



1 The APSIM FodderBeet Model

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The APSIM Fodder Beet Model has been developed using the Plant Modelling Framework (PMF) of [Brown et al., 2014](#). This 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, barley, sorghum) can be achieved by the model developer without additional coding.

The model consists of:

- * A phenology model to simulate development between growth phases
- * A structure model to simulate plant morphology
- * A collection of organs to simulate the various plant parts
- * An arbitrator to allocate resources (N, biomass) to various plant organs.

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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
Arbitrator	Models.PMF.OrganArbitrator
Phenology	Models.PMF.Phen.Phenology
Structure	Models.PMF.Struct.Structure
StorageRoot	Models.PMF.Organs.GenericOrgan
Leaf	Models.PMF.Organs.Leaf
Petiole	Models.PMF.Organs.GenericOrgan
Root	Models.PMF.Organs.Root
MortalityRate	Models.Functions.LinearInterpolationFunction
SCS	Models.Functions.AddFunction

1.1 Arbitrator

1.1.1 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 DoPotentialDMAAllocation() method which works out how much biomass each organ would be allocated assuming N supply is not limiting and sends these allocations to the organs. Each organ then uses their potential DM allocation to determine their N demand (how much N is needed to produce that much DM) and the arbitrator calls DoNSetup() to gather the N supplies and demands from each organ and begin N arbitration. Firstly DoNReallocation() is called to redistribute N that the plant has available from senescing organs. After this step any unmet N demand is considered as plant demand for N uptake from the soil (N Uptake Demand).

2. **doNutrientArbitration**. When this event occurs, the soil arbitrator gets the N uptake demands from each plant (where multiple plants are growing in competition) and their potential uptake from the soil and determines how much of their demand that the soil is able to provide. This value is then passed back to each plant instance as their Nuptake and doNUptakeAllocation() is called to distribute this N between organs.

3. **doActualPlantPartitioning**. On this event the arbitrator call DoNRetranslocation() and DoNFixation() to satisfy any unmet N demands from these sources. Finally, DoActualDMAAllocation is called where DM allocations to each organ are reduced if the N allocation is insufficient to achieve the organs minimum N concentration and final allocations are sent to organs.

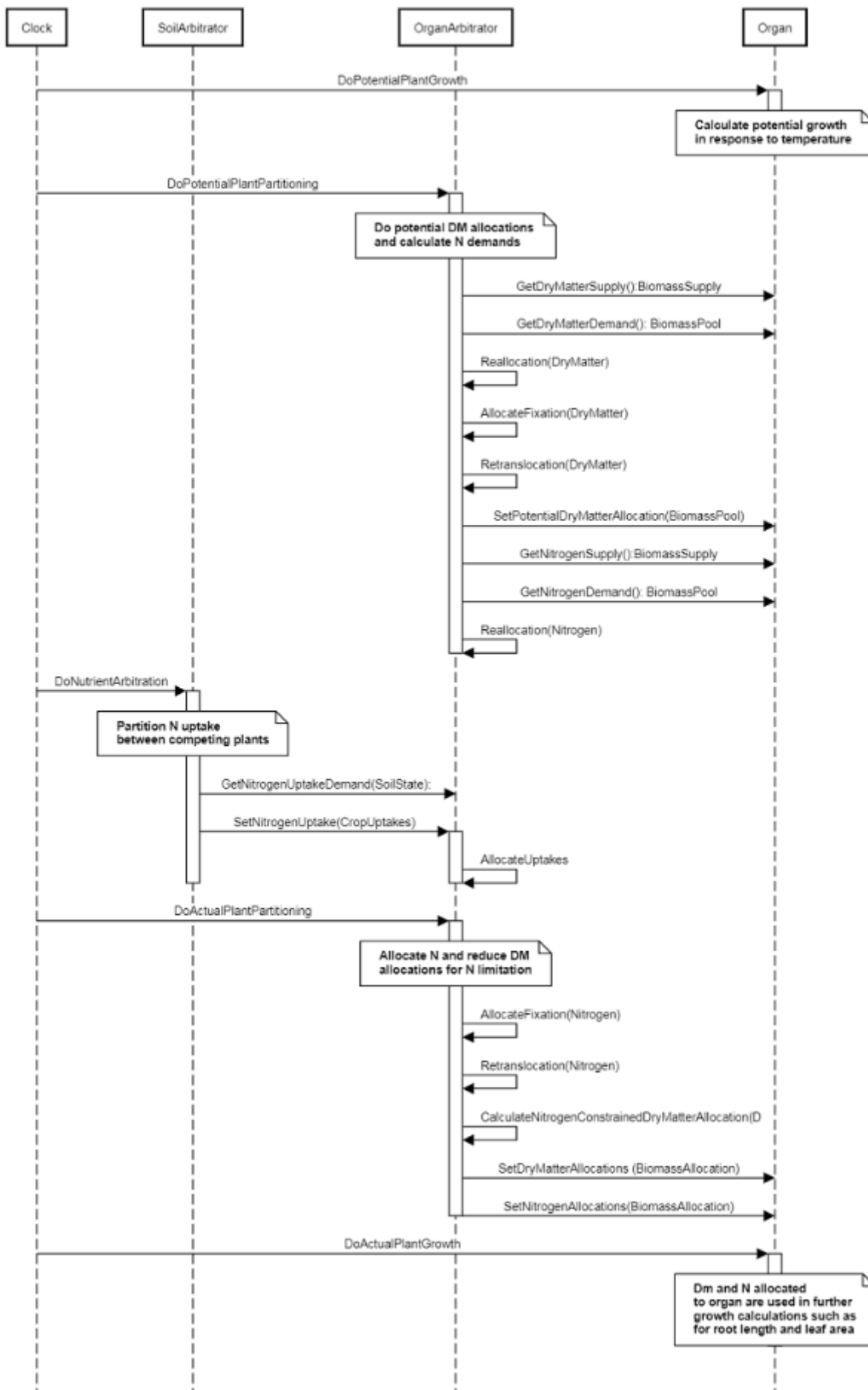


Figure 1: Schematic showing the procedure for arbitration of biomass partitioning. Pink boxes represent events that occur every day and their numbering shows the order of calculations. Blue boxes represent the methods that are called when these events occur. Orange boxes contain properties that make up the organ/arbitrator interface. Green boxes are organ specific properties.

1.2 Phenology

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

The fodder beet model is described for growth and dry matter production using solar radiation and temperature as driving functions. The effect of temperature is quantified using a thermal-time accumulation function. Thermal-time is calculated in degree days for ambient temperature above a base temperature (T_{base}). T_{base} is assumed to be 0°C (Chakwizira et al., 2016).

1.2.1 ThermalTime

$$\text{ThermalTime} = \text{PhaseLookup} \times \text{DroughtPhenologyAcceleration}$$

PhaseLookup is calculated using specific values or functions for various growth phases. The function will use a value of zero for phases not specified below.

The effect of soil temperature can go beyond germination as has been demonstrated in previous studies (Stone et al., 1998).

SoilTemperature has a value between Sowing and Germination calculated as:

$$\text{ThermalTime} = 15$$

The effect of soil temperature can go beyond germination as has been demonstrated in previous studies (Stone et al., 1998).

Temperature is extrapolated to 3-hourly values from daily maximum and minimum using a sinusoidal function, and thermal-time accumulation is calculated for each period and combined to give daily values (Jones et al., 1986). The optimum temperature was set at $25\text{--}30^{\circ}\text{C}$ with a maximum of 45°C , targets assumed similar to those of sugar beet reported by (Ober et al., 2010) and (Sanghera et al., 2016).

AirTemperature has a value between Germination and Maturity calculated as:

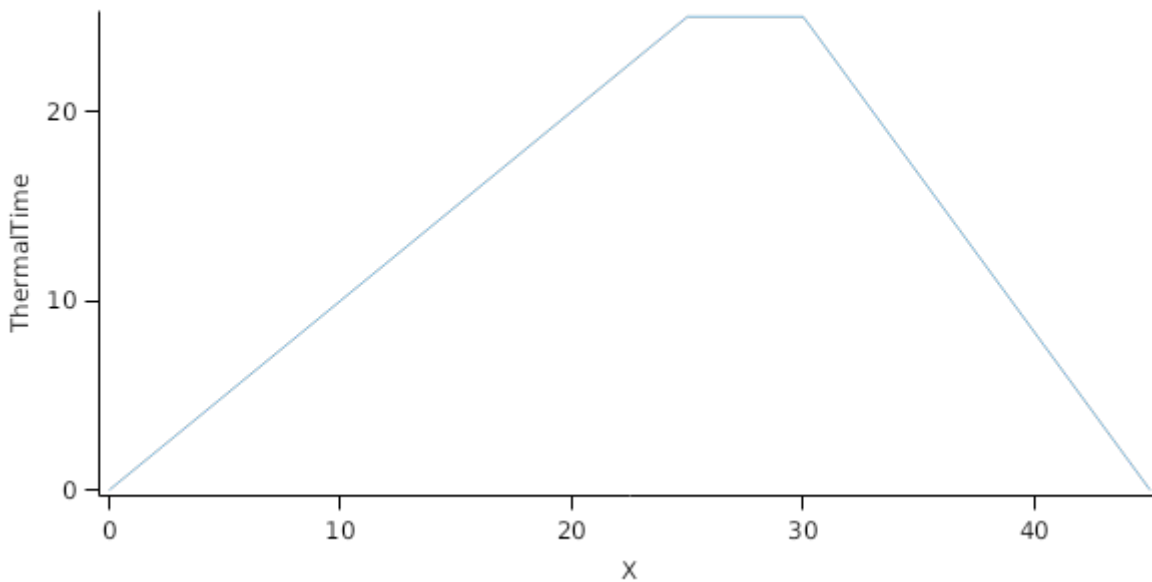
ThermalTime is the average of sub-daily values from a XYPairs.

Firstly 3-hourly estimates of air temperature (T_a) are interpolated using the method of Jones et al., 1986 which assumes a sinusoidal temperature. pattern between T_{max} and T_{min} .

Each of the interpolated air temperatures are then passed into the following Response and the Average taken to give daily ThermalTime

X	ThermalTime
0.0	0.0
25.0	25.0
30.0	25.0
45.0	0.0

ThermalTime



Temperature is extrapolated to 3-hourly values from daily maximum and minimum using a sinusoidal function, and thermal-time accumulation is calculated for each period and combined to give daily values (Jones et al., 1986). The optimum temperature was set at 25–30°C with a maximum of 45°C, targets assumed similar to those of sugar beet reported by (Ober et al., 2010) and (Sanghera et al., 2016).

$$\text{DroughtPhenologyAcceleration} = 1 + \text{Stress}$$

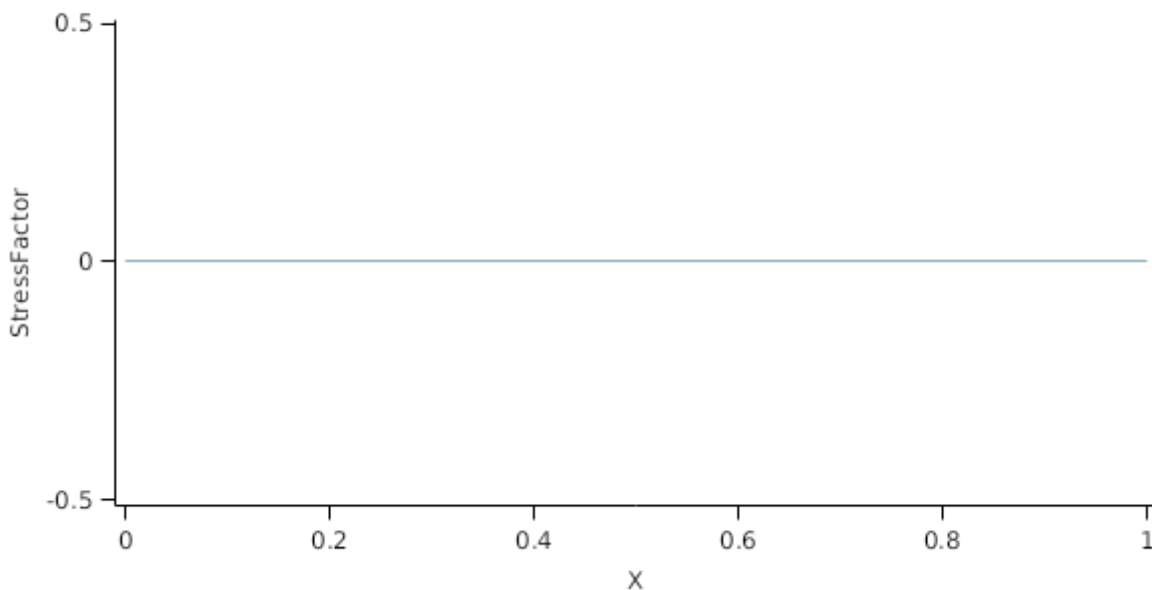
$$\text{Stress} = \text{StressResponseCoefficient} \times \text{StressFactor}$$

$$\text{StressResponseCoefficient} = 2$$

StressFactor is calculated using linear interpolation

X	StressFactor
0.0	0.0
1.0	0.0

StressFactor



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

Phase Number	Phase Name	Initial Stage	Final Stage
1	Planted	Sowing	Germination
2	Germinating	Germination	PreEmerge
3	Emerging	PreEmerge	Established
4	Vegetative	Established	InitRepro
5	EarlyReproductive	InitRepro	PreBolt
6	Bolt	PreBolt	StartBolt
7	Maturity	Bolting	Maturity

1.2.2 Planted

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.

1.2.3 Germinating

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

$$Target = SowingDepth \times ShootRate + ShootLag$$

Where:

$$ShootRate = 12.5 \text{ (deg day/mm),}$$

$$ShootLag = 0 \text{ (deg day),}$$

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

This is an empirical fit where 12.5°Cd per mm sowing depth is assumed based on the 2014 sowing date trial results ([Khaembah et al., 2017](#)).

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

$$ThermalTime = [Phenology].ThermalTime$$

1.2.4 Emerging

This phase goes from preemerge to established.

This an empirical fit of 400°Cd estimated from the October data of the 2014 sowing date trial ([Khaembah et al., 2017](#)).

The *Target* for completion is calculated as:

$$Target = 400 \text{ (oCd)}$$

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

$$Progression = [Phenology].ThermalTime$$

1.2.5 Vegetative

This phase goes from established to initrepro.

The *Target* for completion is calculated as:

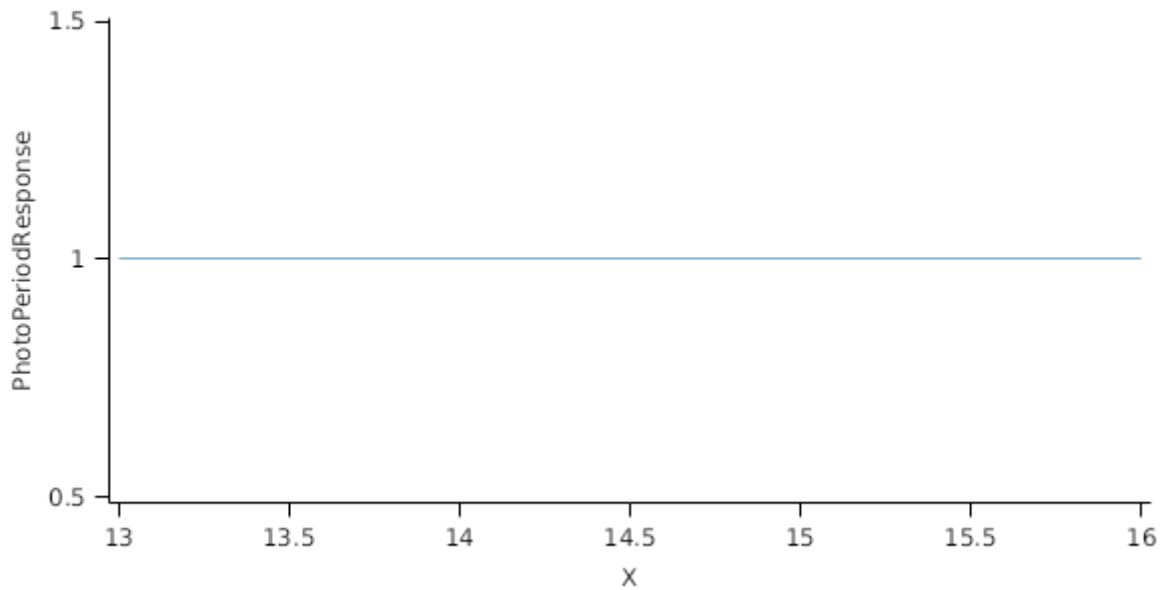
The effect of photoperiod on the vegetative phase is assumed negligible. The maximum TT of 3200°Cd based on the 2014 October sowing date data([Khaembah et al., 2017](#)) is used here.

$$Target = PhotoPeriodResponse \times MaxThermalTimeToBolt$$

PhotoPeriodResponse is calculated using linear interpolation

X	PhotoPeriodResponse
13.0	1.0
16.0	1.0

PhotoPeriodResponse



MaxThermalTimeToBolt = 2700 (oCd)

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

Progression = [Phenology].ThermalTime

1.2.6 EarlyReproductive

This phase goes from initrepro to prebolt.

This an empirical fit - 400°Cd estimated from the 2014 sowing date trial (Khaembah et al., 2017).

The *Target* for completion is calculated as:

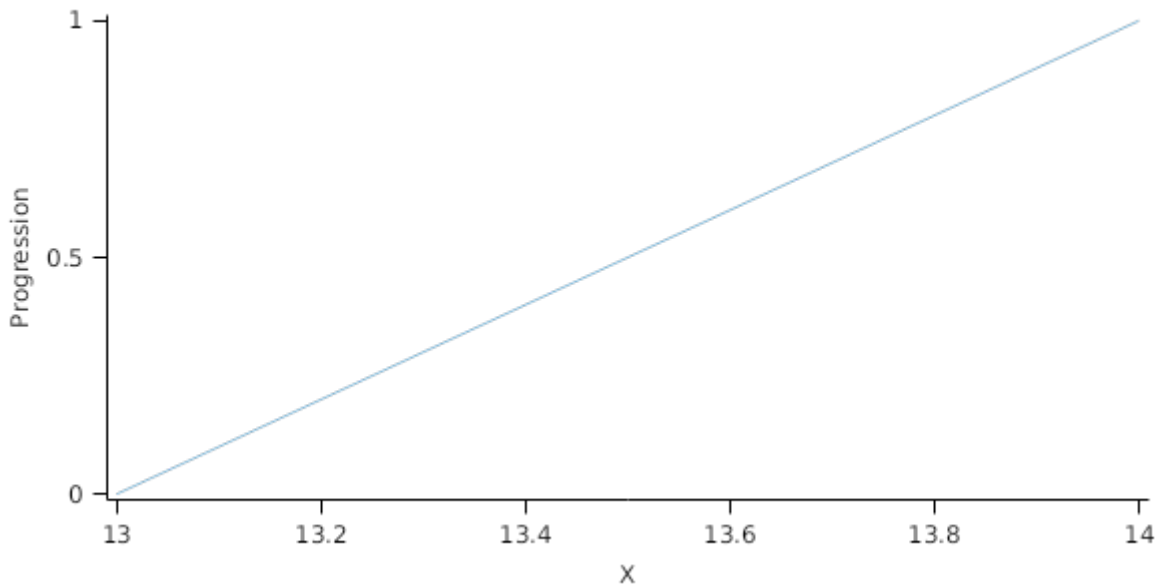
Target = 1 (oCd)

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

Progression is calculated using linear interpolation

X	Progression
13.0	0.0
14.0	1.0

Progression



1.2.7 Bolt

This phase goes from prebolt to startbolt.

The 800°Cd is an empirical fit based on the 2014 sowing date trial ([Khaembah et al., 2017](#)).

The *Target* for completion is calculated as:

Target = 800 (oD)

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

Progression = $[Phenology].ThermalTime$

1.2.8 Maturity

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

1.2.9 AccumulatedThermalTime

AccumulatedThermalTime = Accumulated *VariableReference* between preemerge and maturity

VariableReference = $[Phenology].ThermalTime$

1.2.10 Photoperiod

Returns the duration of the day, or photoperiod, in hours. This is calculated using the specified latitude (given in the weather file) and twilight sun angle threshold. If a variable called `ClimateControl.PhotoPeriod` is found in the simulation, it will be used instead.

The day length is calculated with `\ref MathUtilities.DayLength`.

Twilight = -6 (degrees)

1.3 Structure

The structure model simulates morphological development of the plant to inform the Leaf class when and how many leaves and branches appear and provides an estimate of height.

1.3.1 Plant and Main-Stem Population

The *Plant.Population* is set at sowing with information sent from a manager script in the Sow method. The *PrimaryBudNumber* is also sent with the Sow method. The main-stem population (*MainStemPopn*) for FodderBeet is calculated as:

$$\text{MainStemPopn} = \text{Plant.Population} \times \text{PrimaryBudNumber}$$

Primary bud number is > 1 for crops like potato and grape vine where there are more than one main-stem per plant

1.3.2 Main-Stem leaf appearance

Each day the number of main-stem leaf tips appeared (*LeafTipsAppeared*) is calculated as:

$$\text{LeafTipsAppeared} += \text{DeltaTips}$$

Where *DeltaTips* is calculated as:

$$\text{DeltaTips} = \text{ThermalTime} / \text{Phyllochron}$$

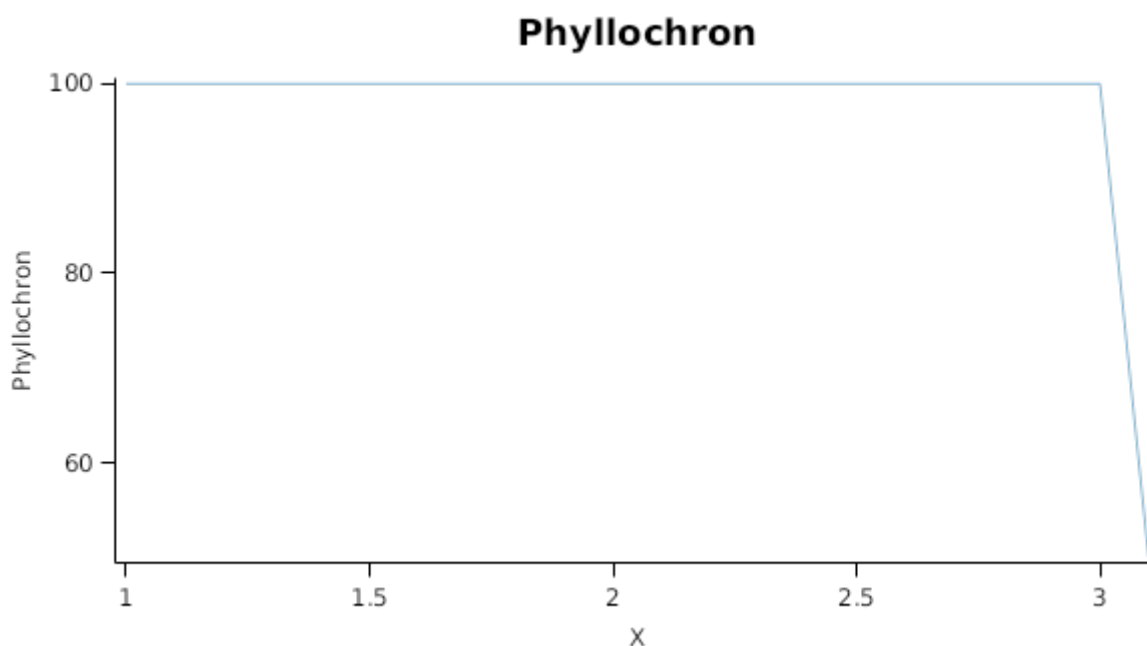
Where *Phyllochron* is the thermal time duration between the appearance of leaf tips given by:

A two stage phyllochron (i.e. 100–50°Cd) is an empirical fit to get faster leaf appearance of the first 3 leaves. The 50°Cd for the fourth and later-formed leaves is estimated from measured values of the 2014-2015 October sowing date treatment (Khaembah et al., 2017).

Phyllochron has a value between PreEmerge and Maturity calculated as:

Phyllochron is calculated using linear interpolation

X	Phyllochron
1.0	100.0
3.0	100.0
3.1	50.0



A two stage phyllochron (i.e. 100–50°Cd) is an empirical fit to get faster leaf appearance of the first 3 leaves. The 50°Cd for the fourth and later-formed leaves is estimated from measured values of the 2014-2015 October sowing date treatment (Khaembah et al., 2017).

ThermalTime is given by

$$\text{ThermalTime} = [\text{Phenology}].\text{ThermalTime}$$

LeafTipsAppeared continues to increase until *FinalLeafNumber* is reached where *FinalLeafNumber* is calculated as:

$$\text{FinalLeafNumber} = 80$$

1.3.3 Branching and Branch Mortality

The total population of stems (*TotalStemPopn*) is calculated as:

$$TotalStemPopn = MainStemPopn + NewBranches - NewlyDeadBranches$$

Where:

$$NewBranches = MainStemPopn \times BranchingRate$$

BranchingRate is given by:

$$BranchingRate = 0$$

NewlyDeadBranches is calculated as:

$$NewlyDeadBranches = (TotalStemPopn - MainStemPopn) \times BranchMortality$$

where *BranchMortality* is given by:

$$BranchMortality = 0$$

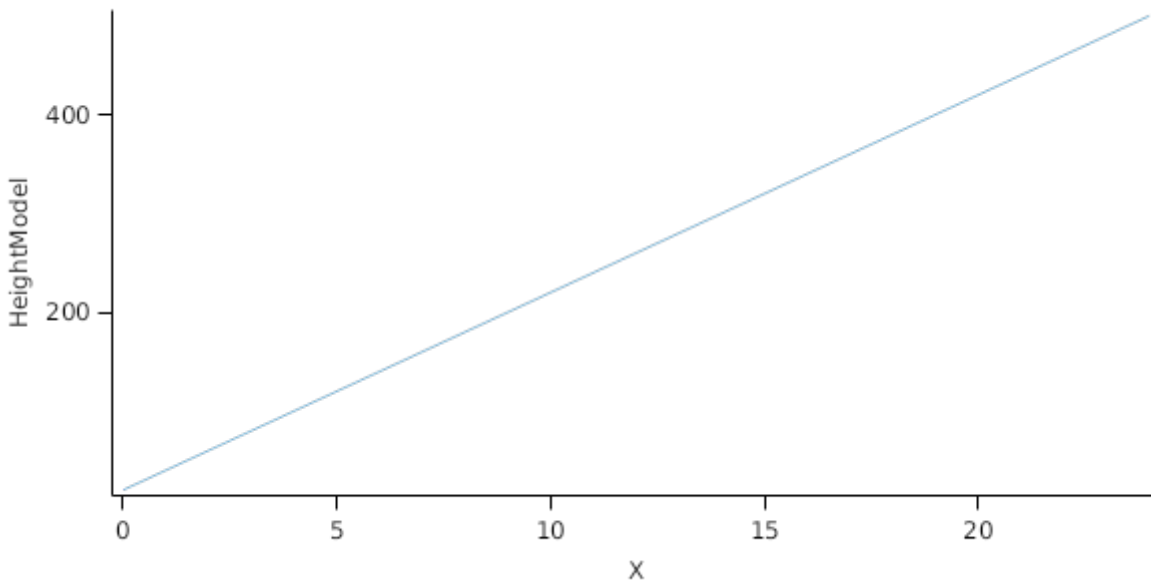
1.3.4 Height

The height of the crop is calculated by the *HeightModel*

HeightModel is calculated using linear interpolation

X	HeightModel
0.0	20.0
24.0	500.0

HeightModel



1.4 StorageRoot

1.4.1 StorageRoot

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.

1.4.2 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.

1.4.2.1 DMDemands

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

$$Structural = DMDemandFunction \times StructuralFraction$$

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

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

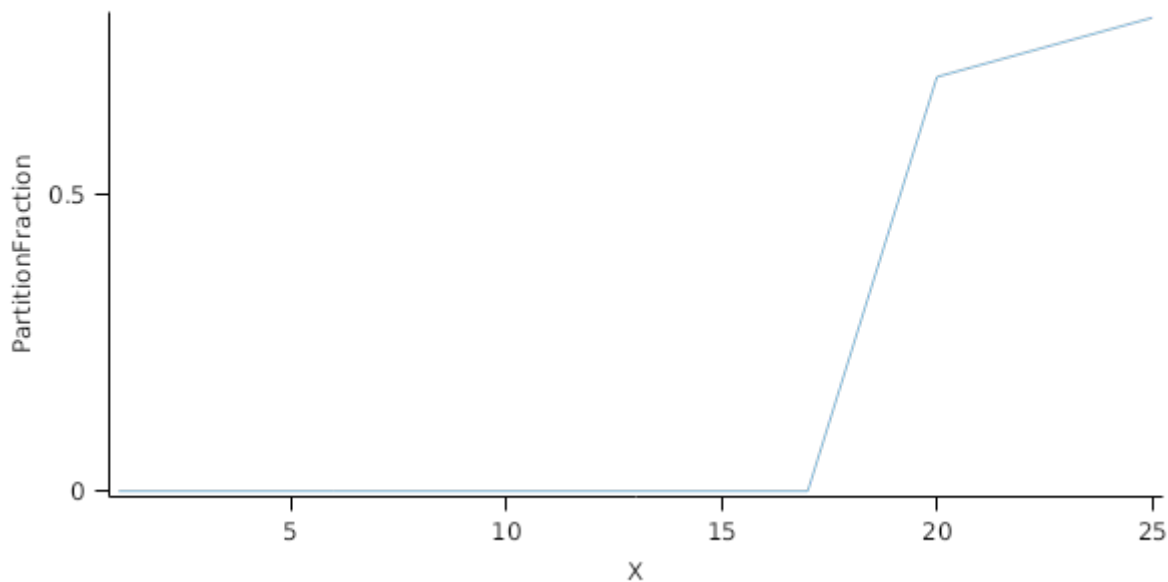
PartitionFraction is calculated using specific values or functions for various growth phases. The function will use a value of zero for phases not specified below.

NonReproductive has a value between PreEmerge and InitRepro calculated as:

PartitionFraction is calculated using linear interpolation

X	PartitionFraction
1.0	0.0
6.0	0.0
17.0	0.0
20.0	0.7
25.0	0.8

PartitionFraction



Reproductive has a value between InitRepro and Maturity calculated as:

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

$$StructuralFraction = 0.4$$

$$Storage = StorageFraction \times [StorageRoot].DMDemands.Structural.DMDemandFunction \times MetabolicFraction$$

$$StorageFraction = 1 - [StorageRoot].DMDemands.Metabolic.MetabolicFraction - [StorageRoot].DMDemands.Structural.StructuralFraction$$

$$MetabolicFraction = 0.45$$

$$Metabolic = MetabolicFraction \times [StorageRoot].DMDemands.Structural.DMDemandFunction$$

$$MetabolicFraction = 0.55$$

$$QStructuralPriority = 1$$

$$QMetabolicPriority = 1$$

$$QStoragePriority = 1$$

1.4.3 Nitrogen Demand

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

1.4.3.1 NDemands

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

$Structural = [StorageRoot].minimumNconc \times [StorageRoot].potentialDMAAllocation.Structural$

$Metabolic = MetabolicNconc \times [StorageRoot].potentialDMAAllocation.Structural$

$MetabolicNconc = [StorageRoot].maximumNconc - 0$

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

$Storage = [StorageRoot].maximumNconc \times ([StorageRoot].Live.Wt + potentialAllocationWt) - [StorageRoot].Live.N$

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

$NitrogenDemandSwitch = [StorageRoot].nitrogenDemandSwitch$

$MaxNconc = [StorageRoot].maximumNconc$

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.4.4 N Concentration Thresholds

MinimumNConc = 0.005

$CriticalNConc = [StorageRoot].MinimumNConc$

MaximumNConc = 0.02

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

NitrogenDemandSwitch has a value between Germination and Maturity calculated as:

Constant = 1

1.4.5 Dry Matter Supply

StorageRoot will reallocate 80% of DM that senesces each day.

StorageRoot does not retranslocate non-structural DM.

1.4.6 Nitrogen Supply

StorageRoot can reallocate up to 5% of N that senesces each day if required by the plant arbitrator to meet N demands.

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

1.4.7 Senescence and Detachment

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

StorageRoot 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	95	0	5	100
Cut	0	0	0	0
Prune	0	0	0	0
Graze	95	0	5	100

1.5 Leaf

The leaves are modelled as a set of leaf cohorts and the properties of each of these cohorts are summed to give overall values for the leaf organ.

A cohort represents all the leaves of a given main- stem node position including all of the branch leaves appearing at the same time as the given main-stem leaf (Lawless et al., 2005).

The number of leaves in each cohort is the product of the number of plants per m² and the number of branches per plant. The *Structure* class models the appearance of main-stem leaves and branches. Once cohorts are initiated the *Leaf* class models the area and biomass dynamics of each.

It is assumed all the leaves in each cohort have the same size and biomass properties. The modelling of the status and function of individual cohorts is delegated to *LeafCohort* classes.

1.5.1 Dry Matter Fixation

The most important DM supply from leaf is the photosynthetic fixation supply. Radiation interception is calculated from LAI using an extinction coefficient of:

$$\text{ExtinctionCoeff} = \text{PotentialExtinctionCoeff} \times \text{WaterStress}$$

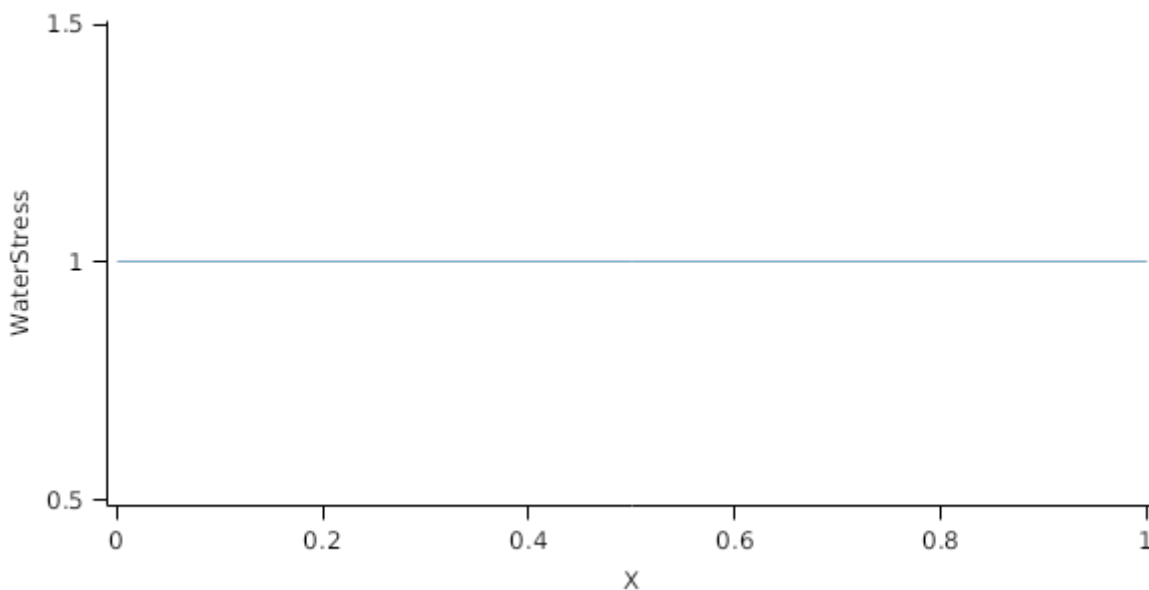
The extinction coefficient value of 0.74 (Chakwizira et al., 2016) was used.

$$\text{PotentialExtinctionCoeff} = 0.74$$

WaterStress is calculated using linear interpolation

X	WaterStress
0.0	1.0
1.0	1.0

WaterStress



Biomass fixation is modelled as the product of intercepted radiation and its conversion efficiency, the radiation use efficiency (RUE) (Monteith et al., 1977).

This approach simulates net photosynthesis rather than providing separate estimates of growth and respiration.

The potential photosynthesis calculated using RUE is then adjusted according to stress factors, these account for plant nutrition (FN), air temperature (FT), vapour pressure deficit (FVPD), water supply (FW) and atmospheric CO₂

concentration (FCO2).

NOTE: RUE in this model is expressed as g/MJ for a whole plant basis, including both above and below ground growth.

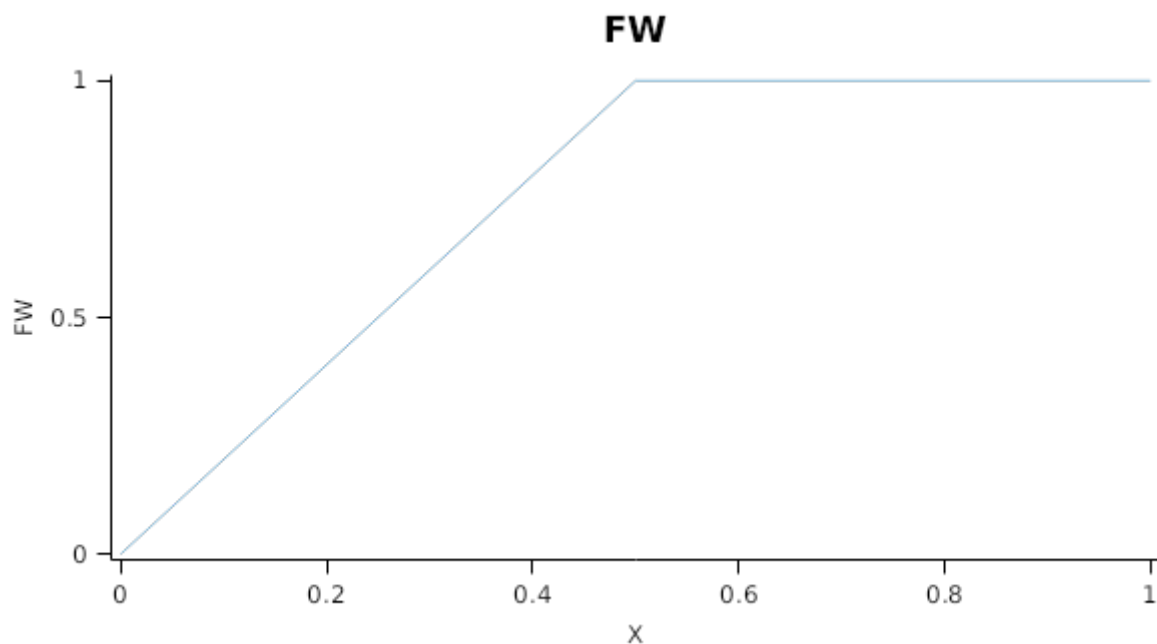
RUE = 1.8

FNconst = 1

FVPD = 1

FW is calculated using linear interpolation

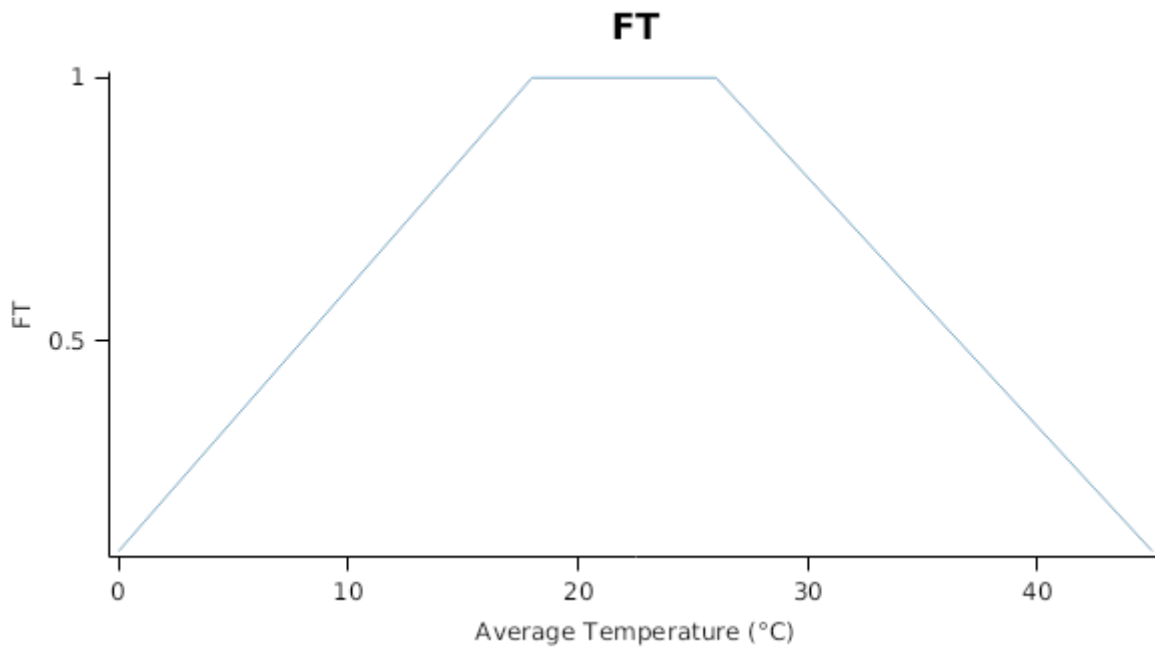
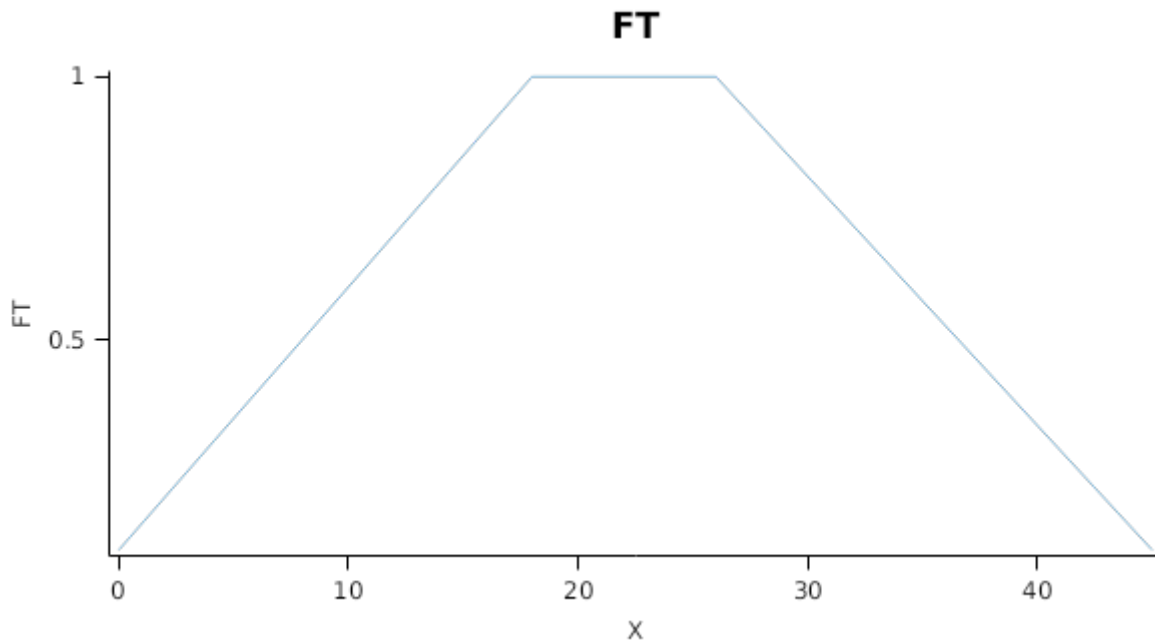
X	FW
0.0	0.0
0.5	1.0
1.0	1.0



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 = 0.75

X	FT
0.0	0.1
18.0	1.0
26.0	1.0
45.0	0.1



This model calculates the CO₂ impact on RUE using the approach of [Reyenga et al., 1999](#).

For C3 plants,

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

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

$$CP = (163.0 - T) / (5.0 - 0.1 \times T)$$

For C4 plants,

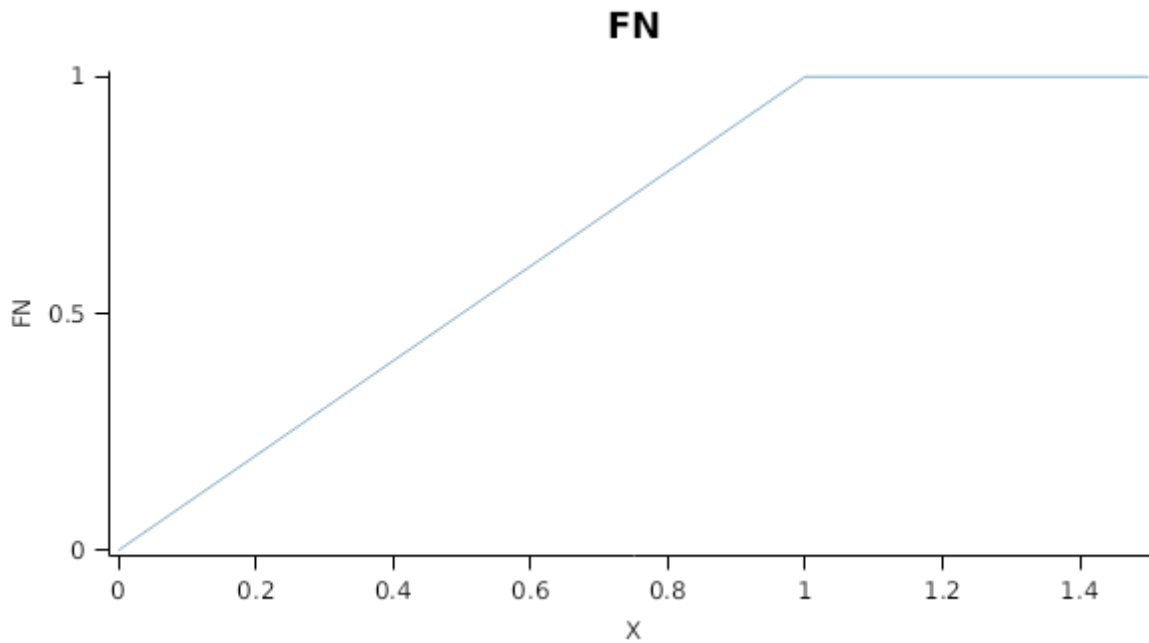
$$F_{CO_2} = 0.000143 \times CO_2 + 0.95$$

$$RadnInt = [Leaf].RadiationIntercepted$$

FN is calculated using linear interpolation

X	FN
0.0	0.0

X	FN
1.0	1.0
1.5	1.0



1.5.2 Constants

StructuralFraction = 0.5

DMConversionEfficiency = 1

RemobilisationCost = 0

CarbonConcentration = 0.4

FrostFraction = 0

WidthFunction = 0

1.5.3 InitialLeaves[1]

Area = 50

1.5.4 Total

1.5.4.1 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

1.5.5 ThermalTime

$ThermalTime = [Phenology].ThermalTime$

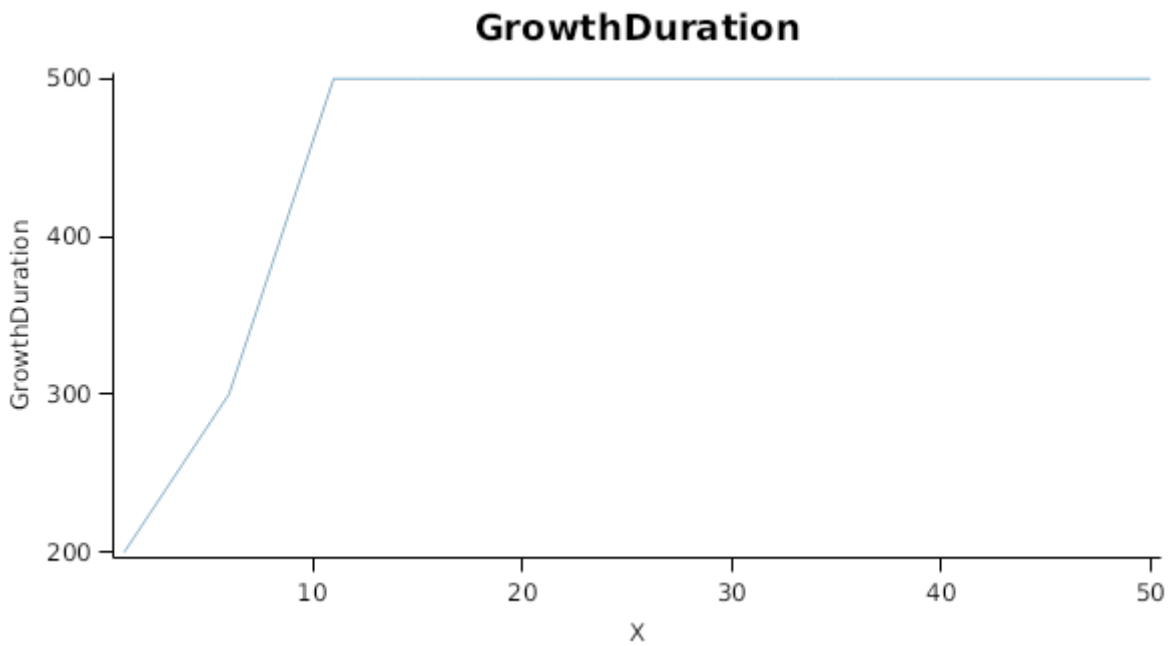
1.5.6 CohortParameters

1.5.6.1 Potential Leaf Area index

Leaf area index is calculated as the sum of the area of each cohort of leaves. The appearance of a new cohort of leaves occurs each time Structure.LeafTipsAppeared increases by one. From tip appearance the area of each cohort will increase for a certain number of degree days defined by the *GrowthDuration*

GrowthDuration is calculated using linear interpolation

X	GrowthDuration
1.0	200.0
6.0	300.0
11.0	500.0
15.0	500.0
21.0	500.0
35.0	500.0
45.0	500.0
50.0	500.0



If no stress occurs the leaves will reach a Maximum area (*MaxArea*) at the end of the *GrowthDuration*. The *MaxArea* is defined by:

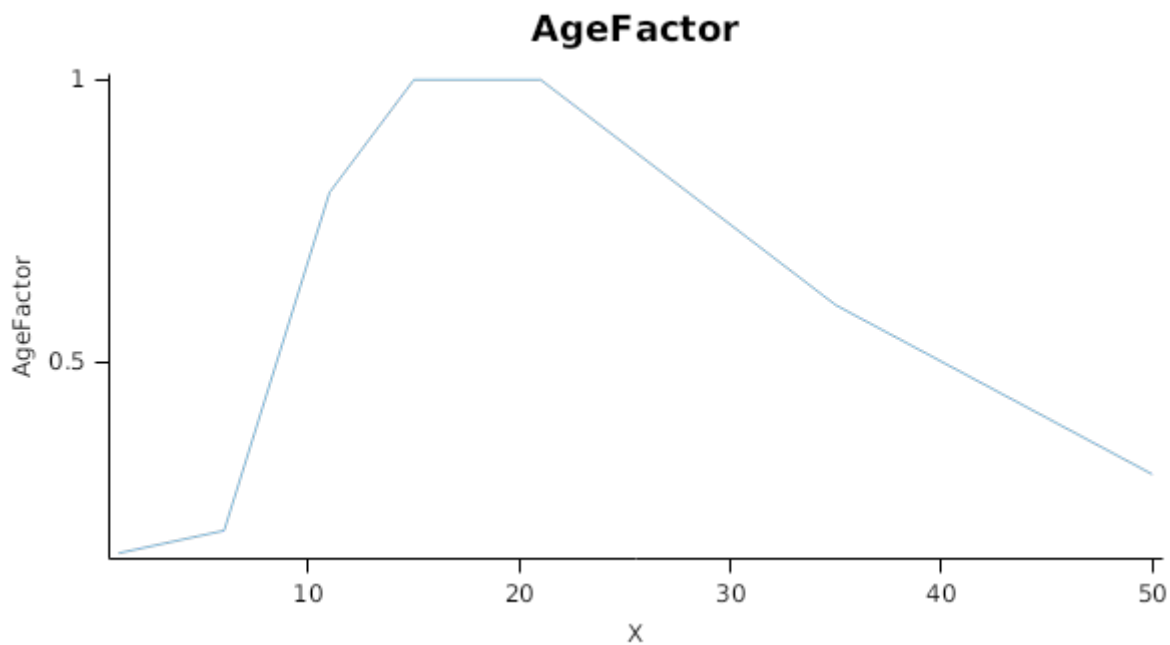
The pattern is assumed to be similar to that of maize (Teixeira et al., 2011).

$$\text{MaxArea} = \text{AreaLargestLeaf} \times \text{AgeFactor}$$

$$\text{AreaLargestLeaf} = 30000 \text{ (mm}^2\text{)}$$

AgeFactor is calculated using linear interpolation

X	AgeFactor
1.0	0.2
6.0	0.2
11.0	0.8
15.0	1.0
21.0	1.0
35.0	0.6
45.0	0.4
50.0	0.3



In the absence of stress the leaf will remain at *MaxArea* for a number of degree days set by the *LagDuration* and then area will senesce to zero at the end of the *SenescenceDuration*

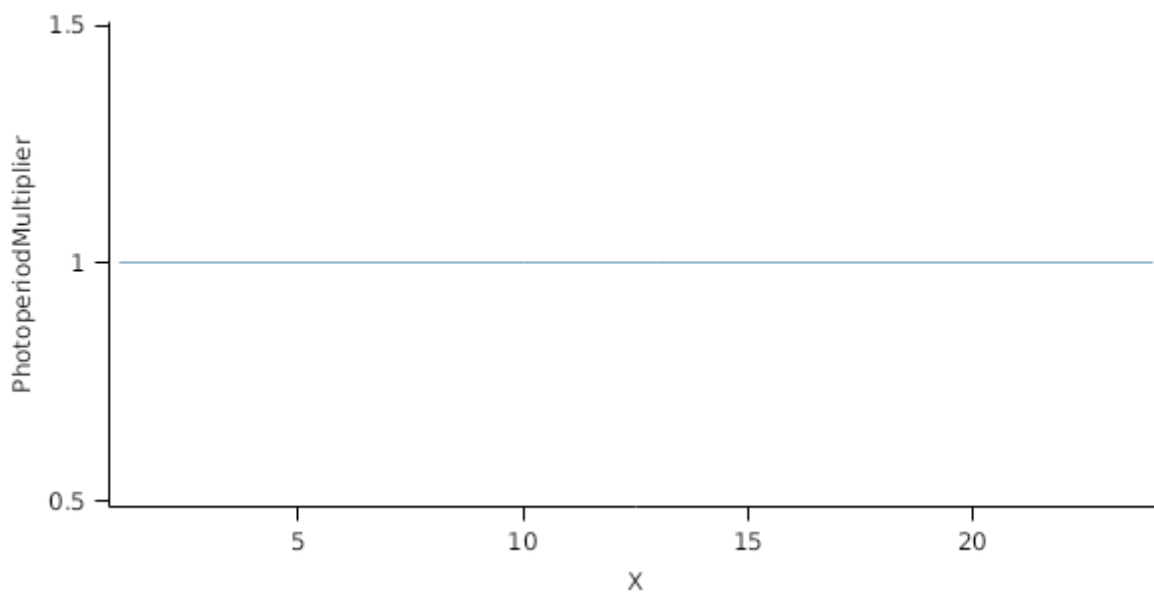
The pattern is assumed to be similar to that of maize ([Teixeira et al., 2011](#)).

$$LagDuration = PhotoperiodMultiplier \times LagDurationBase$$

PhotoperiodMultiplier is calculated using linear interpolation

X	PhotoperiodMultiplier
1.0	1.0
10.0	1.0
13.0	1.0
24.0	1.0

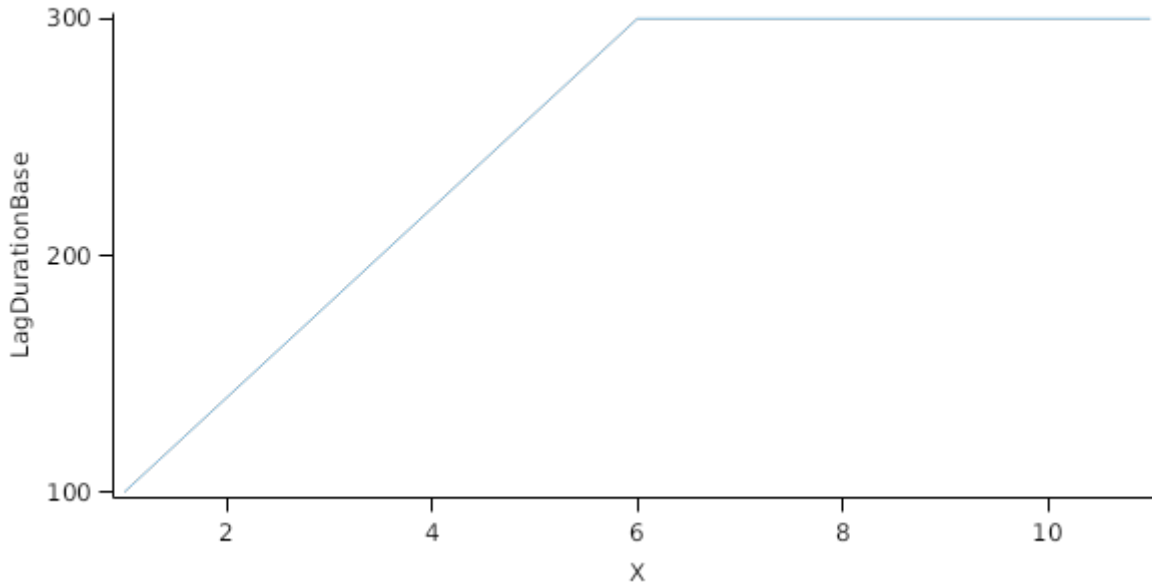
PhotoperiodMultiplier



LagDurationBase is calculated using linear interpolation

X	LagDurationBase
1.0	100.0
6.0	300.0
11.0	300.0

LagDurationBase

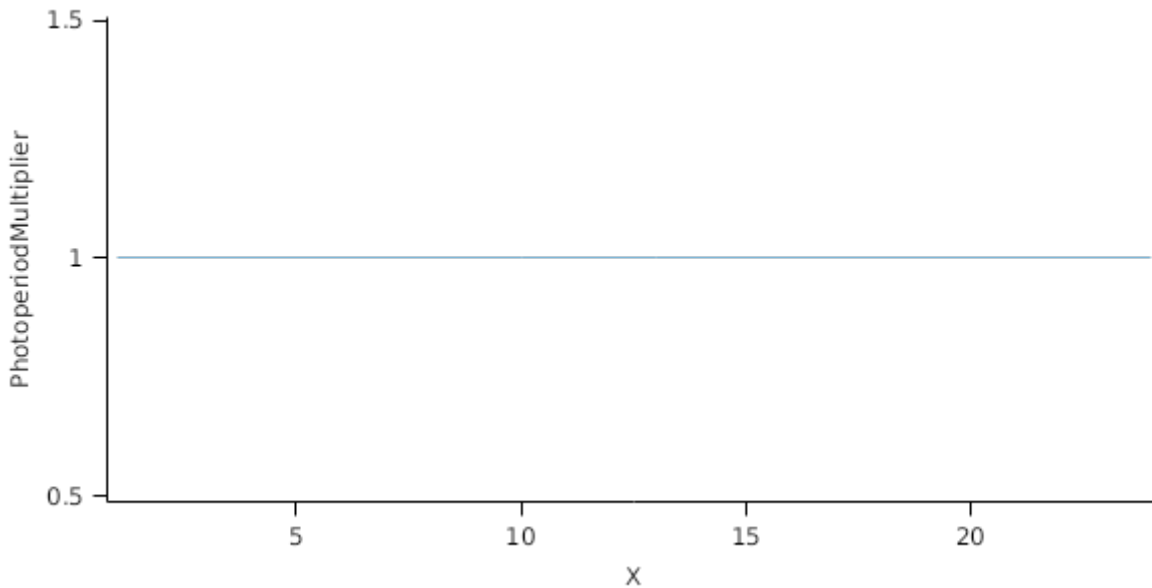


$$\text{SenescenceDuration} = \text{PhotoperiodMultiplier} \times \text{BaseValue}$$

PhotoperiodMultiplier is calculated using linear interpolation

X	PhotoperiodMultiplier
1.0	1.0
10.0	1.0
13.0	1.0
24.0	1.0

PhotoperiodMultiplier



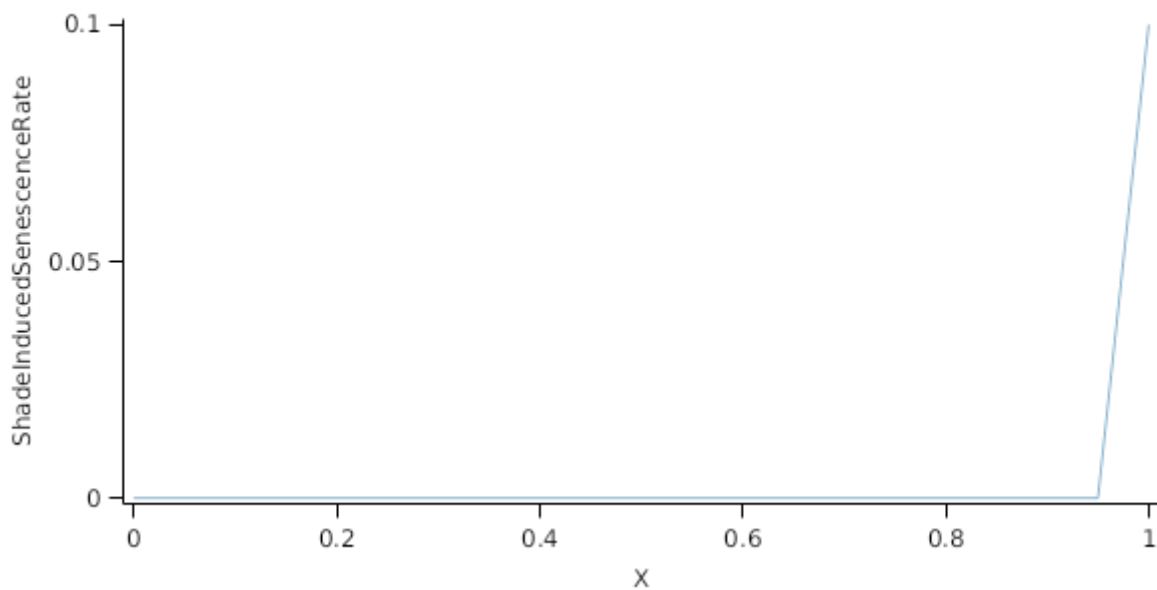
BaseValue = 1200 (oCd)

Mutual shading can cause premature senescence of cohorts if the leaf area above them becomes too great. Each cohort models the proportion of its area that is lost to shade induced senescence each day as:

ShadeInducedSenescenceRate is calculated using linear interpolation

X	ShadeInducedSenescenceRate
0.0	0.0
0.5	0.0
0.9	0.0
1.0	0.1

ShadeInducedSenescenceRate



1.5.6.2 Stress effects on Leaf Area Index

Stress reduces leaf area in a number of ways. Firstly, stress occurring prior to the appearance of the cohort can reduce cell division, so reducing the maximum leaf size. Leaf captures this by multiplying the *MaxSize* of each cohort by a *CellDivisionStress* factor which is calculated as:

$CellDivisionStress = 1 (0-1)$

Leaf.FN quantifies the N stress status of the plant and represents the concentration of metabolic N relative the maximum potential metabolic N content of the leaf calculated as $(Leaf.NConc - MinimumNConc)/(CriticalNConc - MinimumNConc)$.

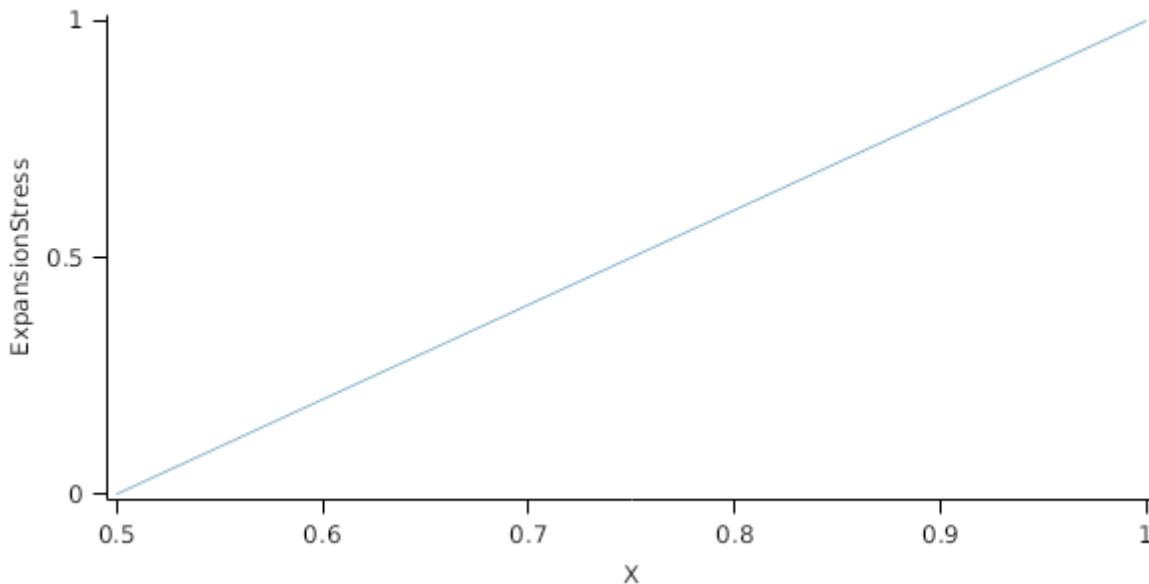
Leaf.FW quantifies water stress and is calculated as $Leaf.Transpiration/Leaf.WaterDemand$, where *Leaf.Transpiration* is the minimum of *Leaf.WaterDemand* and *Root.WaterUptake*

Stress during the $\langle i \rangle GrowthDuration^*$ of the cohort reduces the size increase of the cohort by multiplying the potential increase by a *ExpansionStress* factor:

ExpansionStress is calculated using linear interpolation

X	ExpansionStress
0.5	0.0
1.0	1.0

ExpansionStress



Stresses can also accelerate the onset and rate of senescence in a number of ways. Nitrogen shortage will cause N to be retranslocated out of lower order leaves to support the expansion of higher order leaves and other organs. When this happens the lower order cohorts will have their area reduced in proportion to the amount of N that is remobilised out of them.

Water stress hastens senescence by increasing the rate of thermal time accumulation in the lag and senescence phases. This is done by multiplying thermal time accumulation by *DroughtInducedLagAcceleration* and *DroughtInducedSenescenceAcceleration* factors, respectively.

1.5.6.3 Dry matter Demand

Leaf calculates the DM demand from each cohort as a function of the potential size increment (*DeltaPotentialArea*) and specific leaf area bounds. Under non-stressed conditions the demand for non-storage DM is calculated as *DeltaPotentialArea* divided by the mean of *SpecificLeafAreaMax* and *SpecificLeafAreaMin*. Under stressed conditions it is calculated as *DeltaWaterConstrainedArea* divided by *SpecificLeafAreaMin*.

Maximum leaf specific leaf area was estimated from the 2014 sowing date trial ([Khaembah et al., 2017](#)).

$\text{SpecificLeafAreaMax} = 16000$

$\text{SpecificLeafAreaMin} = 10000$

Non-storage DM Demand is then separated into structural and metabolic DM demands using the *StructuralFraction*:

$\text{StructuralFraction} = 0.5$

The storage DM demand is calculated from the sum of metabolic and structural DM (including today's demands) multiplied by a *NonStructuralFraction*.

1.5.6.4 Nitrogen Demand

Leaf calculates the N demand from each cohort as a function of the potential DM increment and N concentration bounds.

Structural N demand = $\text{PotentialStructuralDMAallocation} * \text{MinimumNConc}$ where:

The minimum, maximum and critical nitrogen concentration were determined in a previous study ([Chakwizira et al., 2016](#)).

$\text{MinimumNConc} = 0.025$

Metabolic N demand is calculated as $\text{PotentialMetabolicDMAallocation} * (\text{CriticalNConc} - \text{MinimumNConc})$ where:

$\text{CriticalNConc} = 0.025$

Storage N demand is calculated as the sum of metabolic and structural wt (including today's demands) multiplied by *LuxuryNConc* ($\text{MaximumNConc} - \text{CriticalNConc}$) less the amount of storage N already present. *MaximumNConc* is given by:

MaximumNConc = 0.04

1.5.6.5 Drymatter supply

In addition to photosynthesis, the leaf can also supply DM by reallocation of senescing DM and retranslocation of storage DM: Reallocation supply is a proportion of the metabolic and non-structural DM that would be senesced each day where the proportion is set by:

DMReallocationFactor = 0.95

Retranslocation supply is calculated as a proportion of the amount of storage DM in each cohort where the proportion is set by :

DMRetranslocationFactor = 0

1.5.6.6 Nitrogen supply

Nitrogen supply from the leaf comes from the reallocation of metabolic and storage N in senescing material and the retranslocation of metabolic and storage N. Reallocation supply is a proportion of the Metabolic and Storage DM that would be senesced each day where the proportion is set by:

NReallocationFactor = 0.95

Retranslocation supply is calculated as a proportion of the amount of storage and metabolic N in each cohort where the proportion is set by :

NRetranslocationFactor = 0

1.5.6.7 Constants

SenescingLeafRelativeSize = 1 (0-1)

DetachmentLagDuration = 1000000

DetachmentDuration = 1

StructuralFraction = 0.5

SpecificLeafAreaMin = 10000

Maximum leaf specific leaf area was estimated from the 2014 sowing date trial ([Khaembah et al., 2017](#)).

SpecificLeafAreaMax = 16000

The minimum, maximum and critical nitrogen concentration were determined in a previous study ([Chakwizira et al., 2016](#)).

MinimumNConc = 0.025

CriticalNConc = 0.025

MaximumNConc = 0.04

NReallocationFactor = 0.95

NRetranslocationFactor = 0

DMRetranslocationFactor = 0

DMReallocationFactor = 0.95

StorageFraction = 0.05

InitialNConc = 0

LeafSizeShapeParameter = 0.01

MaintenanceRespirationFunction = 0

CellDivisionStress = 1 (0-1)

RemobilisationCost = 0

CarbonConcentration = 0.4

1.5.7 FRGRFunction

$FRGRFunction = \text{Min}(RUE_FT, Others)$

Where:

$RUE_FT = [Leaf].Photosynthesis.FT$

$Others = \text{Min}(RUE_FN, RUE_FVPD)$

Where:

$RUE_FN = [Leaf].Photosynthesis.FN$

$RUE_FVPD = [Leaf].Photosynthesis.FVPD$

1.5.8 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	100	100
Cut	80	0	0	0
Prune	0	0	60	0
Graze	95	95	5	5

1.5.9 CO2internal

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

1.5.10 StomatalConductanceCO2Modifier

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

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

1.5.11 DepthFunction

$DepthFunction = [Leaf].Height$

1.5.12 DMDemandPriorityFactors

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

Structural = 1

Metabolic = 1

Storage = 1

1.5.13 NDemandPriorityFactors

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

Structural = 1

Metabolic = 1

Storage = 1

1.6 Petiole

1.6.1 Petiole

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.

1.6.2 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.

1.6.2.1 DMDemands

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

$Structural = DMDemandFunction \times StructuralFraction$

$DMDemandFunction = \text{Max}(\text{MinDemand}, \text{PotentialDemand})$

Where:

$\text{MinDemand} = 0$

$\text{PotentialDemand} = \text{Ratio} \times \text{SubtractFunction}$

$\text{Ratio} = 1.2$

$\text{SubtractFunction} = [\text{FodderBeet}].\text{Leaf}.\text{Live}.\text{Wt} - [\text{FodderBeet}].\text{Petiole}.\text{Wt}$

$\text{StructuralFraction} = 0.5$

$\text{Metabolic} = 0$

$\text{Storage} = [\text{Petiole}].\text{DMDemands}.\text{Structural}.\text{DMDemandFunction} \times \text{StorageFraction}$

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

$\text{QStructuralPriority} = 1$

$\text{QMetabolicPriority} = 1$

$\text{QStoragePriority} = 1$

1.6.3 Nitrogen Demand

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

1.6.3.1 NDemands

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

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

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

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

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

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

The demand for storage N is further reduced by a factor specified by the $[\text{Petiole}].\text{NitrogenDemandSwitch}$.

$\text{NitrogenDemandSwitch} = [\text{Petiole}].\text{nitrogenDemandSwitch}$

$\text{MaxNconc} = [\text{Petiole}].\text{maximumNconc}$

$\text{QStructuralPriority} = 1$

$\text{QMetabolicPriority} = 1$

QStoragePriority = 1

1.6.4 N Concentration Thresholds

MinimumNConc = 0.015

$CriticalNConc = [Petiole].MinimumNConc$

MaximumNConc = 0.02

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

NitrogenDemandSwitch has a value between Germination and Maturity calculated as:

Constant = 1

1.6.5 Dry Matter Supply

Petiole will reallocate 80% of DM that senesces each day.

Petiole does not retranslocate non-structural DM.

1.6.6 Nitrogen Supply

Petiole can reallocate up to 94% of N that senesces each day if required by the plant arbitrator to meet N demands.

Petiole does not retranslocate non-structural N.

1.6.7 Senescence and Detachment

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

$SenescenceRate = \text{Max}(SenescenceRate, Zero)$

Where:

$SenescenceRate = [Leaf].FractionDied$

Zero = 0

Petiole 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
Graze	95	95	5	5

1.7 Root

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

1.7.1 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.

$$\text{Root Depth Increase} = \text{RootFrontVelocity} \times X_{F_i} \times \text{RootDepthStressFactor}$$

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

Root depth is also constrained by a maximum root depth.

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

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

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

$$DM_{\text{Allocated}_i} = \text{TotalDMAllocated} \times RA_{w_i} / \text{TotalRA}_w$$

1.7.2 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.

1.7.3 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 than zero.

1.7.4 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 (k_{NO3} or k_{NH4}), the concentration of N form (ppm), and a soil moisture factor ($NU_{\text{uptakeSWFactor}}$) which typically decreases as the soil dries. $NO3 \text{ uptake} = NO3_i \times k_{NO3} \times NO3_{ppm, i} \times NU_{\text{uptakeSWFactor}}$ $NH4 \text{ uptake} = NH4_i \times k_{NH4} \times NH4_{ppm, i} \times NU_{\text{uptakeSWFactor}}$ As can be seen from the above equations, the values of k_{NO3} and k_{NH4} 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 ($MaxDailyNU_{\text{uptake}}$) and the plant's N demand. The former provides a means to constrain N uptake to a maximum value observed in the field for the crop as a whole. The demand for soil N is then passed to the soil arbitrator which determines how much of the N uptake demand each plant instance will be allowed to take up.

1.7.5 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 KL_{modifier} function. $SW \text{ uptake} = (SW_i - LL_i) \times KL_i \times KL_{\text{modifier}}$

1.7.6 Constants

$$\text{SoilWaterEffect} = 1$$

$$\text{MaximumRootDepth} = 1500$$

$$\text{MaximumNConc} = 0.01$$

$$\text{MinimumNConc} = 0.005$$

$$K_{NO3} = 0.02 \text{ (g/plant)}$$

$$K_{NH4} = 0.01 \text{ (g/plant)}$$

$$\text{SpecificRootLength} = 40 \text{ (m/g)}$$

$$\text{DMConversionEfficiency} = 1$$

$$\text{MaintenanceRespirationFunction} = 1$$

$$\text{RemobilisationCost} = 0$$

CarbonConcentration = 0.4

RootDepthStressFactor = 1

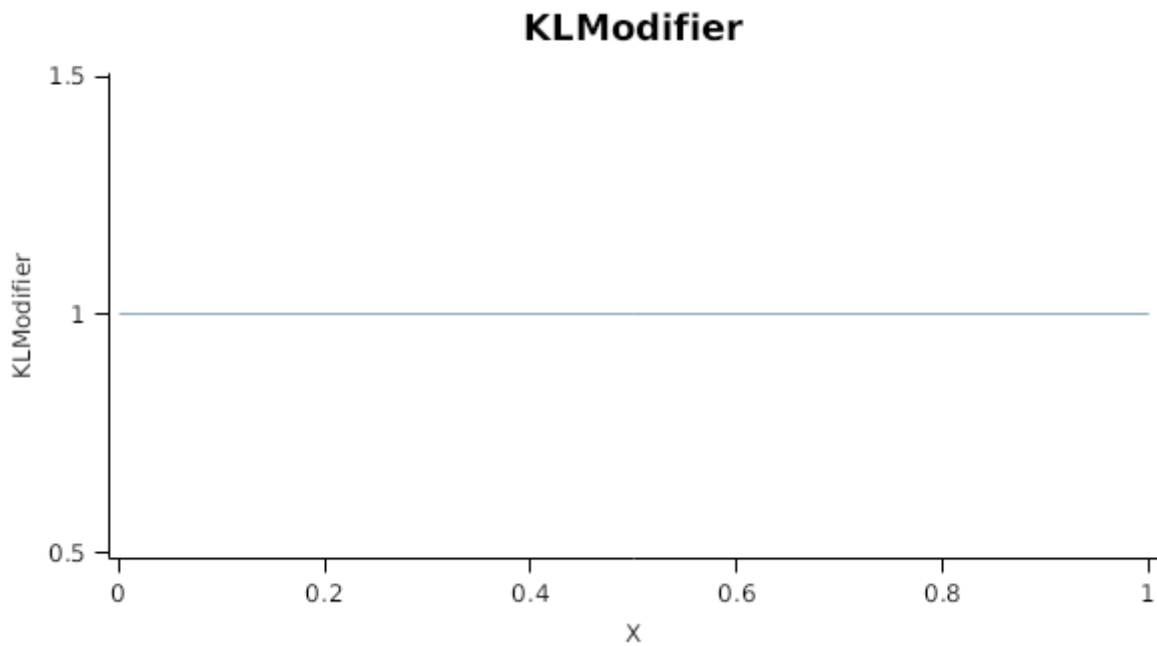
1.7.7 RootShape

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

1.7.8 KLModifier

KLModifier is calculated using linear interpolation

X	KLModifier
0.0	1.0
1.0	1.0



1.7.9 RootFrontVelocity

RootFrontVelocity is calculated using specific values or functions for various growth phases. The function will use a value of zero for phases not specified below.

PhaseLookupValue has a value between Germination and Maturity calculated as:

Constant = 10

1.7.10 NitrogenDemandSwitch

NitrogenDemandSwitch has a value between PreEmerge and Maturity calculated as:

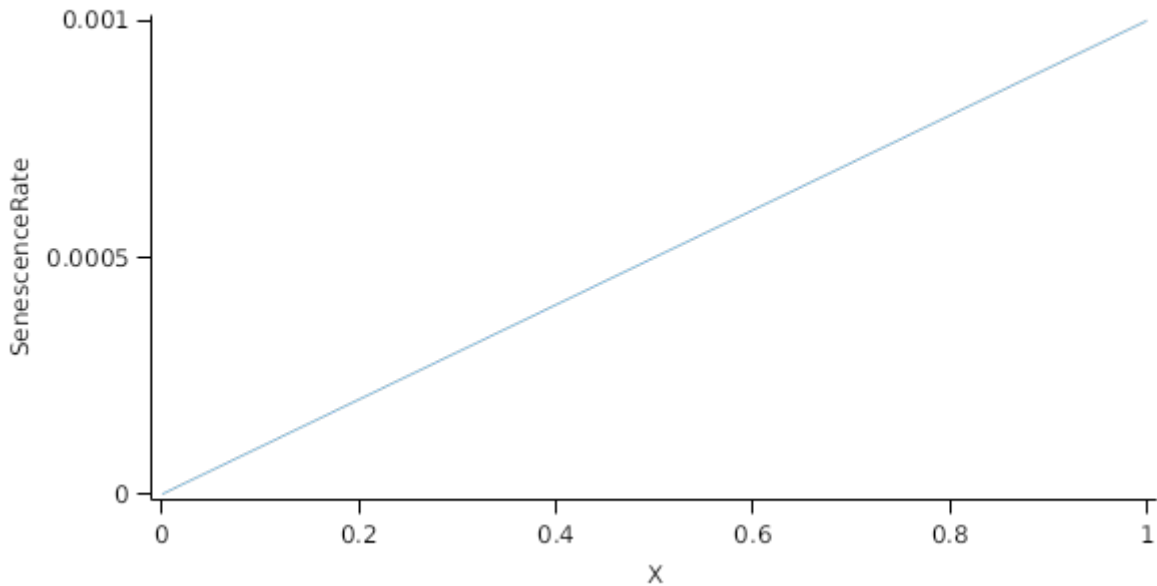
Constant = 1

1.7.11 SenescenceRate

SenescenceRate is calculated using linear interpolation

X	SenescenceRate
0.0	0.0
1.0	0.0

SenescenceRate



1.7.12 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.

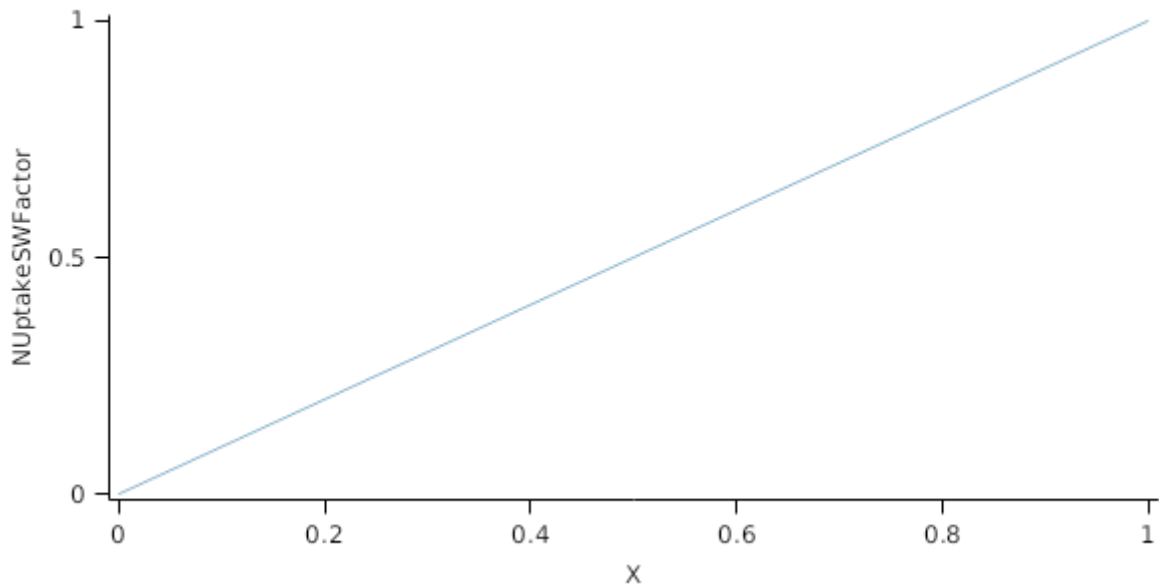
Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	50	0	10	0
Cut	80	0	0	0
Prune	0	0	60	0
Graze	60	0	20	0

1.7.13 NUptakeSWFactor

NUptakeSWFactor is calculated using linear interpolation

X	NUptakeSWFactor
0.0	0.0
1.0	1.0

NUptakeSWFactor

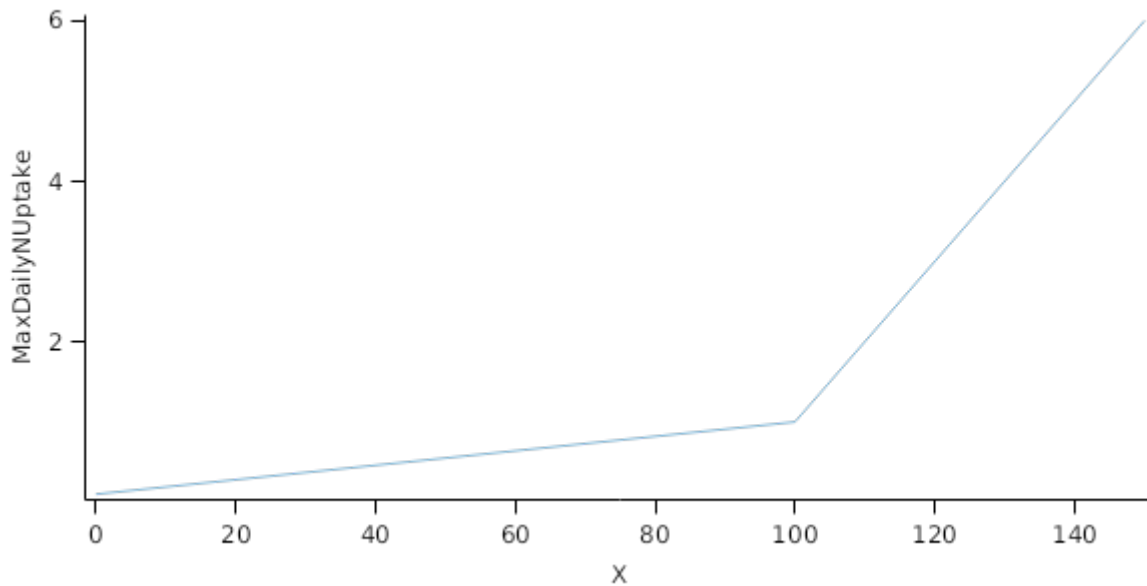


1.7.14 MaxDailyNUptake

MaxDailyNUptake is calculated using linear interpolation

X	MaxDailyNUptake
0.0	0.1
100.0	1.0
150.0	6.0

MaxDailyNUptake



1.7.15 DMDemands

1.7.15.1 DMDemands

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

$Structural = DMDemandFunction \times StructuralFraction$

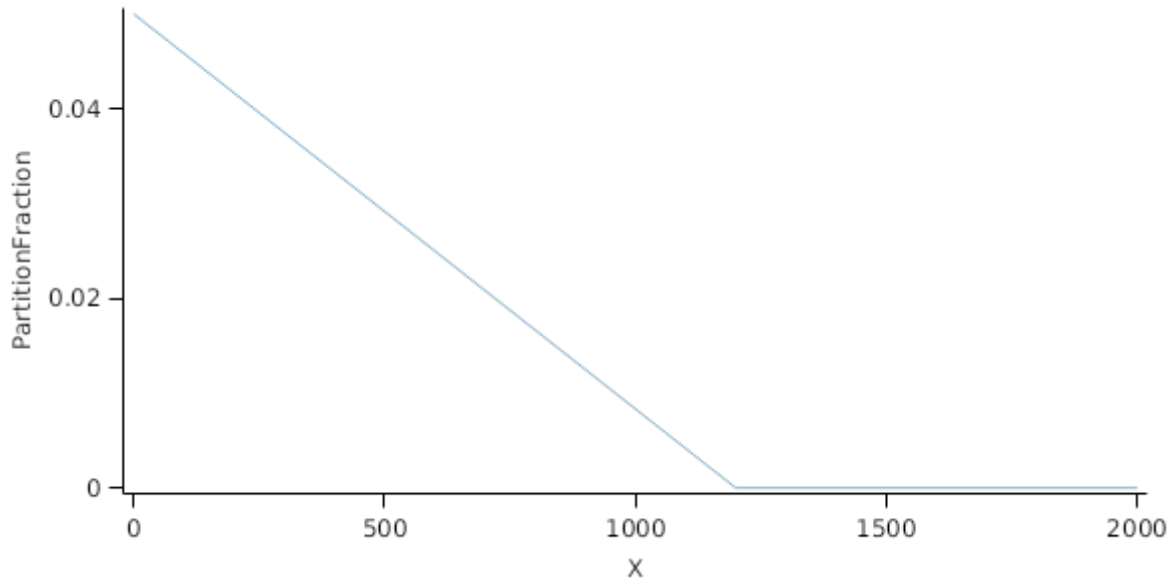
Returns the product of its PartitionFraction and the total DM supplied to the arbitrator by all organs.

$DM_{DemandFunction} = PartitionFraction \times [Arbitrator].DM.TotalFixationSupply$

PartitionFraction is calculated using linear interpolation

X	PartitionFraction
0.0	0.1
1200.0	0.0
2000.0	0.0

PartitionFraction



StructuralFraction = 1

Metabolic = 0

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

$StorageFraction = 1 - [Root].DMDemands.Structural.StructuralFraction$

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.7.16 NDemands

1.7.16.1 NDemands

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

$Structural = [Root].minimumNconc \times [Root].potentialDMAAllocation.Structural$

$Metabolic = MetabolicNconc \times [Root].potentialDMAAllocation.Structural$

$MetabolicNconc = [Root].criticalNConc - [Root].minimumNconc$

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

$Storage = [Root].maximumNconc \times ([Root].Live.Wt + potentialAllocationWt) - [Root].Live.N$

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

$NitrogenDemandSwitch = [Root].nitrogenDemandSwitch$

$MaxNconc = [Root].maximumNconc$

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.7.17 CriticalNConc

CriticalNConc = [Root].MinimumNConc

1.7.18 InitialWt

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

Structural = 5 (g/plant)

Metabolic = 0

Storage = 0

1.8 AboveGround

1.8.1 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:

- * Leaf
- * StorageRoot
- * Petiole

1.9 BelowGround

1.9.1 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:

- * Root

1.10 Total

1.10.1 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
- * StorageRoot
- * Petiole
- * Root

1.11 TotalLive

1.11.1 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
- * Petiole
- * StorageRoot
- * Root

1.12 TotalDead

1.12.1 TotalDead

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

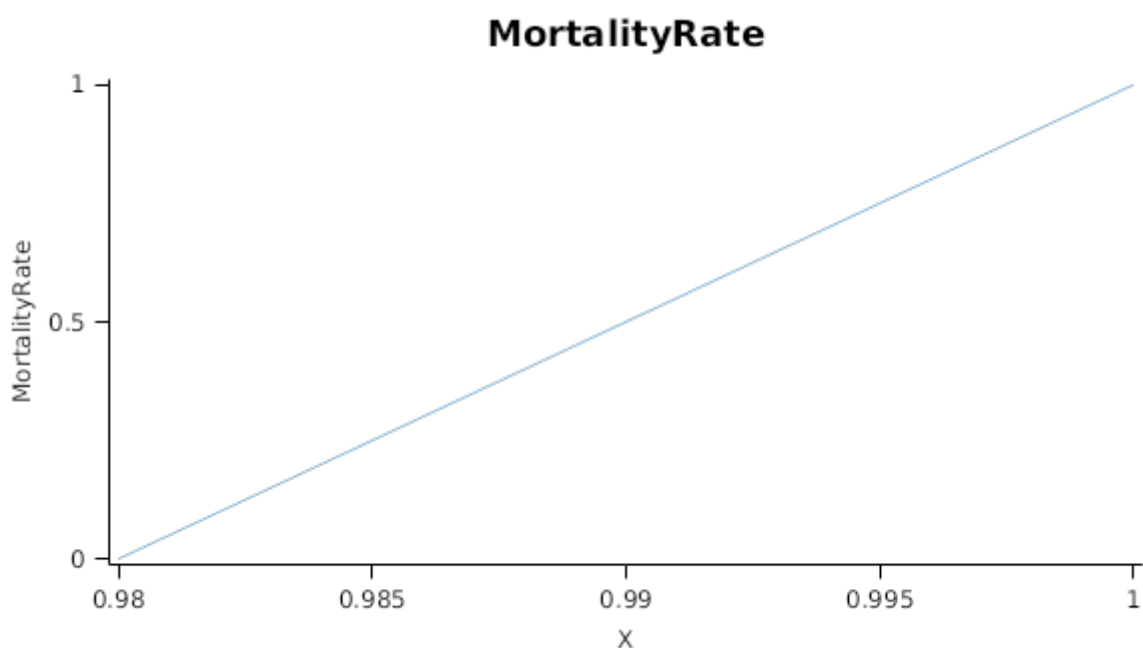
TotalDead summarises the following biomass objects:

- * Leaf
- * Petiole
- * StorageRoot
- * Root

1.13 MortalityRate

MortalityRate is calculated using linear interpolation

X	MortalityRate
1.0	0.0
1.0	1.0



1.14 SCS

Non structural carbohydrates and sugars

$$SCS = [\text{StorageRoot}].\text{Live}.\text{MetabolicWt} + [\text{StorageRoot}].\text{Live}.\text{StorageWt}$$

1.15 Cultivars

1.15.1 Brigadier

Brigadier overrides the following properties:

1.15.2 Rivage

Rivage overrides the following properties:

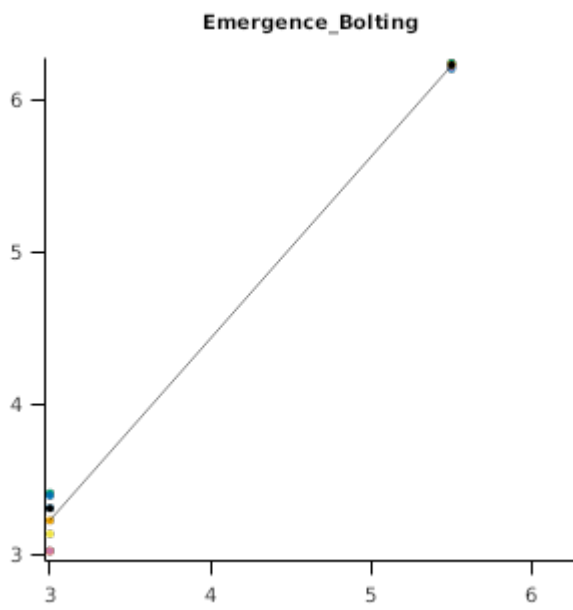
1.15.3 Jamon

Jamon overrides the following properties:

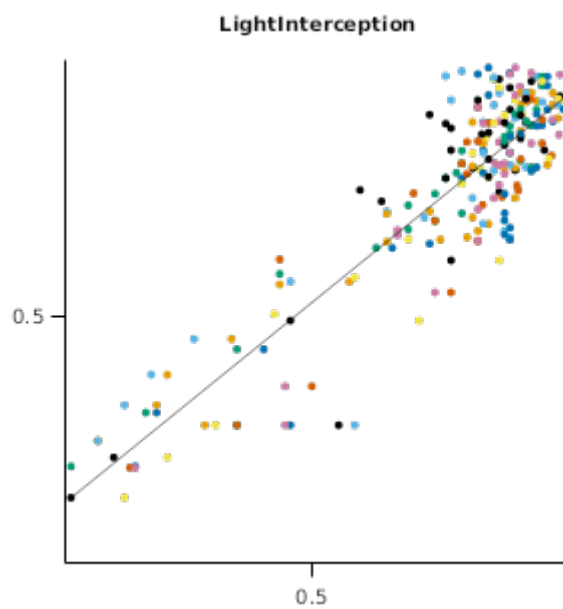
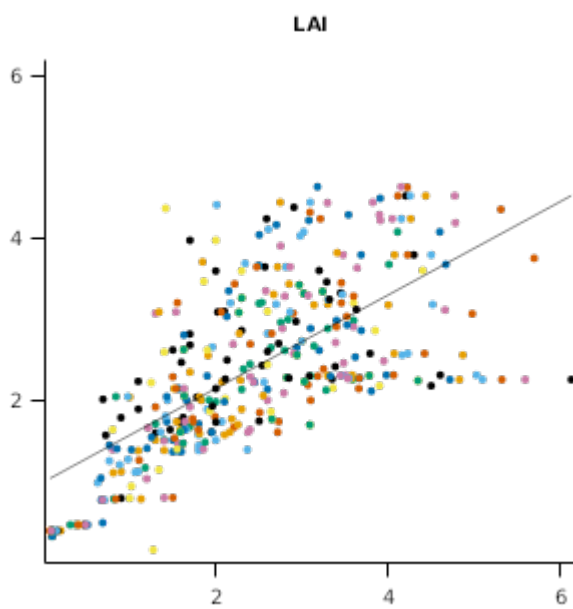
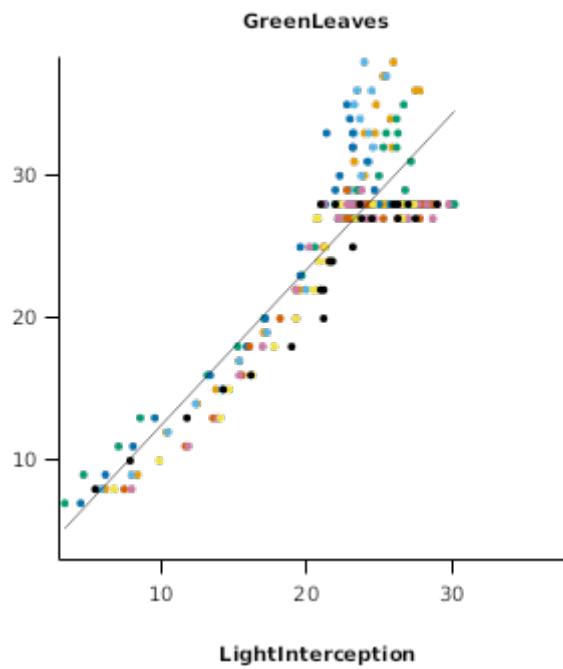
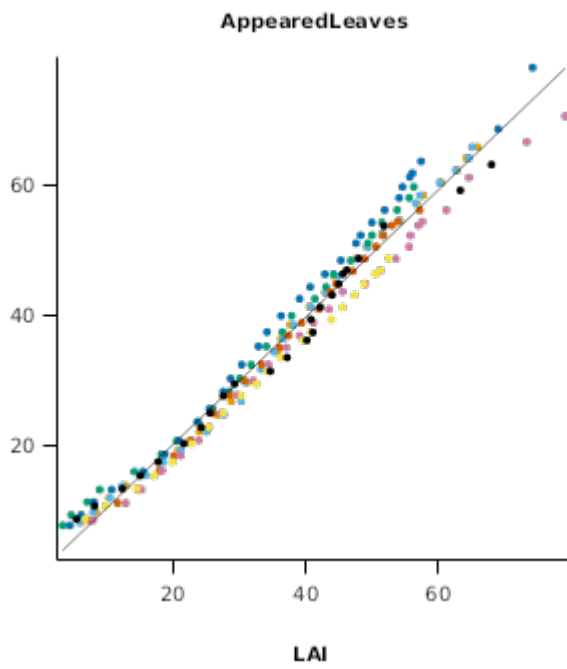
2 FodderBeetValidation

2.1 CombinedStatistics

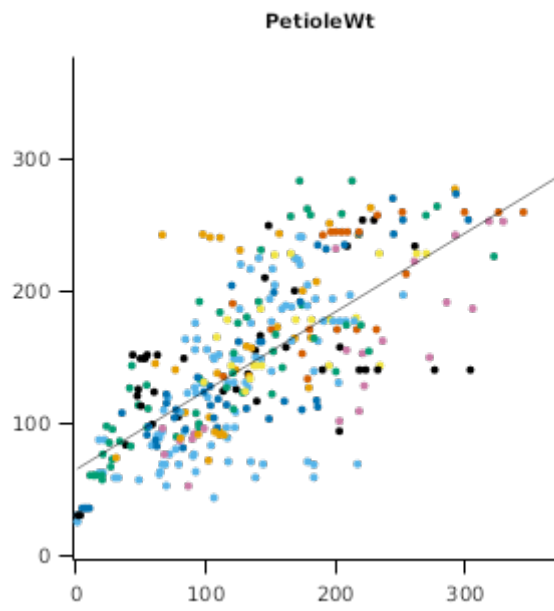
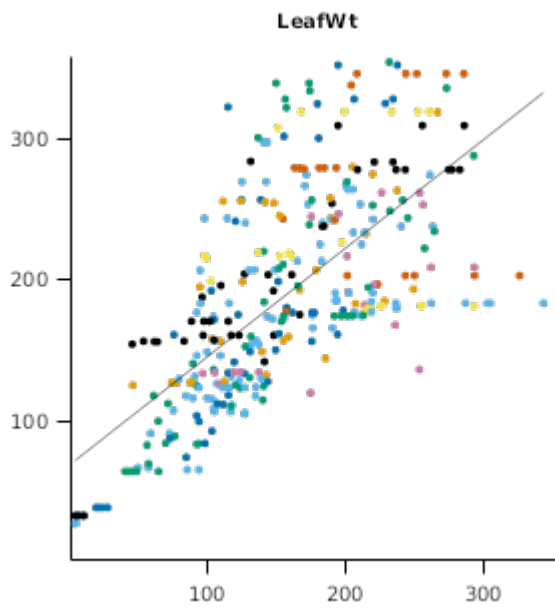
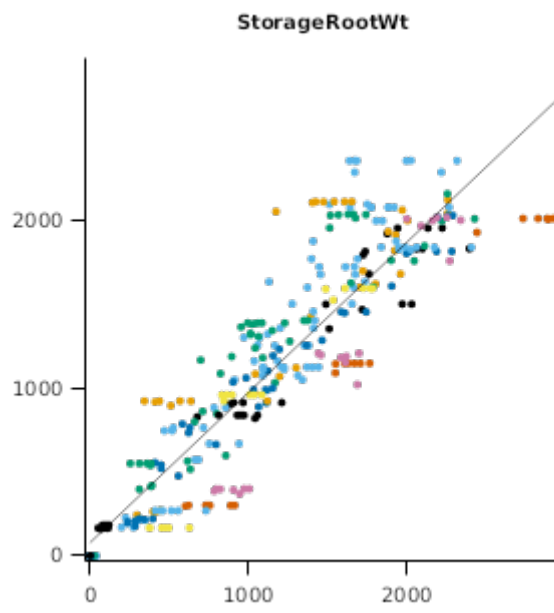
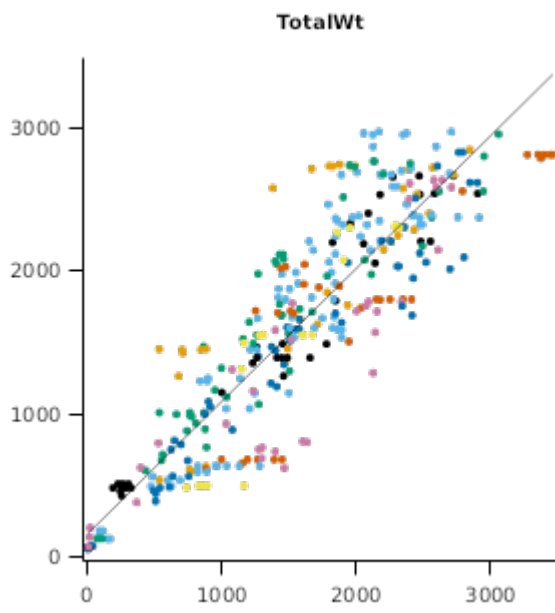
2.1.1 PhenologyStatistics



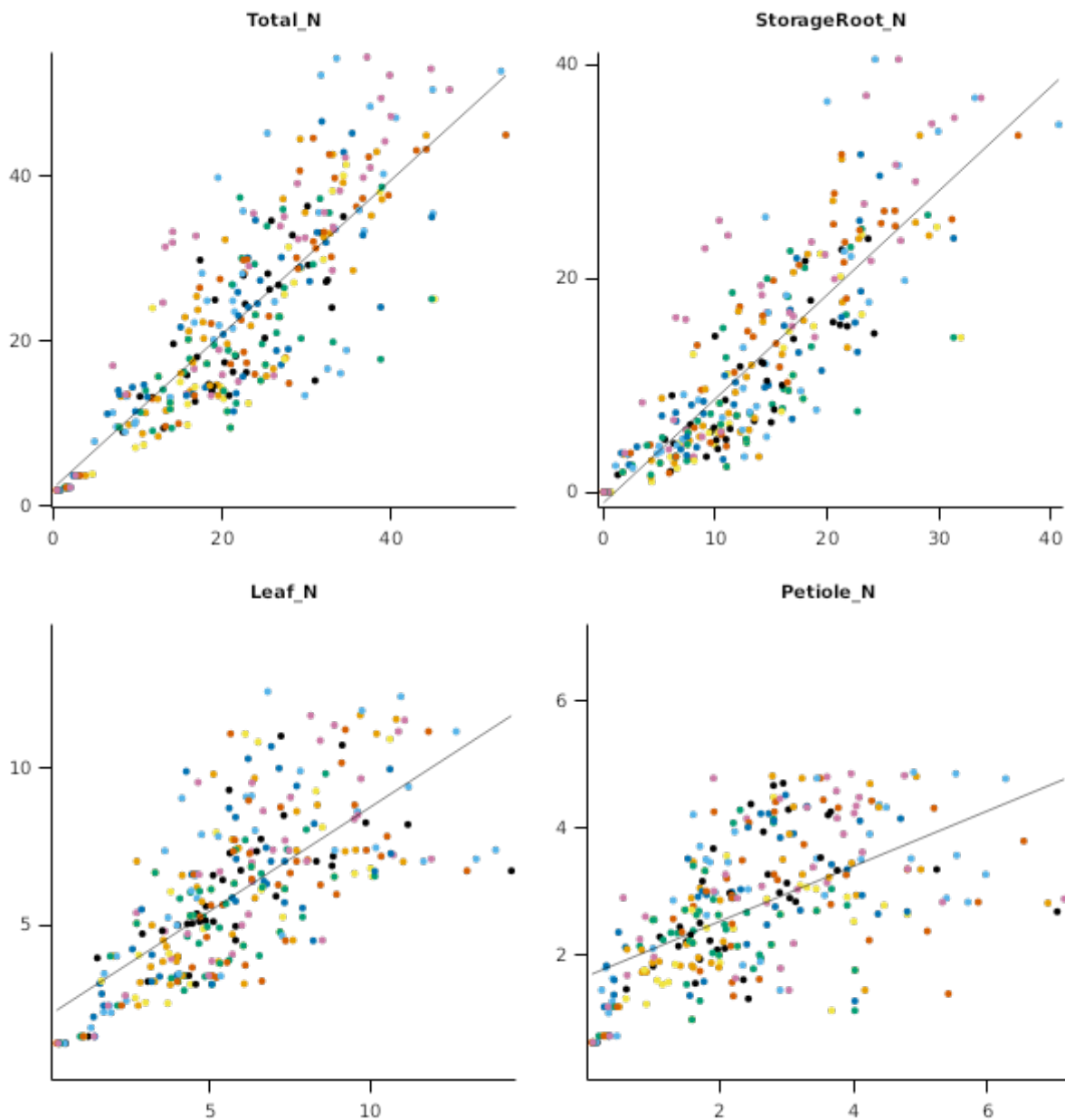
2.1.2 CanopyStatistics



2.1.3 BiomassStatistics



2.1.4 N_uptakeStatistics



2.2 NewZealand

2.2.1 Lincoln

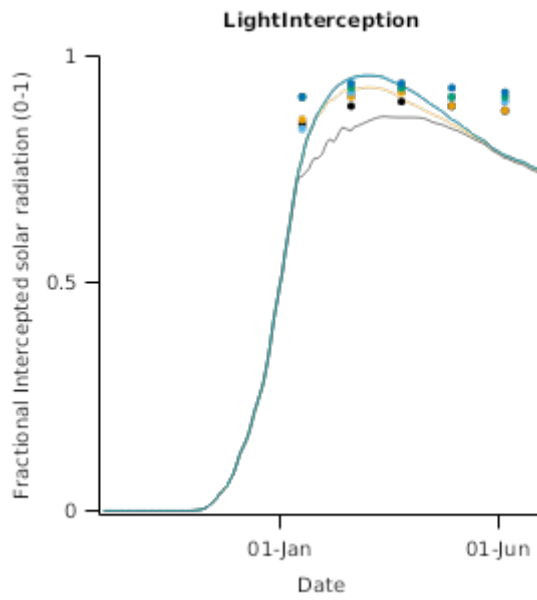
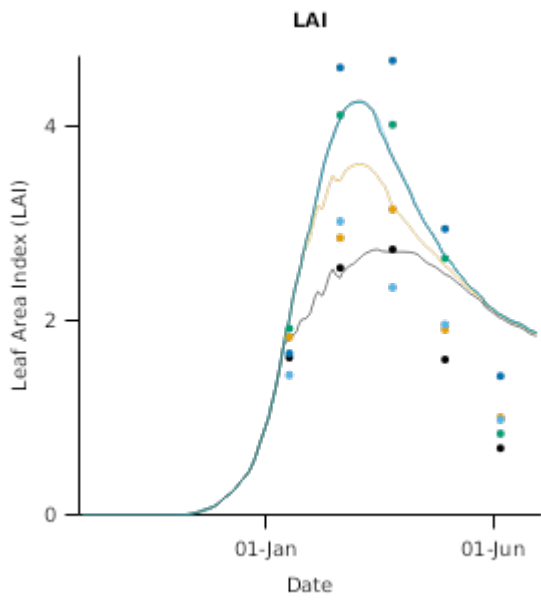
List of experiments.

Experiment Name	Design (Number of Treatments)
Lincoln2011	Nit (5)
Lincoln2012	Irr (4)
Lincoln2014	Cv x SD (8)
LincolnRS2016	Irr x Nit (6)

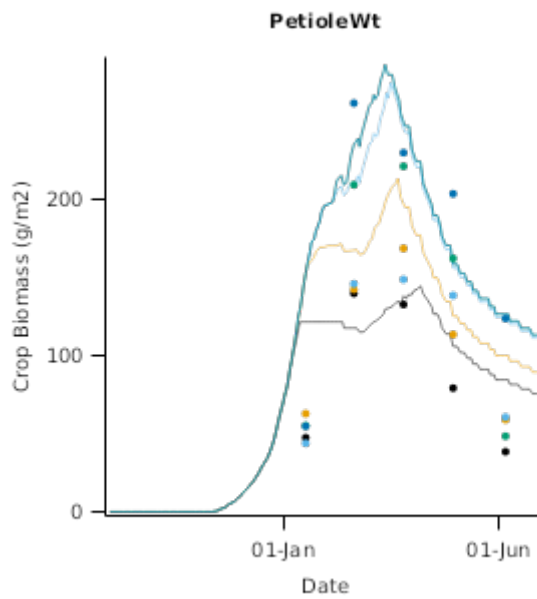
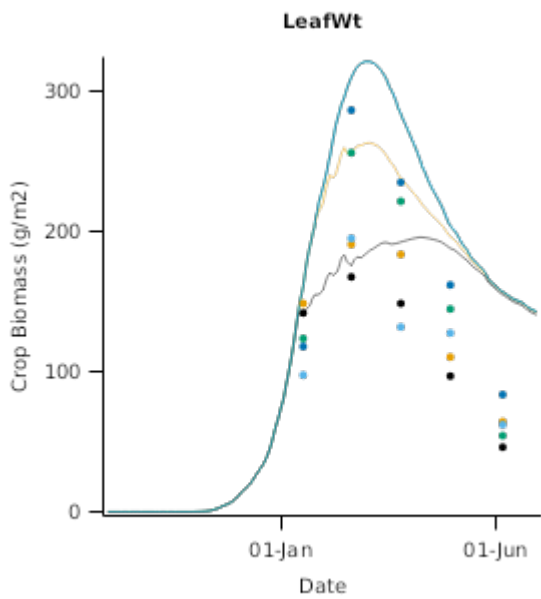
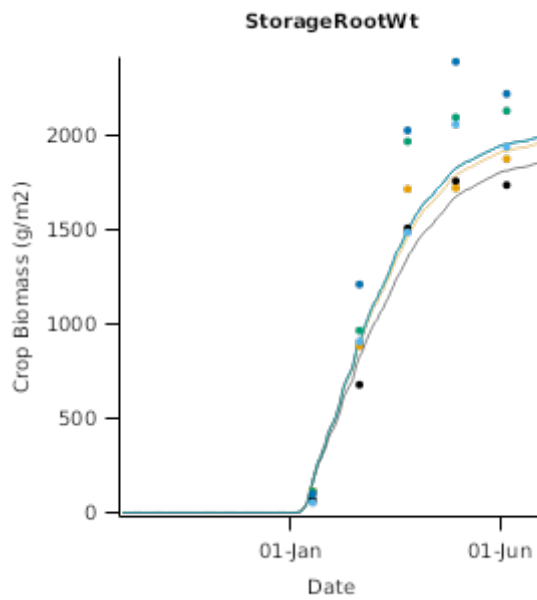
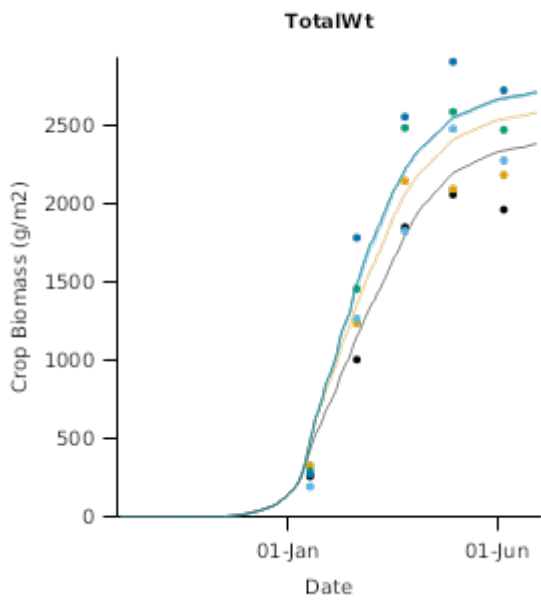
2.2.1.1 Lincoln2011

This was a nitrogen fertiliser treatment trial conducted at Lincoln in 2011 ([Chakwizira et al., 2014](#)).

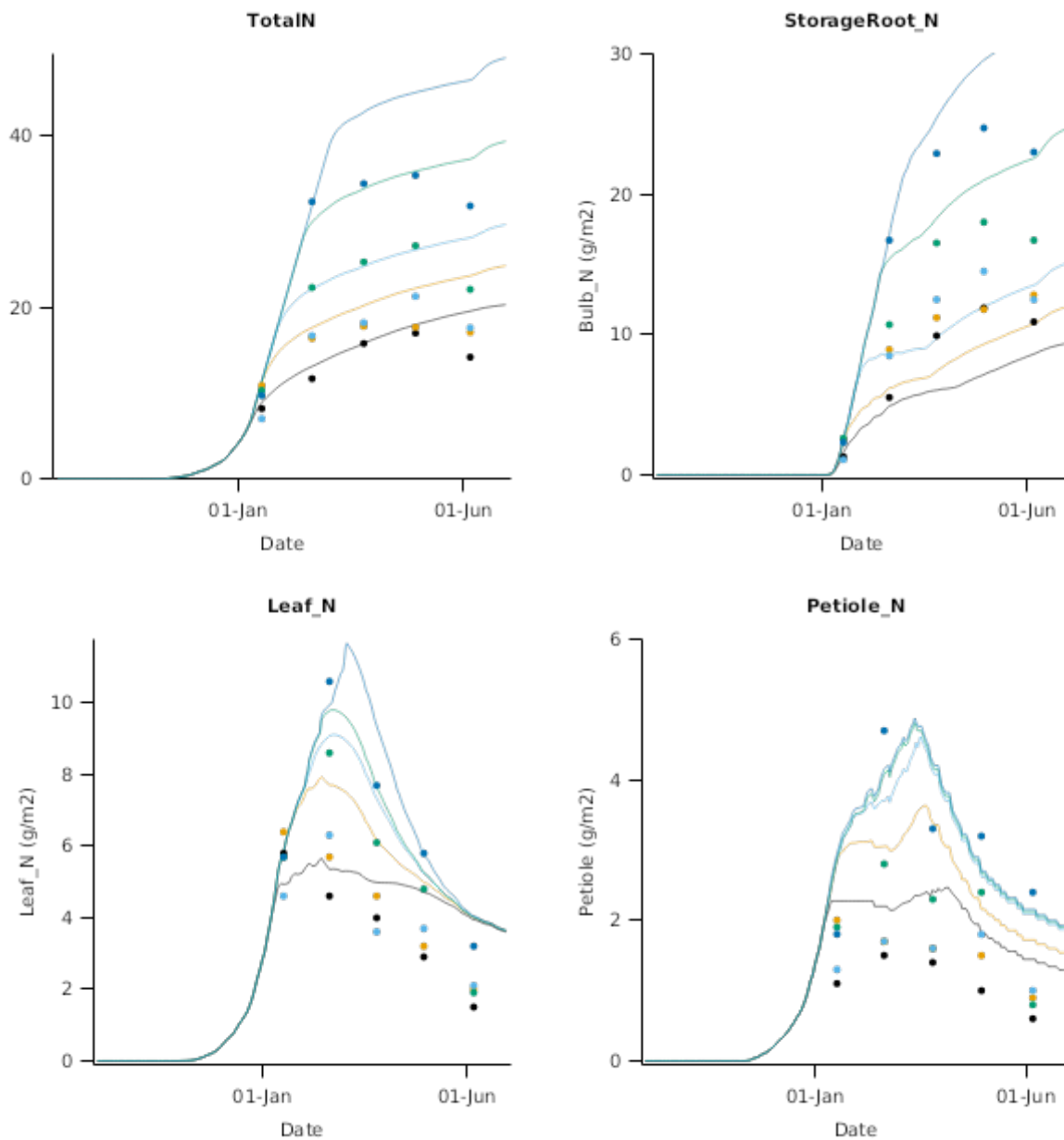
2.2.1.1.1 LeafGraphs



2.2.1.1.2 BiomassGraphs



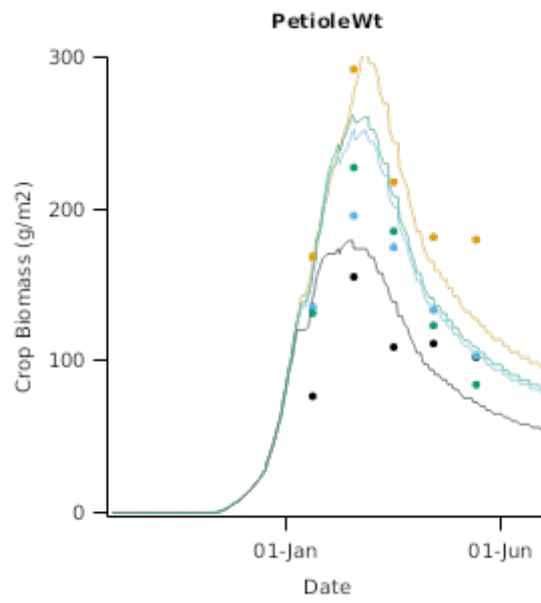
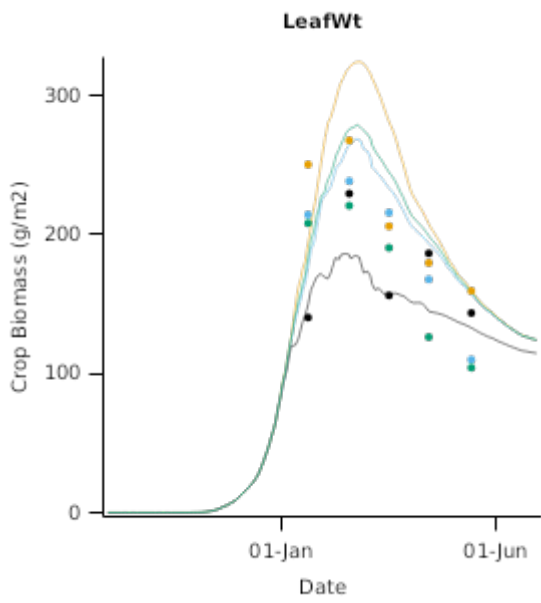
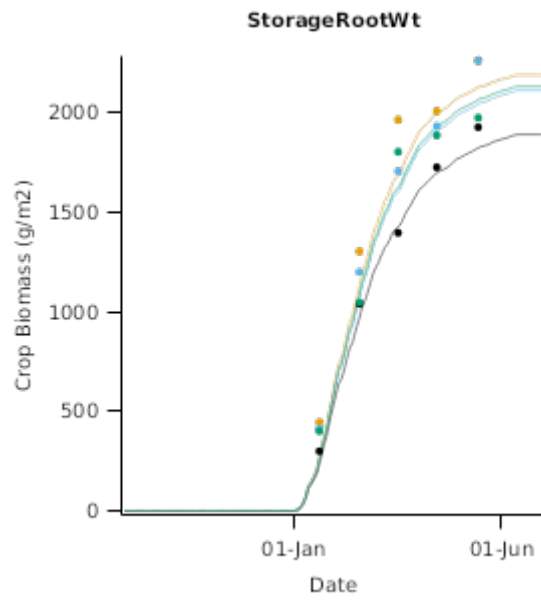
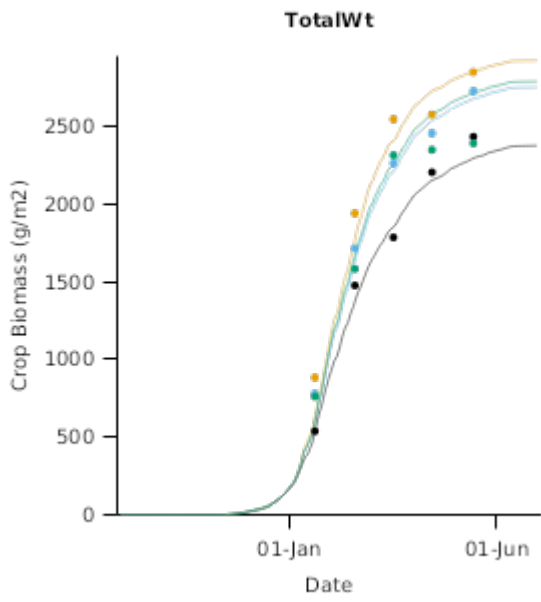
2.2.1.1.3 N_Uptake



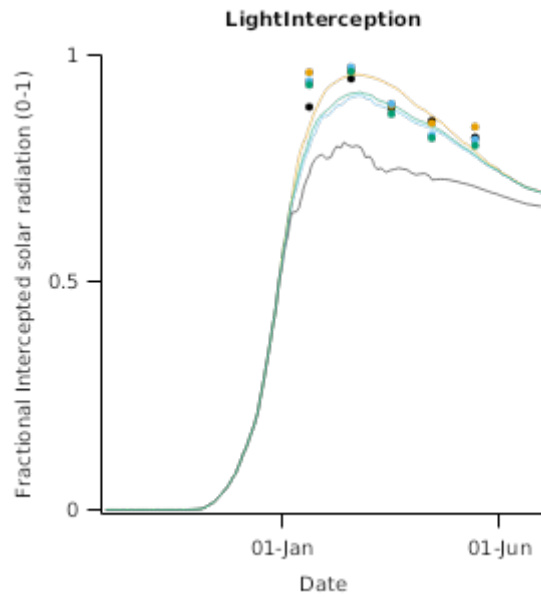
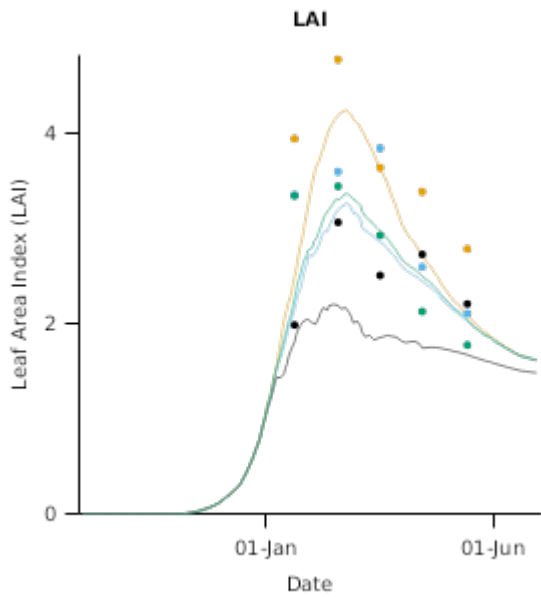
2.2.1.2 Lincoln2012

This was an irrigation treatment trial conducted at Lincoln in 2012 ([Chakwizira et al., 2014](#)).

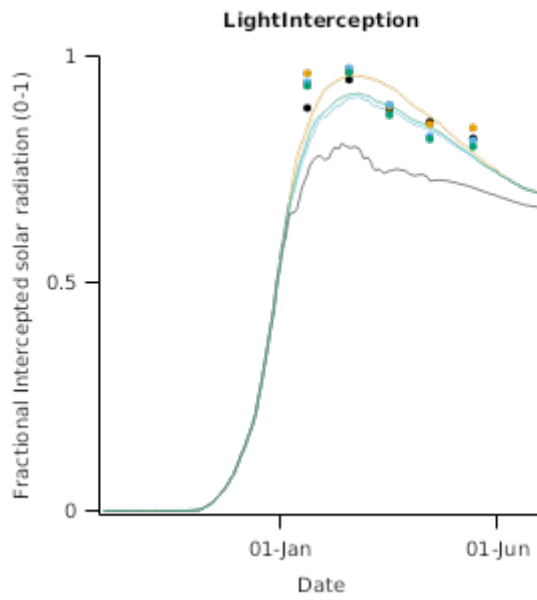
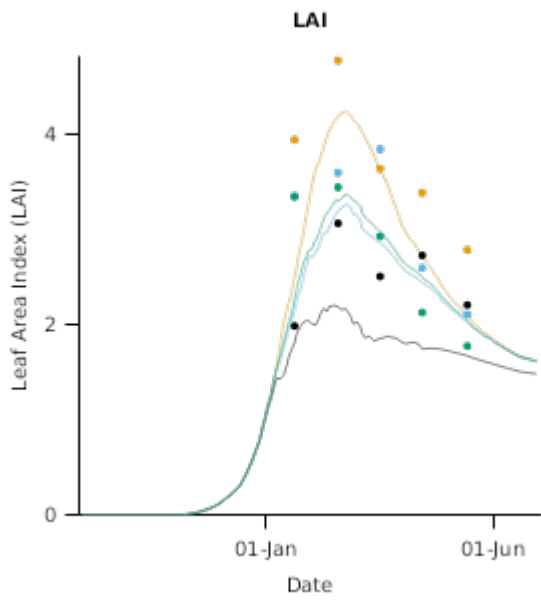
2.2.1.2.1 BiomassGraphs



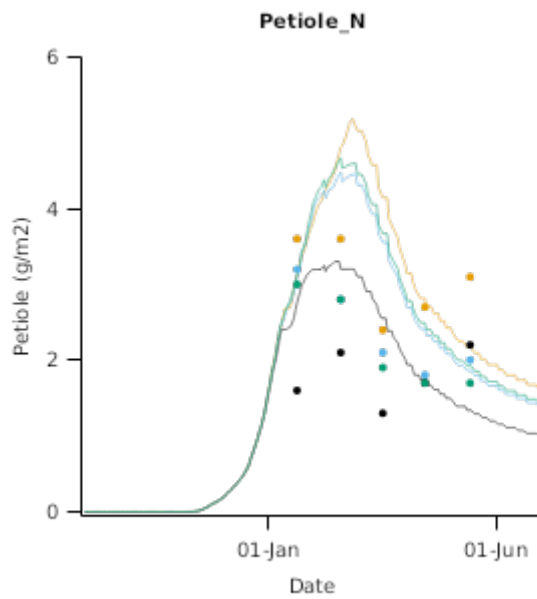
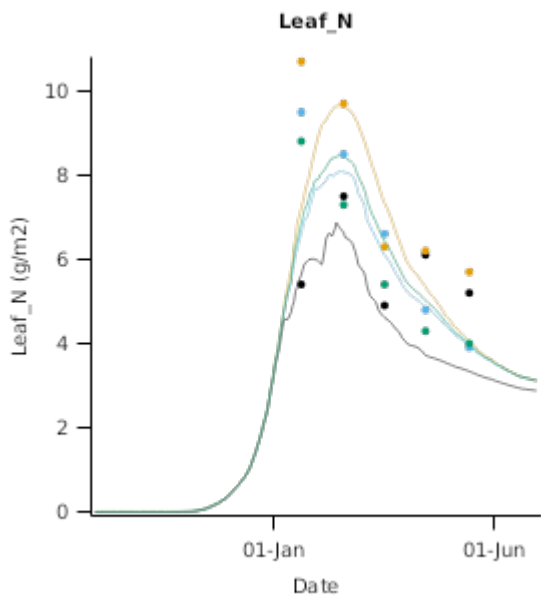
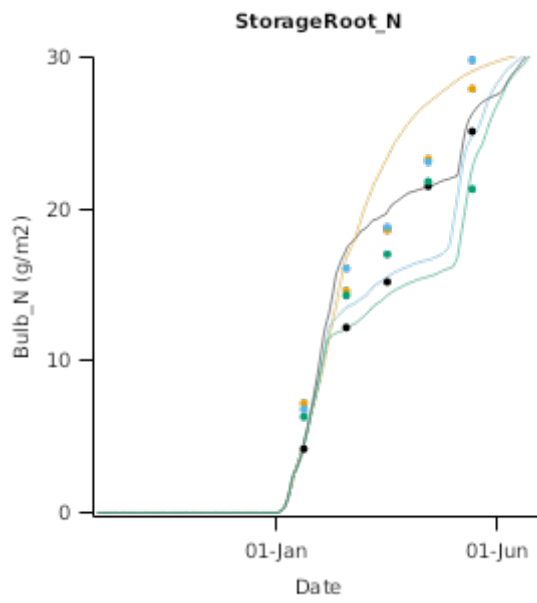
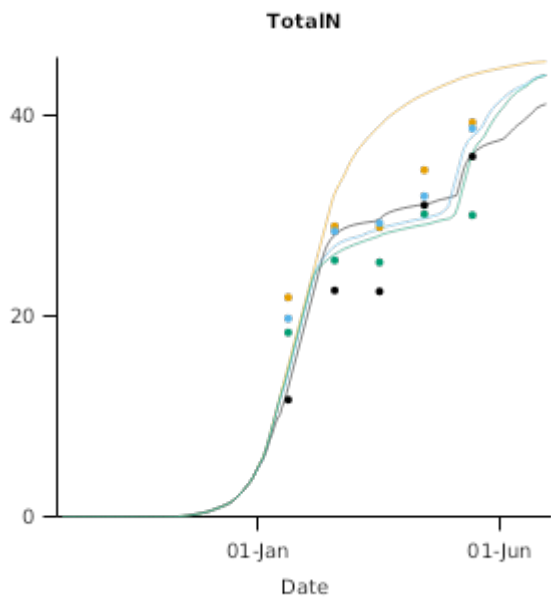
2.2.1.2.2 LeafGraphs



2.2.1.2.2.1 LeafGraphs



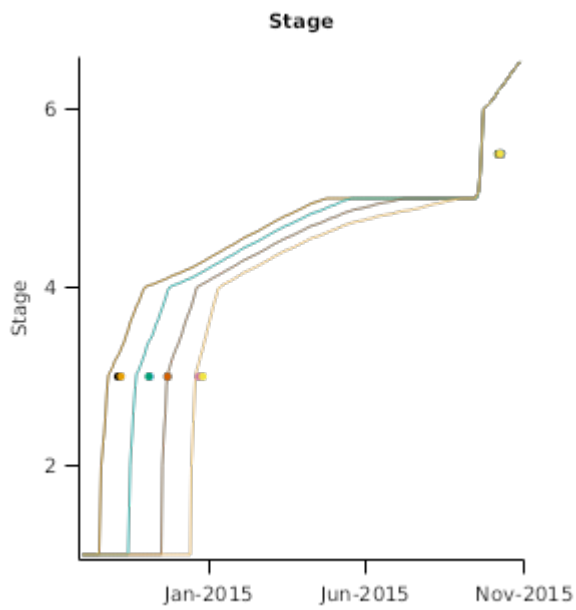
2.2.1.2.3 N_Uptake



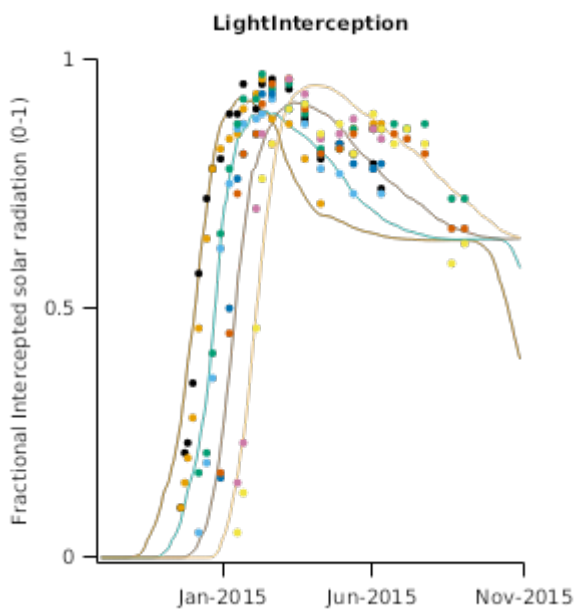
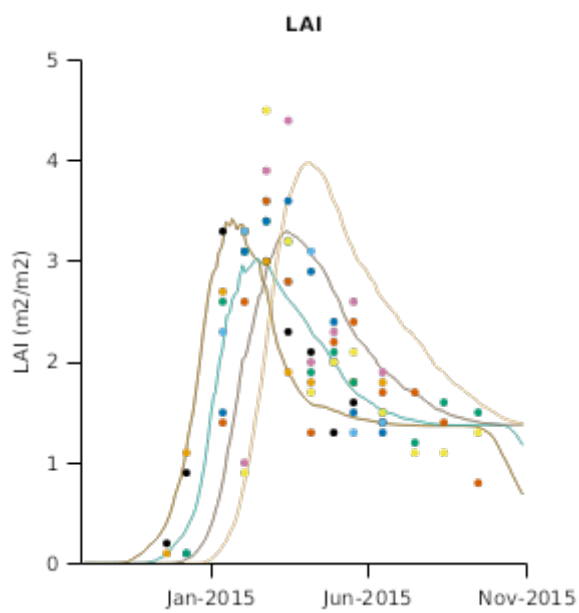
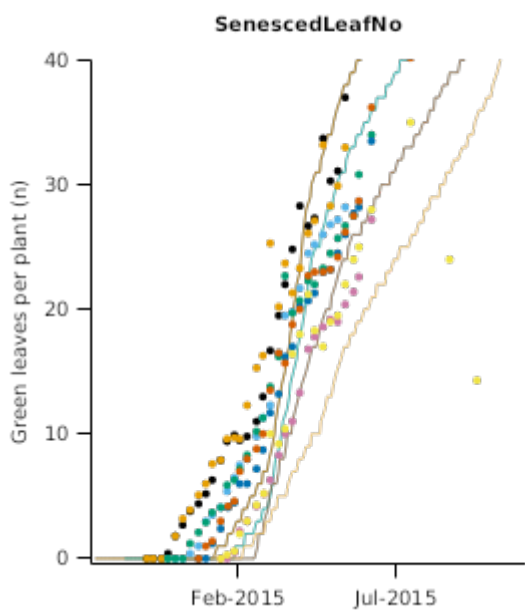
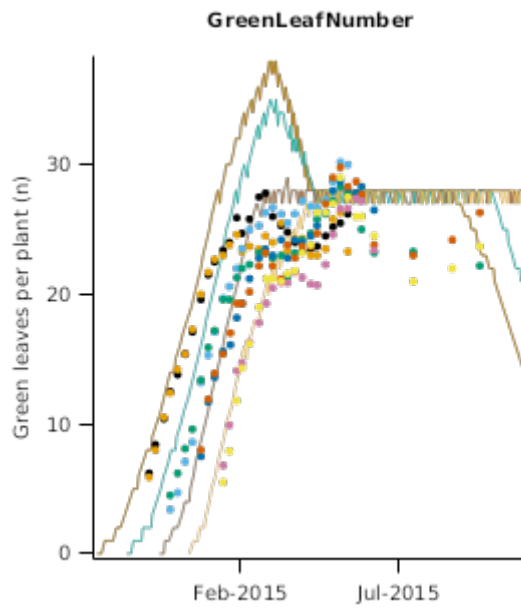
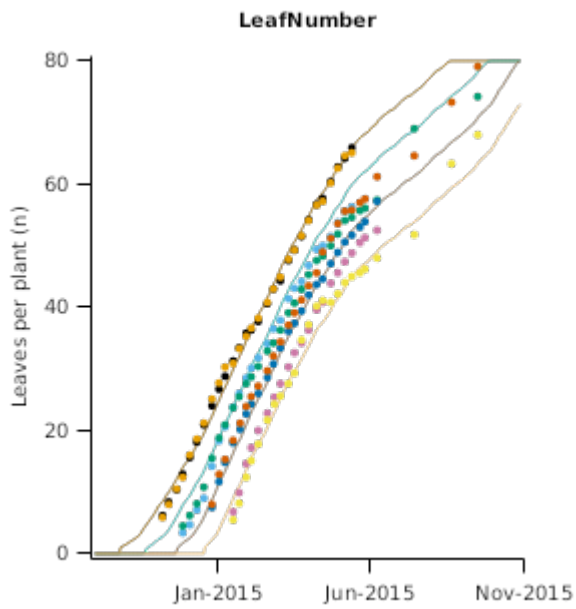
2.2.1.3 Lincoln2014

The data used here is from a sowing date experiment conducted at Lincoln, Canterbury, New Zealand. The experiment was established in the field as a Randomised Complete Block Design with four replicates. Two cultivars ("Rivage" and "Brigadier") were evaluated over four sowing dates (19 September, 17 October, 17 November and 15 December in 2014). The first phase i.e. calibration/parameterisation of a potential yield model was completed using cultivar "Rivage" data from the October sowing date ([Khaembah et al., 2017](#)).

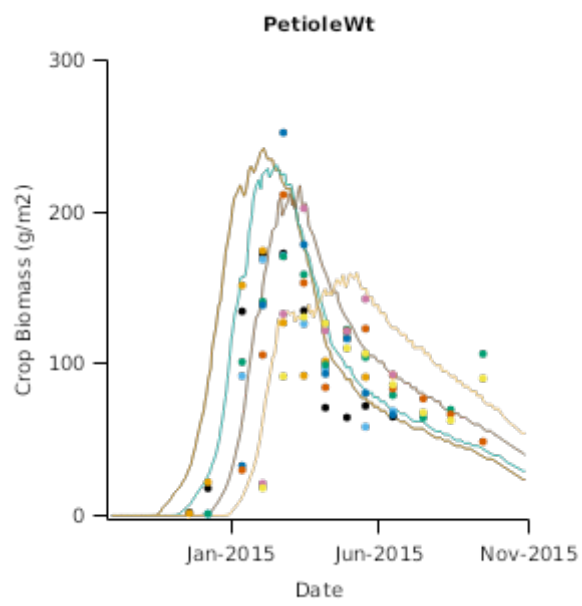
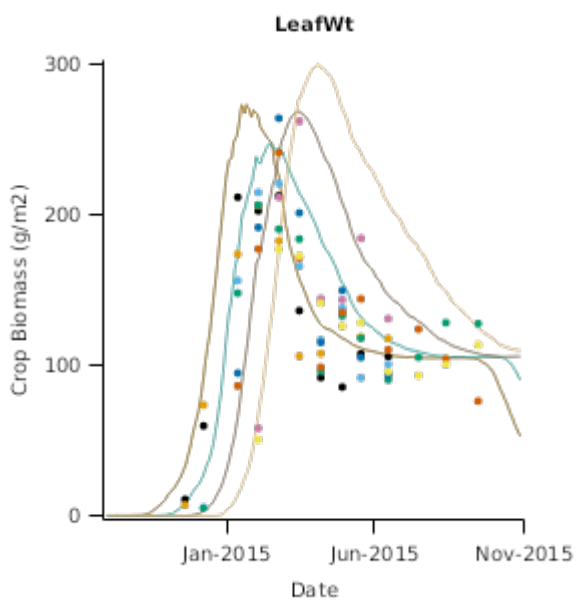
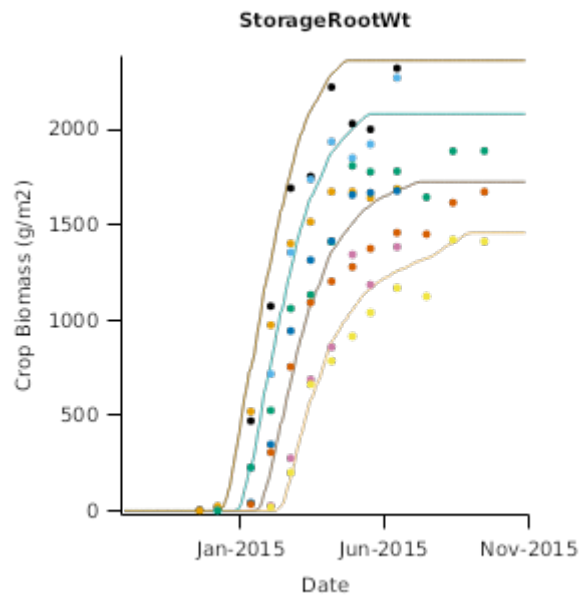
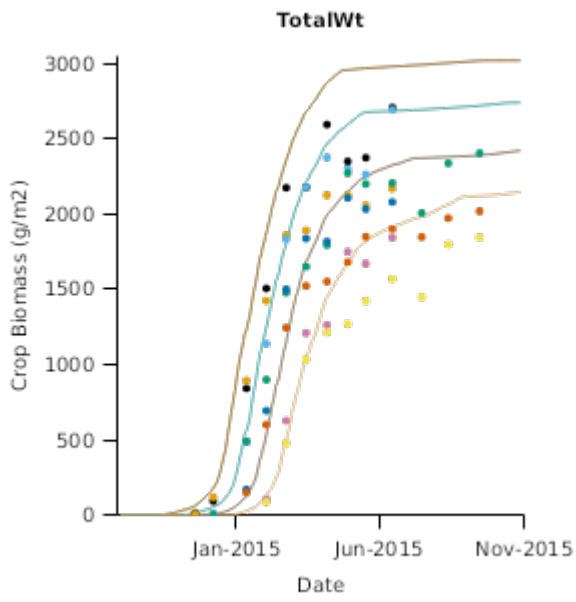
2.2.1.3.1 PhenologyGraphs



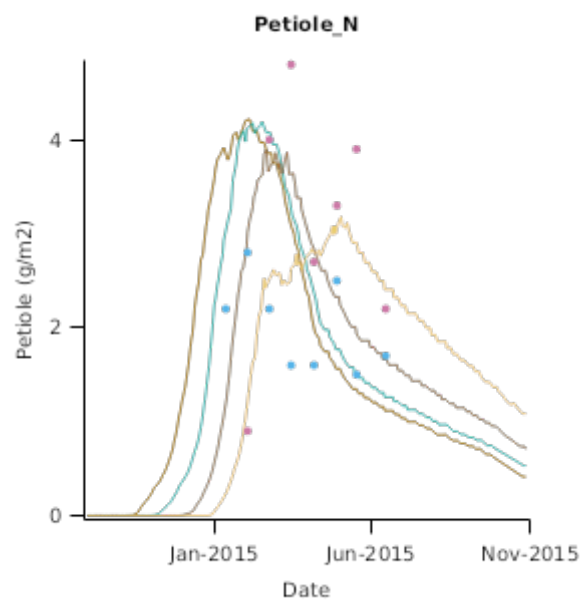
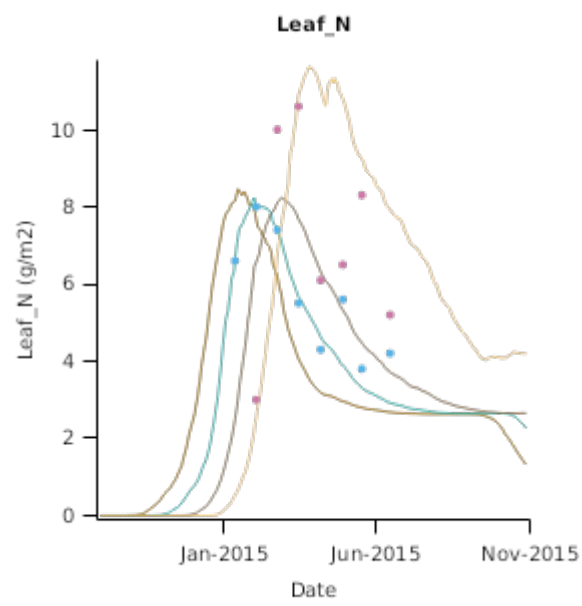
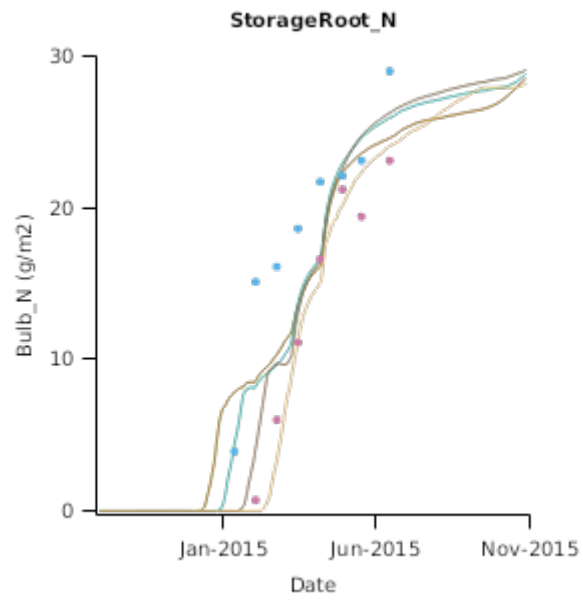
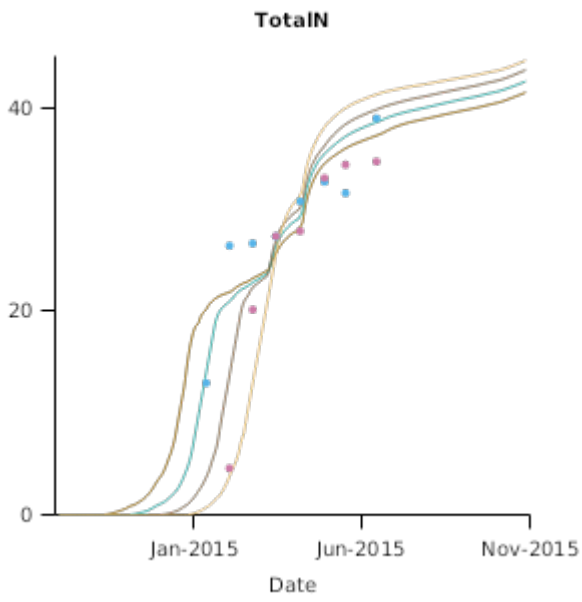
2.2.1.3.2 LeafGraphs



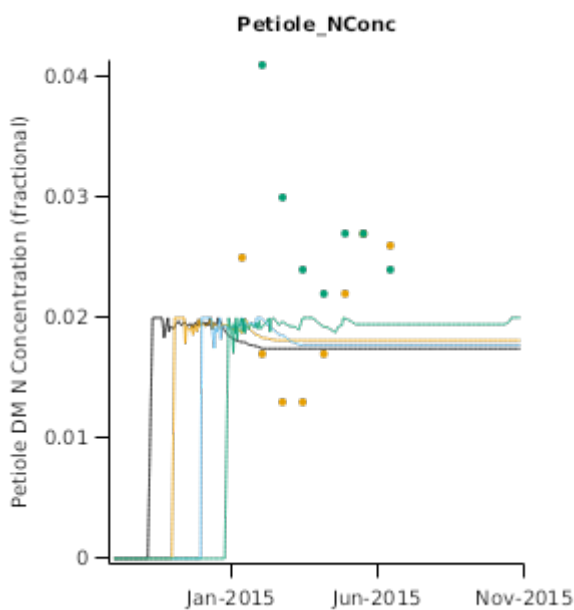
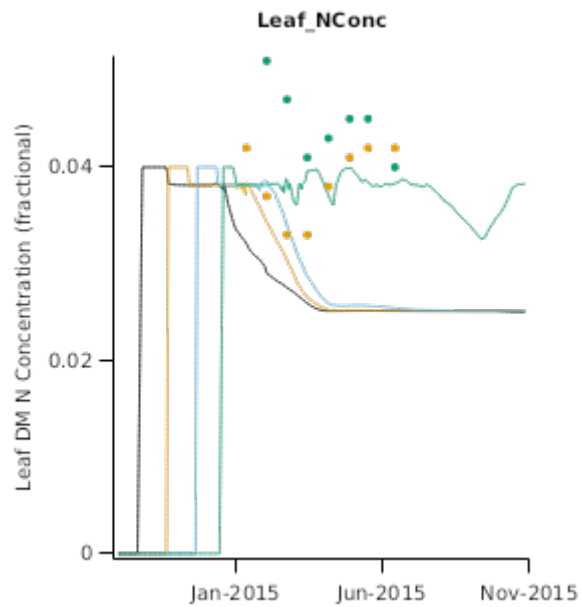
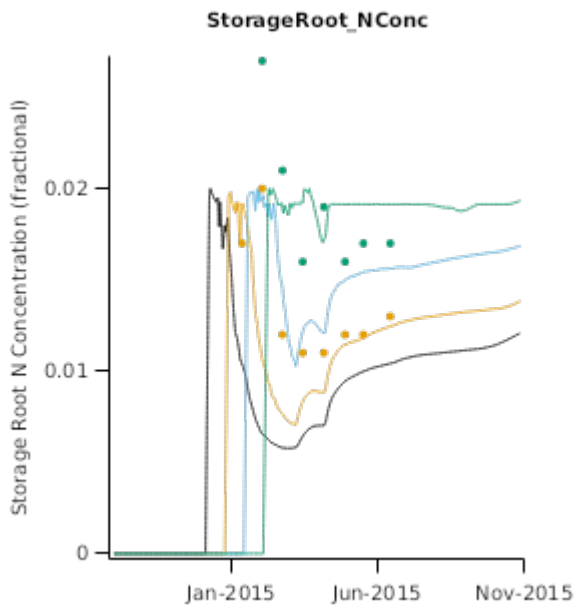
2.2.1.3.3 BiomassGraphs



2.2.1.3.4 N_Uptake



2.2.1.3.5 N_Conc



2.2.1.4 LincolnRS2016

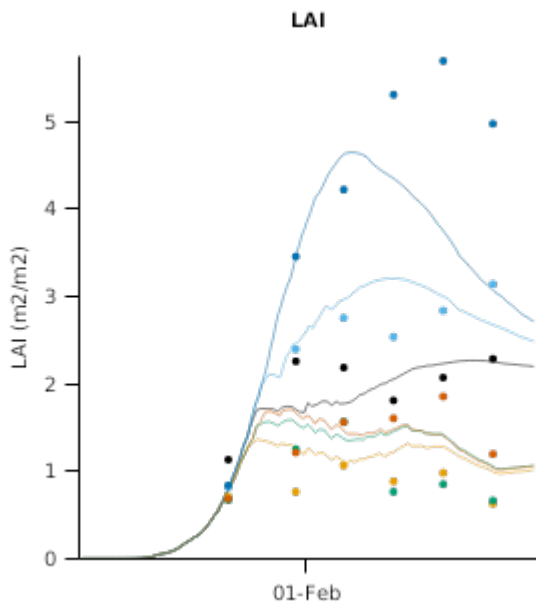
This trial was conducted in the rainshelter at Plant and Food Research in Lincoln, New Zealand in 2016. The objective was to evaluate the effect of nitrogen and irrigation on the development and growth of fodder beet crops. Details:

- Three nitrogen treatments: 0 kg N/ha, 50 kg N/ha & 300 kg N/ha applied as dissolved urea with fertigation
- Two irrigation treatments: Nil and full irrigation

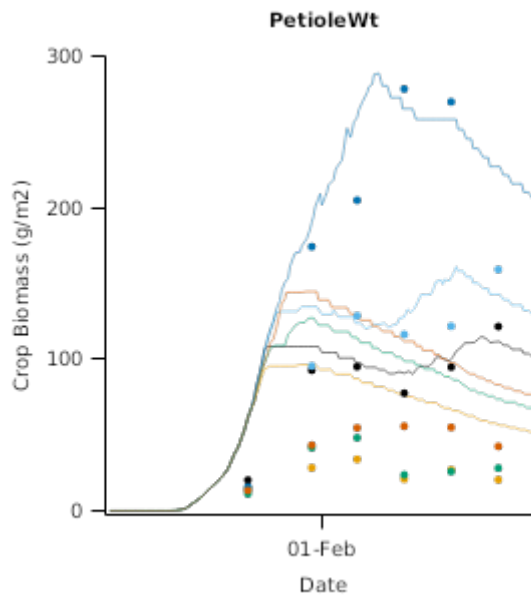
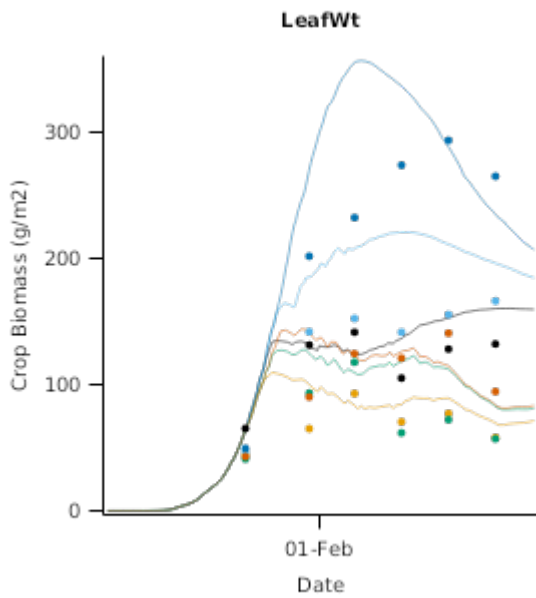
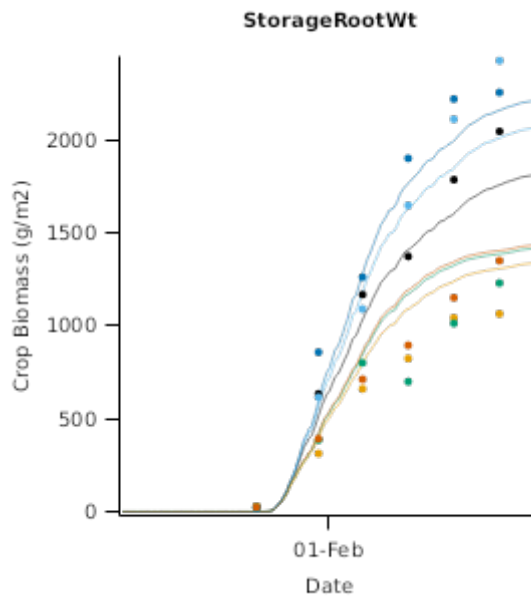
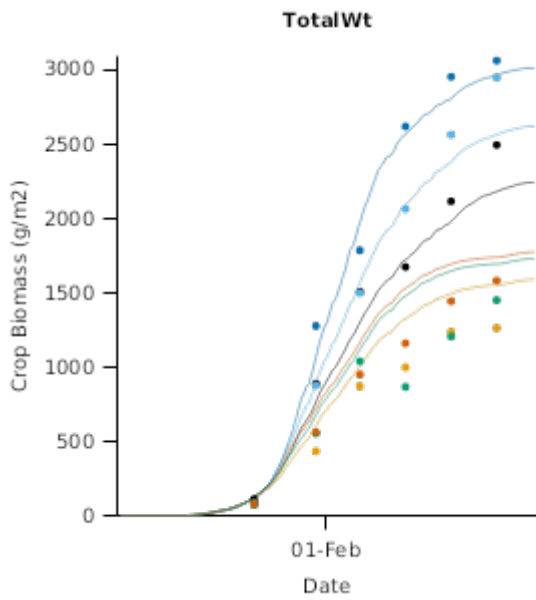
Fodder beet (cultiva "Rivage") was precision drilled on 18 October 2016. Sowing density was 11 plants/m² and row spacing was 0.45m.

2.2.1.4.1 Graphs

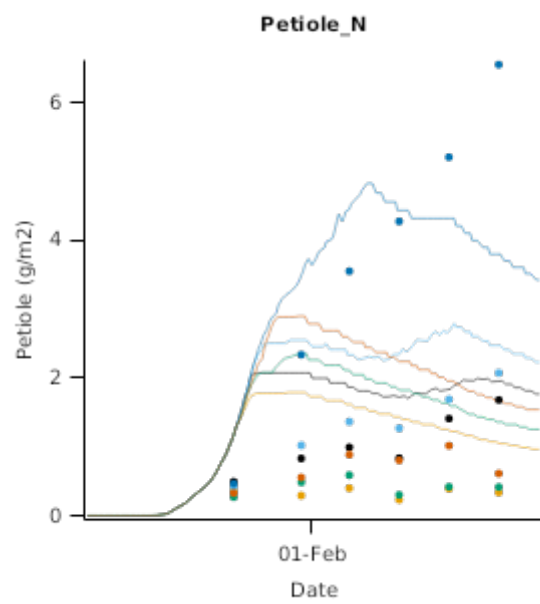
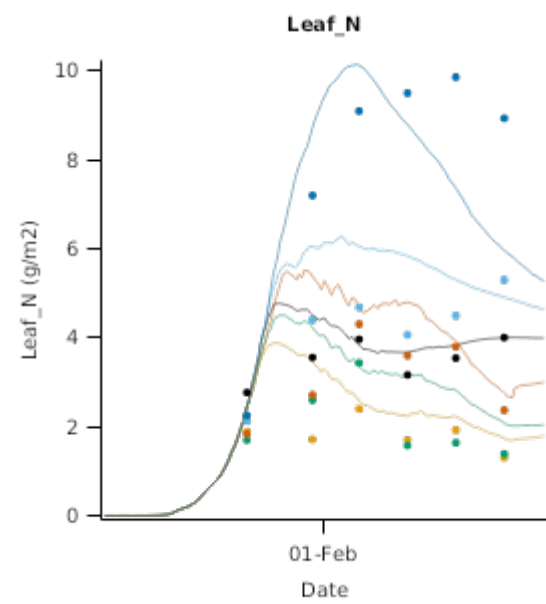
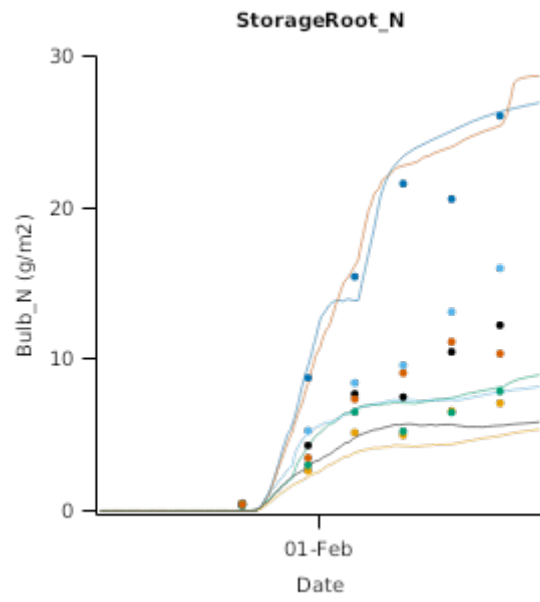
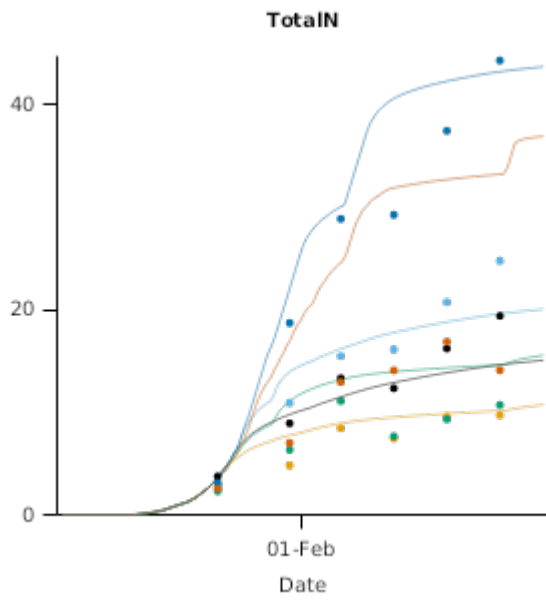
2.2.1.4.1.1 LeafGraphs



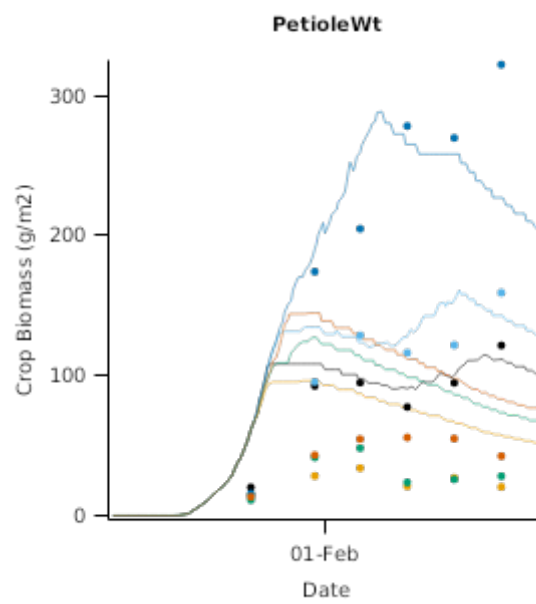
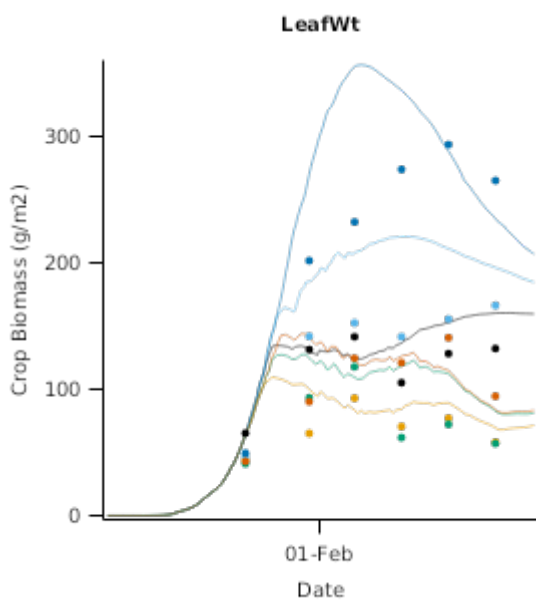
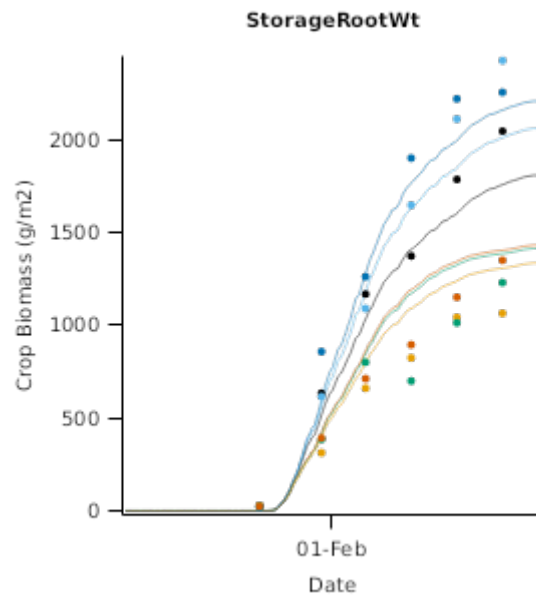
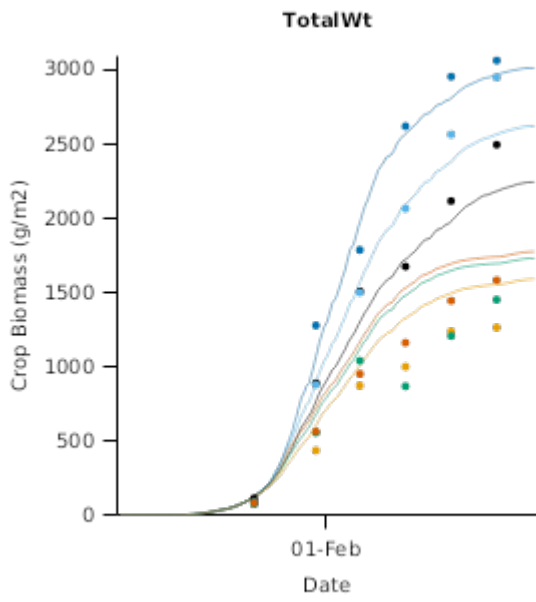
2.2.1.4.1.2 BiomassGraphs



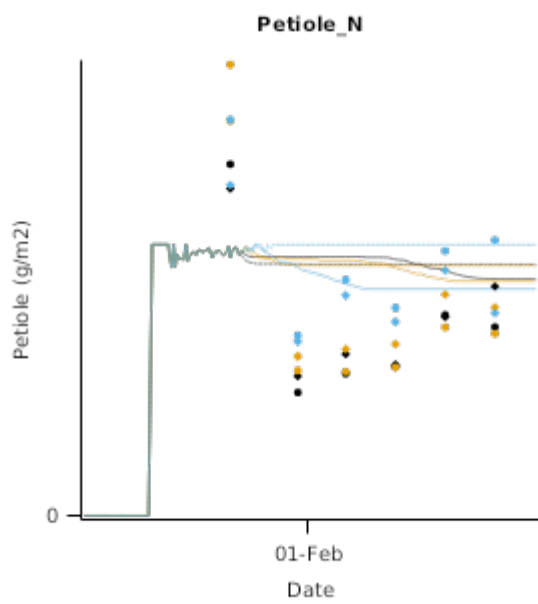
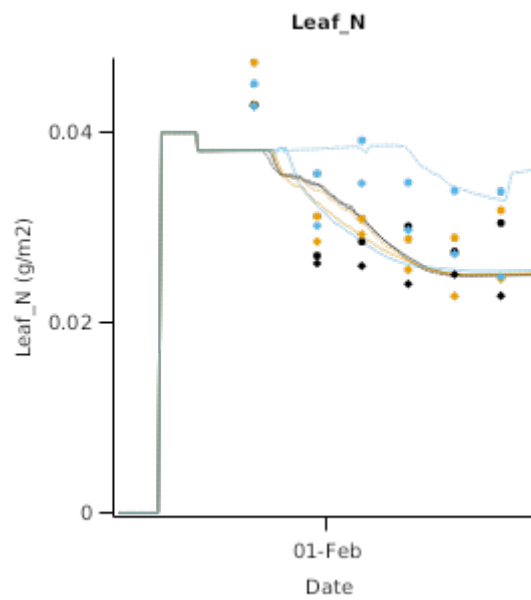
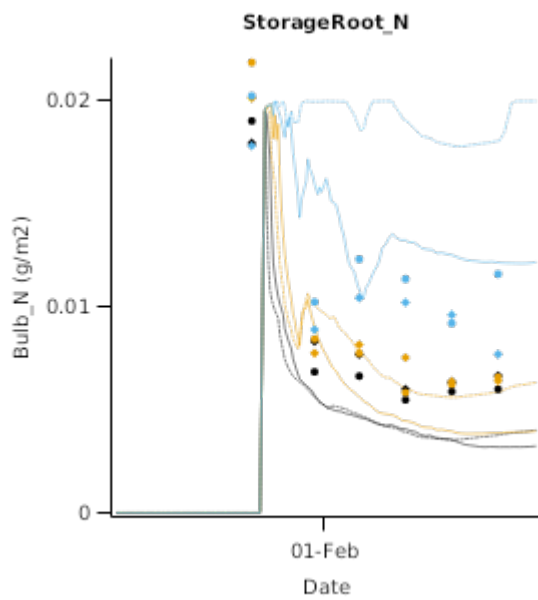
2.2.1.4.1.3 N_Uptake



2.2.1.4.1.4 BiomassGraphsHighN



2.2.1.4.1.5 N_Conc



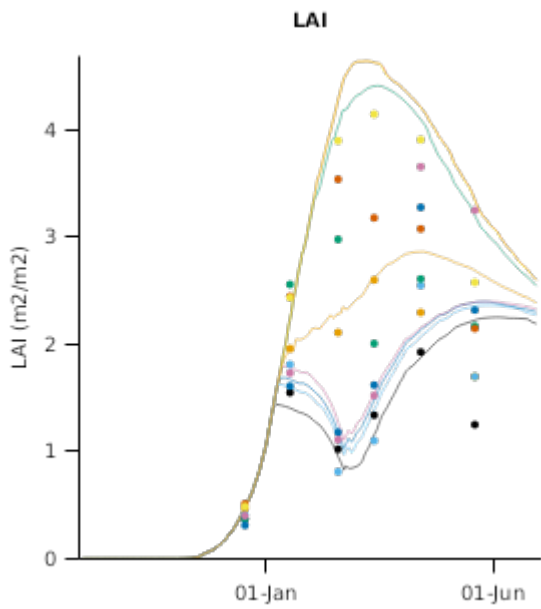
2.2.2 AshleyDene

This is a nitrogen fertiliser by irrigation trial conducted at Ashley Dene in 2013 ([Chakwizira et al., 2016](#)).

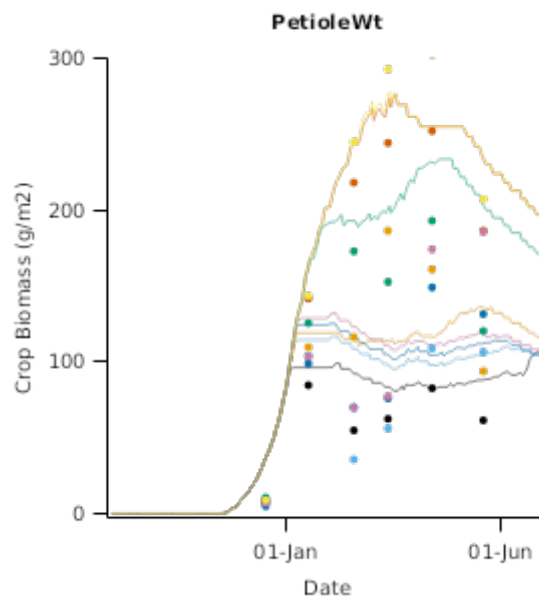
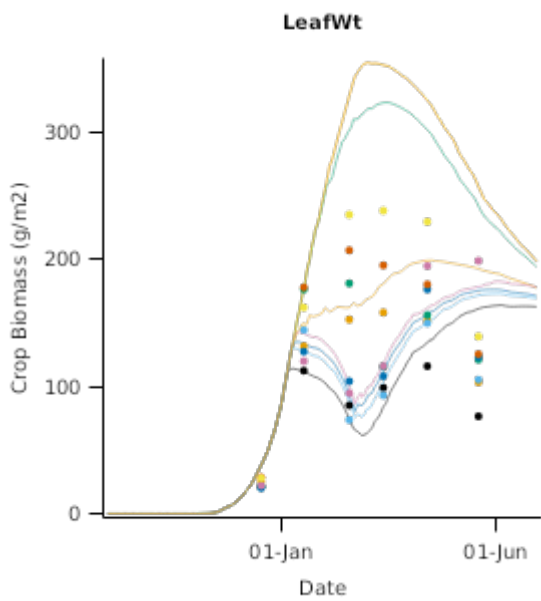
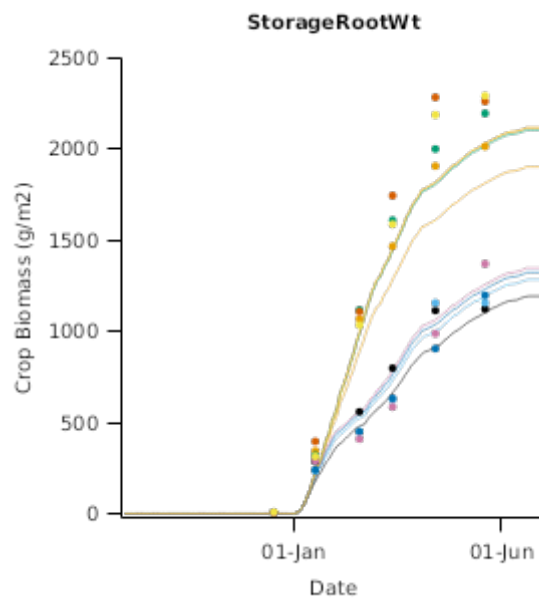
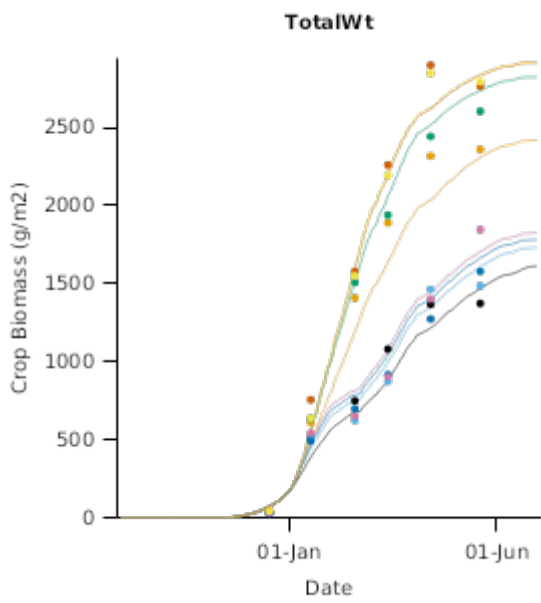
List of experiments.

Experiment Name	Design (Number of Treatments)
Ashley2013	Irr x Nit (8)

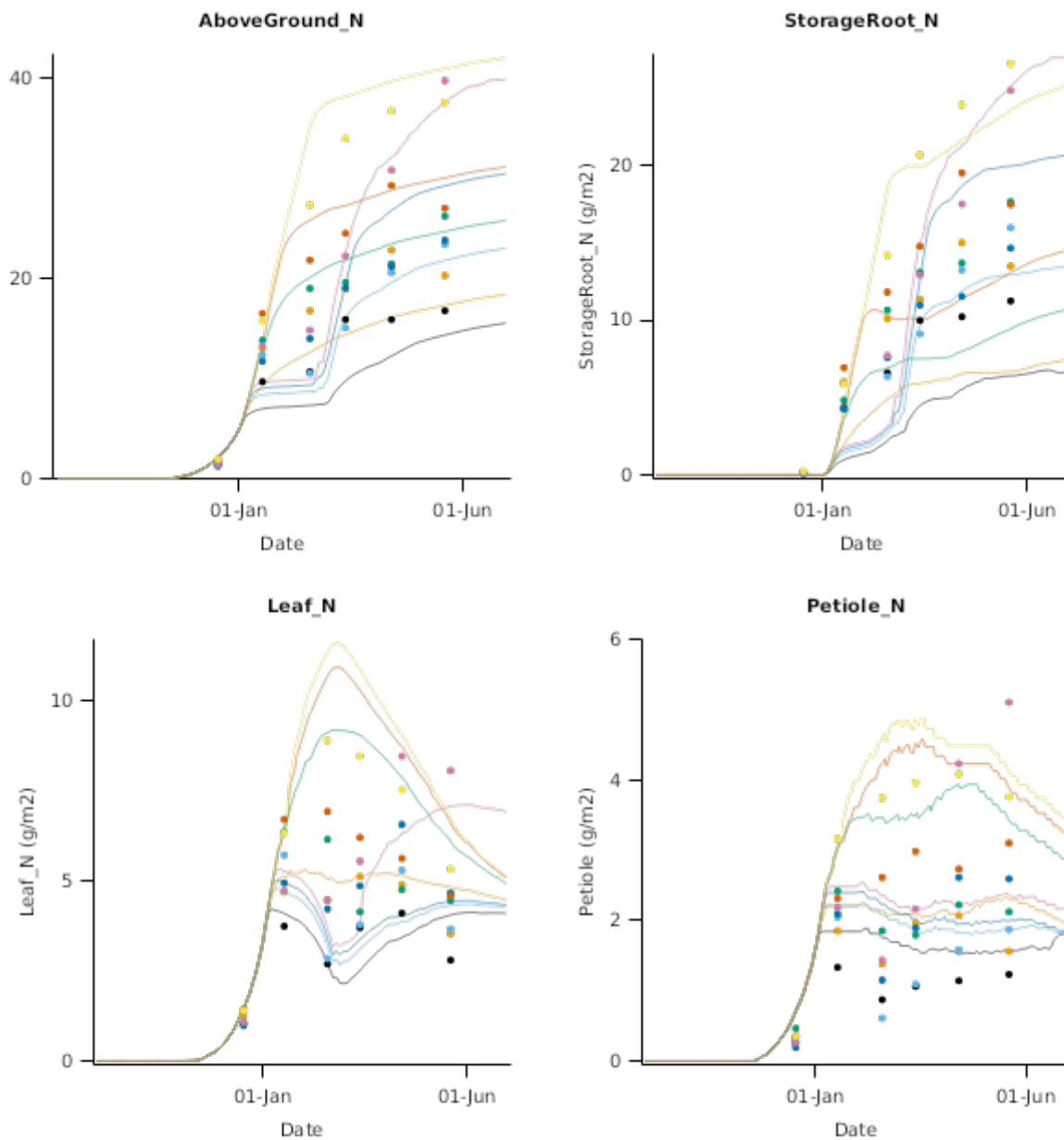
2.2.2.1 LeafGraphs



2.2.2.2 BiomassGraphs



2.2.2.3 N_Uptake



2.2.3 SFF

The data (unpublished) used here is from a SFF experiment managed by de Ruiter et al.

2.2.3.1 Canterbury

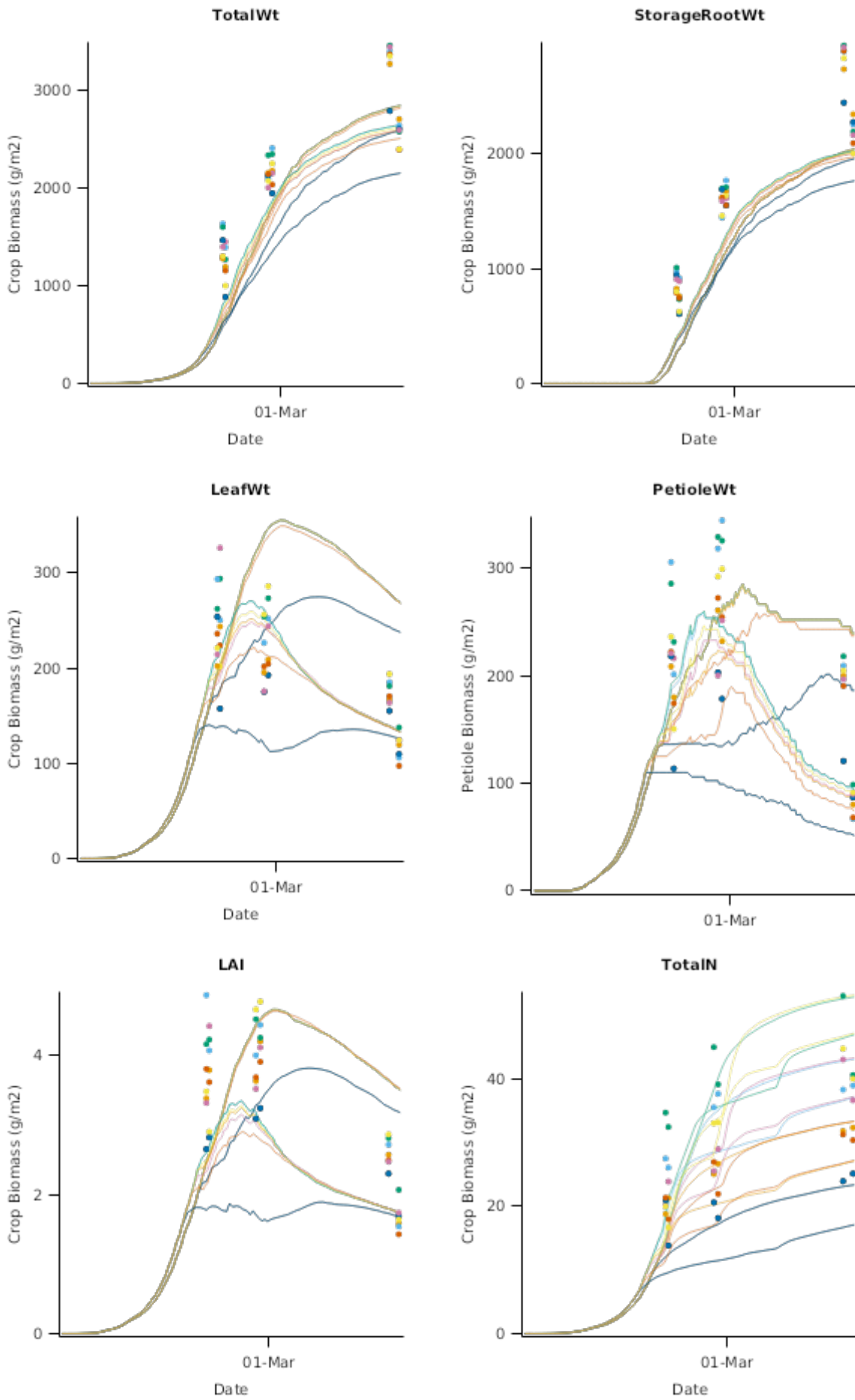
List of experiments.

Experiment Name	Design (Number of Treatments)
Orari	Nit x Splits (8)
Rakaia	Nit x Splits (8)

2.2.3.1.1 Orari

The data used here is from a SFF experiment (Batty; Winchester) managed by de Ruiter et al.

2.2.3.1.2 Graphs

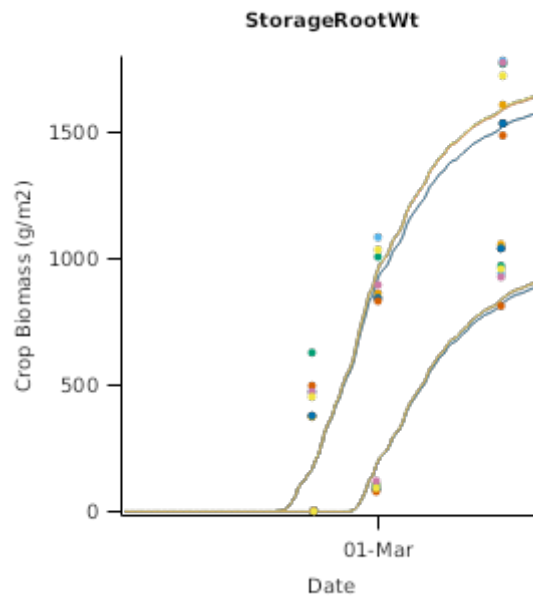
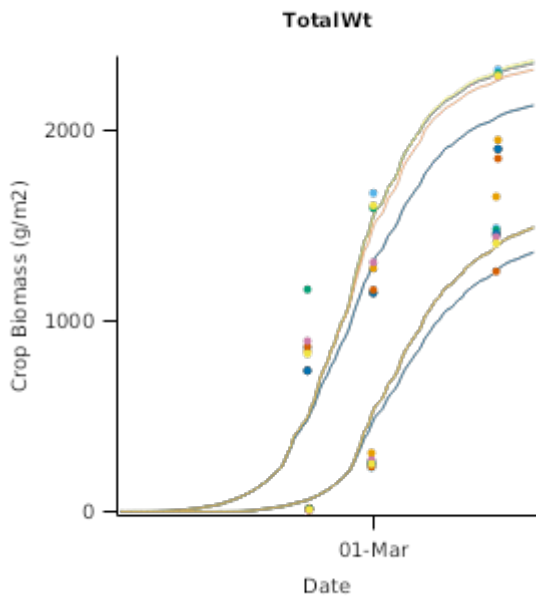


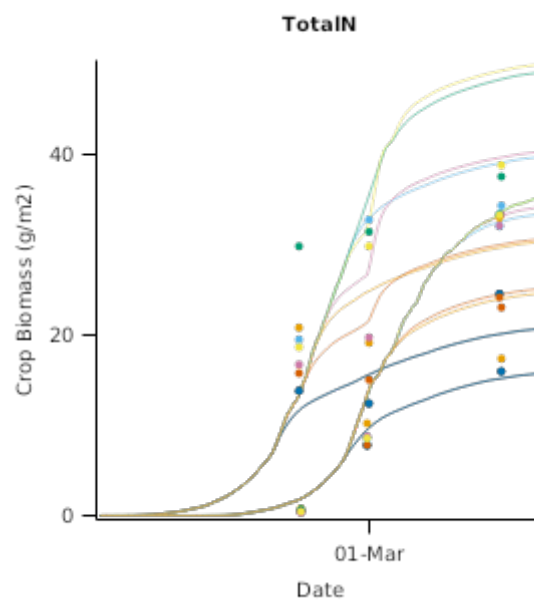
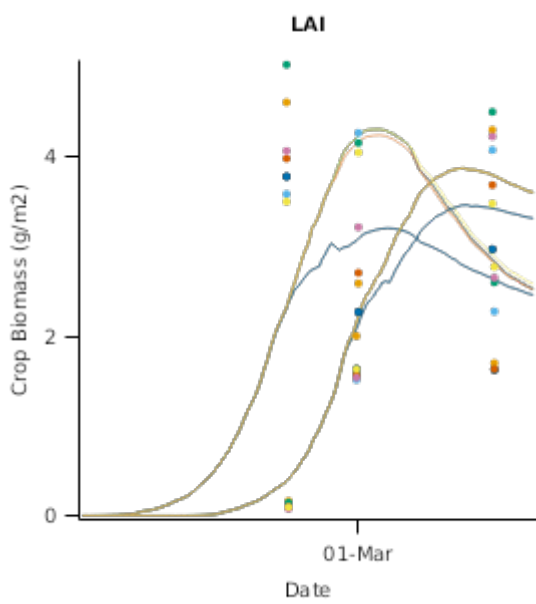
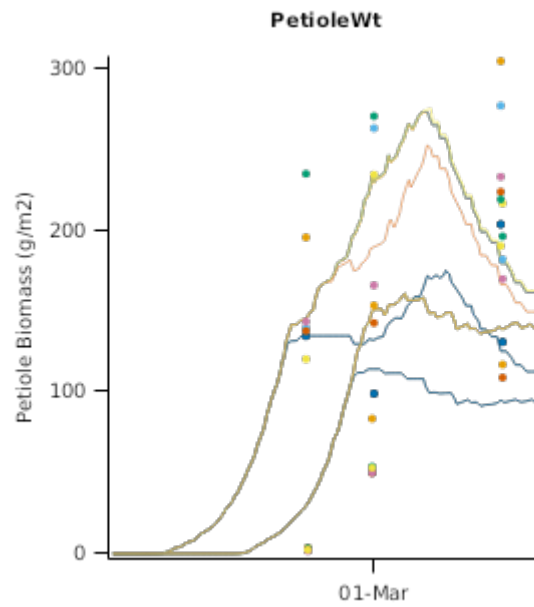
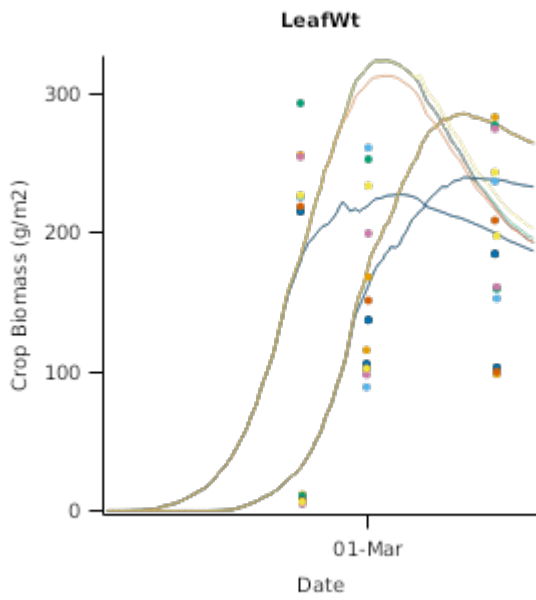
2.2.3.2 Southland

List of experiments.

Experiment Name	Design (Number of Treatments)
Gore	Nit x Splits (8)
Riverton	Nit x Splits (8)

2.2.3.2.1 Graphs



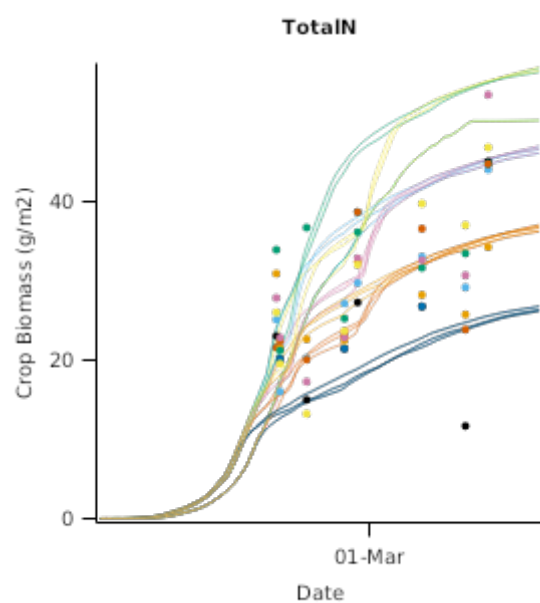
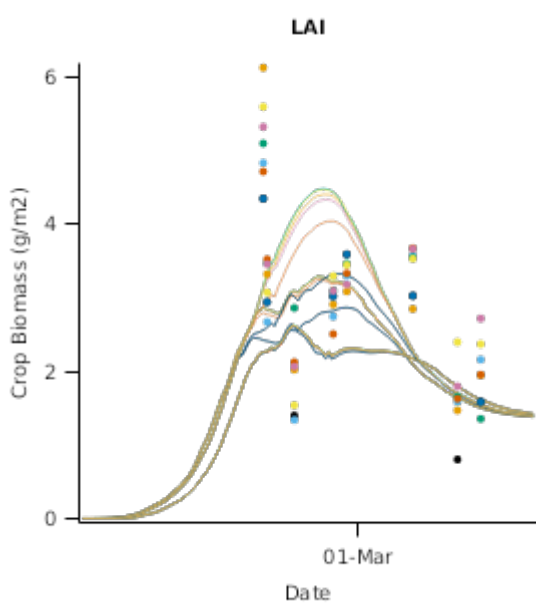
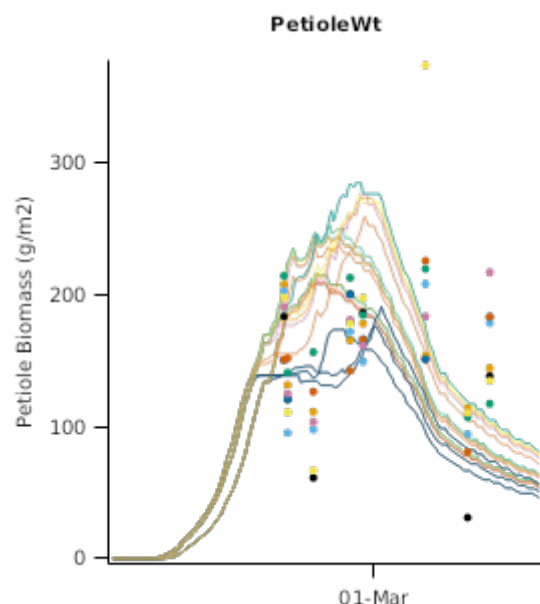
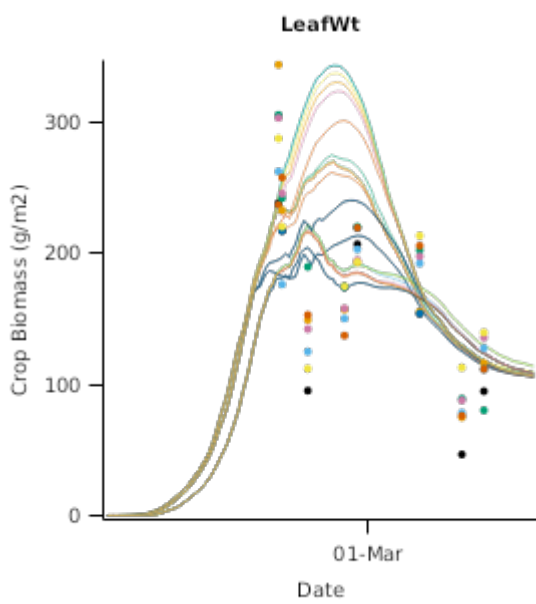
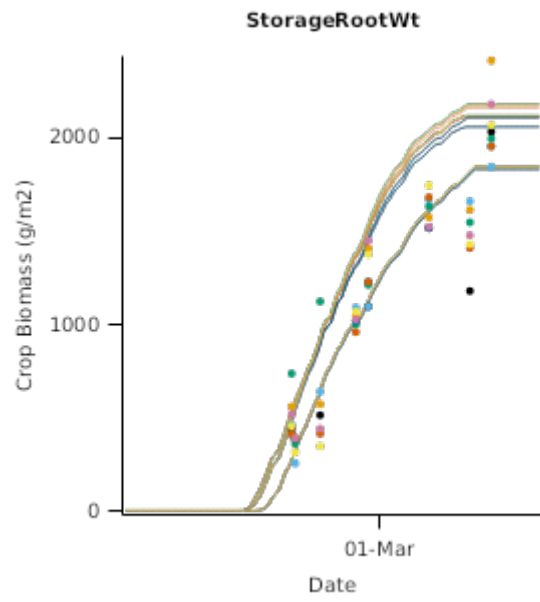
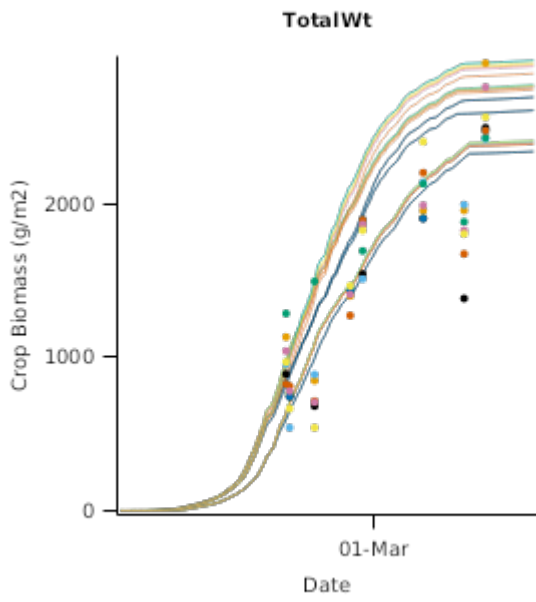


2.2.3.3 Northisland

List of experiments.

Experiment Name	Design (Number of Treatments)
Taranaki	Nit x Splits (8)
Waikato	Nit x Splits (8)
Whanganui	Nit x Splits (8)

2.2.3.3.1 Graphs

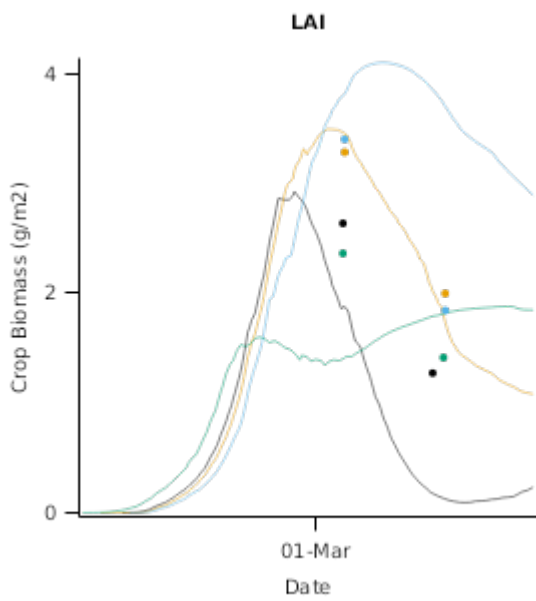
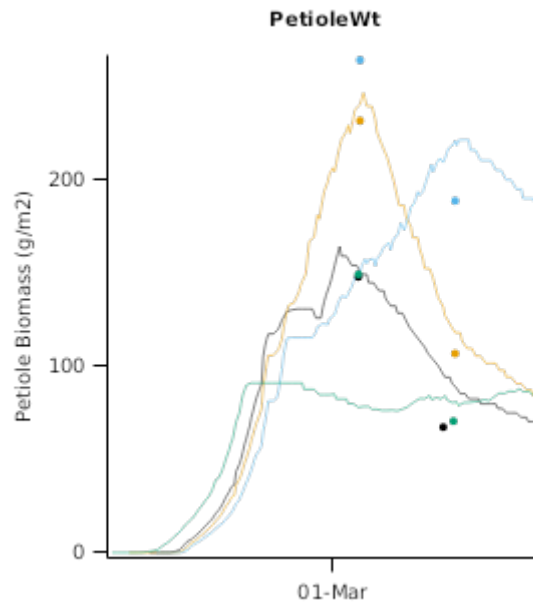
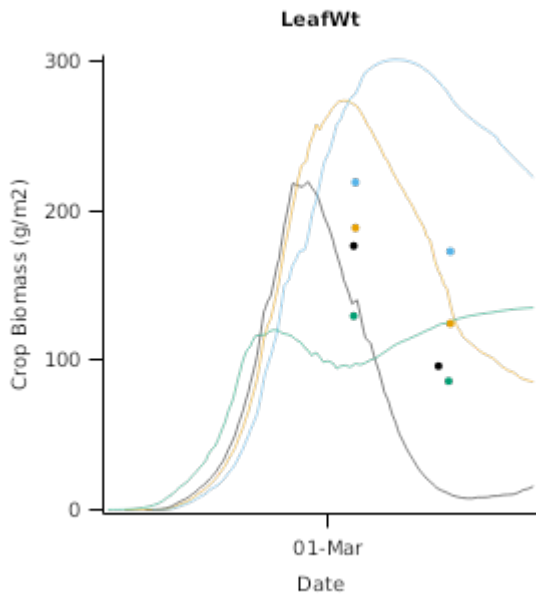
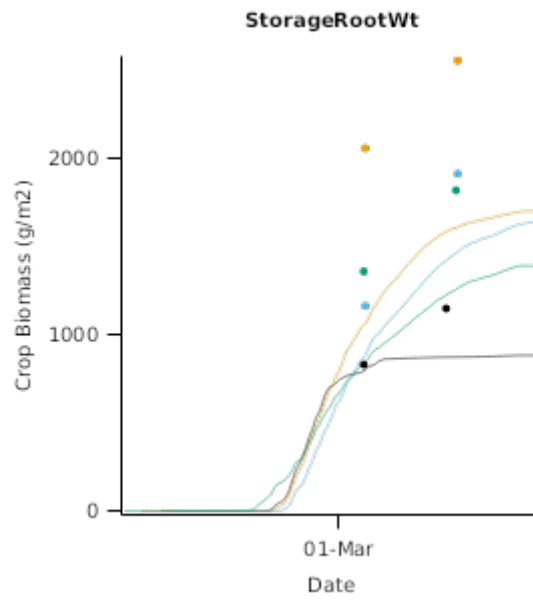
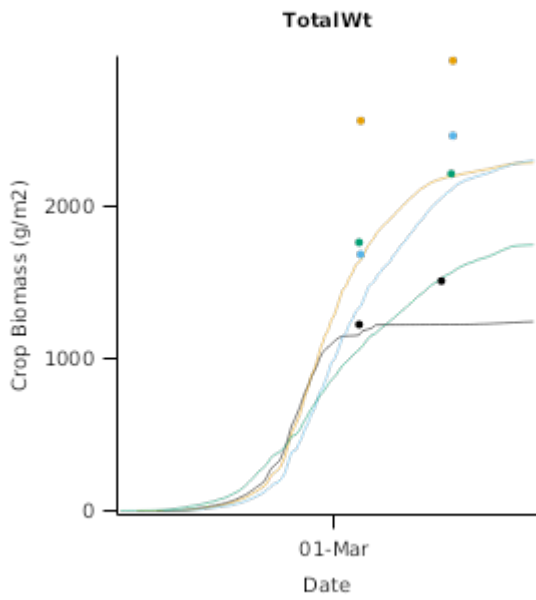


2.2.4 P21EXT

This was an extension of the P21 project

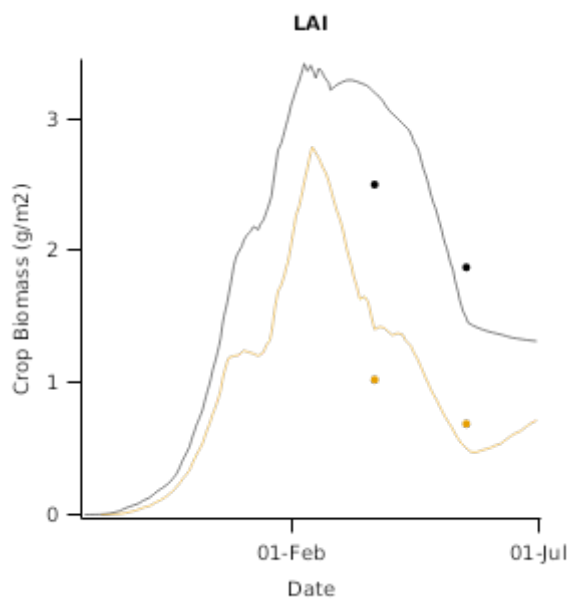
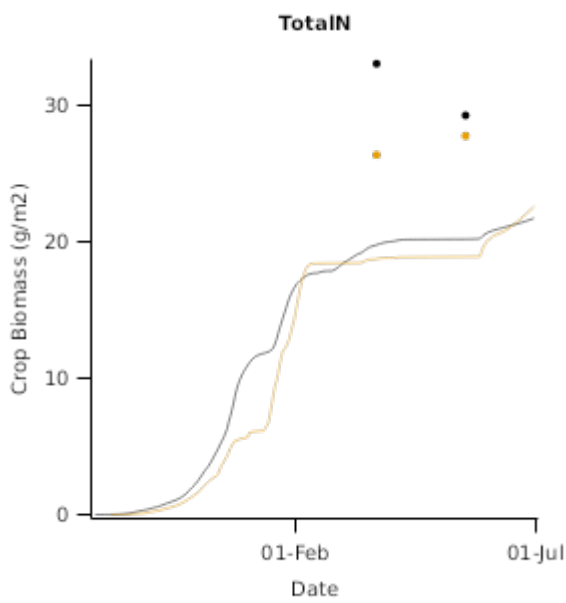
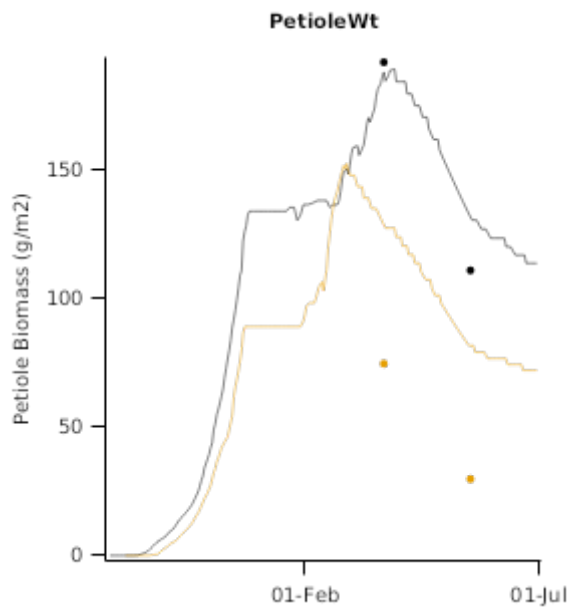
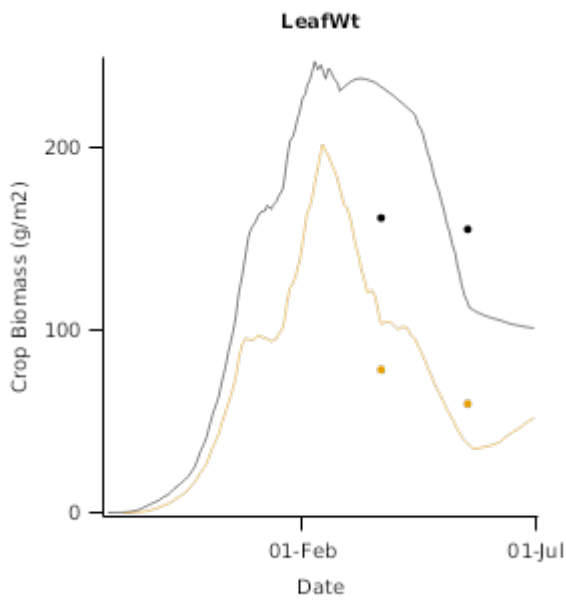
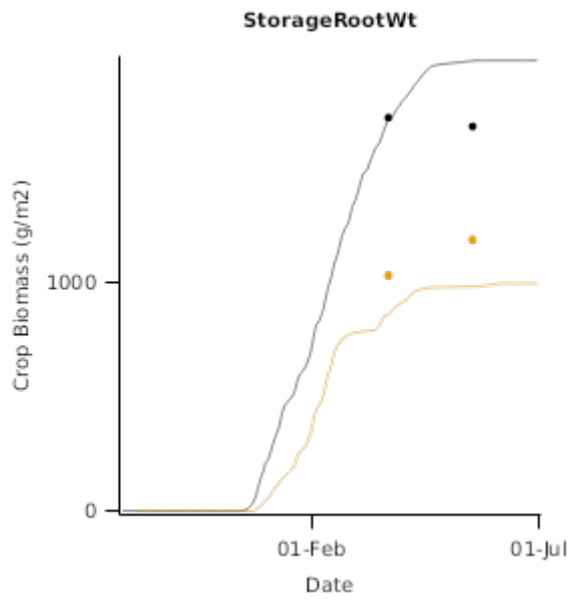
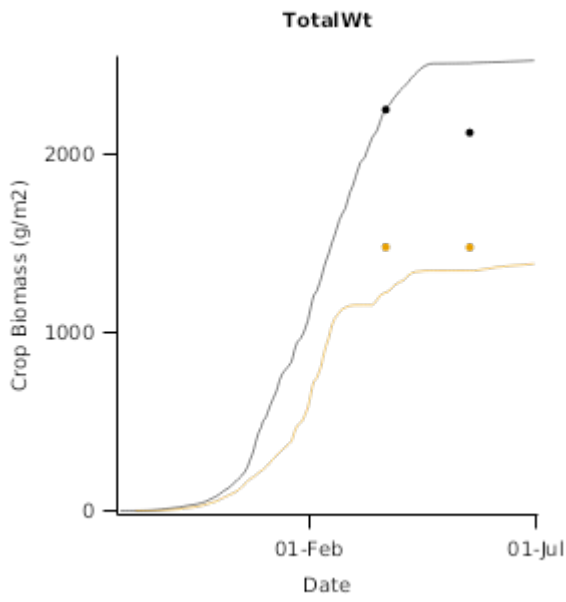
2.2.4.1 Canterbury

2.2.4.1.1 Graphs



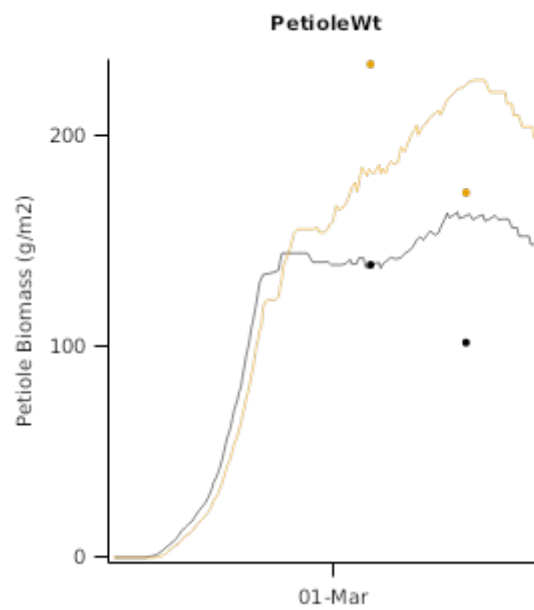
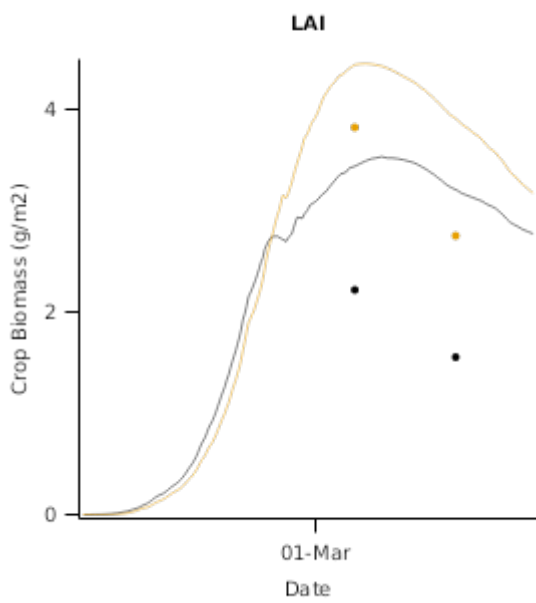
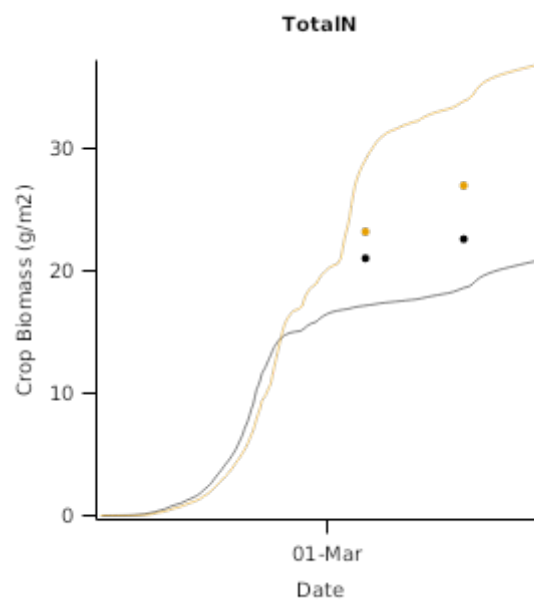
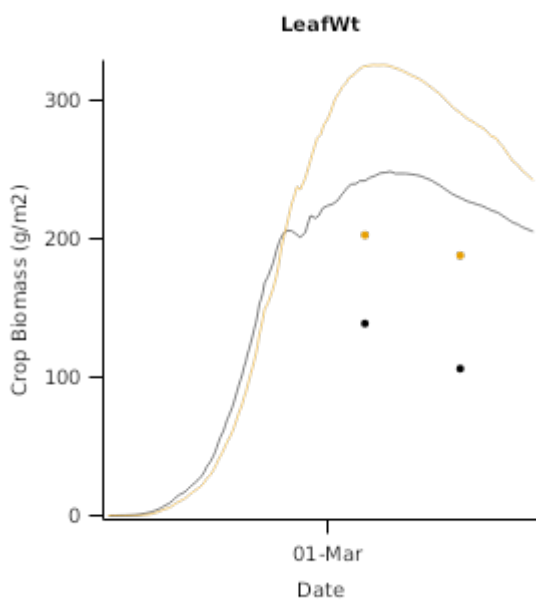
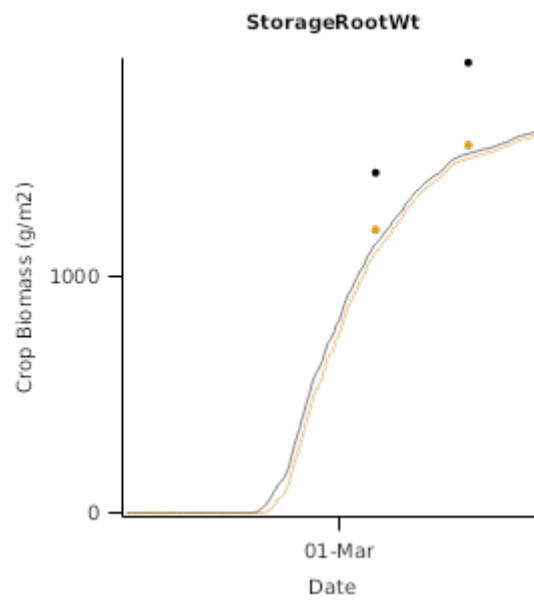
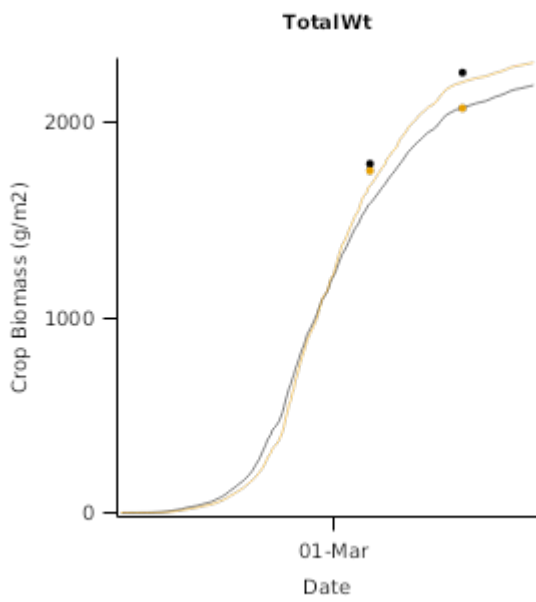
2.2.4.2 NorthOtago

2.2.4.2.1 Graphs



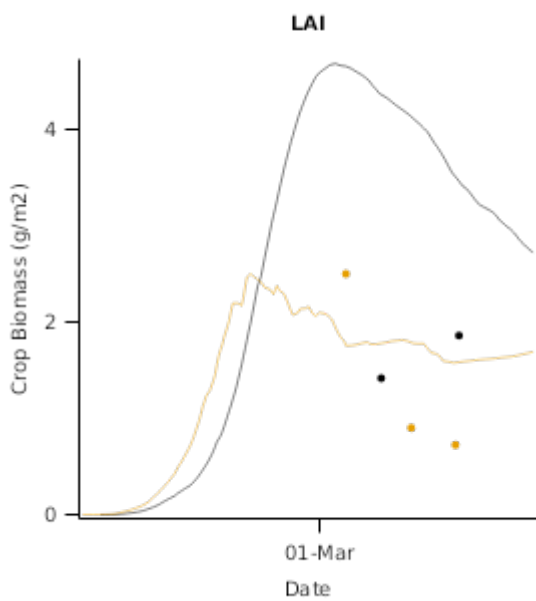
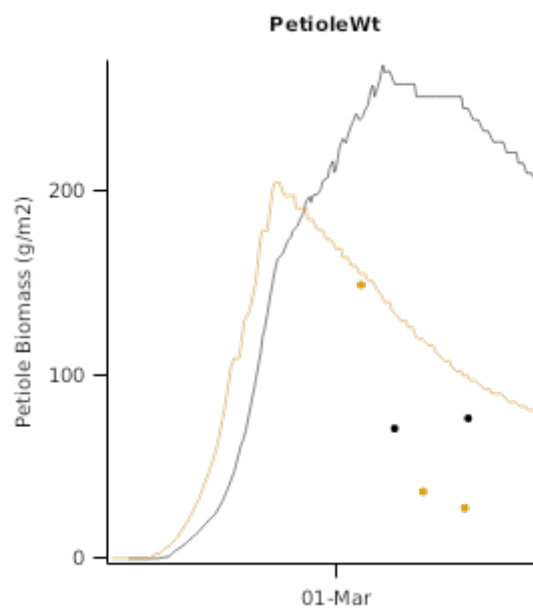
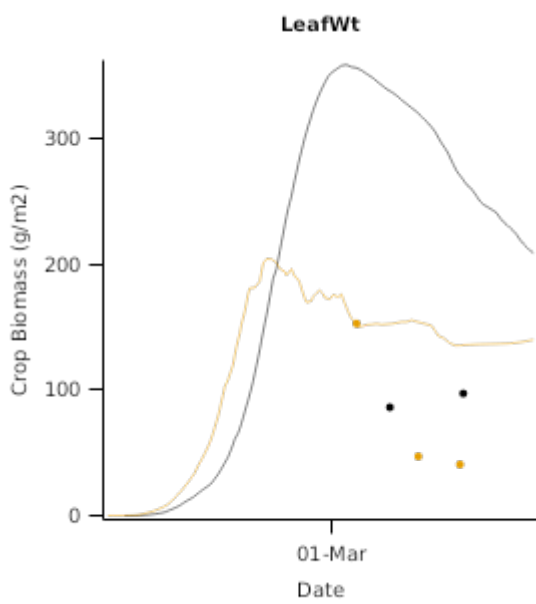
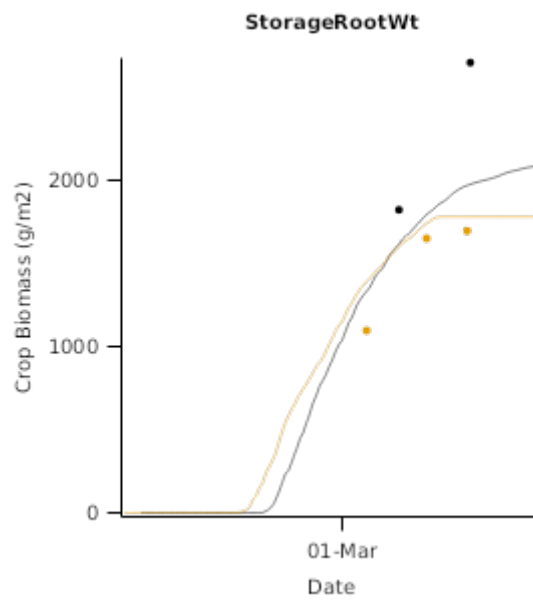
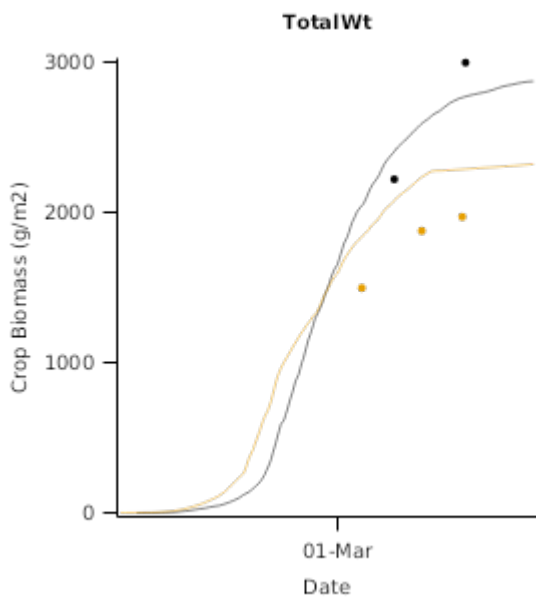
2.2.4.3 Southland

2.2.4.3.1 Graphs



2.2.4.4 NorthIsland

2.2.4.4.1 Graphs



2.2.5 FRNL_NCRS

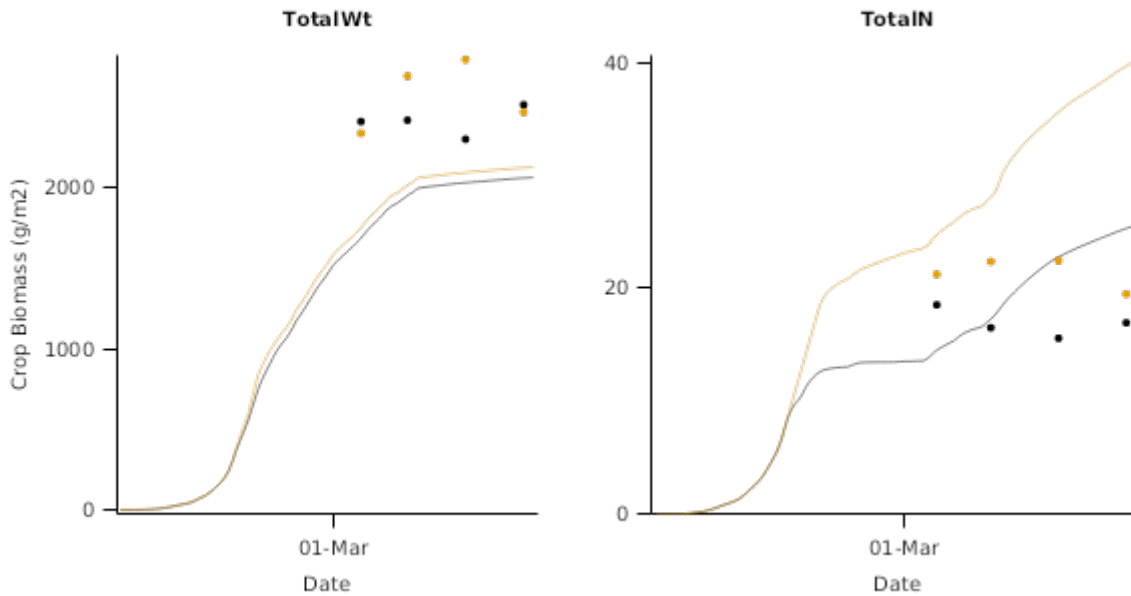
The data used here is from the FRNL trials managed by de Ruiter et al.

List of experiments.

Experiment Name	Design (Number of Treatments)
FRNL_NCRS2014	Nit (2)
FRNL_NCRS2015	SD (4)

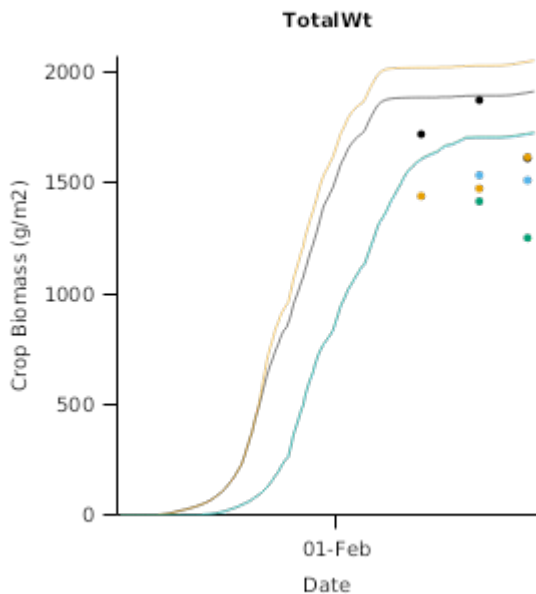
2.2.5.1 FRNL_NCRS2014

2.2.5.1.1 Graphs



2.2.5.2 FRNL_NCRS2015

2.2.5.2.1 Graphs



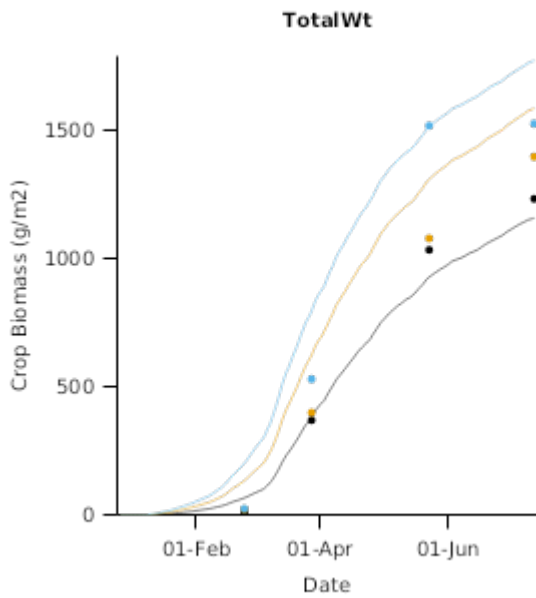
2.3 Australia

Fodder beet population experiment based on Pembleton & Rawnsley (2011) report. Three sowing (precision) rates (4, 8, 12 plants/m²) were evaluated.

List of experiments.

Experiment Name	Design (Number of Treatments)
Irishtown	Pop (3)

2.3.1 BiomassGraphs



2.4 NewZealand_Sensitivity

2.4.1 LincolnSens

List of experiments.

Experiment Name	Design (Number of Treatments)
Lincoln2016Temp	Temperature (5)
Lincoln2016Extinc	KCoefficient (8)

2.4.1.1 Lincoln2016Temp

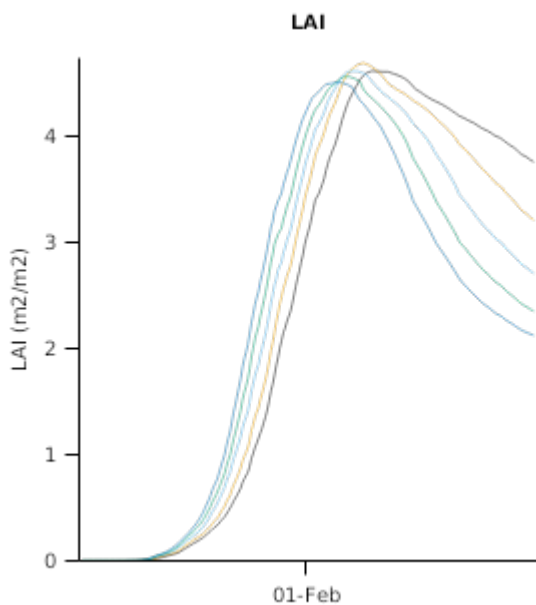
This trial was conducted in the rainshelter at Plant and Food Research in Lincoln, New Zealand in 2016. The objective was to evaluate the effect of nitrogen and irrigation on the development and growth of fodder beet crops.

Details:

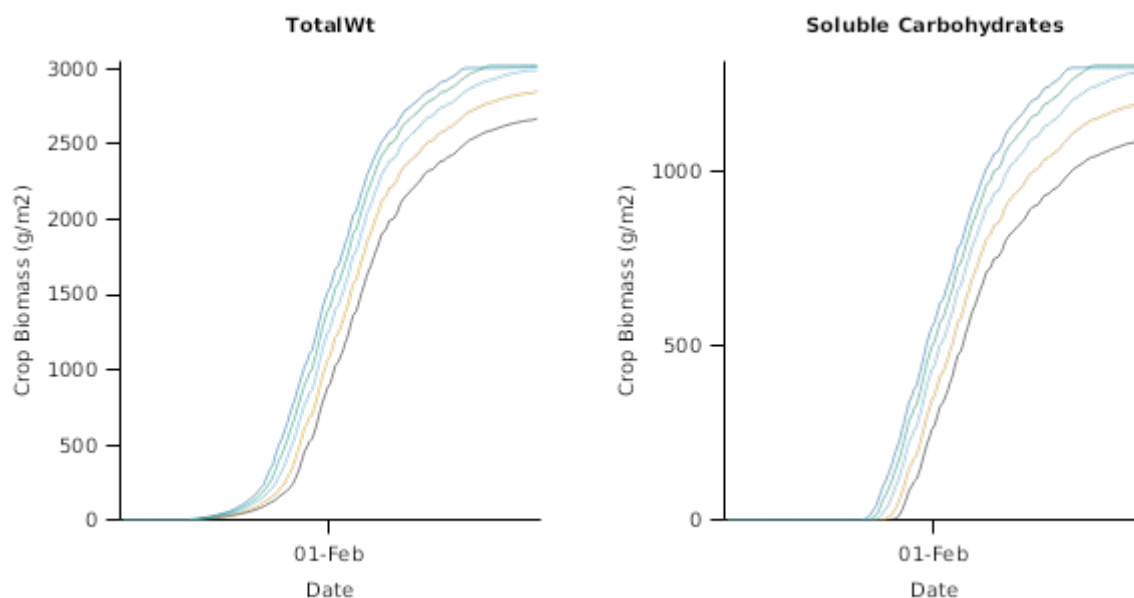
- Three nitrogen treatments: 0 kg N/ha, 50 kg N/ha & 300 kg N/ha applied as dissolved urea with fertigation
- Two irrigation treatments: Nil and full irrigation

Fodder beet (cultiva "Rivage") was precision drilled on 18 October 2016. Sowing density was 11 plants/m² and row spacing was 0.45m.

2.4.1.1.1 LeafGraphs



2.4.1.1.2 BiomassGraphs



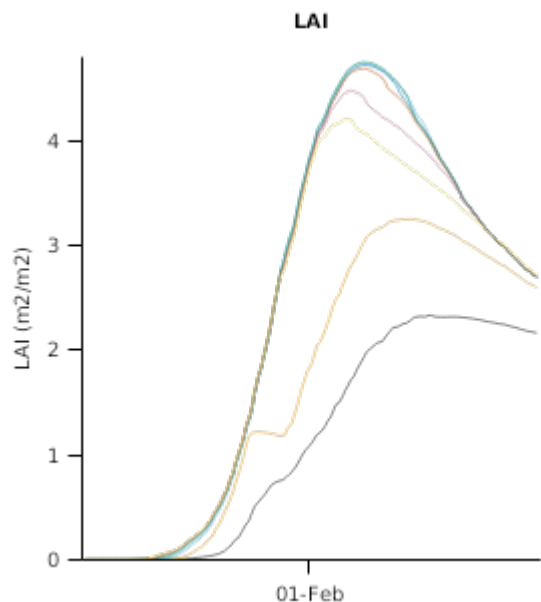
2.4.1.2 Lincoln2016Extinc

This trial was conducted in the rainshelter at Plant and Food Research in Lincoln, New Zealand in 2016. The objective was to evaluate the effect of nitrogen and irrigation on the development and growth of fodder beet crops. Details:

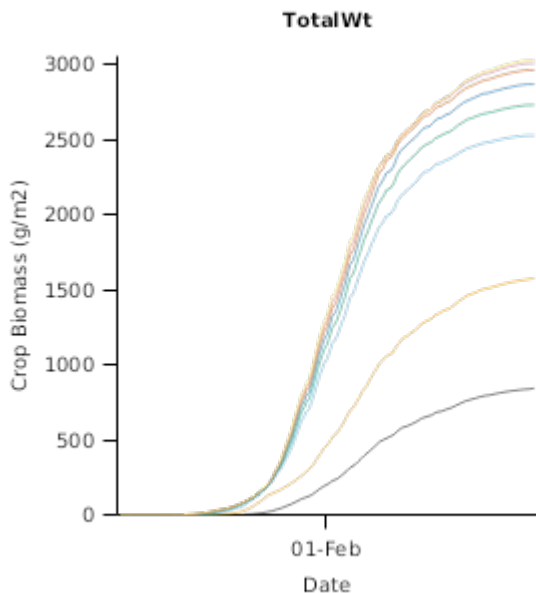
- Three nitrogen treatments: 0 kg N/ha, 50 kg N/ha & 300 kg N/ha applied as dissolved urea with fertigation
- Two irrigation treatments: Nil and full irrigation

Fodder beet (cultiva "Rivage") was precision drilled on 18 October 2016. Sowing density was 11 plants/m² and row spacing was 0.45m.

2.4.1.2.1 LeafGraphs



2.4.1.2.2 BiomassGraphs



3 References

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