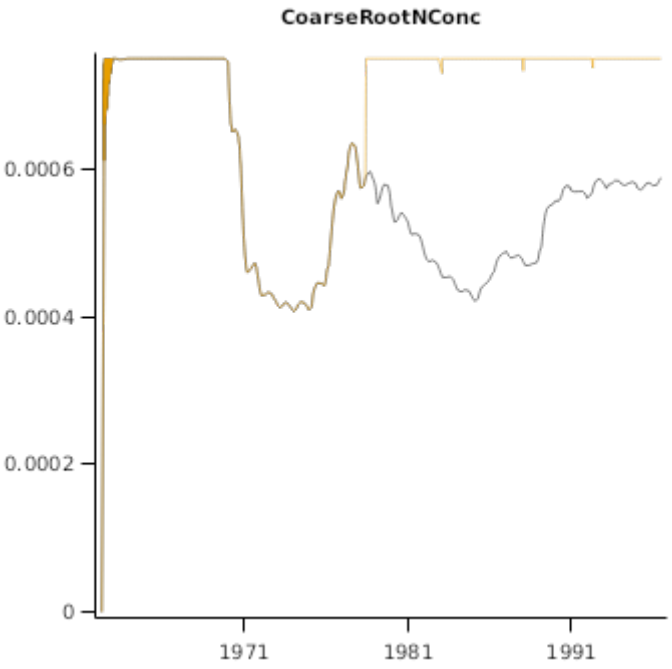

MineralNTotalkgpha
500
0
1971
1981
1991

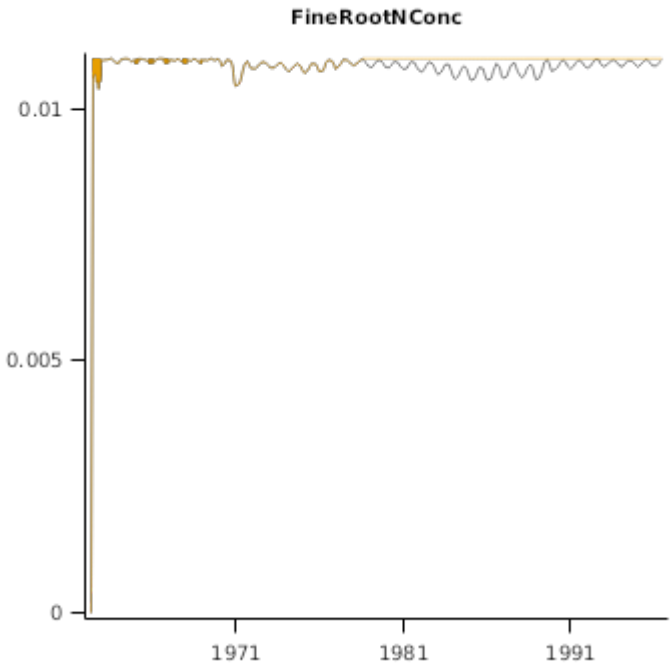

ConeNConc
0.002
0.001
0
1971
1981
1991


FoliarNConc
0.01
0.005
0
1971
1981
1991

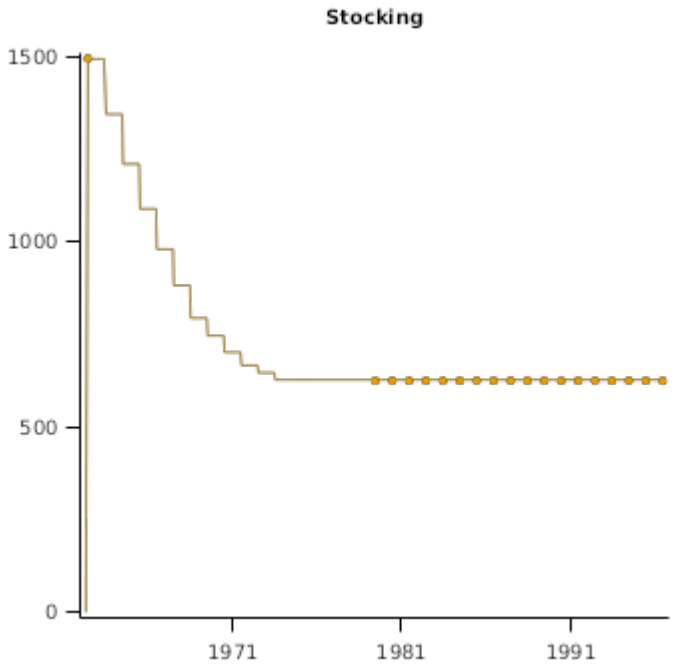

BranchNConc
0.002
0.001
0
1971
1981
1991

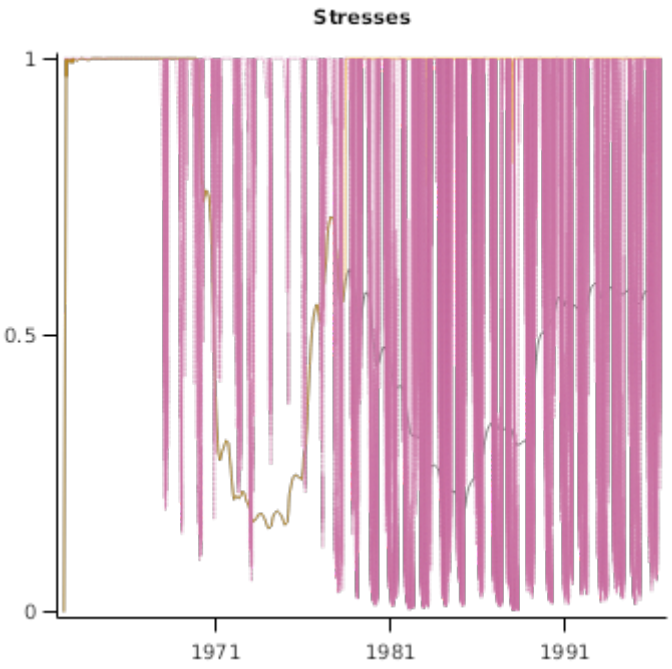


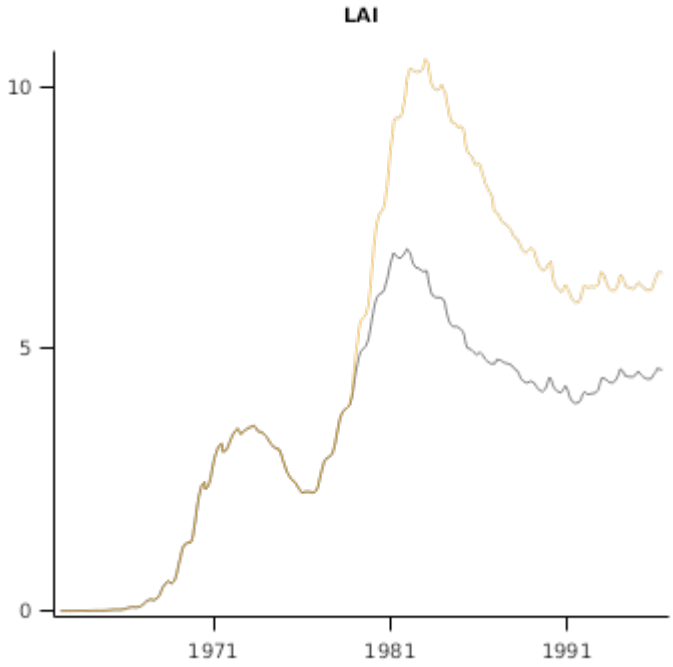


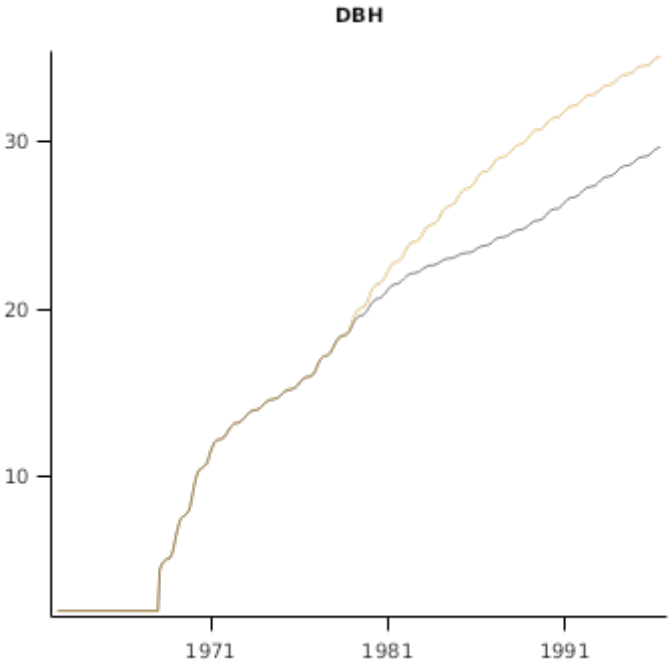


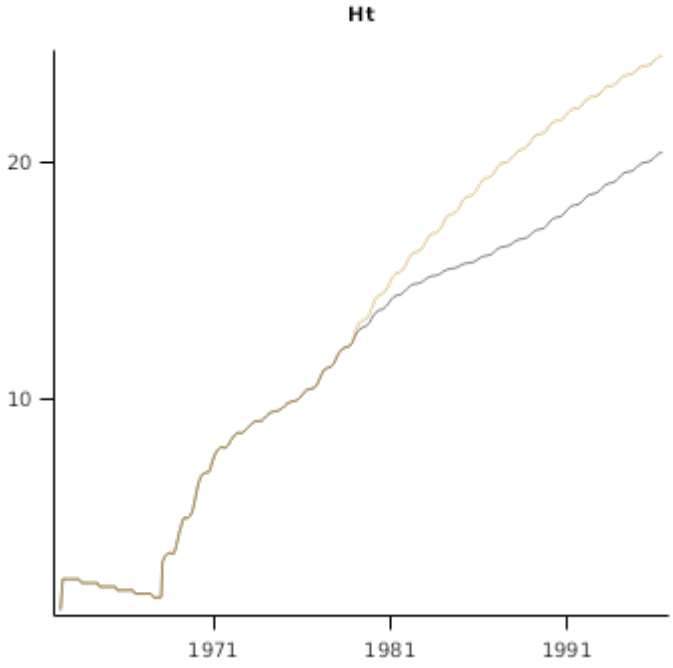
5.2.5.3 GraphsMetrics

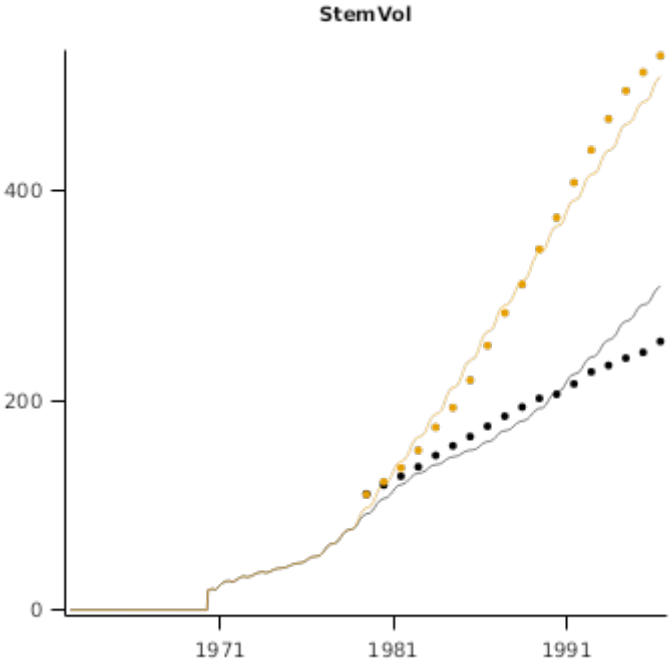

Stocking
1500
1000
500
0
1971
1981
1991

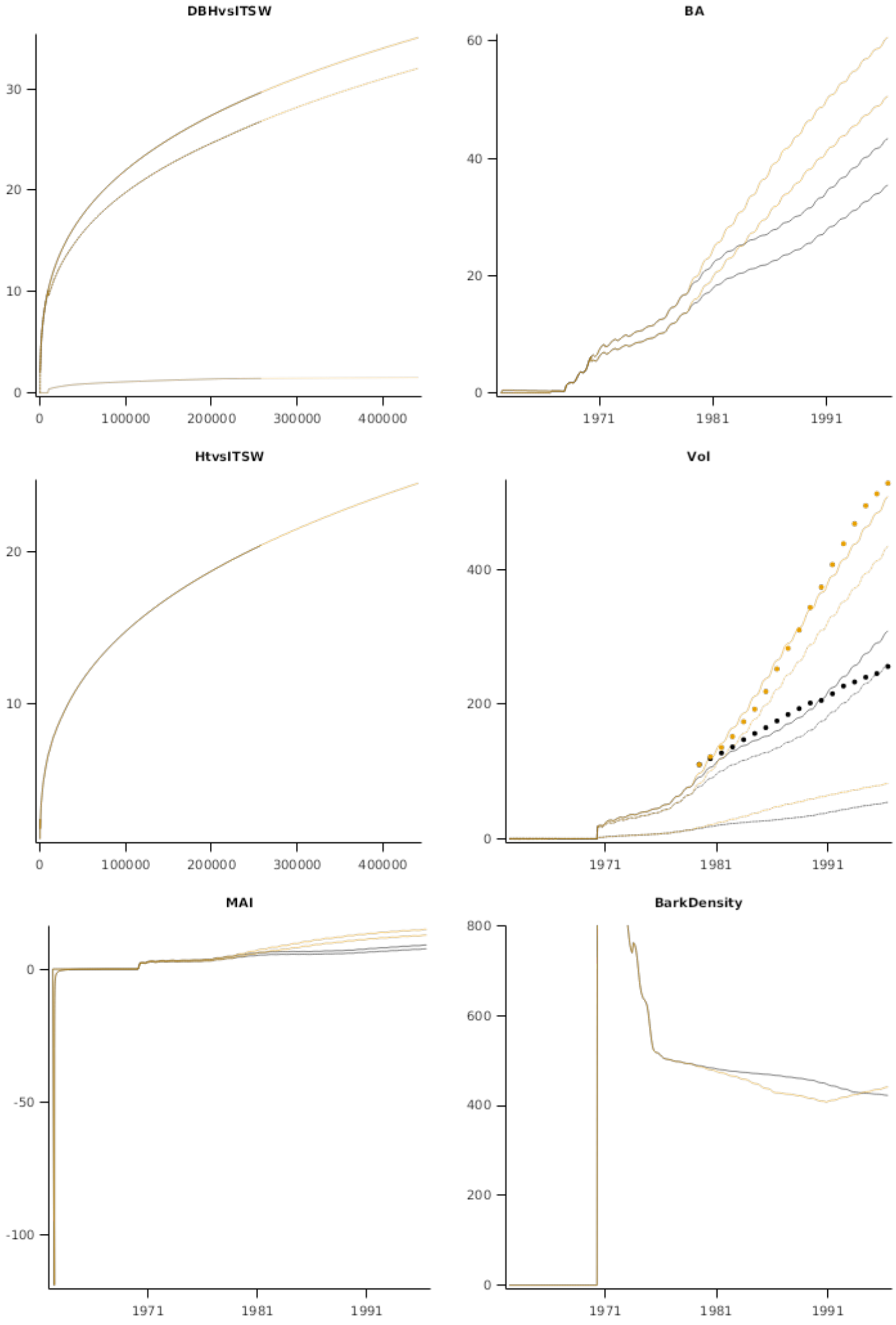

Stresses
1
0.5
0
1971
1981
1991


LAI
10
5
0
1971
1981
1991


DBH
30
20
10
1971
1981
1991


Ht
20
10
1971
1981
1991


StemVol
400
200
0
1971
1981
1991


DBHvsITSW
30
20
10
0
0
100000
200000
300000
400000
BA
60
40
20
0
1971
1981
1991
HtvsITSW
20
10
0
100000
200000
300000
400000
Vol
400
200
0
1971
1981
1991
MAI
0
-50
-100
1971
1981
1991
BarkDensity
800
600
400
200
0
1971
1981
1991

5.2.6 GraphsOvP

Test! These observed versus predicted graphs include all validation datasets and timesteps within a site for which observed data were available.

5.3 Tropical and SubTropical

These are the Tropical and SubTropical datasets.

5.3.1 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).

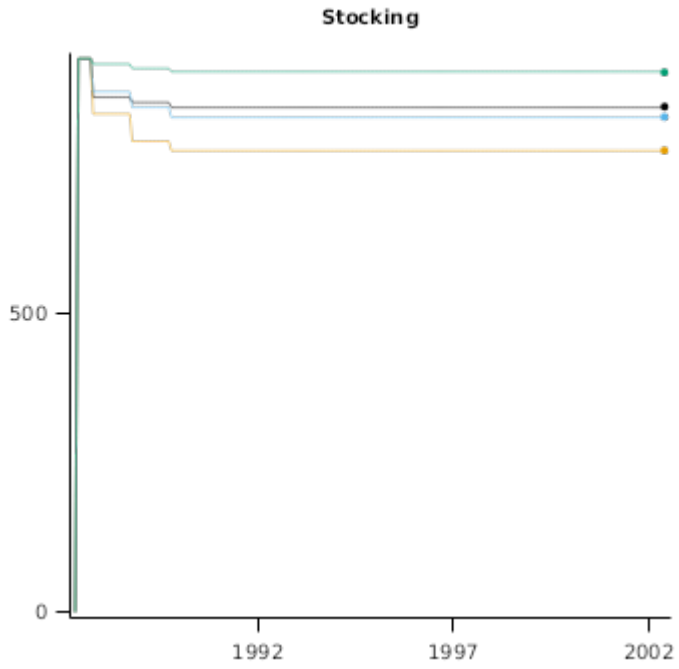
5.3.1.1 FPQBeerwah

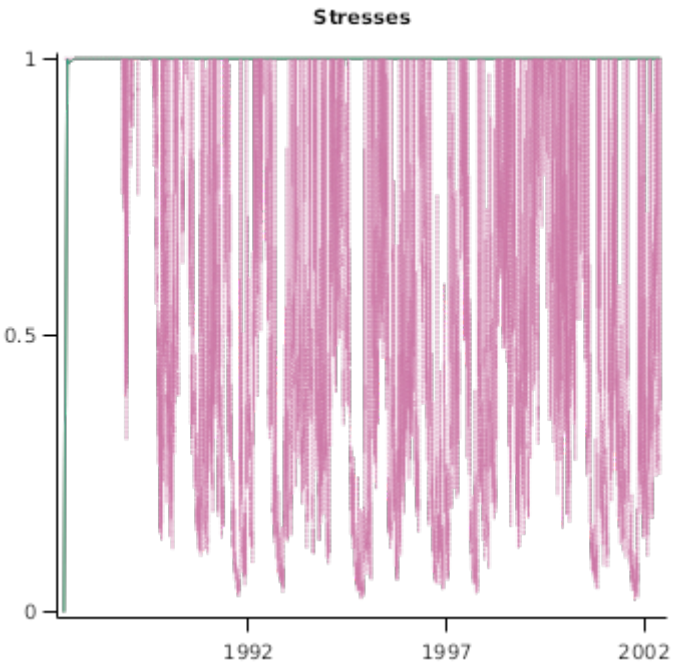
These data are from a genetics experiment in south-east Queensland described by Dieters et al., 2007. Four genotypes are compared: *P. elliottii* var. elliottii (PEE), *P. caribaea* var. hondurensis (PCH), the F1 hybrid, and the F2 hybrid. As only stem metrics were provided in the paper, genotypes were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

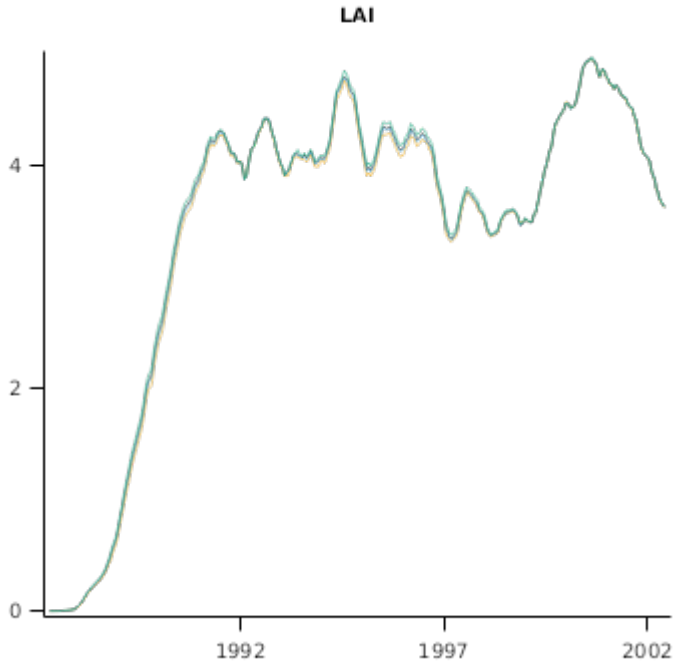
List of experiments.

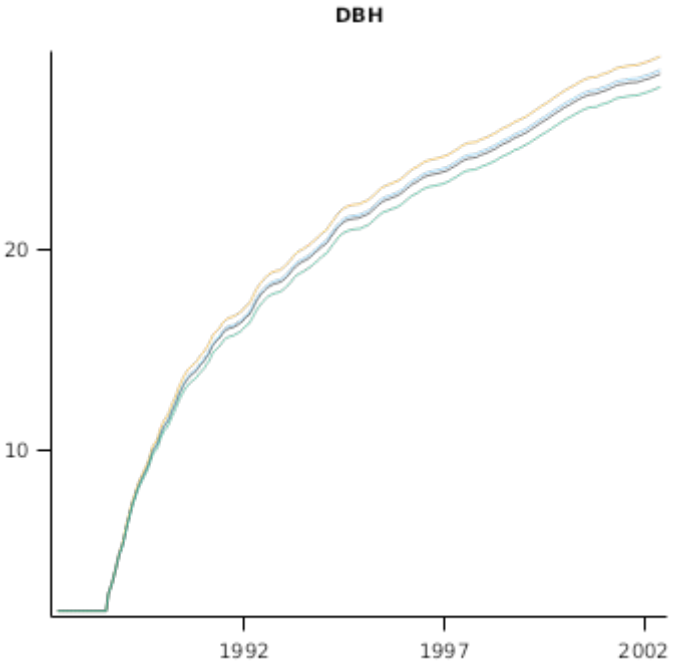
Experiment Name	Design (Number of Treatments)
FPQBeerwah	_ (4)

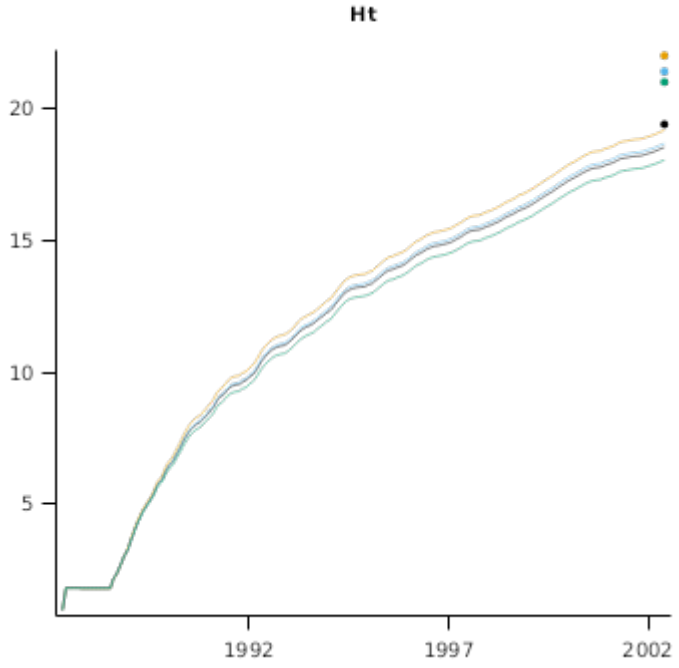
5.3.1.1.1 GraphsMetrics

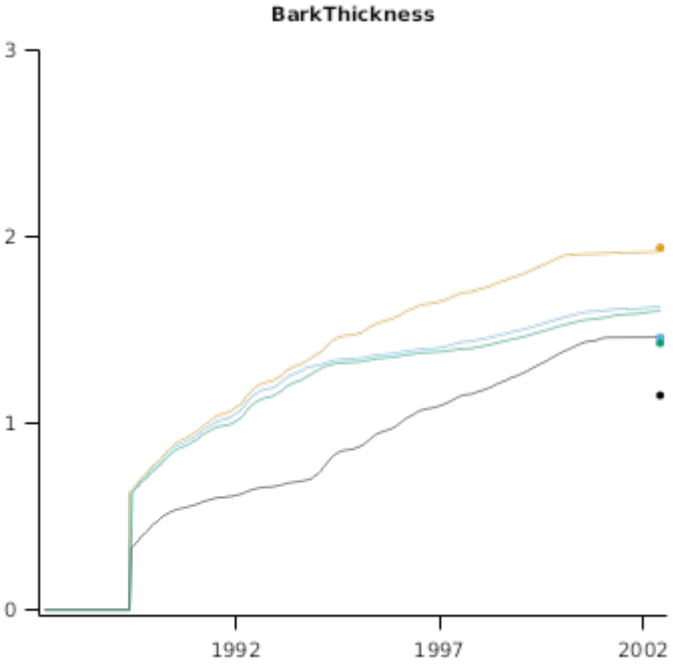

Stocking
500
0
1992
1997
2002

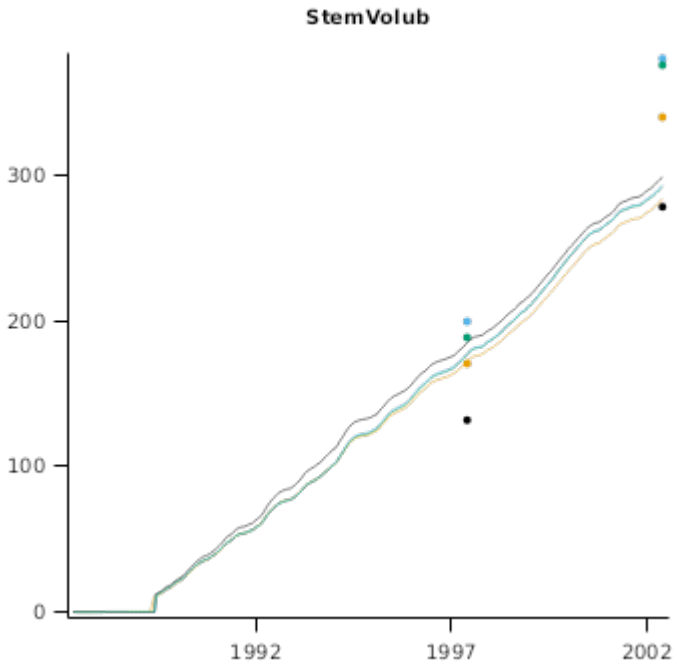

Stresses
1
0.5
0
1992
1997
2002

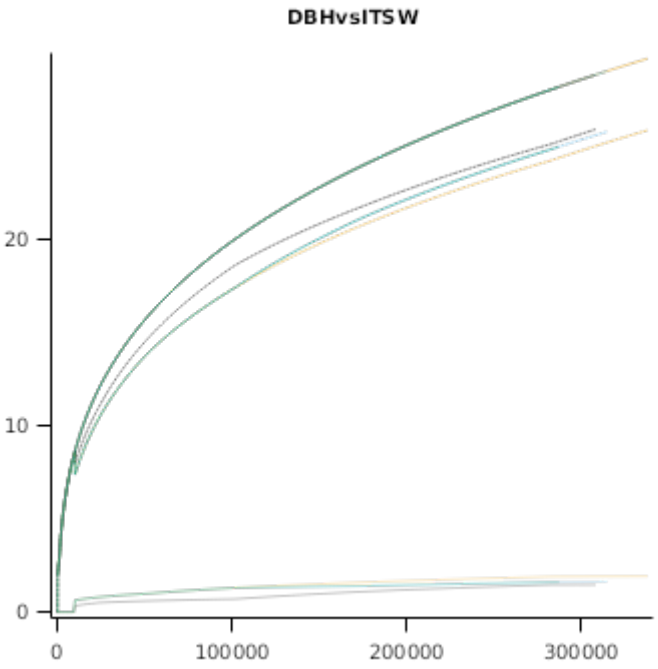

LAI
4
2
0
1992
1997
2002

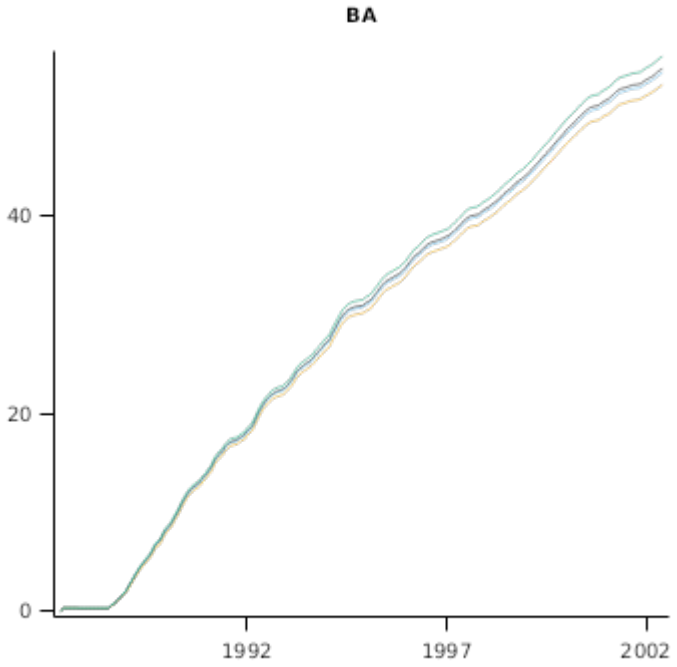

DBH
20
10
1992
1997
2002

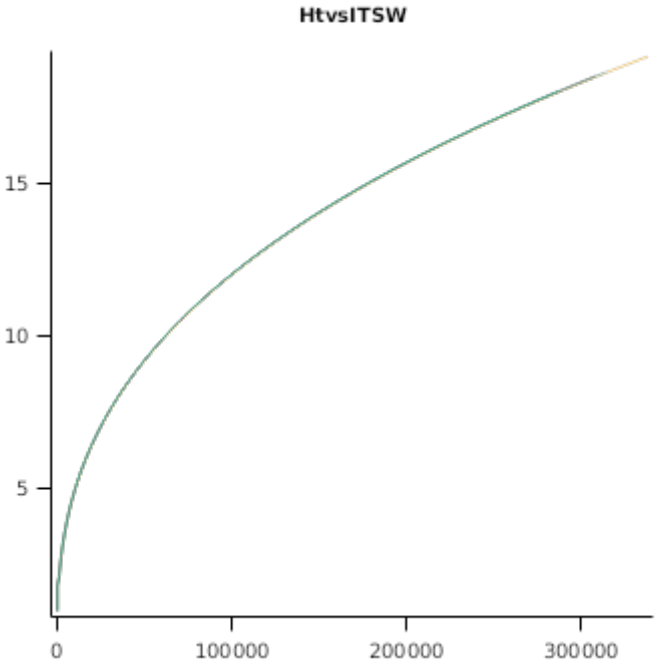

Ht
20
15
10
5
1992
1997
2002

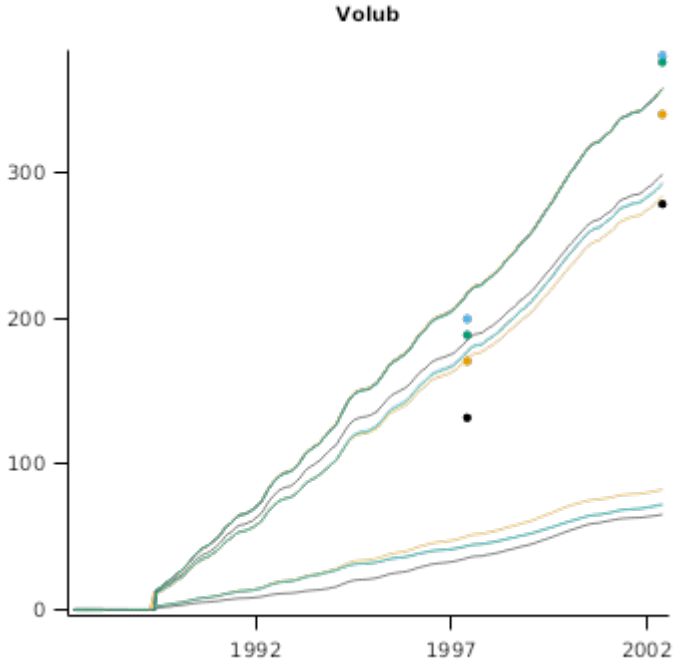

BarkThickness
3
2
1
0
1992
1997
2002

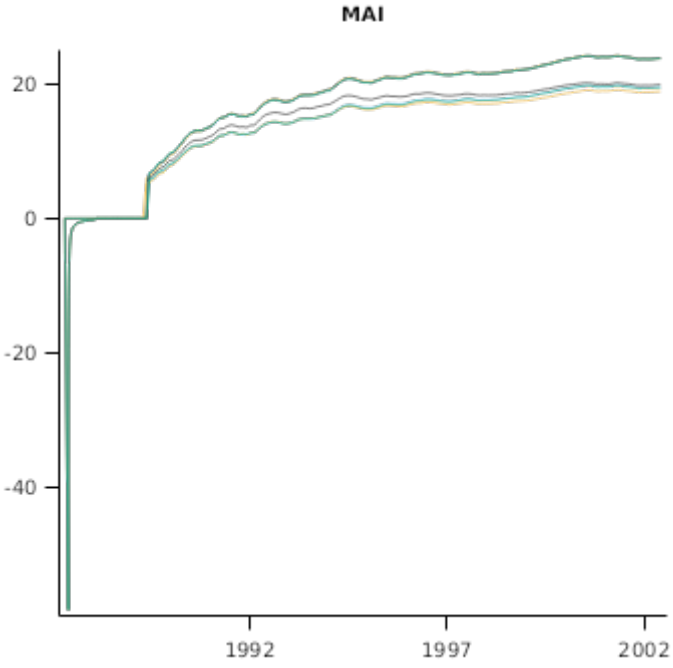

StemVolub
300
200
100
0
1992
1997
2002

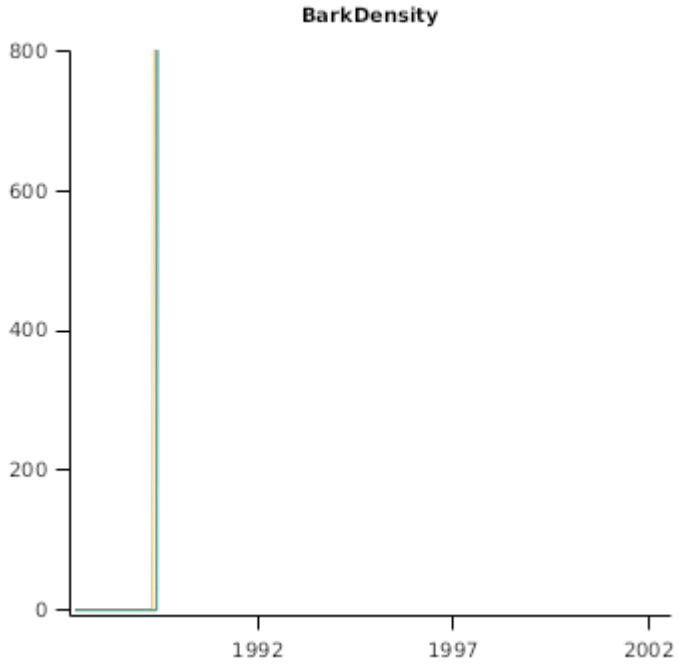

DBHvsITSW
20
10
0
0
100000
200000
300000

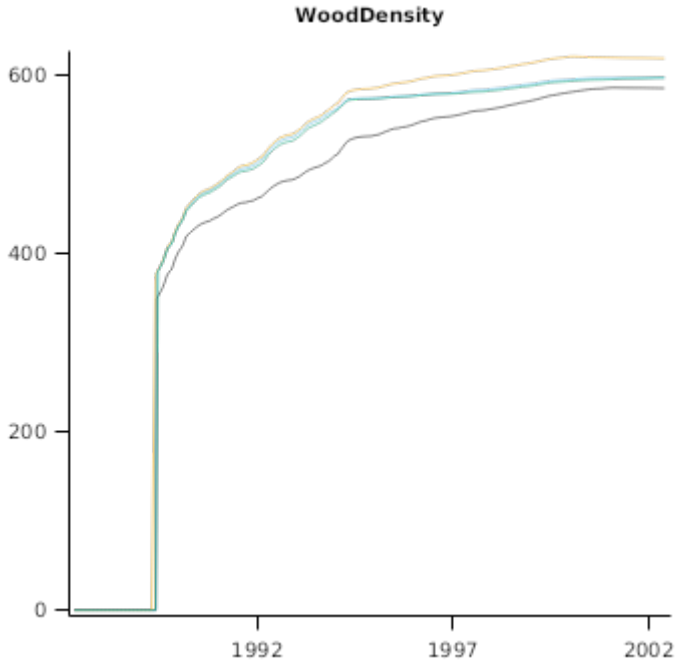

BA
40
20
0
1992
1997
2002


HtvsITSW
15
10
5
0
100000
200000
300000


Volub
300
200
100
0
1992
1997
2002


MAI
20
0
-20
-40
1992
1997
2002





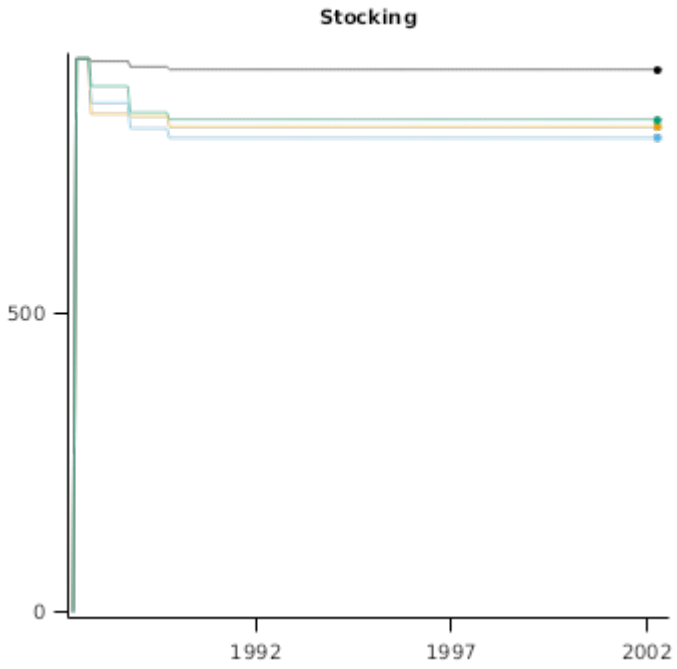
5.3.1.2 FPQToolara

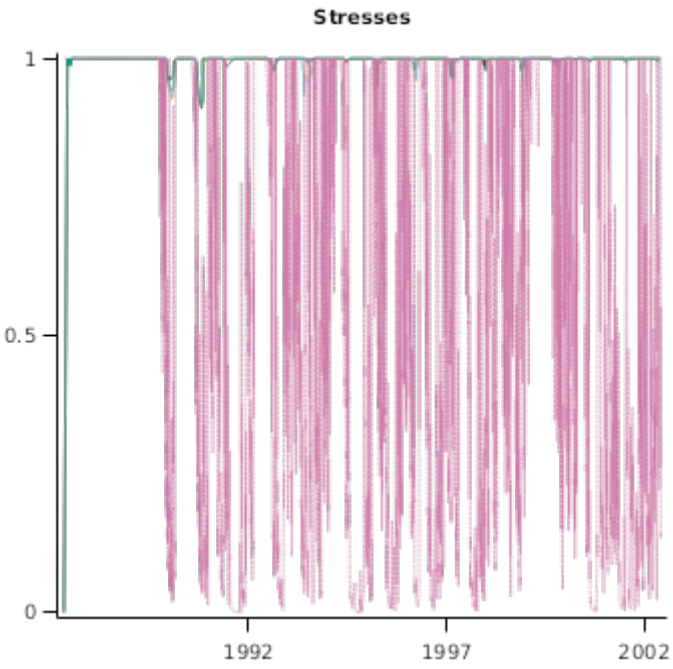
These data are from a genetics experiment in south-east Queensland described by Dieters et al., 2007. Four genotypes are compared: *P. elliottii* var. elliottii (PEE), *P. caribaea* var. hondurensis (PCH), the F1 hybrid, and the F2 hybrid. As only stem metrics were provided in the paper, genotypes were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

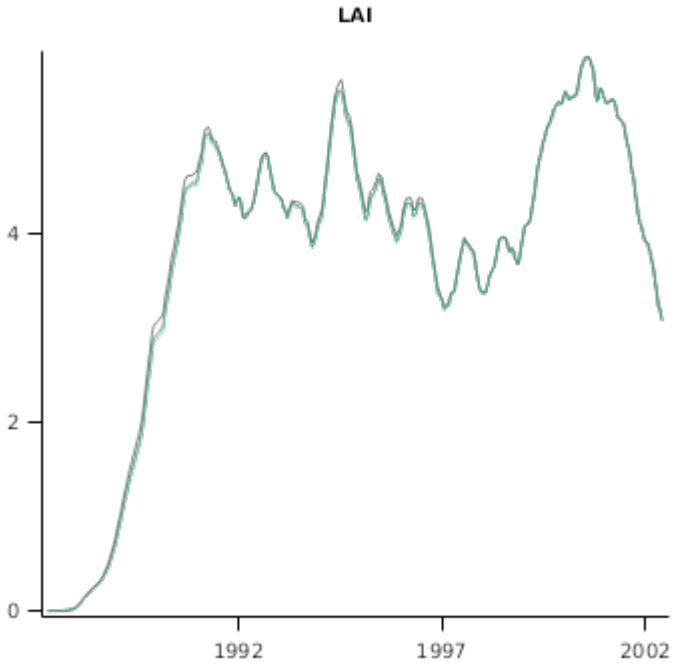
List of experiments.

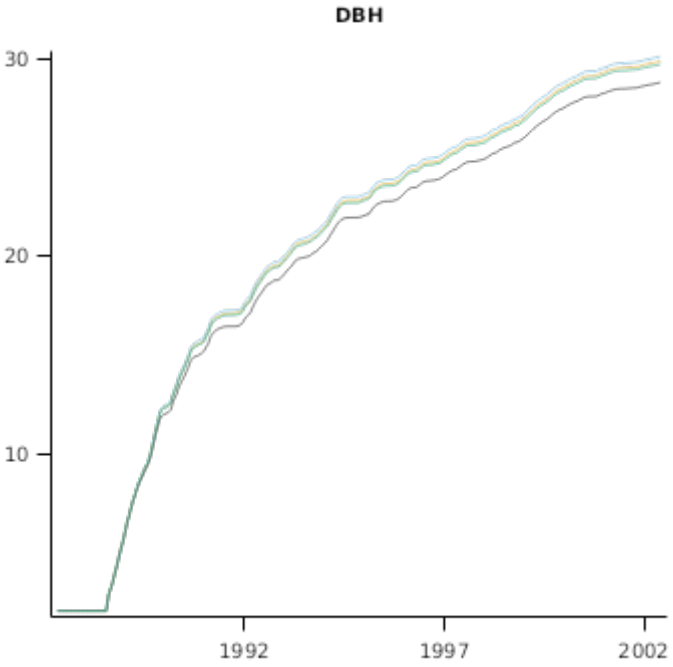
Experiment Name	Design (Number of Treatments)
FPQToolara	_ (4)

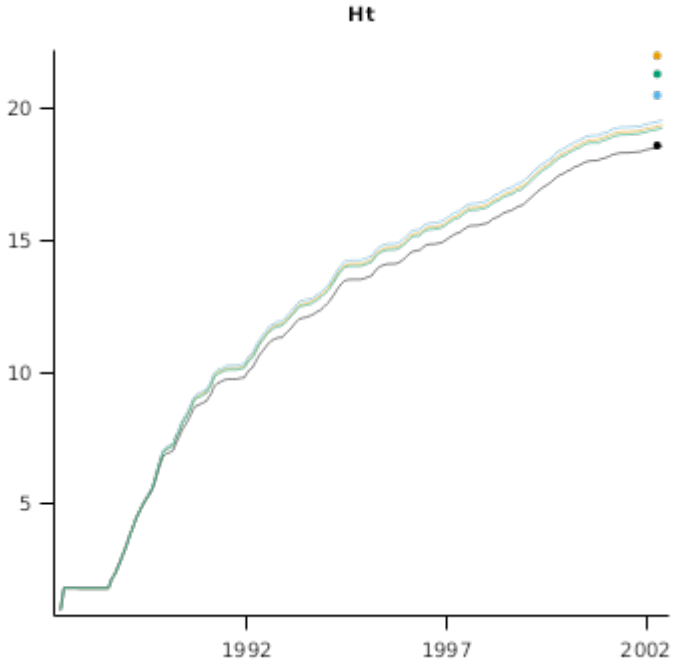
5.3.1.2.1 GraphsMetrics


Stocking
500
0
1992
1997
2002


Stresses
1
0.5
0
1992
1997
2002


LAI
4
2
0
1992
1997
2002


DBH
30
20
10
1992
1997
2002


Ht
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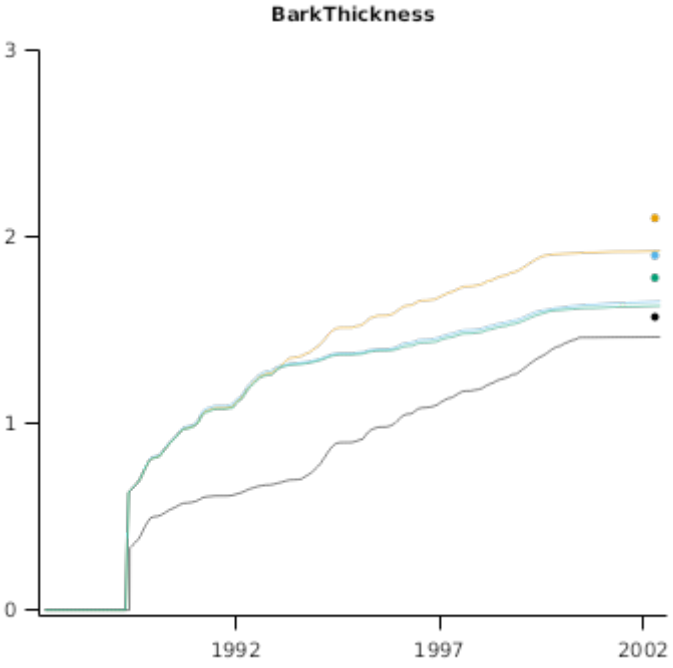
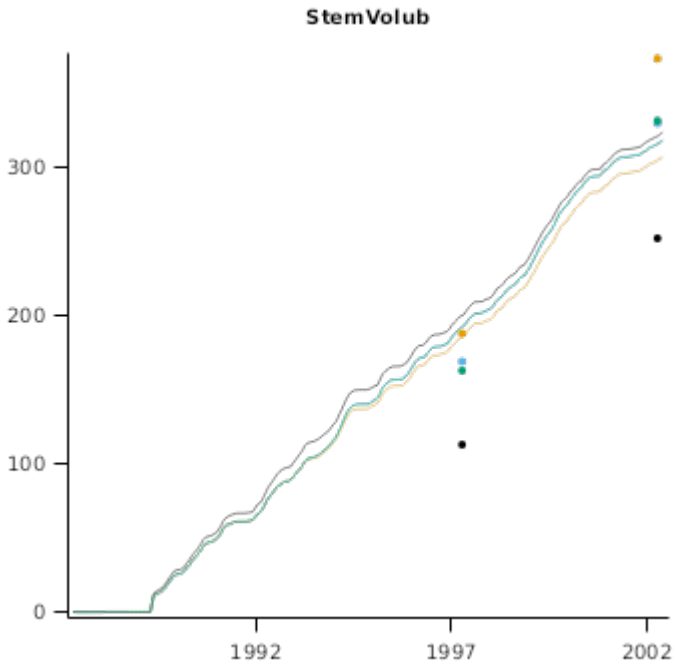
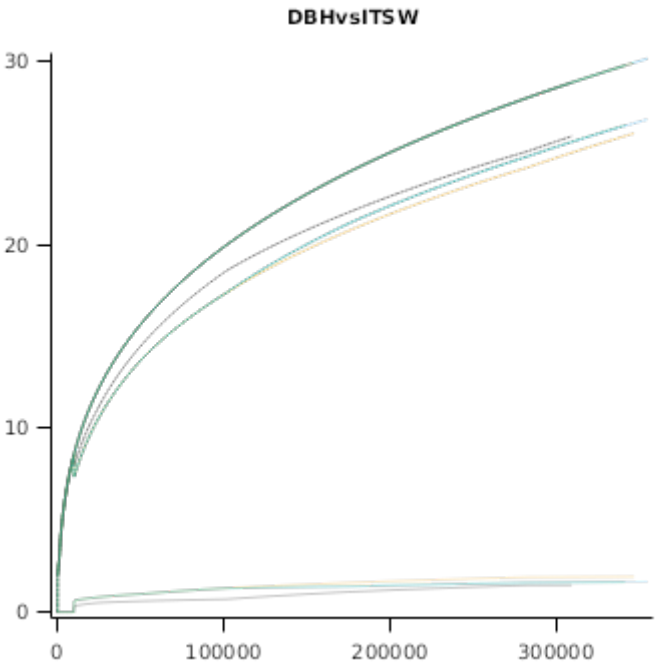
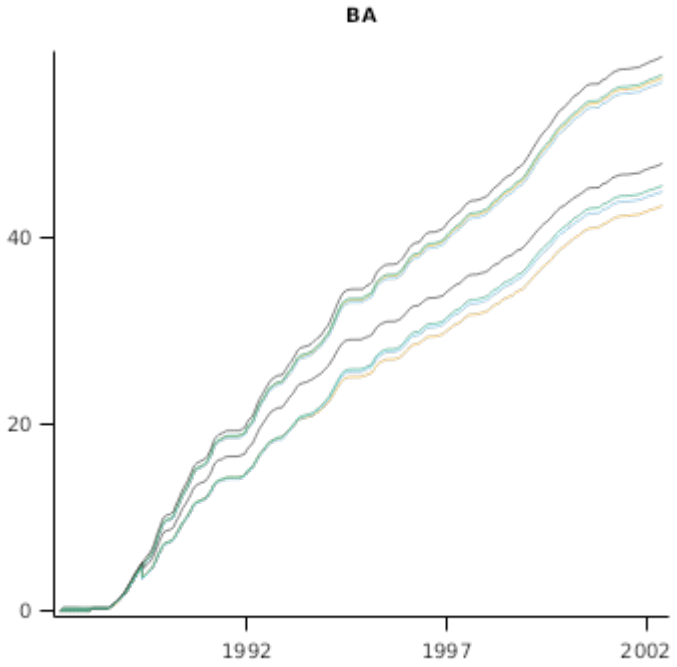
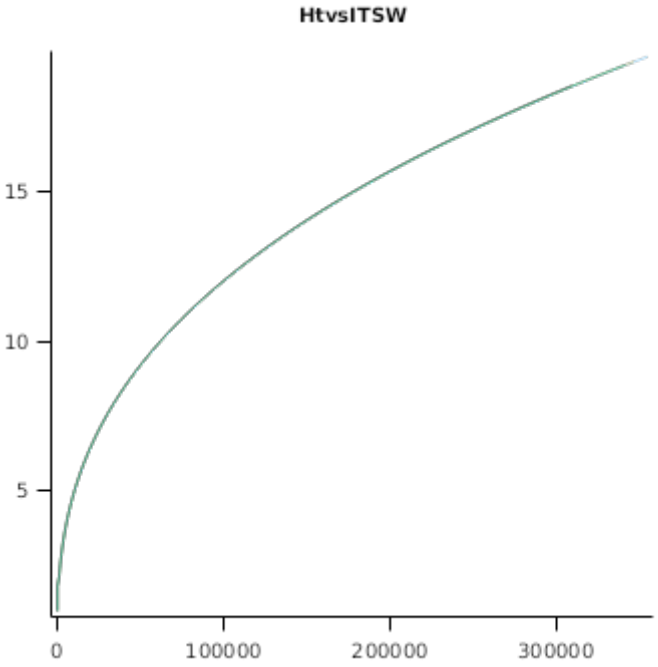
15
10
5
1992
1997
2002

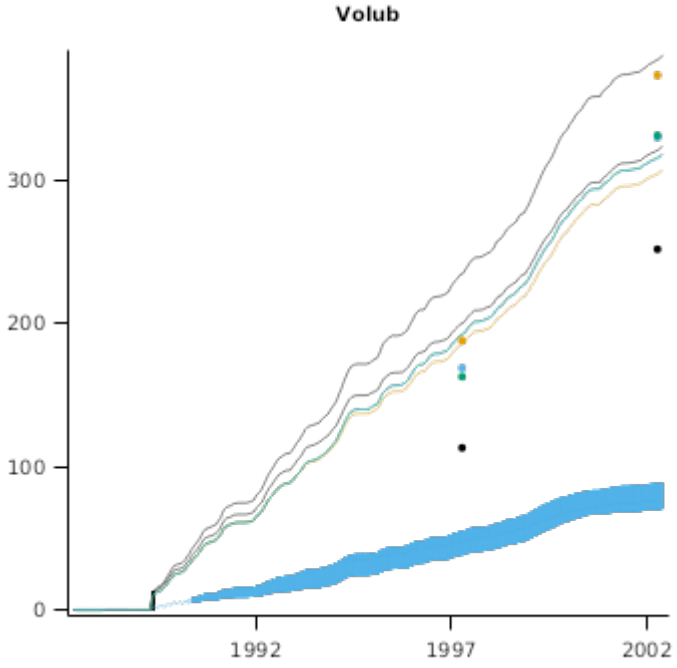

BarkThickness
3
2
1
0
1992
1997
2002

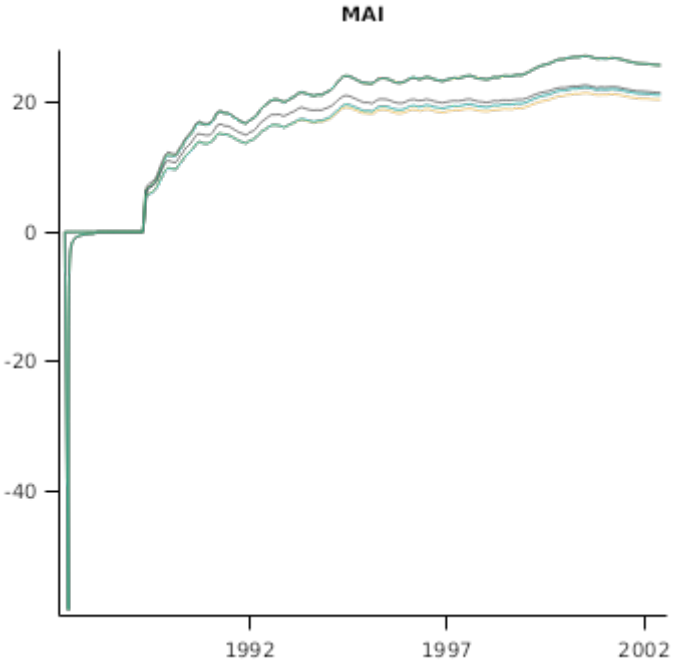

StemVolub
300
200
100
0
1992
1997
2002

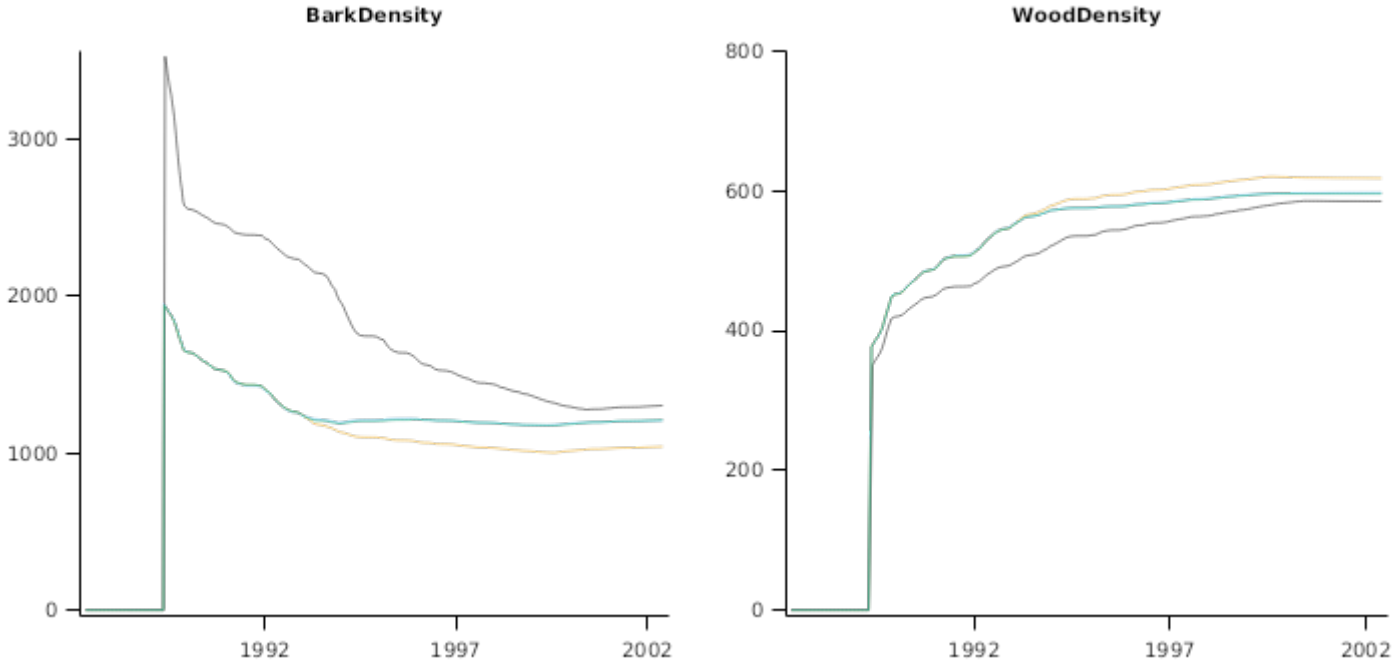

DBHvsITSW
30
20
10
0
0
100000
200000
300000


BA
40
20
0
1992
1997
2002


HtvsITSW
15
10
5
0
100000
200000
300000


Volub
300
200
100
0
1992
1997
2002


MAI
20
0
-20
-40
1992
1997
2002



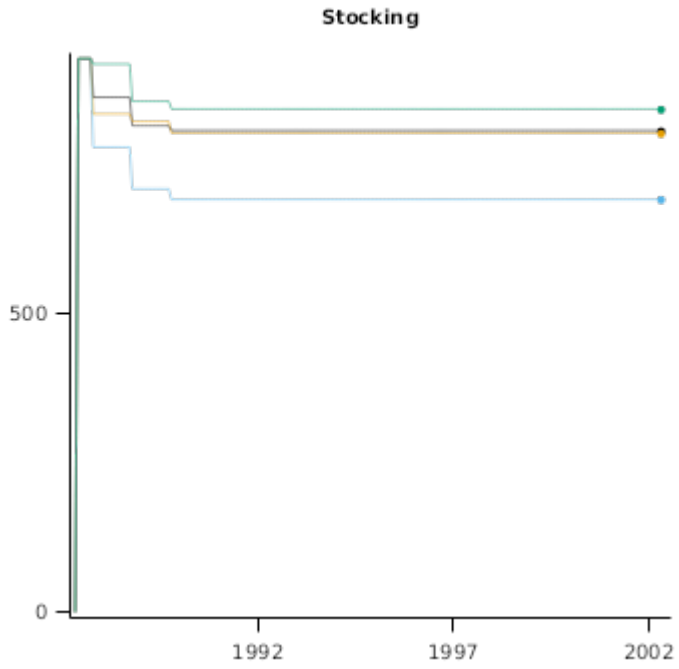
5.3.1.3 FPQTuan

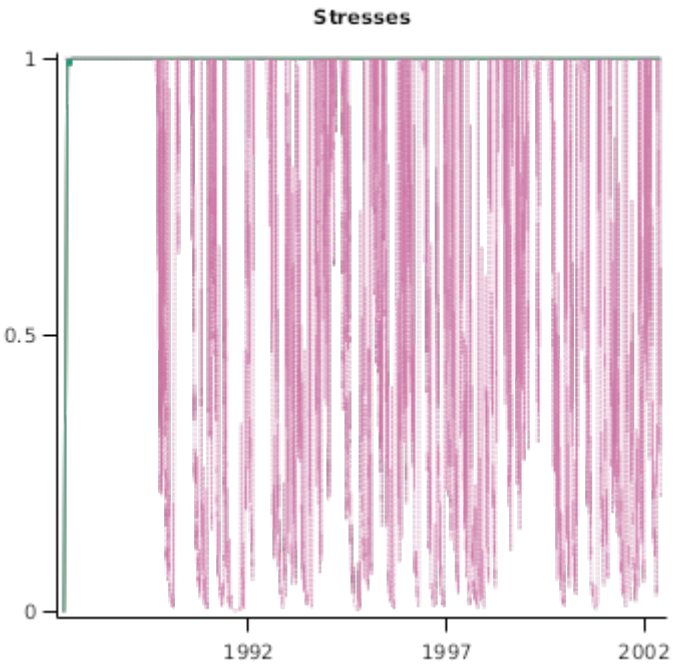
These data are from a genetics experiment in south-east Queensland described by Dieters et al., 2007. Four genotypes are compared: *P. elliottii* var. elliottii (PEE), *P. caribaea* var. hondurensis (PCH), the F1 hybrid, and the F2 hybrid. As only stem metrics were provided in the paper, genotypes were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

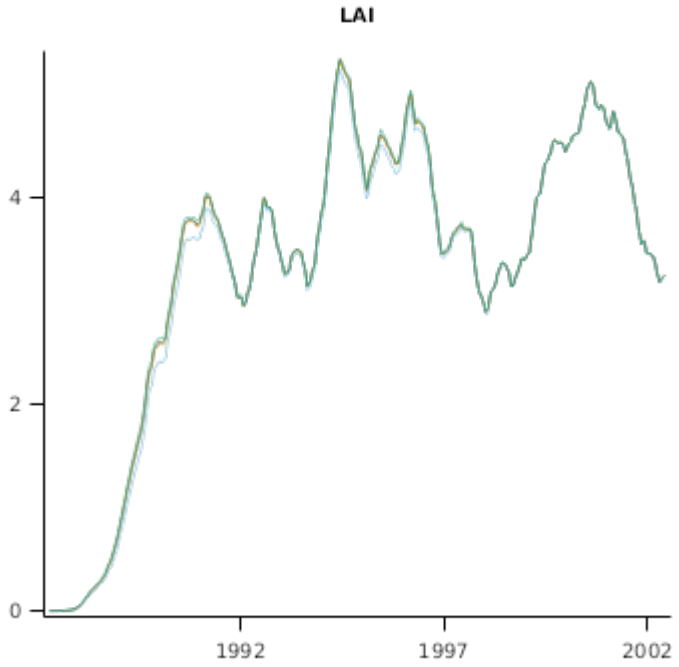
List of experiments.

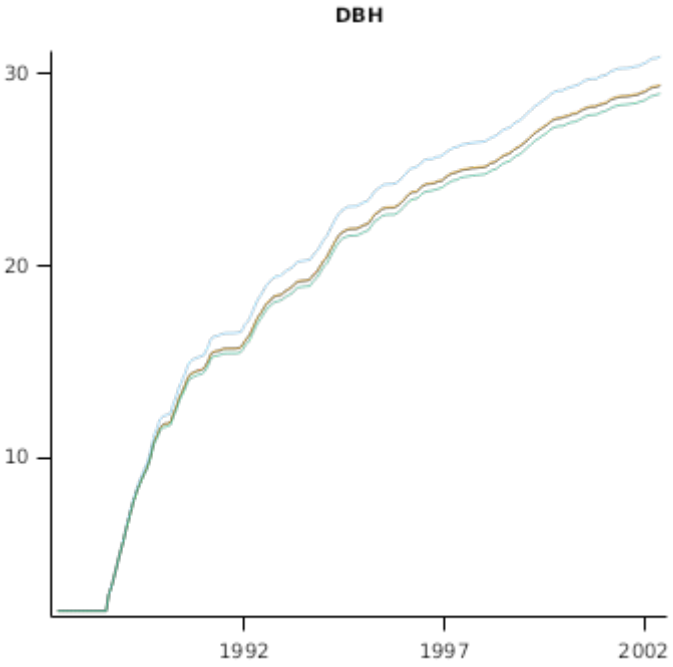
Experiment Name	Design (Number of Treatments)
FPQTuan	_ (4)

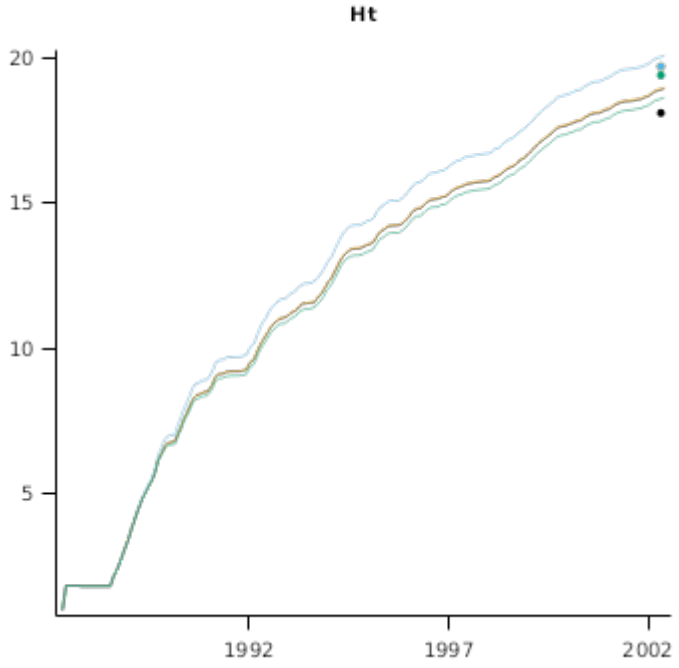
5.3.1.3.1 GraphsMetrics

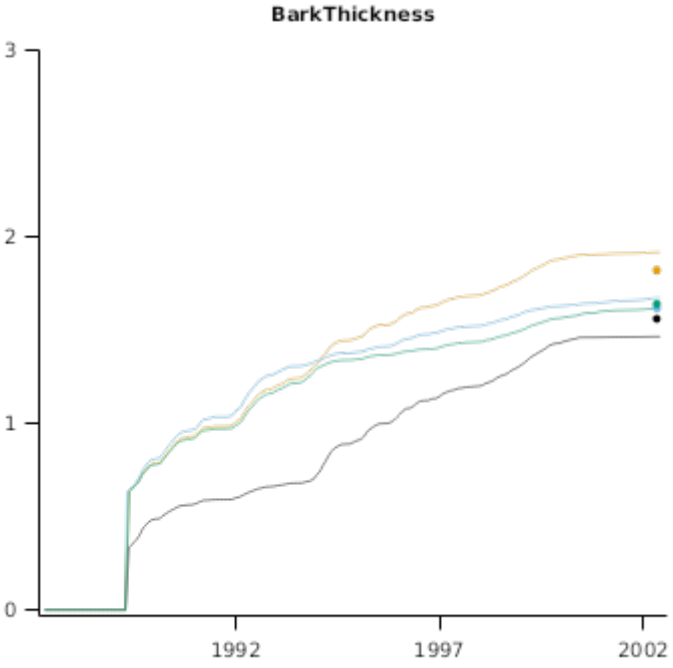

Stocking
500
0
1992
1997
2002

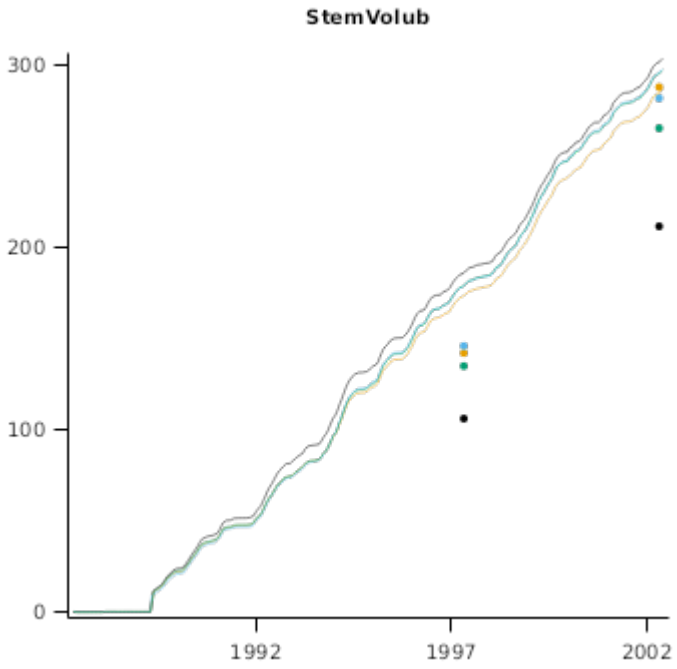

Stresses
1
0.5
0
1992
1997
2002

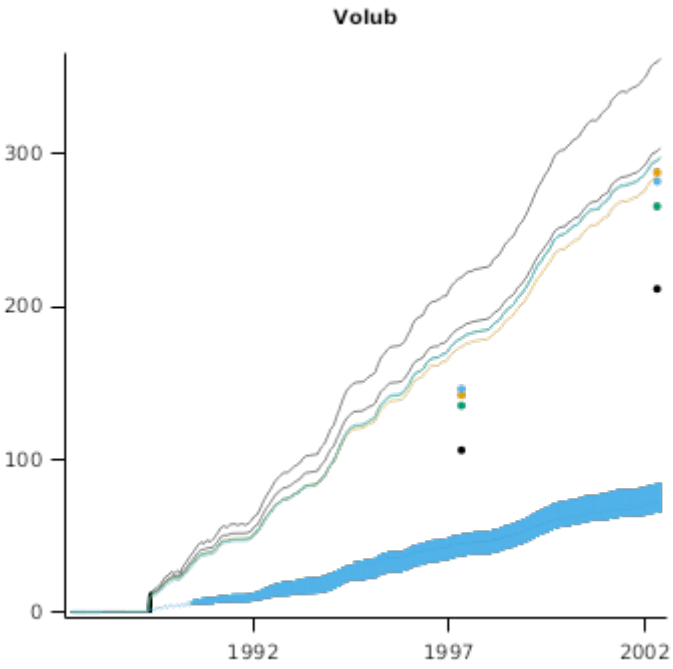

LAI
4
2
0
1992
1997
2002

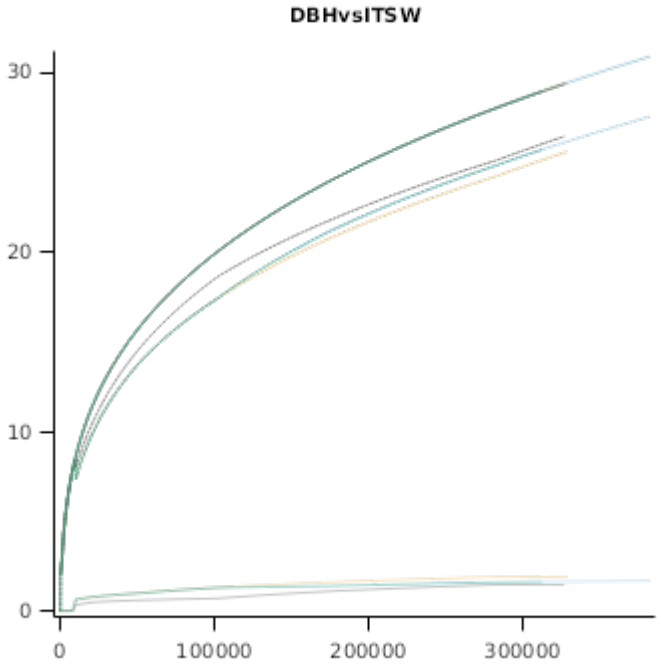

DBH
30
20
10
1992
1997
2002

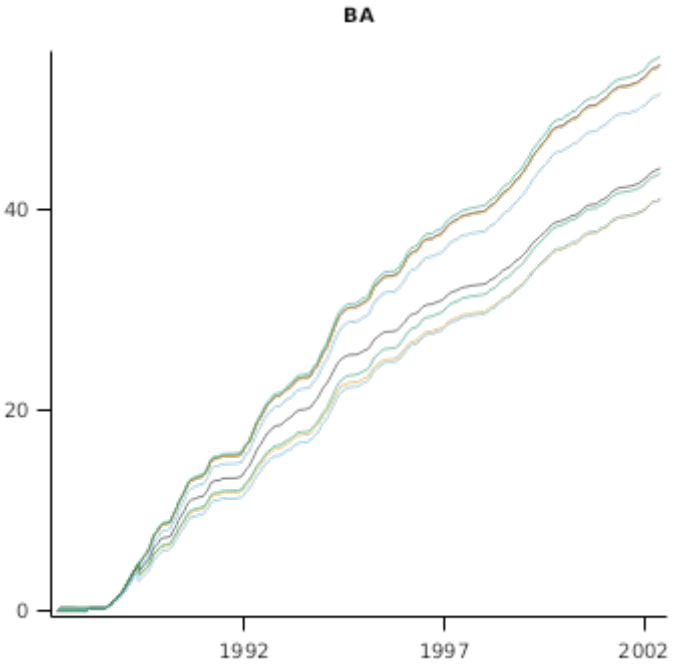

Ht
20
15
10
5
1992
1997
2002

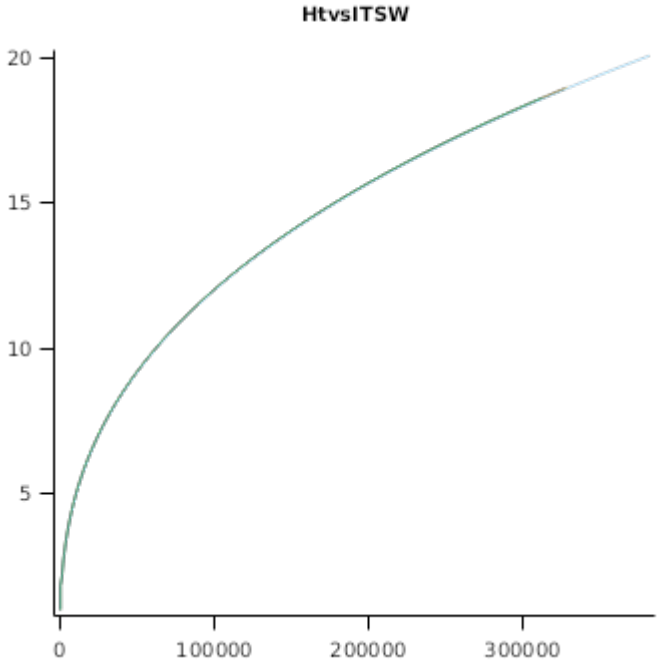

BarkThickness
3
2
1
0
1992
1997
2002

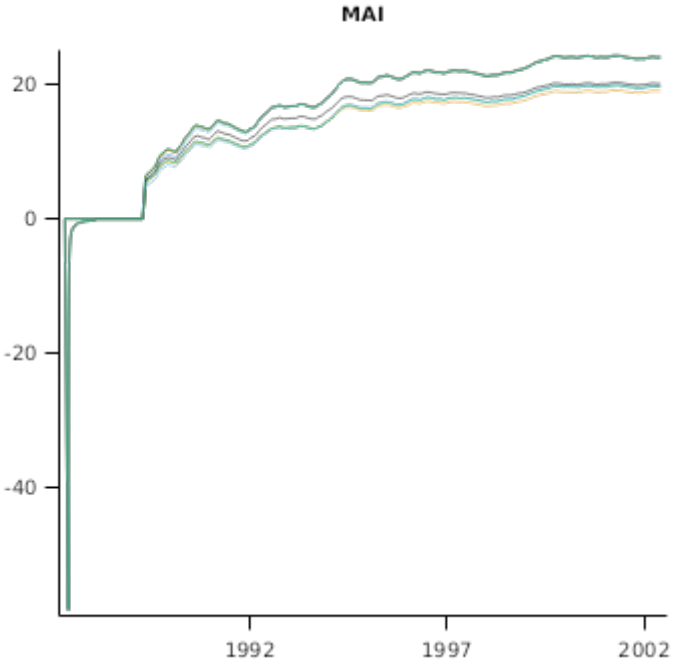

StemVolub
300
200
100
0
1992
1997
2002

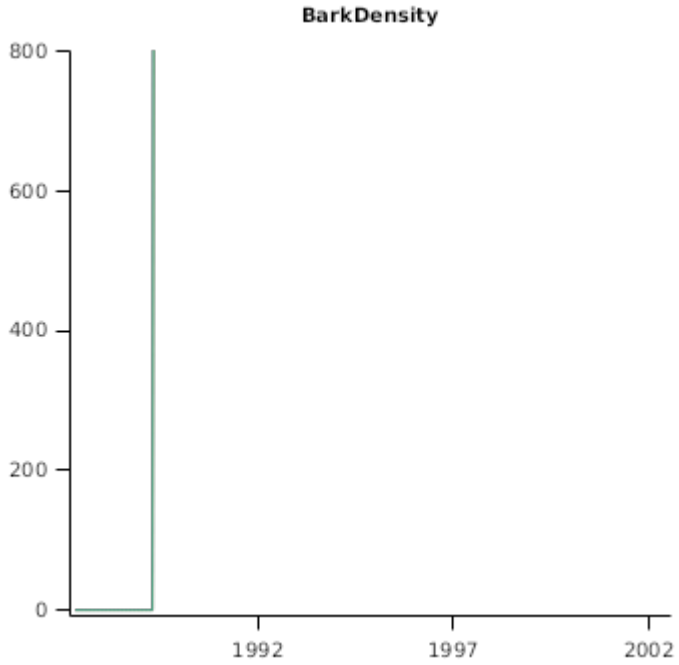

Volub
300
200
100
0
1992
1997
2002

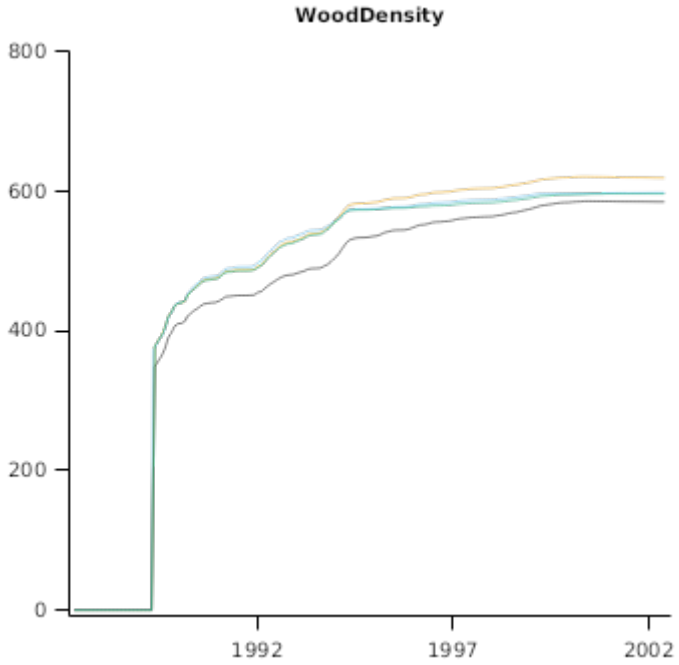

DBHvsITSW
30
20
10
0
0
100000
200000
300000


BA
40
20
0
1992
1997
2002


HtvsITSW
20
15
10
5
0
100000
200000
300000


MAI
20
0
-20
-40
1992
1997
2002



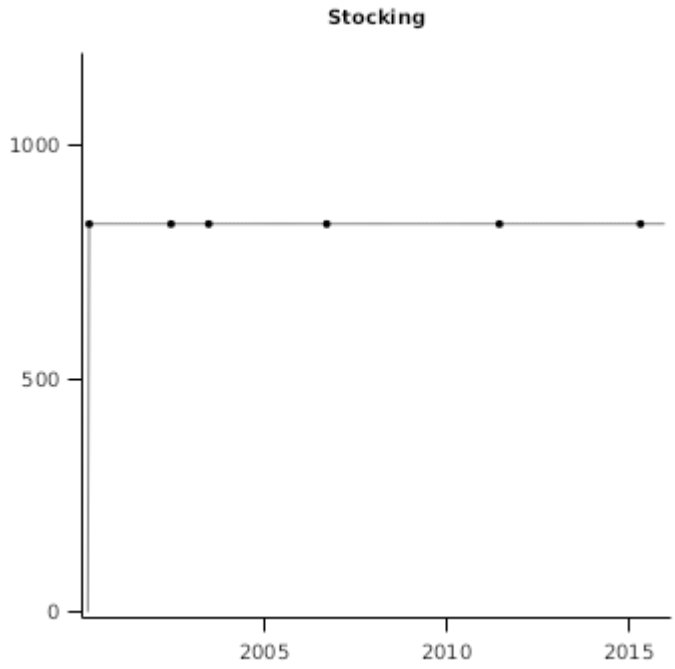


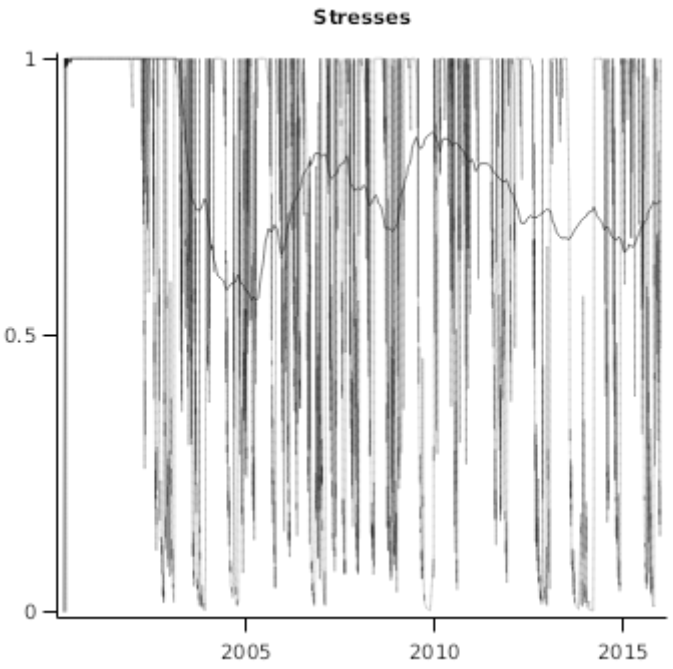
5.3.1.4 HQP248

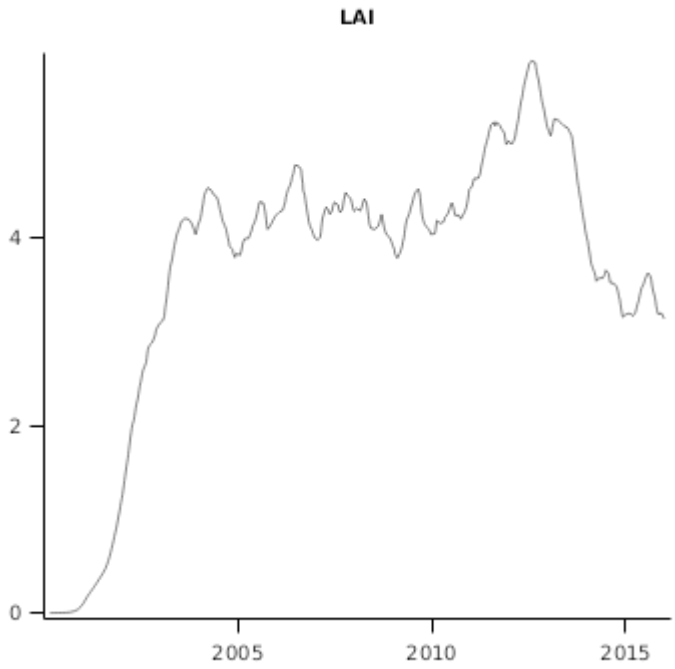
These data were kindly provided by Hancock Queensland Plantations (HQPlantations, HQP) from Experiment 248 MBR, which was established to determine the most appropriate taxa (including stock production systems) and site preparation prescription(s) for use on wet sites in south-east Queensland. As the 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).

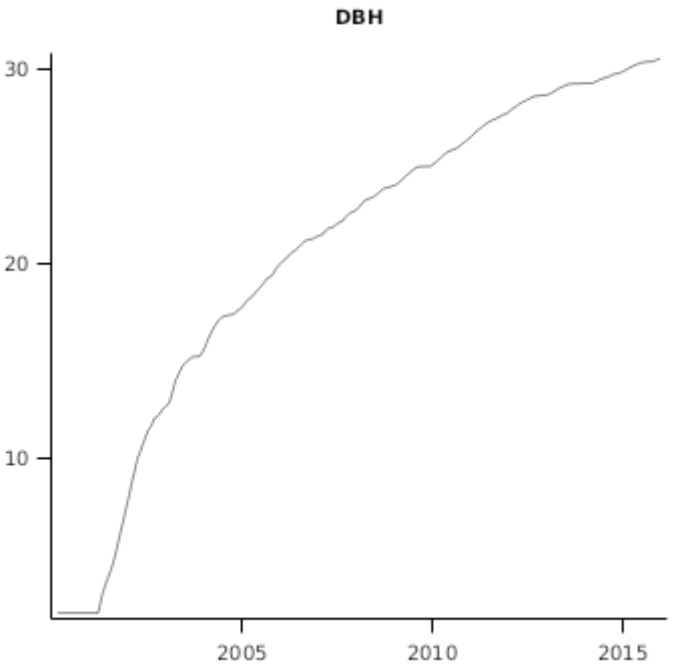
5.3.1.4.1 Graphs

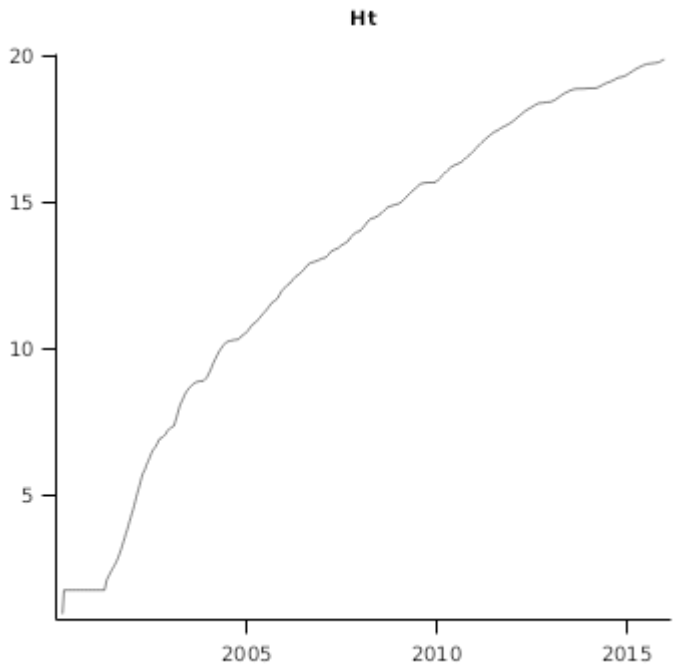
5.3.1.4.1.1 GraphsMetrics

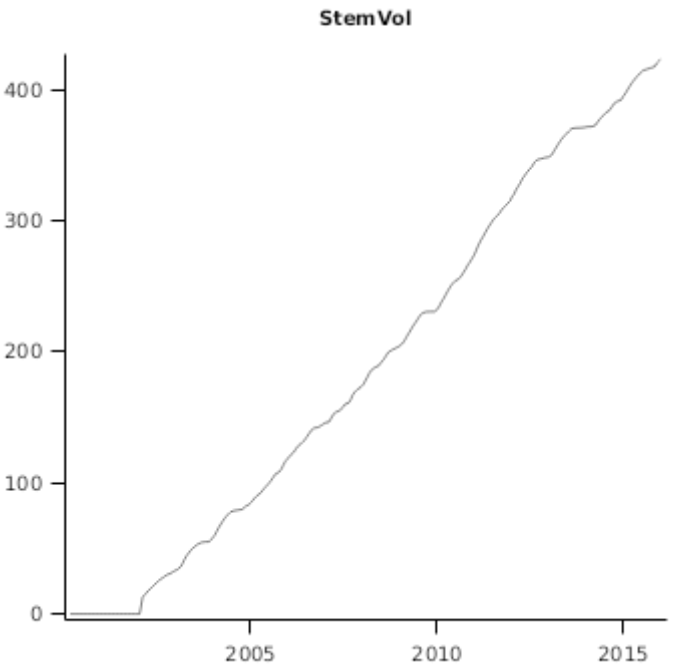

Stocking
1000
500
0
2005
2010
2015

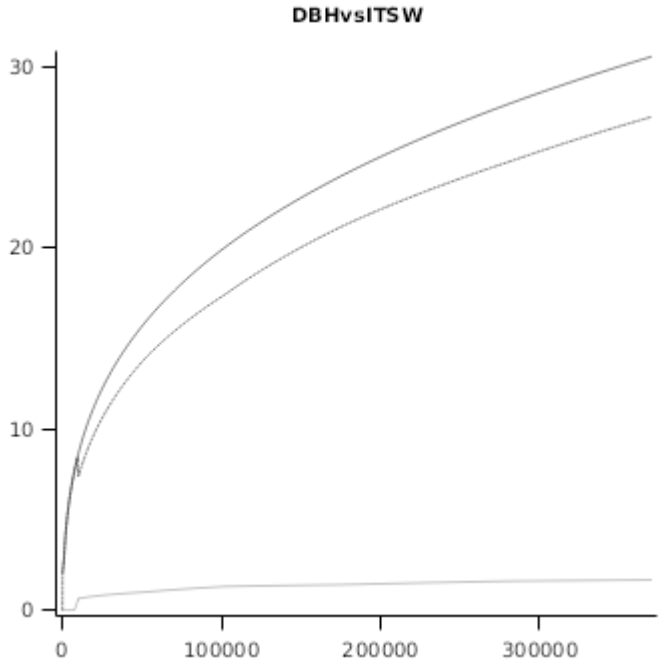

Stresses
1
0.5
0
2005
2010
2015

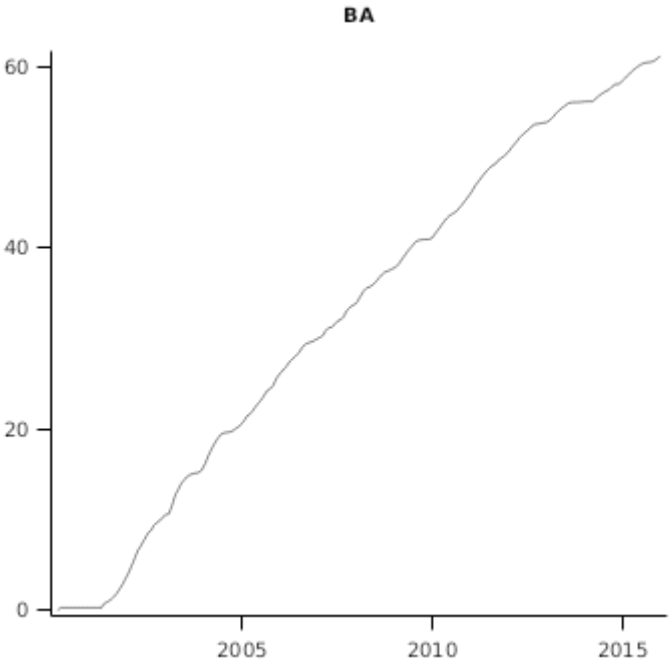

LAI
4
2
0
2005
2010
2015

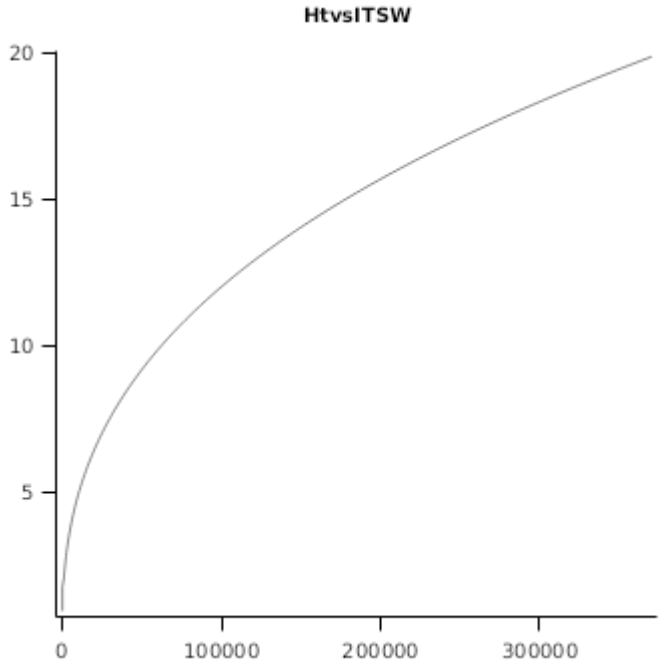

DBH
30
20
10
2005
2010
2015

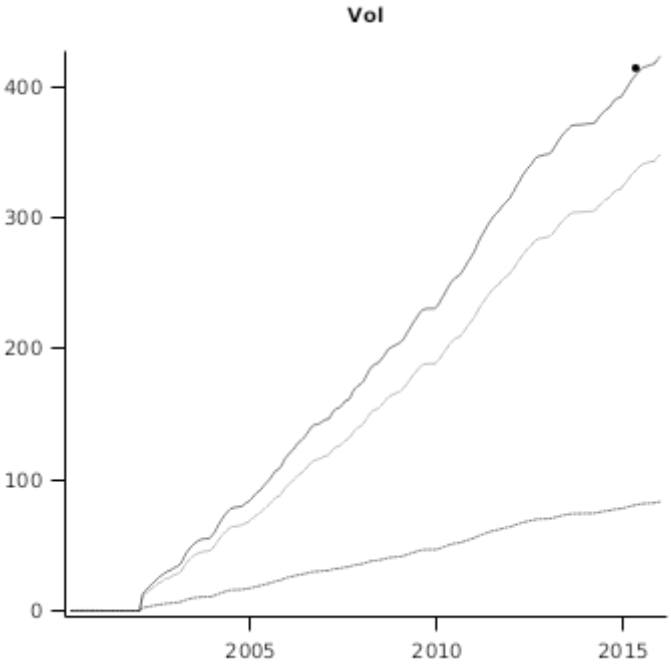

Ht
20
15
10
5
2005
2010
2015

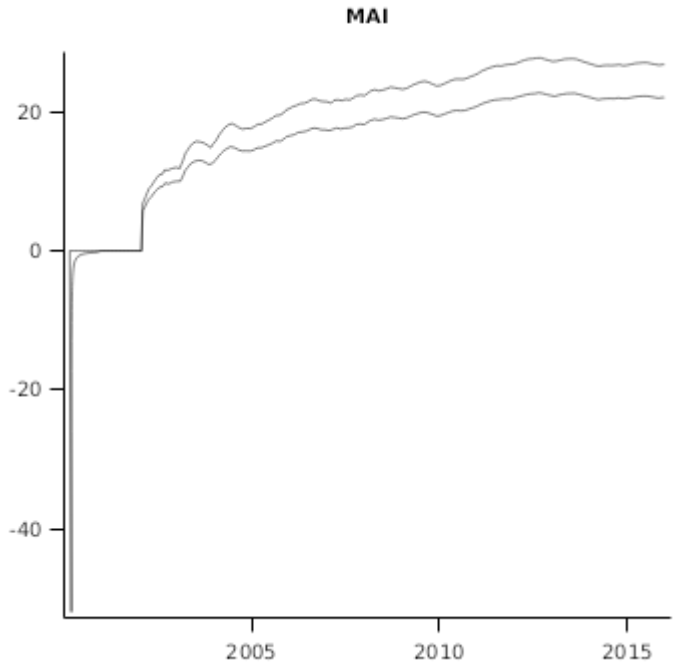

StemVol
400
300
200
100
0
2005
2010
2015

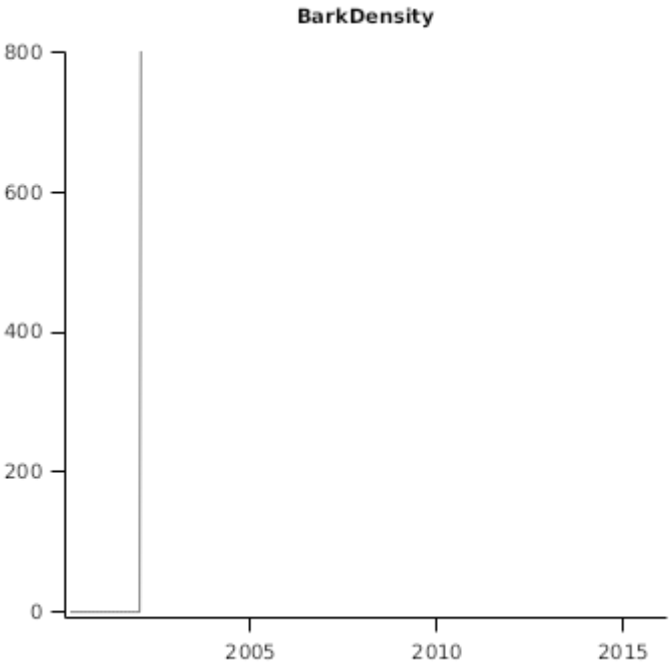

DBHvsITSW
30
20
10
0
0
100000
200000
300000

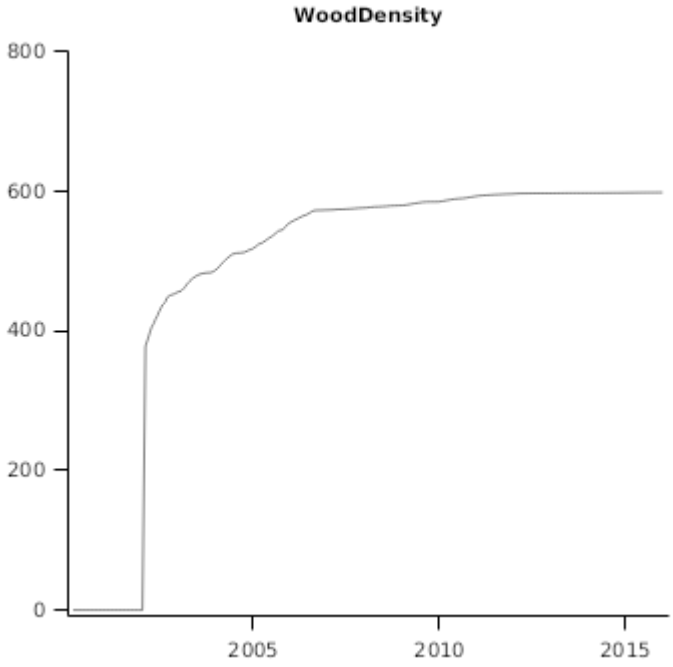

BA
60
40
20
0
2005
2010
2015


HtvsITSW
20
15
10
5
0
100000
200000
300000


Vol
400
300
200
100
0
2005
2010
2015


MAI
20
0
-20
-40
2005
2010
2015


BarkDensity
800
600
400
200
0
2005
2010
2015

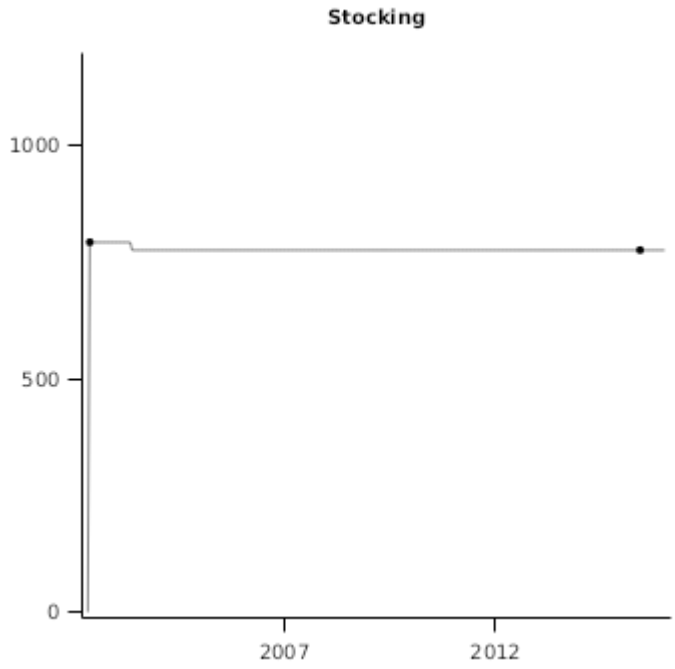


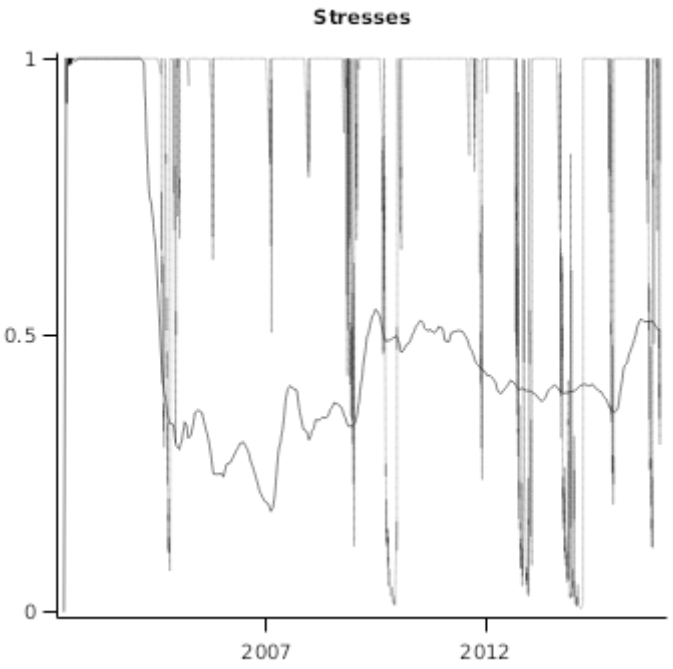
5.3.1.5 HQP251

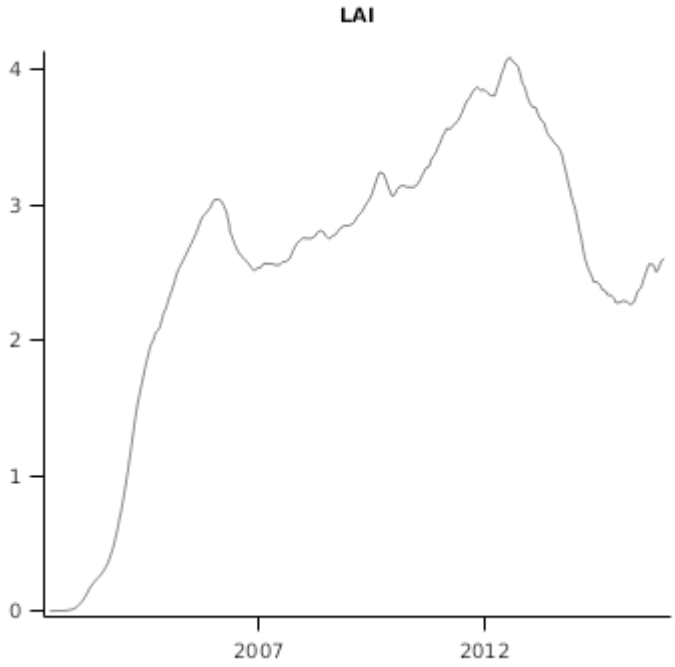
These data were kindly provided by Hancock Queensland Plantations (HQPlantations) from Experiment 251 MBR, which was established to investigate the impact of various 2R site preparation methods at a high-mounded first rotation (1R) site with hard-setting soil in south-east Queensland. As the model was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

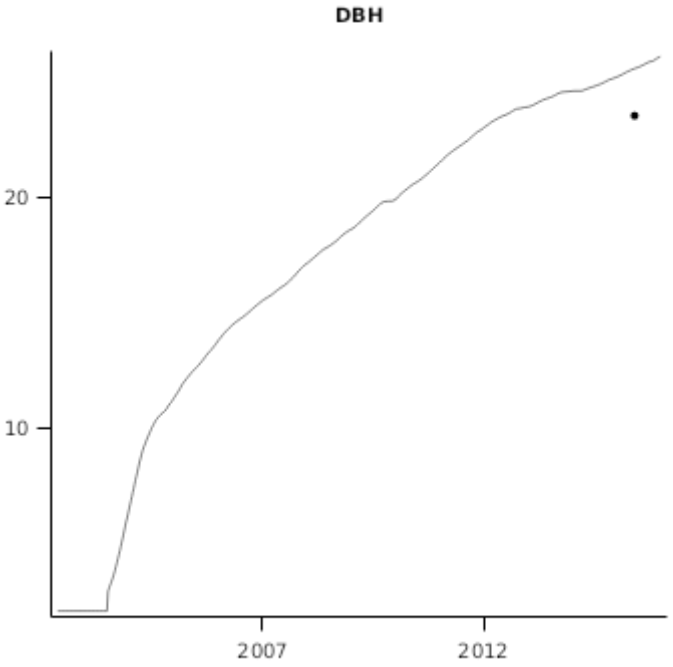
5.3.1.5.1 Graphs

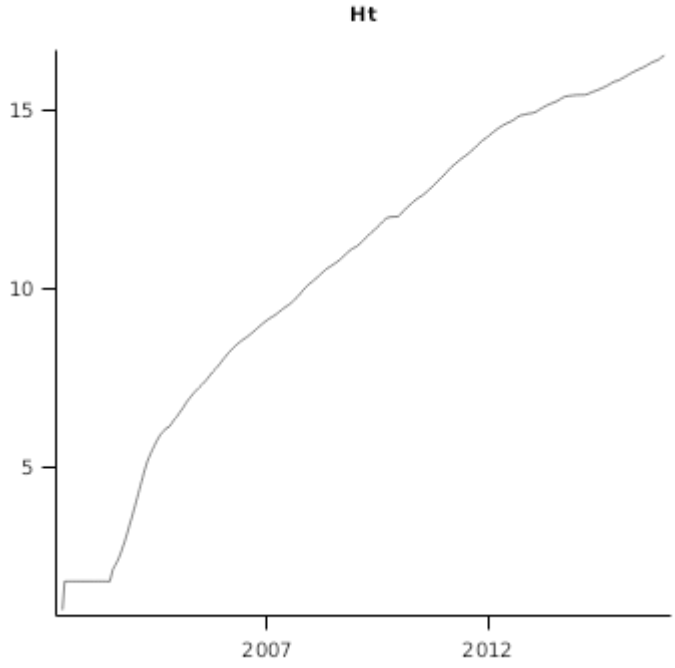
5.3.1.5.1.1 GraphsMetrics

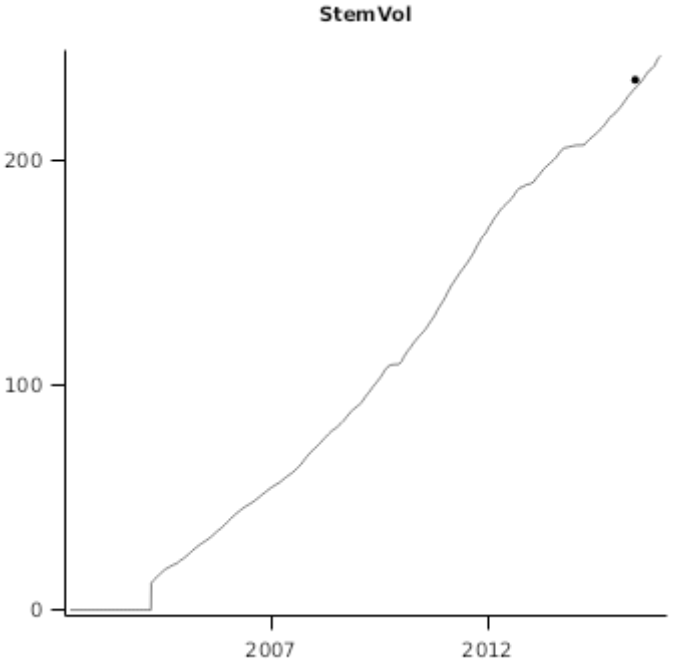

Stocking
1000
500
0
2007
2012

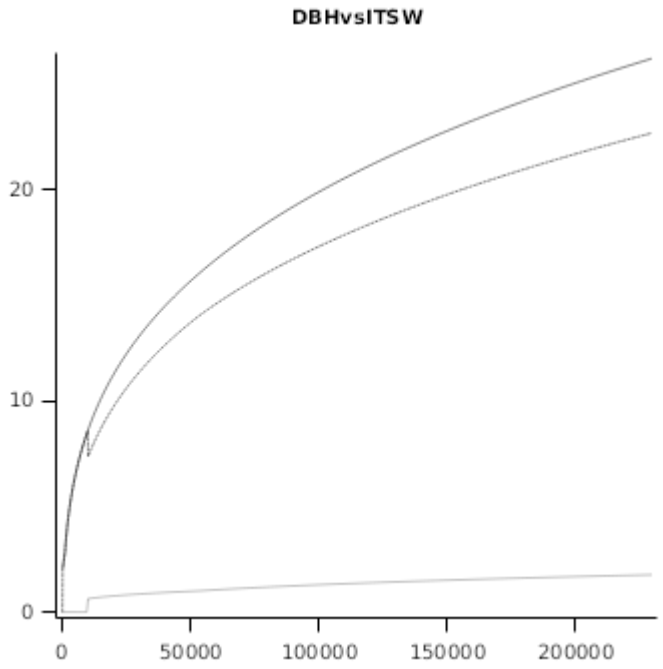

Stresses
1
0.5
0
2007
2012

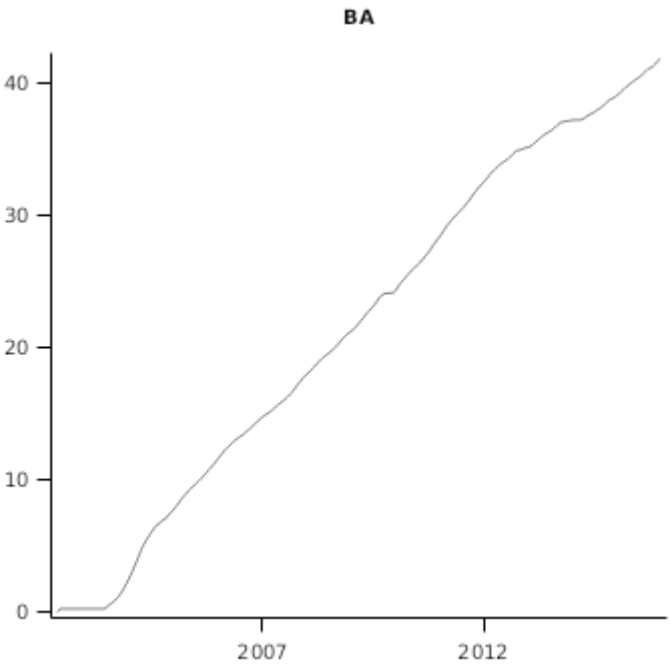

LAI
4
3
2
1
0
2007
2012

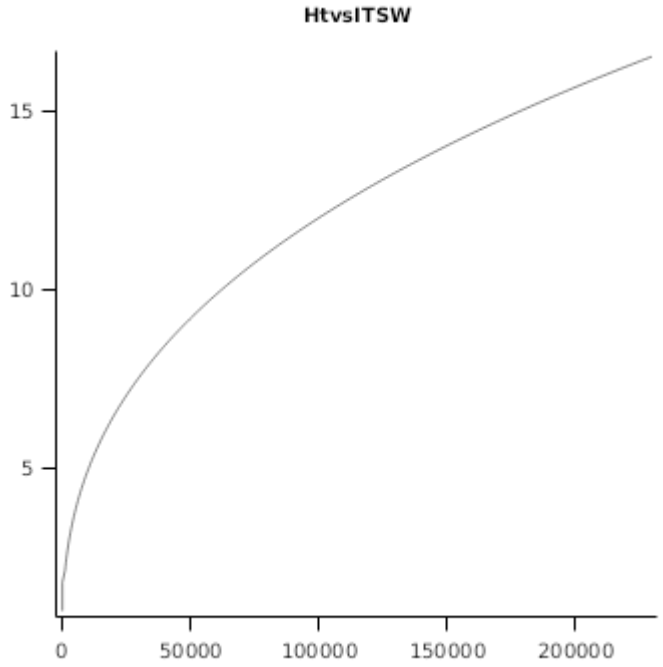

DBH
20
10
2007
2012

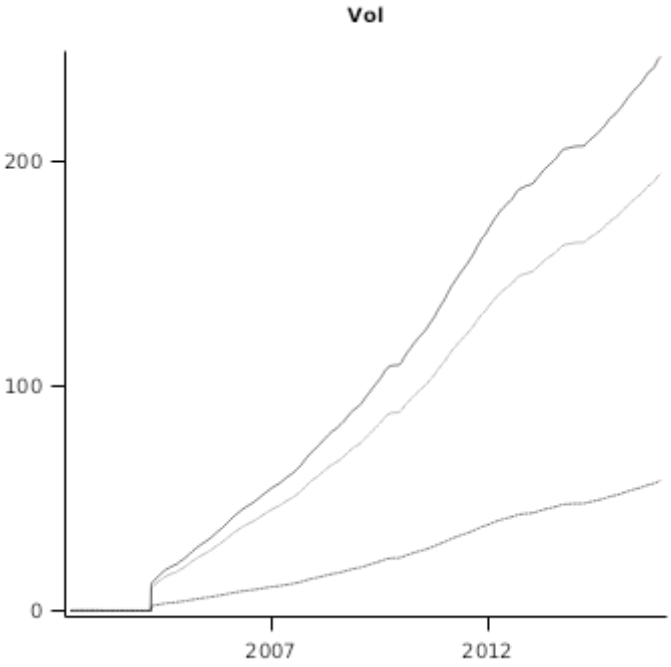

Ht
15
10
5
2007
2012

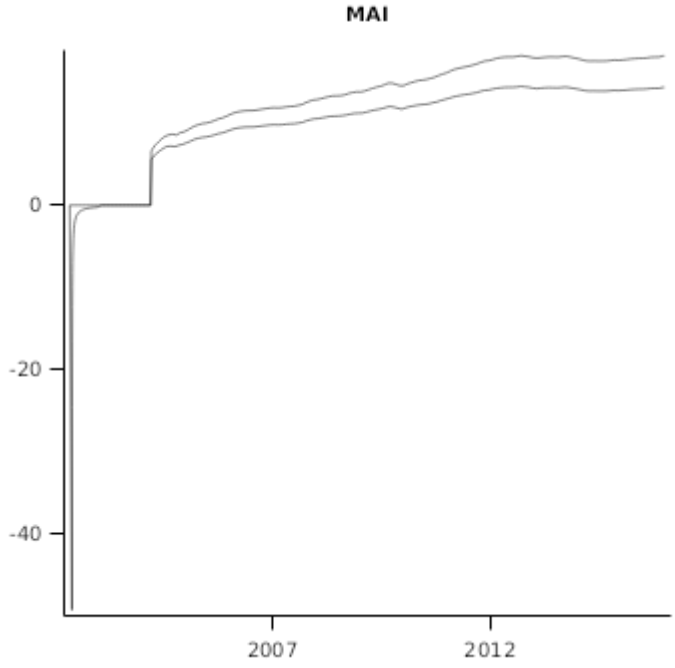

StemVol
200
100
0
2007
2012

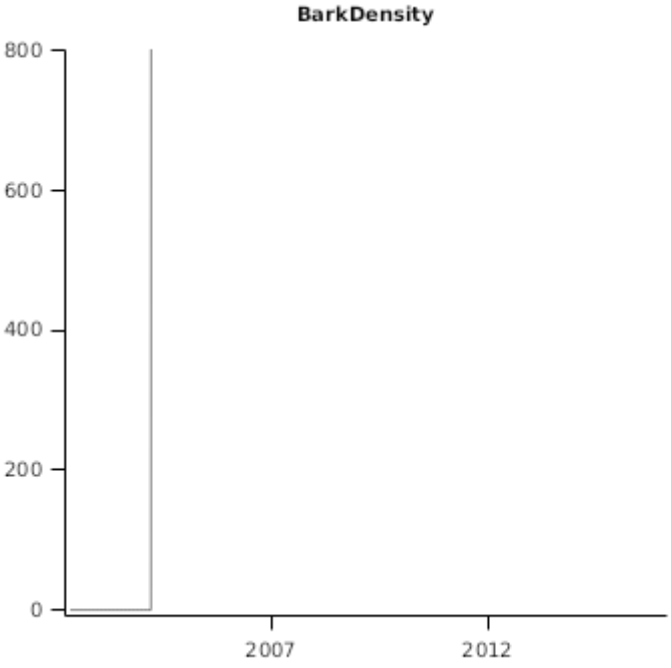

DBHvsITSW
20
10
0
0
50000
100000
150000
200000

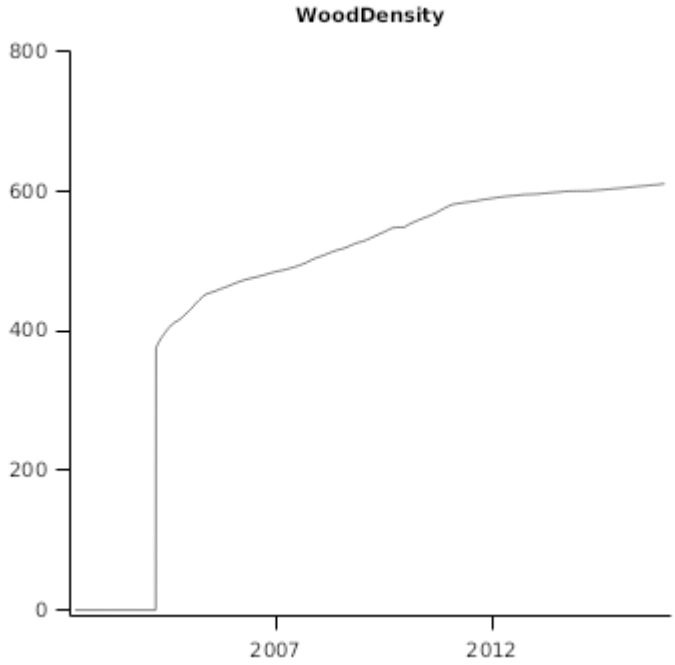

BA
40
30
20
10
0
2007
2012


HtvsITSW
15
10
5
0
50000
100000
150000
200000


Vol
200
100
0
2007
2012


MAI
0
-20
-40
2007
2012


BarkDensity
800
600
400
200
0
2007
2012



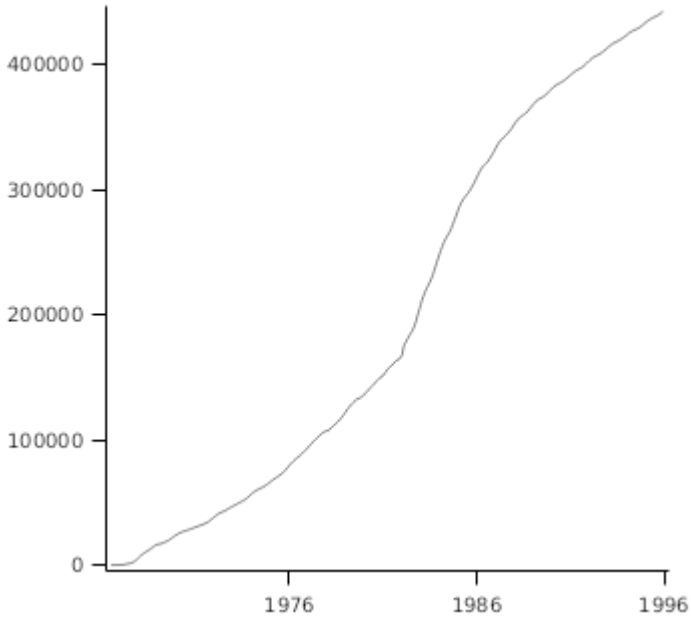
5.3.1.6 HQP321R1

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.

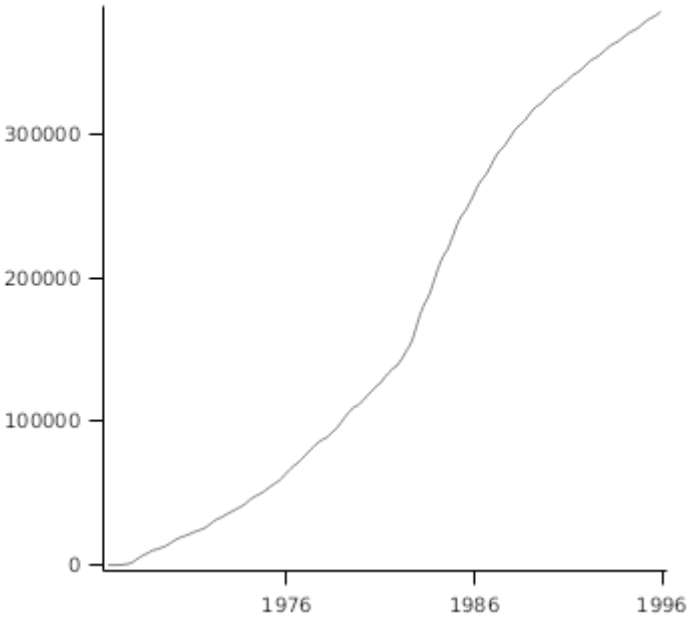
5.3.1.6.1 Graphs

5.3.1.6.1.1 GraphsWeights

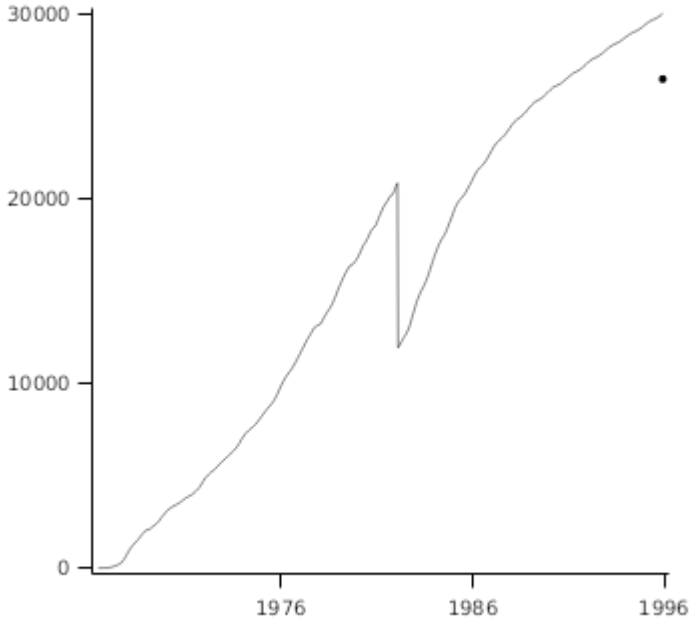
IndividualTreeLiveWt



IndividualStemWt

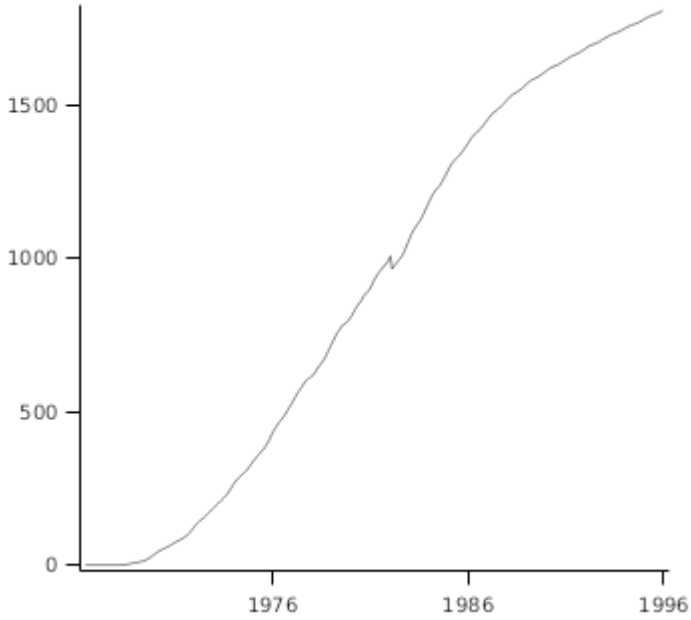


AboveGroundWt

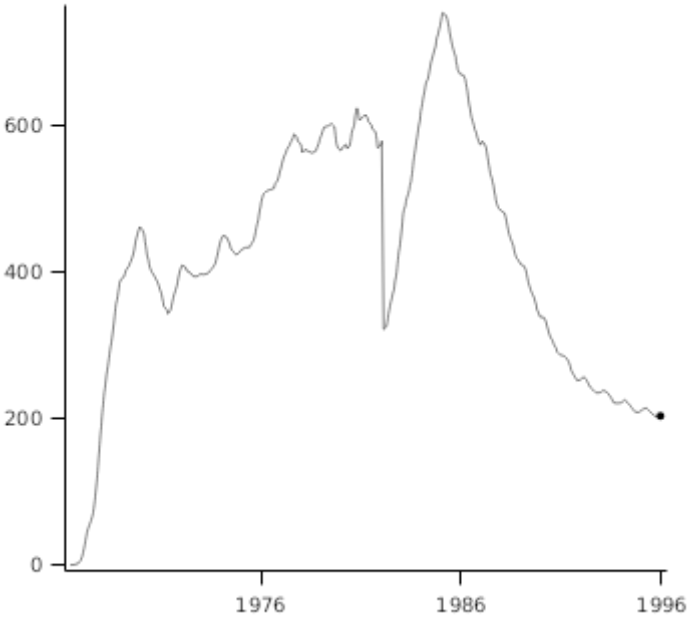


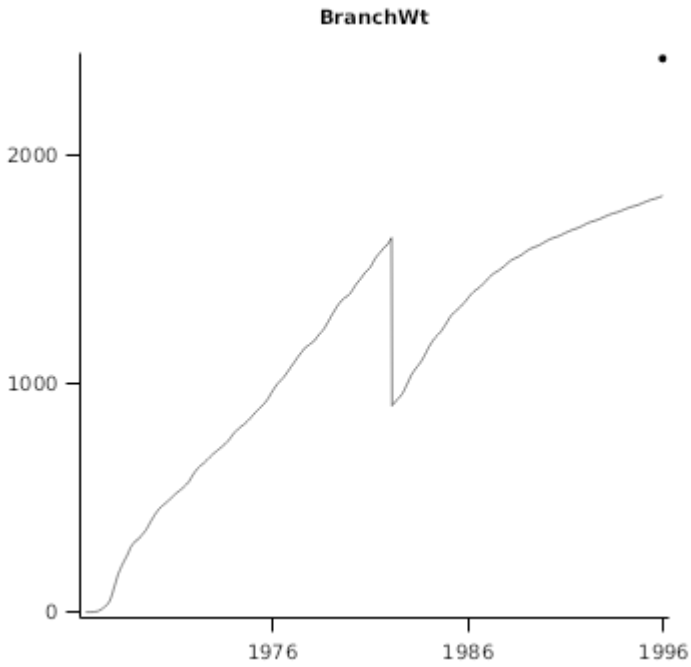
ComponentWts

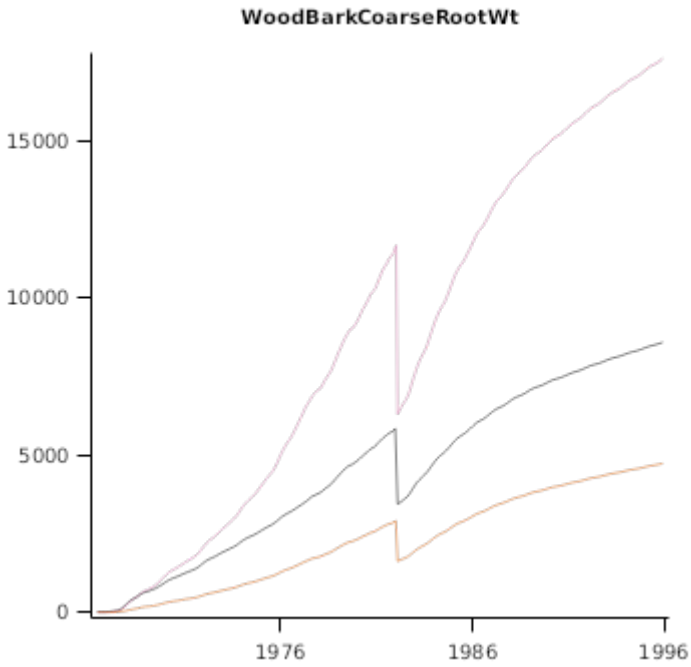
ConeWt

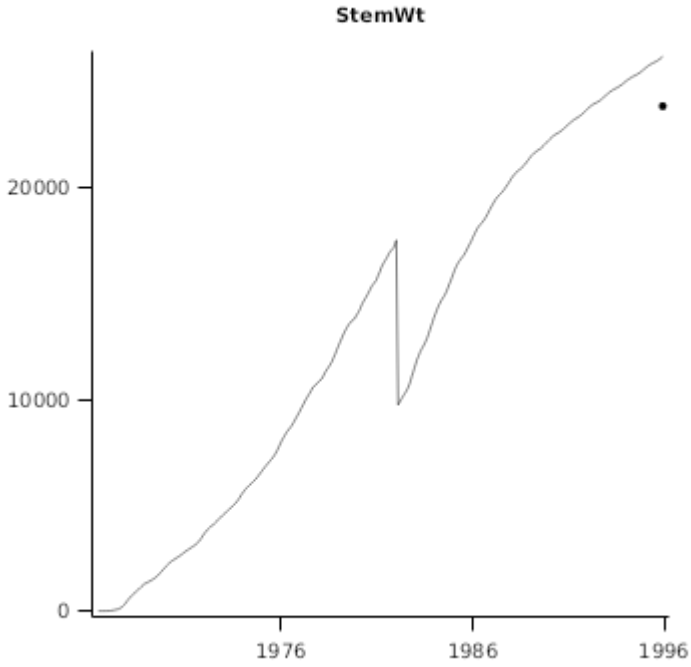


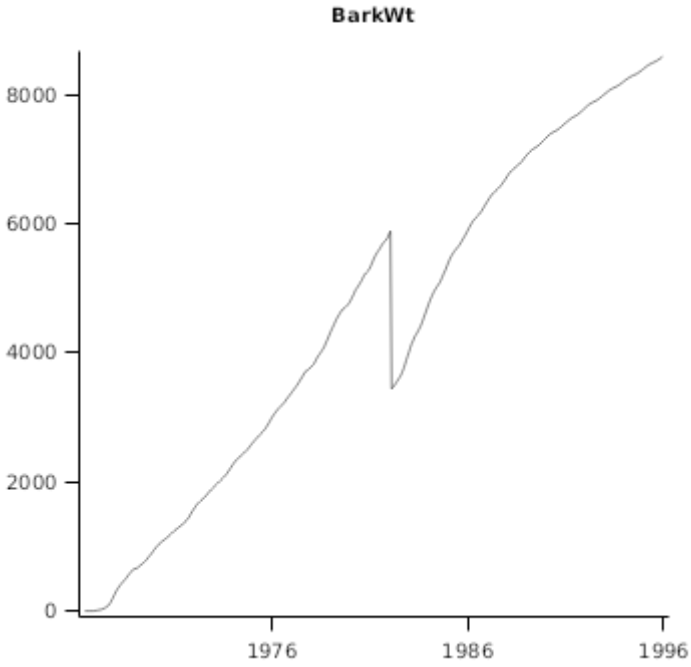
LeafWt

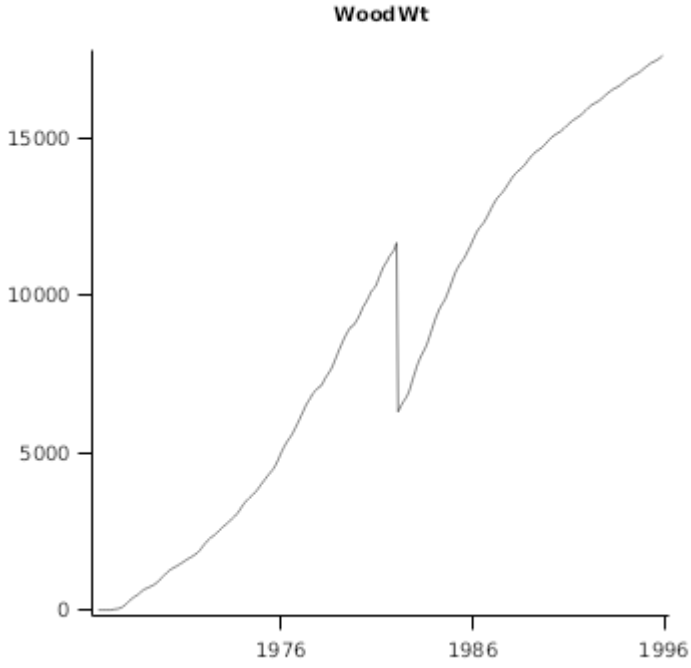


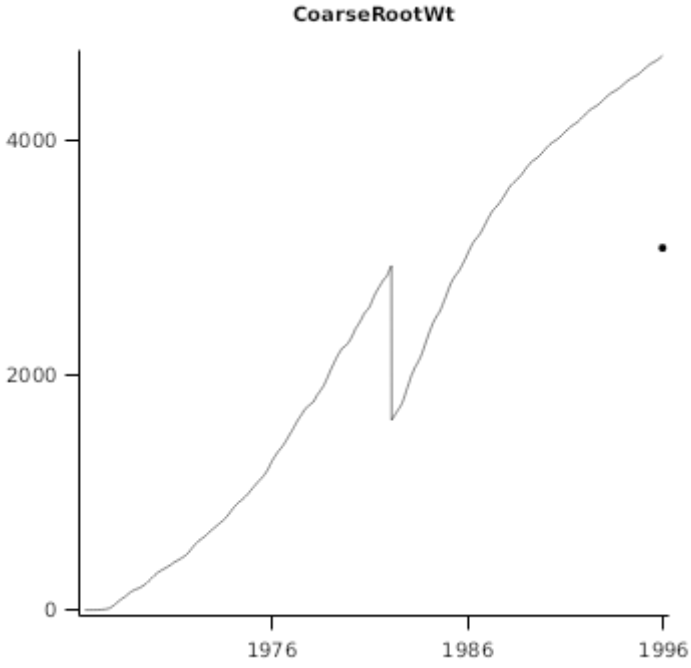

BranchWt
2000
1000
0
1976
1986
1996

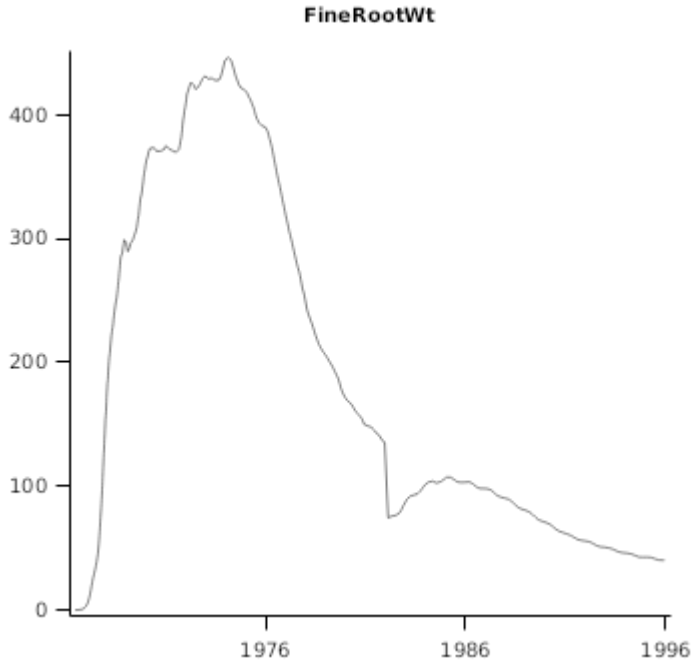

WoodBarkCoarseRootWt
15000
10000
5000
0
1976
1986
1996

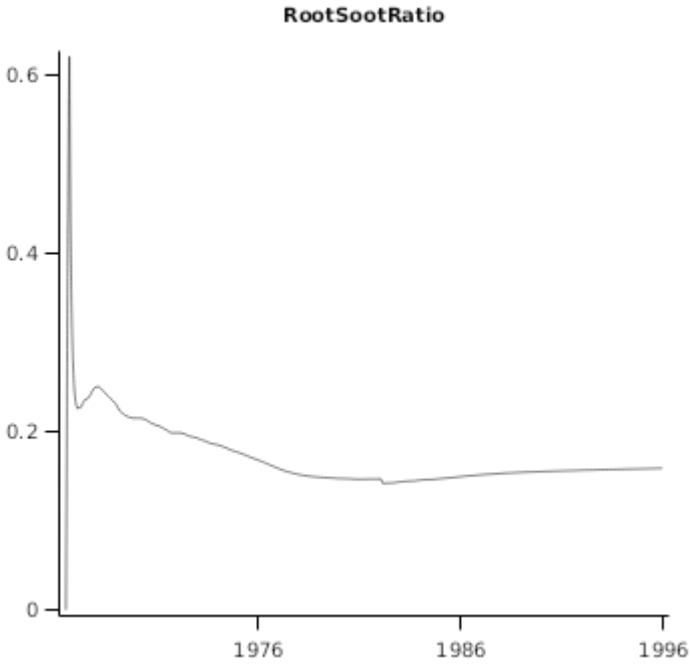

StemWt
20000
10000
0
1976
1986
1996


BarkWt
8000
6000
4000
2000
0
1976
1986
1996


WoodWt
15000
10000
5000
0
1976
1986
1996

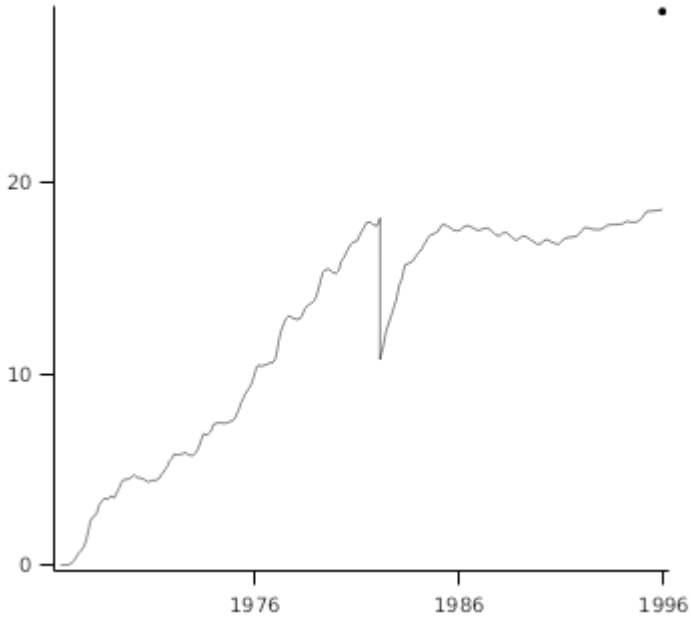

CoarseRootWt
4000
2000
0
1976
1986
1996





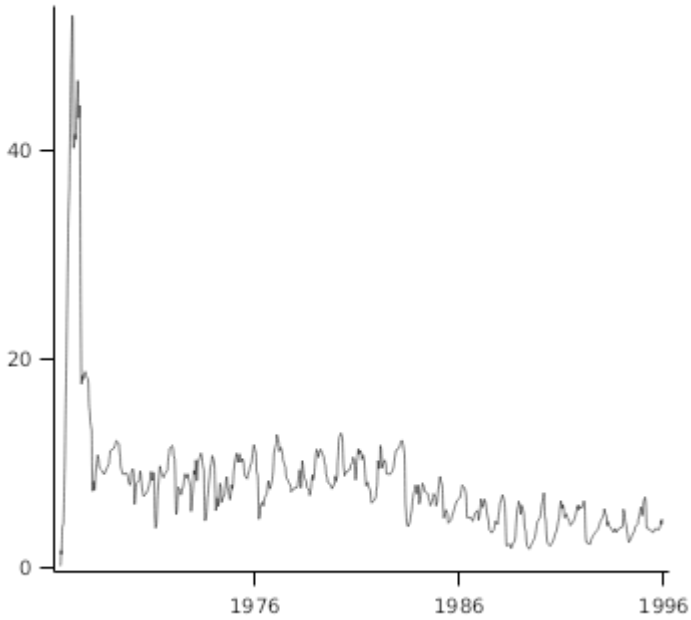
5.3.1.6.1.2 GraphsN

AboveGroundN

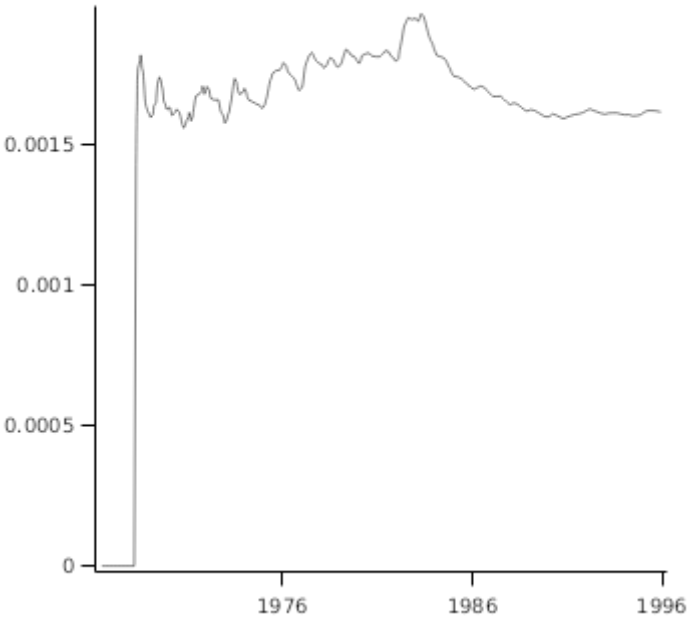


NNM

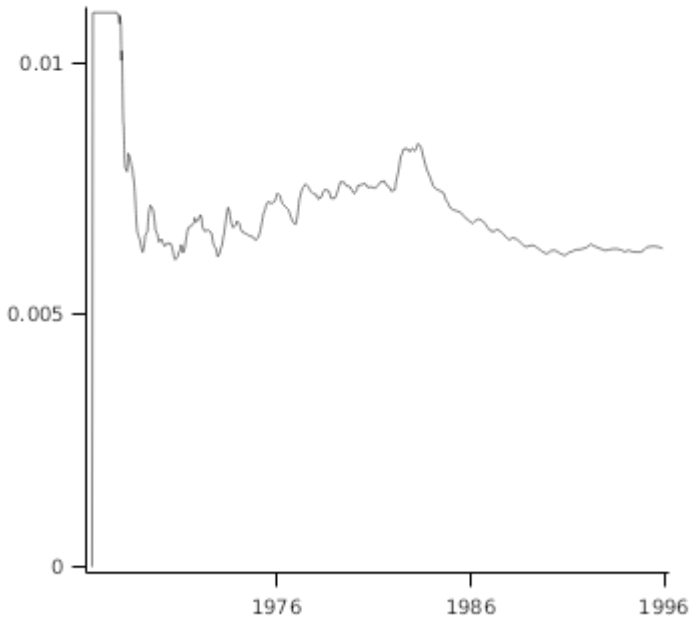
MineralNTotalkgpha



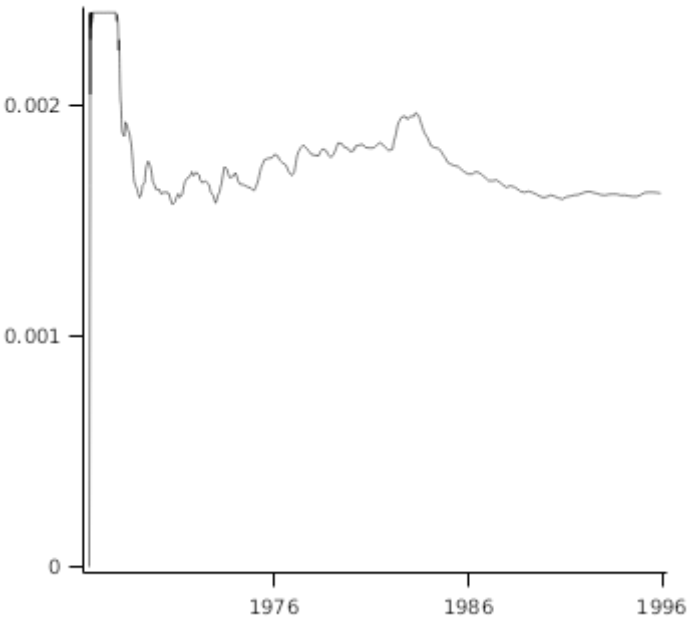
ConeNConc

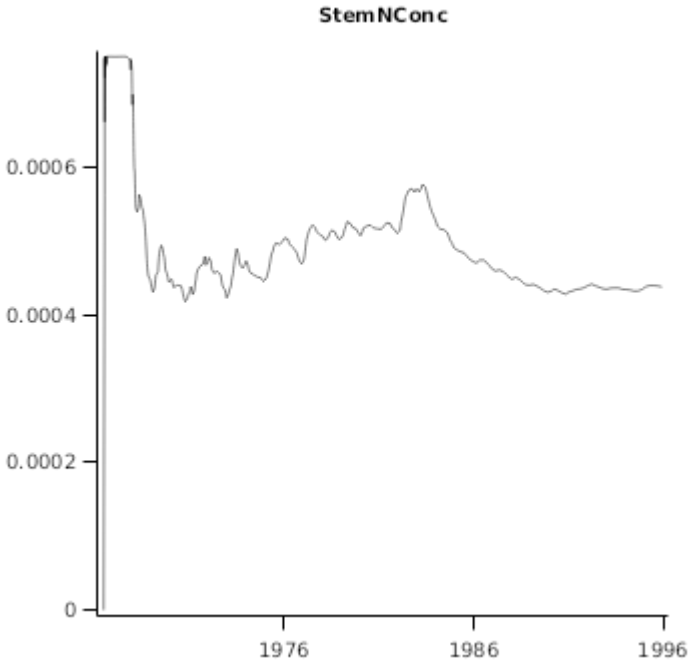


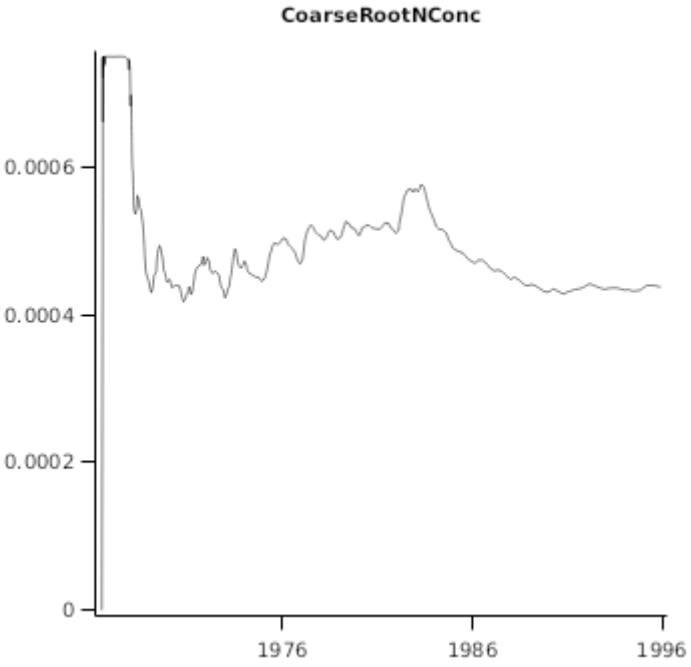
FoliarNConc

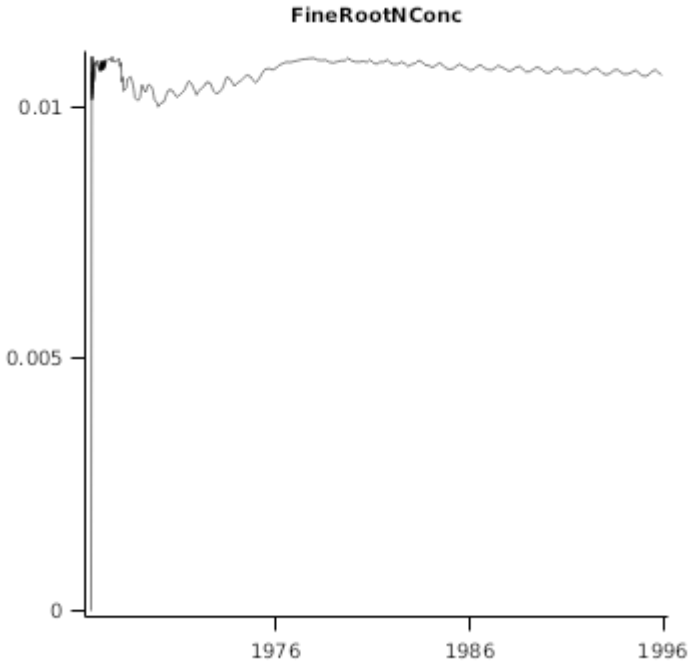


BranchNConc

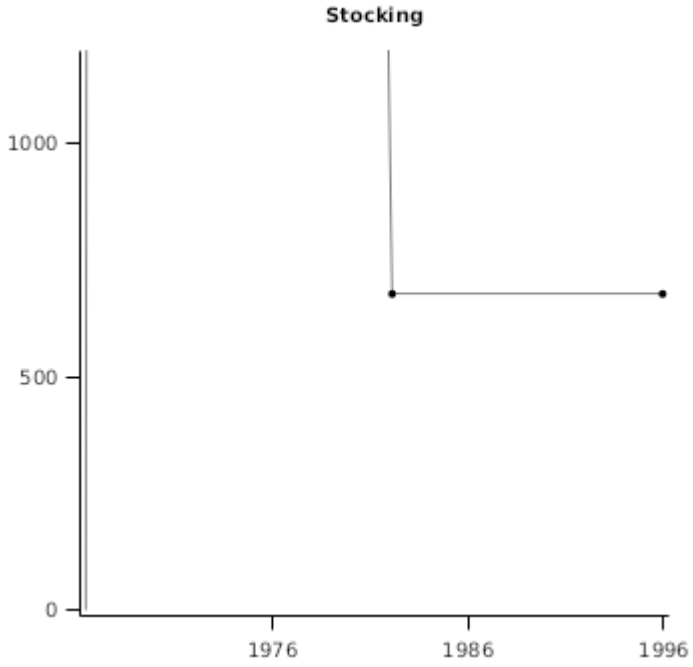


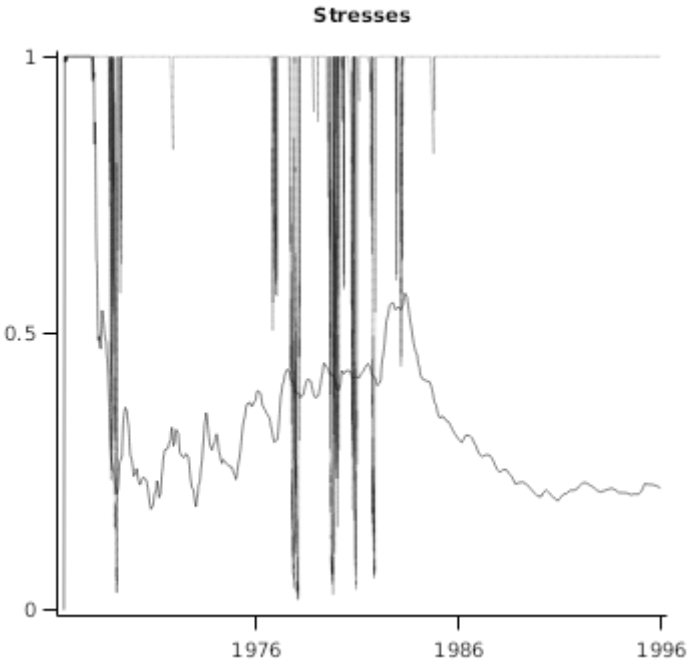






5.3.1.6.1.3 GraphsMetrics


Stocking
1000
500
0
1976
1986
1996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0
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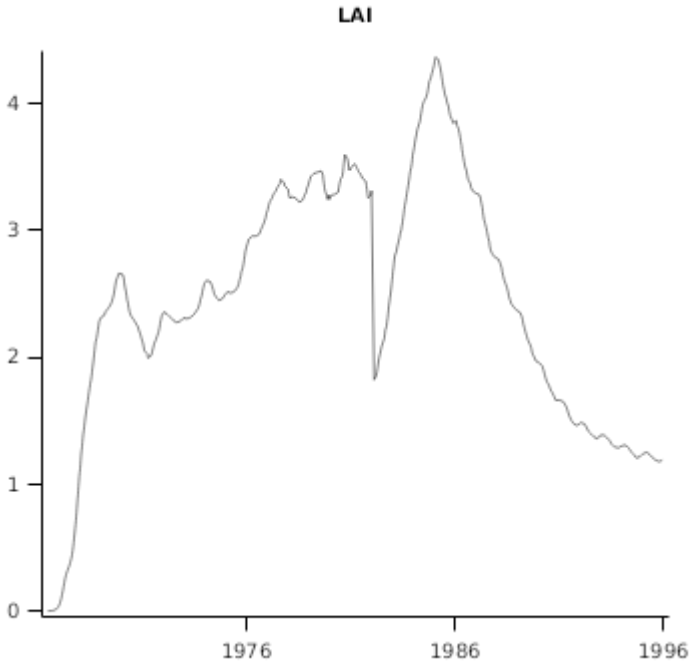
1986
1996


LAI
4
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2
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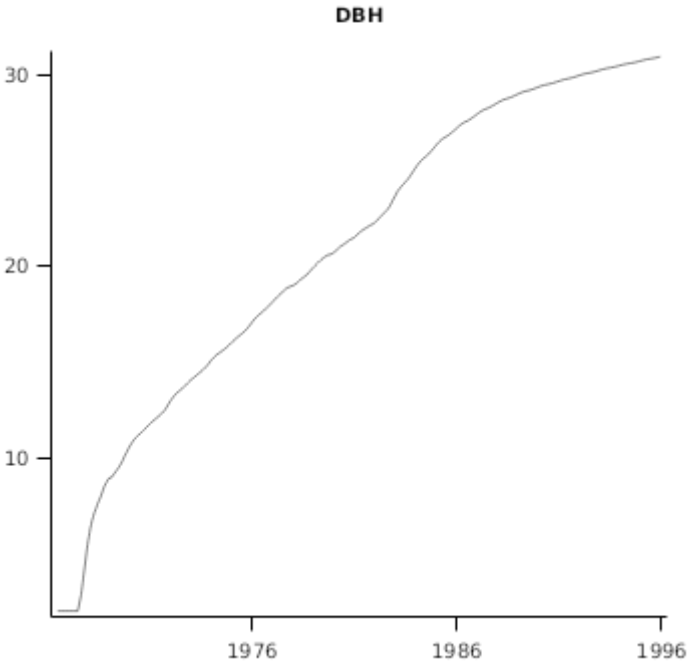
0
1976
1986
1996


DBH
30
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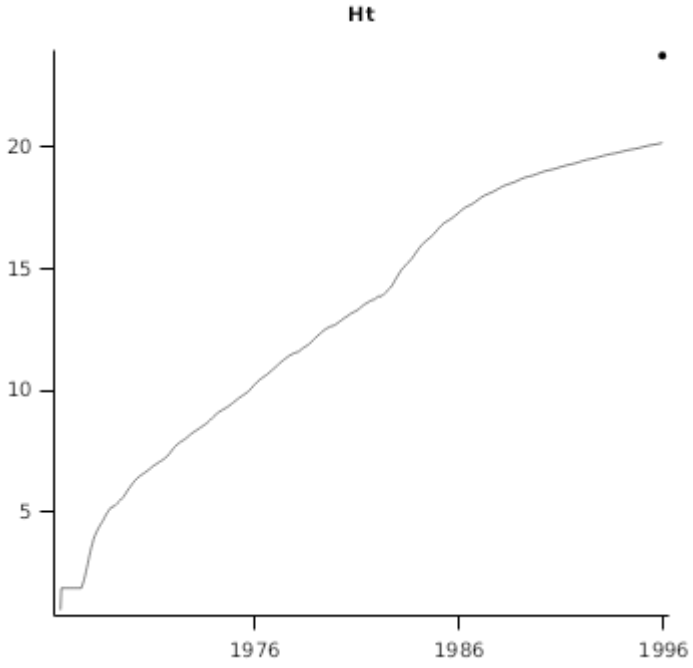
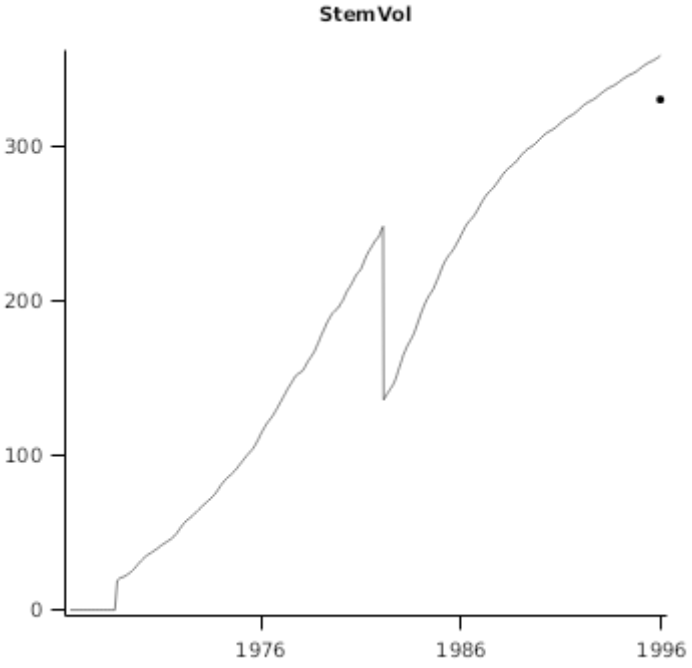
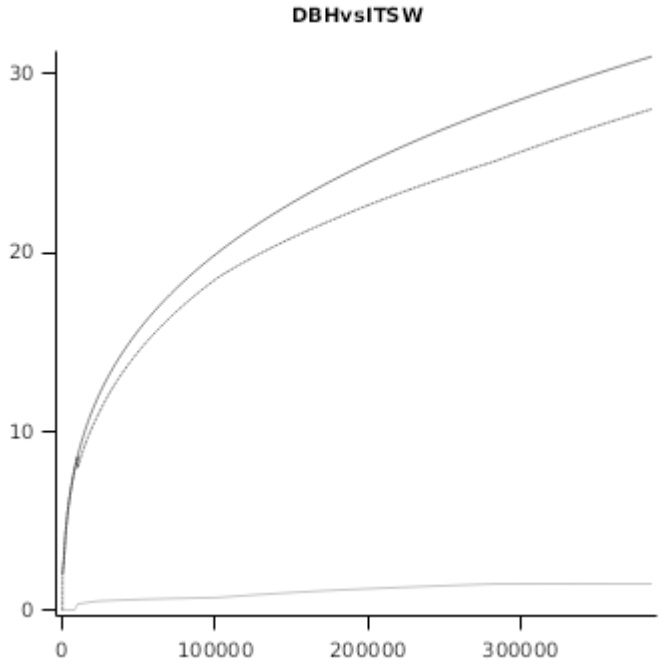
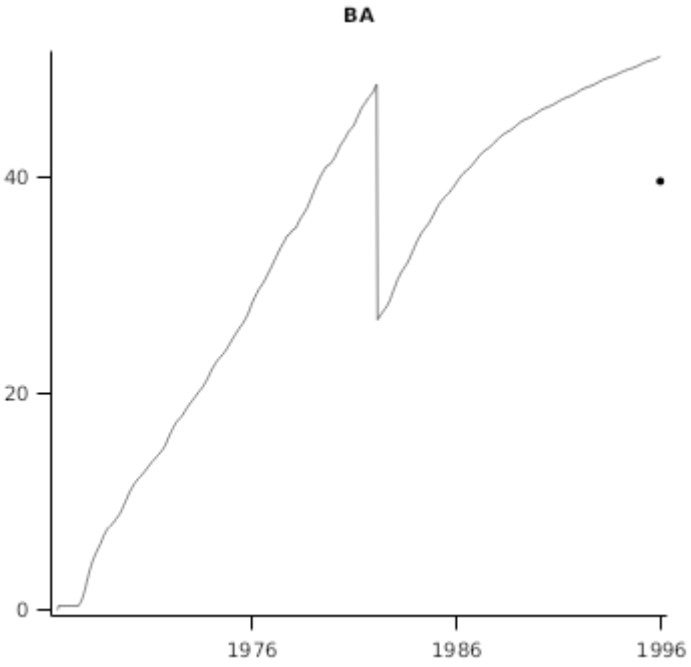
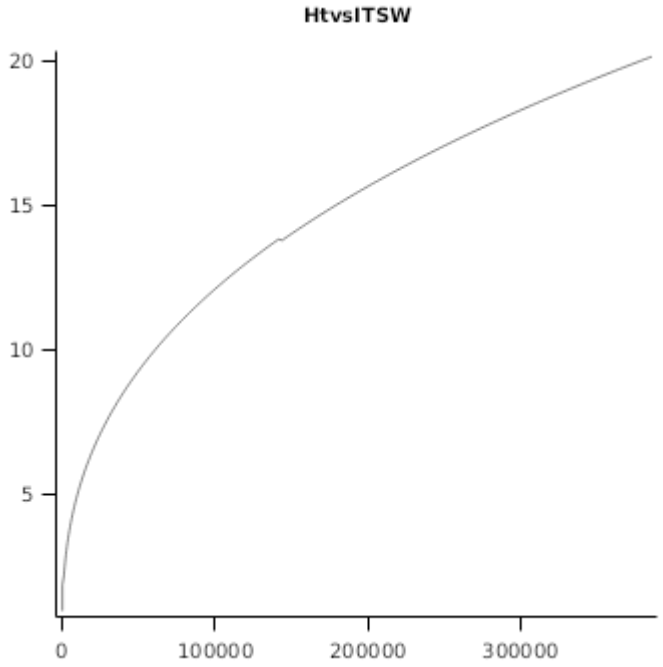
10
1976
1986
1996

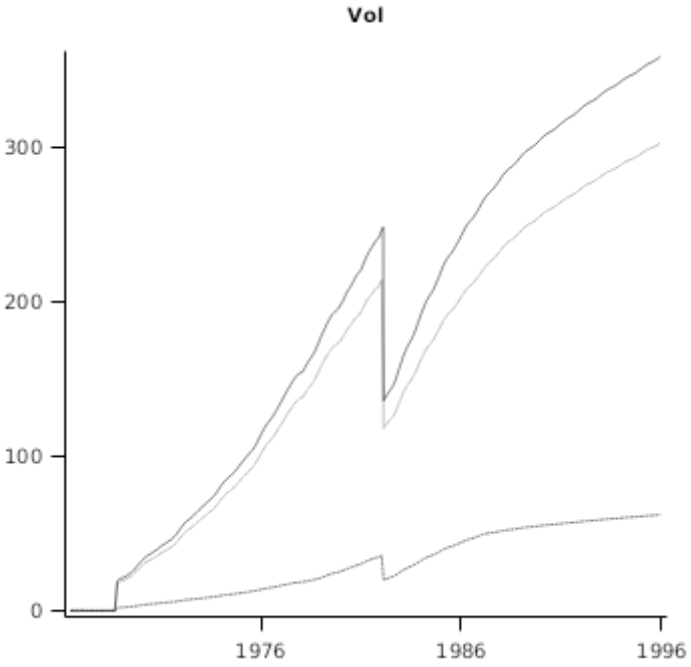

Ht
20
15
10
5
1976
1986
1996

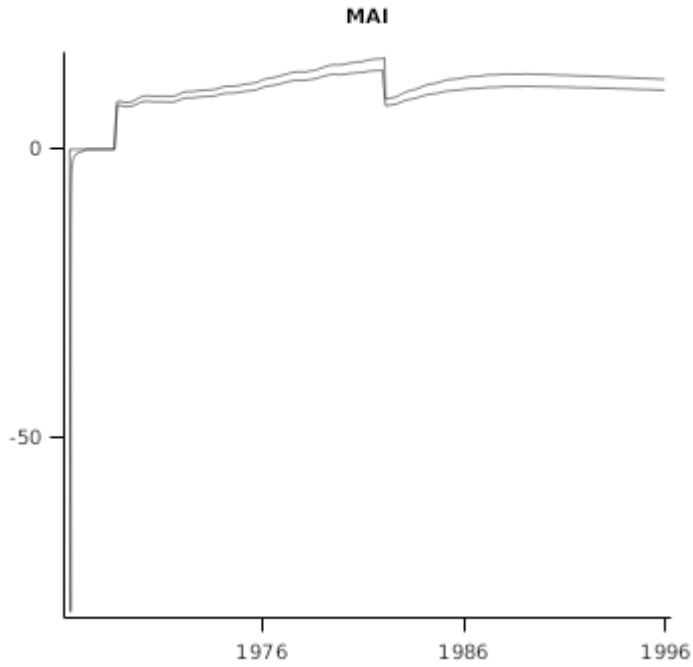

StemVol
300
200
100
0
1976
1986
1996

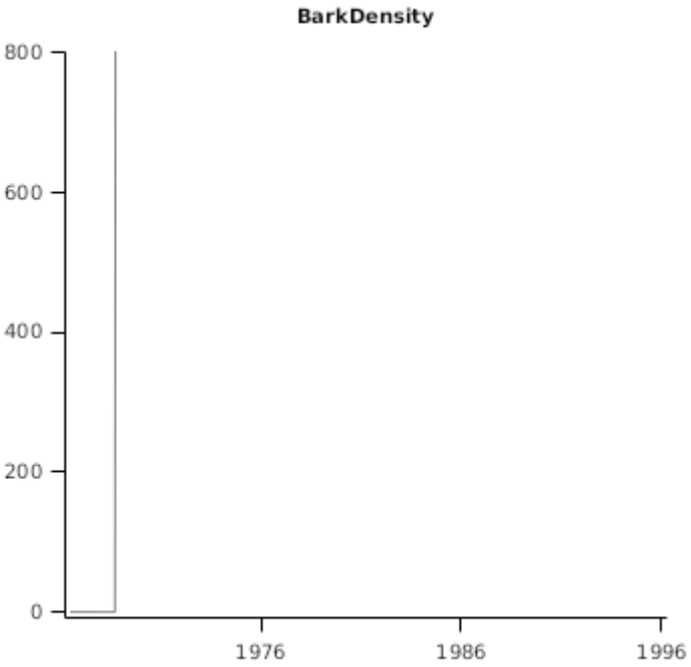

DBHvsITSW
30
20
10
0
0
100000
200000
300000

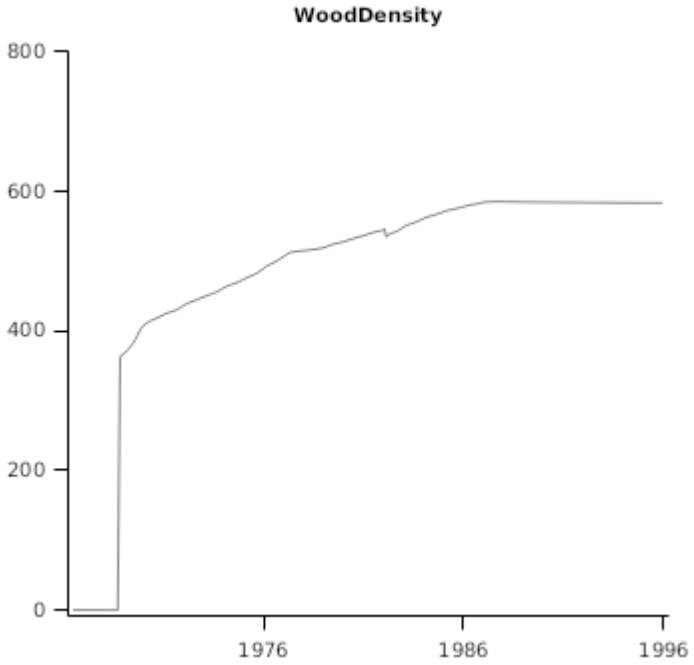

BA
40
20
0
1976
1986
1996


HtvsITSW
20
15
10
5
0
100000
200000
300000


Vol
300
200
100
0
1976
1986
1996


MAI
0
-50
1976
1986
1996


BarkDensity
800
600
400
200
0
1976
1986
1996

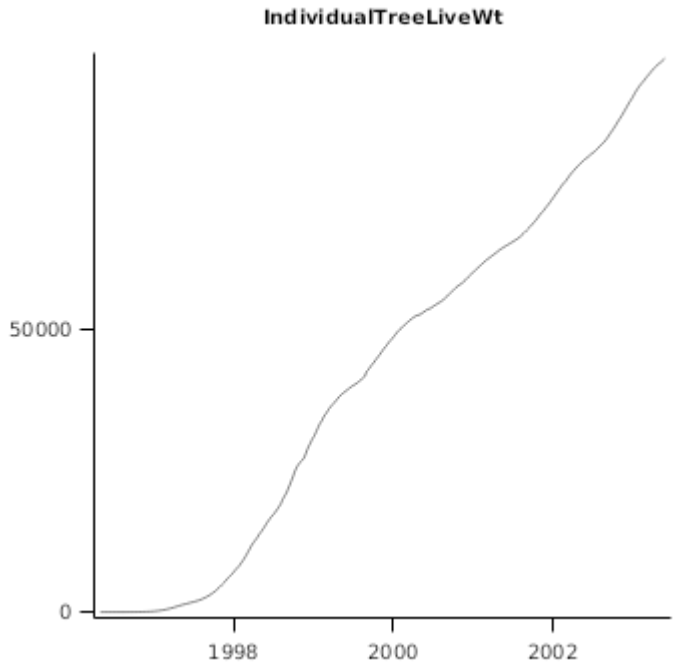


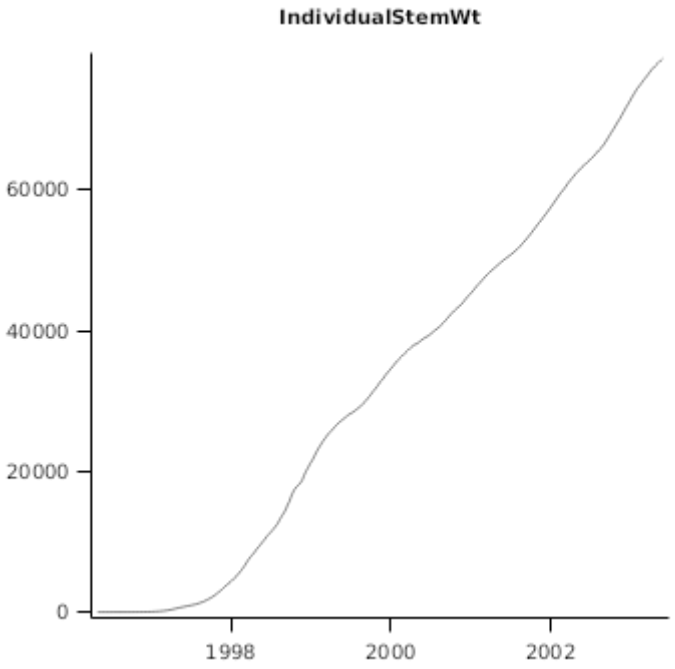
5.3.1.7 HQP321R2

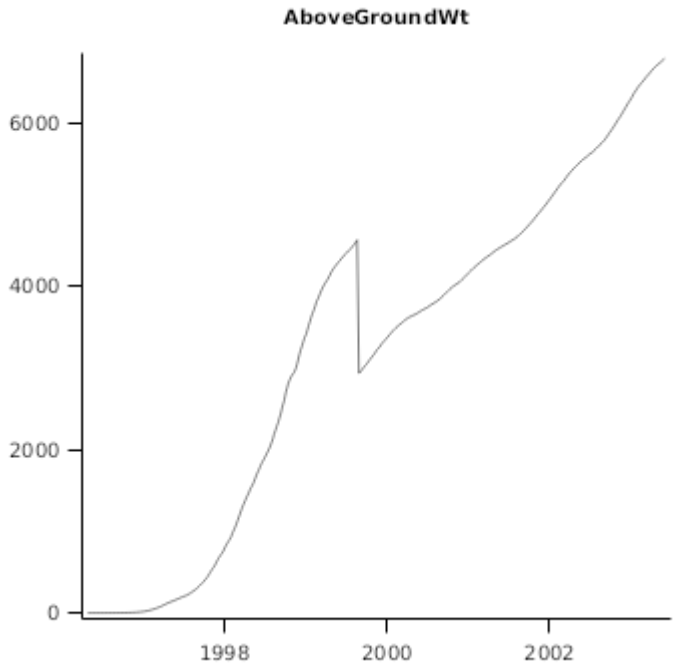
These data were kindly provided by Hancock Queensland Plantations (HQPlantations) from Experiment 321GYM, which was established to:(1) examine the impacts of slash management, fertilization and cover crops on tree growth and nutrient status; (2) quantify the effects on soil properties; and (3) contribute 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, Treatement BL2-TWC).

5.3.1.7.1 Graphs

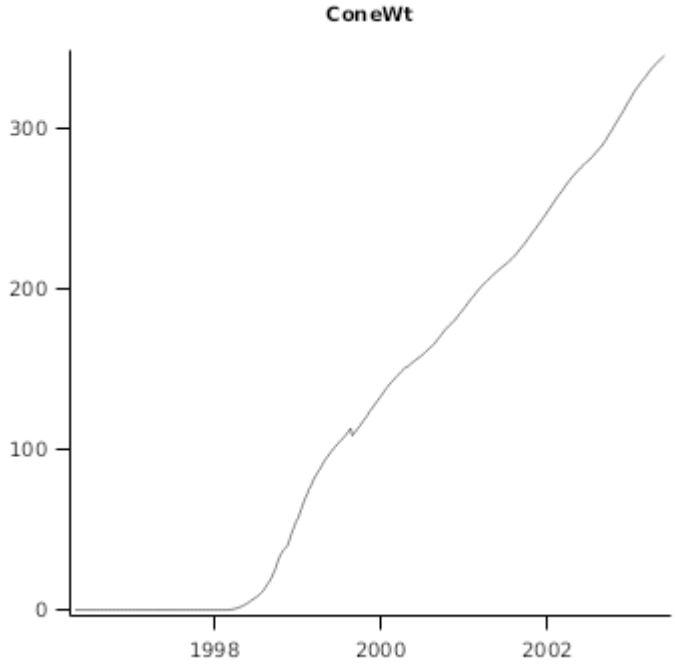
5.3.1.7.1.1 GraphsWeights

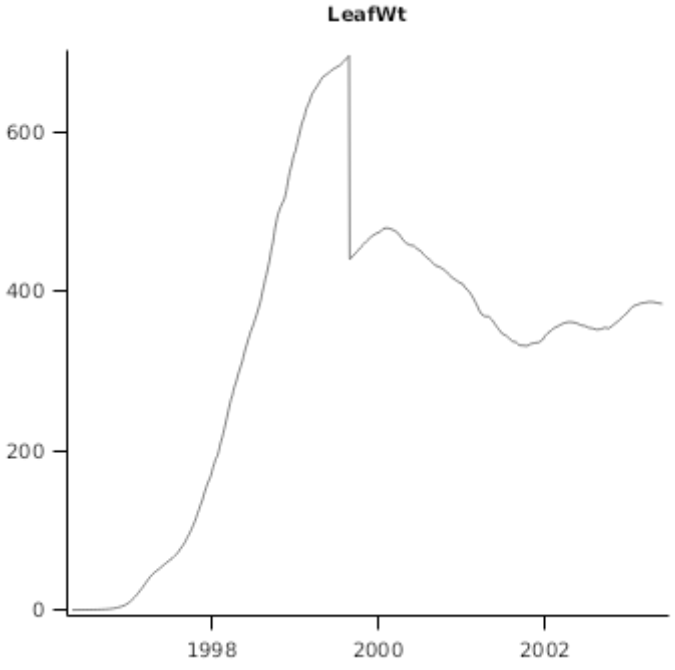


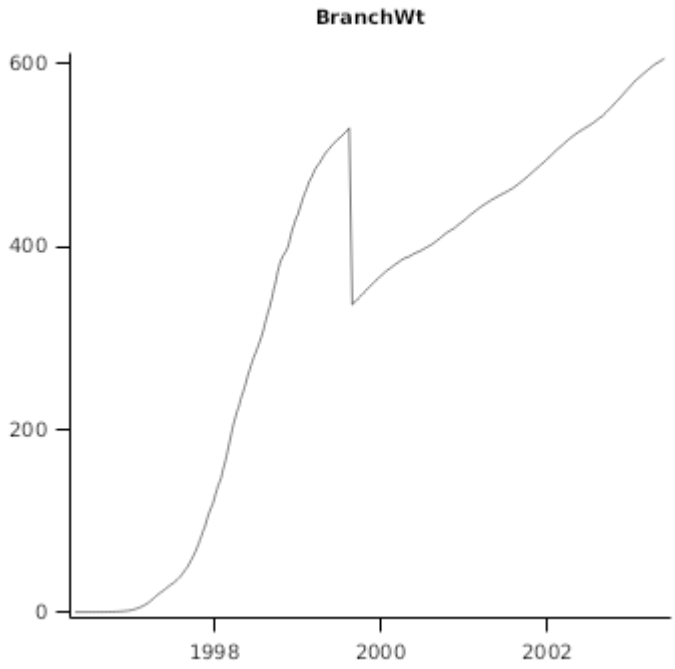


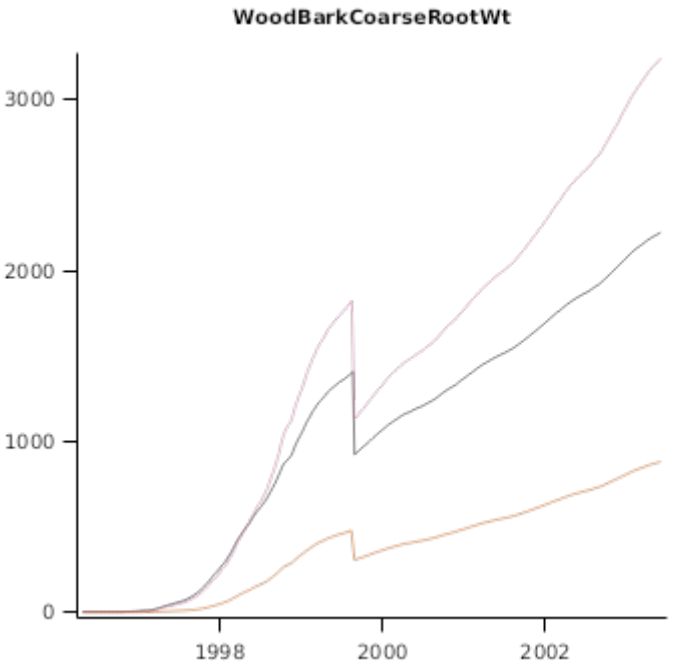


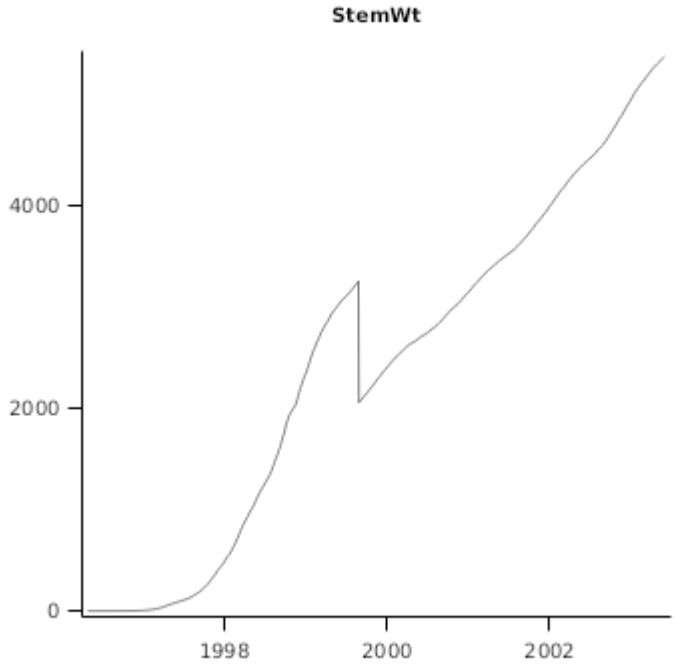
ComponentWts

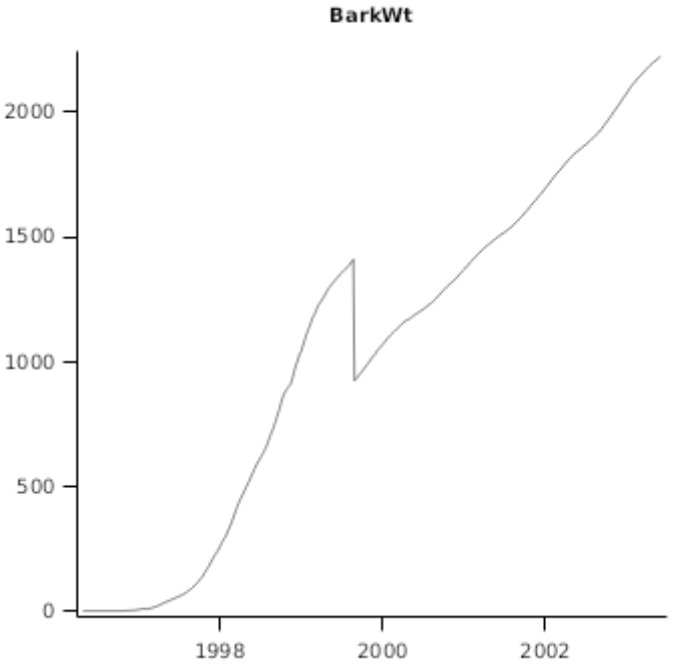


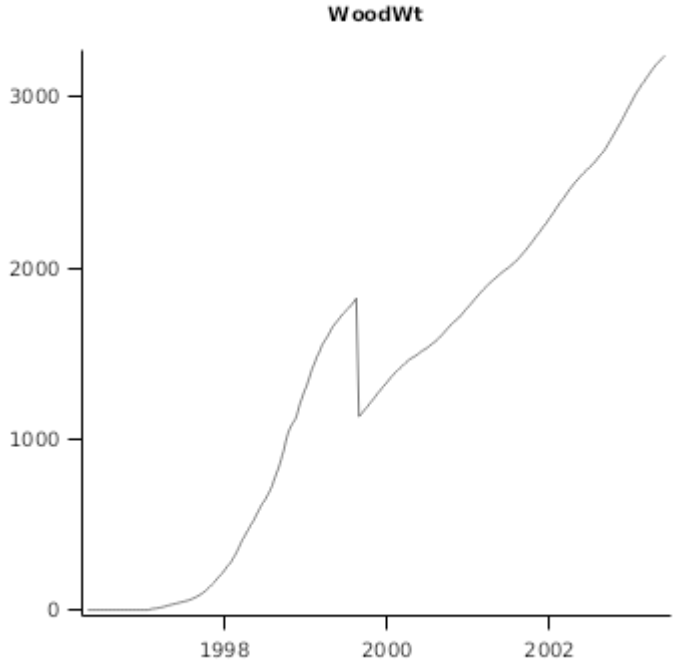


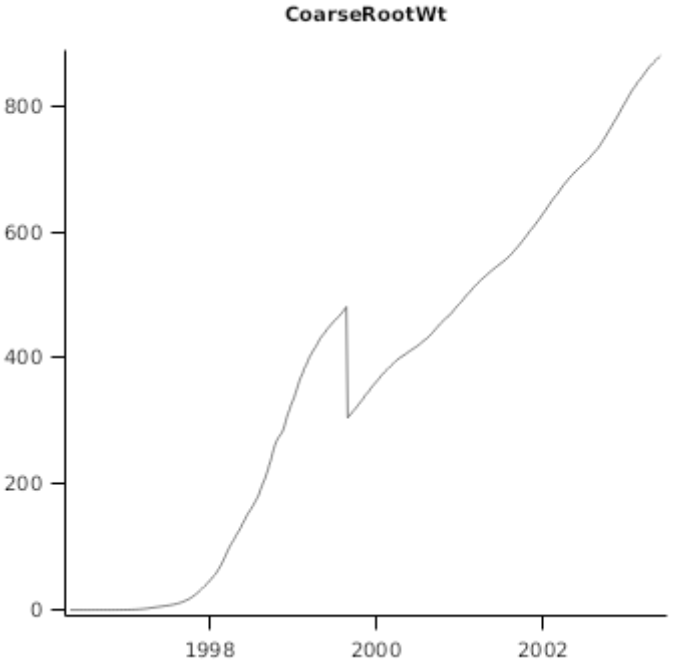

BranchWt
600
400
200
0
1998
2000
2002

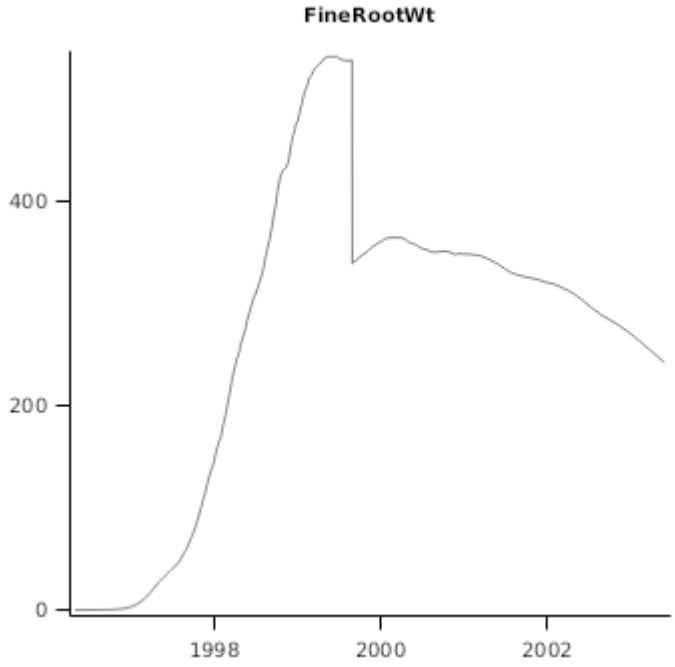

WoodBarkCoarseRootWt
3000
2000
1000
0
1998
2000
2002

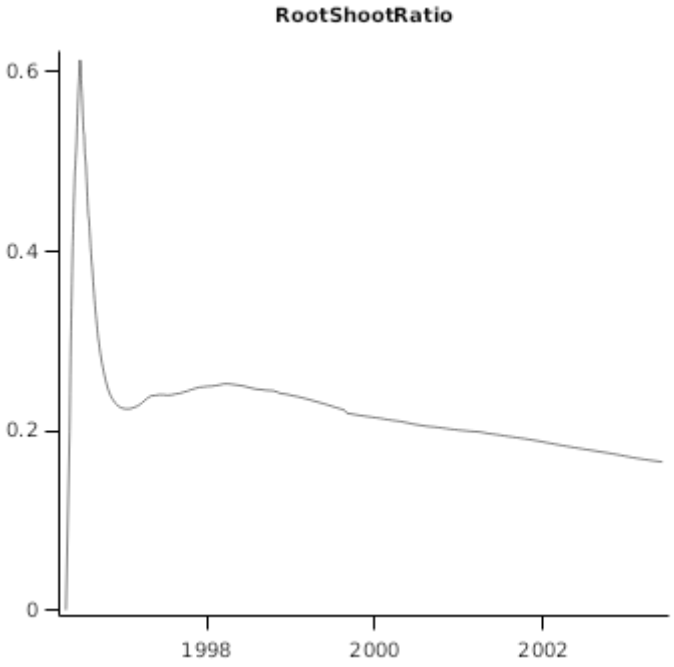

StemWt
4000
2000
0
1998
2000
2002


BarkWt
2000
1500
1000
500
0
1998
2000
2002

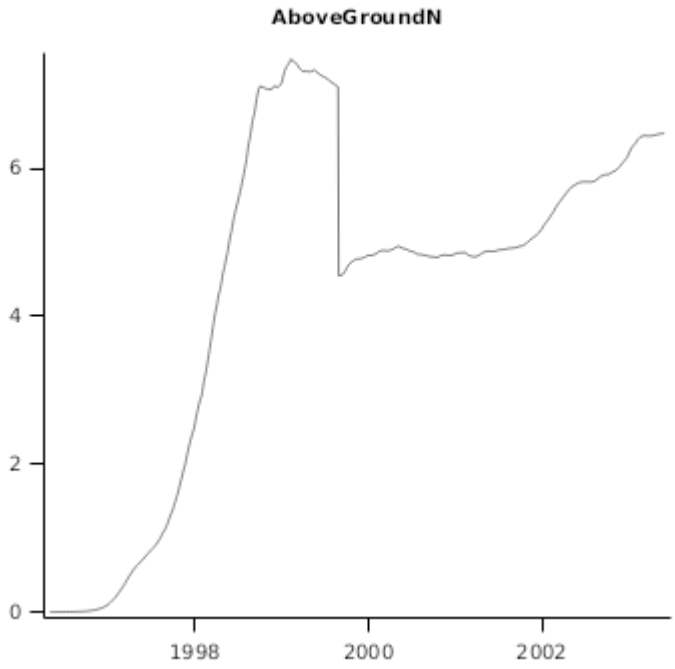

WoodWt
3000
2000
1000
0
1998
2000
2002

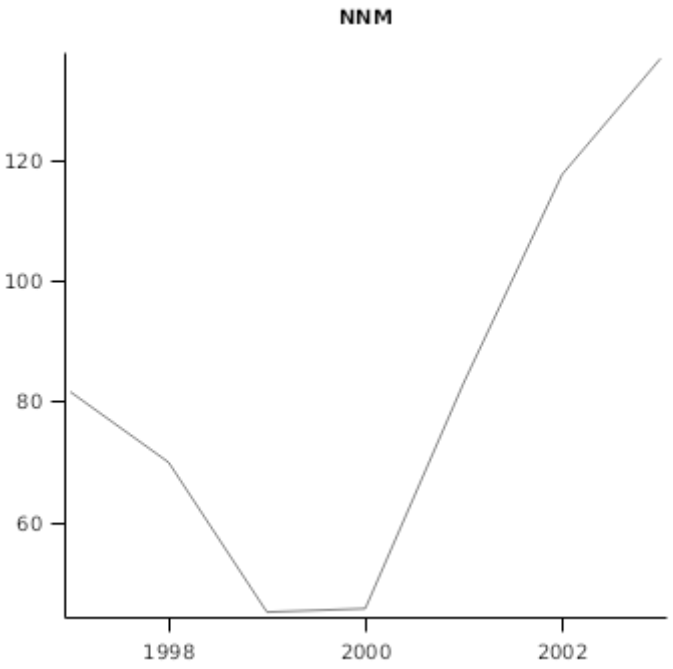

CoarseRootWt
800
600
400
200
0
1998
2000
2002

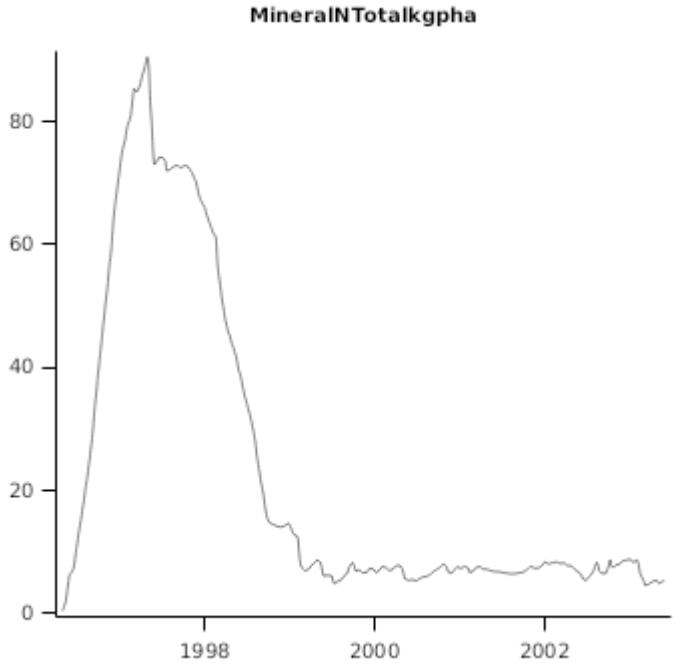


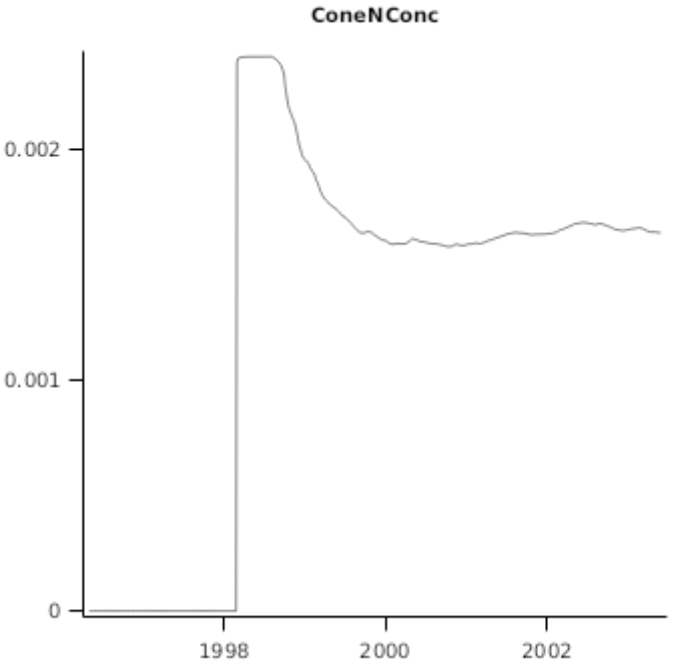


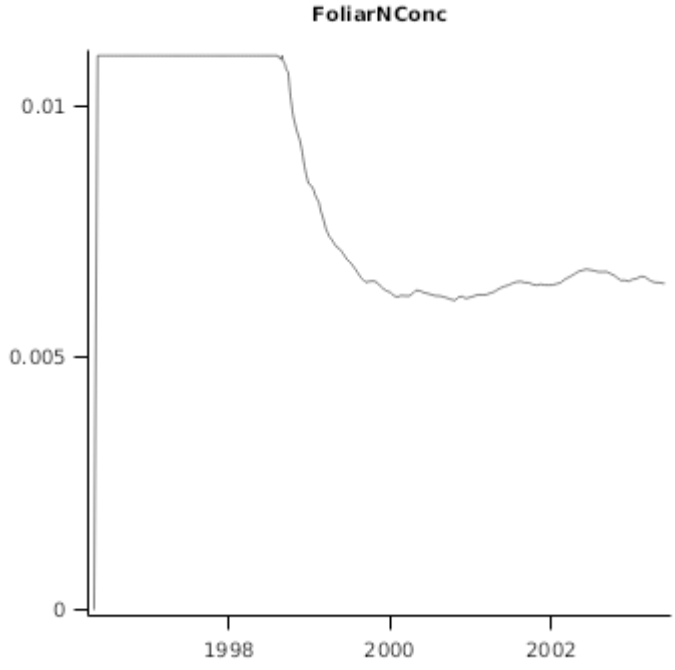
5.3.1.7.1.2 GraphsN

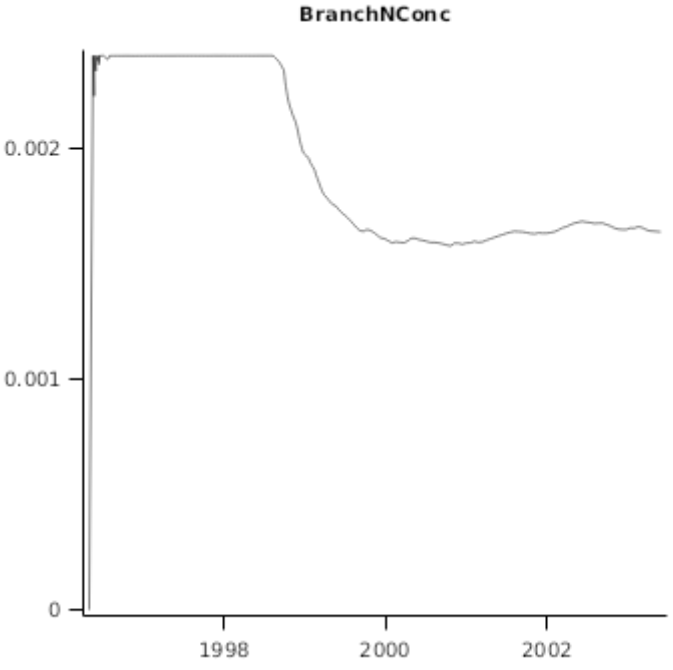

AboveGroundN
6
4
2
0
1998
2000
2002

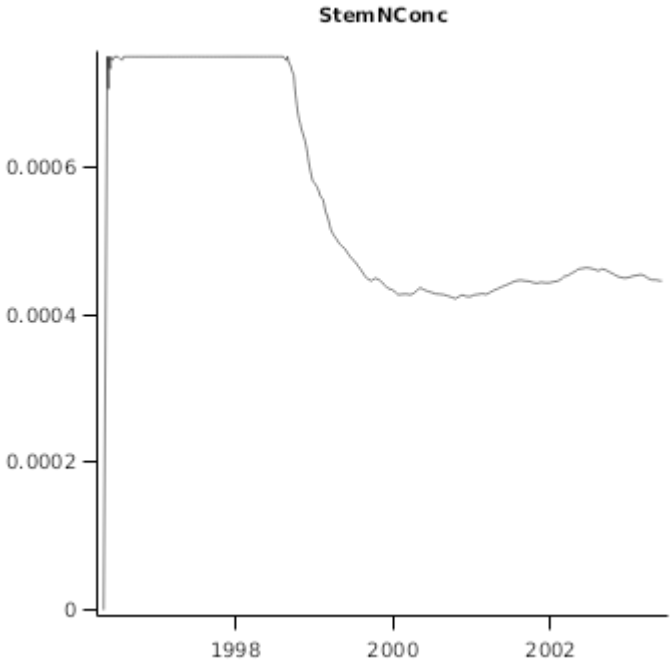

NNM
120
100
80
60
1998
2000
2002

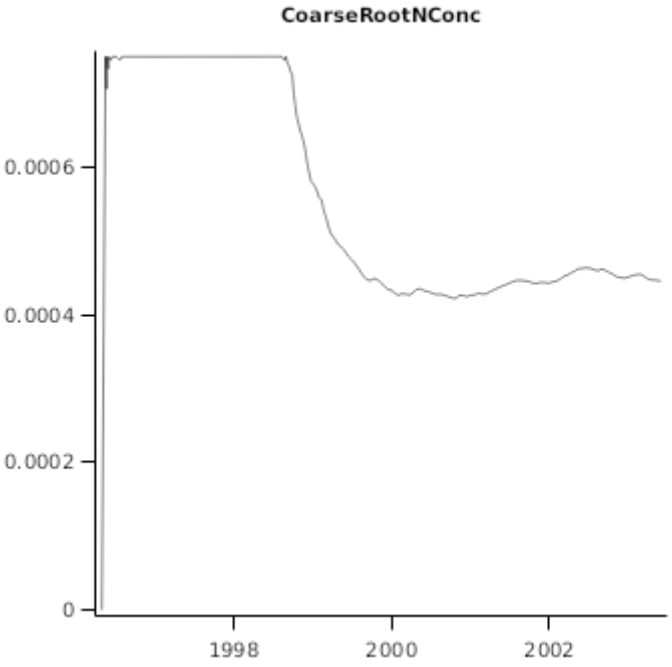

MineralNTotalkgpha
80
60
40
20
0
1998
2000
2002

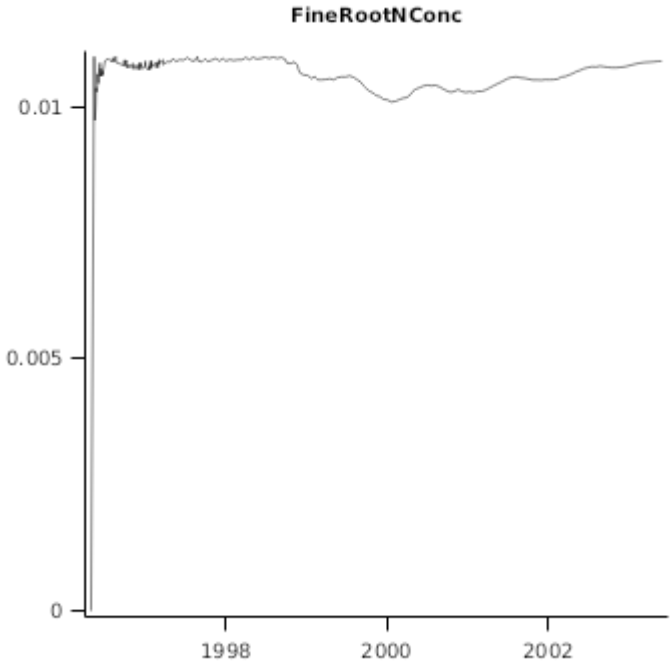

ConeNConc
0.002
0.001
0
1998
2000
2002


FoliarNConc
0.01
0.005
0
1998
2000
2002

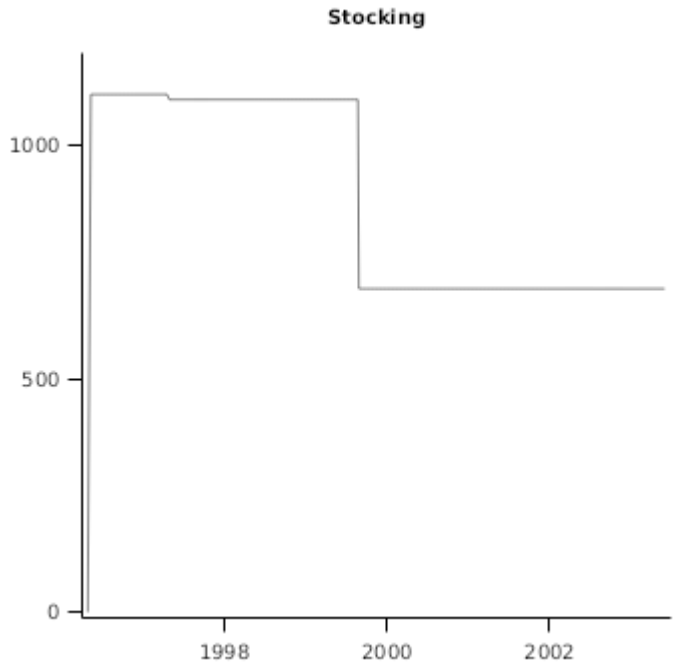

BranchNConc
0.002
0.001
0
1998
2000
2002

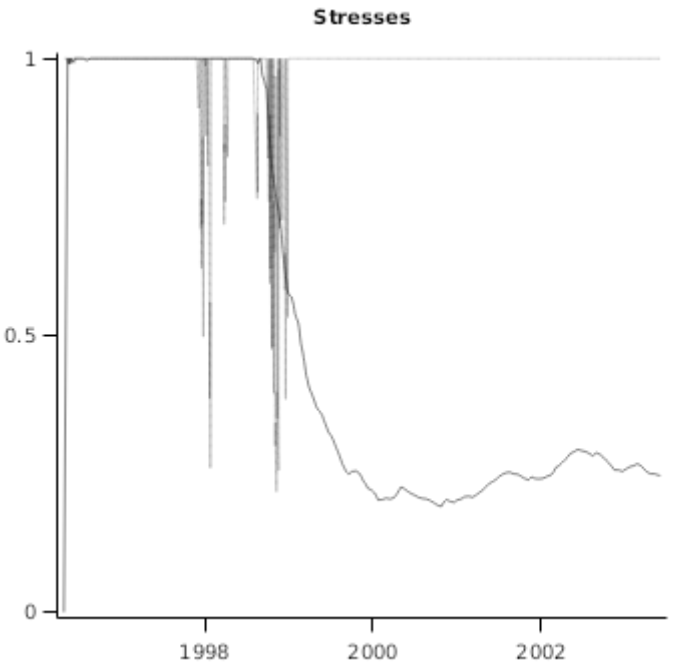


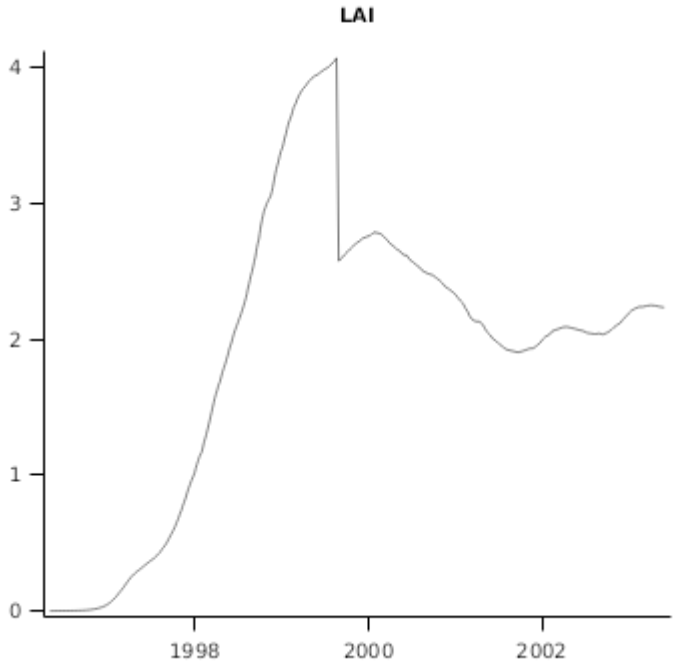


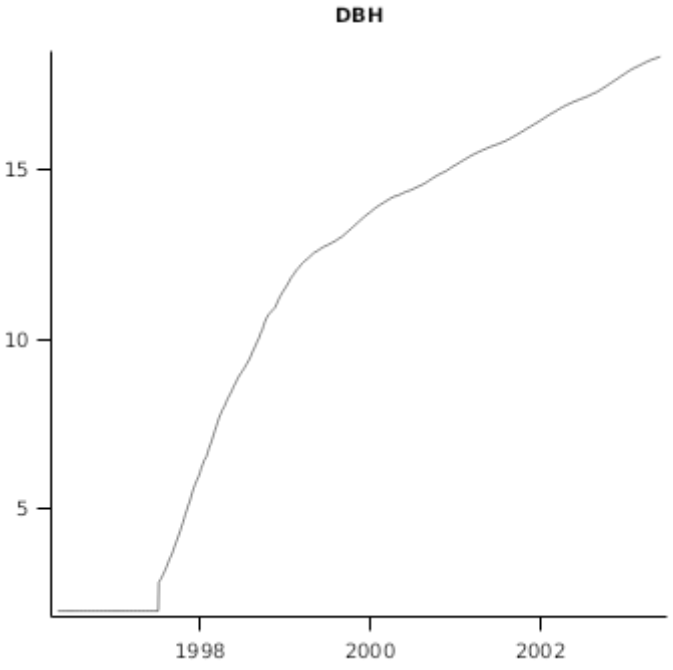


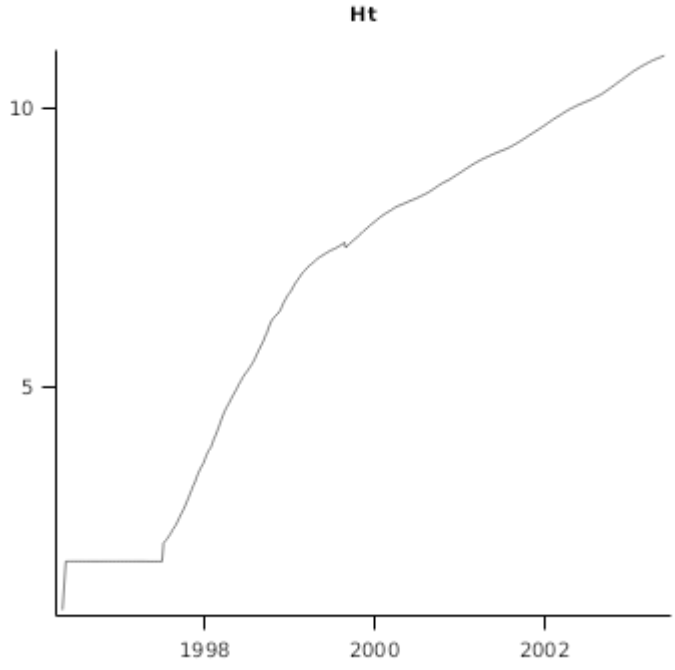
5.3.1.7.1.3 GraphsMetrics

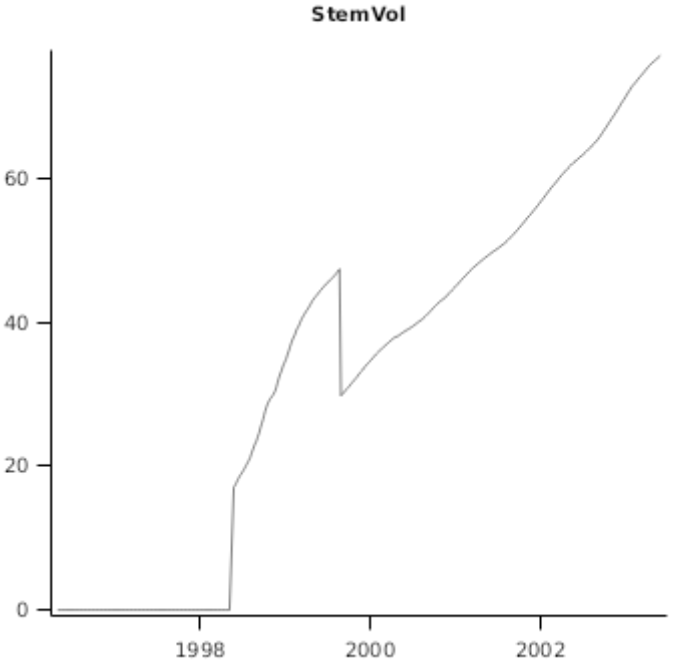

Stocking
1000
500
0
1998
2000
2002

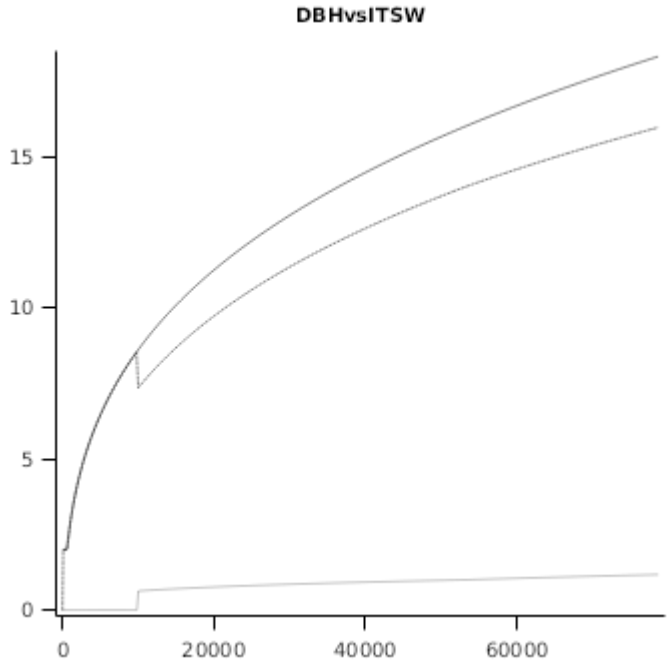

Stresses
1
0.5
0
1998
2000
2002


LAI
4
3
2
1
0
1998
2000
2002


DBH
15
10
5
1998
2000
2002


Ht
10
5
1998
2000
2002


StemVol
60
40
20
0
1998
2000
2002


DBHvsITSW
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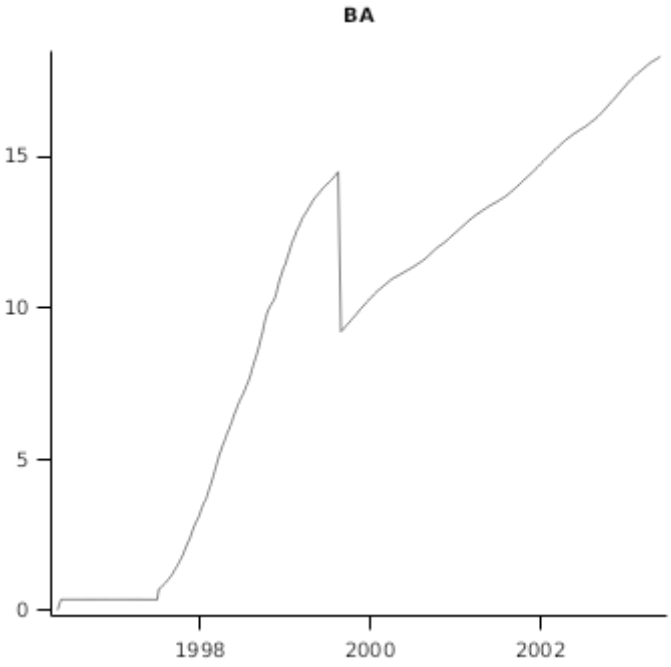
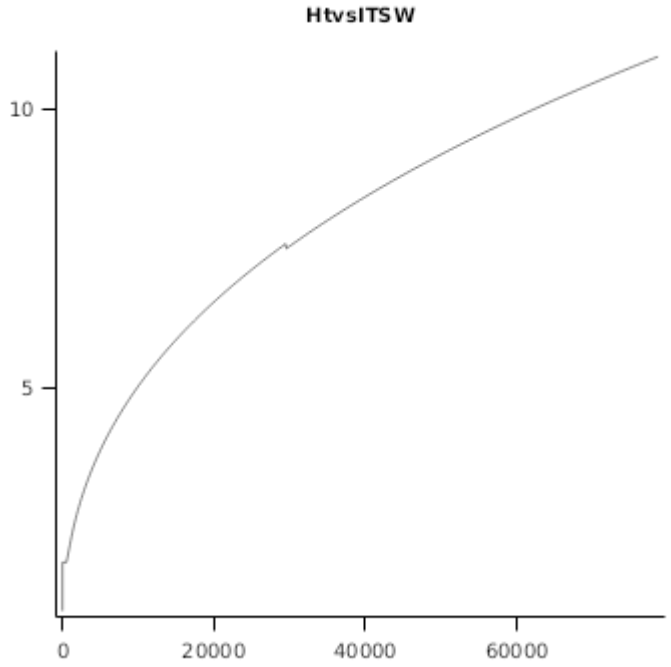
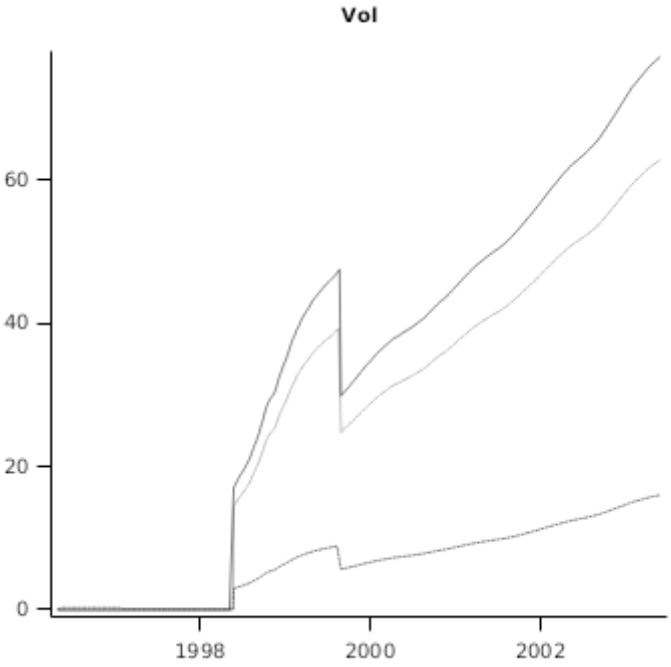
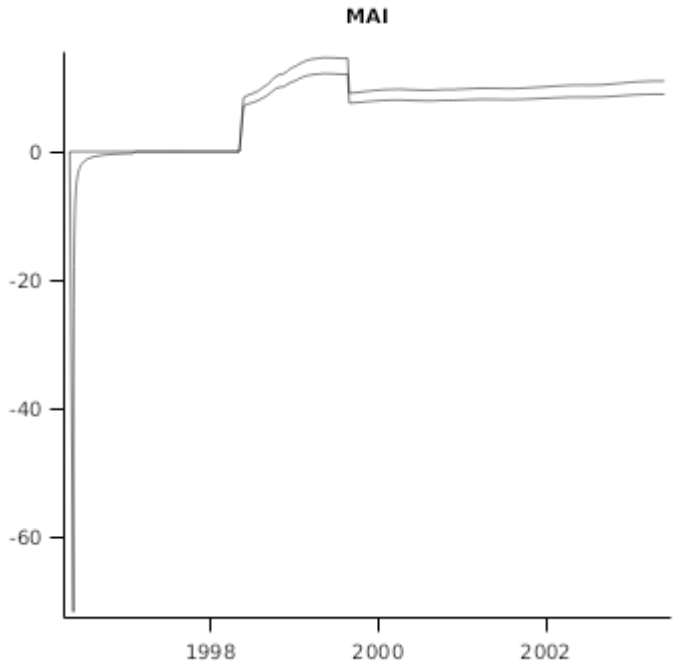
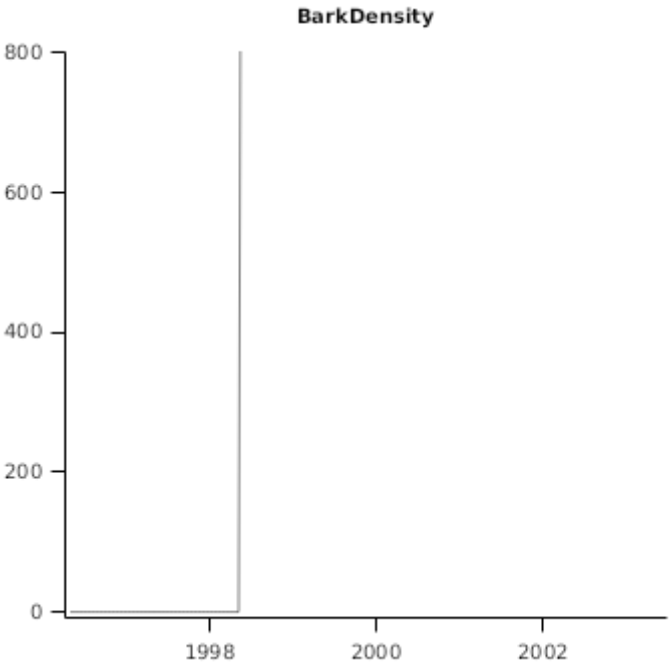
10
5
0
0
20000
40000
60000


BA
15
10
5
0
1998
2000
2002


HtvsITSW
10
5
0
20000
40000
60000


Vol
60
40
20
0
1998
2000
2002


MAI
0
-20
-40
-60
1998
2000
2002

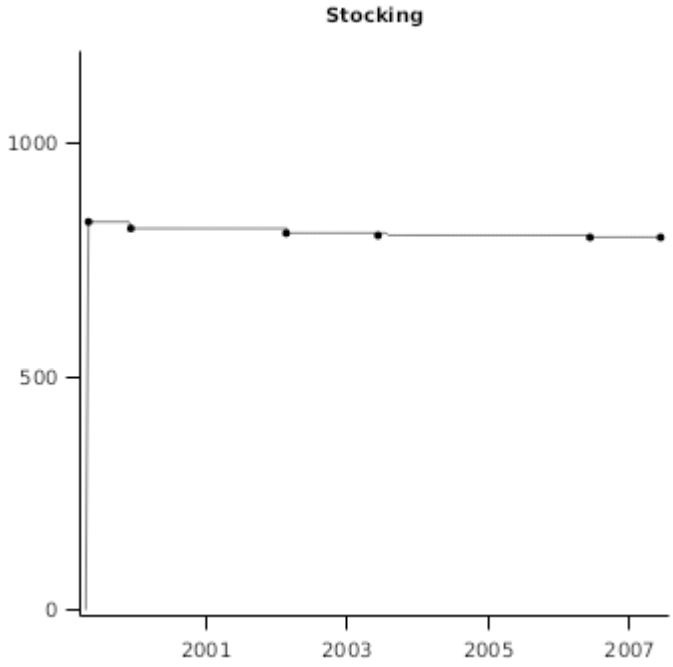

BarkDensity
800
600
400
200
0
1998
2000
2002

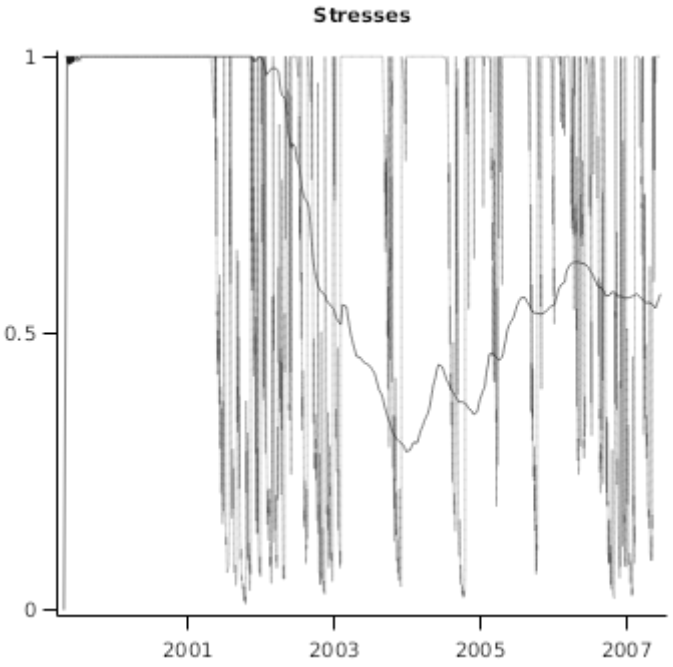
5.3.1.8 HQP350

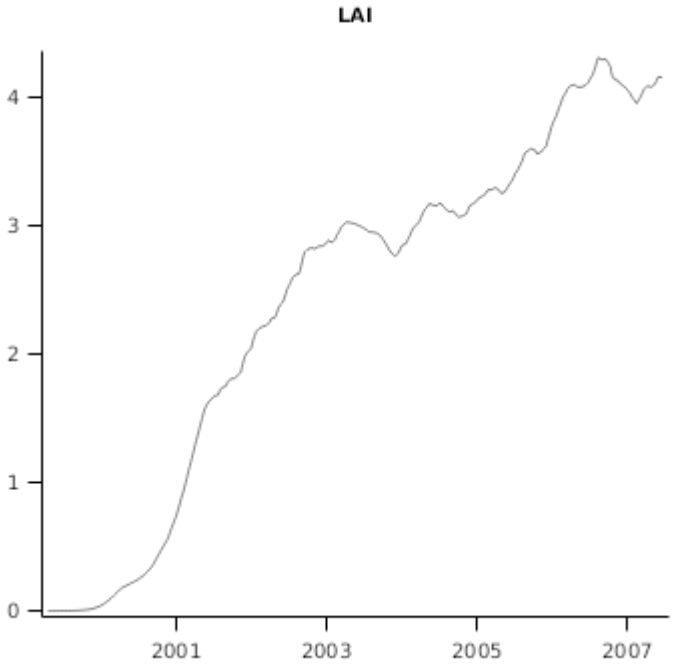
These data were kindly provided by Hancock Queensland Plantations (HQPlantations) from Experiment 350GYM, which was established to assess the relative benefits, both short-term and long-term, of major factors and their interactions on PEE x PCH hybrid plantations when grown on an average site in the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

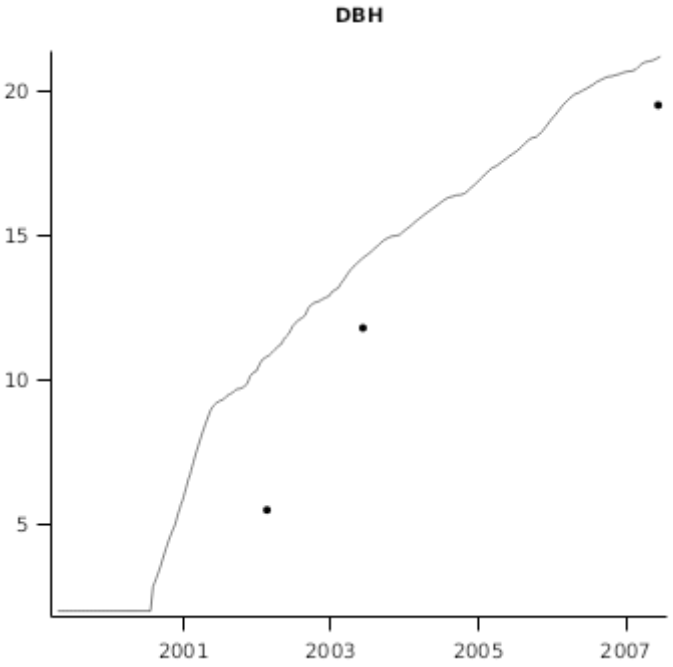
5.3.1.8.1 Graphs

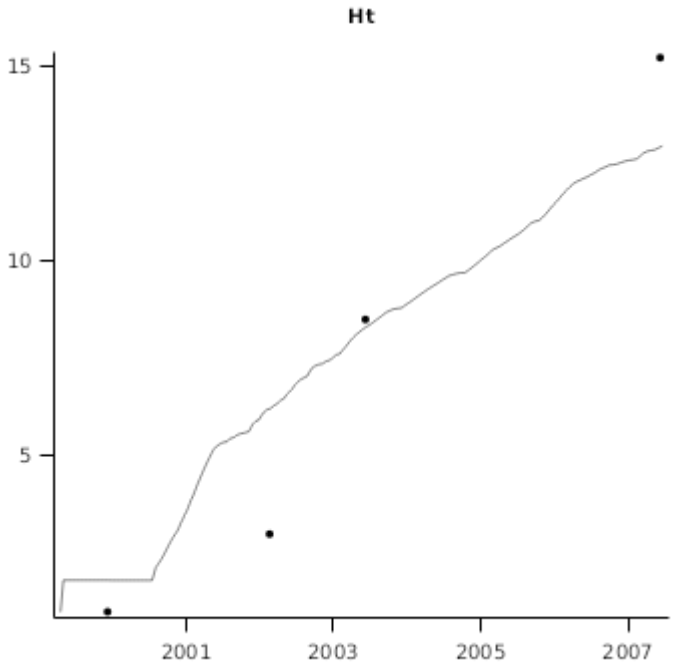
5.3.1.8.1.1 GraphsMetrics

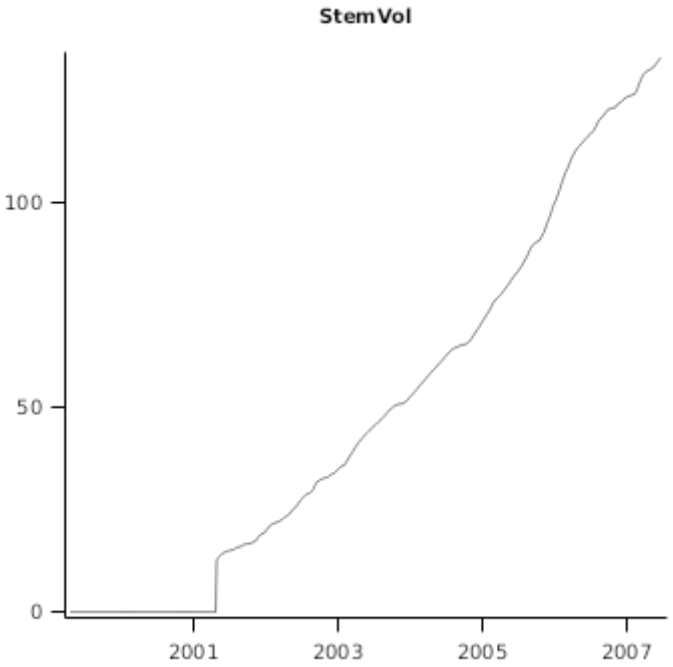

Stocking
1000
500
0
2001
2003
2005
2007

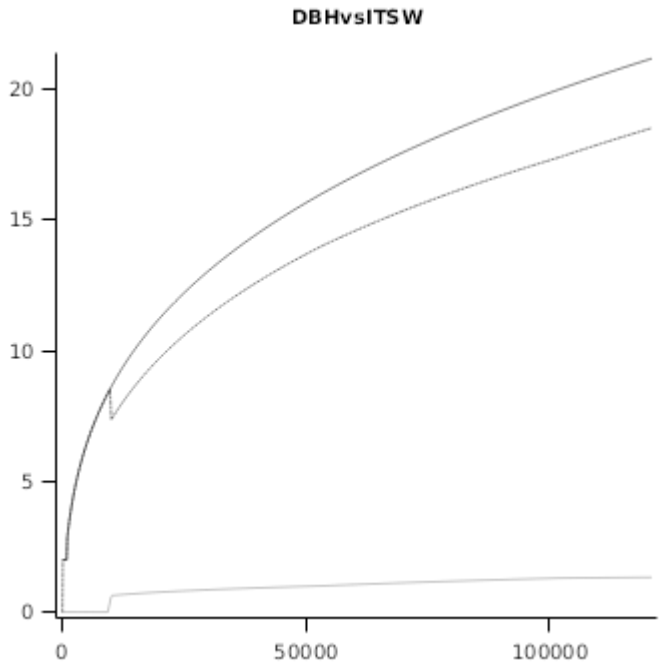

Stresses
1
0.5
0
2001
2003
2005
2007

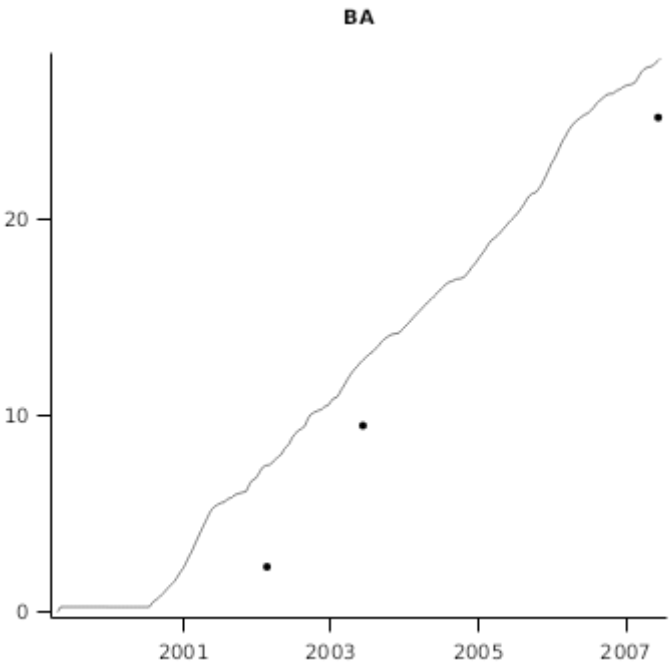

LAI
4
3
2
1
0
2001
2003
2005
2007

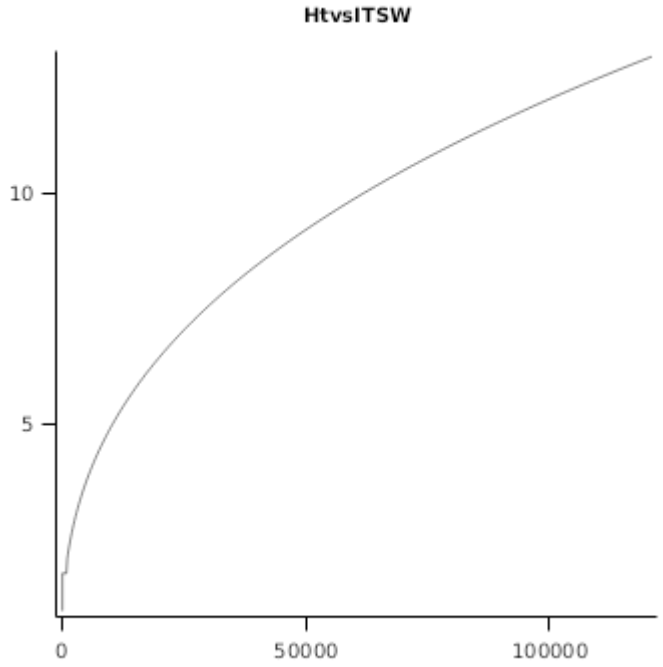

DBH
20
15
10
5
2001
2003
2005
2007

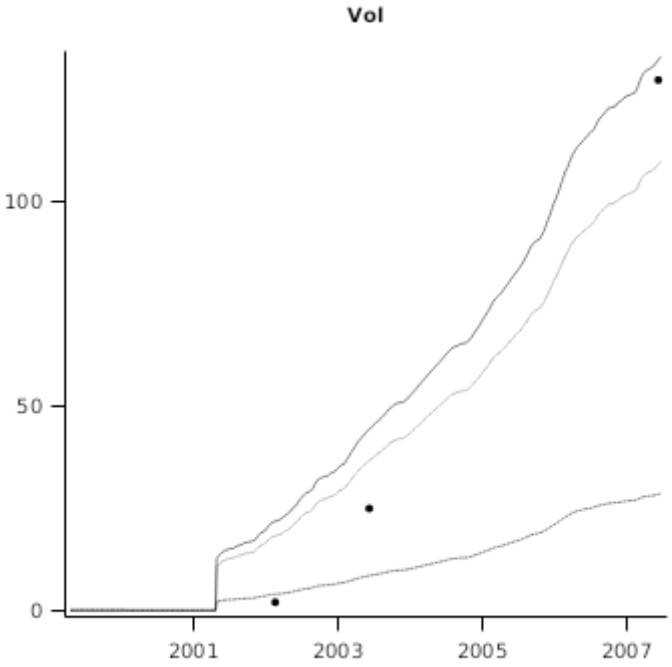

Ht
15
10
5
2001
2003
2005
2007

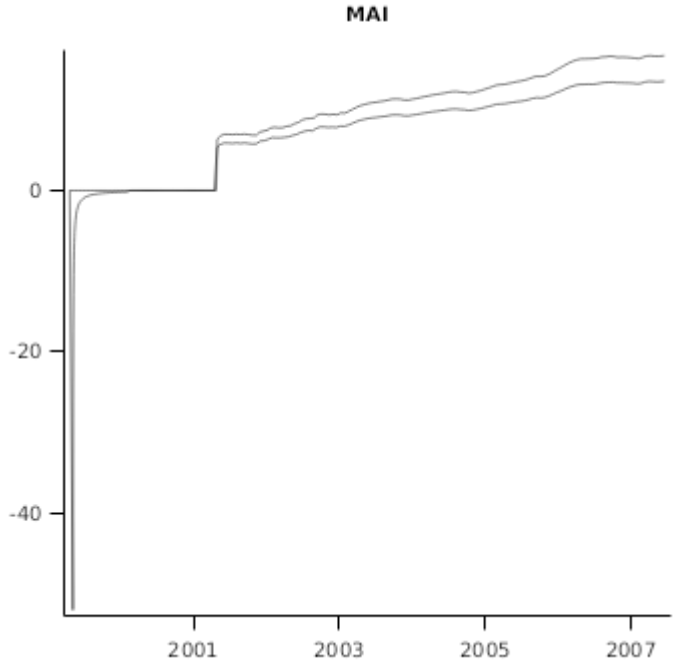

StemVol
100
50
0
2001
2003
2005
2007

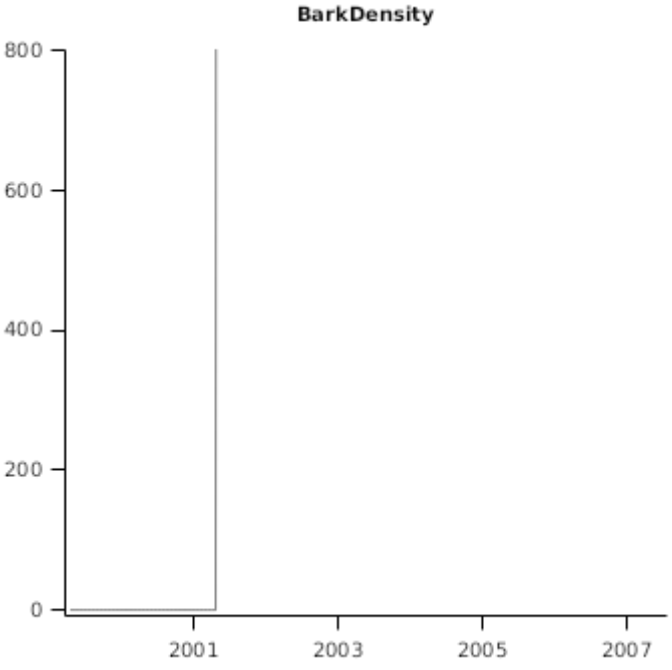

DBHvsITSW
20
15
10
5
0
0
50000
100000

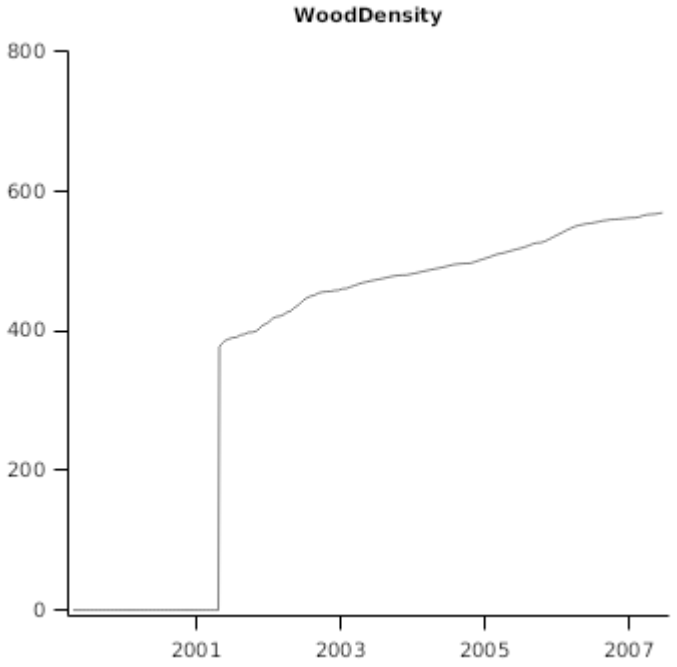

BA
20
10
0
2001
2003
2005
2007


HtvsITSW
10
5
0
50000
100000


Vol
100
50
0
2001
2003
2005
2007


MAI
0
-20
-40
2001
2003
2005
2007


BarkDensity
800
600
400
200
0
2001
2003
2005
2007



5.3.1.9 GraphsOvP

Test! These observed versus predicted graphs include all validation datasets and timesteps within a site for which observed data were available.

5.3.2 USA

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

5.3.2.1 IMPAC

These data are from an experiment with ferilizer 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 the model couold not be expected to simulate, only the high input treatment was simualted.

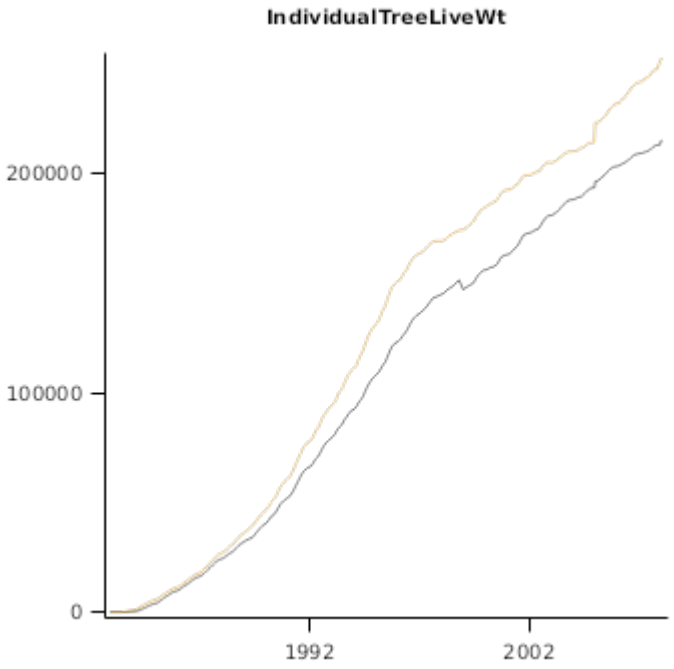
Numerous publications report on this experiment: Jokela et al., 2000, Vogel et al., 2011, Martin et al., 2004, Gonzalez-Benecke et al., 2012, Jokela et al., 2010, Subedi et al., 2019, Jokela et al., 2004, and Gonzalez-Benecke et al., 2016. A consolidated dataset was kindly provided by Eric Jokela and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

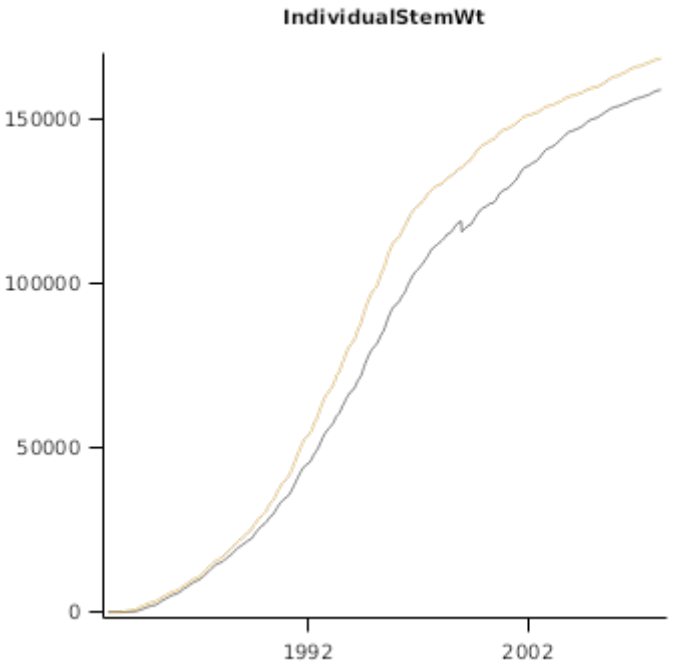
List of experiments.

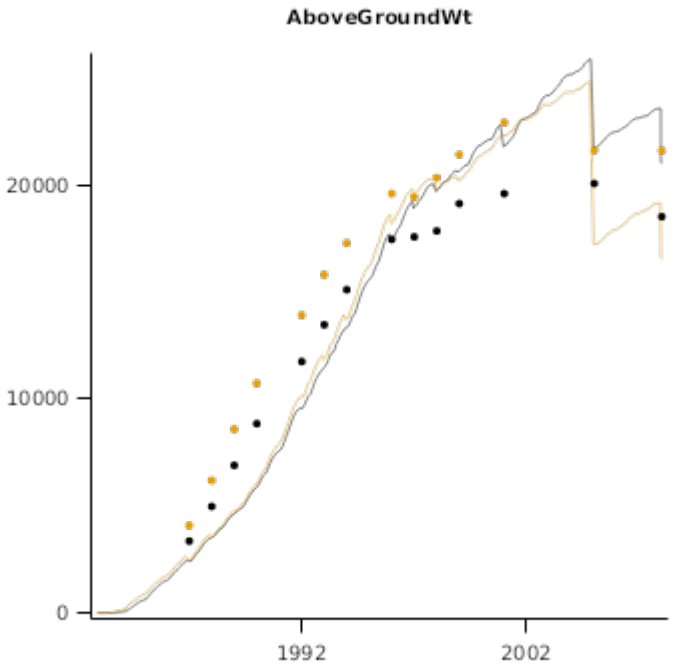
Experiment Name	Design (Number of Treatments)
IMPAC	L x S (2)

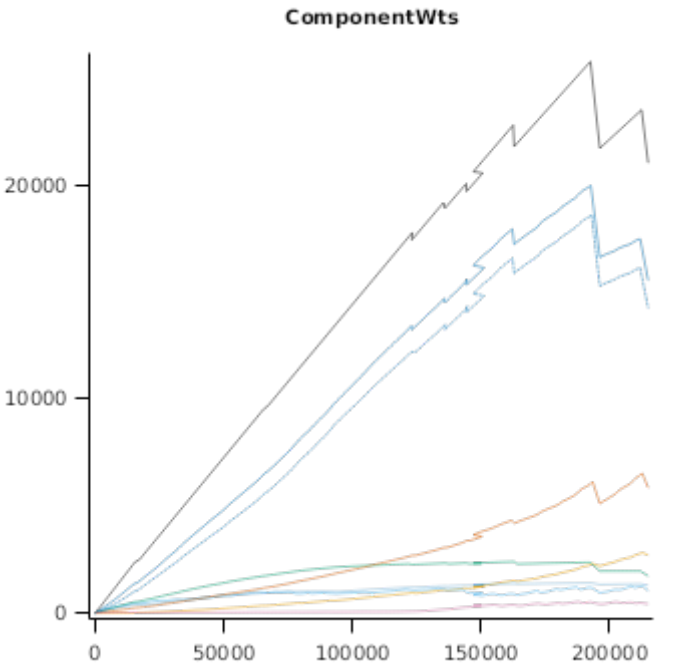
5.3.2.1.1 Graphs

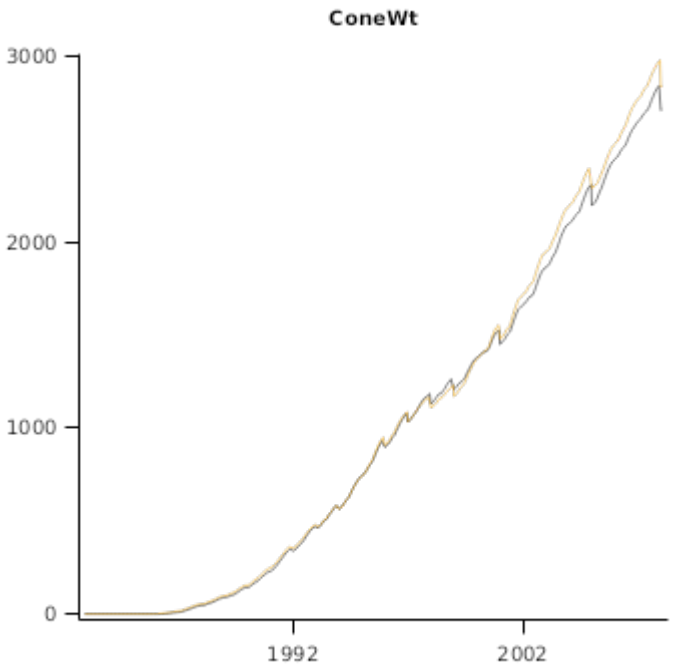
5.3.2.1.1.1 GraphsWeights

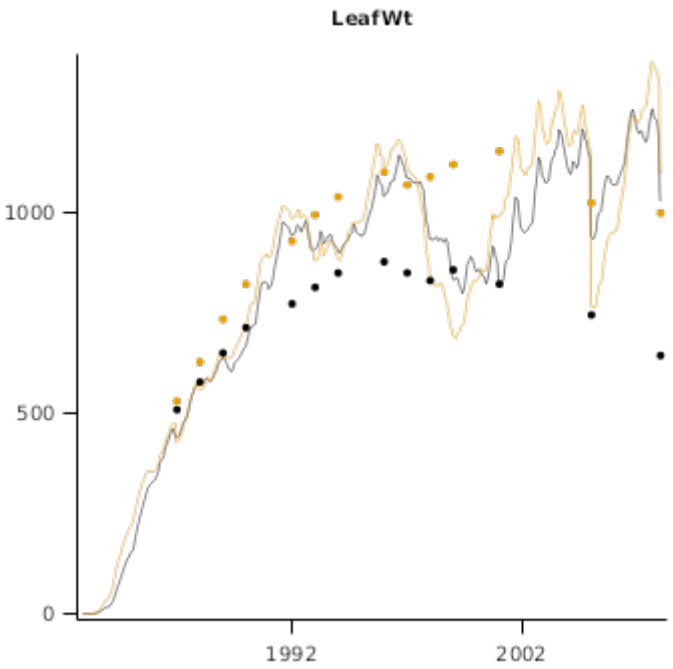

IndividualTreeLiveWt
200000
100000
0
1992
2002

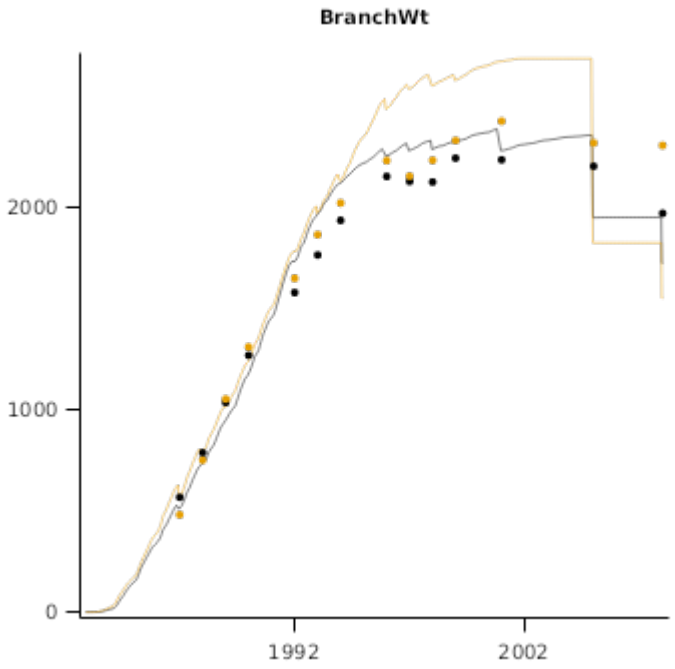

IndividualStemWt
150000
100000
50000
0
1992
2002


AboveGroundWt
20000
10000
0
1992
2002

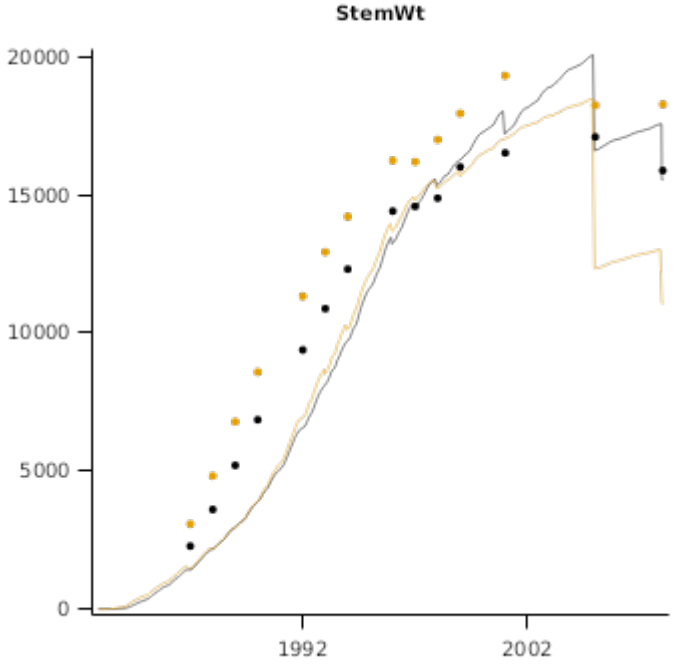

ComponentWts
20000
10000
0
0
50000
100000
150000
200000

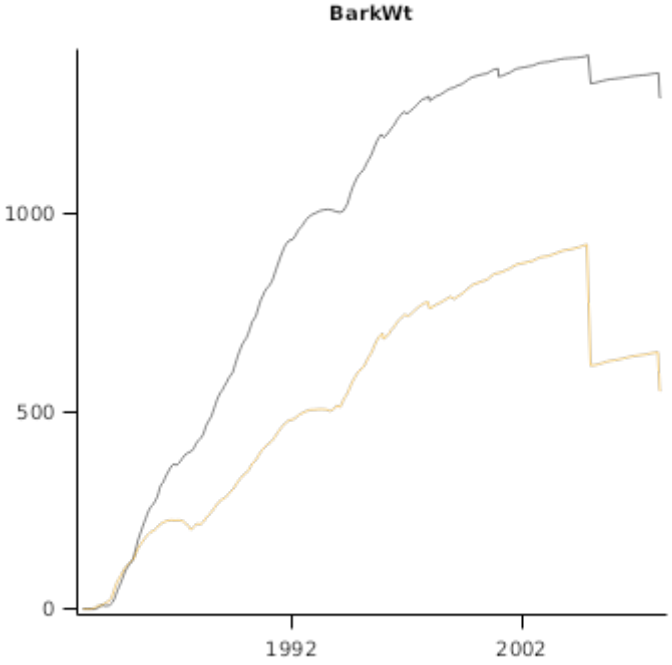

ConeWt
3000
2000
1000
0
1992
2002

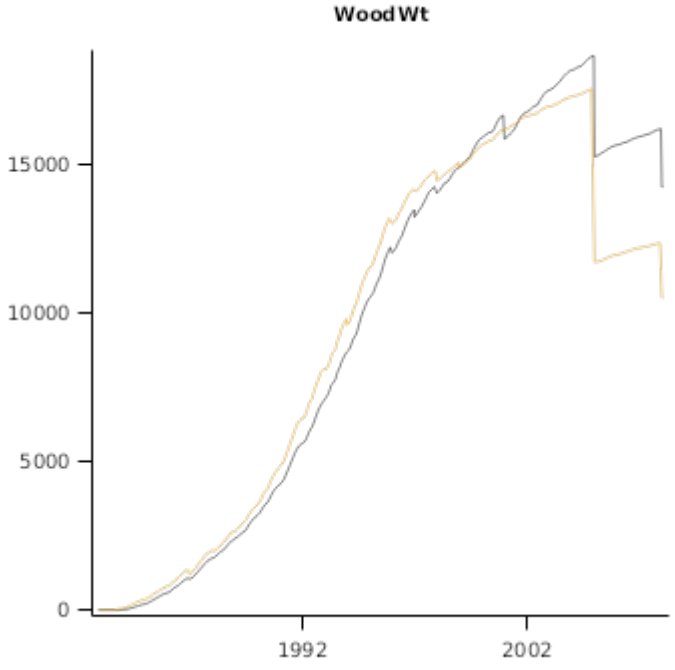

LeafWt
1000
500
0
1992
2002

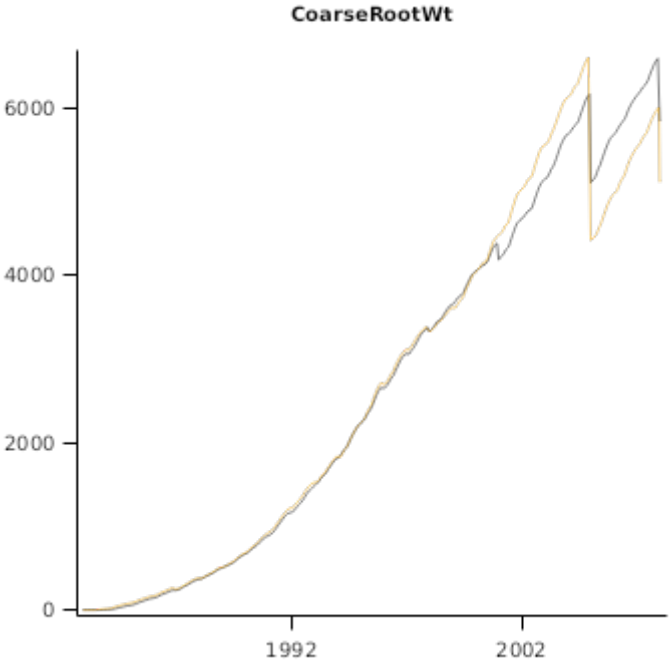

BranchWt
2000
1000
0
1992
2002

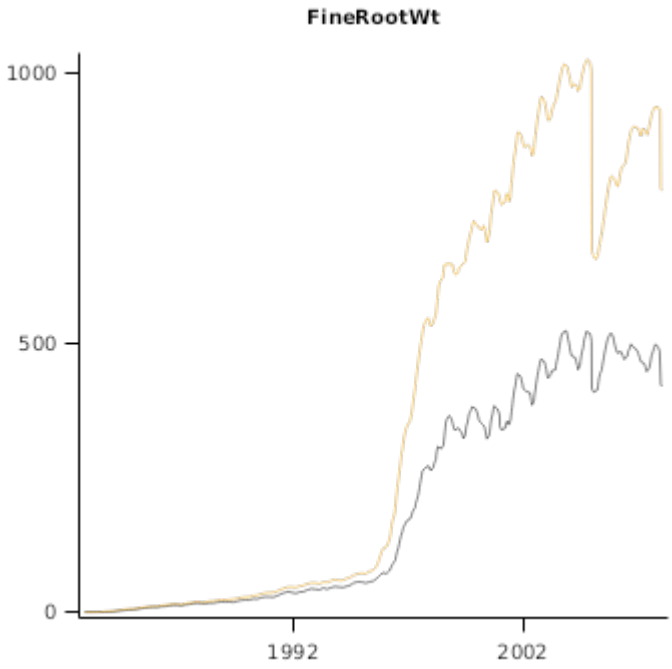
WoodBarkCoarseRootWt
15000
10000
5000
0
1992
2002

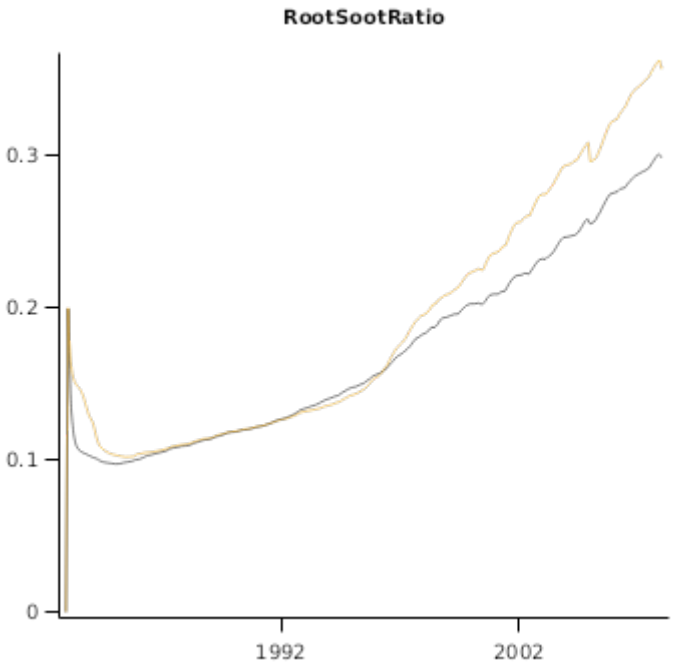

StemWt
20000
15000
10000
5000
0
1992
2002


BarkWt
1000
500
0
1992
2002

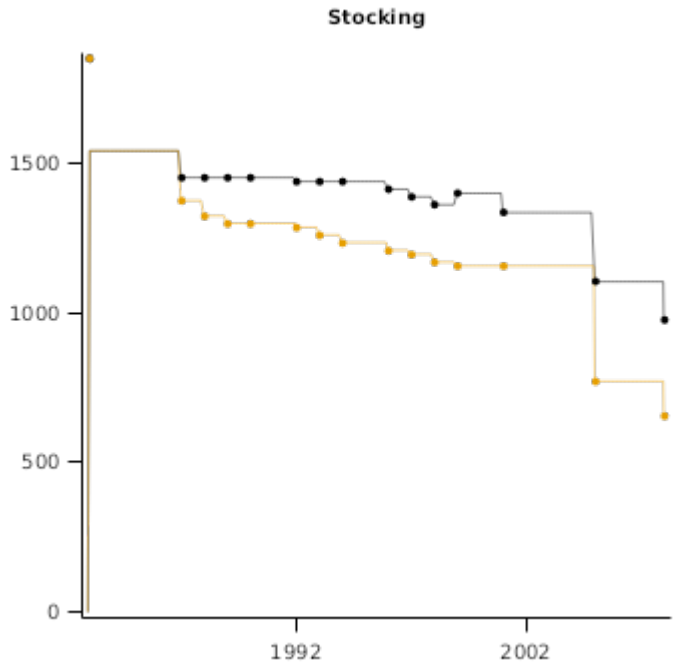

WoodWt
15000
10000
5000
0
1992
2002

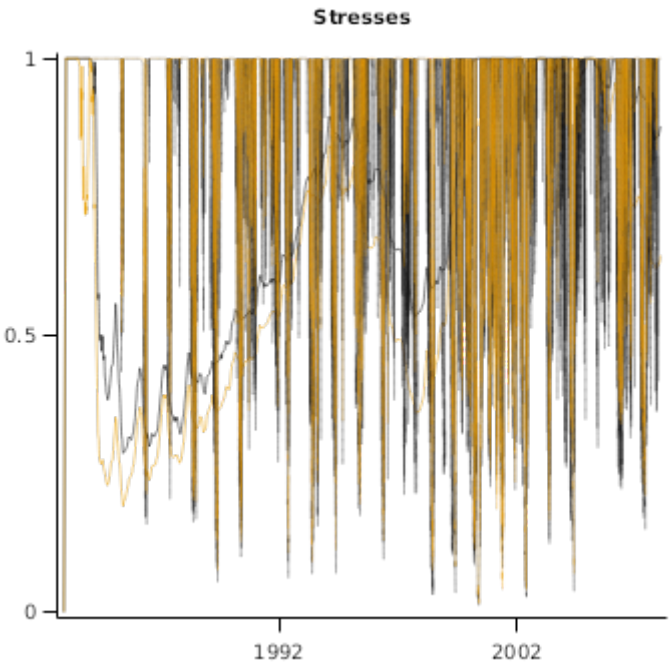

CoarseRootWt
6000
4000
2000
0
1992
2002

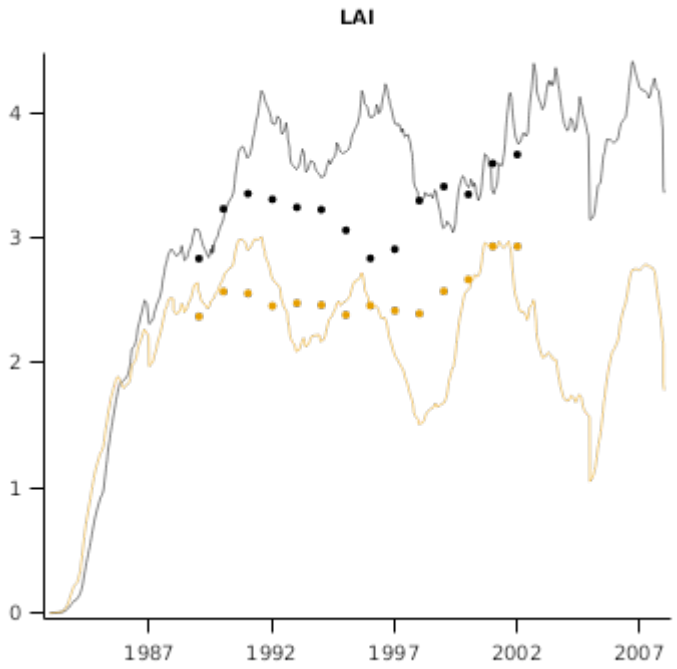


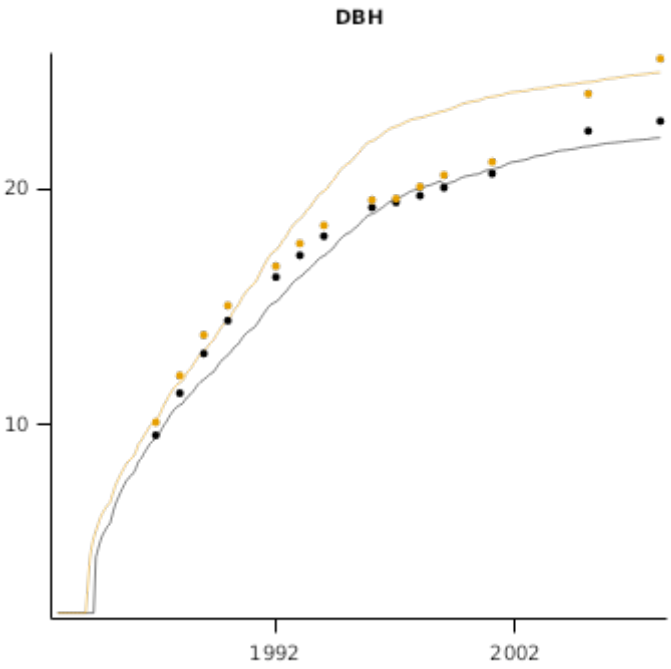


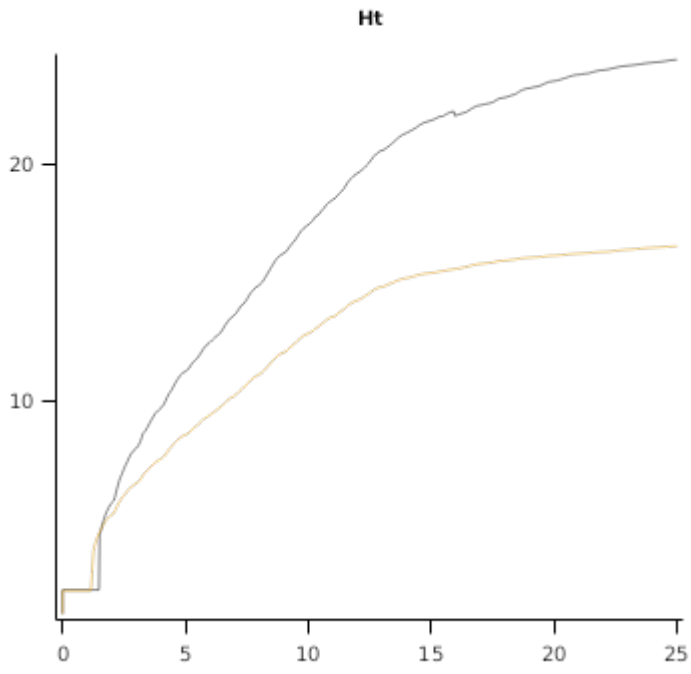
5.3.2.1.1.2 GraphsMetrics

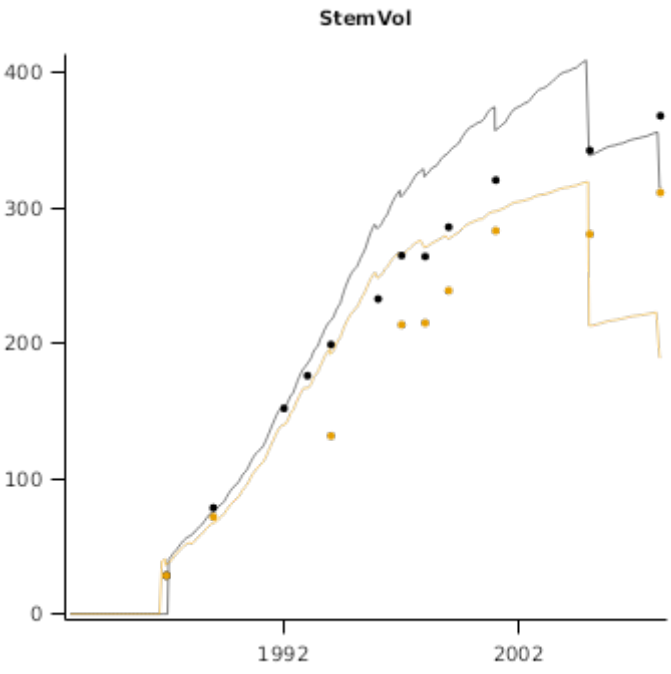

Stocking
1500
1000
500
0
1992
2002

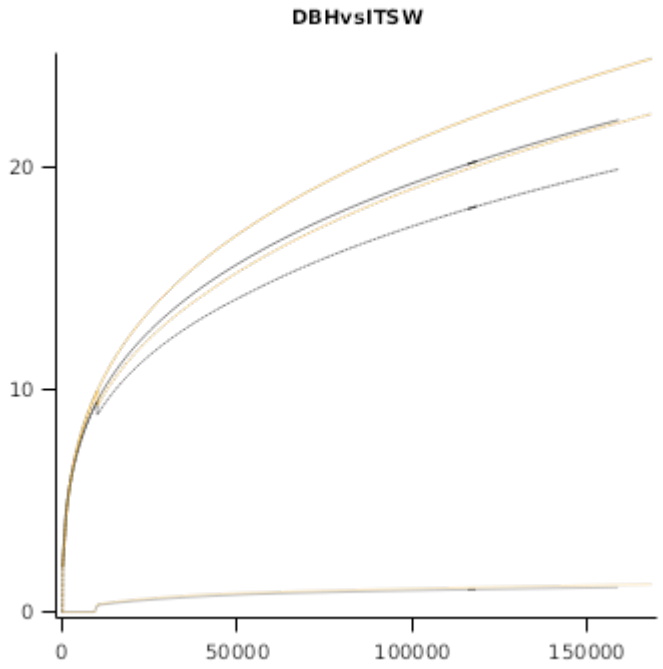

Stresses
1
0.5
0
1992
2002

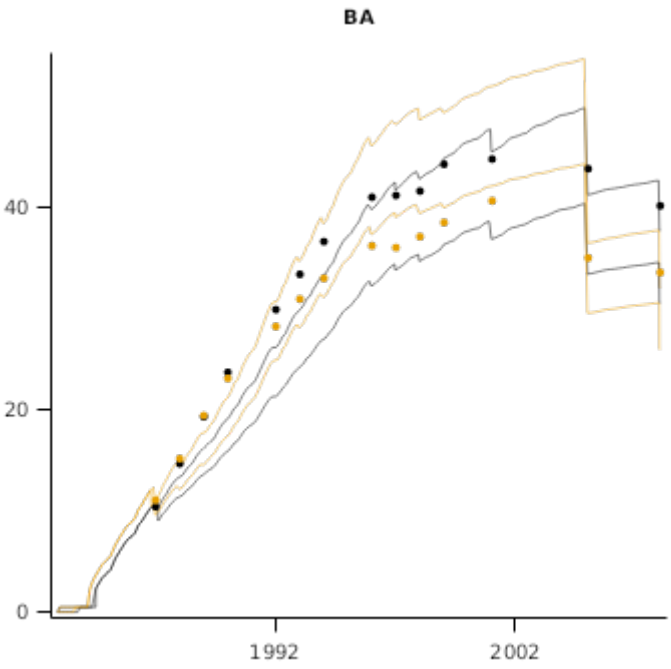

LAI
4
3
2
1
0
1987
1992
1997
2002
2007

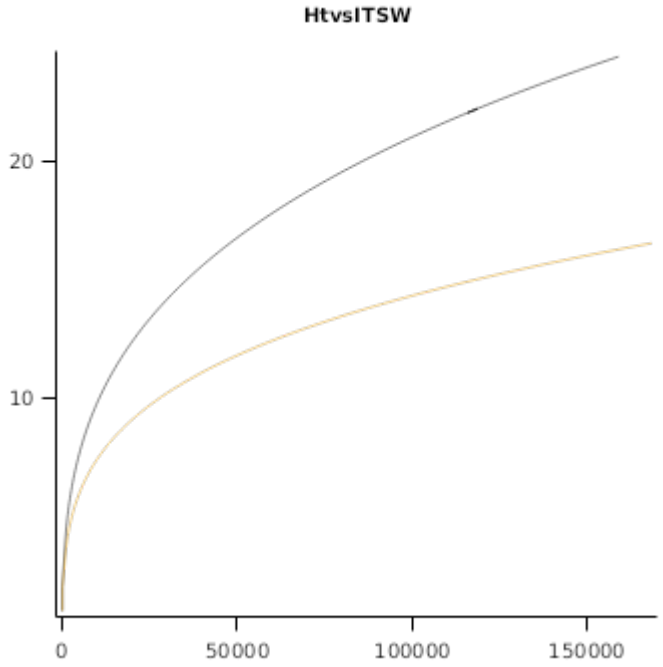

DBH
20
10
1992
2002

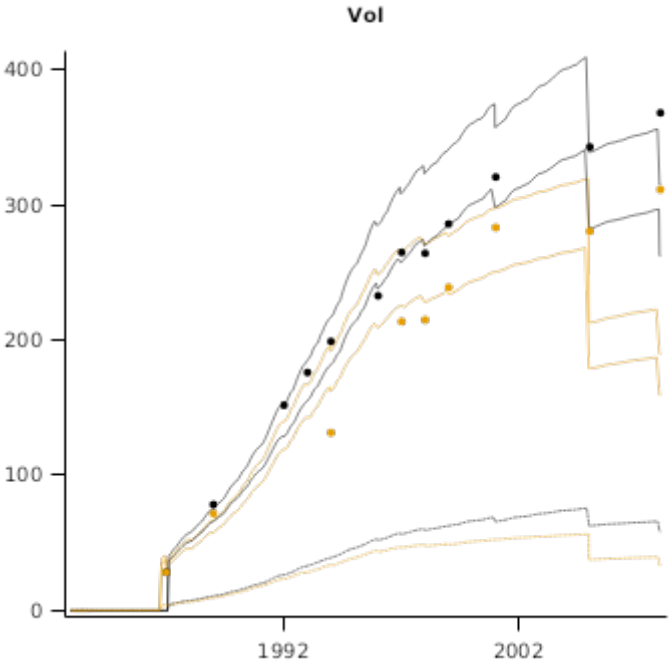

Ht
20
10
0
5
10
15
20
25

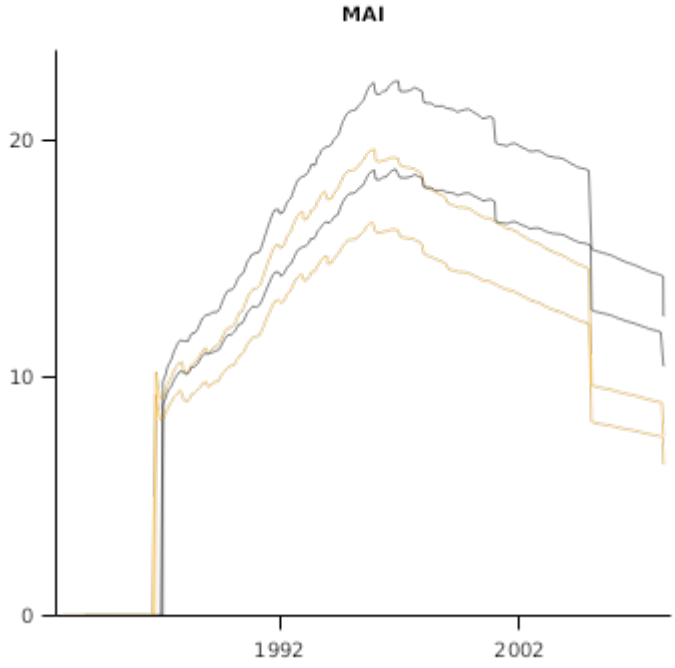

StemVol
400
300
200
100
0
1992
2002

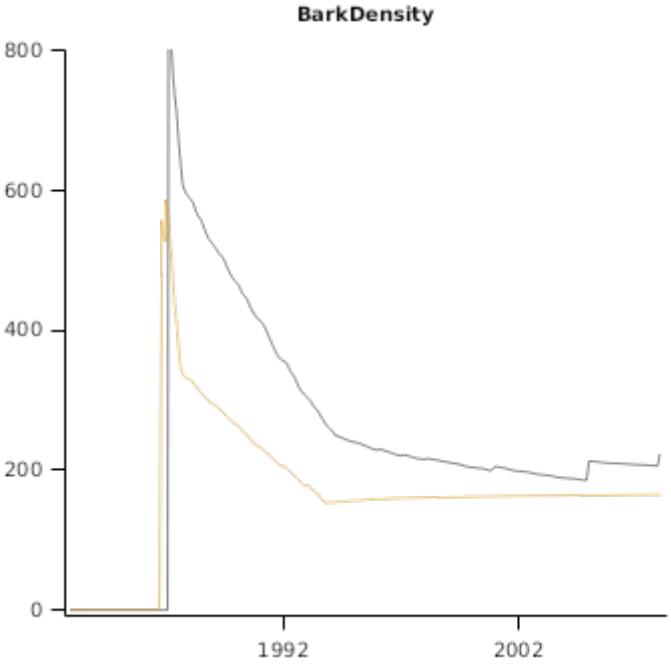

DBHvsITSW
20
10
0
0
50000
100000
150000

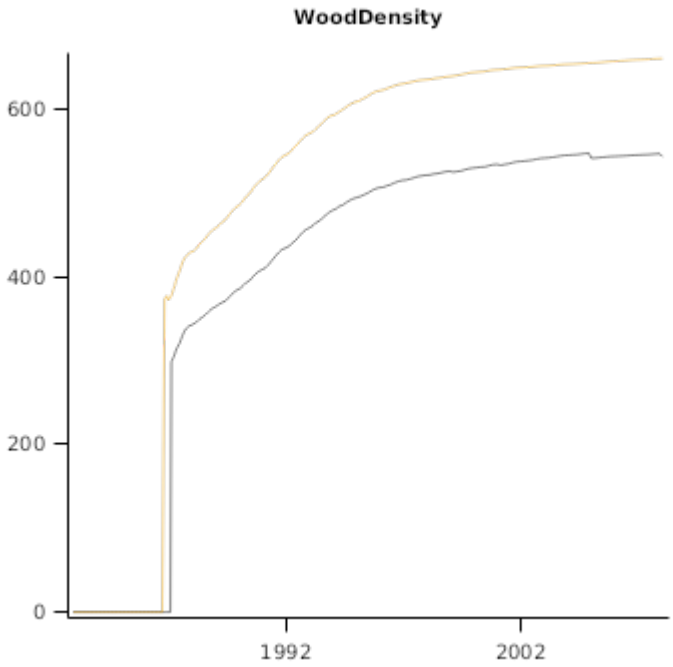

BA
40
20
0
1992
2002


HtvsITSW
20
10
0
50000
100000
150000


Vol
400
300
200
100
0
1992
2002


MAI
20
10
0
1992
2002


BarkDensity
800
600
400
200
0
1992
2002



5.3.2.2 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 couold not be expected to simulate, only the high input treatment was simualted.

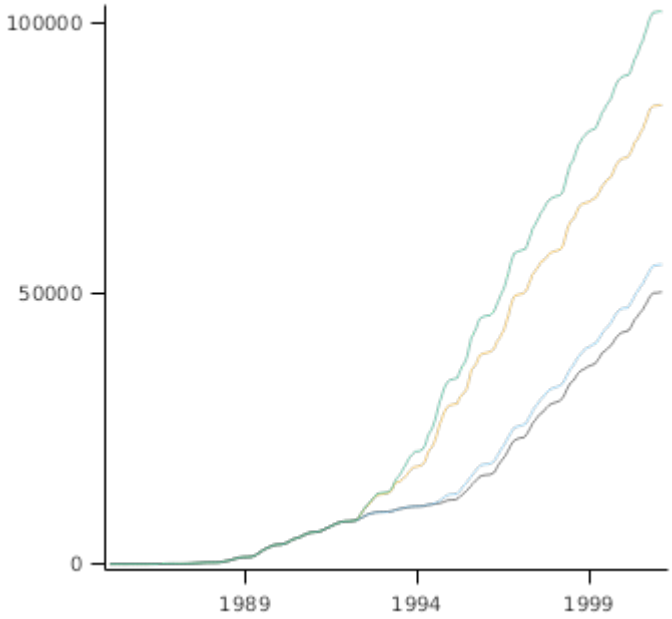
Numerous publications report on this experiment, of which we drew on Zhao et al., 2016, Landsberg et al., 2001, Albaugh et al., 2009, Albaugh et al., 2004, and Albaugh et al., 1998.

List of experiments.

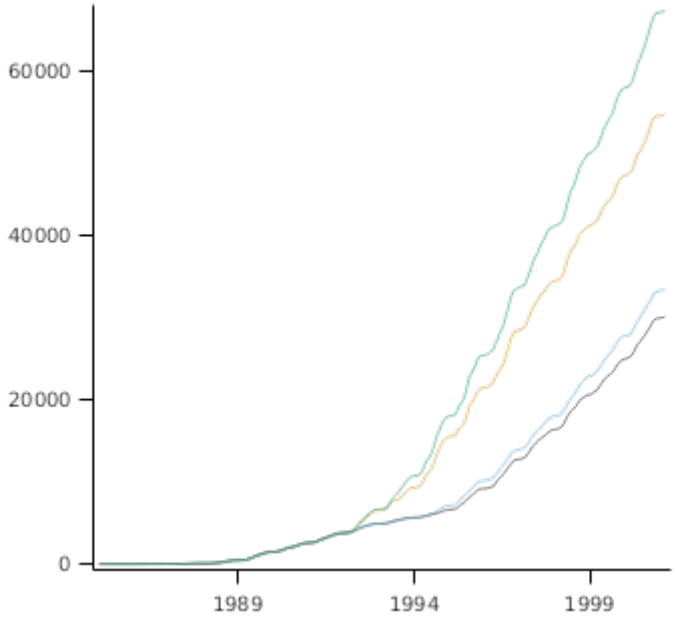
Experiment Name	Design (Number of Treatments)
SETRE	S (4)

5.3.2.2.1 GraphsWeights

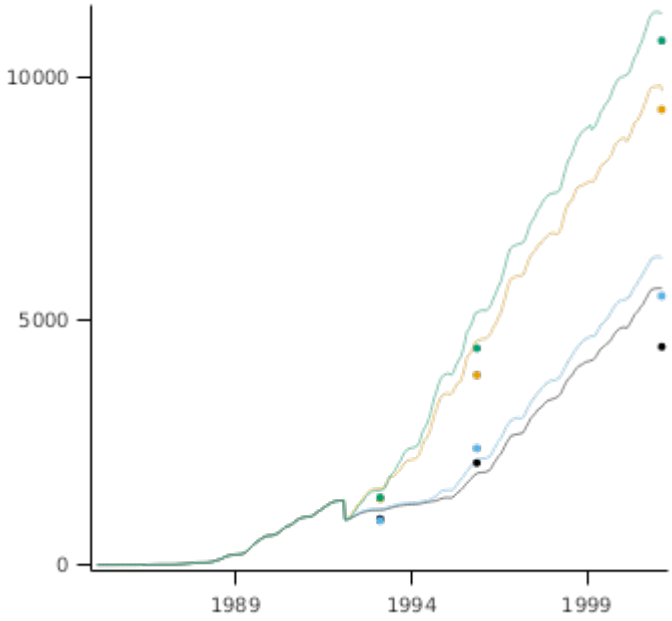
IndividualTreeLiveWt



IndividualStemWt

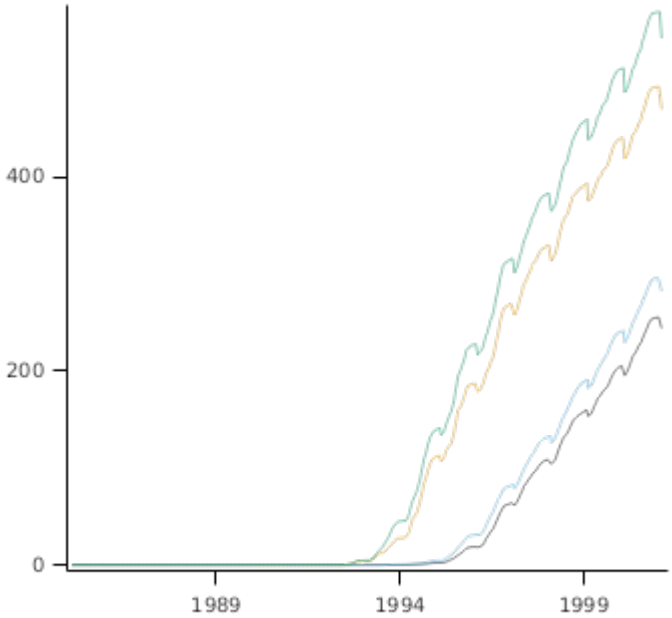


AboveGroundWt

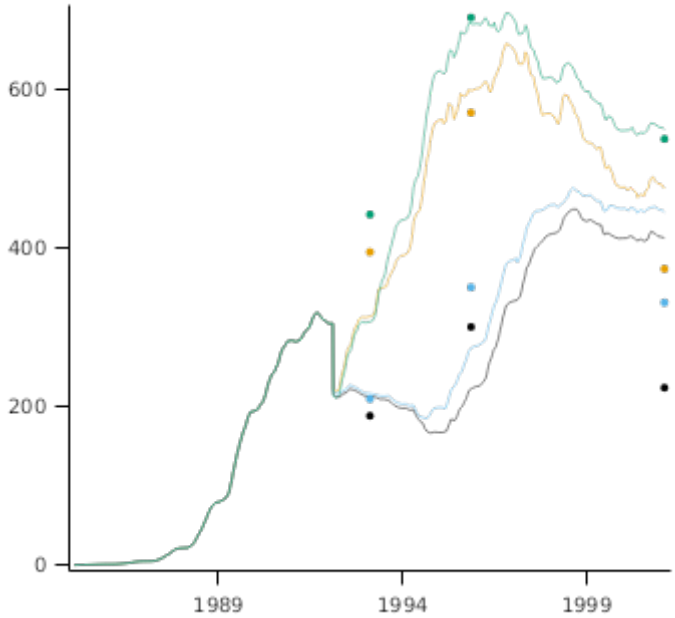


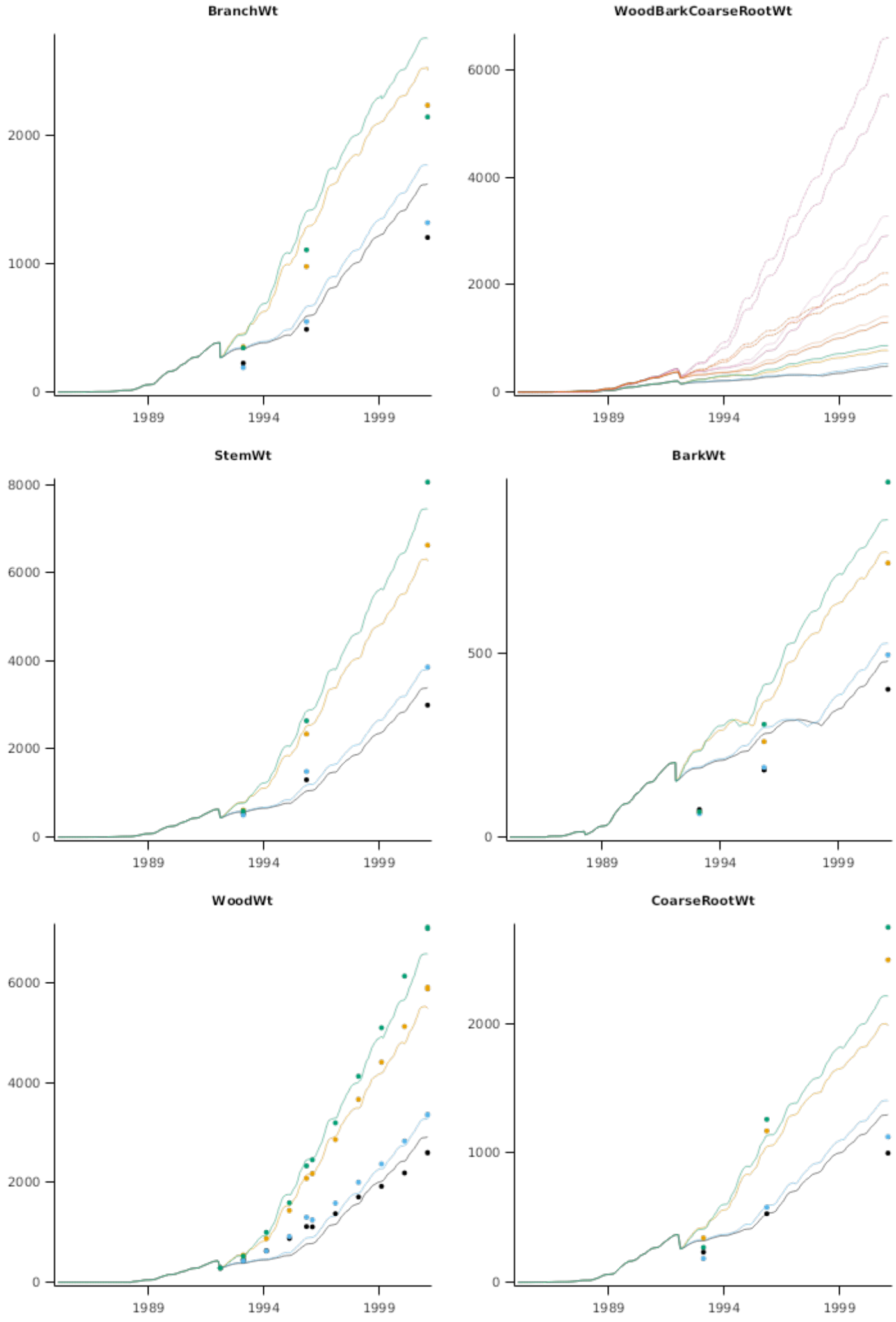
ComponentWts

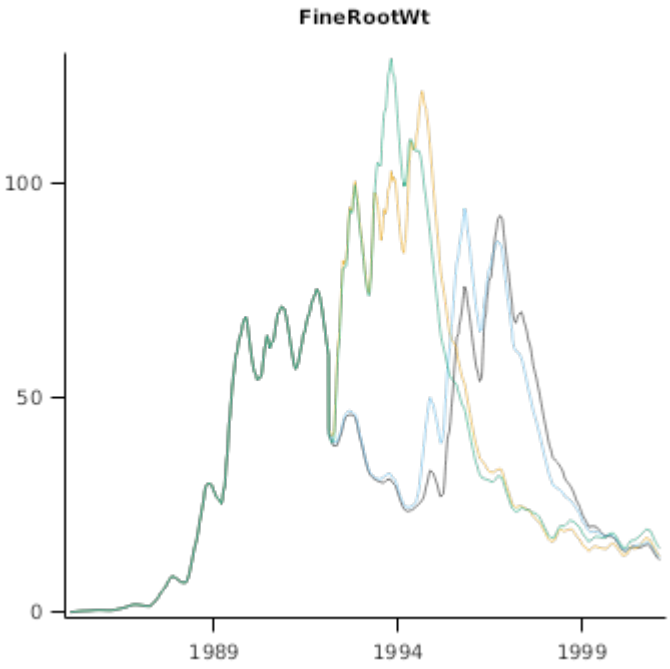
ConeWt

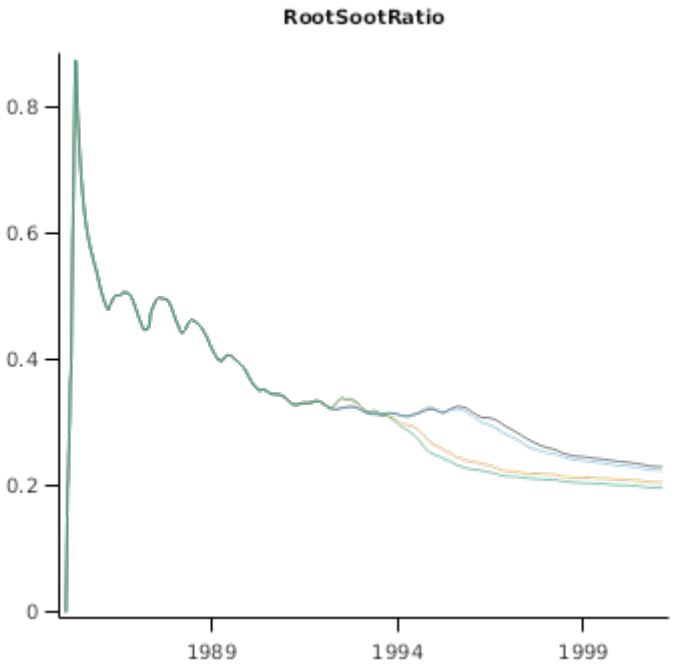


LeafWt




BranchWt
WoodBarkCoarseRootWt
StemWt
BarkWt
WoodWt
CoarseRootWt
0
1000
2000
4000
6000
8000
500
1989
1994
1999





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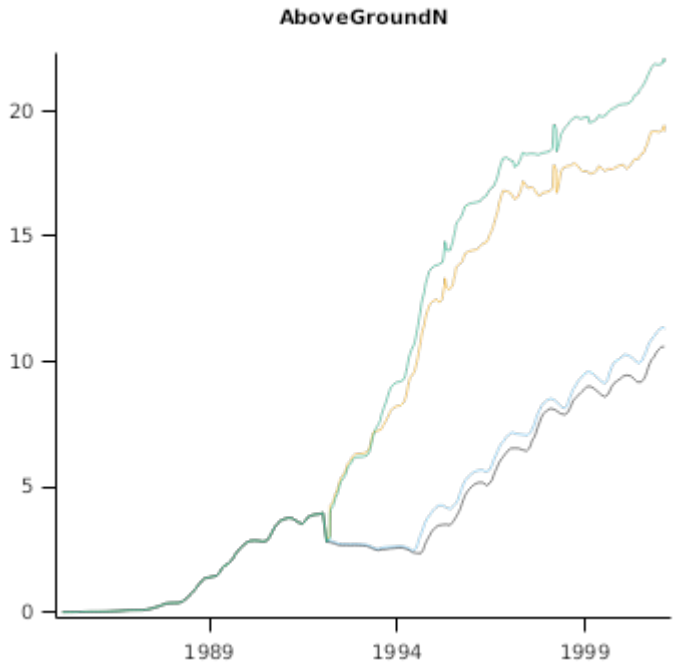
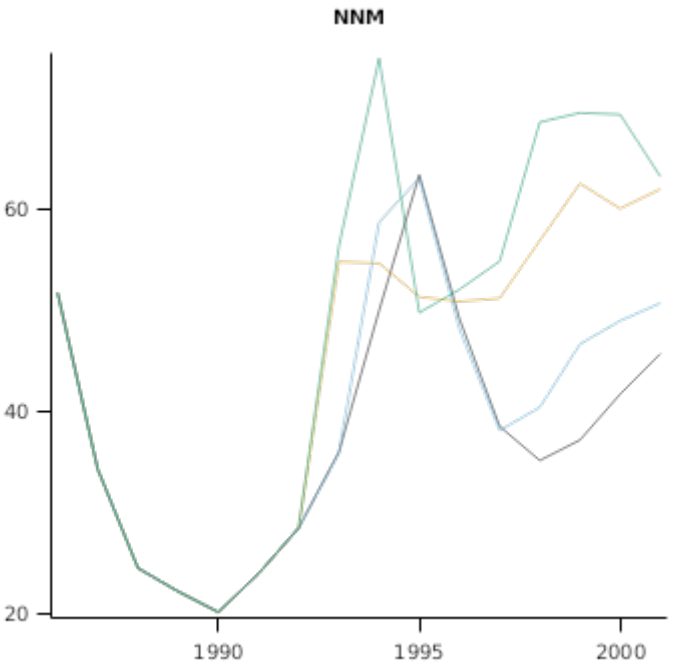
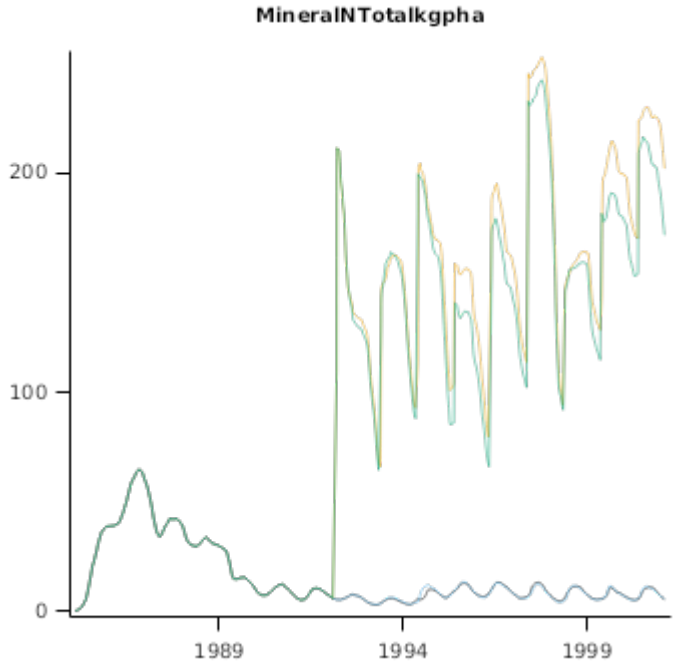
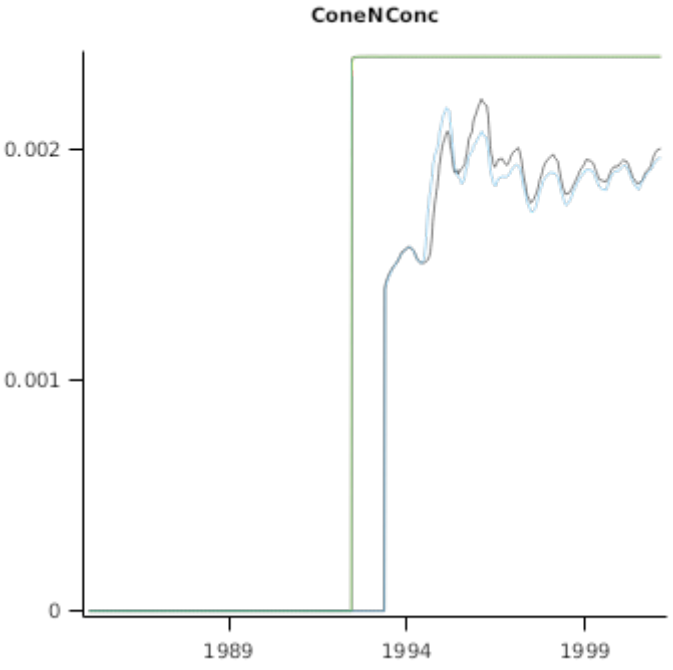
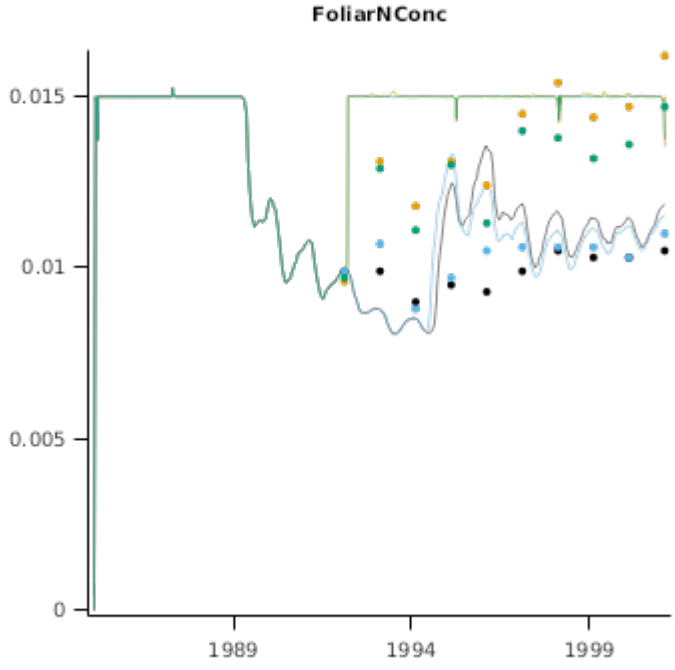
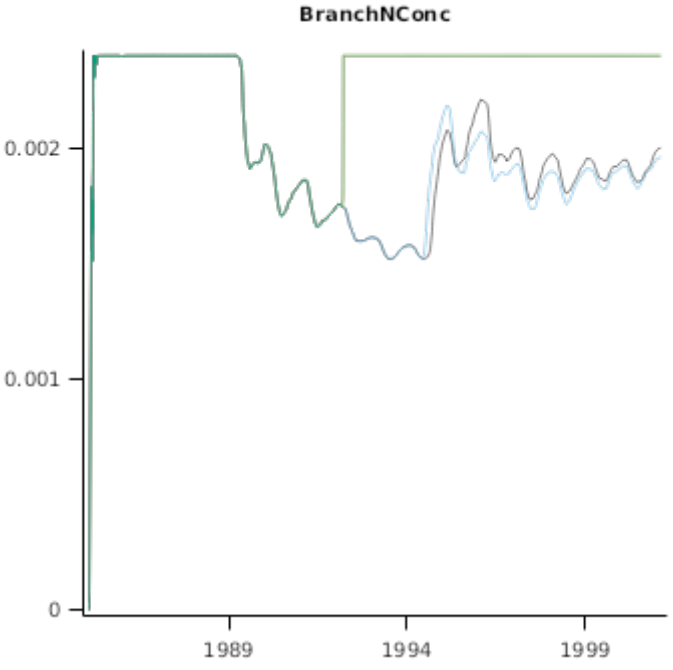

AboveGroundN
20
15
10
5
0
1989
1994
1999

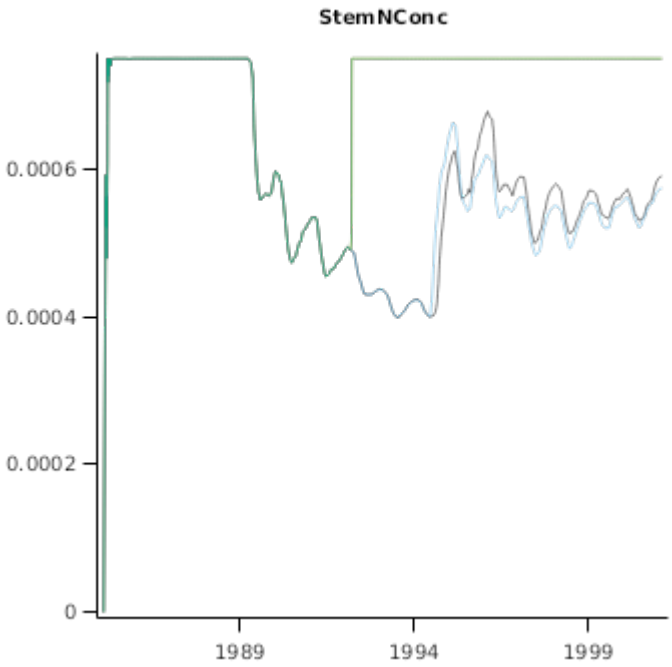

NNM
60
40
20
1990
1995
2000

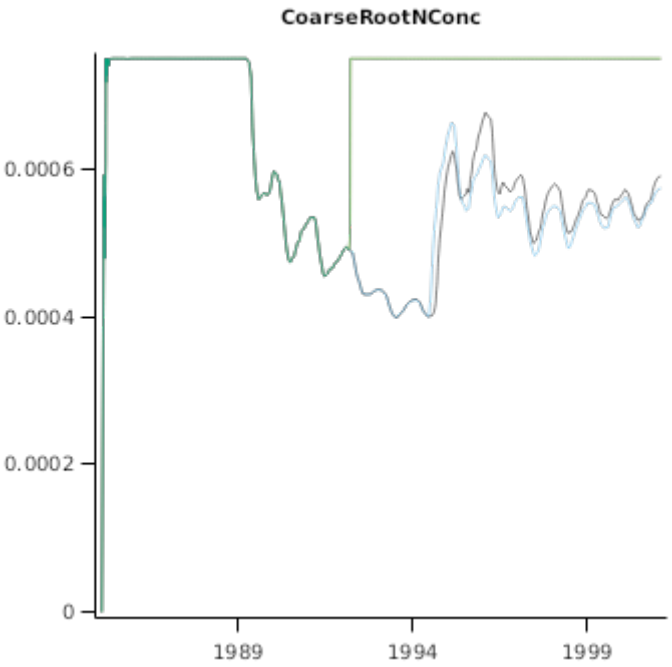

MineralNTotalkgpha
200
100
0
1989
1994
1999

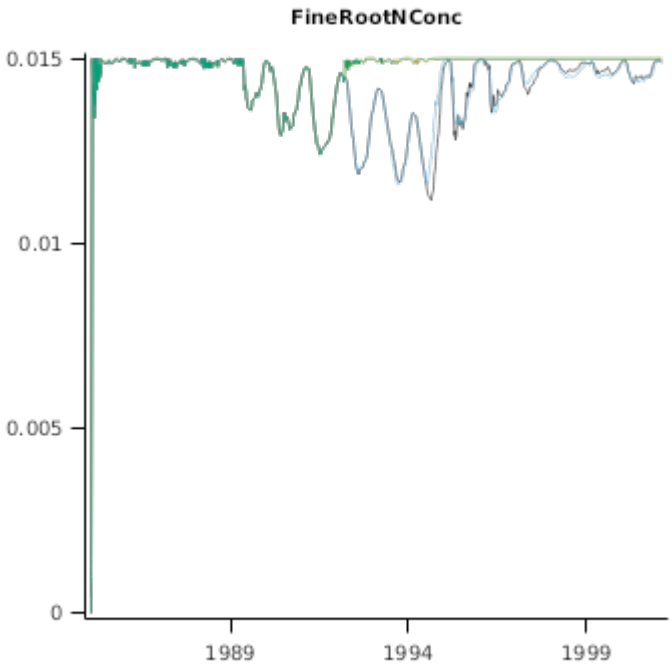

ConeNConc
0.002
0.001
0
1989
1994
1999


FoliarNConc
0.015
0.01
0.005
0
1989
1994
1999

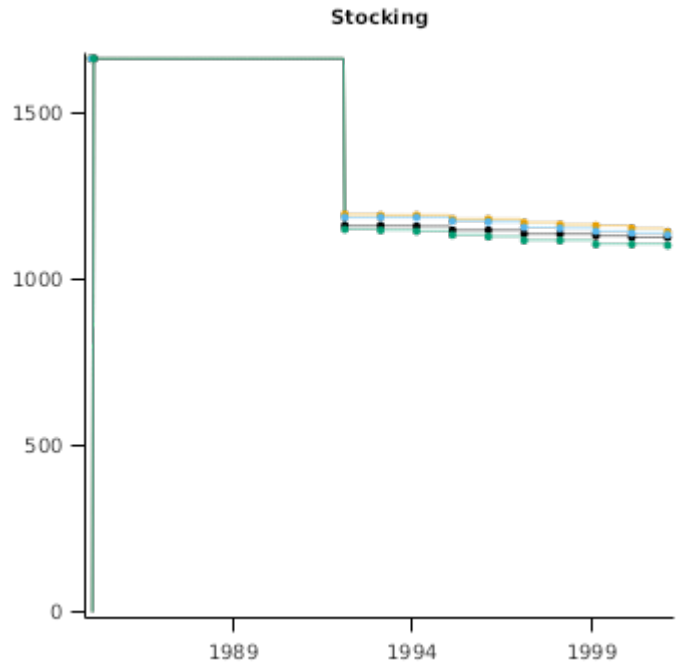

BranchNConc
0.002
0.001
0
1989
1994
1999

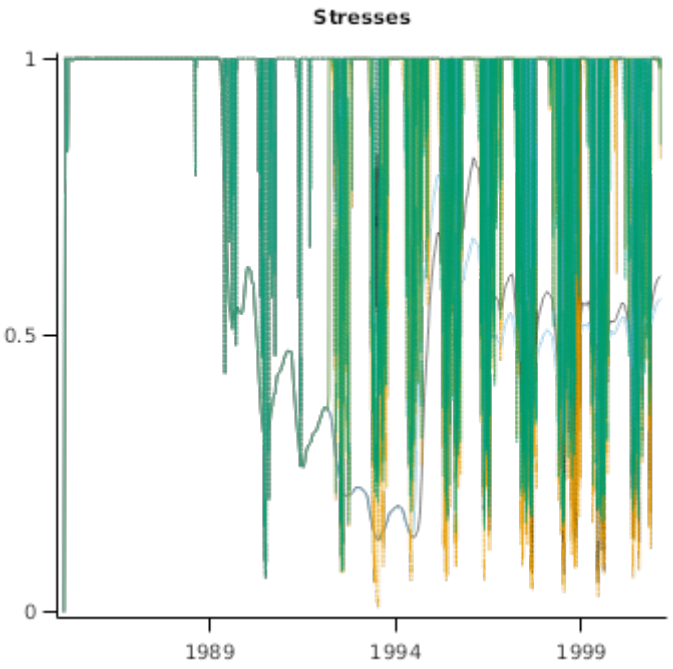


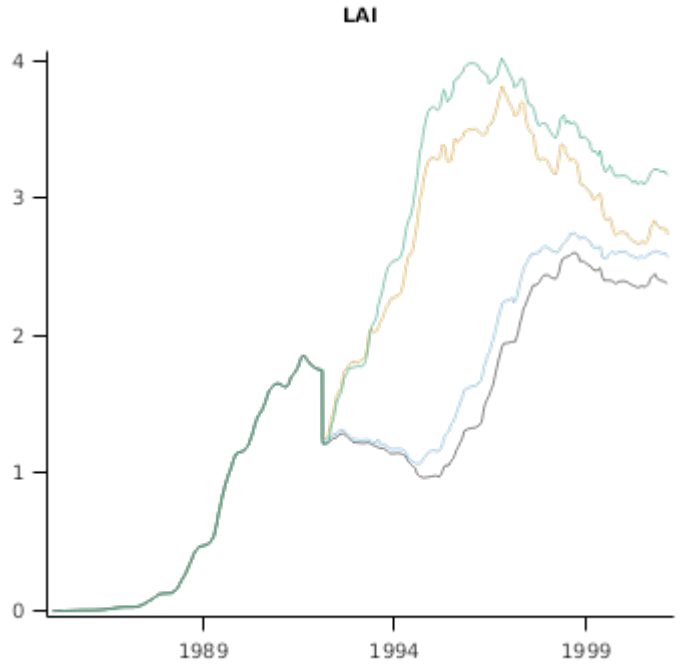


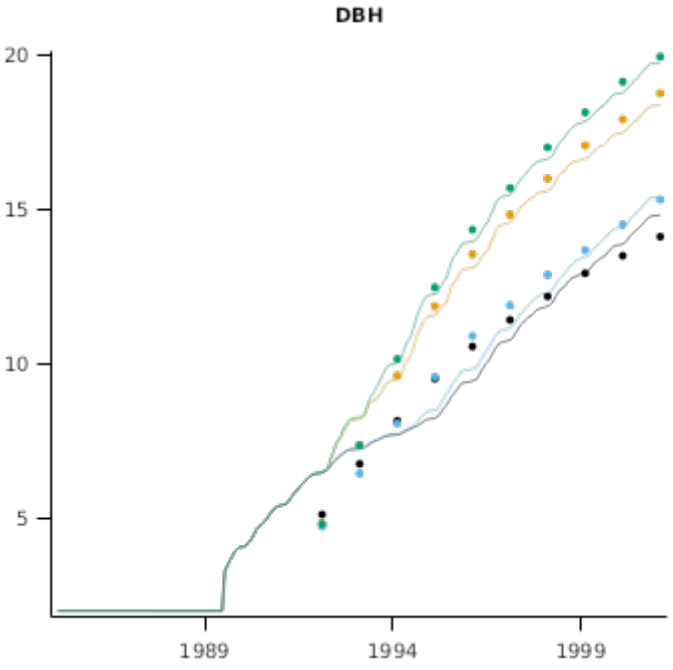


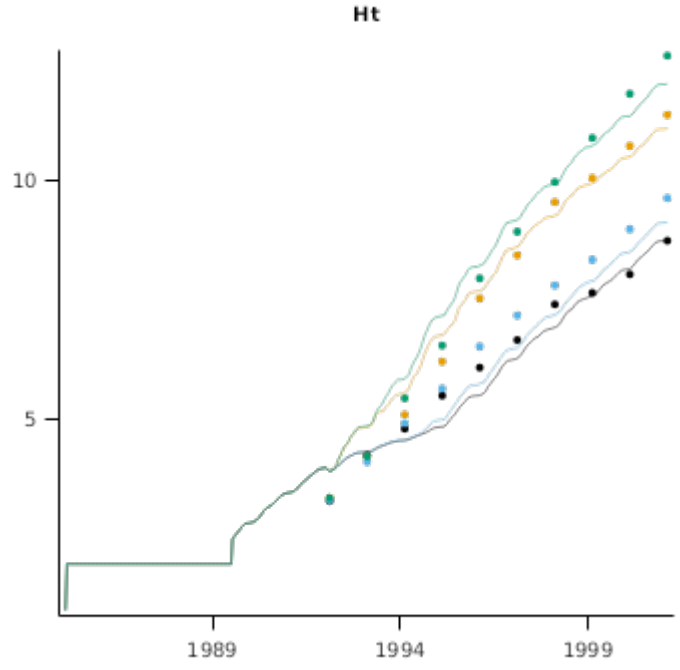
5.3.2.2.3 GraphsMetrics

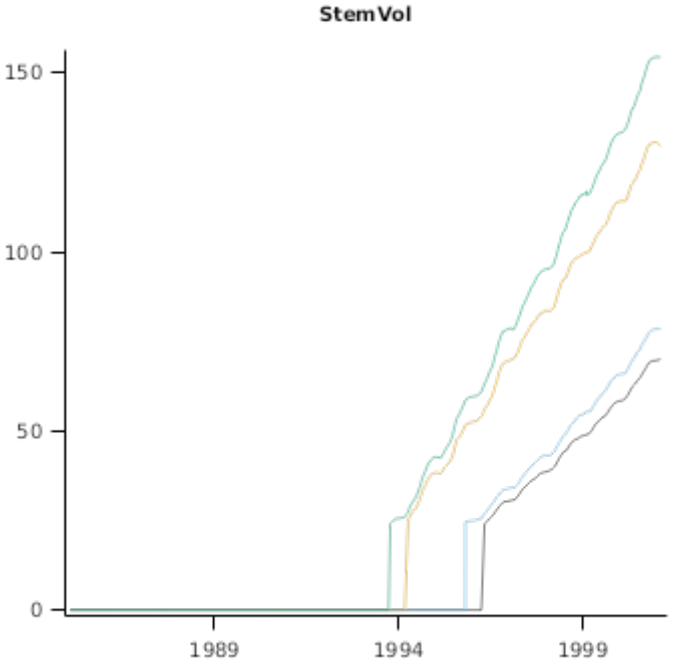

Stocking
1500
1000
500
0
1989
1994
1999

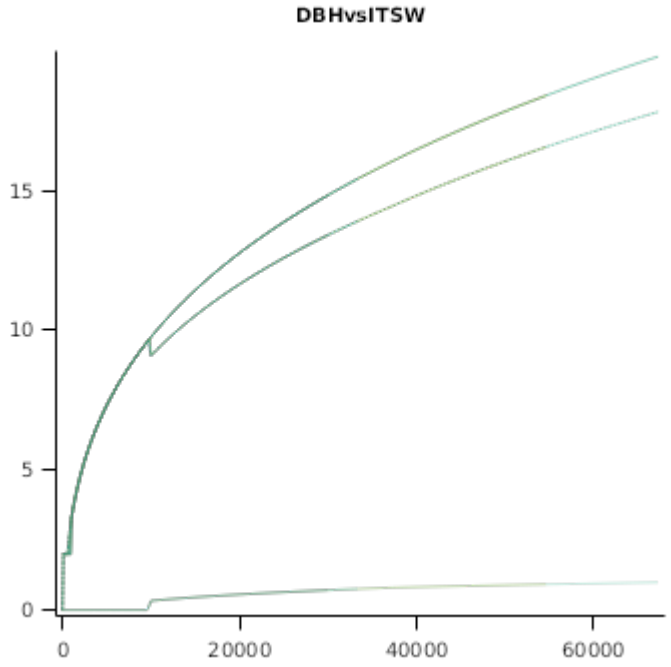

Stresses
1
0.5
0
1989
1994
1999

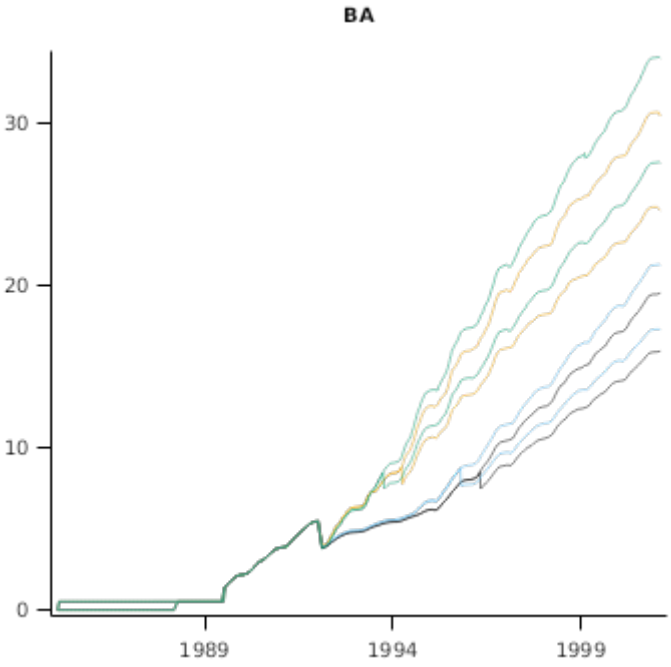

LAI
4
3
2
1
0
1989
1994
1999

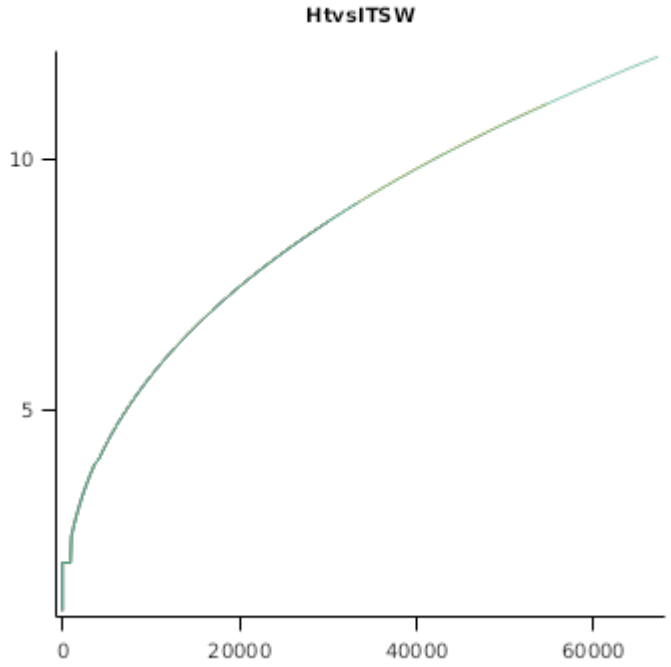

DBH
20
15
10
5
1989
1994
1999

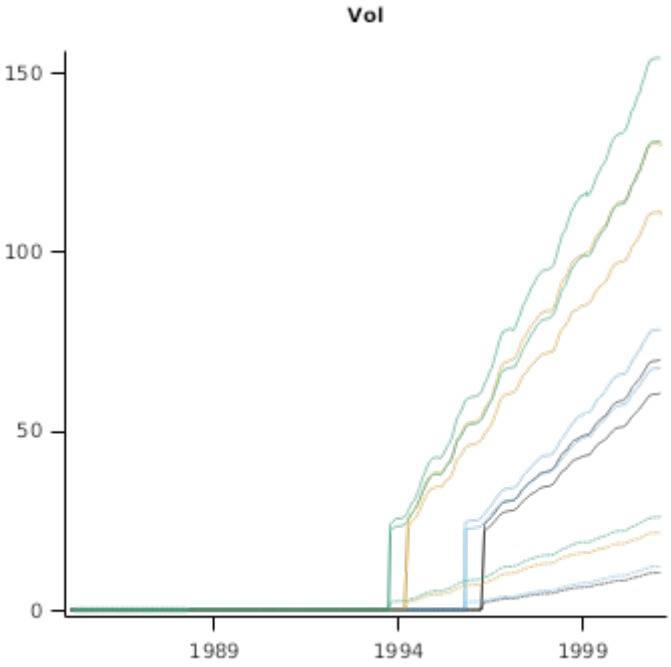

Ht
10
5
1989
1994
1999

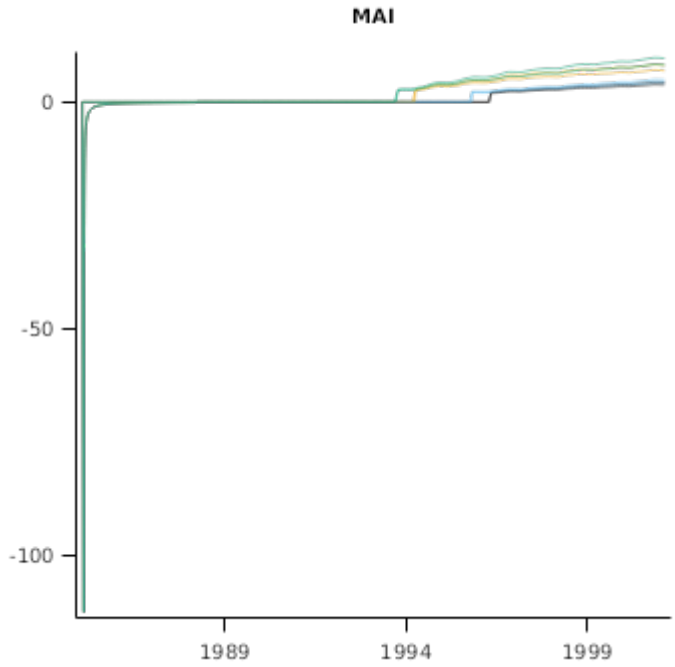

StemVol
150
100
50
0
1989
1994
1999

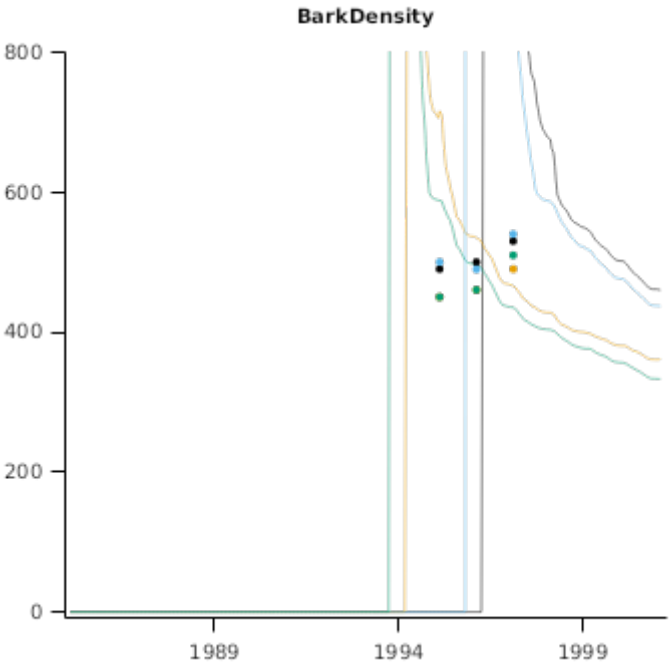

DBHvsITSW
15
10
5
0
0
20000
40000
60000

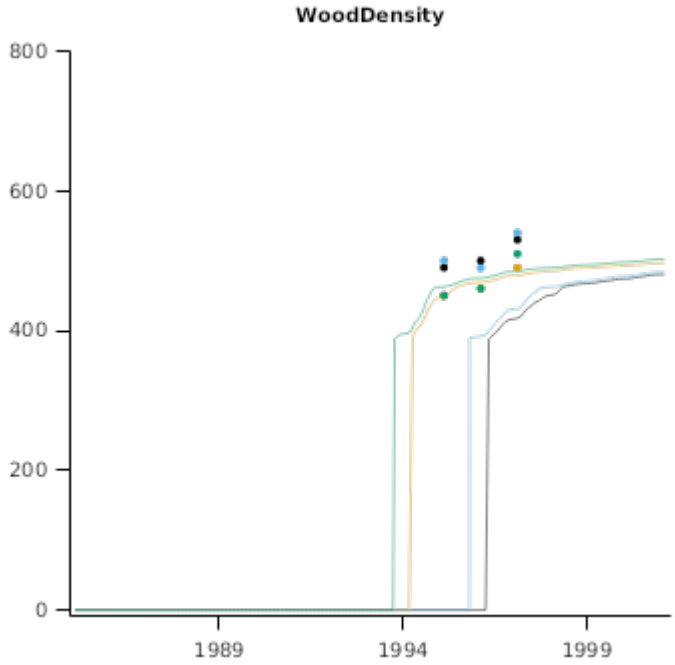

BA
30
20
10
0
1989
1994
1999


HtvsITSW
10
5
0
20000
40000
60000


Vol
150
100
50
0
1989
1994
1999


MAI
0
-50
-100
1989
1994
1999


BarkDensity
800
600
400
200
0
1989
1994
1999

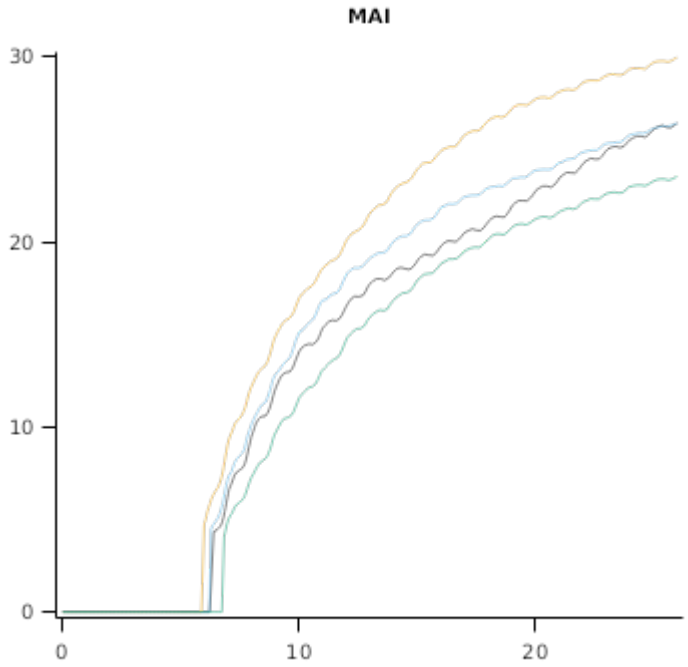


6 Sensibility

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.

6.1 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.



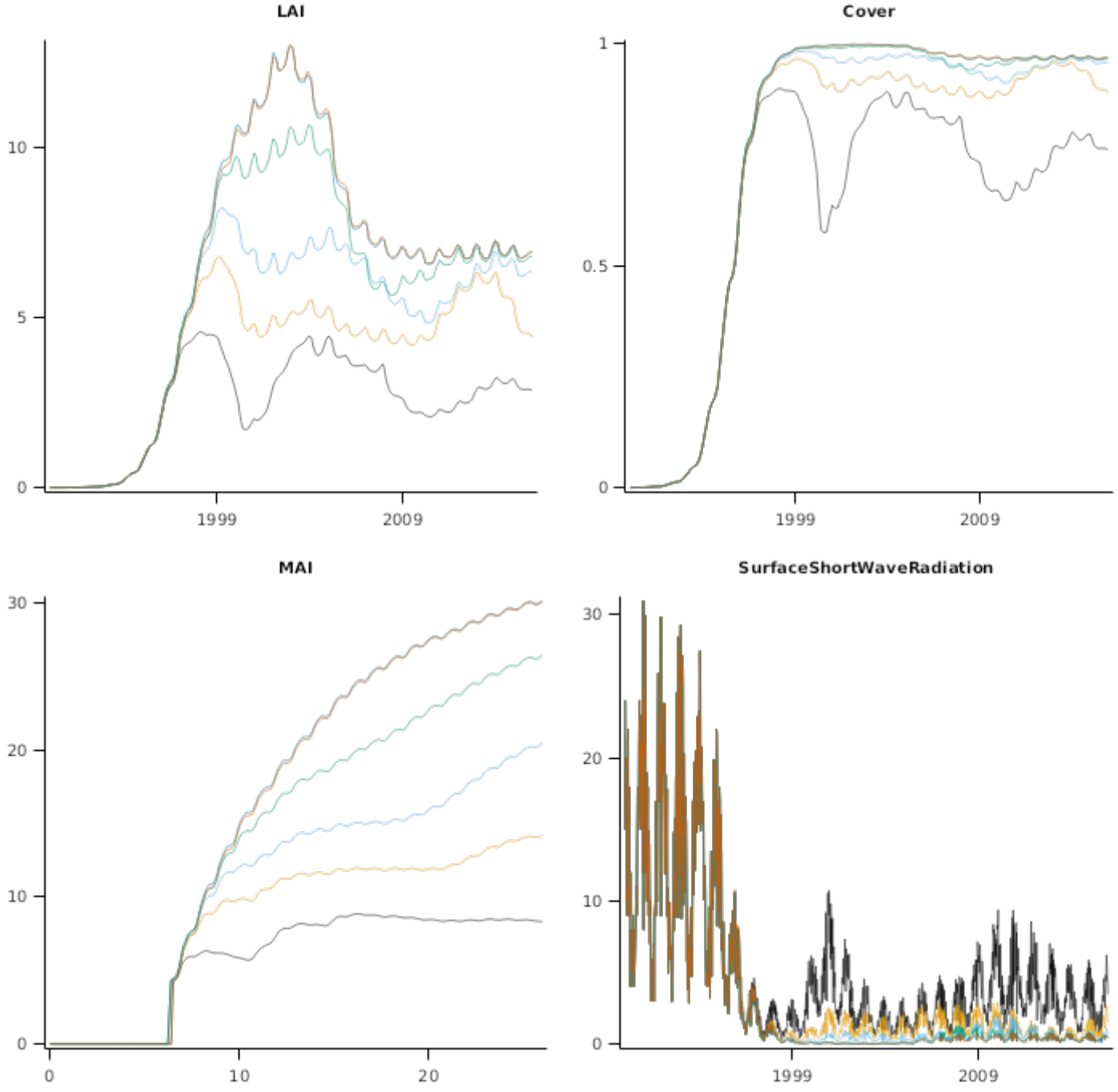
6.2 Response to Rainfall

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)

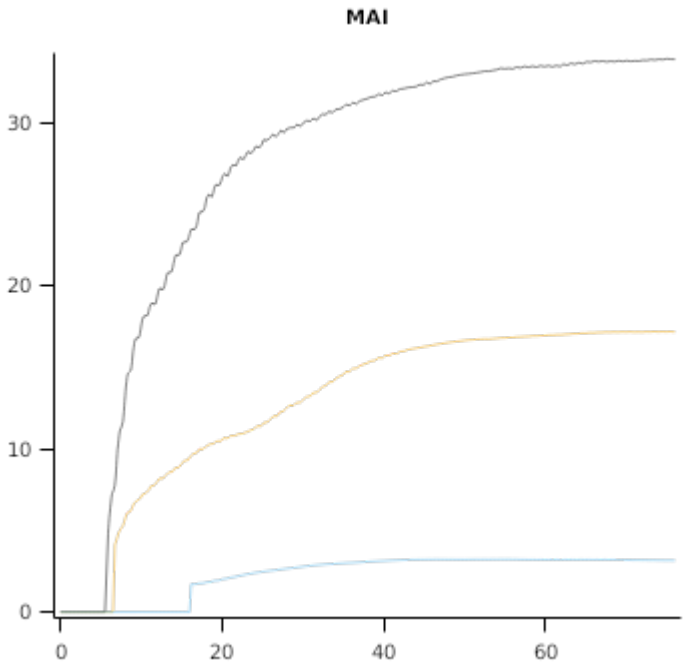


6.3 Response to Soil Fertility

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)



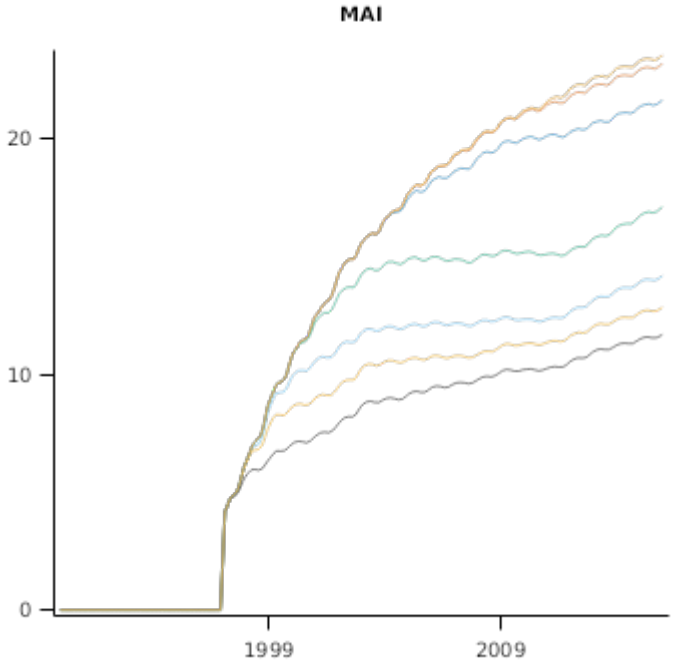
6.4 Reponse to N Fertilizer

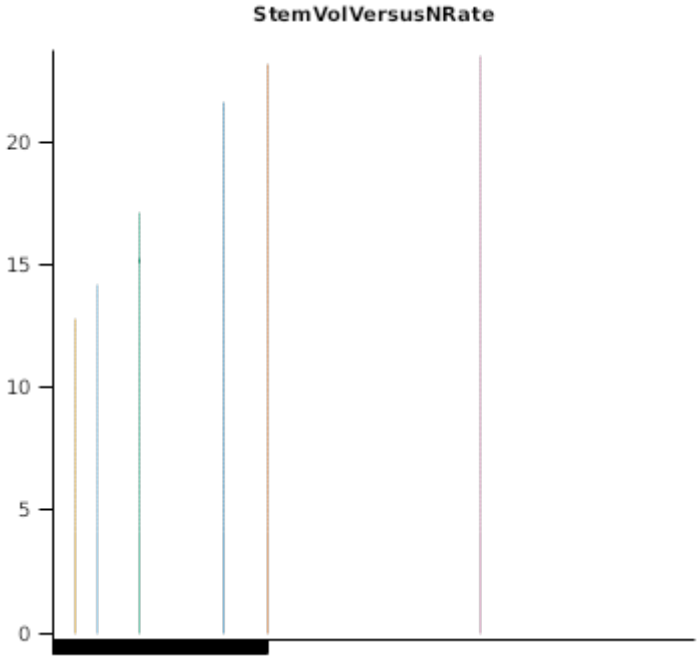
Pinus response to rate of N fertiliser are often asymptotic, the plateau of which is determined by other limiting factors. In the sensibility test presented here, an infertile soil at Stockdale, Victoria, Australia, was used as the basis for the simulations *P. radiata* was fertilised at 3 years of age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

Operationally, *P. radiata* plantations in Australia receive several hundered 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.

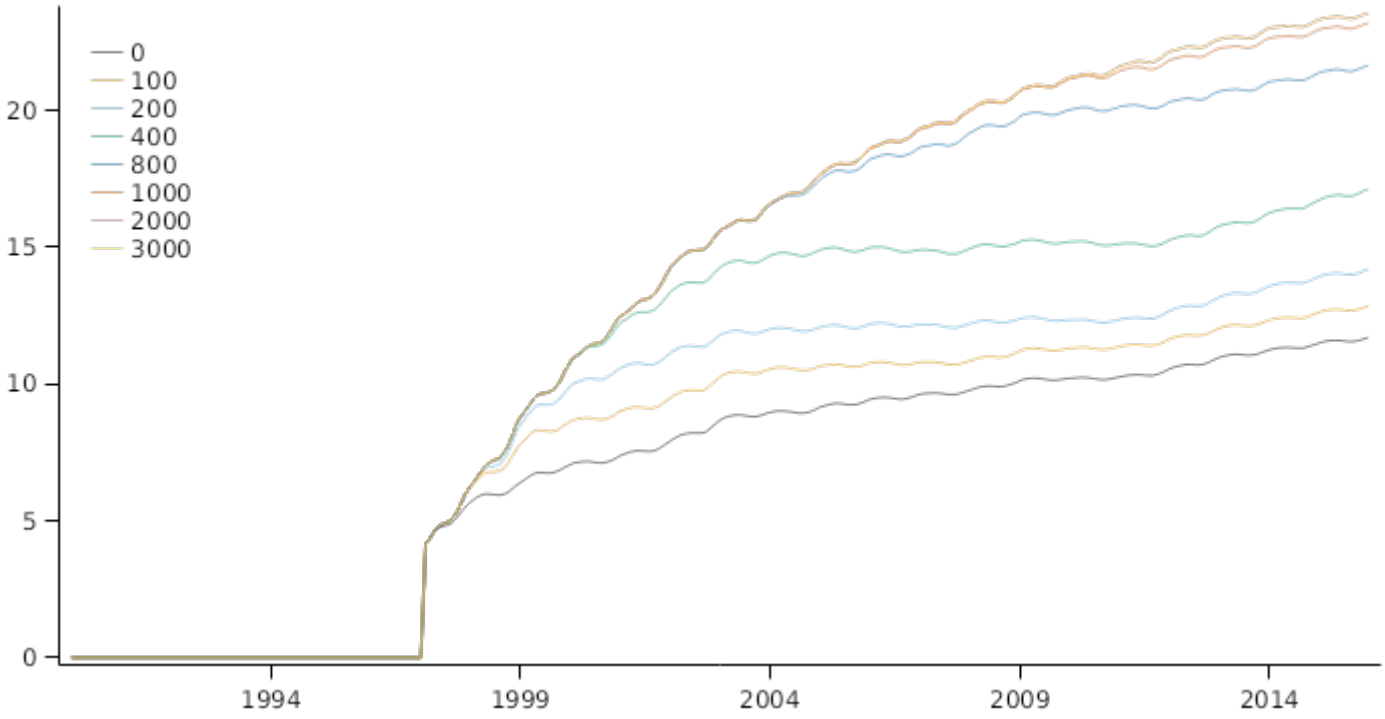
Experiment Name	Design (Number of Treatments)
Stockdale	N (8)



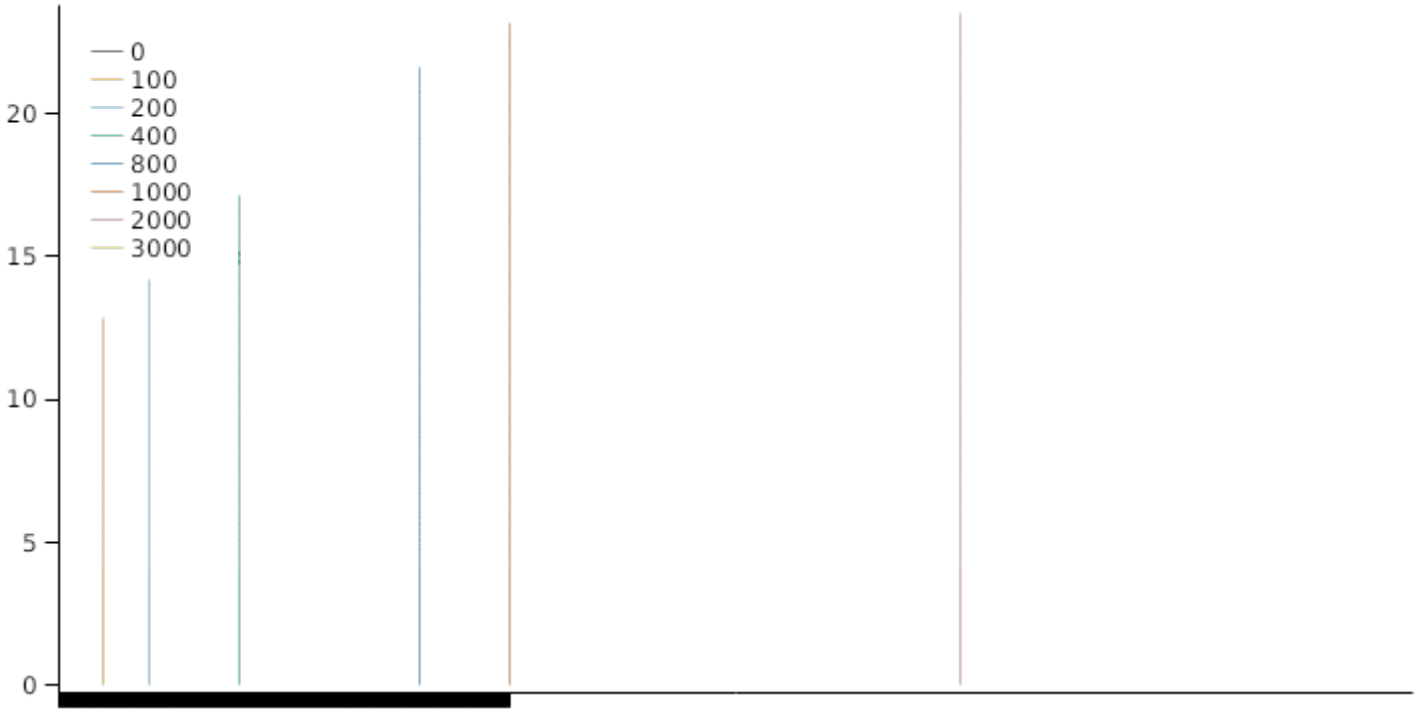


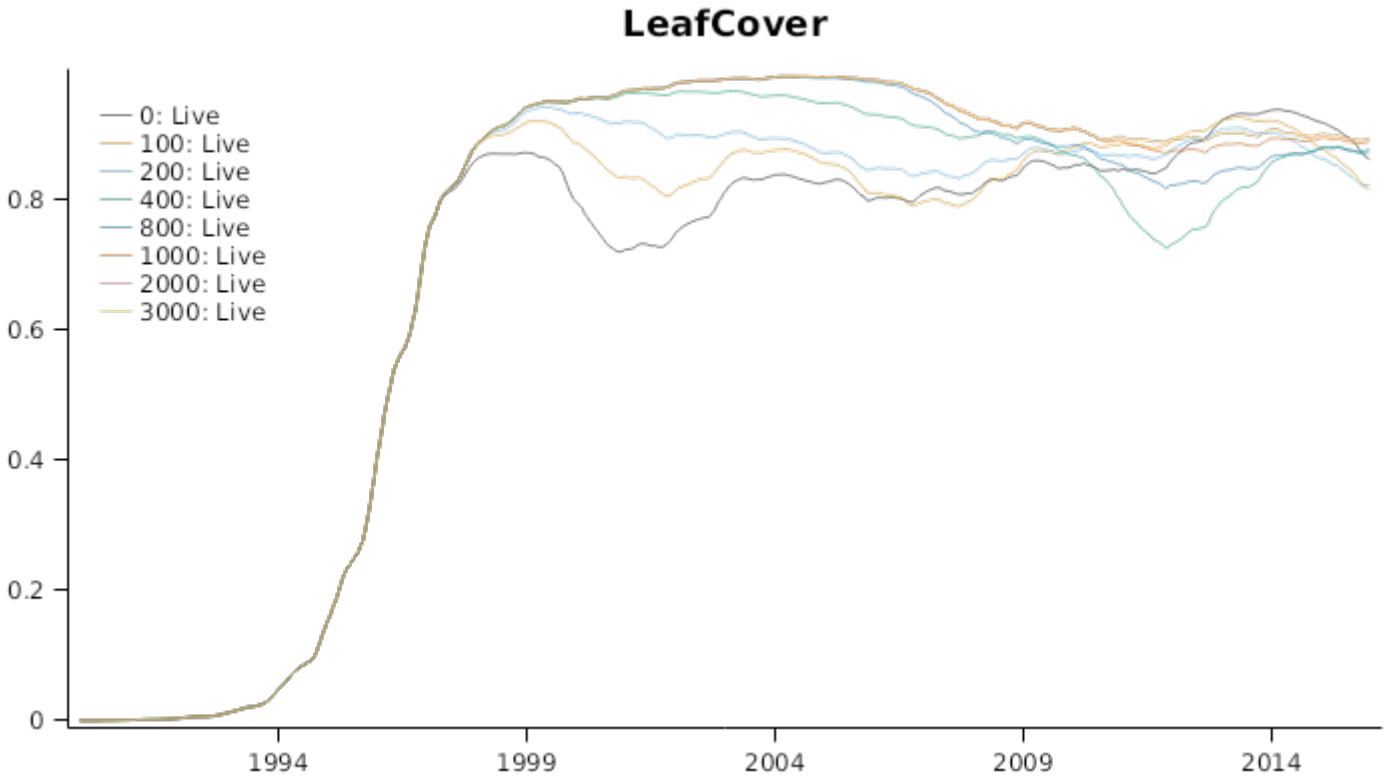
6.4.1 Stockdale

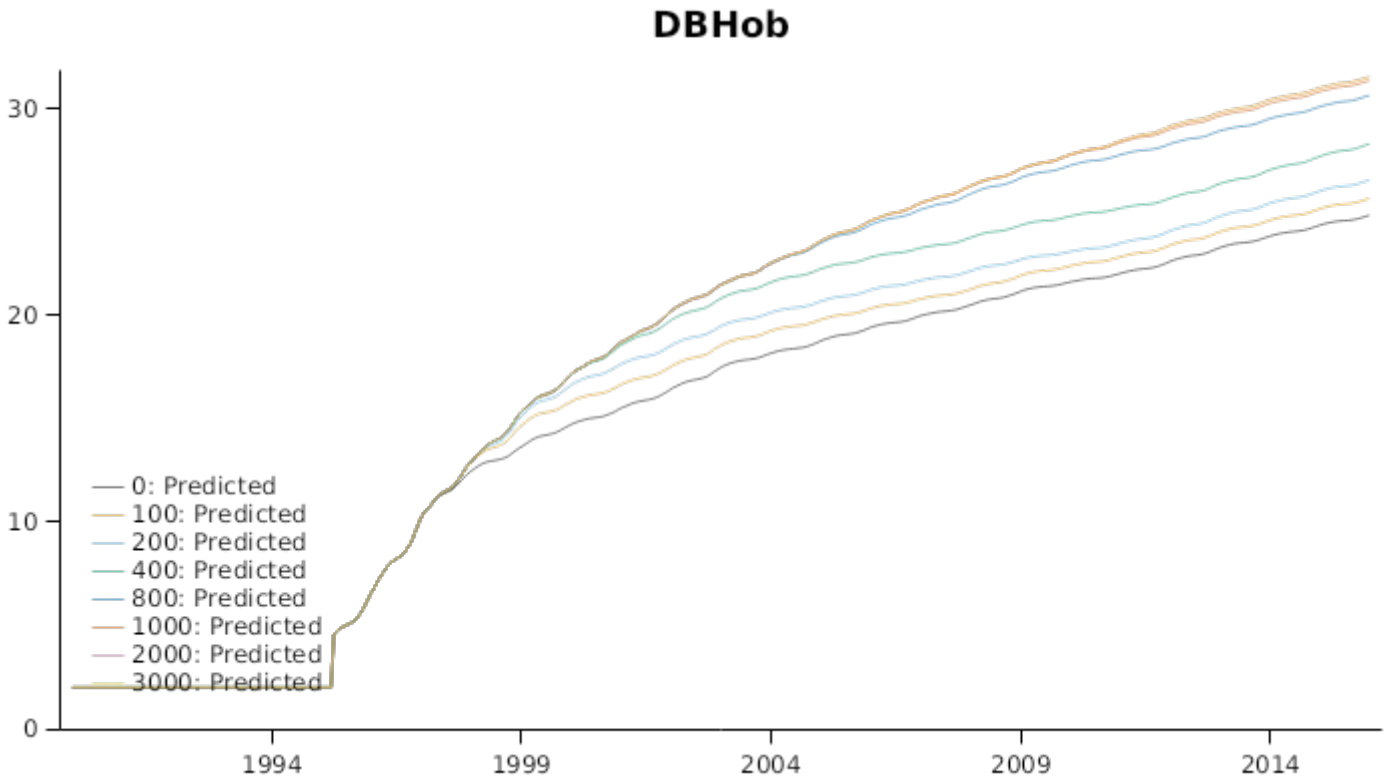
MAI



StemVolVersusNRate




LeafCover
0: Live
100: Live
200: Live
400: Live
800: Live
1000: Live
2000: Live
3000: Live
0
0.2
0.4
0.6
0.8
1994
1999
2004
2009
2014


DBHob
0: Predicted
100: Predicted
200: Predicted
400: Predicted
800: Predicted
1000: Predicted
2000: Predicted
3000: Predicted
0
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20
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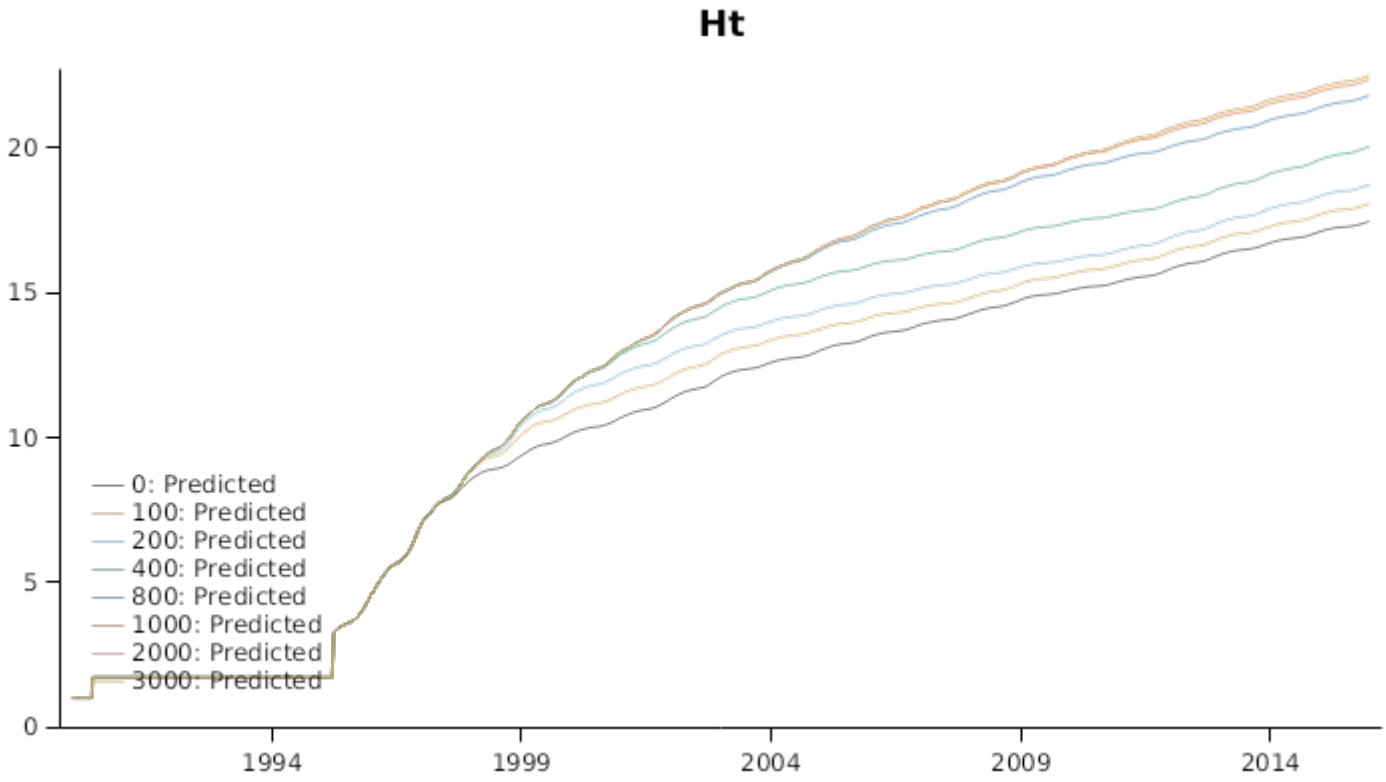
1999
2004
2009
2014



6.5 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 conersely Australian tropical and sub-tropical genotypes (e.g. elliottiiXcaribaeaF1) 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 ranage of yield potentials and patterns are therefore available.

Although the MAI values are generally as expected for all genotypes of *P. radaita*[[turvey1983soil] and others, this analysis raises some questions that could help focus further model improvements.

Calibration of the model focussed on Australian datasets.

The elliottiiIMPAC and taedaIMPAC genotypes simulate noticably reduced preformace 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.

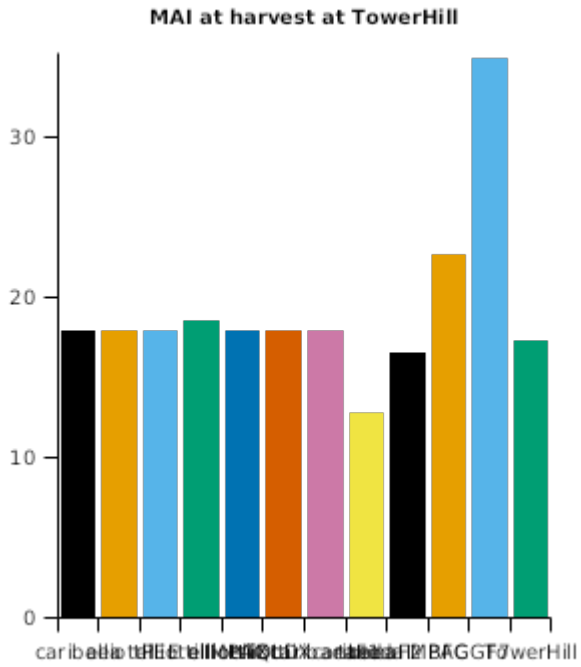
Several Australian genotypes performed similarly during simulations, indicating little practical difference in their calibration and therefore scope for merging, e.g. the elliottiiXcaribaeaF1 and elliottiiXcaribaeaF2 genotypes.

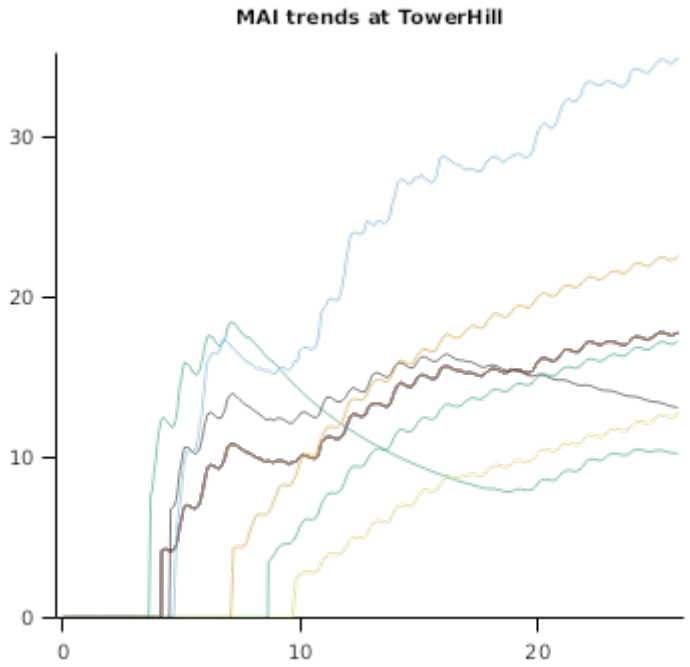
One would expect more discrimination than simulated between temperate and other genotypes when simulating growth at these northern and southern extremes of commercial plantations in Australia. To achieve that though model capability might be need for disease occurance and impacts on survival and growth,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

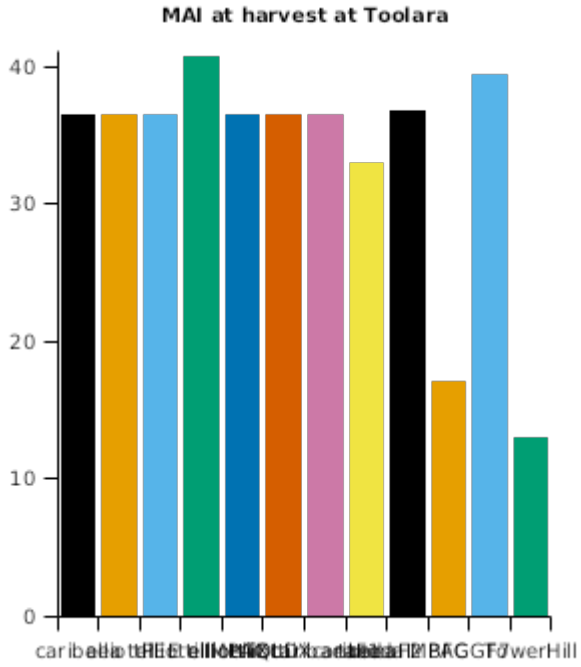
Note that due to the long-term nature of plantation forestry, observed datasets are necessarily old and probably using out-dated genotypes. Therefore, using the genotypes curently available in the model might not be appropriate for simulating the performance of current or future plantations.

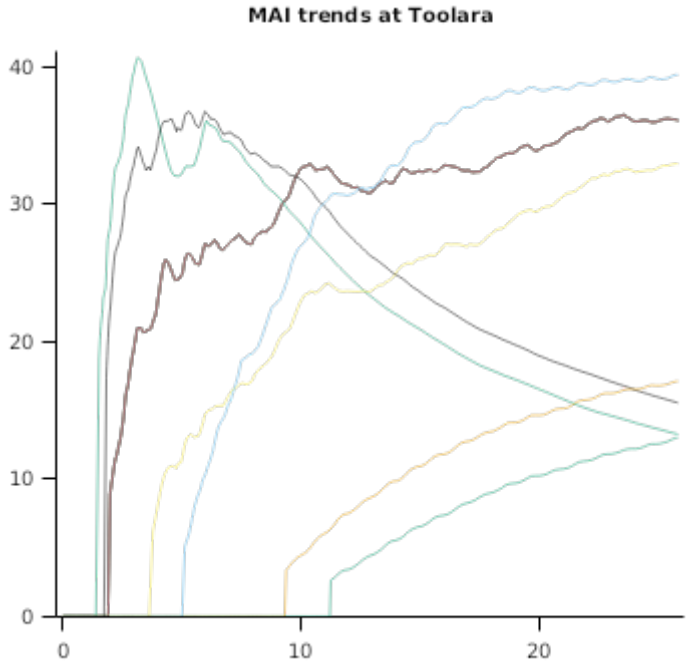
List of experiments.

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









7 References

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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.

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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.

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