



## 1 The APSIM Oats Model

*Allan Peake, Hamish Brown, Rob Zyskowski, Edmar I. Teixeira, Neil Huth*

The APSIM oats 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 oats model consists of:

- \* a phenology model to simulate development through sequential 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 the various plant organs

This work builds upon an earlier APSIM Oats model that was constructed in 2007 and then published at the Australian Agronomy Conference in 2008 using data from Gatton, Tarlee and Pinery ([Peake et al., 2008](#)). However numerous changes have been made in the APSIM NextGen version, so simulations run under APSIM 7.10 and previous versions will give different predictions when run with APSIM NextGen.

The Oats model is broadly based on APSIM Wheat models such as NWheat ([S Asseng et al., 2002](#), [BA Keating, 2001](#)), NWheatS ([S Asseng et al., 1998](#)), Cropmod-Wheat ([Wang et al., 2002](#)), and the earlier versions developed within the Plant Modelling Framework ([Brown et al., 2014](#)).

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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
Grain	Models.PMF.Organs.ReproductiveOrgan
Leaf	Models.PMF.Organs.Leaf
Stem	Models.PMF.Organs.GenericOrgan
Root	Models.PMF.Organs.Root
Panicle	Models.PMF.Organs.GenericOrgan
MortalityRate	Models.Functions.Constant

### 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.

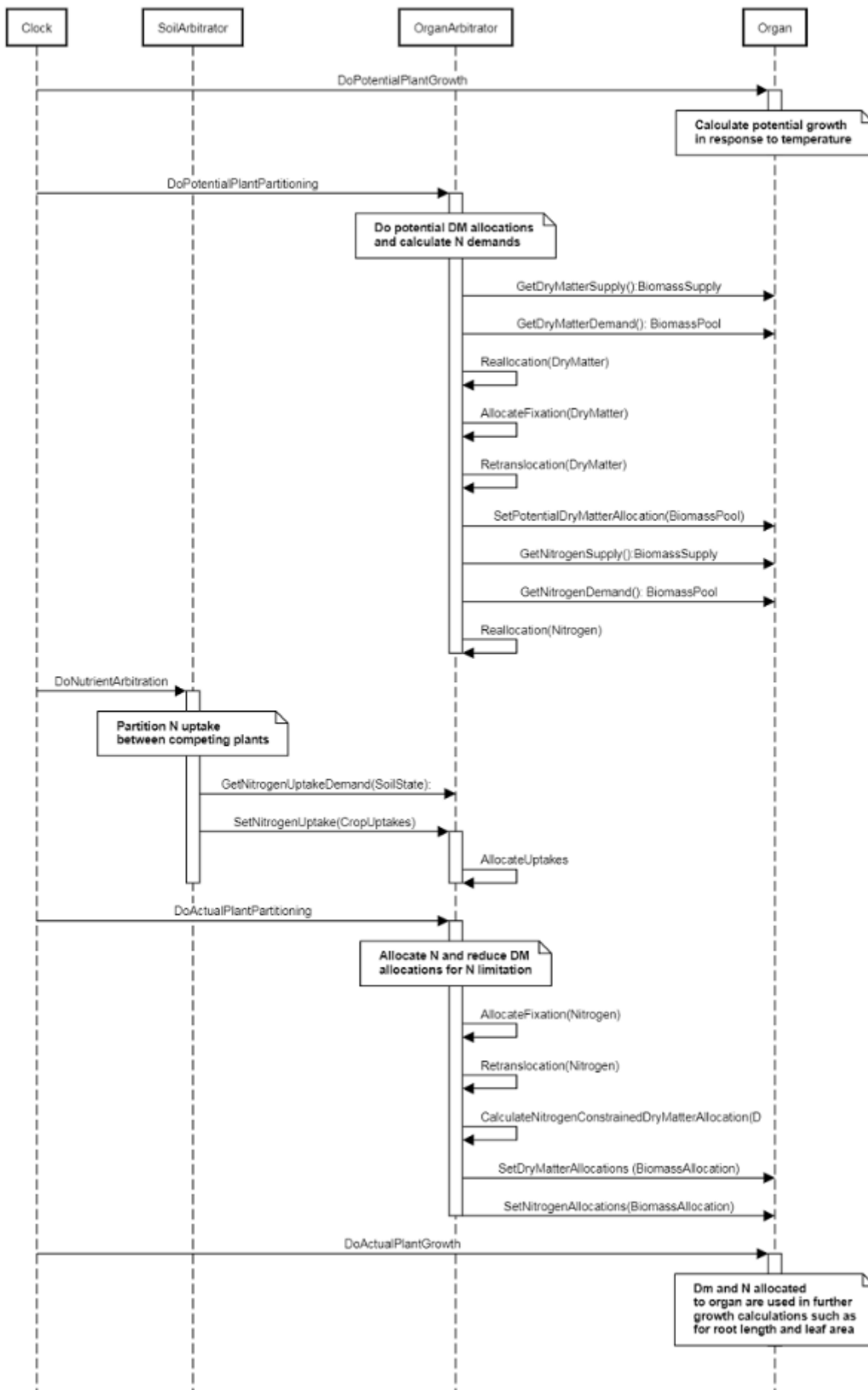
1. **doPotentialPlantGrowth**. When this event occurs, each organ class executes code to determine their potential growth, biomass supplies and demands. In addition to demands for structural, non-structural and metabolic biomass (DM and N) each organ may have the following biomass supplies:

- \* **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.

Oat crops exhibit a range of developmental responses to environment and these are strongly influenced by genotype characteristics. Temperature effects development increasing development rates and decreasing phase durations as temperatures increase. These effects are captured by thermal time. However, Oat crops also exhibit vernalisation and photoperiod sensitivities in their Vegetative phase and further photoperiod sensitivity in the EarlyReproductive phase. Photoperiod responses are seen as a reduction in the length of a phase for a photoperiod sensitive genotype in response to a longer photoperiod. Vernalisation responses are more complicated as they are driven by temperature but interact with photoperiod. For vernalisation sensitive varieties (Winter types) exposure to cool temperatures or short photoperiods during the Vegetative phase will reduce the thermal time duration of the vegetative phase.

As used in the APSIM wheat model, we draw on the Kirby Framework to capture these vernalisation and photoperiod responses. This framework assumes that the timing of anthesis is a result of the timing of flag leaf and an additional thermal time passage from there to anthesis. It also assumes the timing of flag leaf is a result of the Final Leaf Number which sets a target, and leaf appearance rate, which sets the rate of progress toward this target. Leaf appearance rate is a function of Thermal time and a genotype specific Phyllochron which changes with Haun stage as described by [Jamieson et al., 1995](#).

Final Leaf Number (FLN) is modelled as the sum of three numbers:

$$\text{FLN} = \text{MinLeafNumber} + \text{VernalLeaves} + \text{PhotoLeaves}$$

Where MinLeafNumber is the number of leaves that a wheat crop will produce when vernalisation is satisfied early in the crop's duration (before 2nd true leaf) and it is grown in a long photoperiod. VernalLeaves are the number of leaves that are added due to vernalisation effects. For insensitive varieties this will always be zero but this is potentially a larger number for sensitive varieties and the number progressively decreases as the crop encounters more vernalisation. PhotoLeaves are the number of leaves that are added to the minimum leaf number as a result of short day exposure. For insensitive varieties this will be zero but is potentially larger for more sensitive varieties and decreases as day length increases. More detailed explanations of the components of phenology are provided below.

### 1.2.1 ThermalTime

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

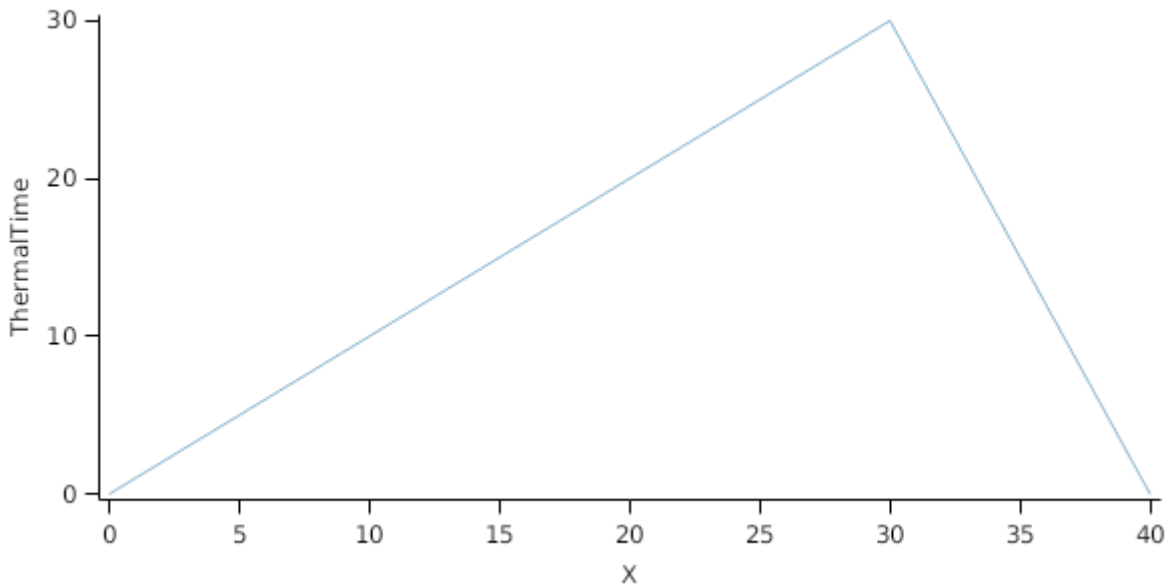
Thermal time determines the rate of developmental progress through many of the crop's phases and is used by organs to determine potential growth rates.

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
30.0	30.0
40.0	0.0

## ThermalTime



### 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	Vegetative	Emergence	TerminalSpikelet
4	StemElongation	TerminalSpikelet	FlagLeaf
5	EarlyReproductive	FlagLeaf	Flowering
6	GrainDevelopment	Flowering	StartGrainFill
7	GrainFilling	StartGrainFill	EndGrainFill
8	Maturing	EndGrainFill	Maturity
9	Ripening	Maturity	HarvestRipe
10	ReadyForHarvesting	HarvestRipe	Unused

#### 1.2.2 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.

#### 1.2.3 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:

$$\text{Target} = \text{SowingDepth} \times \text{ShootRate} + \text{ShootLag}$$

Where:

$$\text{ShootRate} = 4 \text{ (deg day/mm)},$$

$$\text{ShootLag} = 40 \text{ (deg day)},$$

*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:

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

## 1.2.4 Vegetative

This phase goes from emergence to terminalspikelet.

The duration of the vegetative phase is set by a target Haun Stage for the occurrence of Terminal Spikelet and the rate of leaf appearance.

HaunStageTerminalSpiklet decreases as vernalisation is accumulated and as photoperiod extends, capturing the effect of these responses on the duration of the Vegetative phase

The *Target* for completion is calculated as:

$$Target = [Structure].MeanPhyllochron \times [Structure].HaunStageTerminalSpikelet$$

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

$$Progression = [Phenology].ThermalTime$$

## 1.2.5 StemElongation

This phase goes from terminalspikelet to flagleaf and it continues until the final main-stem leaf has finished expansion. The duration of this phase is determined by leaf appearance rate (Structure.Phylochron) and the number of leaves produced on the mainstem (Structure.FinalLeafNumber)

The Final leaf number is fixed at Terminal Spikelet and leaves continue to appear at a rate set by thermal time and phyllochron until flag leaf ligule appears and this phase is completed.

$$ThermalTime = [Phenology].ThermalTime$$

$$FinalLeafNumber = [Structure].FinalLeafNumber$$

$$LeafNumber = [Leaf].ExpandedCohortNo + [Leaf].NextExpandingLeafProportion$$

$$FullyExpandedLeafNo = [Leaf].ExpandedCohortNo$$

$$InitialisedLeafNumber = [Leaf].InitialisedCohortNo$$

## 1.2.6 EarlyReproductive

This phase goes from flagleaf to flowering.

The *Target* for completion is calculated as:

$$Target = [Structure].Phyllochron.BasePhyllochron \times Phyllochrons$$

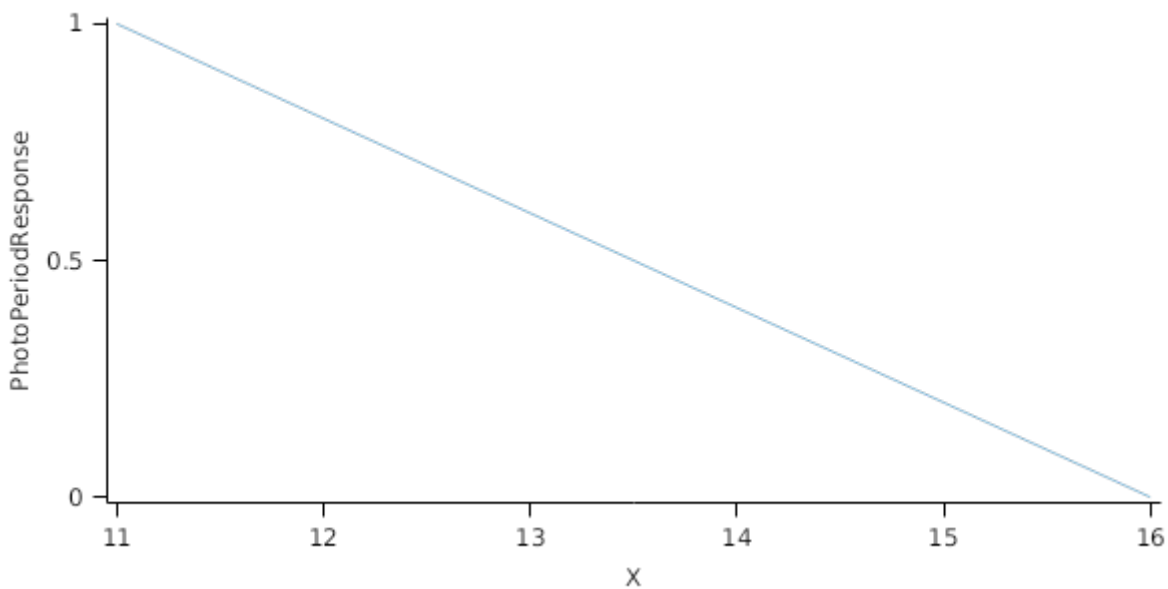
$$Phyllochrons = [Phenology].EarlyReproductiveLongDayBase + IncreaseDueToShortPhotoPeriod$$

$$IncreaseDueToShortPhotoPeriod = PhotoPeriodResponse \times [Phenology].EarlyReproductivePpSensitivity$$

*PhotoPeriodResponse* is calculated using linear interpolation

X	PhotoPeriodResponse
11.0	1.0
16.0	0.0

## PhotoPeriodResponse



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

*Progression* = [Phenology].ThermalTime

### 1.2.7 GrainDevelopment

This phase goes from flowering to startgrainfill.

The *Target* for completion is calculated as:

Target = 20 (oD)

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

*Progression* = [Phenology].ThermalTime

### 1.2.8 GrainFilling

This phase goes from startgrainfill to endgrainfill.

The *Target* for completion is calculated as:

Target = 650 (oD)

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

*Progression* = [Phenology].ThermalTime

### 1.2.9 Maturing

This phase goes from endgrainfill to maturity.

The *Target* for completion is calculated as:

Target = 30 (oD)

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

*Progression* = [Phenology].ThermalTime

### 1.2.10 Ripening

This phase goes from maturity to harvestripe.

The *Target* for completion is calculated as:

Target = 100 (oD)

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

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

### 1.2.11 ReadyForHarvesting

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

### 1.2.12 Constants

Number of leaves the plant will produce when fully vernalised early and grown in long photoperiod

$$\text{MinimumLeafNumber} = 7 \text{ (Leaves)}$$

The difference between Inherent earlyness leaf number and the number of leaves produced when the plant is unvernalsed and grown in long photoperiod

$$\text{VrnSensitivity} = 0 \text{ (Leaves)}$$

The amount of vernalising temperature required before vernalisation response will be evident. Value of relative to the amount offl vernalisation temperature required from the end of the lag until vernalisation saturation. A value of 0 means there is no lag, a value of 1 means the lag is the same (in vernal time) as the vernalisation requirement and a value of 2 means the lag is twice as long as the vernalisation response phase

$$\text{VernLag} = 1 \text{ (Unitless)}$$

The reduction in leaf number going from 8 to 16 h Pp

$$\text{PpSensitivity} = 3 \text{ (Leaves)}$$

The phyllochrons duration for the plant to go from flag leaf ligual appearance at 16 h Pp compared to the phyllochron duration for the same phase at 8 h Pp.

$$\text{EarlyReproductivePpSensitivity} = 3$$

The phyllochrons duration for the plant to go from flag leaf ligual appearance at 16 h Pp.

$$\text{EarlyReproductiveLongDayBase} = 3$$

### 1.2.13 MeanTemp

$$\text{MeanTemp} = \text{TempSum} / 2$$

$$\text{TempSum} = [\text{Weather}].\text{MaxT} + [\text{Weather}].\text{MinT}$$

### 1.2.14 DailyVernalisation

Vernalisation responses are based on those described by [Brown et al., 2013](#). Vernalisation is assumed to be related to the expression of the Vrn1 Gene. Its experssion is accumulated daily and daily upregulation as a function of development (DeltaHaunStage) and a TempResponseProfile that declines exponentially from a maximum at 1°C to zero at 0°C and at 20°C.

$$\text{DailyVernalisation} = [\text{Structure}].\text{DeltaHaunStage} \times \text{TempResponseProfile}$$

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

Firstly 3-hourly estimates of air temperature (Ta) are interpolated using the method of [Jones et al., 1986](#) which assumes a sinusoidal temperature. pattern between Tmax and Tmin.

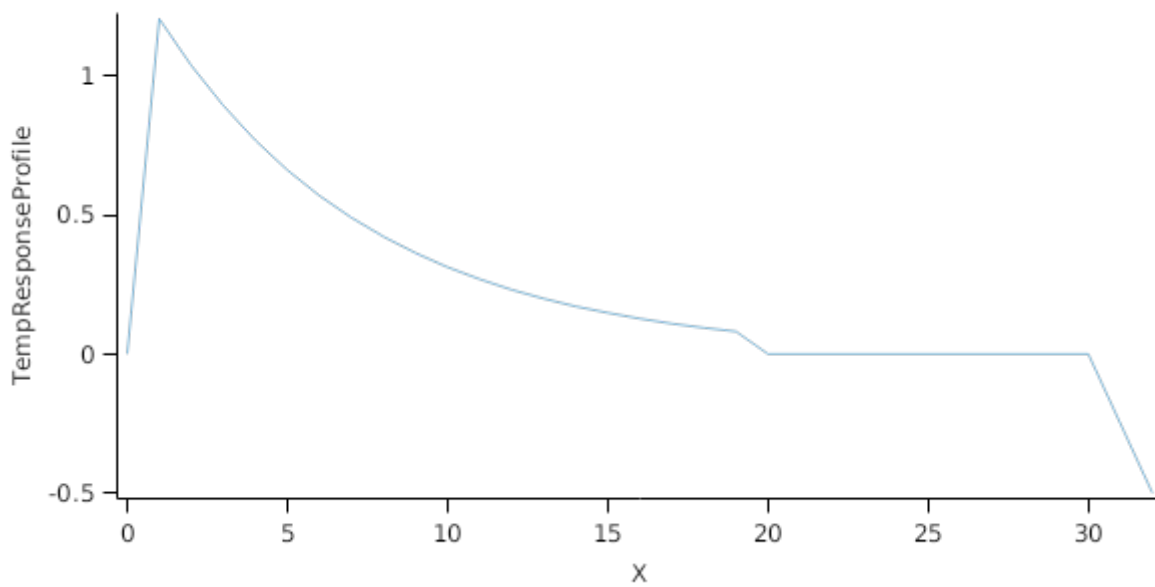
Each of the interpolated air temperatures are then passed into the following Response and the Average taken to give daily TempResponseProfile

X	TempResponseProfile
0.0	0.0
1.0	1.2
2.0	1.0



X	TempResponseProfile
3.0	0.9
4.0	0.8
5.0	0.7
6.0	0.6
7.0	0.5
8.0	0.4
9.0	0.4
10.0	0.3
11.0	0.3
12.0	0.2
13.0	0.2
14.0	0.2
15.0	0.1
16.0	0.1
17.0	0.1
18.0	0.1
19.0	0.1
20.0	0.0
30.0	0.0
32.0	-0.5

**TempResponseProfile**



### 1.2.15 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)*

### 1.2.16 PerceivedPhotoPeriod

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

ApexBelowGround has a value between Germination and Emergence calculated as:

Photoperiod = 0 (h)

ApexAboveGround has a value between Emergence and HarvestRipe calculated as:

*Photoperiod = [Phenology].Photoperiod*

### 1.2.17 Vrn1

Vrn1 accumulation begins when Vrn4 expression is down-regulated to zero and stops, assuming vernalisation saturation, at a value of 1

*Vrn1 = Min(Saturation, CurrentExpression)*

Where:

Saturation = 1 (Relative Expression)

*CurrentExpression = Accumulated Vernalisation* between germination and terminalspikelet

IF [Phenology].Vrn4 < [Phenology].VernLag THEN

Return\_Zero = 0

ELSE

*elseReturn\_Vernalisation = [Phenology].DailyVernalisation*

### 1.2.18 Vrn4

*Vrn4 = Min(MaxExpression, CurrentExpression)*

Where:

*MaxExpression = [Phenology].VernLag*

*CurrentExpression = Accumulated VernalisationConditioning* between germination and terminalspikelet

*VernalisationConditioning = [Phenology].DailyVernalisation*

### 1.2.19 Zadok

#### 1.2.19.1 Zadok

This model calculates a Zadok growth stage value based upon the current phenological growth stage within the model. The model uses information regarding germination, emergence, leaf appearance and tiller appearance for early growth stages (Zadok stages 0 to 30). The model then uses simulated phenological growth stages for Zadok stages 30 to 100.

Growth Phase	Description
Germinating	ZadokStage = 5 x FractionThroughPhase
Emerging	ZadokStage = 5 + 5 x FractionThroughPhase
Vegetative	ZadokStage = 10 + Structure.LeafTipsAppeared
Reproductive	ZadokStage is interpolated from values of

Growth Phase	Description
	stage number using the following table.
Growth Stage	ZadokStage
3.9	30
4.9	33
5.0	39
6.0	65
7.0	71
8.0	87
9.0	90

### 1.2.20 FlagLeafDAS

Before FlagLeaf

PreEventValue = 0

On FlagLeaf the value is set to:

*PostEventValue = [Plant].DaysAfterSowing*

### 1.2.21 FloweringDAS

Before Flowering

PreEventValue = 0

On Flowering the value is set to:

*PostEventValue = [Plant].DaysAfterSowing*

### 1.2.22 MaturityDAS

Before Maturity

PreEventValue = 0

On Maturity the value is set to:

*PostEventValue = [Plant].DaysAfterSowing*

## 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 Oats is calculated as:

*MainStemPopn = Plant.Population x 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:

*LeafTipsAppeared += DeltaTips*

Where *DeltaTips* is calculated as:

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

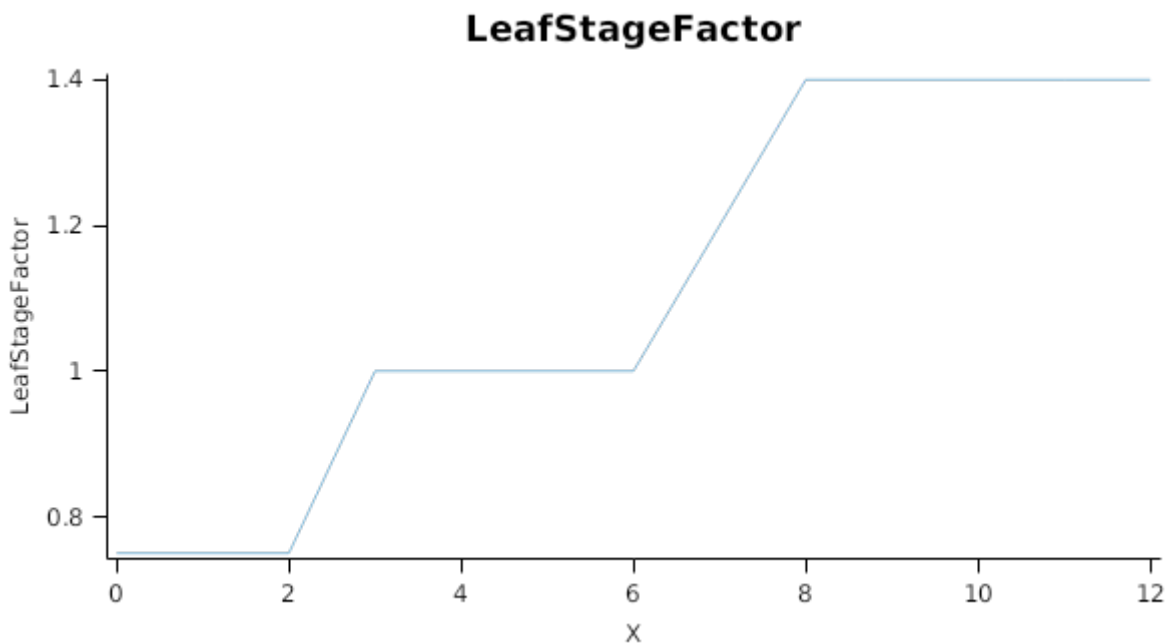
Where *Phyllochron* is the thermal time duration between the appearance of leaf tips given by:

This is the thermal time between the emergence of leaf tips. The model used here is based on [Jamieson et al., 1998](#) where leaf appearance could be described by a base phyllochron determined between leaves 2 and 7 and a phyllochron that was 70% of base phyllochron for leaves < 2 and 130% of base phyllochron for leaves > 7

$$\text{Phyllochron} = \text{LeafStageFactor} \times \text{BasePhyllochron} \times \text{PhotoPeriodEffect}$$

*LeafStageFactor* is calculated using linear interpolation

X	LeafStageFactor
0.0	0.8
2.0	0.8
3.0	1.0
6.0	1.0
8.0	1.4
11.0	1.4
12.0	1.4

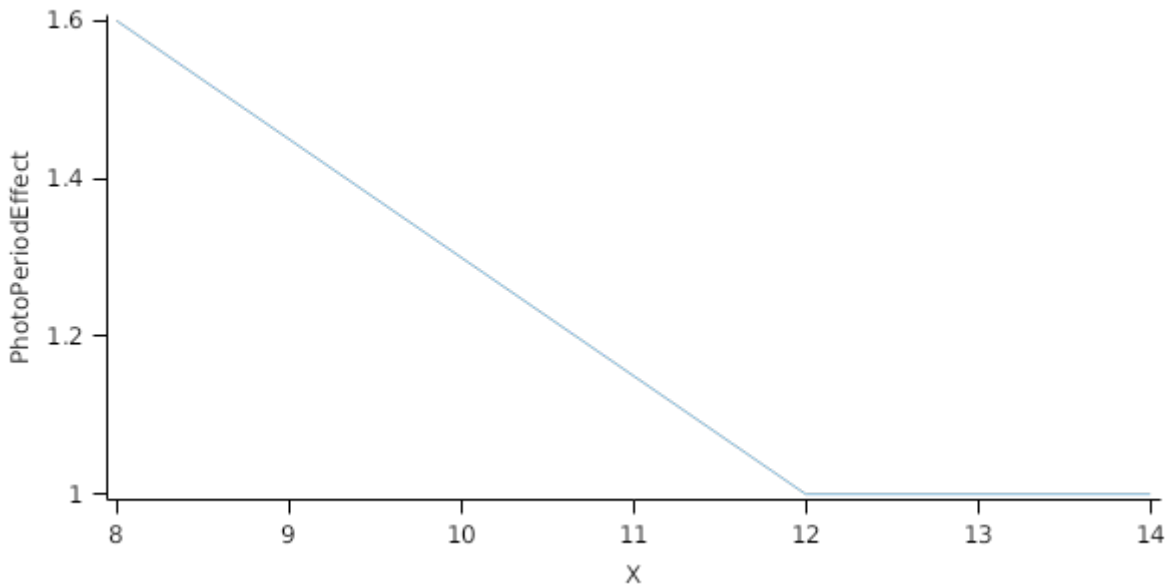


BasePhyllochron = 90 (oC.d)

*PhotoPeriodEffect* is calculated using linear interpolation

X	PhotoPeriodEffect
8.0	1.6
12.0	1.0
14.0	1.0

## PhotoPeriodEffect



*ThermalTime* is given by

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

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

$$\text{FinalLeafNumber} = \text{FinalNodeNumber} \text{ until TerminalSpikelet after which the value is fixed.}$$

$$\text{FinalNodeNumber} = [\text{Phenology}].\text{MinimumLeafNumber} + \text{VernalLeaves} + \text{PhotoPLeaves}$$

$$\text{VernalLeaves} = [\text{Phenology}].\text{VrnSensitivity} \times \text{VernalisationReductionFactor}$$

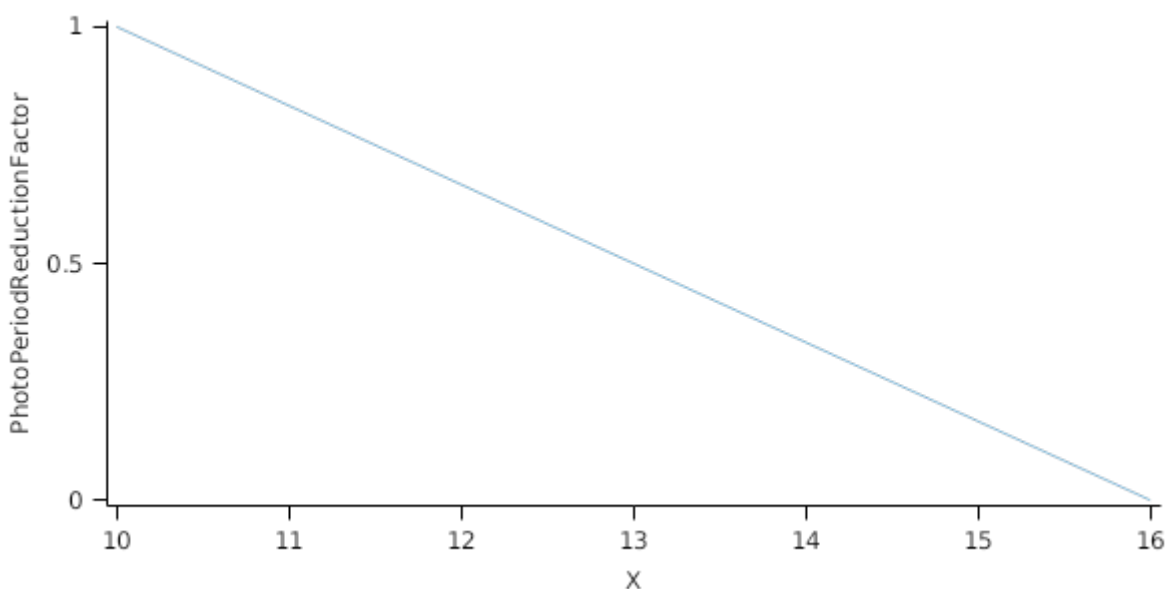
$$\text{VernalisationReductionFactor} = 1 - [\text{Phenology}].\text{Vrn1}$$

$$\text{PhotoPLeaves} = [\text{Phenology}].\text{PpSensitivity} \times \text{PhotoPeriodReductionFactor}$$

*PhotoPeriodReductionFactor* is calculated using linear interpolation

X	PhotoPeriodReductionFactor
10.0	1.0
16.0	0.0

## PhotoPeriodReductionFactor



### 1.3.3 Branching and Branch Mortality

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

$$\text{TotalStemPopn} = \text{MainStemPopn} + \text{NewBranches} - \text{NewlyDeadBranches}$$

Where:

$$\text{NewBranches} = \text{MainStemPopn} \times \text{BranchingRate}$$

*BranchingRate* is given by:

Potential branching rate is determined by the commonly observed pattern of tillering in wheat, in which each tiller emerges with the third leaf on its parent axis (e.g. first tiller emerges at the same time as the third leaf on the main stem, the first secondary tiller appears with the third leaf on tiller 1). This is described as a simple function of main stem leaf number. This function is varied occasionally between Oat cultivars due to the wide range of plant habits.

$$\text{BranchingRate} = \text{PotentialBranchingRate} \times \text{StressFactors}$$

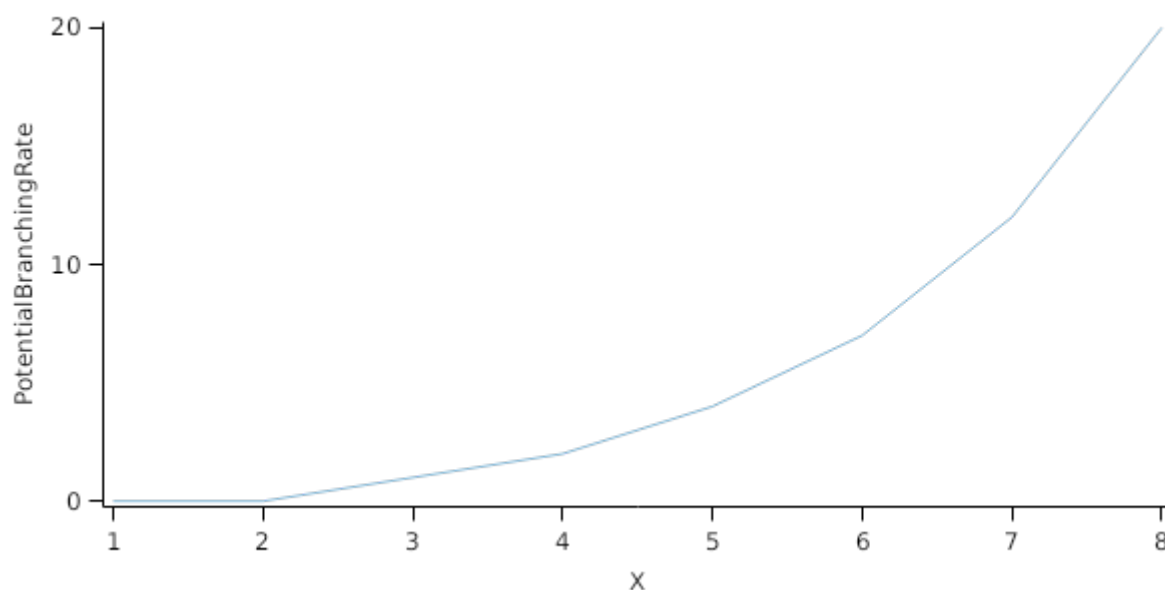
PotentialBranchingRate is calculated using specific values or functions for various growth phases. The function will use a value of zero for phases not specified below.

Vegetative has a value between Emergence and TerminalSpikelet calculated as:

*PotentialBranchingRate* is calculated using linear interpolation

X	PotentialBranchingRate
1.0	0.0
2.0	0.0
3.0	1.0
4.0	2.0
5.0	4.0
6.0	7.0
7.0	12.0
8.0	20.0

**PotentialBranchingRate**



Reproductive has a value between TerminalSpikelet and HarvestRipe calculated as:

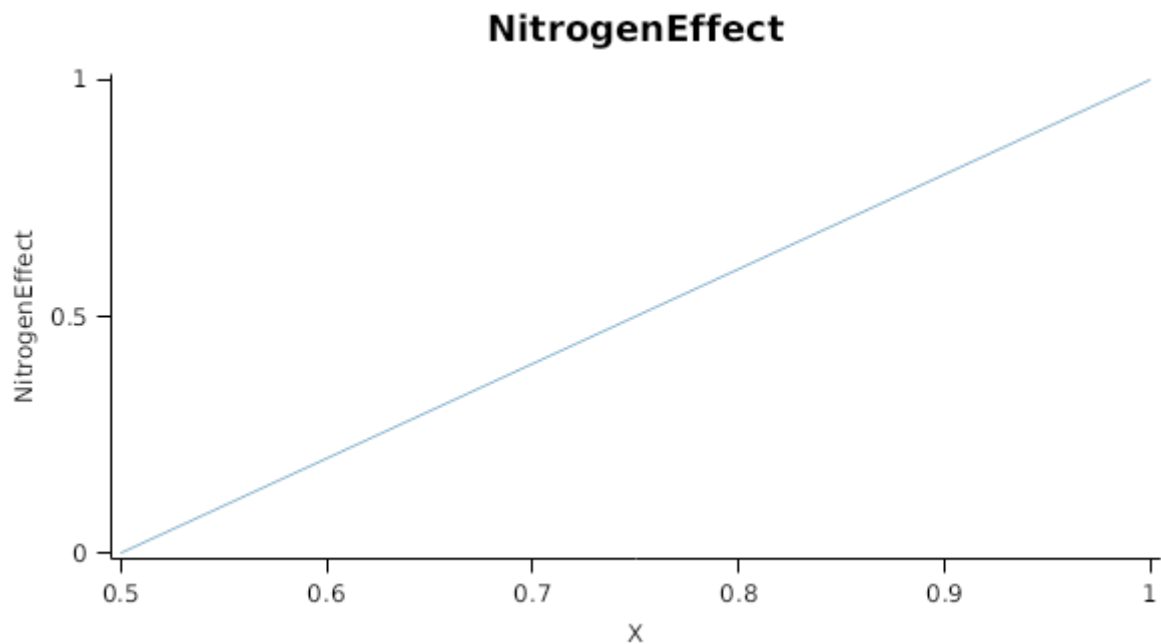
Zero = 0

$StressFactors = \text{Min}(NitrogenEffect, CoverEffect, WaterStressEffect)$

Where:

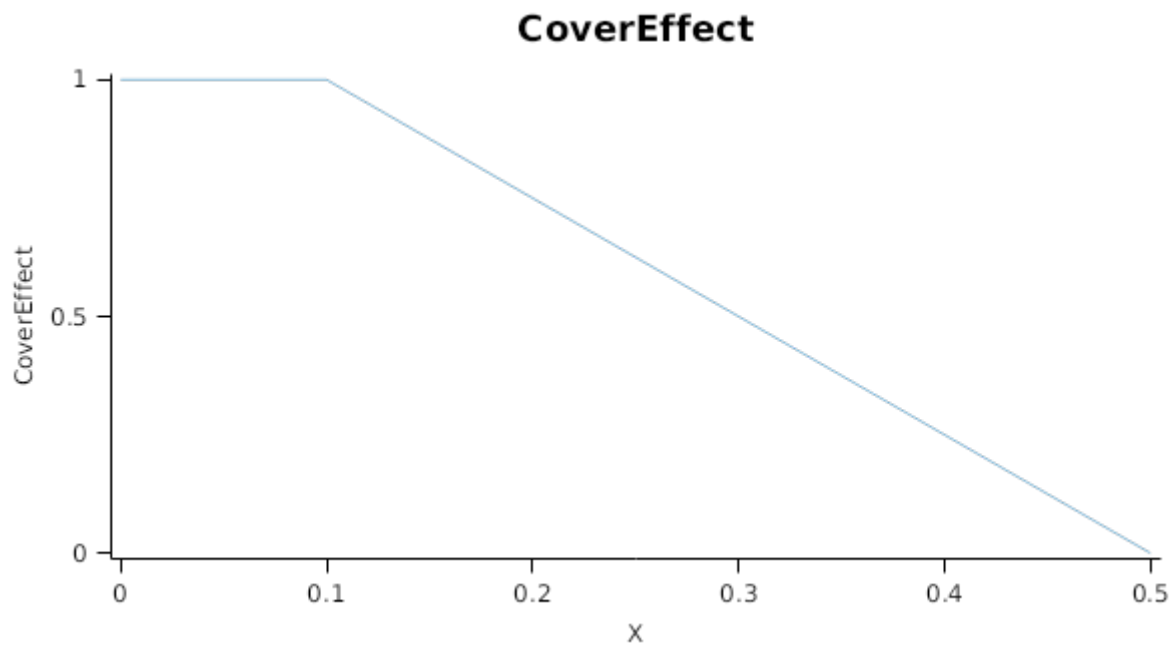
*NitrogenEffect* is calculated using linear interpolation

X	NitrogenEffect
0.5	0.0
1.0	1.0



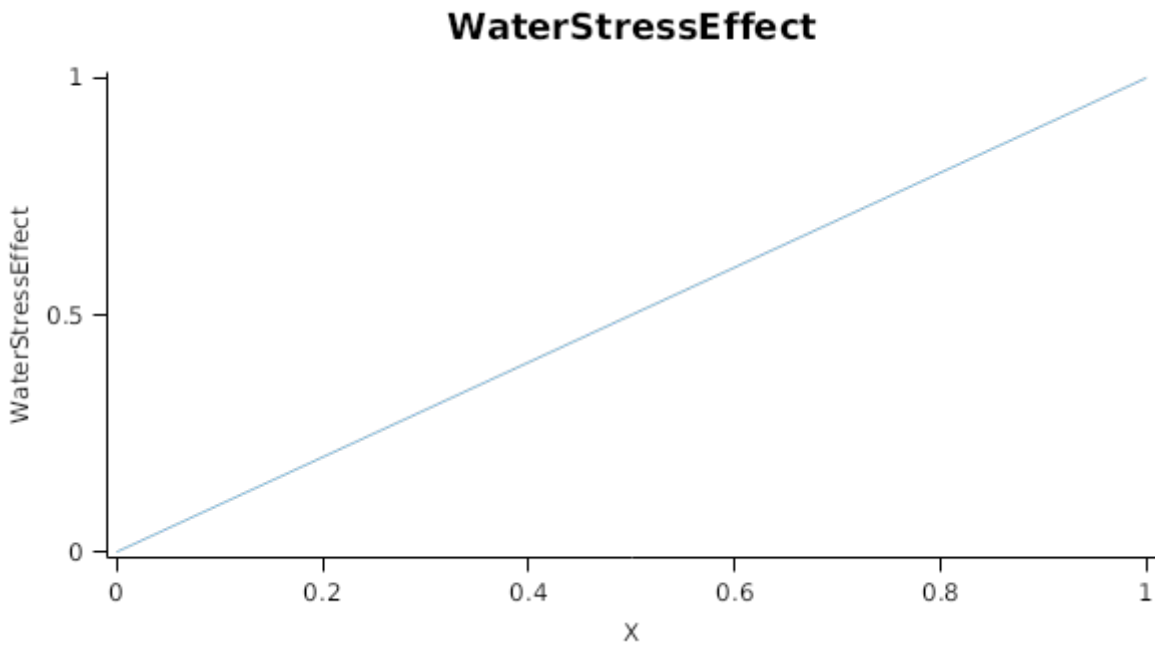
*CoverEffect* is calculated using linear interpolation

X	CoverEffect
0.0	1.0
0.1	1.0
0.5	0.0



*WaterStressEffect* is calculated using linear interpolation

X	WaterStressEffect
0.0	0.0
1.0	1.0



*NewlyDeadBranches* is calculated as:

$$\text{NewlyDeadBranches} = (\text{TotalStemPopn} - \text{MainStemPopn}) \times \text{BranchMortality}$$

where *BranchMortality* is given by:

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

*MortalityPhase* has a value between *TerminalSpikelet* and *Flowering* calculated as:

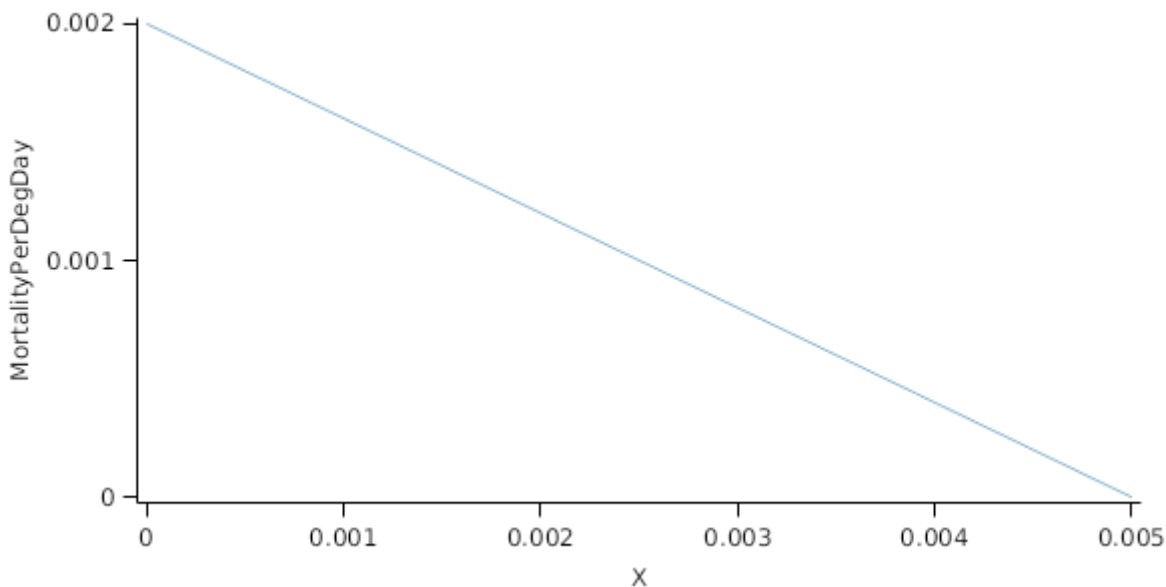
$$\text{Mortality} = \text{MortalityPerDegDay} \times [\text{Phenology}].\text{ThermalTime}$$

*MortalityPerDegDay* is calculated using linear interpolation

X	MortalityPerDegDay
0.0	0.0
0.0	0.0



## MortalityPerDegDay



### 1.3.4 Height

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

Height is used by the MicroClimate model to calculate the aerodynamic resistance used for calculation of potential transpiration. Calculates the potential height increment and then multiplies it by the smallest of any children functions (Child functions represent stress).

### 1.4 Grain

This organ uses a generic model for plant reproductive components. Yield is calculated from its components in terms of organ number and size (for example, grain number and grain size).

#### 1.4.1 Constants

InitialGrainProportion = 0.05

MaximumPotentialGrainSize = 0.032 (g)

MinimumNConc = 0.0123

MaxNConcDailyGrowth = 0.03

MaximumNConc = 0.03

WaterContent = 0.12

DMConversionEfficiency = 1

RemobilisationCost = 0

CarbonConcentration = 0.4

#### 1.4.2 Memo

As with Barley, Oats grain is typically harvested by farmers still in its husk (i.e. the palea and lemma remain attached to the kernel/caryopsis), while the kernel proper is typically smaller than a wheat grain grown under similar conditions. For simplicity (and in the absence of an extensive grain-oats data set) the Oats model uses the same grain size model as wheat, with the assumption that the weight of the oats kernel includes the weight of the husk (which is not included within kernel weight in the wheat model).

Grain number prediction is also derived directly from the wheat model, estimated as a constant number of grains (default=26) per unit of stem+spike dry matter at anthesis. This approach has known limitations and investigation is underway to improve this function in the future.

#### 1.4.3 NumberFunction

*NumberFunction* = *GrainNumber* until Flowering after which the value is fixed.

*GrainNumber* = *GrainsPerGramOfStem* x [*StemPlusPanicle*].*Wt*

*GrainsPerGramOfStem* = 26 (grains)

#### 1.4.4 DMDemandFunction

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

InitialPhase has a value between Flowering and StartGrainFill calculated as:

Filling rate is calculated from grain number, a maximum mass to be filled and the duration of the filling process.

*NumberFunction* = [*Grain*].*NumberFunction*

*FillingDuration* = [*Phenology*].*GrainDevelopment.Target*

*ThermalTime* = [*Phenology*].*ThermalTime*

*PotentialSizeIncrement* = [*Grain*].*InitialGrainProportion* x [*Grain*].*MaximumPotentialGrainSize*

LinearPhase has a value between StartGrainFill and EndGrainFill calculated as:

Filling rate is calculated from grain number, a maximum mass to be filled and the duration of the filling process.

*NumberFunction* = [*Grain*].*NumberFunction*

*FillingDuration* = [*Phenology*].*GrainFilling.Target*

*ThermalTime* = [*Phenology*].*ThermalTime*

*PotentialSizeIncrement* = *ProportionLinearPhase* x [*Grain*].*MaximumPotentialGrainSize*

*ProportionLinearPhase* = 1 - [*Grain*].*InitialGrainProportion*

#### 1.4.5 NFillingRate

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

GrainFilling has a value between FlagLeaf and EndGrainFill calculated as:

Filling rate is calculated from grain number, a maximum mass to be filled and the duration of the filling process.

*NumberFunction* = [*Grain*].*NumberFunction*

*FillingDuration* = [*Phenology*].*GrainDevelopment.Target* + [*Phenology*].*GrainFilling.Target*

*ThermalTime* = [*Phenology*].*ThermalTime*

*PotentialSizeIncrement* = [*Grain*].*MaximumPotentialGrainSize* x [*Grain*].*MaximumNConc*

#### 1.4.6 AccumThermalTime

*AccumThermalTime* = Accumulated *DailyThermalTimeValue* between flagleaf and maturity

*DailyThermalTimeValue* = [*Phenology*].*ThermalTime*

#### 1.4.7 Protein

*Protein* = ([*Grain*].*Live.N* + [*Grain*].*Dead.N*)/([*Grain*].*Live.Wt* + [*Grain*].*Dead.Wt*) x 100 x 5.71

#### 1.4.8 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	100	100	0	0
Cut	100	100	0	0
Prune	0	0	0	0
Graze	0	0	0	0
Thin	0	0	0	0

#### 1.4.9 DM Demand Priority Factors

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

Structural = 1

Metabolic = 1

Storage = 1

#### 1.4.10 ND Demand Priority Factors

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

Structural = 1

Metabolic = 1

Storage = 1

### 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 m<sup>2</sup> 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:

Using extinction coefficient as per measured at Gatton in 2007 (0.45).

ExtinctionCoeff = 0.45

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<sub>2</sub> concentration (FCO<sub>2</sub>).

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

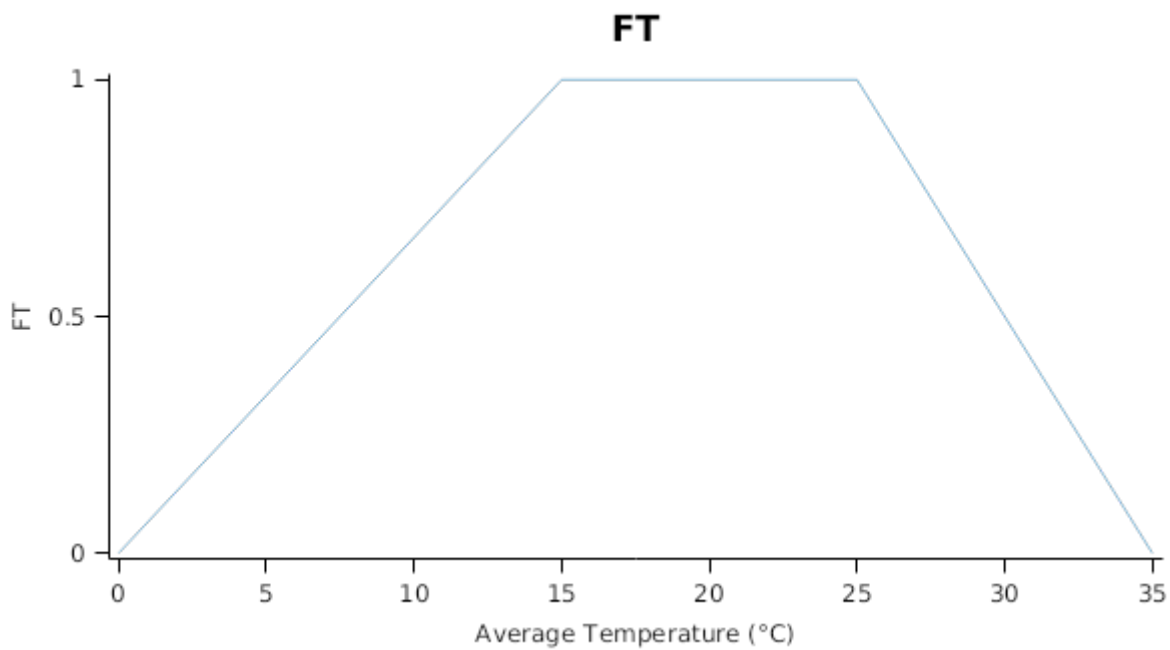
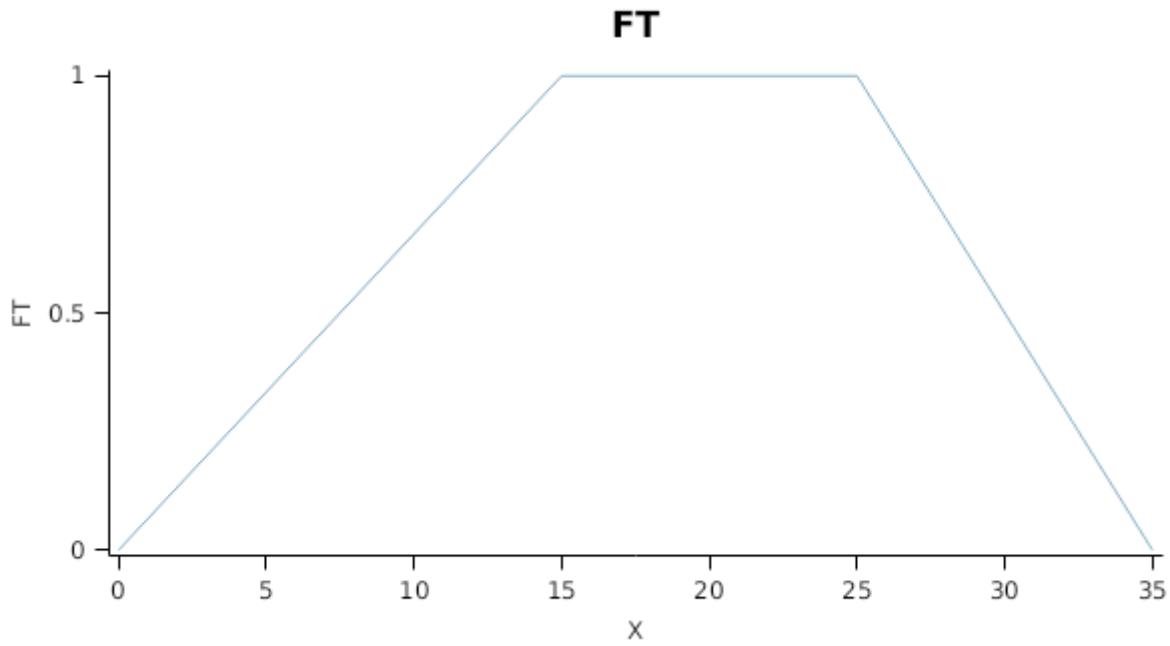
WHOLE PLANT RUE = bigger than RUE calculated using above ground biomass. 1.35 measured for Oats at Gatton 2007 (Above ground biomass only) so assume 20% more for root biomass.

RUE = 1.6

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

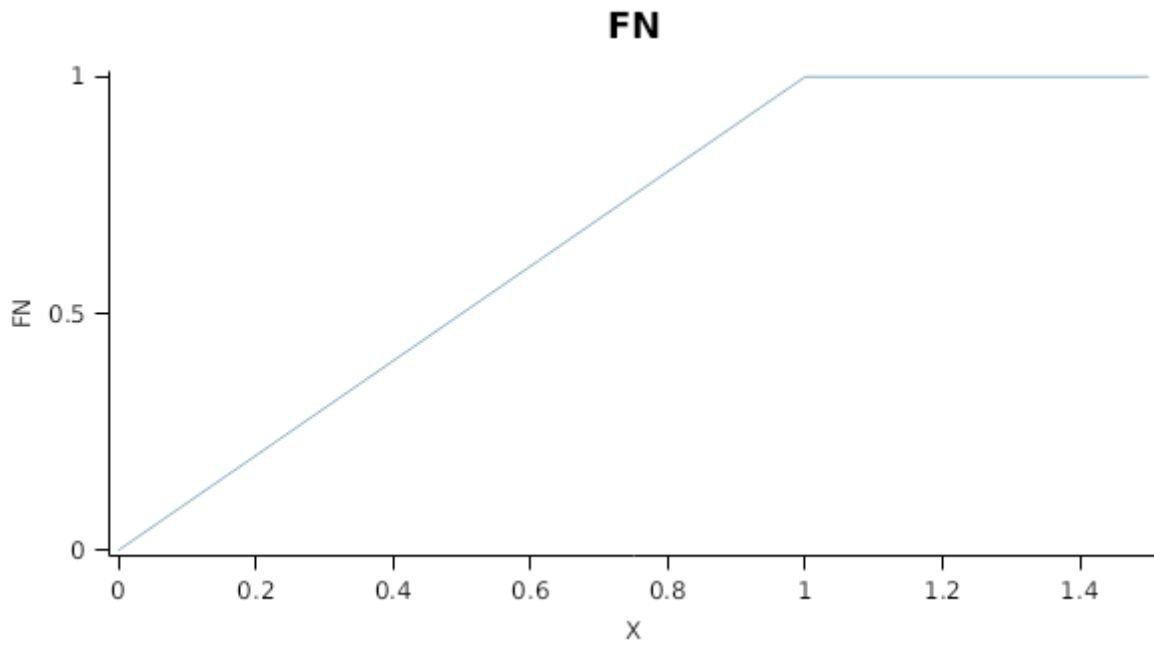
X	FT
0.0	0.0
15.0	1.0
25.0	1.0
35.0	0.0



FN is calculated using linear interpolation

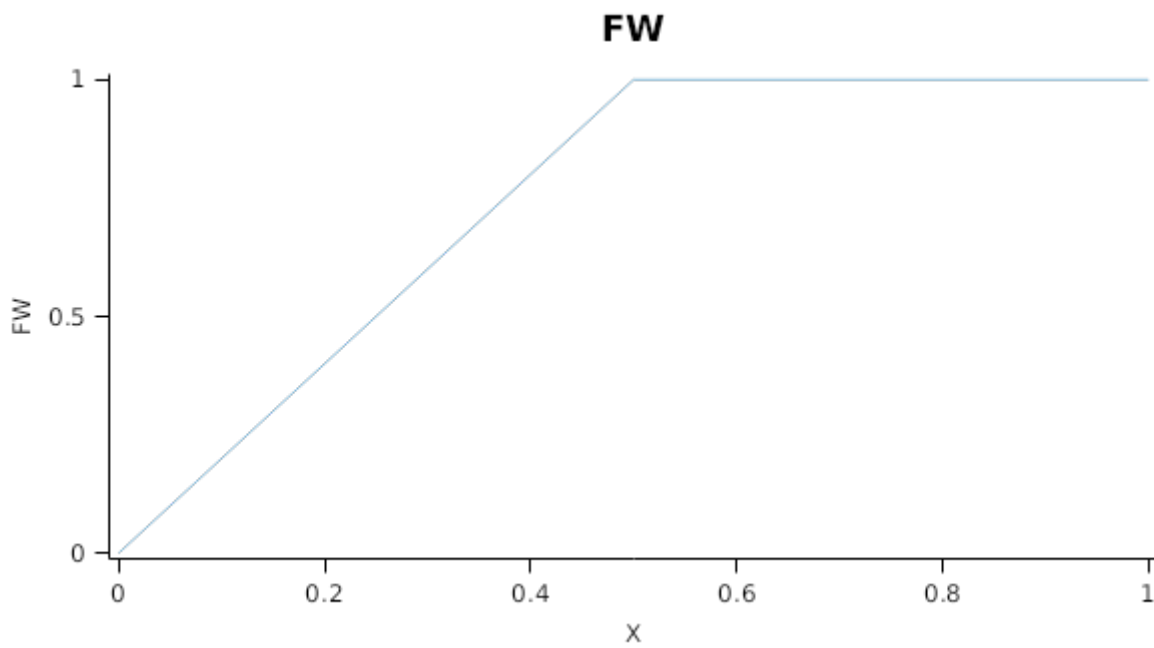
X	FN
0.0	0.0

X	FN
1.0	1.0
1.5	1.0



FW is calculated using linear interpolation

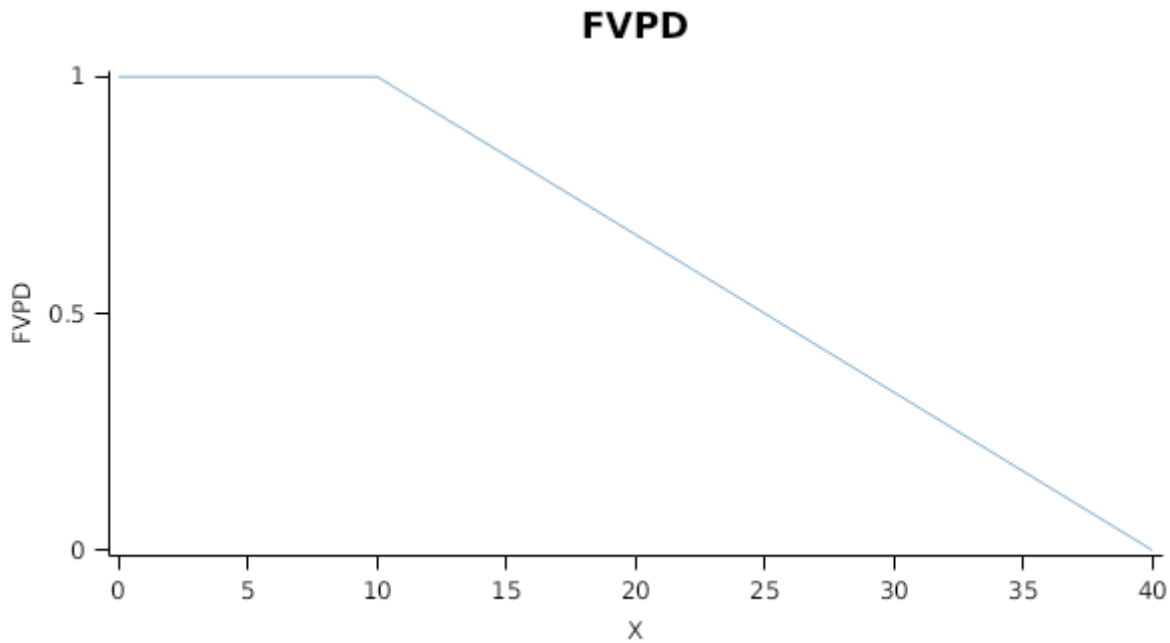
X	FW
0.0	0.0
0.5	1.0
1.0	1.0



FVPD is calculated using linear interpolation

X	FVPD
0.0	1.0

X	FVPD
10.0	1.0
40.0	0.0



This model calculates the CO<sub>2</sub> 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,

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

$$RadInt = [Leaf].RadiationIntercepted$$

### 1.5.2 Constants

FrostFraction = 0

Using extinction coefficient as per measured at Gatton in 2007 (0.45).

ExtinctionCoeff = 0.45

StructuralFraction = 0.5

DMConversionEfficiency = 1

RemobilisationCost = 0

CarbonConcentration = 0.4

WidthFunction = 0

### 1.5.3 CO<sub>2</sub>internal

$$CO_2internal = (163 - [IWeather].MeanT) / (5 - 0.1 \times [IWeather].MeanT)$$

### 1.5.4 StomatalConductanceCO<sub>2</sub>Modifier

$$StomatalConductanceCO_2Modifier = [Leaf].Photosynthesis.FCO_2 / RelativeCO_2Gradient$$

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

### 1.5.5 InitialLeaves[1]

Area = 200

### 1.5.6 InitialLeaves[2]

Area = 0

### 1.5.7 CohortParameters

#### 1.5.7.1 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*

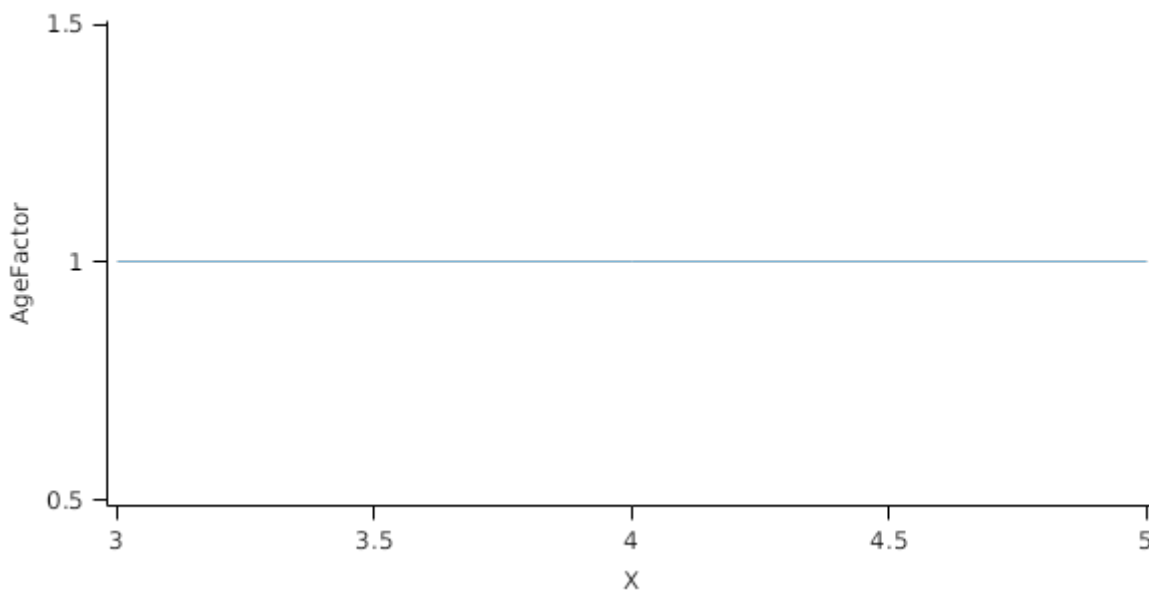
$$\text{GrowthDuration} = \text{Multiplier} \times [\text{Structure}].\text{Phyllochron} \times \text{AgeFactor}$$

Multiplier = 1.75

*AgeFactor* is calculated using linear interpolation

X	AgeFactor
3.0	1.0
4.0	1.0
5.0	1.0

### AgeFactor



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

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

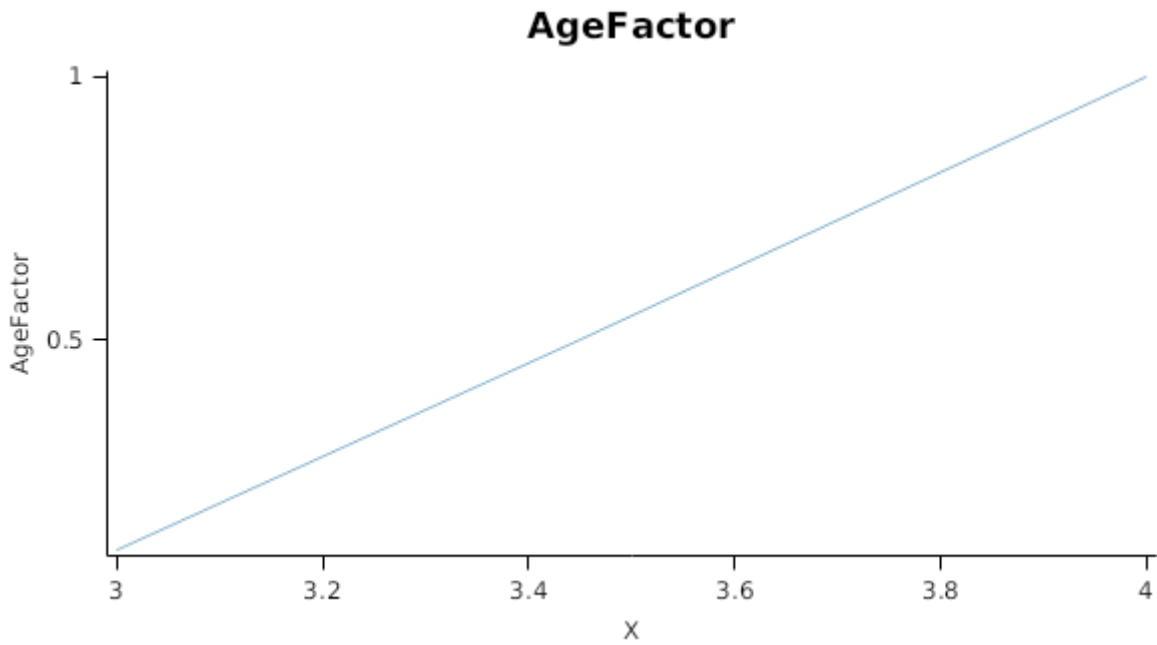
Default as per NZ Lincoln data set. Amended between varieties due to large variation in Oats plant type.

AreaLargestLeaves = 4000 (mm<sup>2</sup>)

*AgeFactor* is calculated using linear interpolation

X	AgeFactor
3.0	0.1

X	AgeFactor
3.5	0.5
4.0	1.0

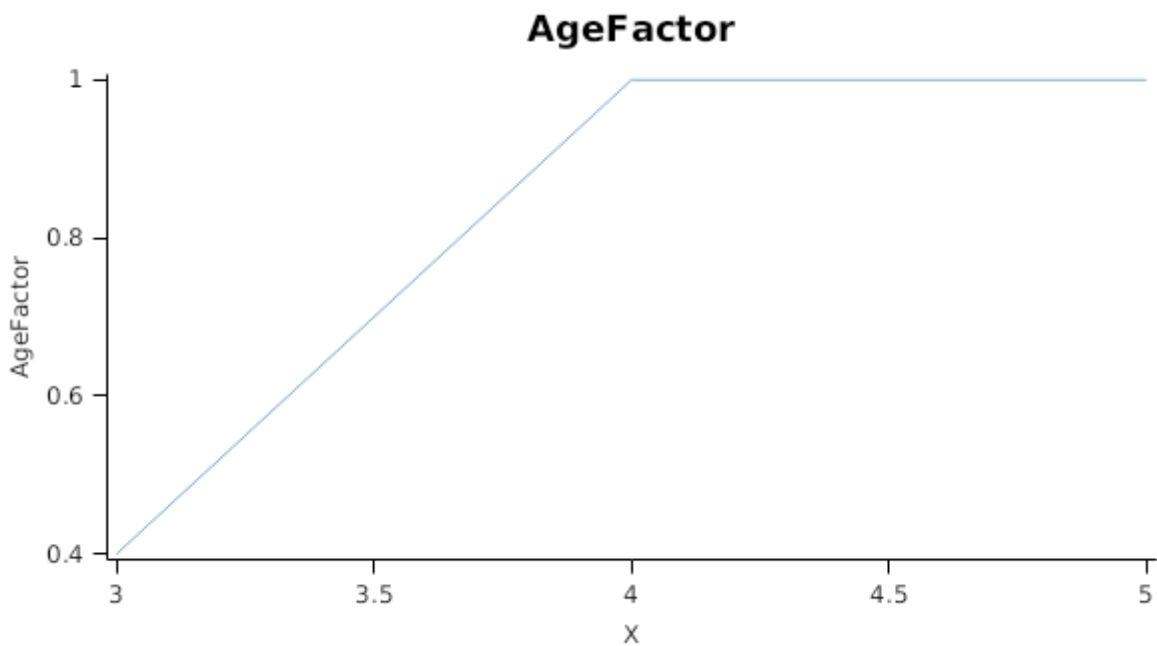


In the absence of stress the leaf will remain at *MaxArea* for a number of degree days set by the *LagDuration* and then area will senesce to zero at the end of the *SenescenceDuration*

$$LagDuration = AgeFactor \times LastLeafDuration$$

*AgeFactor* is calculated using linear interpolation

X	AgeFactor
3.0	0.4
4.0	1.0
5.0	1.0



$$LastLeafDuration = ThermalTimeToRipe - [Leaf].CohortParameters.SenescenceDuration$$



$ThermalTimeToRipe = [Phenology].EarlyReproductive.Target + [Phenology].GrainDevelopment.Target + [Phenology].GrainFilling.Target + [Phenology].Maturing.Target + [Phenology].Ripening.Target$

$SenescenceDuration = Multiplier \times [Structure].Phyllochron$

Multiplier = 6

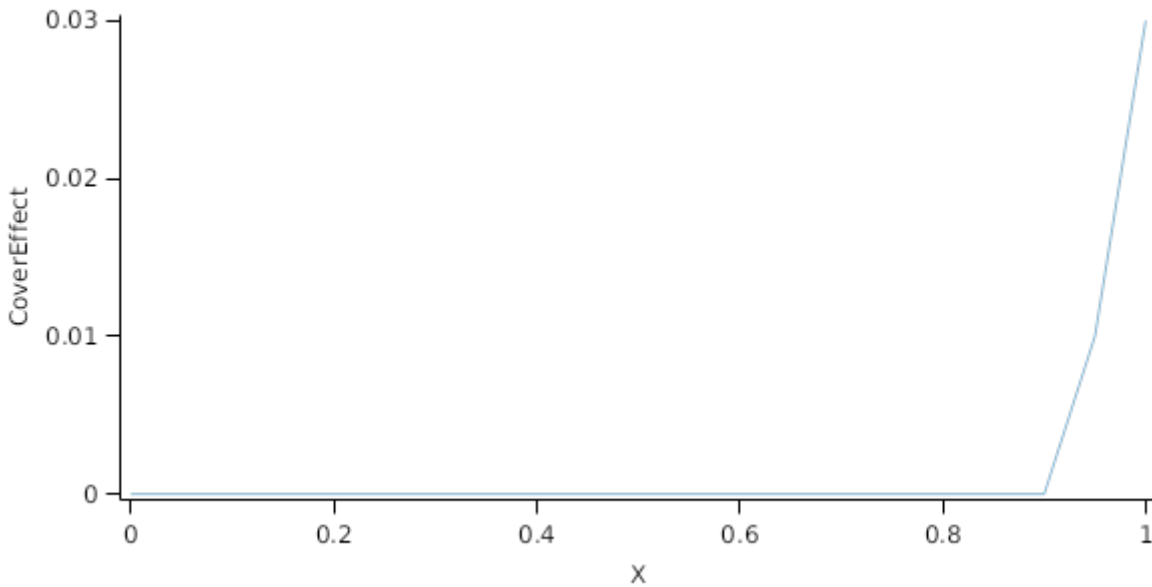
Mutual shading can cause premature senescence of cohorts if the leaf area above them becomes too great. Each cohort models the proportion of its area that is lost to shade induced senescence each day as:

$ShadeInducedSenescenceRate = CoverEffect \times [Phenology].ThermalTime$

CoverEffect is calculated using linear interpolation

X	CoverEffect
0.0	0.0
0.9	0.0
0.9	0.0
1.0	0.0

**CoverEffect**



### 1.5.7.2 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:

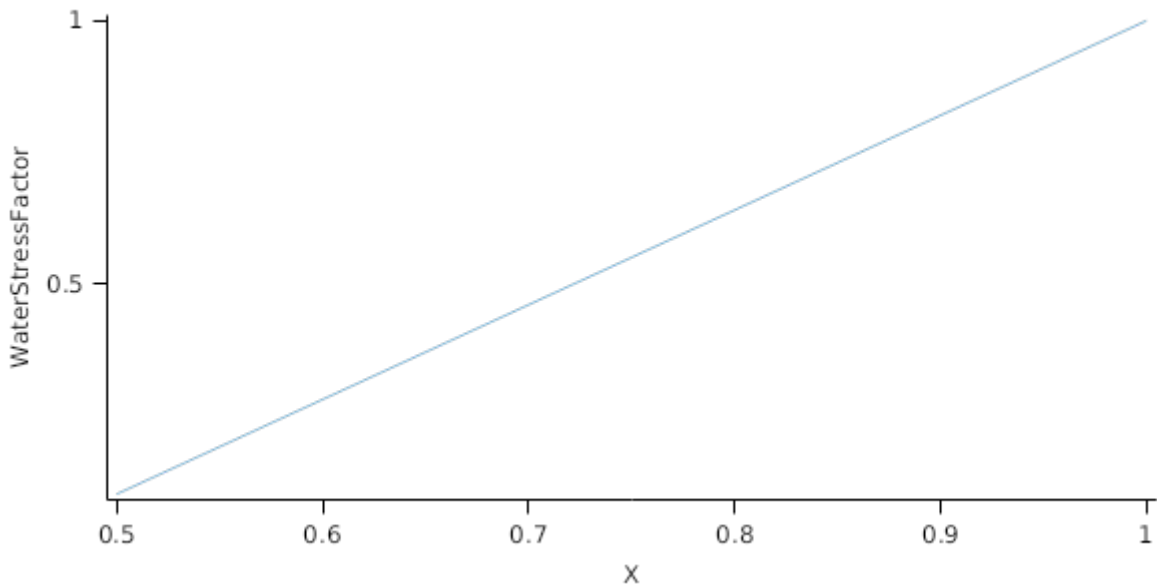
$CellDivisionStress = \text{Min}(WaterStressFactor, NitrogenStressFactor)$

Where:

*WaterStressFactor* is calculated using linear interpolation

X	WaterStressFactor
0.5	0.1
1.0	1.0

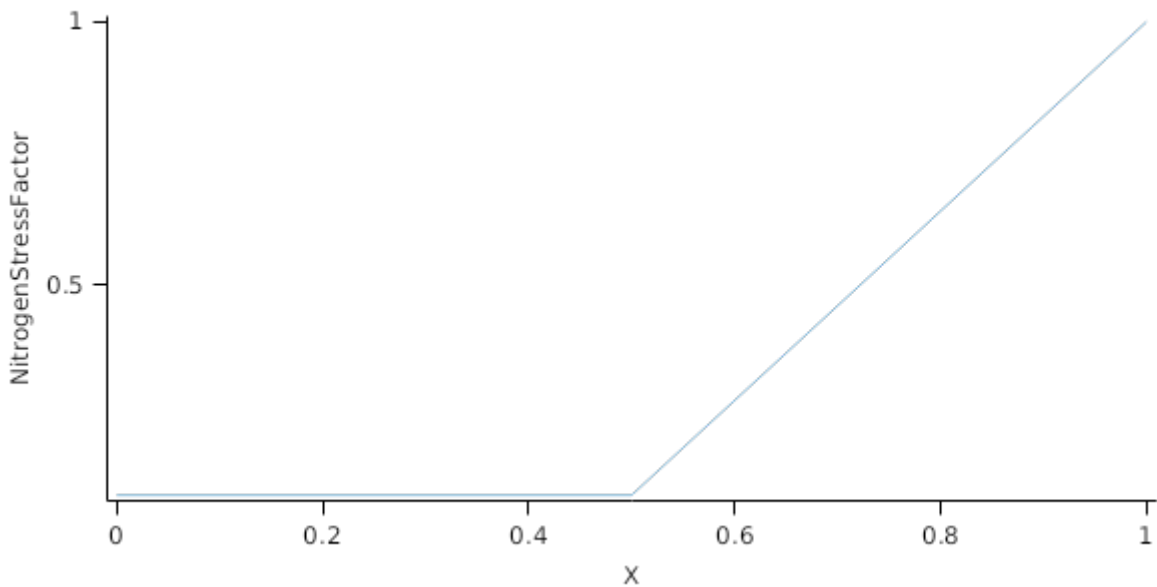
## WaterStressFactor



*NitrogenStressFactor* is calculated using linear interpolation

X	NitrogenStressFactor
0.0	0.1
0.5	0.1
1.0	1.0

## NitrogenStressFactor



*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*

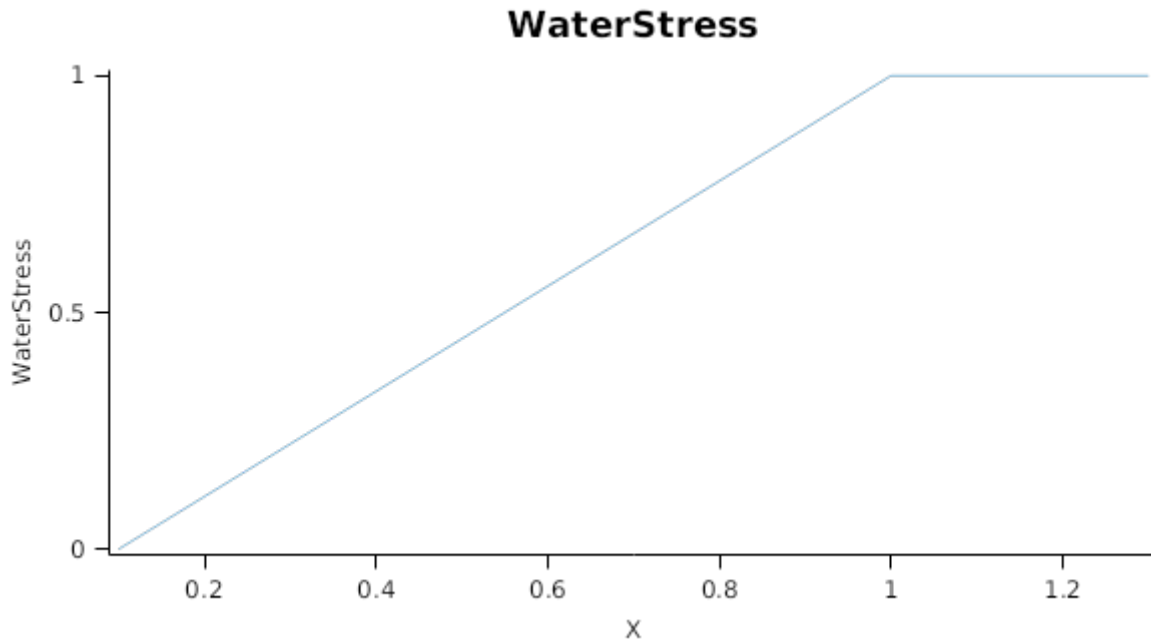
Stress during the *GrowthDuration*\* of the cohort reduces the size increase of the cohort by multiplying the potential increase by a *ExpansionStress* factor:

$$ExpansionStress = \text{Min}(WaterStress, TemperatureEffect, NitrogenStressFactor)$$

Where:

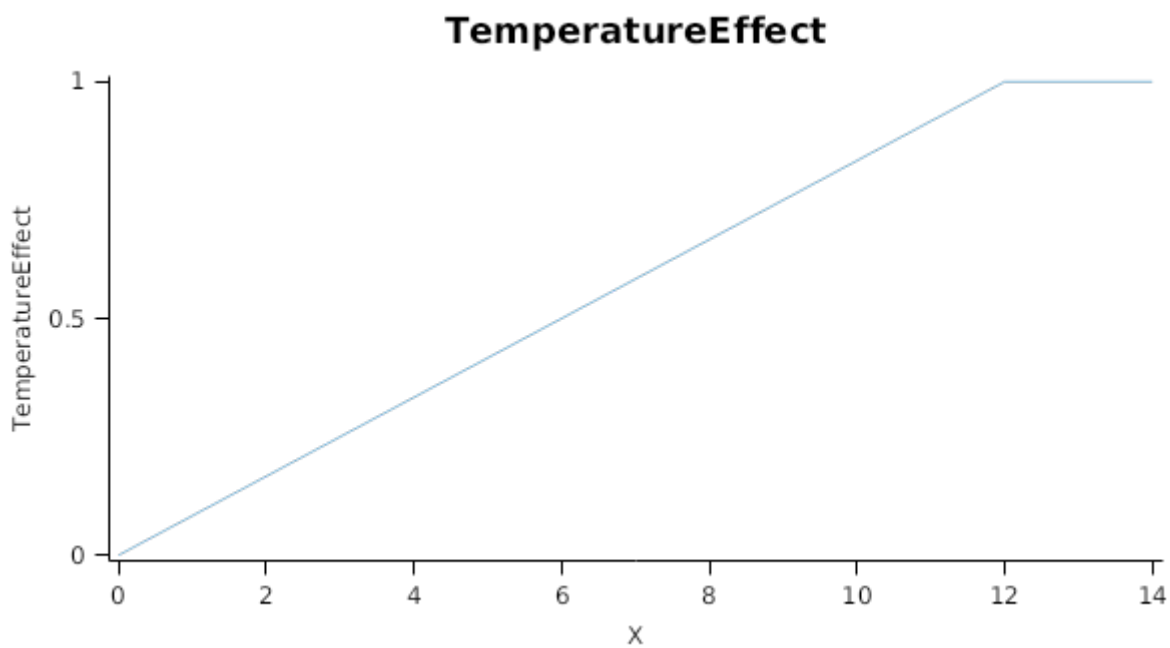
*WaterStress* is calculated using linear interpolation

X	WaterStress
0.1	0.0
1.0	1.0
1.3	1.0



*TemperatureEffect* is calculated using linear interpolation

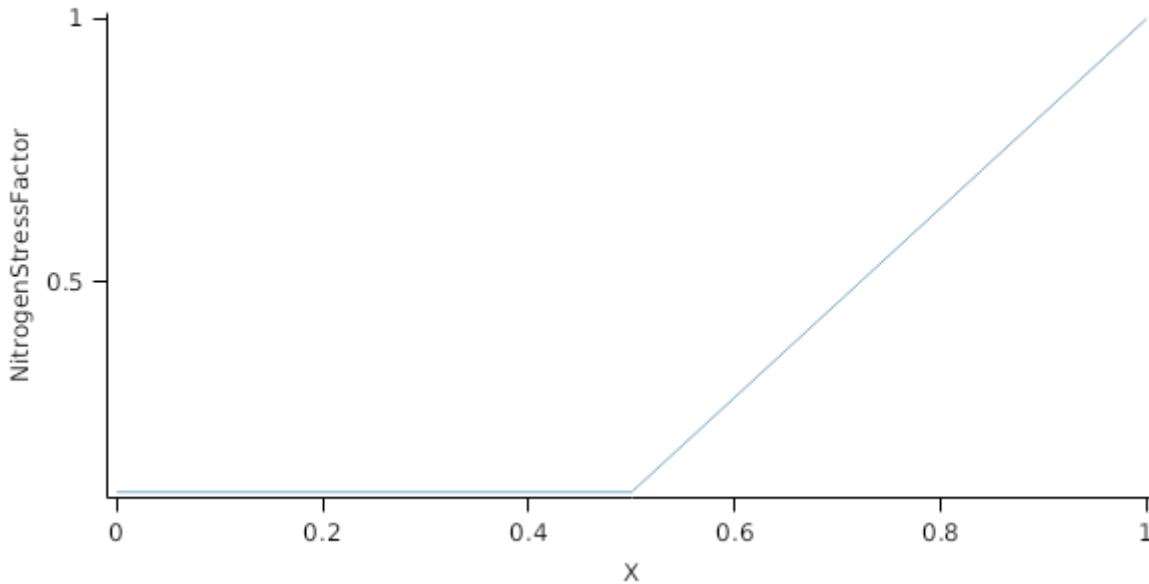
X	TemperatureEffect
0.0	0.0
12.0	1.0
14.0	1.0



*NitrogenStressFactor* is calculated using linear interpolation

X	NitrogenStressFactor
0.0	0.1
0.5	0.1
1.0	1.0

**NitrogenStressFactor**



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.

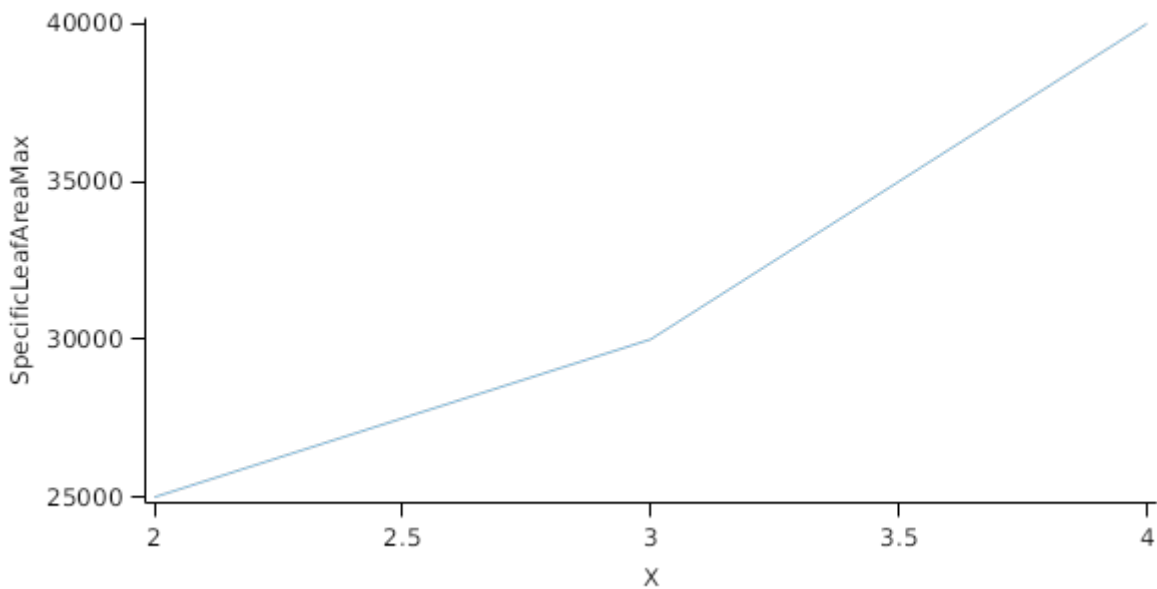
### 1.5.7.3 Dry matter Demand

Leaf calculates the DM demand from each cohort as a function of the potential size increment (*DeltaPotentialArea*) and a 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*.

*SpecificLeafAreaMax* is calculated using linear interpolation

X	SpecificLeafAreaMax
2.0	25000.0
3.0	30000.0
4.0	40000.0

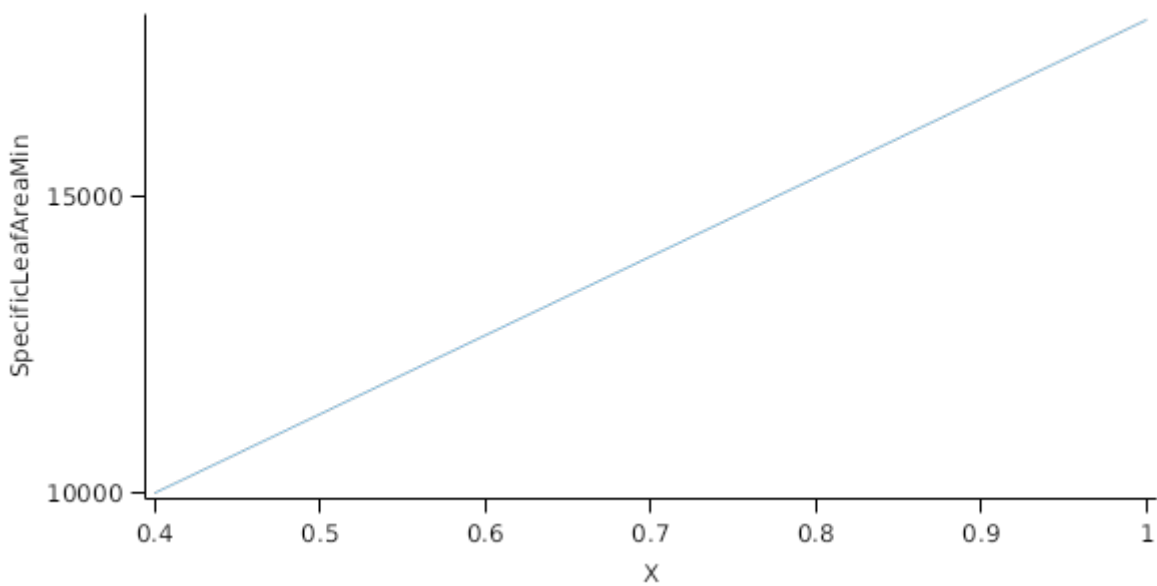
## SpecificLeafAreaMax



*SpecificLeafAreaMin* is calculated using linear interpolation

X	SpecificLeafAreaMin
0.4	10000.0
1.0	18000.0

## SpecificLeafAreaMin



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

$StructuralFraction = 0.3$

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

### 1.5.7.4 Nitrogen Demand

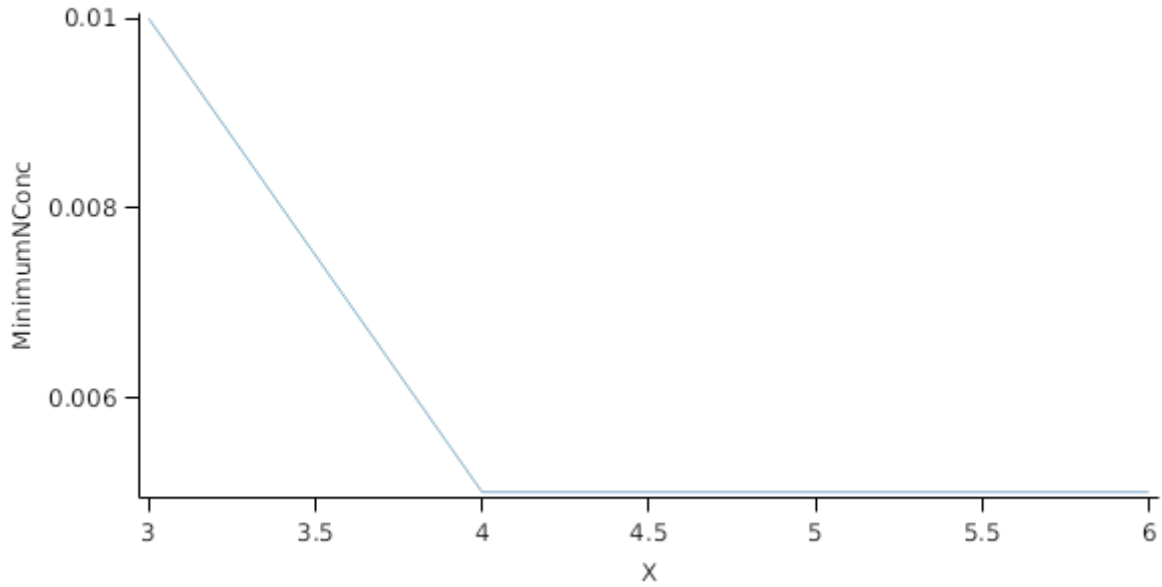
Leaf calculates the N demand from each cohort as a function of the potential DM increment and N concentration bounds.

Structural N demand =  $PotentialStructuralDMAllocation * MinimumNConc$  where:

*MinimumNConc* is calculated using linear interpolation

X	MinimumNConc
3.0	0.0
4.0	0.0
6.0	0.0

**MinimumNConc**



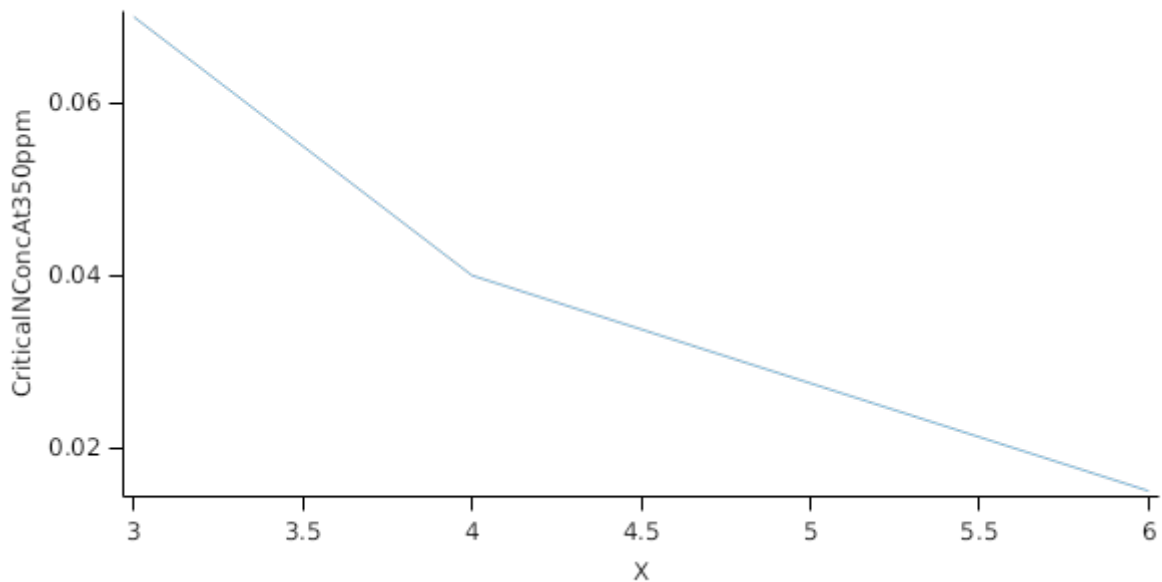
Metabolic N demand is calculated as  $PotentialMetabolicDMAAllocation * (CriticalNConc - MinimumNConc)$  where:

$CriticalNConc = CriticalNConcAt350ppm * CO2Factor$

$CriticalNConcAt350ppm$  is calculated using linear interpolation

X	CriticalNConcAt350ppm
3.0	0.1
4.0	0.0
6.0	0.0

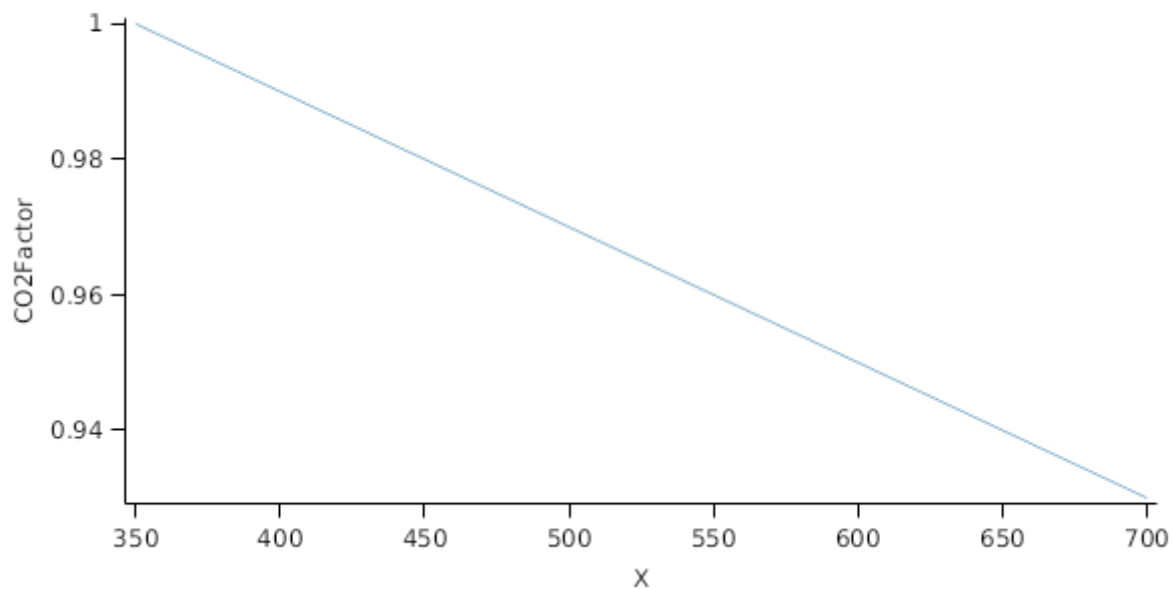
**CriticalNConcAt350ppm**



CO2Factor is calculated using linear interpolation

X	CO2Factor
350.0	1.0
700.0	0.9

**CO2Factor**

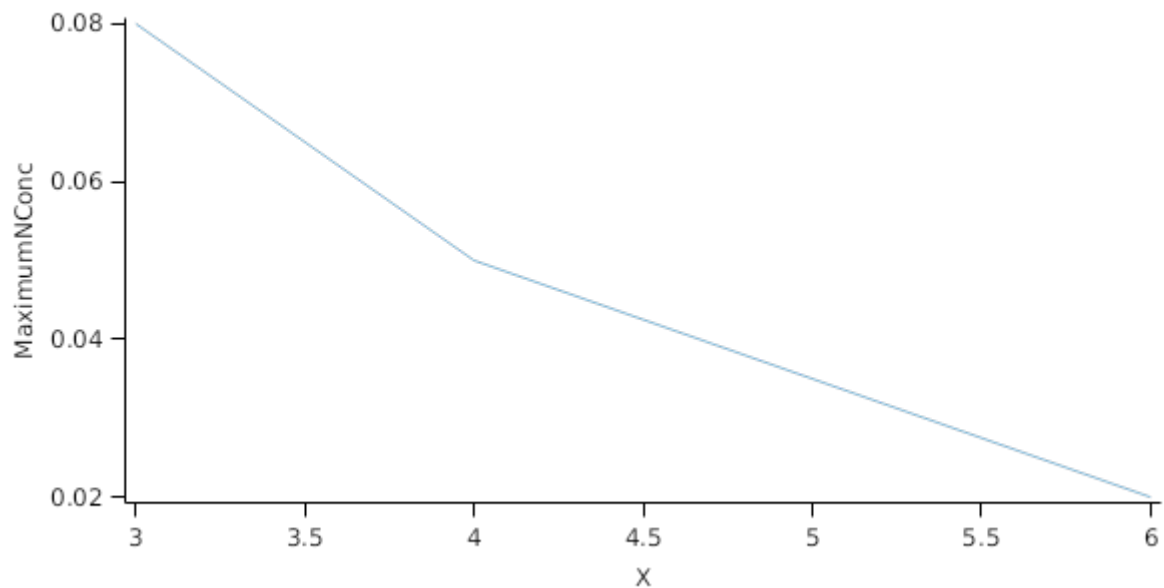


Storage N demand is calculated as the sum of metabolic and structural wt (including today's demands) multiplied by *LuxaryNconc* ( $MaximumNConc - CriticalNConc$ ) less the amount of storage N already present. *MaximumNConc* is given by:

*MaximumNConc* is calculated using linear interpolation

X	MaximumNConc
3.0	0.1
4.0	0.1
6.0	0.0

**MaximumNConc**



### 1.5.7.5 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:

$DM_{\text{ReallocationFactor}} = 1$

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

$DM_{\text{RetranslocationFactor}} = 0.8$

### 1.5.7.6 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:

$N_{\text{ReallocationFactor}} = 1$

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

$N_{\text{RetranslocationFactor}} = 0.03$

### 1.5.7.7 Constants

$N_{\text{ReallocationFactor}} = 1$

$\text{MaintenanceRespirationFunction} = 0$

$N_{\text{RetranslocationFactor}} = 0.03$

$DM_{\text{ReallocationFactor}} = 1$

$DM_{\text{RetranslocationFactor}} = 0.8$

$\text{DetachmentLagDuration} = 1000000$

$\text{DetachmentDuration} = 1000000$

$\text{RelativeBranchLeafSize} = 1$

$\text{InitialNConc} = 0$

$\text{StructuralFraction} = 0.3$

$\text{StorageFraction} = 0$

$\text{LeafSizeShapeParameter} = 0.3$

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

$\text{RemobilisationCost} = 0$

$\text{CarbonConcentration} = 0.4$

### 1.5.8 ThermalTime

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

### 1.5.9 FRGRFunction

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

Where:

$\text{RUE\_FT} = [\text{Leaf}].\text{Photosynthesis.FT}$

$\text{Others} = \text{Min}(\text{RUE\_FN}, \text{RUE\_FVPD})$



Where:

$$RUE\_FN = [Leaf].Photosynthesis.FN$$

$$RUE\_FVPD = [Leaf].Photosynthesis.FVPD$$

### 1.5.10 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	80	80
Cut	80	50	10	10
Prune	0	0	0	0
Graze	0	0	0	0
Thin	0	0	0	0

### 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 Stem

### 1.6.1 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.

### 1.6.2 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.

$$Structural = DMDemandFunction \times StructuralFraction$$

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.

PreStemElongation has a value between Emergence and TerminalSpikelet calculated as:

StemFraction = 0.4

StemElongation has a value between TerminalSpikelet and FlagLeaf calculated as:

StemFraction = 0.7

EarEmergence has a value between FlagLeaf and Flowering calculated as:

StemFraction = 0.7

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

VegetativeGrowth has a value between Sowing and Flowering calculated as:

Fraction = 0.7

ReproductiveGrowth has a value between Flowering and HarvestRipe calculated as:

Fraction = 0.5

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

### 1.6.3 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.

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

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

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

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

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

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

### 1.6.4 N Concentration Thresholds

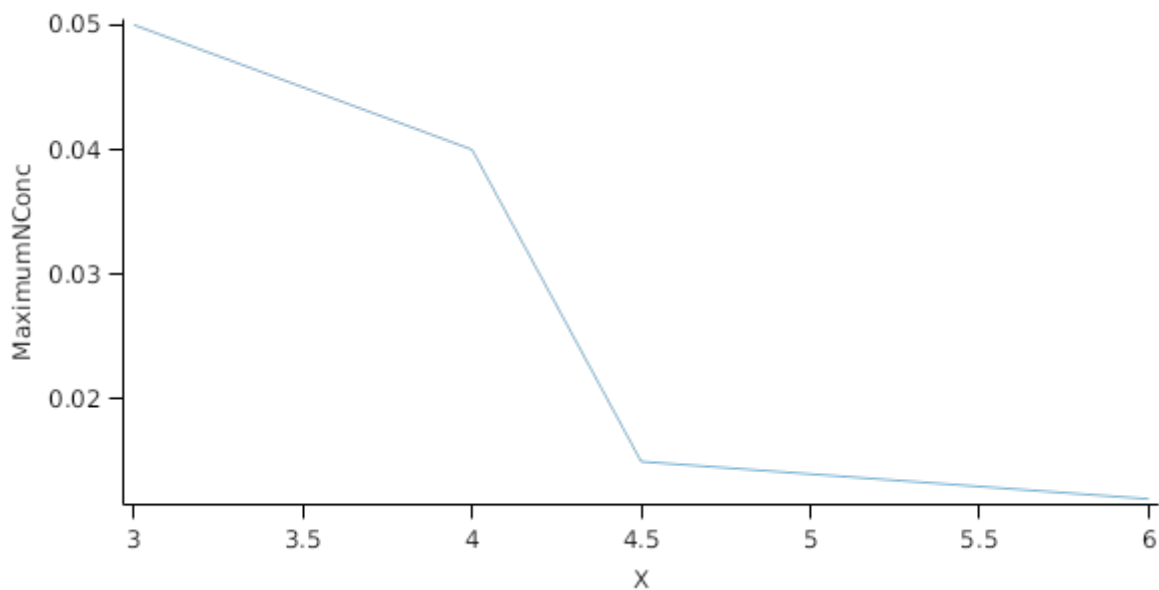
MinimumNConc = 0.0018

$CriticalNConc = [Stem].MinimumNConc$

MaximumNConc is calculated using linear interpolation

X	MaximumNConc
3.0	0.1
4.0	0.0
4.5	0.0
6.0	0.0

### MaximumNConc



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

NitrogenDemandSwitch has a value between Emergence and StartGrainFill calculated as:

Constant = 1

### 1.6.5 Dry Matter Supply

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

The proportion of non-structural DM that is allocated each day is quantified by the DMReallocationFactor.

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

VegetativeGrowth has a value between Emergence and StartGrainFill calculated as:

DMRetranslocationFactor = 0

ReproductiveGrowth has a value between StartGrainFill and EndGrainFill calculated as:

DMRetranslocationFactor = 0

### 1.6.6 Nitrogen Supply

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

The proportion of non-structural N that is allocated each day is quantified by the NReallocationFactor.

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

VegetativeGrowth has a value between Sowing and Flowering calculated as:

Fraction = 0

ReproductiveGrowth has a value between Flowering and HarvestRipe calculated as:

Fraction = 0.5

### 1.6.7 Senescence and Detachment

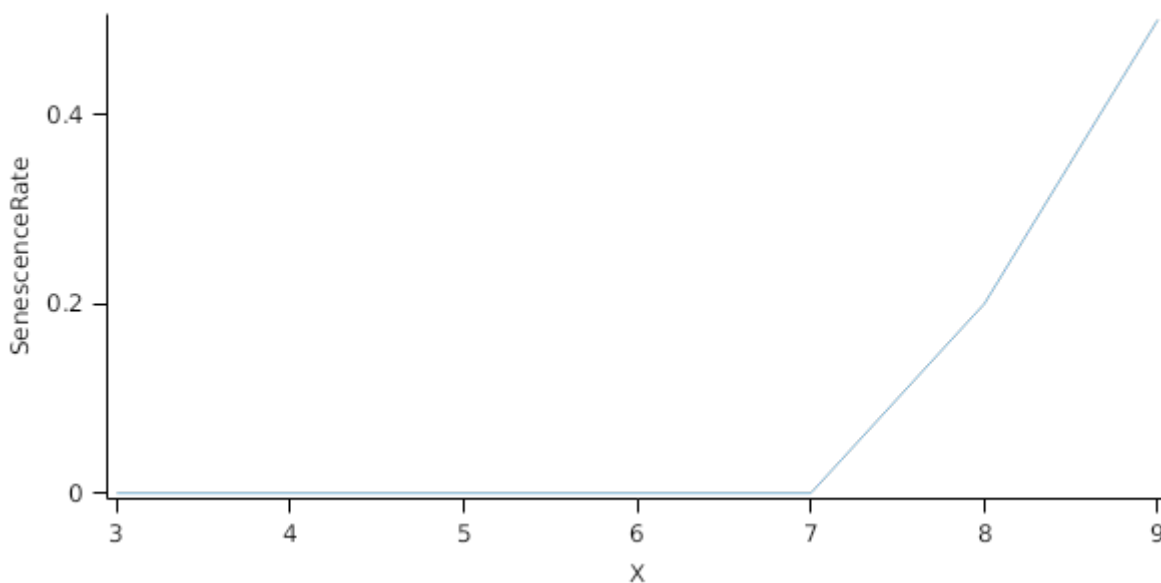
The proportion of live biomass that senesces and moves into the dead pool each day is quantified by the SenescenceRate.

$SenescenceRate = SenescenceRate$

SenescenceRate is calculated using linear interpolation

X	SenescenceRate
3.0	0.0
7.0	0.0
8.0	0.2
9.0	0.5

### SenescenceRate



Stem 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	60	60
Cut	70	50	10	10
Prune	0	0	0	0
Graze	0	0	0	0

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Thin	0	0	0	0

## 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.

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

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

Root depth is also constrained by a maximum root depth.

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

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

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

$$\text{DMAllocated}_i = \text{TotalDMAllocated} \times \text{RAw}_i / \text{TotalRAw}$$

### 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 (kNO3 or kNH4), the concentration of N form (ppm), and a soil moisture factor (NUptakeSWFactor) which typically decreases as the soil dries.  $\text{NO}_3 \text{ uptake} = \text{NO}_3 \times \text{kNO}_3 \times \text{NO}_{3\text{ppm},i} \times \text{NUptakeSWFactor}$   $\text{NH}_4 \text{ uptake} = \text{NH}_4 \times \text{kNH}_4 \times \text{NH}_{4\text{ppm},i} \times \text{NUptakeSWFactor}$  As can be seen from the above equations, the values of kNO3 and kNH4 equate to the potential fraction of each mineral N pool which can be taken up per day for wet soil when that pool has a concentration of 1 ppm. Nitrogen uptake demand is limited to the maximum daily potential uptake (MaxDailyNUptake) and the plant's N demand. The former provides a means to constrain N uptake to a maximum value observed in the field for the crop as a whole. The demand for soil N is then passed to the soil arbitrator which determines how much of the N uptake demand each plant instance will be allowed to take up.

### 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 KLModifier function.  $\text{SW uptake} = (\text{SW}_i - \text{LL}_i) \times \text{KL}_i \times \text{KLModifier}$

### 1.7.6 Constants

KLModifier = 1

SoilWaterEffect = 1

MaxDailyNUptake = 20

SenescenceRate = 0.005

MaximumRootDepth = 1000000

MaximumNConc = 0.01

MinimumNConc = 0.01

KNO3 = 0.02

KNH4 = 0.01

SpecificRootLength = 105 (m/g)

DMConversionEfficiency = 1

MaintenanceRespirationFunction = 1

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 NitrogenDemandSwitch

NitrogenDemandSwitch has a value between Germination and Maturity calculated as:

Constant = 1

### 1.7.9 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	0	0	50	50
Prune	0	0	0	0
Graze	0	0	0	0
Thin	0	0	0	0

### 1.7.10 RootFrontVelocity

$RootFrontVelocity = PotentialRootFrontVelocity \times TemperatureFactor \times WaterFactor$

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

PreEmergence has a value between Germination and Emergence calculated as:

Value = 5 (mm/d)

PostEmergence has a value between Emergence and Maturity calculated as:

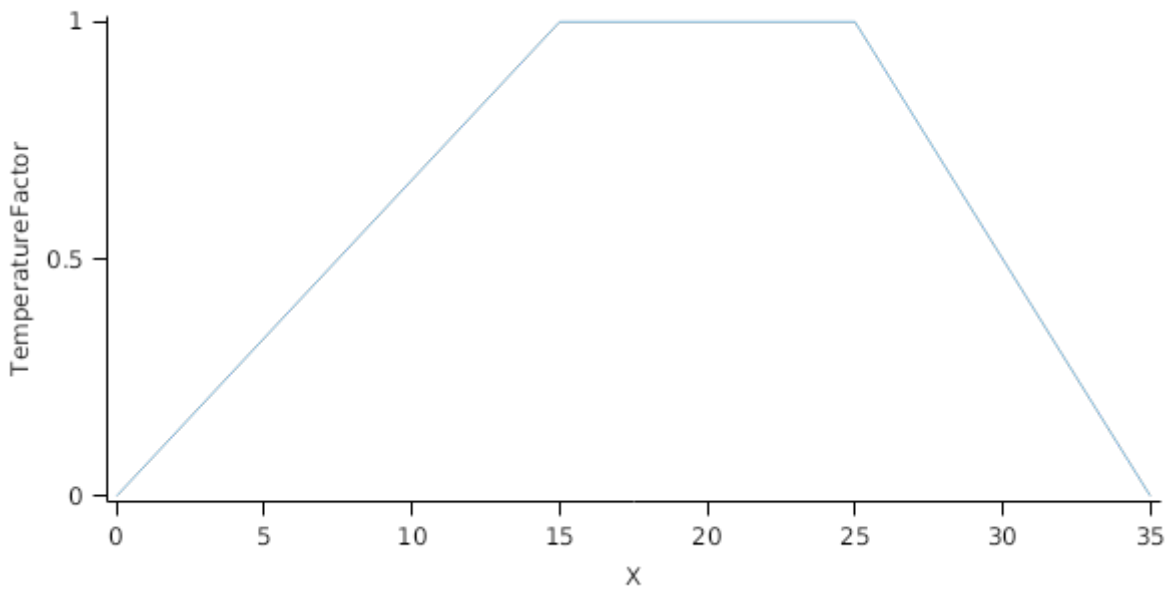
Value = 20 (mm/d)

*TemperatureFactor* 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.

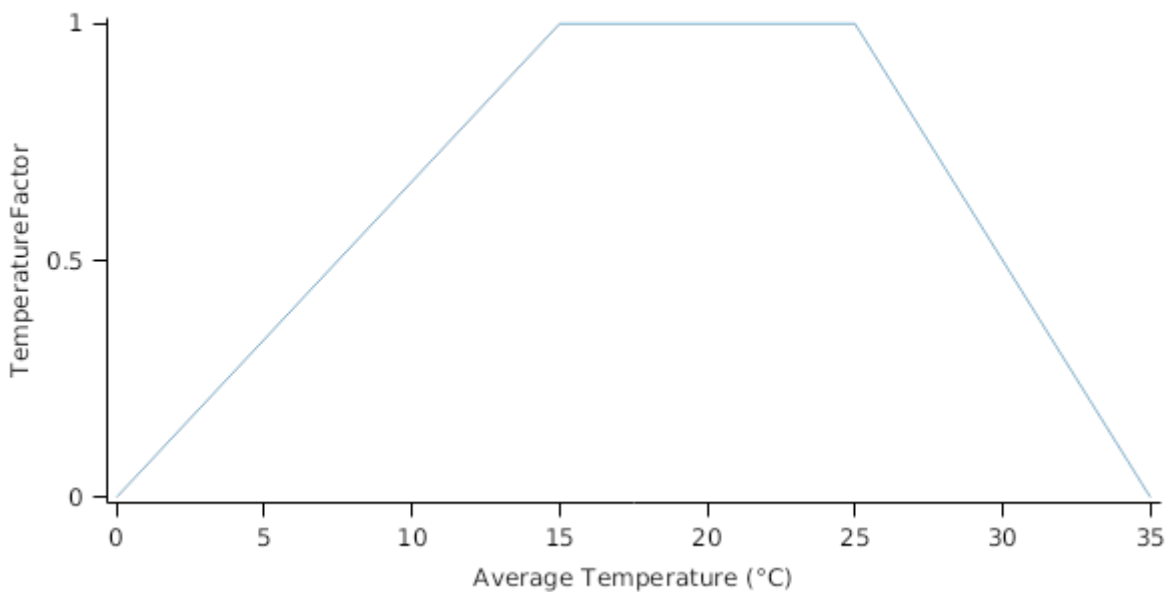
*MaximumTemperatureWeighting* = 0.5

X	TemperatureFactor
0.0	0.0
15.0	1.0
25.0	1.0
35.0	0.0

**TemperatureFactor**



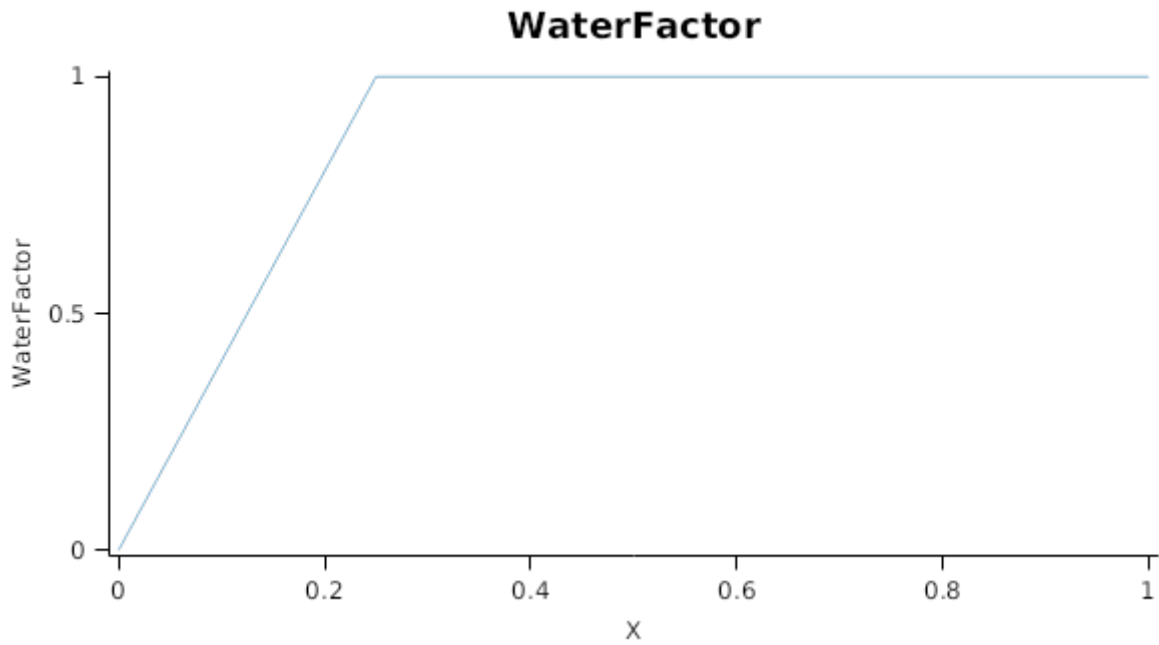
**TemperatureFactor**



*WaterFactor* is calculated using linear interpolation

X	WaterFactor
0.0	0.0

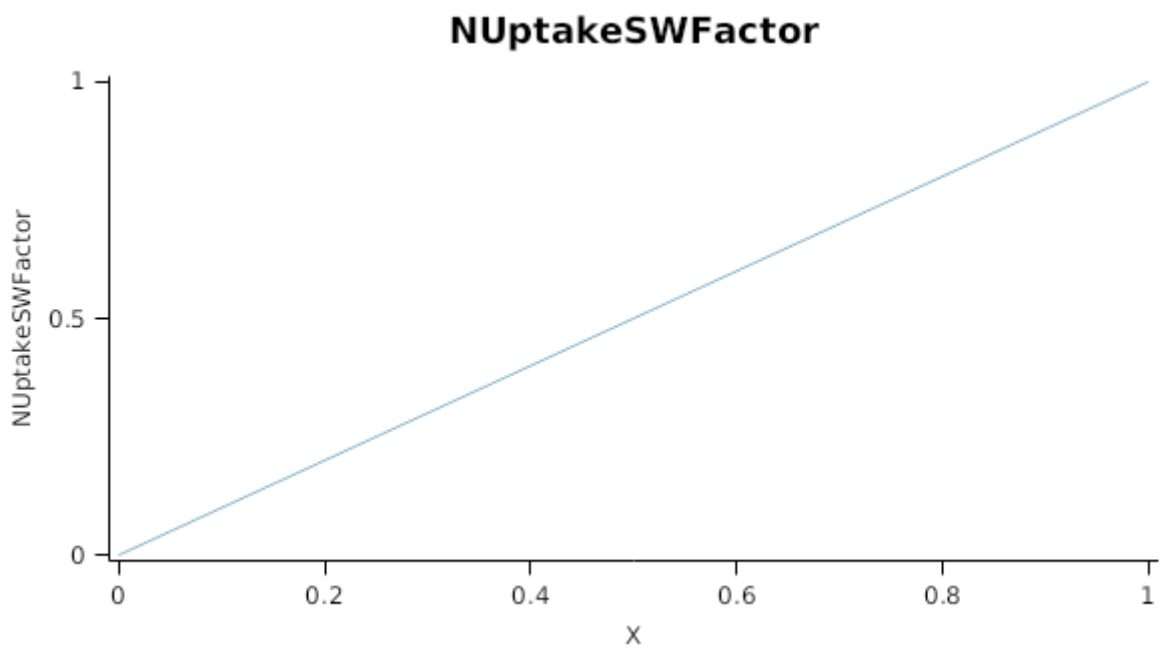
X	WaterFactor
0.2	1.0
1.0	1.0



#### 1.7.11 NUptakeSWFactor

*NUptakeSWFactor* is calculated using linear interpolation

X	NUptakeSWFactor
0.0	0.0
1.0	1.0



#### 1.7.12 DMDemands

##### 1.7.12.1 DMDemands

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



$Structural = DM_{DemandFunction} \times StructuralFraction$

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

PreEmergence has a value between Germination and Emergence calculated as:

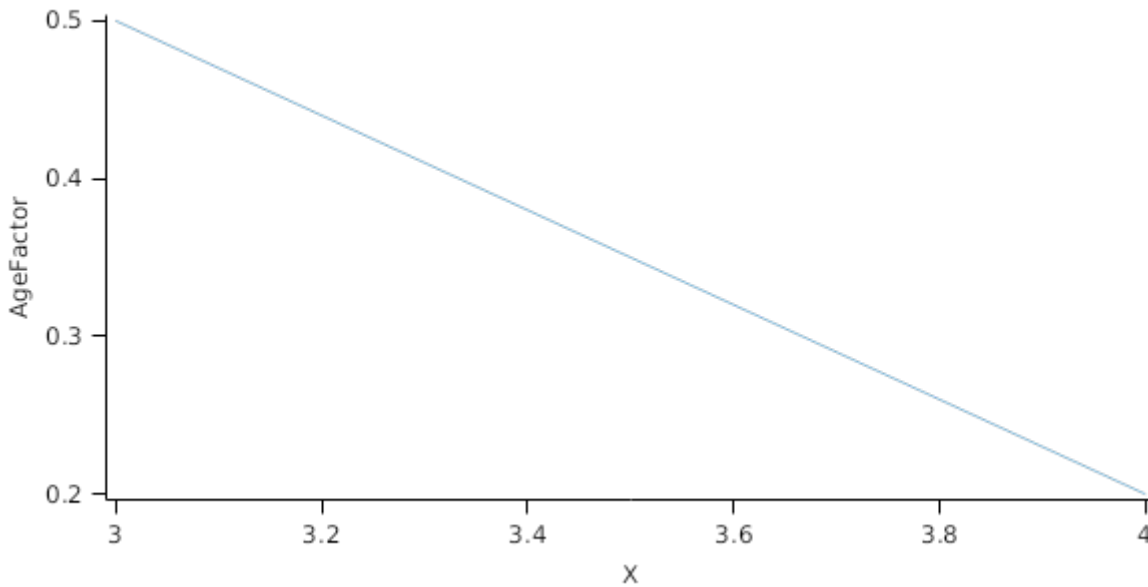
Value = 0

PreFlowering has a value between Emergence and Flowering calculated as:

AgeFactor is calculated using linear interpolation

X	AgeFactor
3.0	0.5
4.0	0.2

**AgeFactor**



PostFlowering has a value between Flowering and EndGrainFill calculated as:

Value = 0.2

StructuralFraction = 1

Metabolic = 0

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

$StorageFraction = 1 - [Root].DM_{Demands}.Structural.StructuralFraction$

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

### 1.7.13 NDemands

#### 1.7.13.1 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

### 1.7.14 CriticalNConc

$CriticalNConc = [Root].MinimumNConc$

### 1.7.15 InitialWt

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

Structural = 0.005 (g/plant)

Metabolic = 0

Storage = 0

## 1.8 Panicle

### 1.8.1 Panicle

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.

### 1.8.2 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.

#### 1.8.2.1 DMDemands

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

$Structural = DMDemandFunction \times StructuralFraction$

Demand is calculated from the product of growth rate, thermal time and population.

$ThermalTime = [Phenology].ThermalTime$

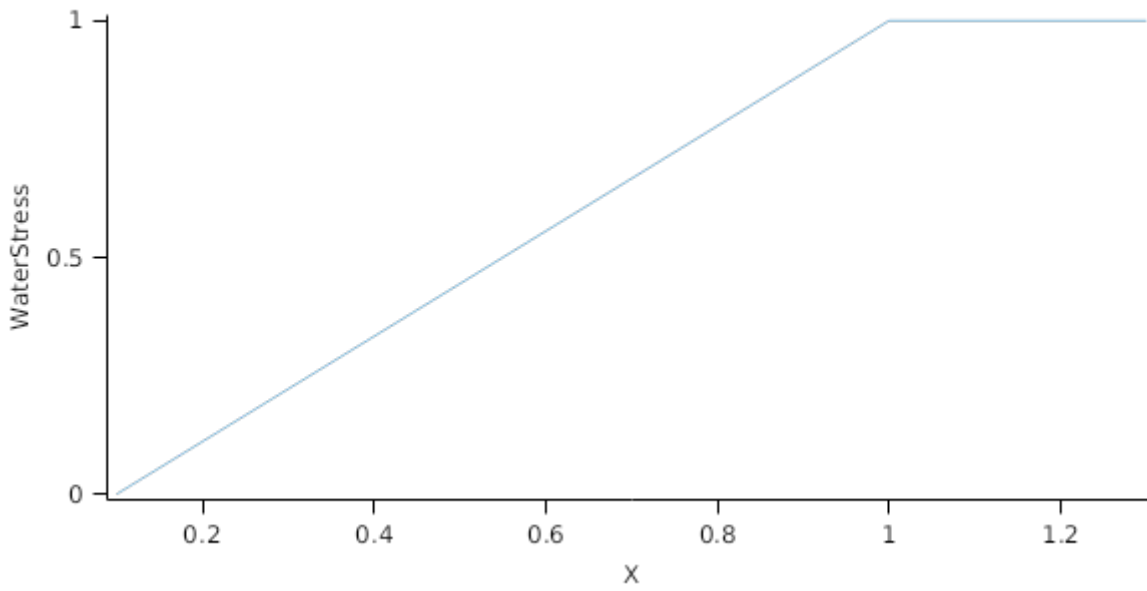
$ExpansionStress = \text{Min}(WaterStress, TemperatureEffect, NitrogenStressFactor)$

Where:

$WaterStress$  is calculated using linear interpolation

X	WaterStress
0.1	0.0
1.0	1.0
1.3	1.0

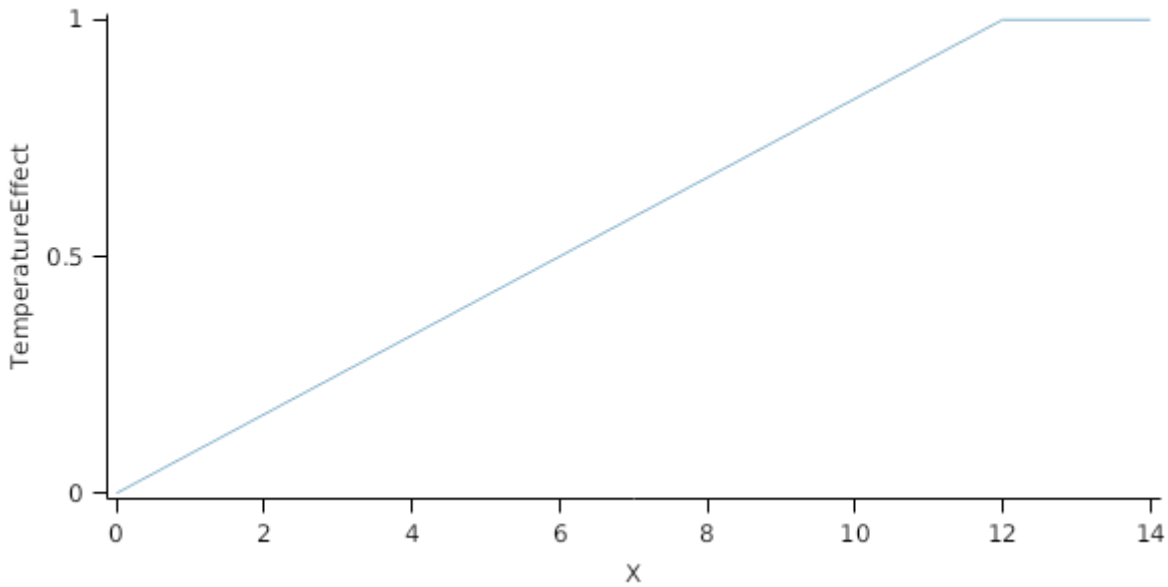
### WaterStress



*TemperatureEffect* is calculated using linear interpolation

X	TemperatureEffect
0.0	0.0
12.0	1.0
14.0	1.0

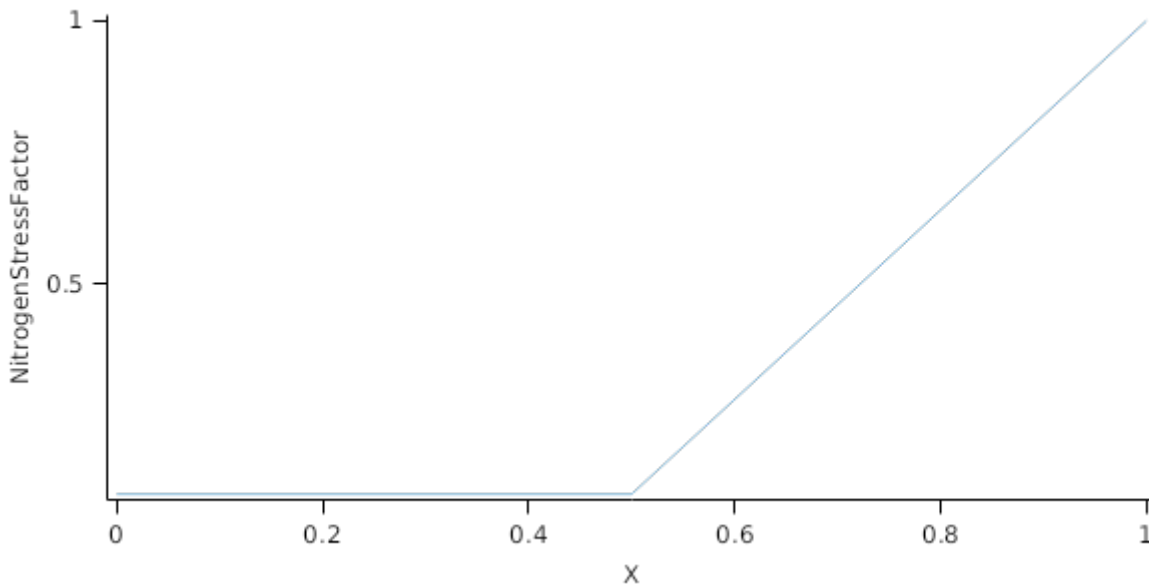
### TemperatureEffect



*NitrogenStressFactor* is calculated using linear interpolation

X	NitrogenStressFactor
0.0	0.1
0.5	0.1
1.0	1.0

## NitrogenStressFactor



$OrganPopulation = [Panicl].HeadNumber$

$StartStage = 4.8$

$MaximumOrganWt = 0.4 \text{ (g)}$

$GrowthDuration = [Phenology].EarlyReproductive.Target + [Phenology].GrainDevelopment.Target$

$StructuralFraction = 0.9$

$Metabolic = 0$

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

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

$QStructuralPriority = 1$

$QMetabolicPriority = 1$

$QStoragePriority = 1$

### 1.8.3 Nitrogen Demand

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

#### 1.8.3.1 NDemands

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

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

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

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

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

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

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

$NitrogenDemandSwitch = [Panicl].nitrogenDemandSwitch$

$MaxNconc = [Panicl].maximumNconc$

$QStructuralPriority = 1$

QMetabolicPriority = 1

QStoragePriority = 1

#### 1.8.4 N Concentration Thresholds

MinimumNConc = 0.02

*CriticalNConc* = [*Panicle*].*MinimumNConc*

MaximumNConc = 0.025

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

NitrogenDemandSwitch has a value between Emergence and StartGrainFill calculated as:

Constant = 1

#### 1.8.5 Dry Matter Supply

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

The proportion of non-structural DM that is allocated each day is quantified by the DMReallocationFactor.

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

VegetativeGrowth has a value between Emergence and StartGrainFill calculated as:

DMRetranslocationFactor = 0

ReproductiveGrowth has a value between StartGrainFill and EndGrainFill calculated as:

DMRetranslocationFactor = 0.5

#### 1.8.6 Nitrogen Supply

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

Panicle can retranslocate up to 30% of non-structural N each day if required by the plant arbitrator to meet N demands.

#### 1.8.7 Senescence and Detachment

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

Panicle 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	100	100	0	0
Prune	0	0	0	0
Graze	0	0	0	0
Thin	0	0	0	0

### 1.9 AboveGround

#### 1.9.1 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
- \* Stem
- \* Panicle
- \* Grain

## **1.10 AboveGroundLive**

### **1.10.1 AboveGroundLive**

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

AboveGroundLive summarises the following biomass objects:

- \* Leaf
- \* Stem
- \* Panicle
- \* Grain

## **1.11 AboveGroundDead**

### **1.11.1 AboveGroundDead**

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

AboveGroundDead summarises the following biomass objects:

- \* Leaf
- \* Stem
- \* Panicle
- \* Grain

## **1.12 BelowGround**

### **1.12.1 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

## **1.13 Total**

### **1.13.1 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
- \* Root
- \* Panicle
- \* Grain

## **1.14 TotalLive**

### **1.14.1 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
- \* Stem
- \* Root

- \* Panicle
- \* Grain

## **1.15 TotalDead**

### **1.15.1 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
- \* Stem
- \* Root
- \* Panicle
- \* Grain

## **1.16 Ear**

### **1.16.1 Ear**

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

Ear summarises the following biomass objects:

- \* Panicle
- \* Grain

## **1.17 StemPlusPanicle**

### **1.17.1 StemPlusPanicle**

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

StemPlusPanicle summarises the following biomass objects:

- \* Stem
- \* Panicle

## **1.18 Cultivars**

### **1.18.1 Drummond**

Drummond overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8.5

[Phenology].VrnSensitivity.FixedValue = 7

[Phenology].PpSensitivity.FixedValue = 3

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].Phyllochron.BasePhyllochron.FixedValue = 75

[Structure].BranchingRate.StressFactors.CoverEffect.XYPairs.X = 0,0.2,0.35

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 4000

[Structure].BranchingRate.PotentialBranchingRate.Vegetative.PotentialBranchingRate.XYPairs.X = 1,2,3.99,4,5,6,7,8,9

[Structure].BranchingRate.PotentialBranchingRate.Vegetative.PotentialBranchingRate.XYPairs.Y = 0,0,0,1,2,4,7,12,20

[Leaf].CohortParameters.GrowthDuration.AgeFactor.XYPairs.Y = 1,1,0.1

[Grain].MaximumPotentialGrainSize.FixedValue = 0.05

[Grain].NumberFunction.GrainNumber.GrainsPerGramOfStem.FixedValue = 40

### **1.18.2 Drummond\_orig**

Drummond\_orig overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].PpSensitivity.FixedValue = 10

[Structure].Phyllochron.BasePhyllochron.FixedValue = 80

[Structure].BranchingRate.StressFactors.CoverEffect.XYPairs.X = 0,0.2,0.35

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 4000

[Structure].BranchingRate.PotentialBranchingRate.Vegetative.PotentialBranchingRate.XYPairs.X = 1,2,3.99,4,5,6,7,8,9

### **1.18.3 Milton**

Milton overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8.5

[Phenology].VrnSensitivity.FixedValue = 7

[Phenology].PpSensitivity.FixedValue = 3

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 2

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 0

[Structure].Phyllochron.BasePhyllochron.FixedValue = 105

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 4000

[Leaf].CohortParameters.SenescenceDuration.Multiplier.FixedValue = 3

[Leaf].CohortParameters.GrowthDuration.AgeFactor.XYPairs.Y = 1,1,0.1

[Grain].MaximumPotentialGrainSize.FixedValue = 0.05

[Grain].NumberFunction.GrainNumber.GrainsPerGramOfStem.FixedValue = 50

[Leaf].ExtinctionCoeff.FixedValue = 0.6

### **1.18.4 Hokonui**

Hokonui overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].PpSensitivity.FixedValue = 10

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

[Leaf].CohortParameters.GrowthDuration.AgeFactor.XYPairs.Y = 1,1,0.1

### **1.18.5 Stampede**

Stampede overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].PpSensitivity.FixedValue = 10

[Structure].Phyllochron.BasePhyllochron.FixedValue = 80



[Leaf].CohortParameters.GrowthDuration.AgeFactor.XYPairs.Y = 1,1,0.1

### **1.18.6 Coolibah**

Coolibah overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 5.3

[Phenology].PpSensitivity.FixedValue = 3.0

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 5000

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 0

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 2

[Structure].BranchingRate.StressFactors.CoverEffect.XYPairs.X = 0,0.25,0.5

### **1.18.7 Taipan**

Taipan overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 10

[Phenology].PpSensitivity.FixedValue = 7.5

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 3

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 8000

### **1.18.8 Wintaroo**

Wintaroo overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 7

[Phenology].VrnSensitivity.FixedValue = 2

[Phenology].PpSensitivity.FixedValue = 2

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 0

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 2

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

### **1.18.9 Kangaroo**

Kangaroo overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 7

[Phenology].VrnSensitivity.FixedValue = 4

[Phenology].PpSensitivity.FixedValue = 4

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 0

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 2

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

### **1.18.10 Brusher**

Brusher overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 7

[Phenology].VrnSensitivity.FixedValue = 1

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 0

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 2

[Structure].Phyllochron.BasePhyllochron.FixedValue = 80

### **1.18.11 Algerian**

Algerian overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 12

[Phenology].PpSensitivity.FixedValue = 6

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 4

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Structure].Phyllochron.BasePhyllochron.FixedValue = 105

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 5000

[Structure].BranchingRate.StressFactors.CoverEffect.XYPairs.X = 0,0.4,0.7

### **1.18.12 Nugene**

Nugene overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 10

[Phenology].PpSensitivity.FixedValue = 7.5

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 3

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 8000

### **1.18.13 Drover**

Drover overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 4

[Phenology].PpSensitivity.FixedValue = 9

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 6

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Structure].Phyllochron.BasePhyllochron.FixedValue = 80

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 8000

#### **1.18.14 Genie**

Genie overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 10

[Phenology].PpSensitivity.FixedValue = 7.5

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 3

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 8000

#### **1.18.15 Aladdin**

Aladdin overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 10

[Phenology].PpSensitivity.FixedValue = 7.5

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 3

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 8000

#### **1.18.16 Comet**

Comet overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 10

[Phenology].PpSensitivity.FixedValue = 7.5

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 3

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 8000

#### **1.18.17 Wizard**

Wizard overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 10

[Phenology].PpSensitivity.FixedValue = 7.5

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 3

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 8000

### **1.18.18 Bond**

Bond overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].VrnSensitivity.FixedValue = 10

[Phenology].PpSensitivity.FixedValue = 7.5

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 3

[Phenology].EarlyReproductiveLongDayBase.FixedValue = 3

[Structure].Phyllochron.BasePhyllochron.FixedValue = 90

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 8000

### **1.19 MortalityRate**

MortalityRate = 0

## **2 Validation**

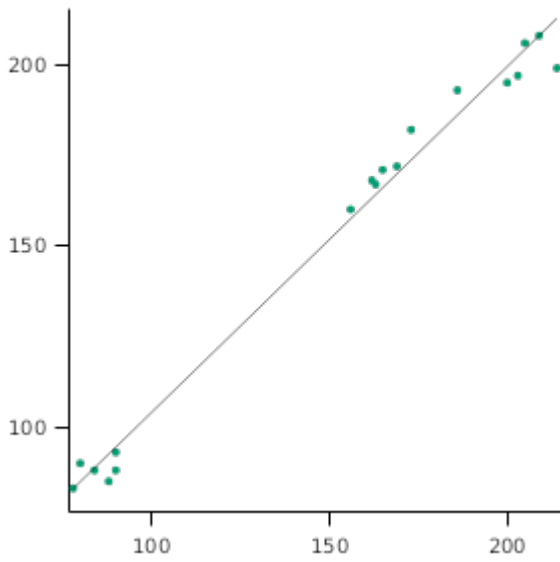
A test dataset has been developed to test the APSIM Oats model for a range of environmental (soil and climate) conditions, management options (sowing dates, populations, nitrogen rates, row spacing, irrigation), genetic backgrounds (different regions, cultivar types) and for special considerations such as defoliation (or simulated grazing). These tests have been grouped into various geographical regions to allow the user to evaluate the suitability of the model for their particular region of interest. Graphs of model performance are provided for yield, biomass production, canopy development, phenological development, water and nitrogen uptake, and grain yield components.



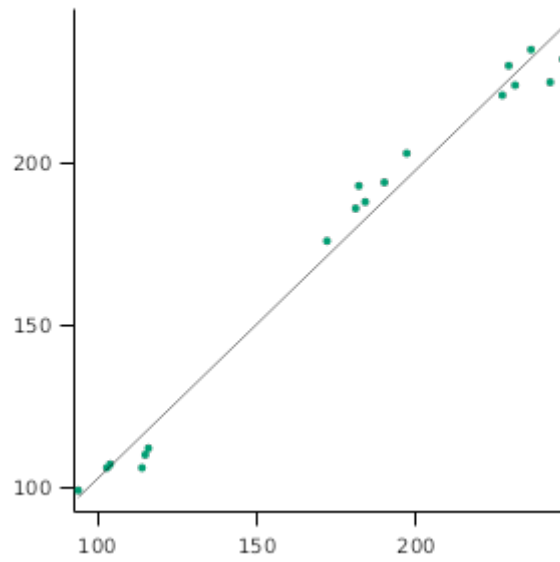
## 2.1 Combined Results

Simulation results for the combined datasets from the various countries are shown in the following graphs. The model is able to adequately capture the influence of growing conditions (soil, climate) and management (population, Nitrogen, irrigation, sowing date).

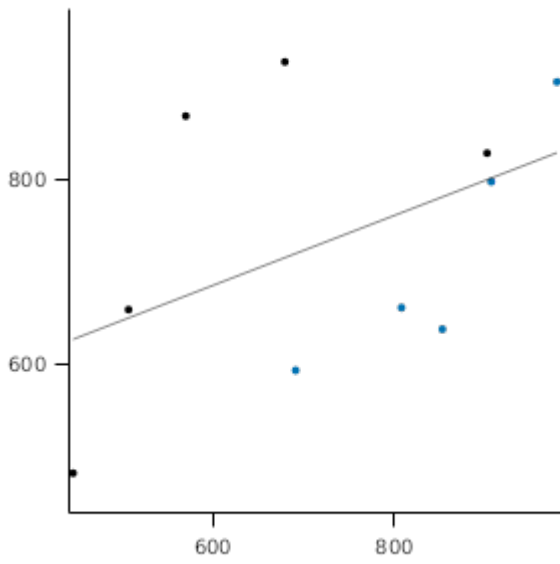
**FlagLeaf Prediction**



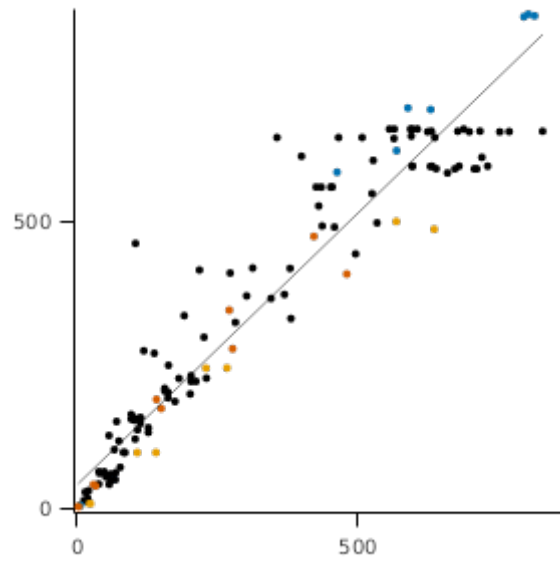
**Flowering Prediction**



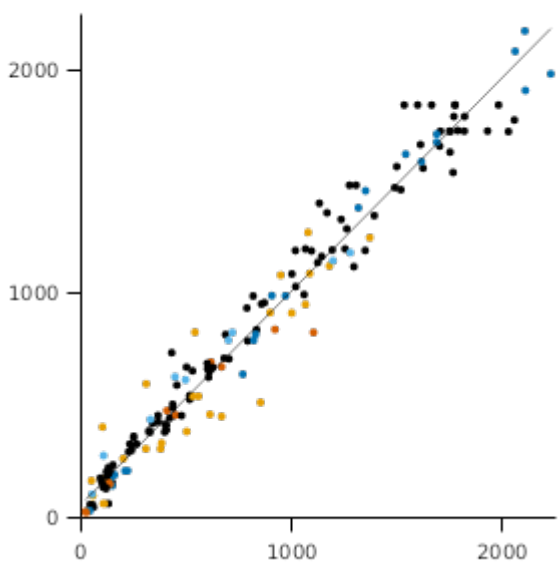
**Harvest Grain Weight**



**Stem Weight**



**Biomass**



## 2.2 New Zealand

List of experiments.

Experiment Name	Design (Number of Treatments)
RS_Oats_9899	_Irrig (5)
WinterSowing2015	Sow x Fert (4)
WinterSowing2016	Sow x Fert (2)
CPT	Sow x Cult (18)
RS_Oats_1718	Nit x Irr (6)

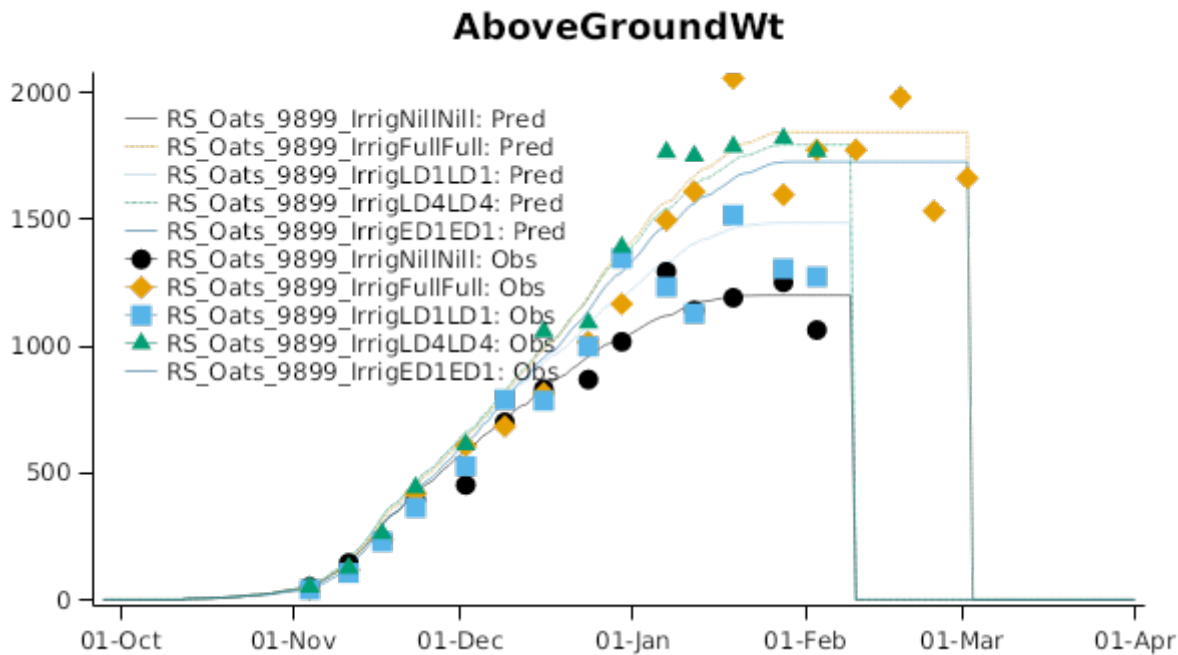
### 2.2.1 RS\_Oats\_9899

Data from:

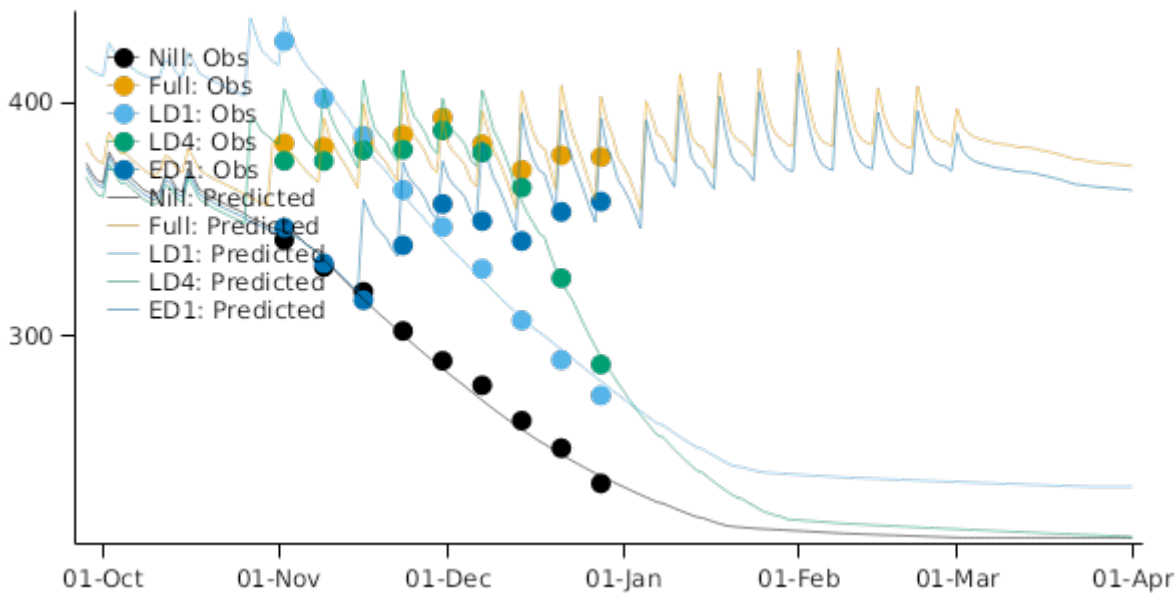
[Martin et al., 2001](#)

The response of oats (*Avena sativa* L.) to timing and intensity of drought was determined in a mobile

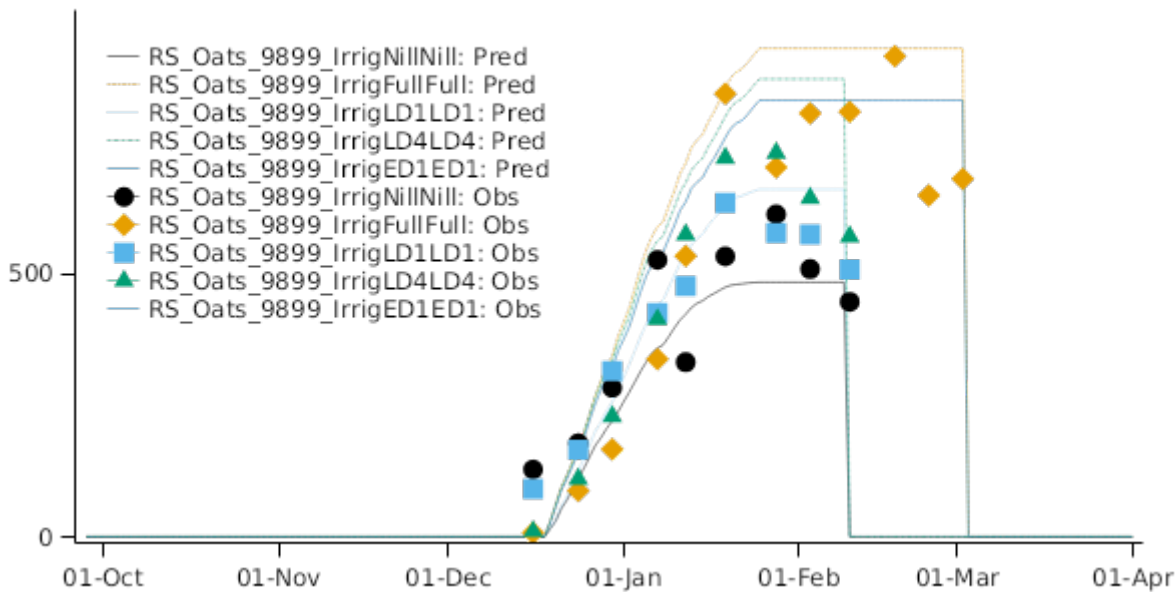
rainshelter, which excluded rainfall during crop growth. Ten irrigation treatments subjected the crops to drought of varying duration at different stages during plant growth; the crops were otherwise fully irrigated. Oat grain yield generally increased linearly with cumulative water use, and decreased linearly as the maximum potential soil moisture deficit experienced during crop growth increased, regardless of the timing of drought. The exception to this was the no drought (fully irrigated) treatment, where lodging reduced panicle number and grain weight compared to early drought treatments. Drought affected yield mainly by reducing panicle and grain number, effects on grain weight were small. . Relieving early drought through late irrigation led to more late tillers, more panicles, heavier grains, and later maturity. Full and late drought increased screenings.



## Water Profile



## Grain



### 2.2.2 WinterSowing2015

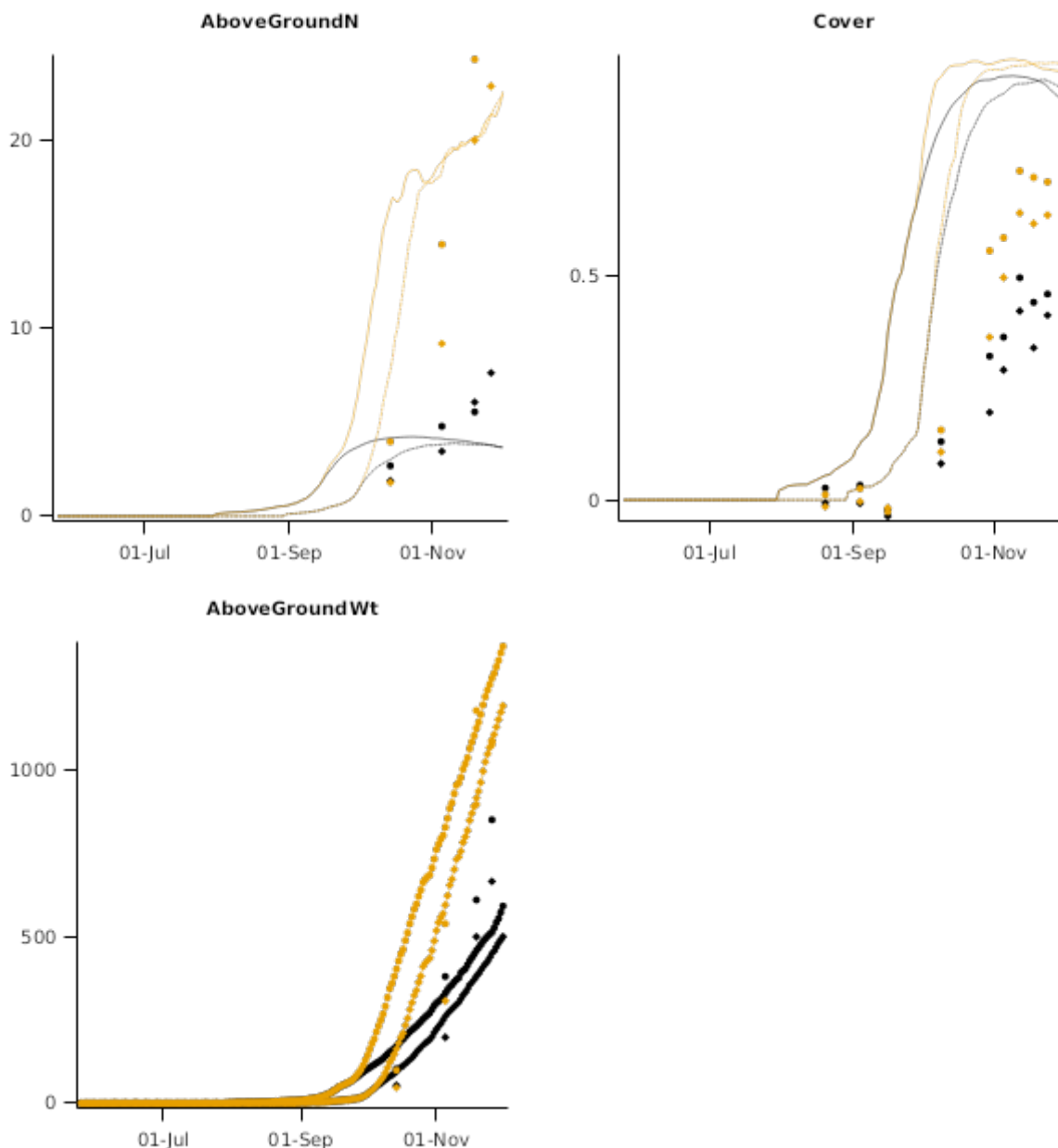
FRNL Experiment: Data from [Malcolm et al., 2016](#)

Note: the 2015 version of this experiment established inconsistently and data is not of the same quality as that generated in 2016.

Grazing winter forage crops is an important management strategy for profitable livestock production in many New Zealand regions where there is commonly a pasture feed deficit during this period. However, the high stocking densities that are often associated with these systems can have negative environmental effects, such as nitrogen (N) leaching losses to groundwater. This field study investigated the potential biomass production and reduced risk of N leaching from establishing oats (*Avena sativa* L.) as a green-chop catch crop after winter-grazed forage kale (*Brassica oleracea* var. *acephala* L.) in Canterbury, New Zealand. Oat crops were direct-drilled on two sowing dates (early: 1 July 2015 and late: 1 August 2015) and were managed under high (400 kg N/ha) and low (0 kg N/ha) N load conditions, representing urine-patch and inter urine-patch areas. For the early-sown crops yields were 6.1 (low N) and 11.8 t DM/ha (high N) at final harvest (50% ear emergence) on 19 November 2015. For the late-sown crops yields were 6.7 (low N) and 10.1 t DM/ha (high N) at the same development stage (26 November 2015). By establishing oats as a catch crop in winter soil profile mineral-N (0-120 cm depth) was reduced by up to 86% (early) and 80% (late) in the high N (simulated urine-patch) treatments compared with the respective fallow treatment. These results indicated the technical feasibility of direct drilling oats as catch crops immediately after winter forage grazing, with likely production and environmental benefits such as the reduced risk of N leaching losses.



### 2.2.2.1 Graphs

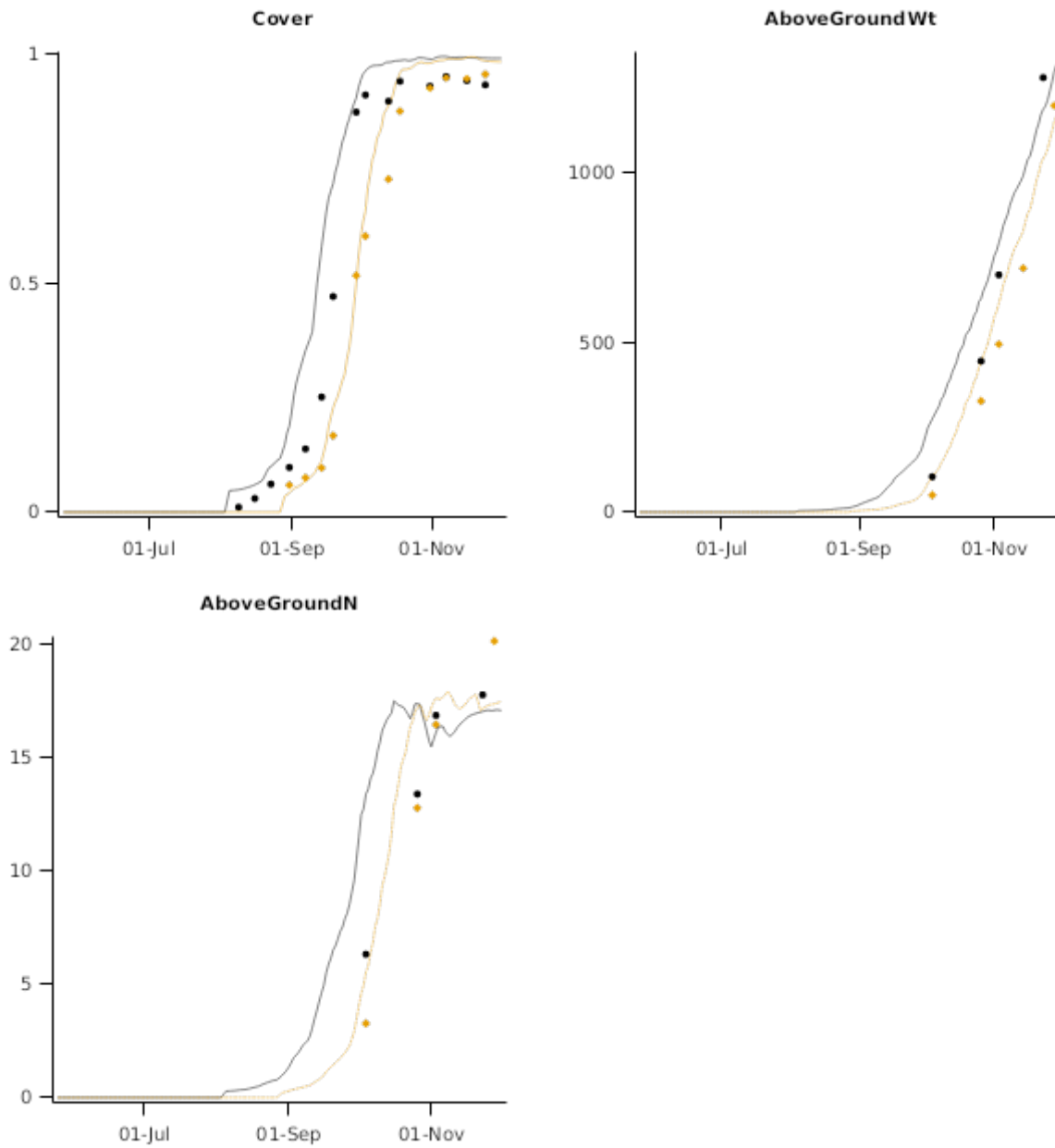


### 2.2.3 WinterSowing2016

FRNL Experiment: Data from [Malcolm et al., 2016](#)

Grazing winter forage crops is an important management strategy for profitable livestock production in many New Zealand regions where there is commonly a pasture feed deficit during this period. However, the high stocking densities that are often associated with these systems can have negative environmental effects, such as nitrogen (N) leaching losses to groundwater. This field study investigated the potential biomass production and reduced risk of N leaching from establishing oats (*Avena sativa* L.) as a green-chop catch crop after winter-grazed forage kale (*Brassica oleracea* var. *acephala* L.) in Canterbury, New Zealand. Oat crops were direct-drilled on two sowing dates (early: 1 July 2015 and late: 1 August 2015) and were managed under high (400 kg N/ha) and low (0 kg N/ha) N load conditions, representing urine-patch and inter urine-patch areas. For the early-sown crops yields were 6.1 (low N) and 11.8 t DM/ha (high N) at final harvest (50% ear emergence) on 19 November 2015. For the late-sown crops yields were 6.7 (low N) and 10.1 t DM/ha (high N) at the same development stage (26 November 2015). By establishing oats as a catch crop in winter soil profile mineral-N (0-120 cm depth) was reduced by up to 86% (early) and 80% (late) in the high N (simulated urine-patch) treatments compared with the respective fallow treatment. These results indicated the technical feasibility of direct drilling oats as catch crops immediately after winter forage grazing, with likely production and environmental benefits such as the reduced risk of N leaching losses.

#### 2.2.3.1 Graphs

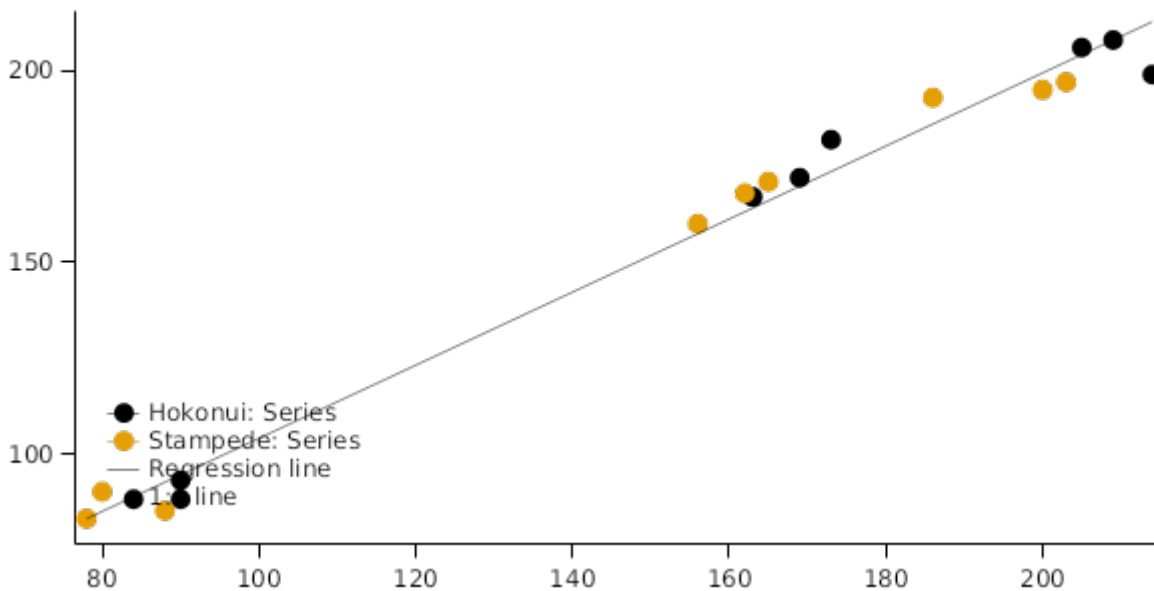


## 2.2.4 CPT

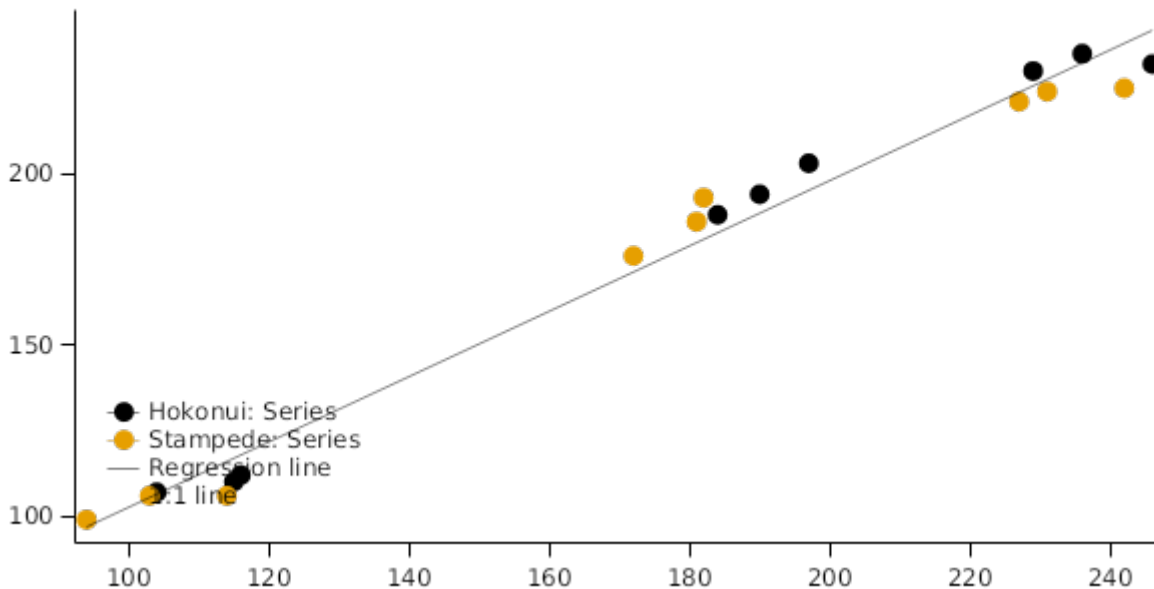
Jamieson, P. D. and C. A. Munro (1999). A simple method for the phenological evaluation of new cereal cultivars. *Agronomy Society of New Zealand - Proceedings, Twenty-Ninth Annual Conference, 1999*. J. G. Hampton and K. M. Pollock. 29: 63-68.

This experiment is part of the ongoing Cultivar Prediction Trial at Plant & Food Lincoln when a Cultivar is planted at 3 sowing dates throughout the year and the time of flowering, Final leaf number and Flag leaf are recorded.

## FlagLeaf Prediction



## Flowering Prediction



### 2.2.5 RS\_Oats\_1718

#Experiment description

#### 2.2.5.1 Introduction

This is a simulation of Oats in a crop rotation consisting of a forage species, fodder beet, grown over spring/summer and harvested in autumn, followed by the catch crop, oats. The actual experiment was done in two parts in the rain shelter facility of Plant and Food Research, Lincoln, NZ. The experiments were designed to help develop the model for the respective plants and here they are used to further demonstrate that ApsimX can simulate water and nitrogen cycling in the field and then to examine whether catch crops are a good option for mitigating N leaching from forages.

Part 1: Co-limitation of water and nitrogen on fodder beet physiology (no detail supplied for this experiment as it is not simulated herein)

Part 2: Ability of oats to act as catch-crops over winter/spring

- Irrigation: 2 treatments, low (enough to keep plants growing) or full irrigation (to match PET)
- Nitrogen: 3 treatments, 80 kg N/ha, 125 kg N/ha & 320 kg N/ha at sowing (urea applied at sowing)

Oats Experiment Management:

- Cultivar: Milton

- Sowing density: 300 plants/m<sup>2</sup>  
row spacing: 15 cm  
depth: 45 mm

General actions:

05/07/2017 - Sowing

05/07/2017 - Fertiliser application (400kg/ha Potash, Urea: treat4=80kgN/ha, treat5=125kgN/ha, treat6=320kgN/ha)

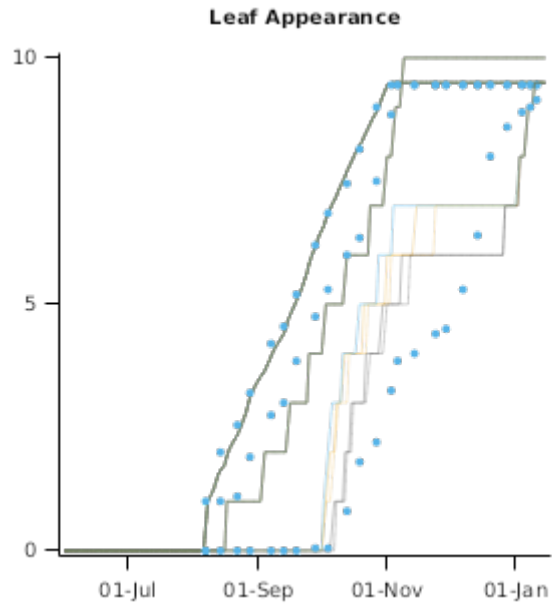
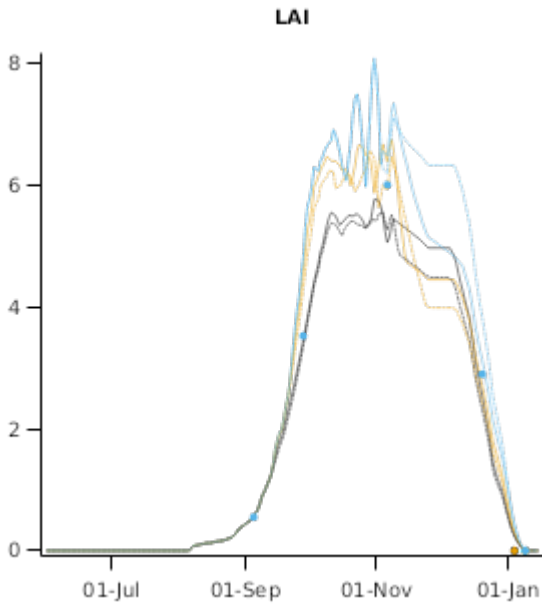
24/07/2017 - Plants started to emerge

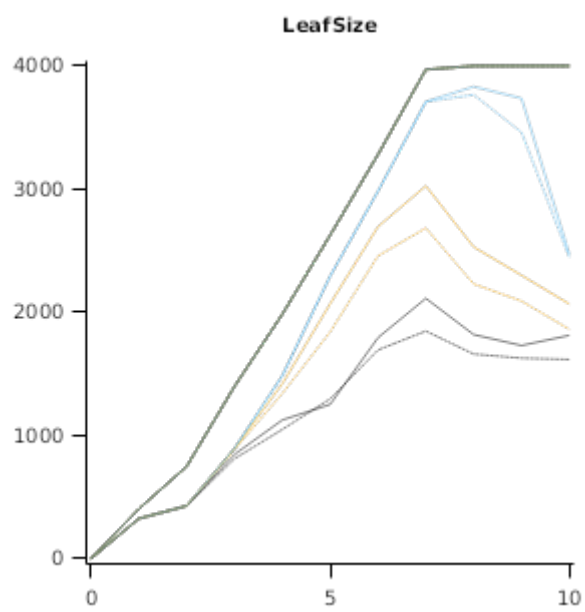
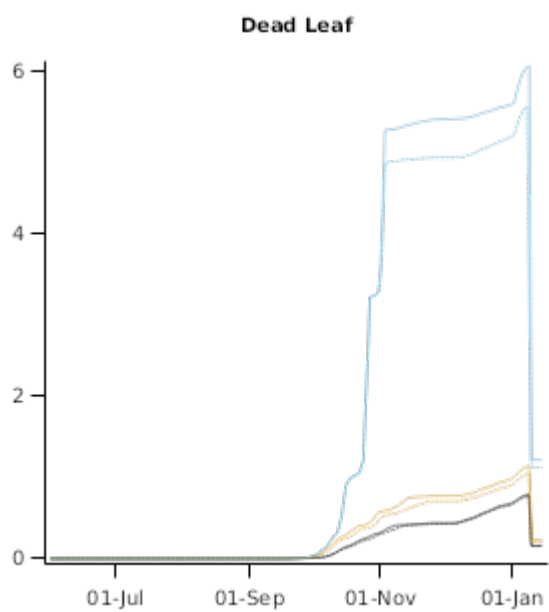
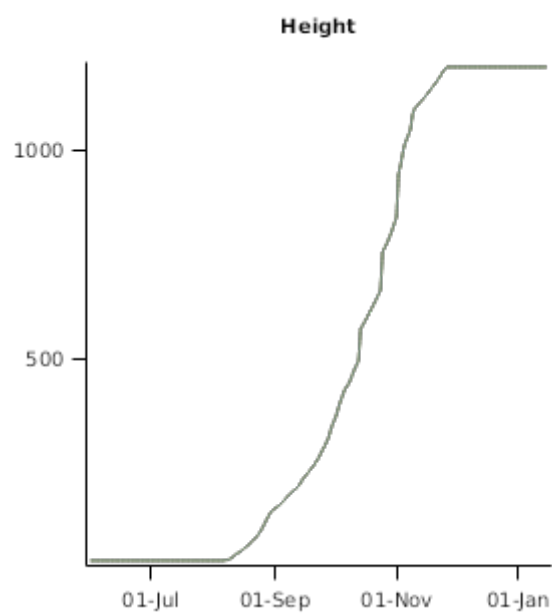
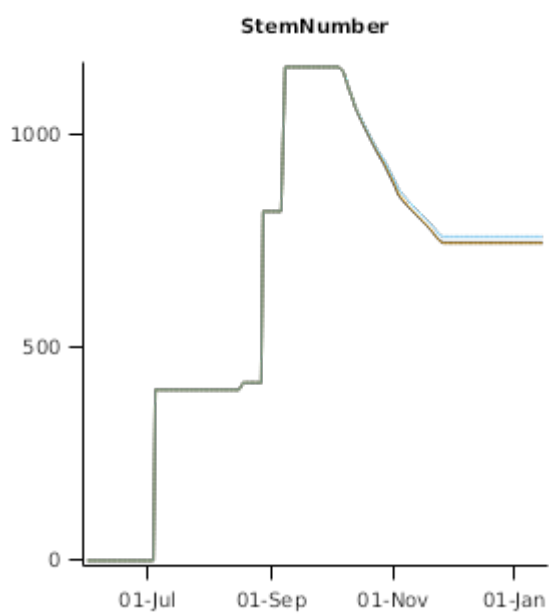
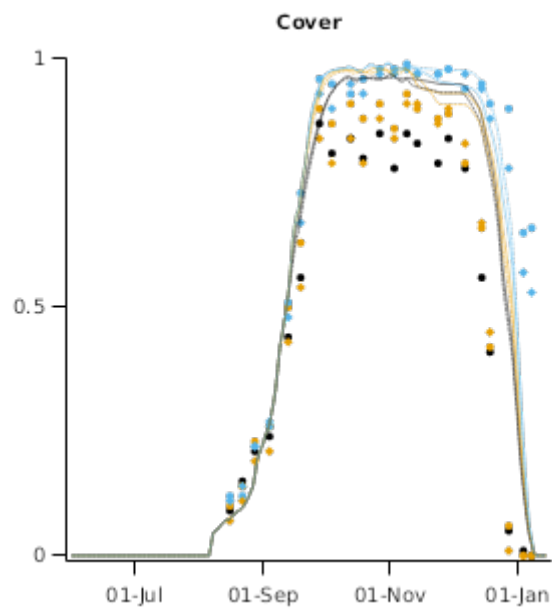
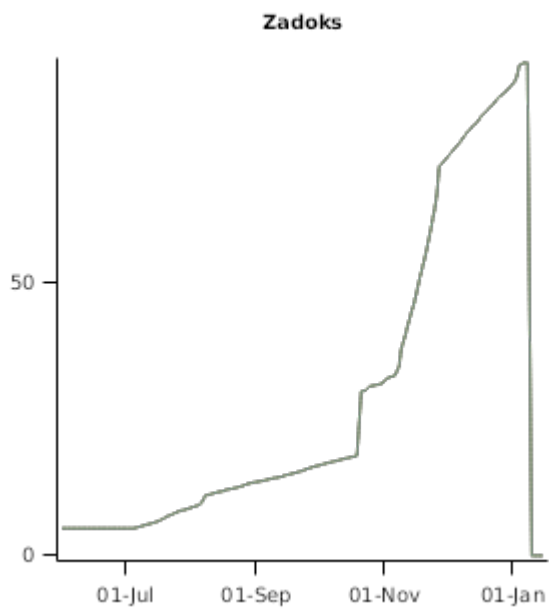
11/09/2017 - Irrigation started in treatments 4, 5, and 6

06/11/2017 - Irrigation extended to all plots

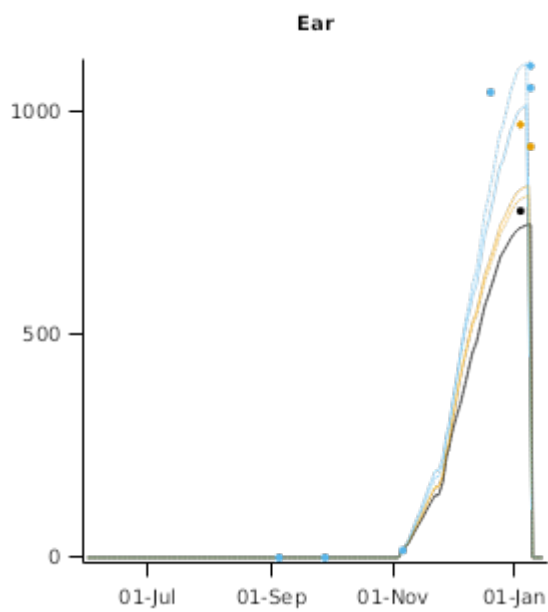
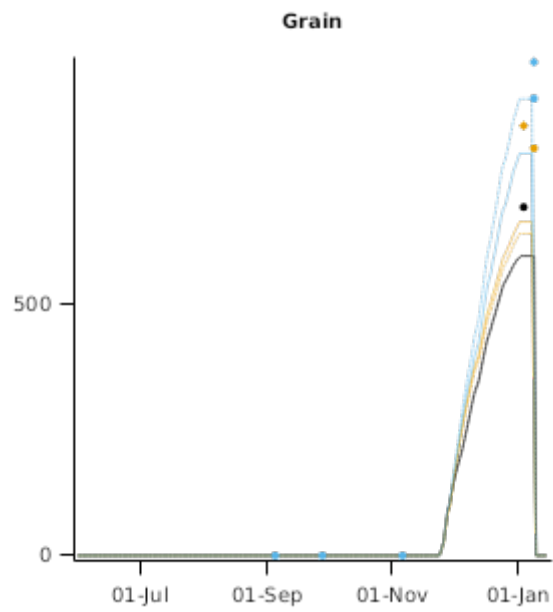
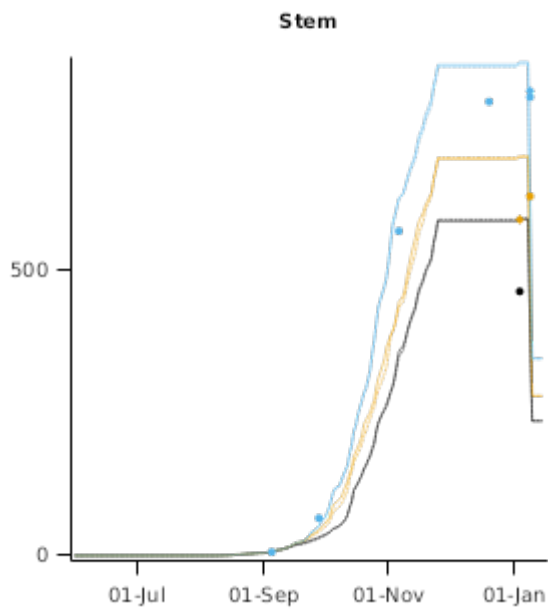
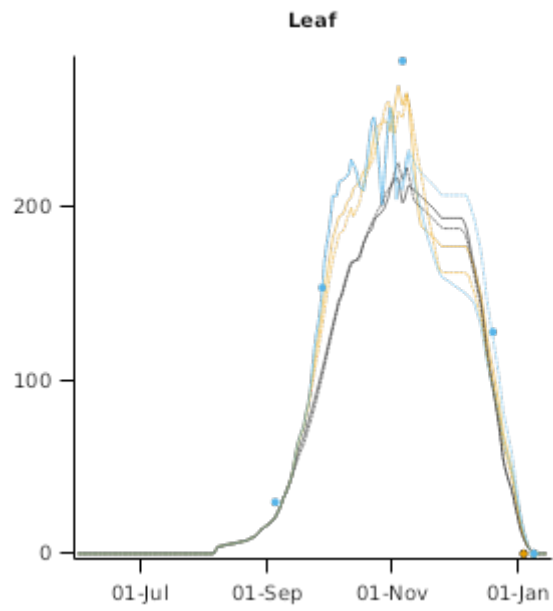
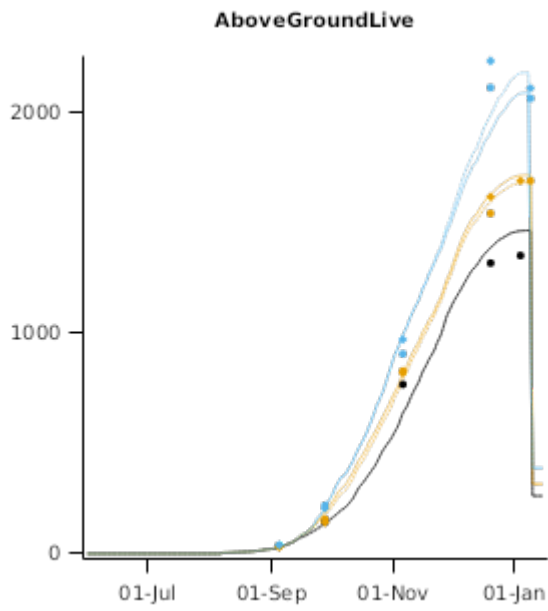
04-09/01/2018 - Plots harvested

### 2.2.5.2 Canopy



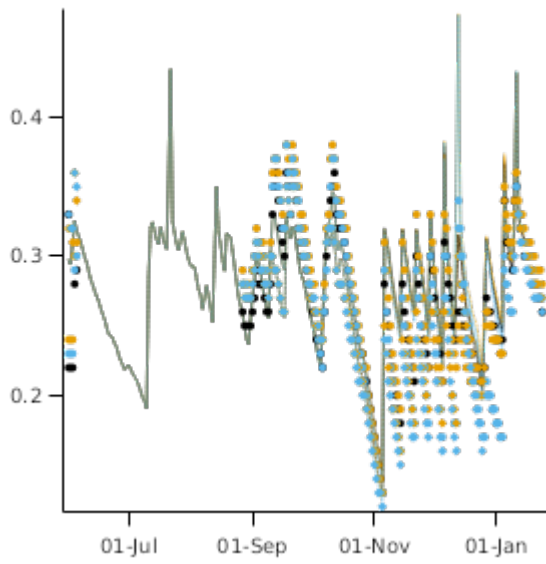


### 2.2.5.3 Biomass

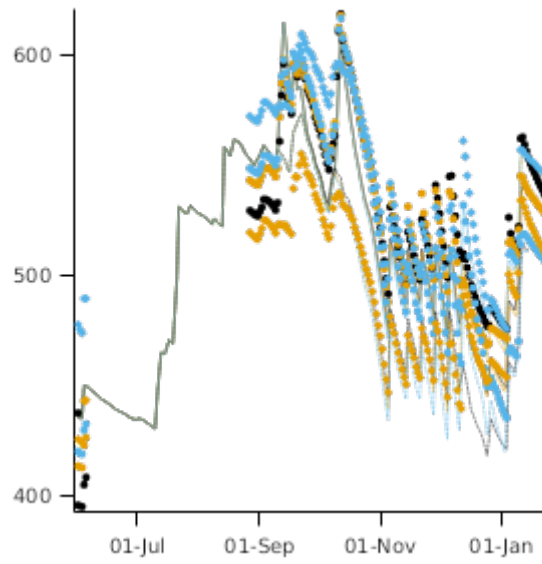


#### 2.2.5.4 SoilOutputs

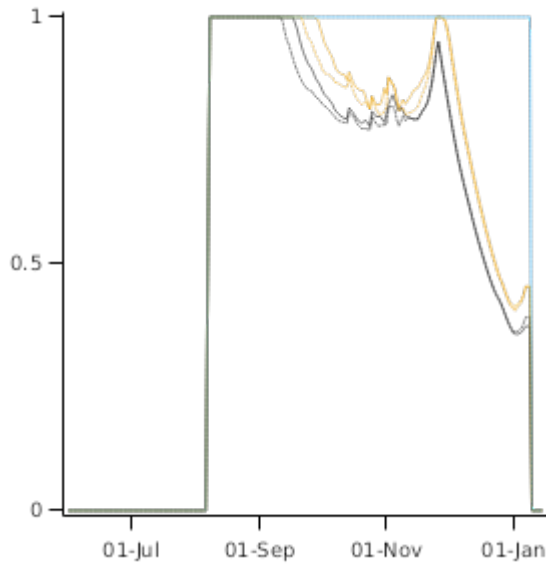
**SWC\_L1**



**ProfileWater**

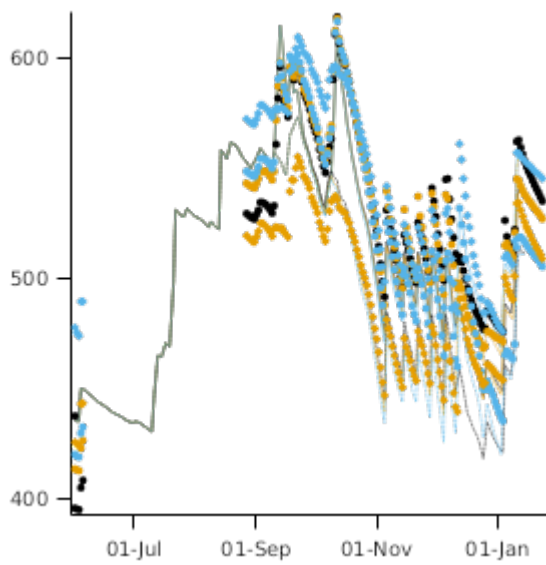


**Fn**

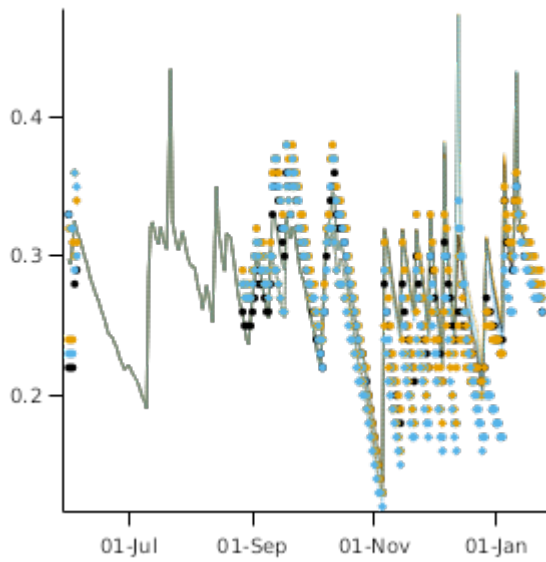
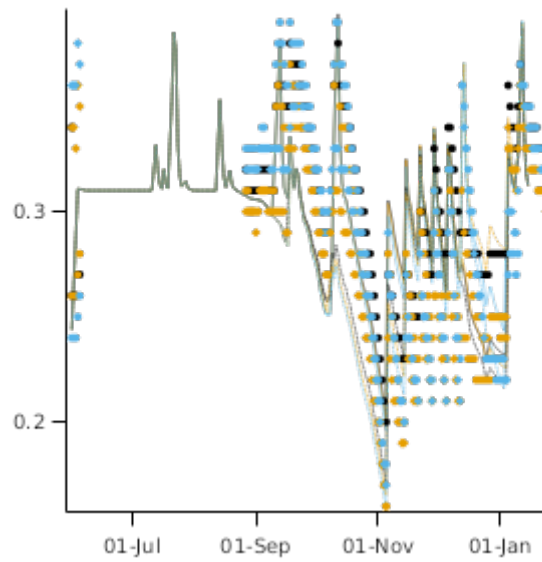
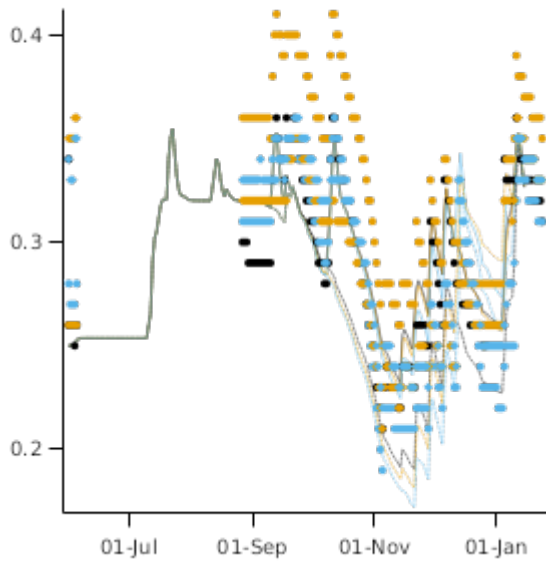
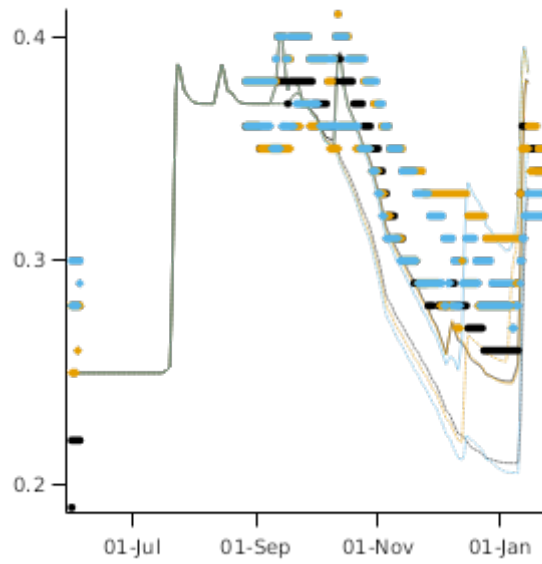
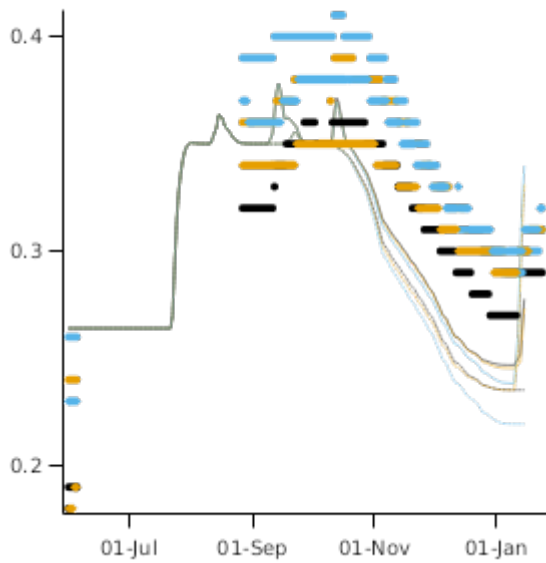
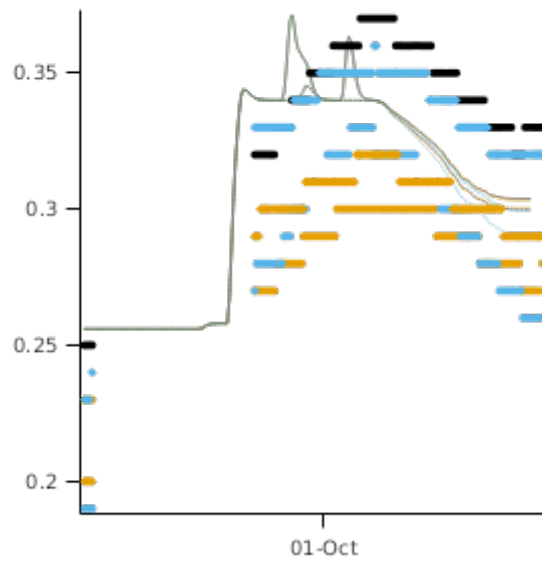


**2.2.5.4.1 Water**

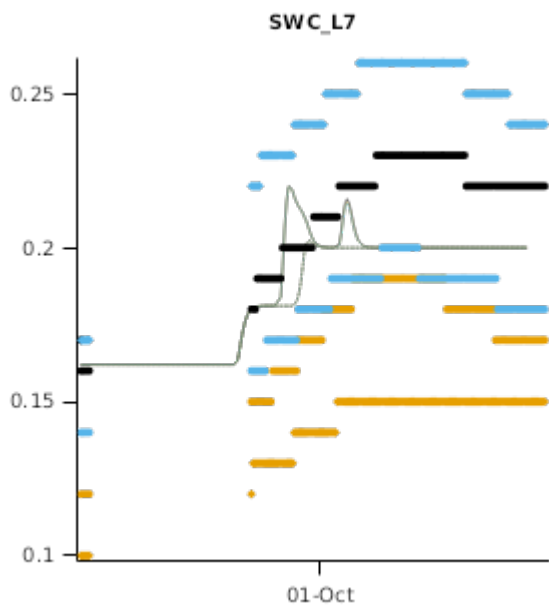
**ProfileWater**



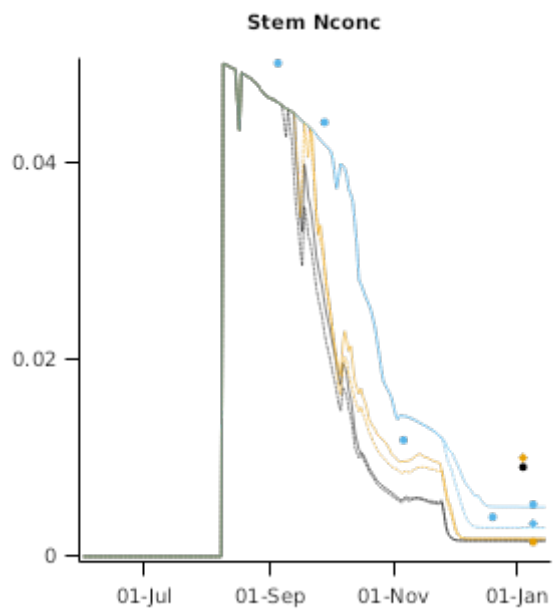
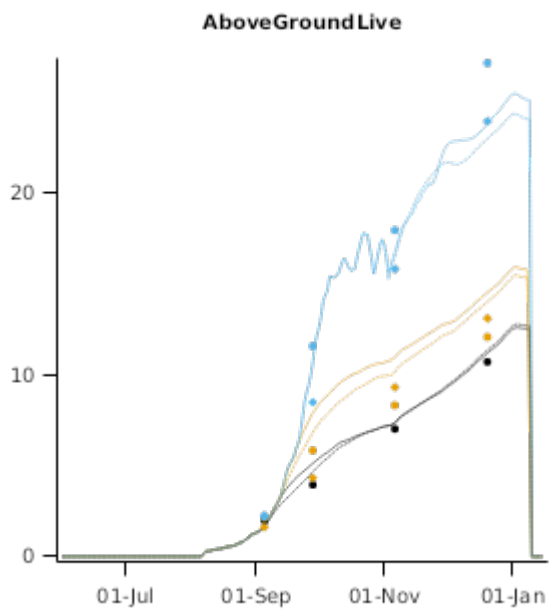
**2.2.5.4.1.1 SWC**

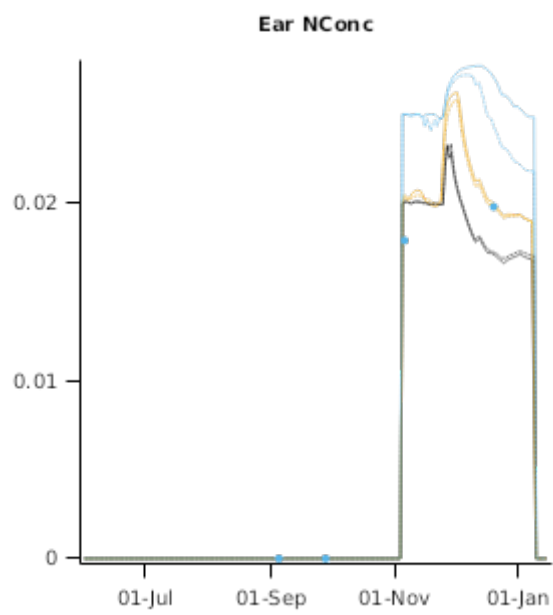
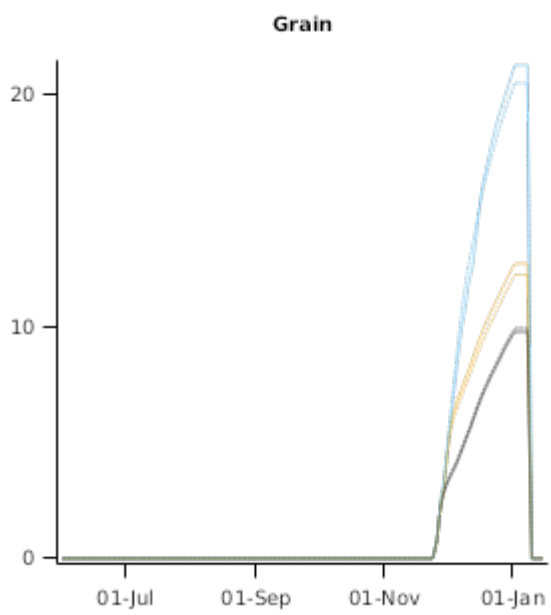
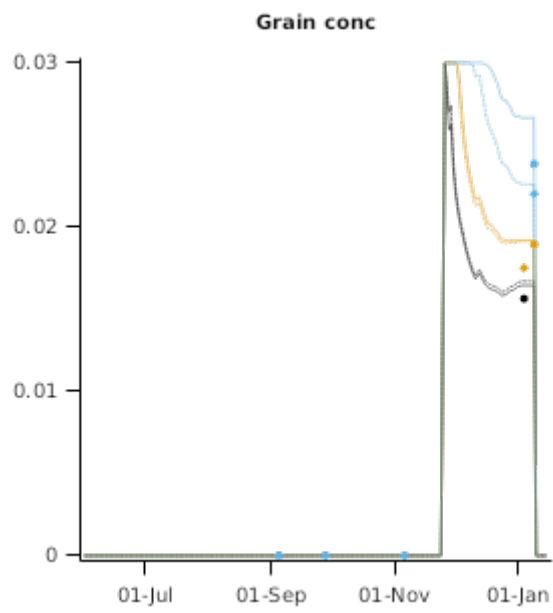
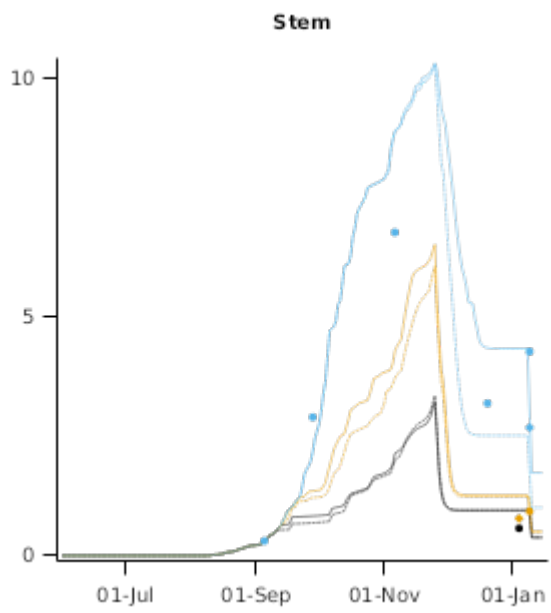
**SWC\_L1****SWC\_L2****SWC\_L3****SWC\_L4****SWC\_L5****SWC\_L6**

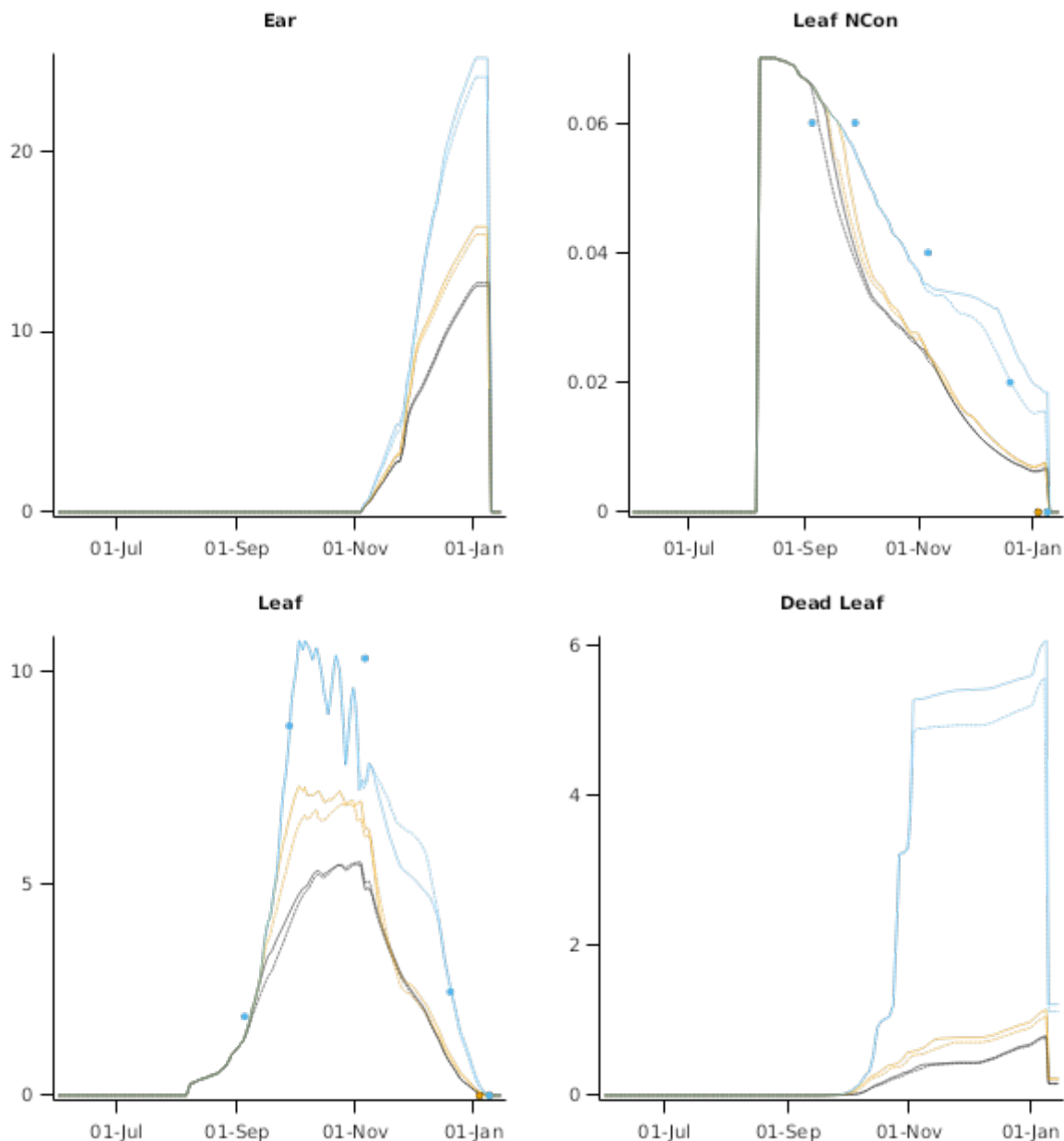




### 2.2.5.5 Nitrogen







## 2.3 Australia

The Oats model construction for Australian varieties was based primarily around the experiment at Gatton in 2007. Supporting phenology data was collected at the Leslie Research Centre (LRC) and Wellcamp Research Station for northern varieties, data kindly supplied by Bruce Winter, Oats Breeder with DAFQ. The model was then extended to data sets at Roma in QLD, and also sites in South Australia (Tarlee, Pinery) where additional adjustments were made to the relevant varieties.

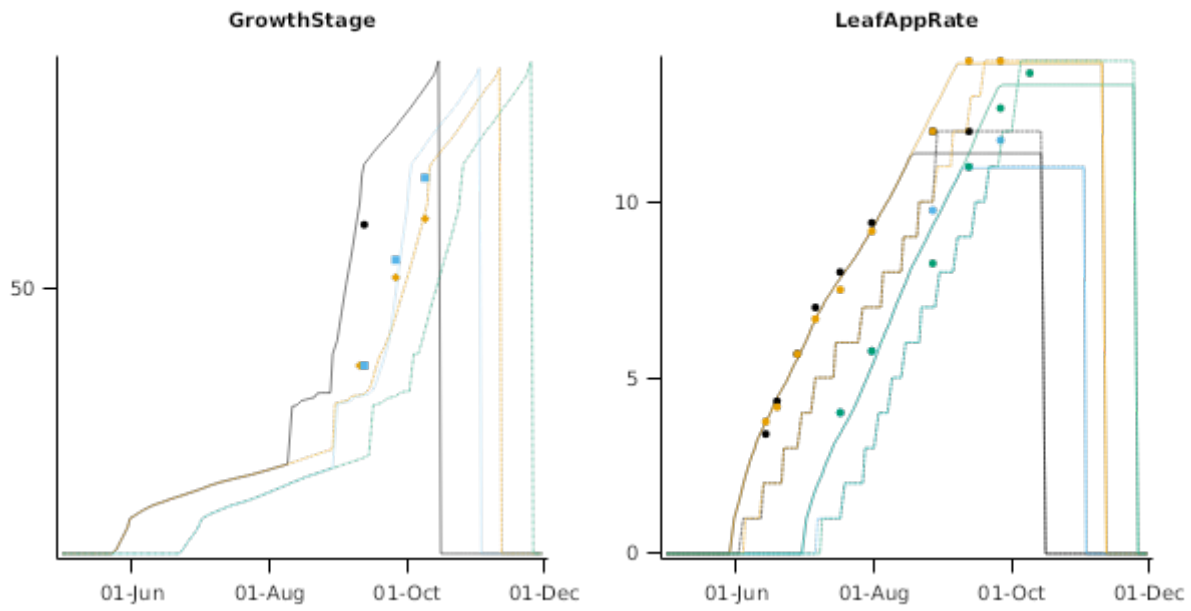
The Gatton, Roma, Tarlee, and Pinery experiments were used to construct the original APSIM Oats model and published at the Australian Agronomy Conference in 2008.

Peake A, Whitbread A, Davoren B, Braun J and Limpus, S. (2008). The development of a model in APSIM for the simulation of grazing oats and oaten hay. In: Global Issues, Paddock Action. Proceedings of the 14th ASA Conference, 21-25 September 2008, Adelaide, South Australia.

### 2.3.1 Gatton2007

This experiment comprised an early and late sowing date, but full growth and soil water data was only collected for the early sowing date. The late sowing date was comprised of observation plots for phenology data collection only.

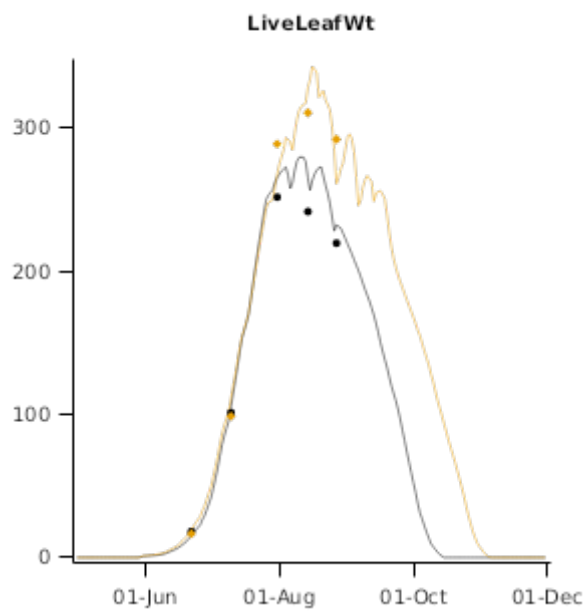
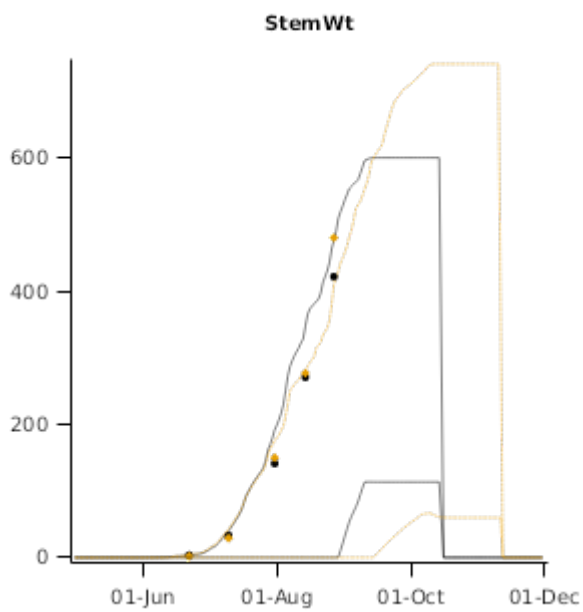
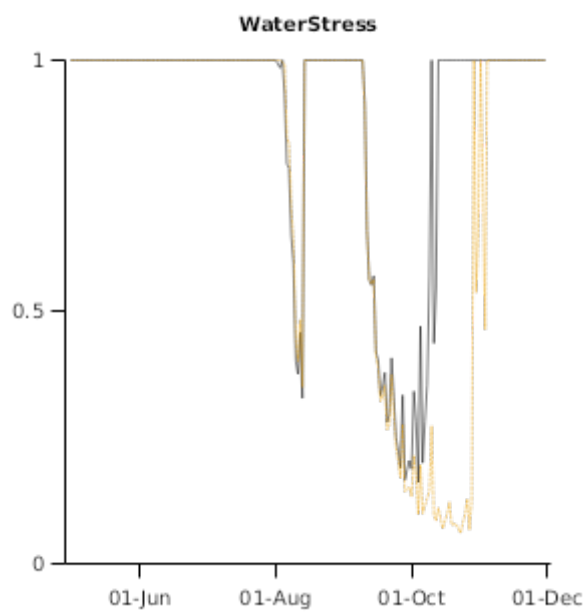
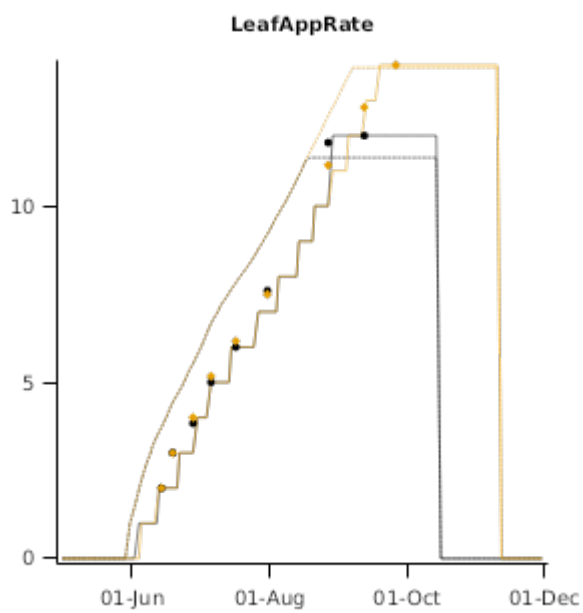
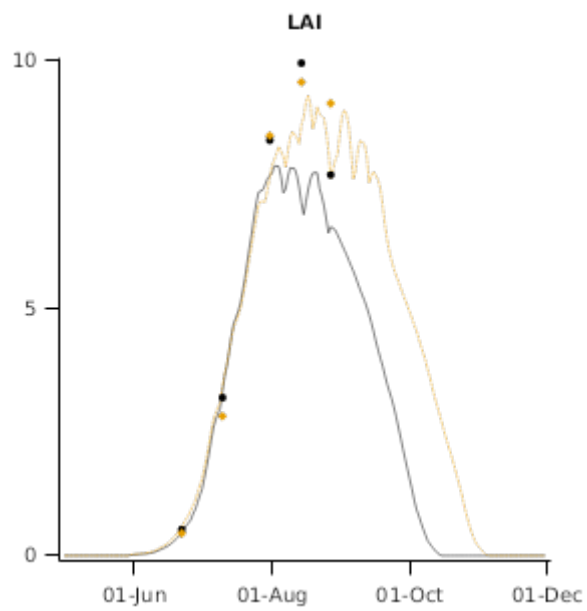
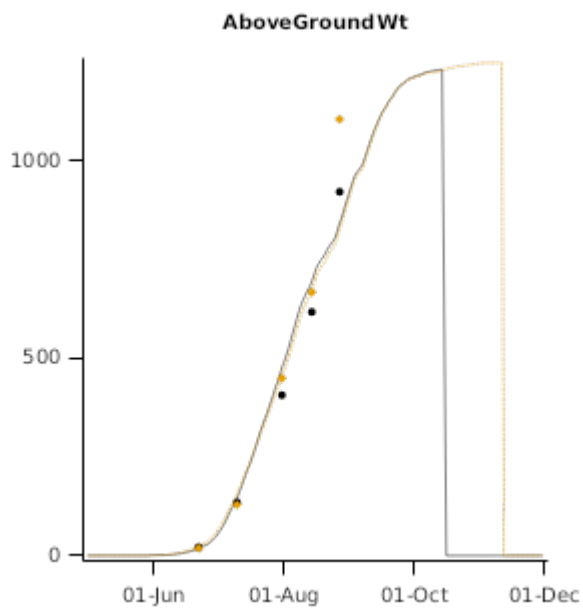
Extinction coefficient and 'kl' values were measured on the early sowing date in addition to partitioned biomass data. Note that the kl values measured and used to simulated this irrigated trial were high, and may not apply to many dryland situations. Other simulations in the Australian validation data sets used the traditional wheat kl values for dryland situations.

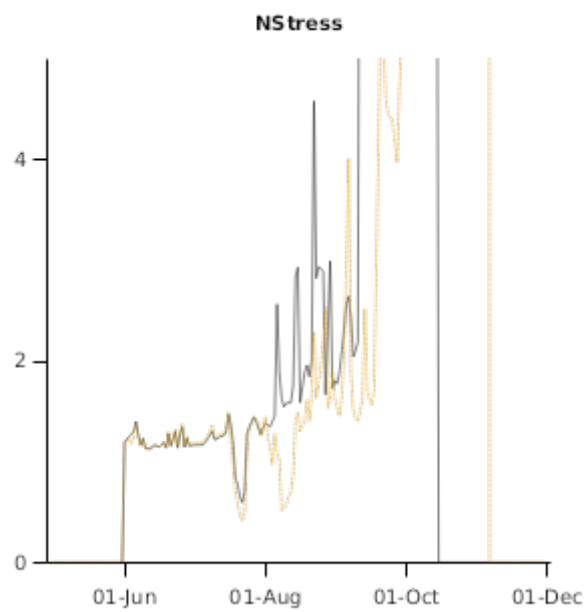
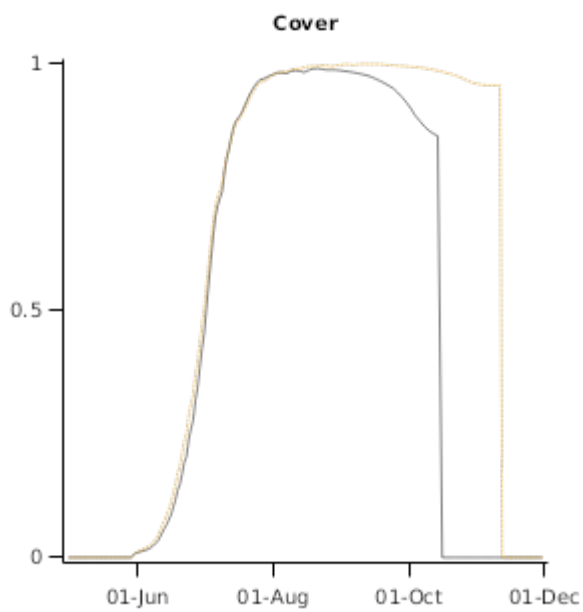
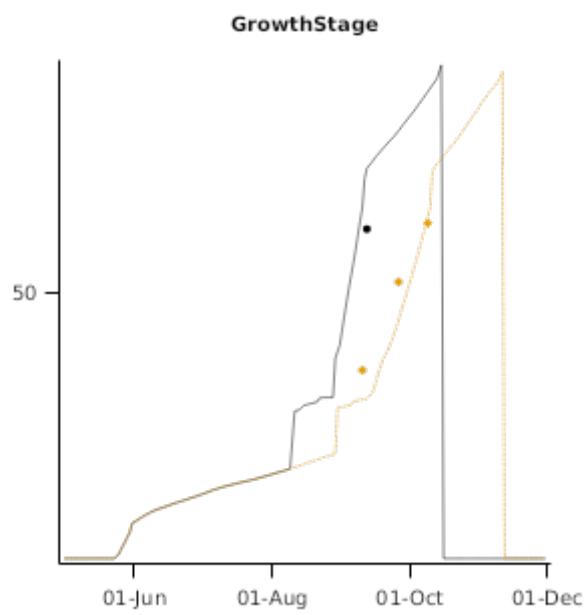
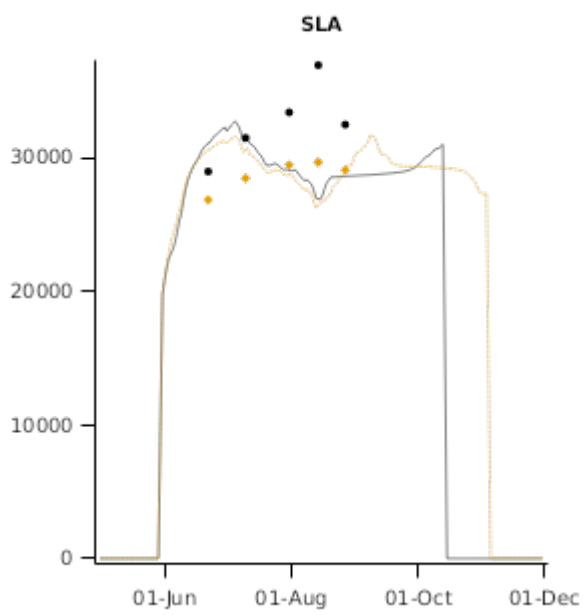
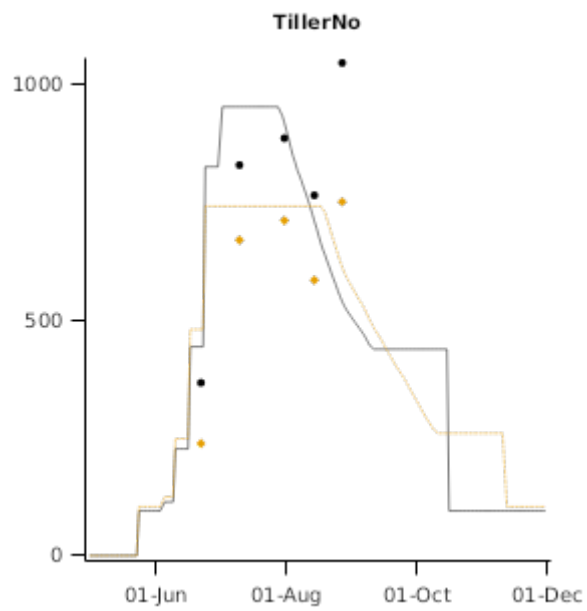
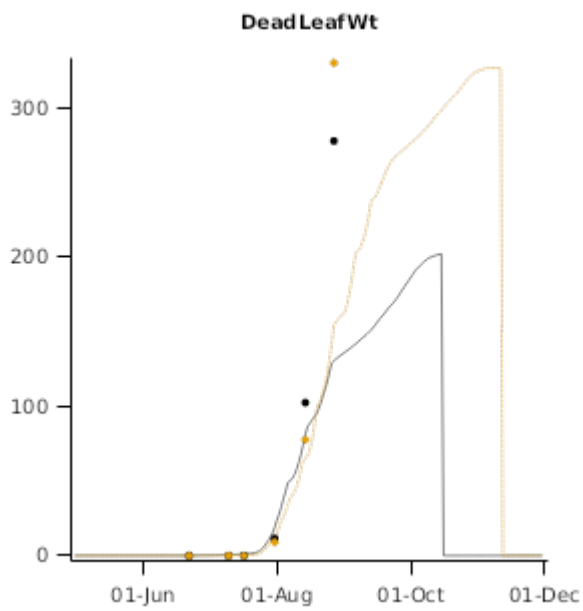


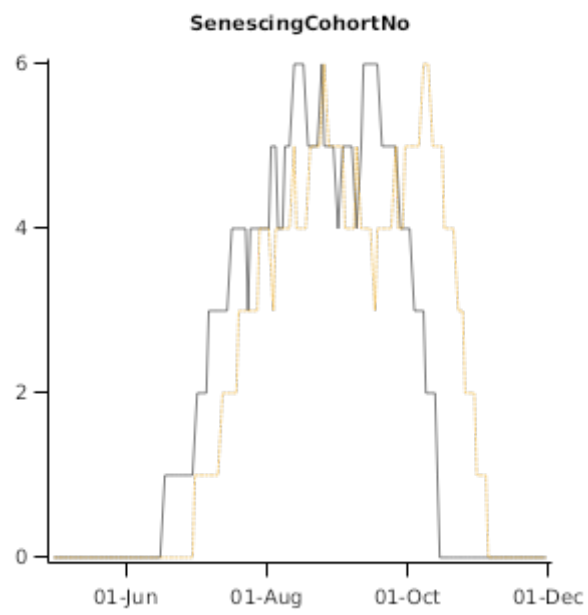
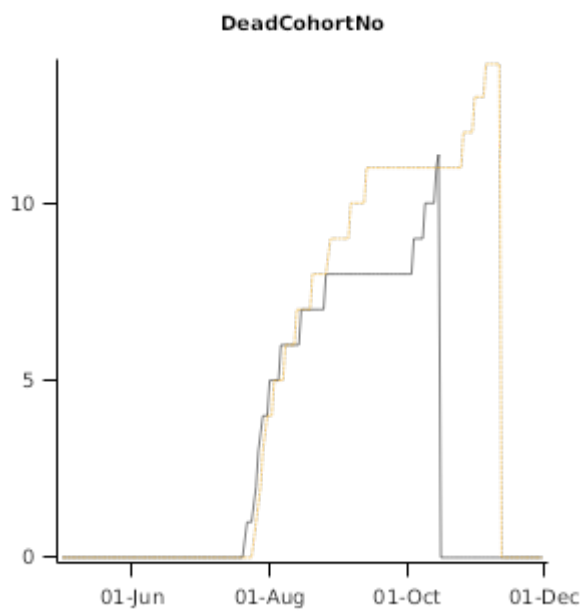
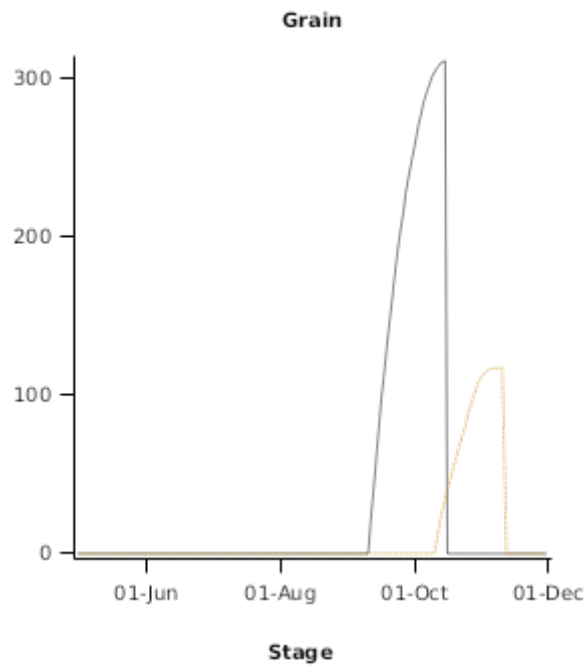
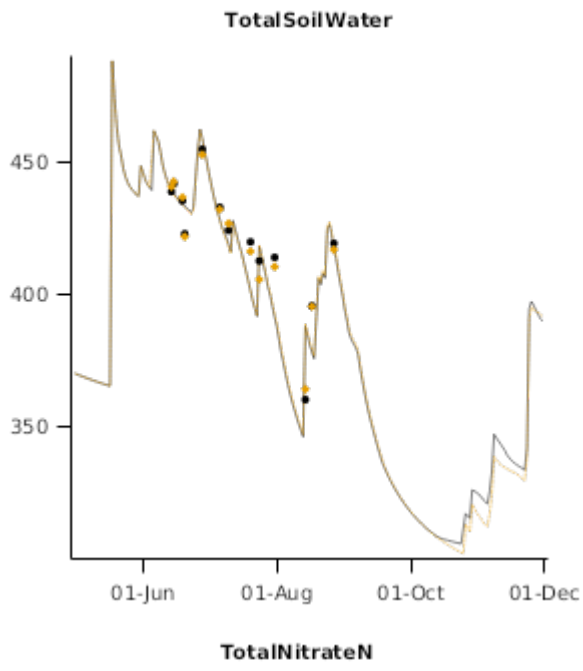
### 2.3.1.1 Gatton2007early

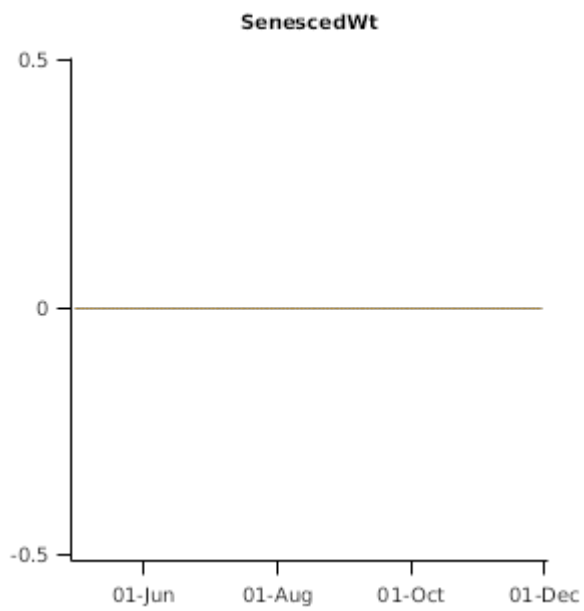
List of experiments.

Experiment Name	Design (Number of Treatments)
Gatton2007	Cv (2)

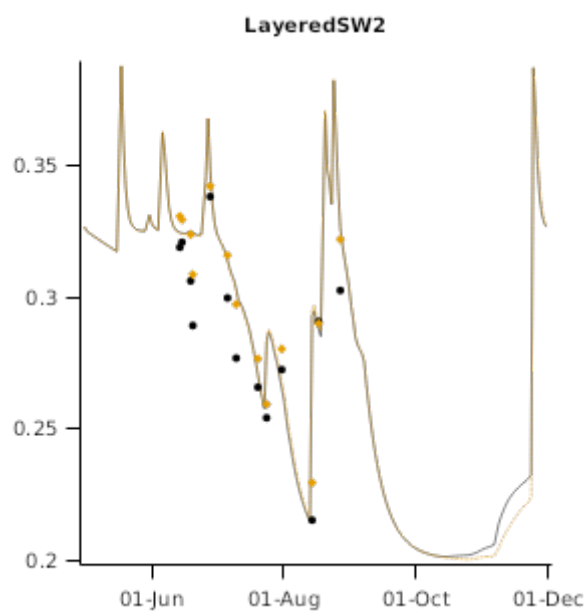
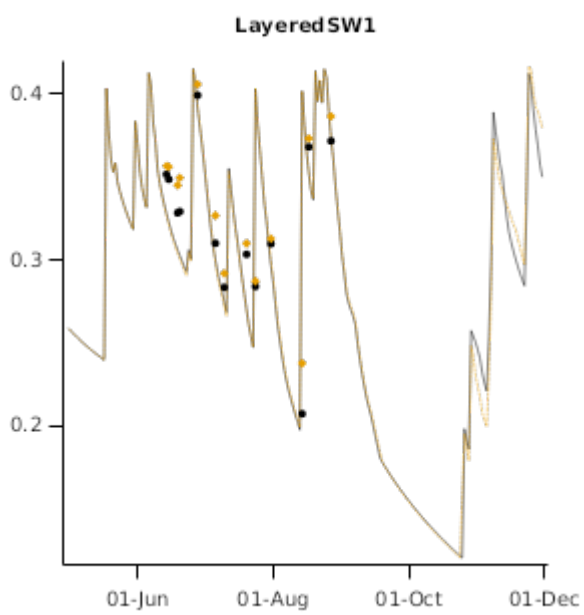




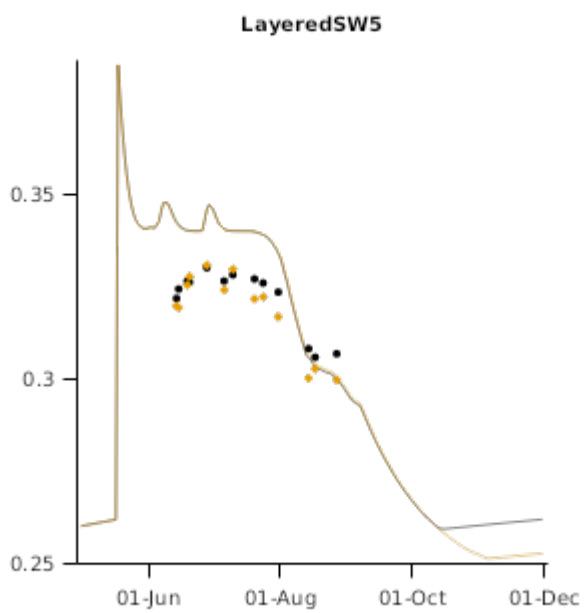
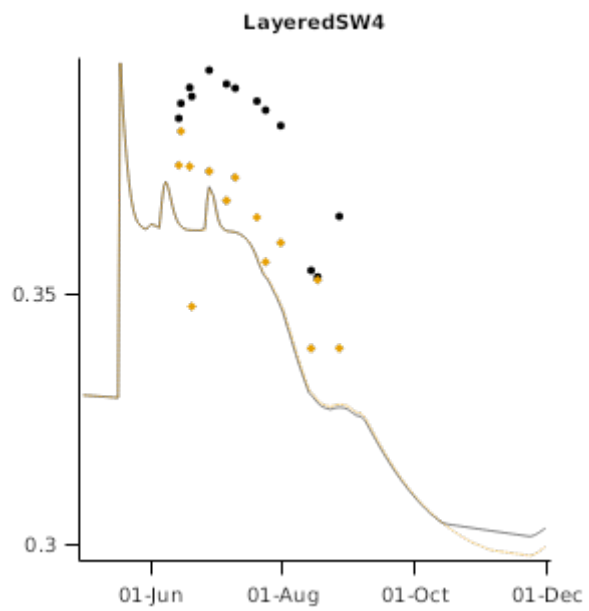
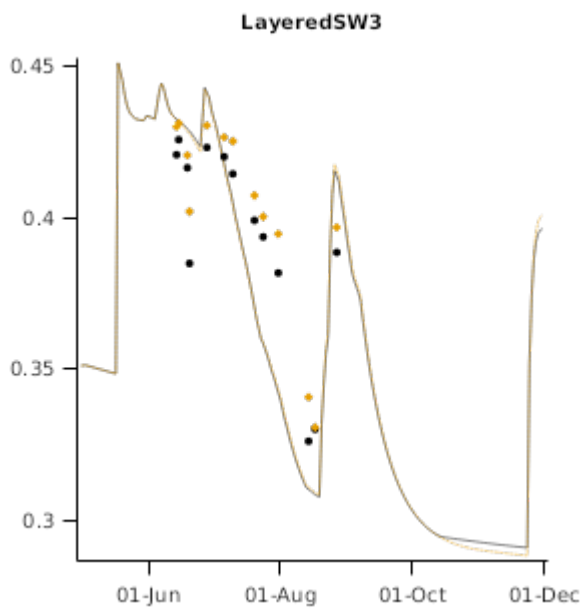




#### 2.3.1.1.1 Layered SW



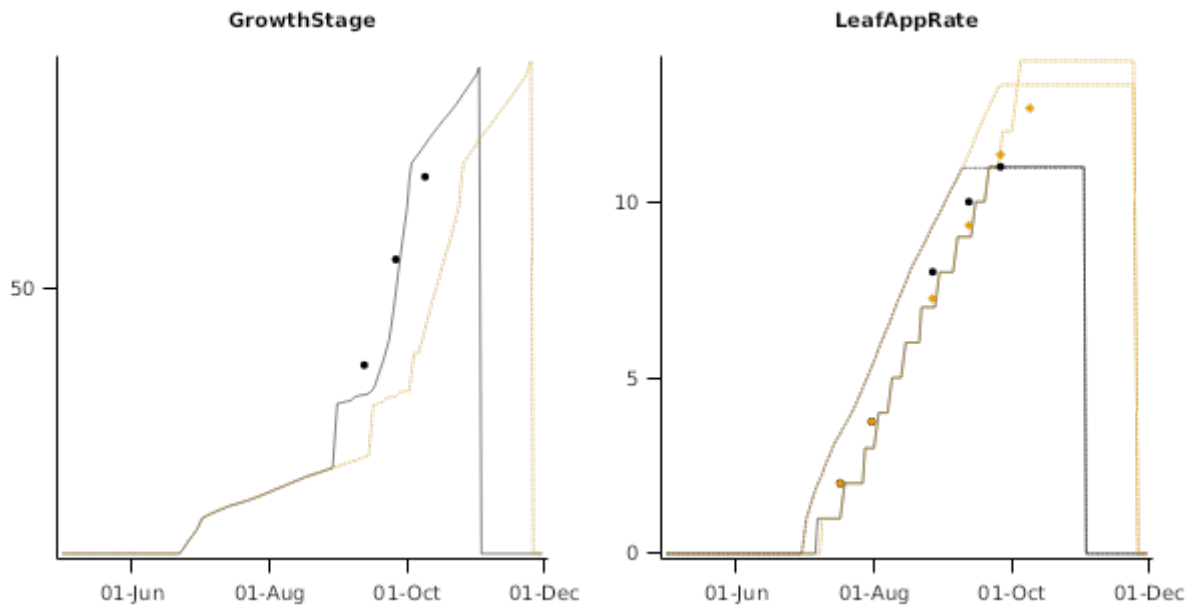




### 2.3.1.2 Gatton2007LATEsown

List of experiments.

Experiment Name	Design (Number of Treatments)
Gatton2007Late	Cv (2)



### 2.3.1.2.1 Gatton2007Late

The late sown experiment at Gatton in 2007 was comprised of observation plots of the two varieties used in the early sowing date. 4 plants were monitored for phenology (Leaf Appearance Rate and Zadoks stage) from each observation plot.

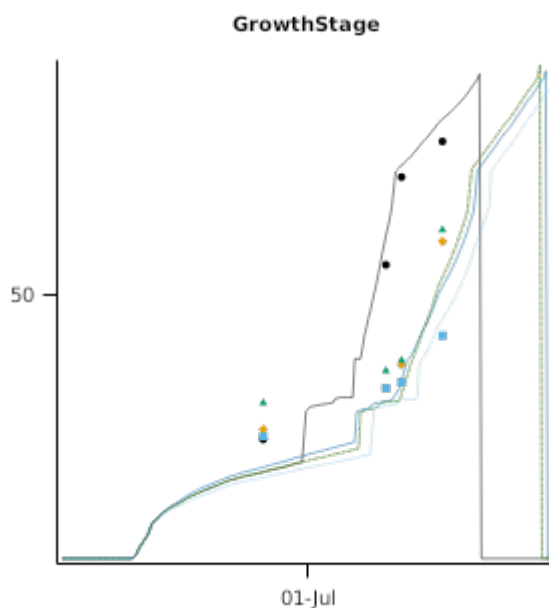
### 2.3.2 Wellcamp2006

This experiment was run at DPI Wellcamp Research Station, Queensland in 2006. Phenology data (Zadok stage) was the only data collected.

This experiment was a phenology experiment based on small and narrow observation plots (4 rows) in conjunction with a QDAF Oats breeding trial. The decision was taken to use a nearby SILO met-data set rather than the onsite weather station, due to the possibility that the onsite met station had not been calibrated for some time.

#### List of experiments.

Experiment Name	Design (Number of Treatments)
Wellcamp2006	Cv x Cut (15)



### 2.3.3 Roma2006

This experiment was run at Roma Research Station, Queensland in 2006. Two reps were used to generate cut and regrowth data (two cuts taken). The third rep was split in two, and one half was used to allow unlimited growth (no

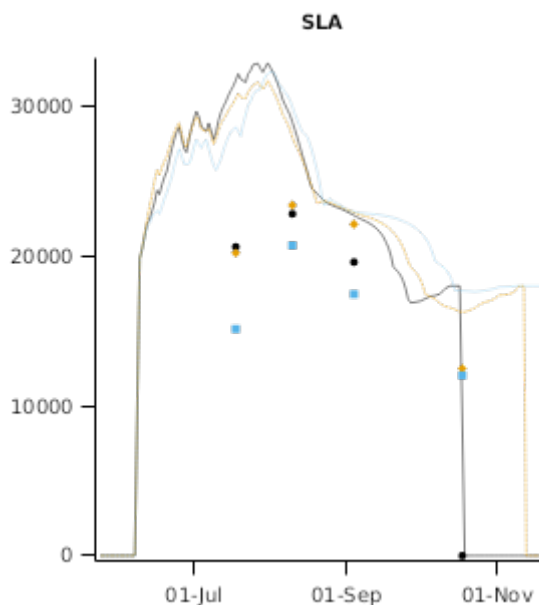
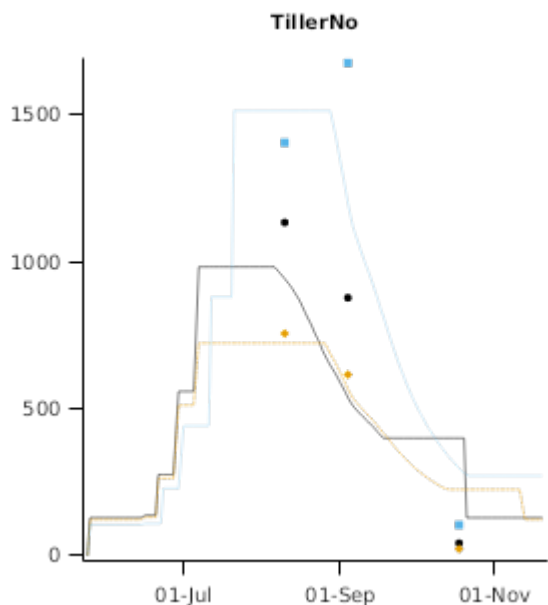
cutting), and the other half was only cut once. Soil water data for the ungrazed treatment was sourced exclusively from rep 3 except for the sowing PAW which was measured bulked across the experiment.

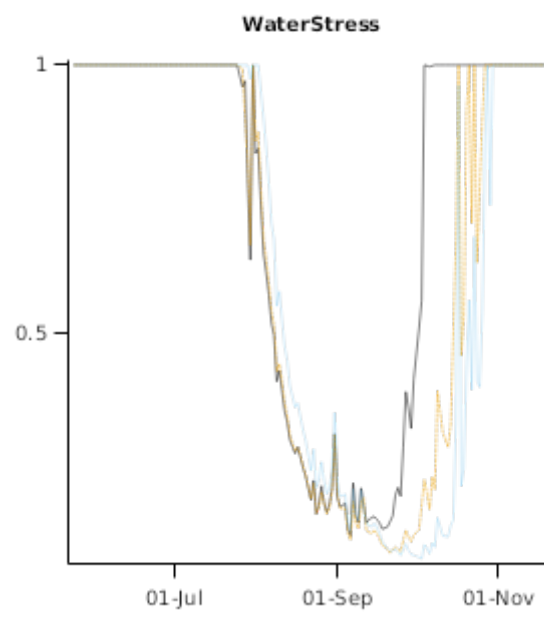
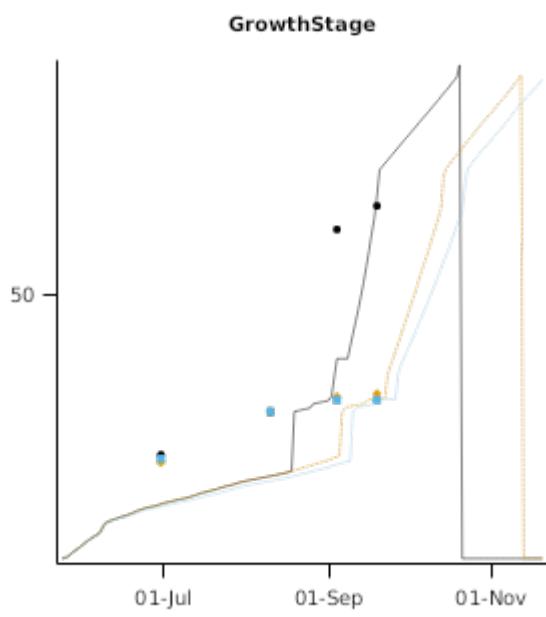
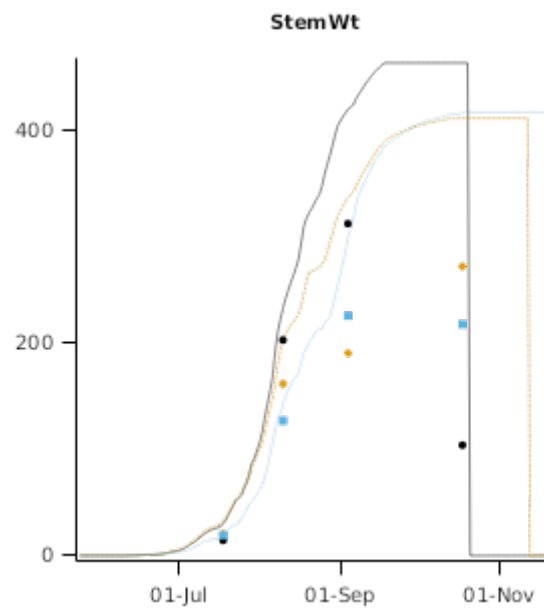
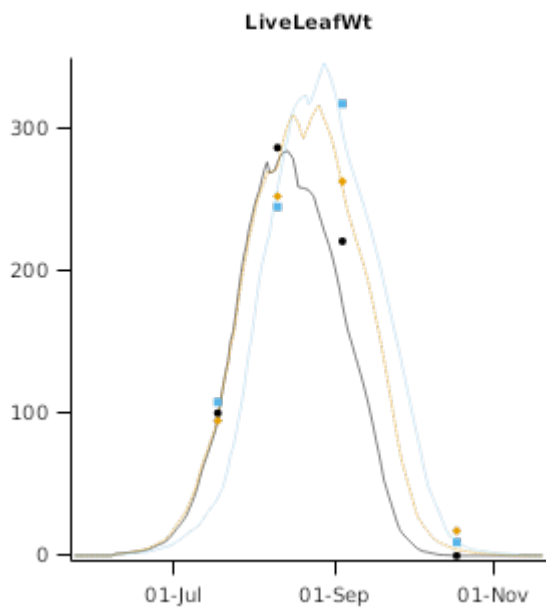
Inaccuracy in the prediction of SLA and LAI was probably due to measurement error. The trial was heavily water stressed and it was difficult to accurately measure leaf area of curled, drought stress leaves, particularly when they were stored overnight.

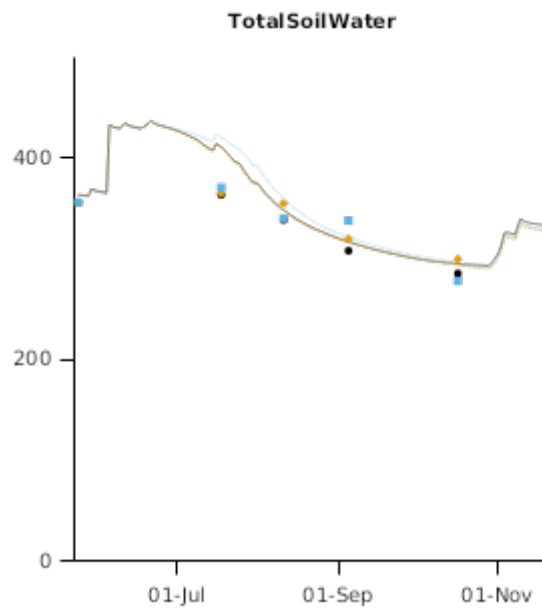
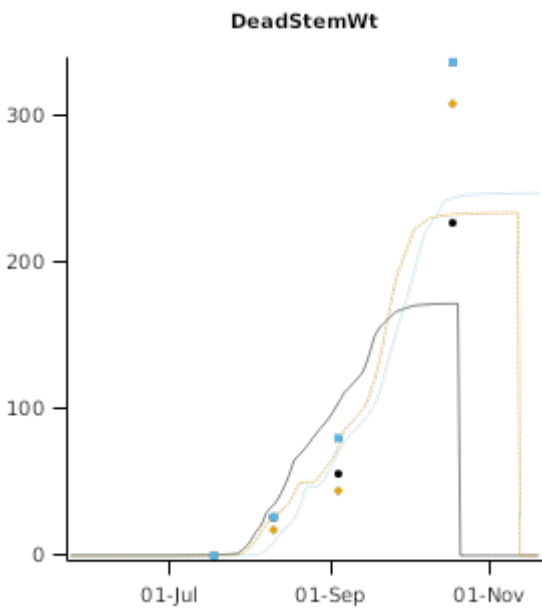
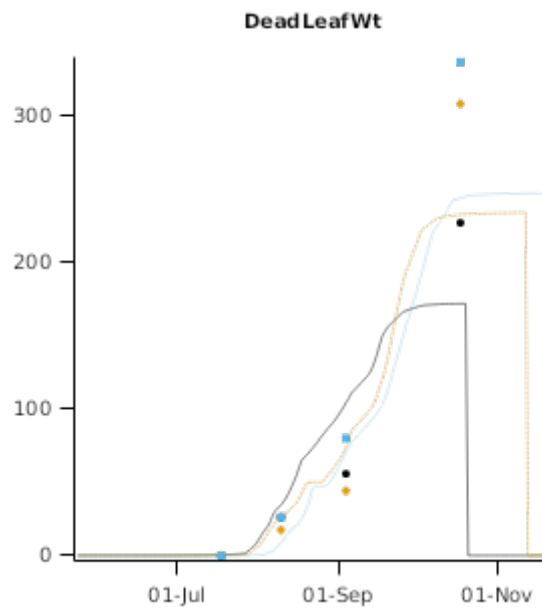
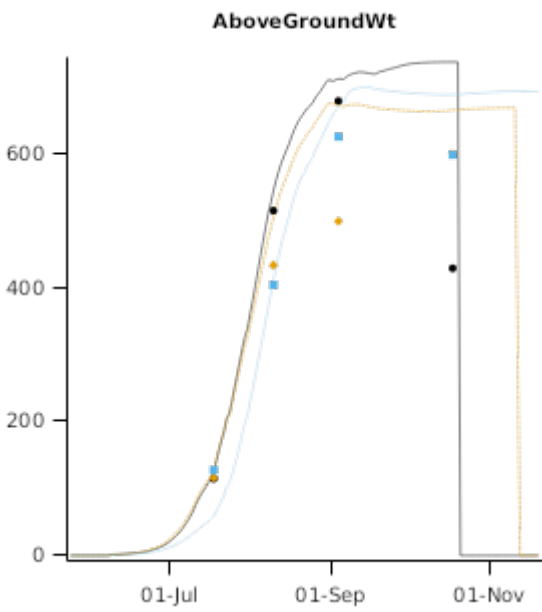
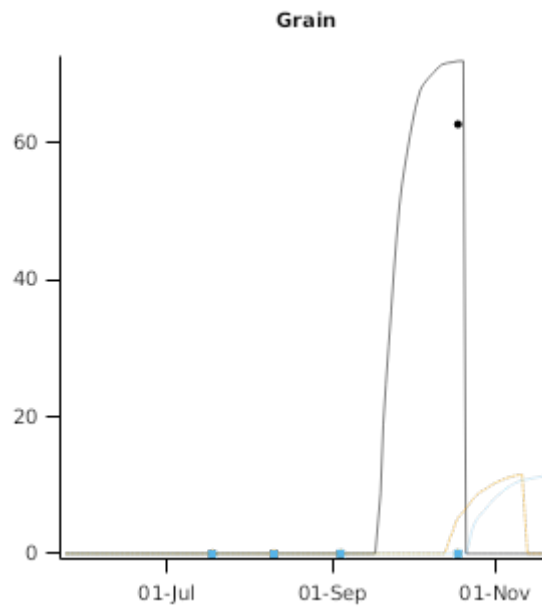
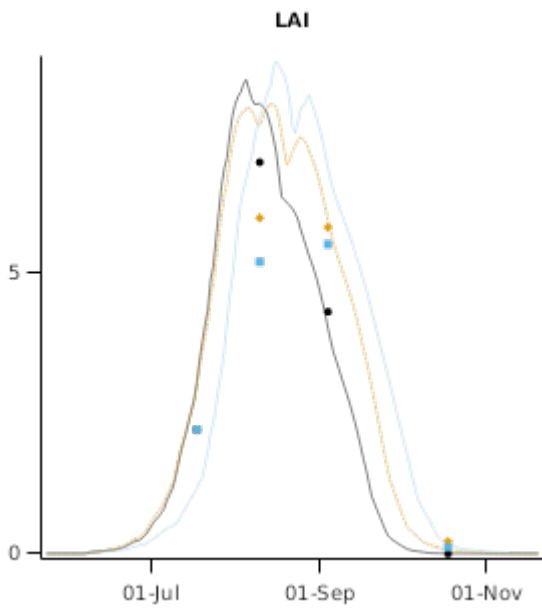
**List of experiments.**

Experiment Name	Design (Number of Treatments)
Roma2006	Cv x Cut (9)

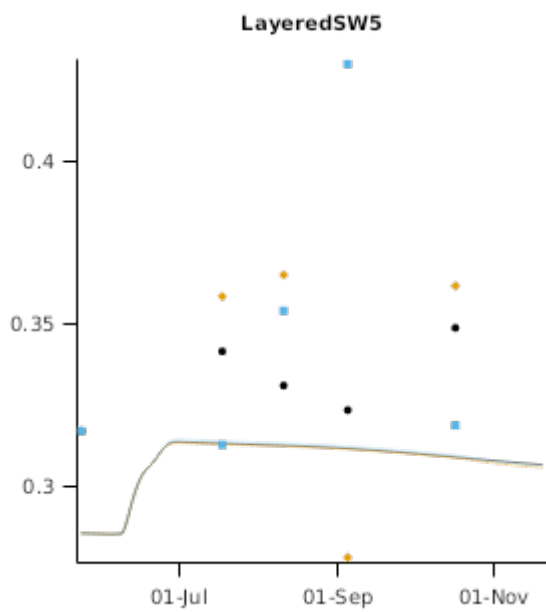
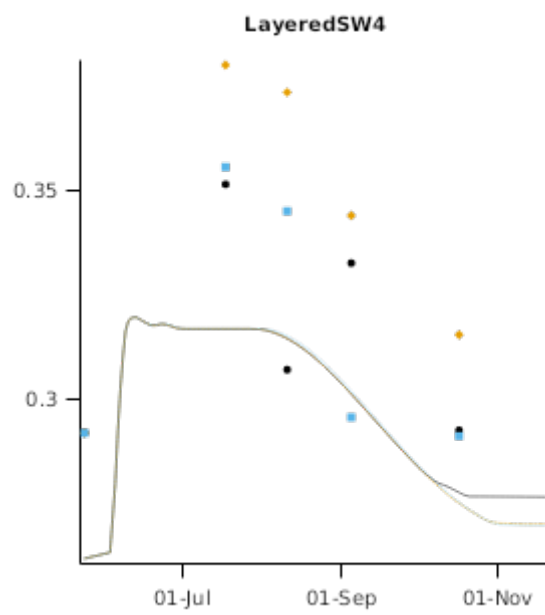
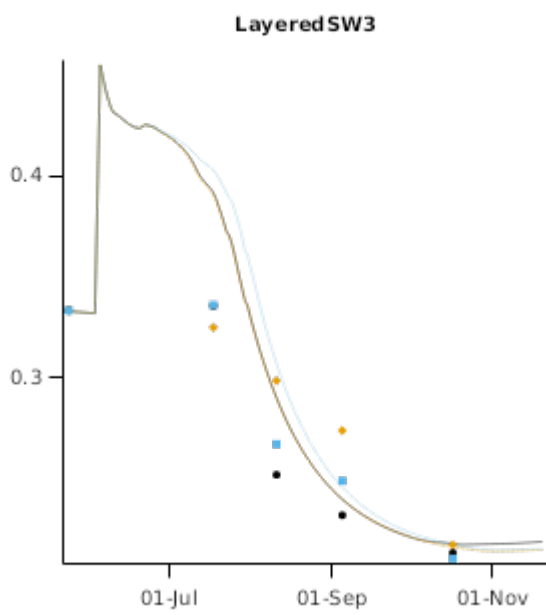
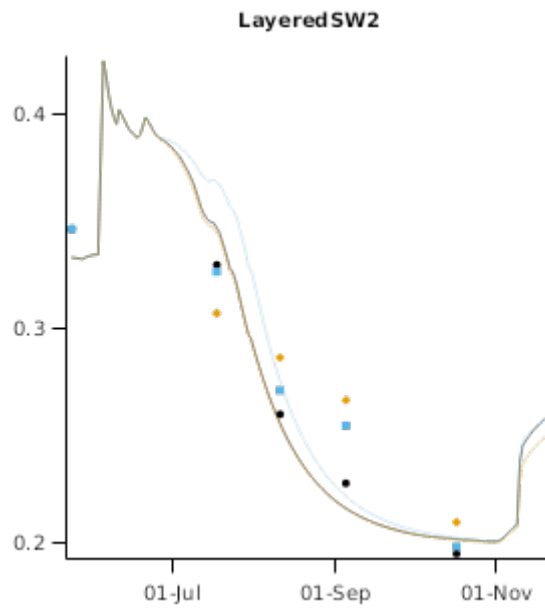
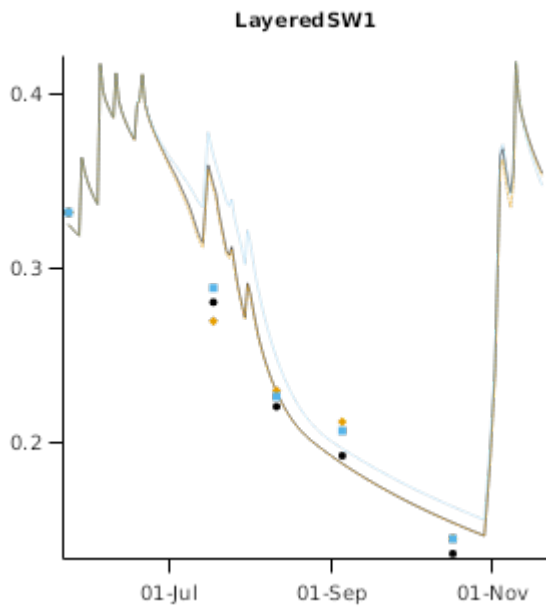
**2.3.3.1 UngrazedGraphs**



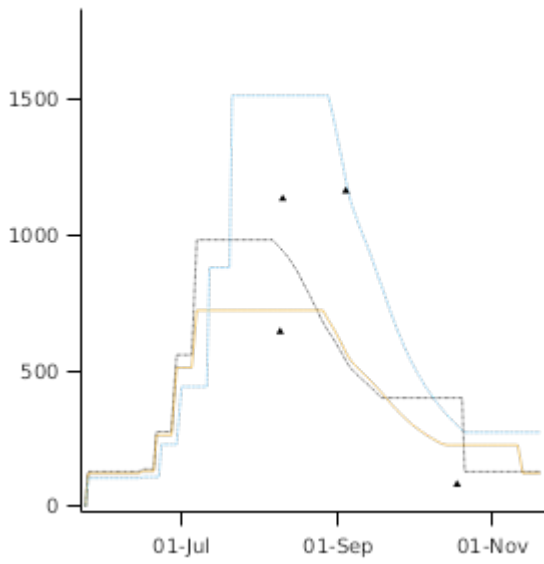
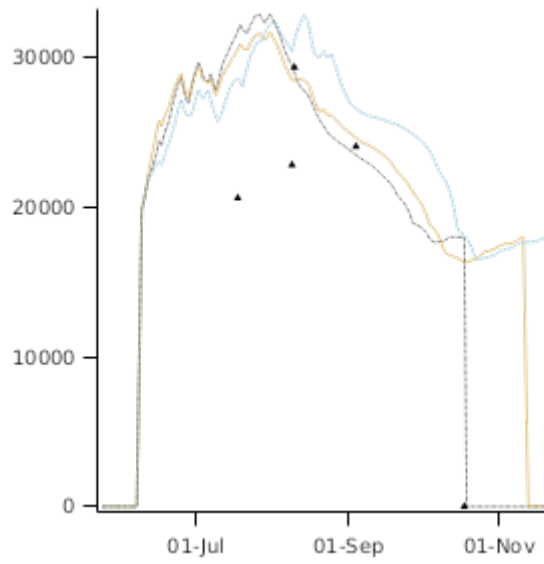
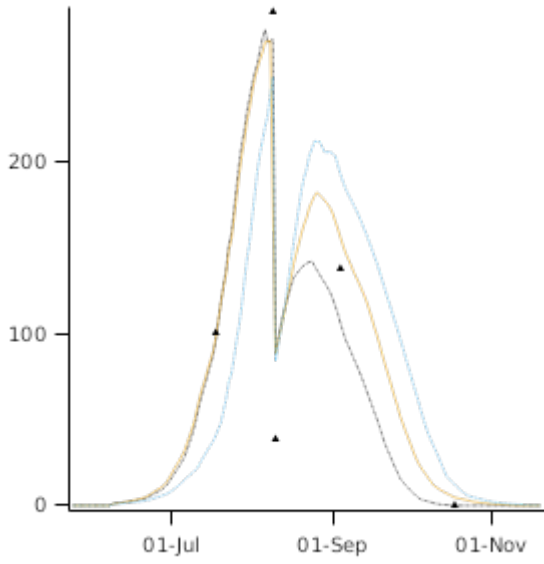
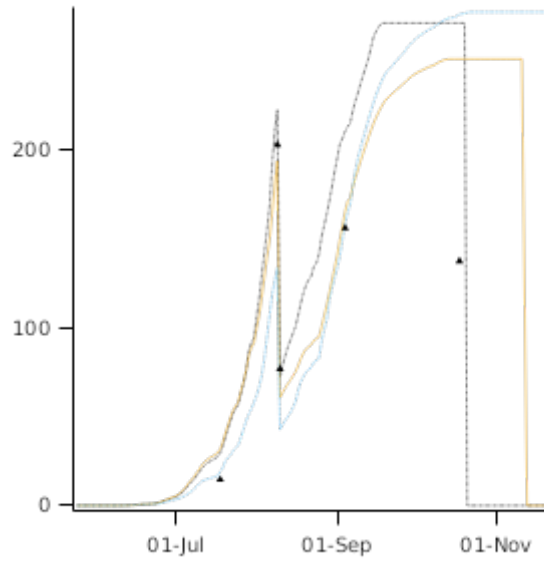
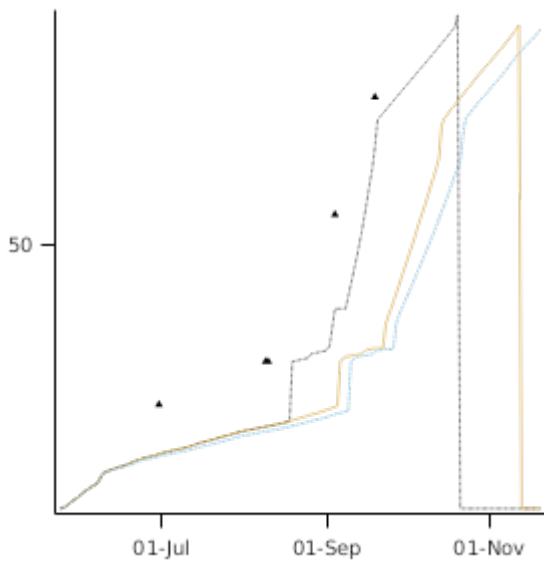
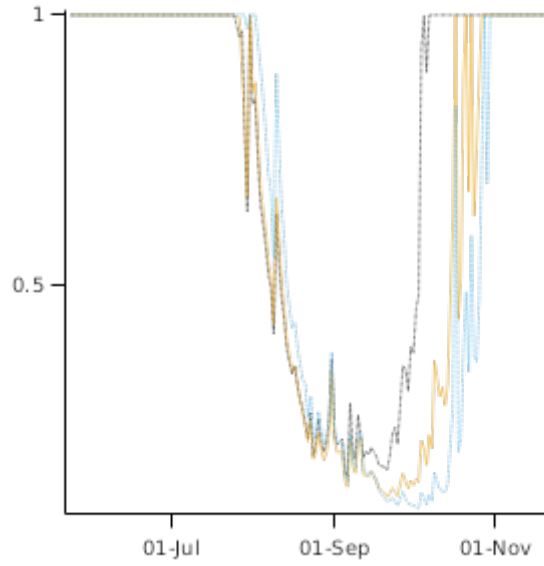


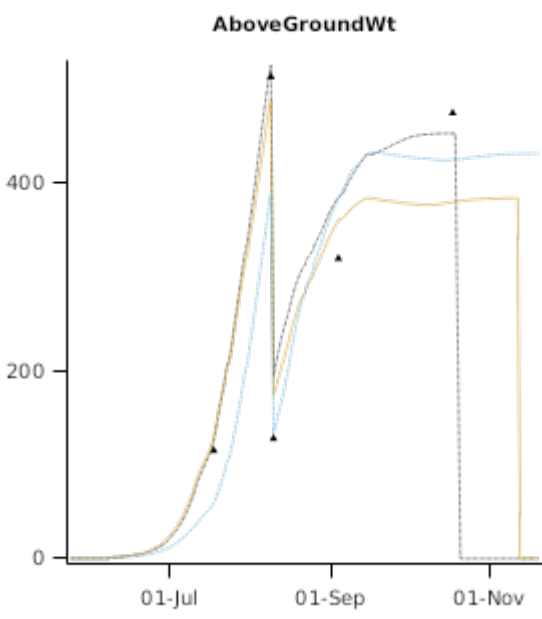
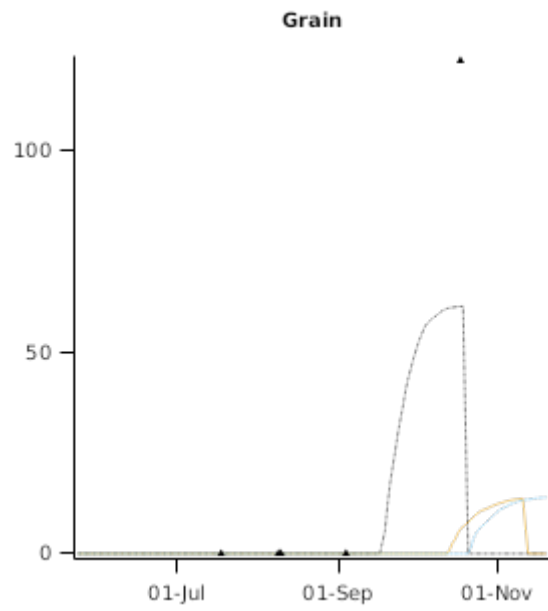
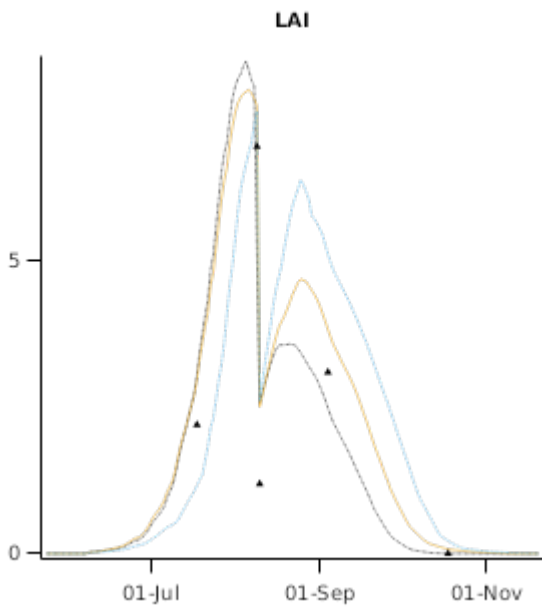


**2.3.3.2 LayeredSWUncut**



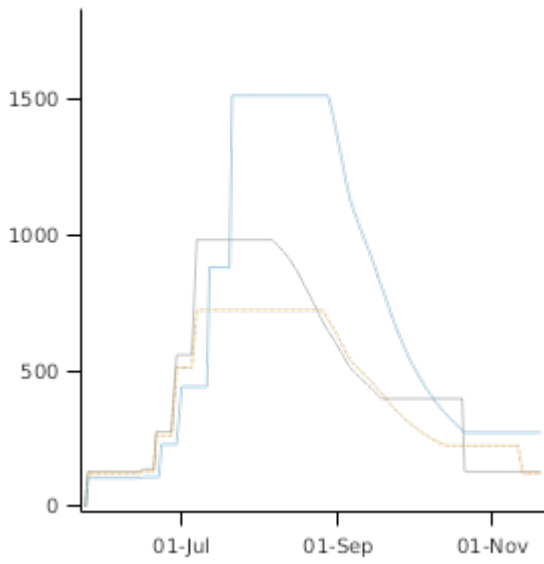
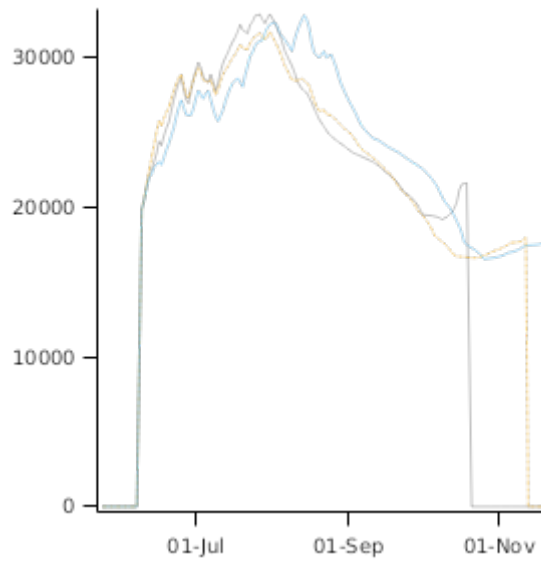
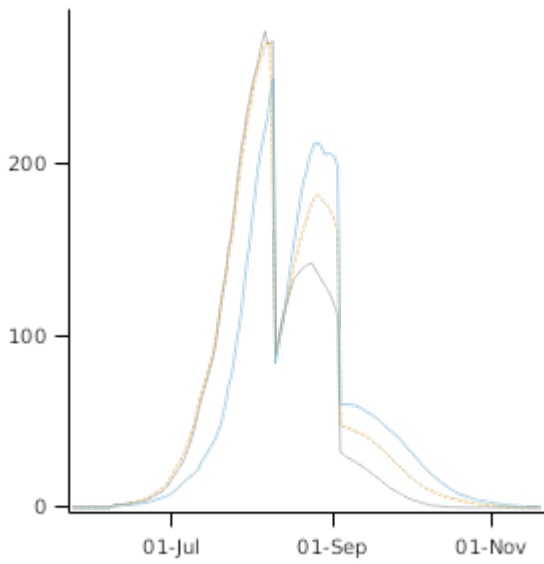
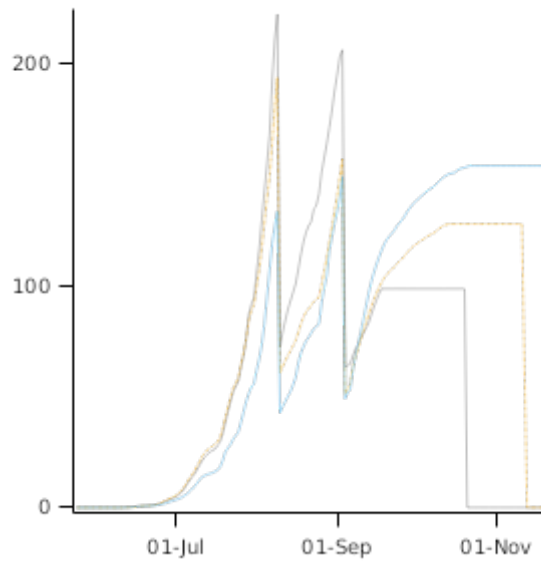
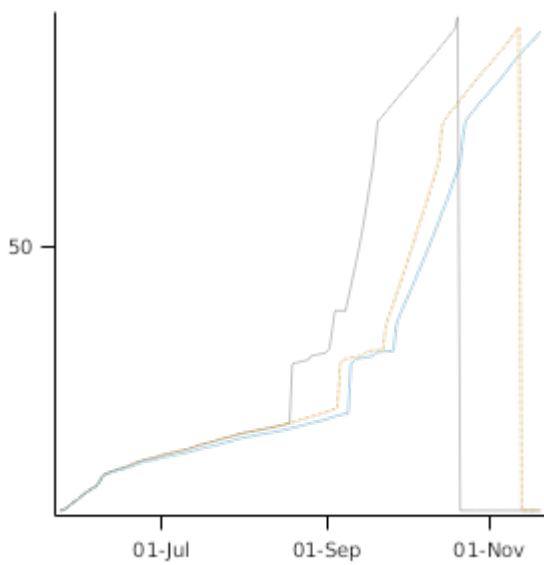
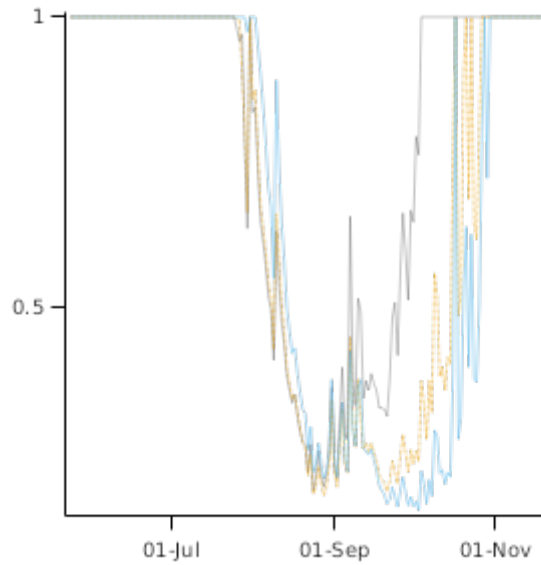
**2.3.3.3 OneCutGraphs**

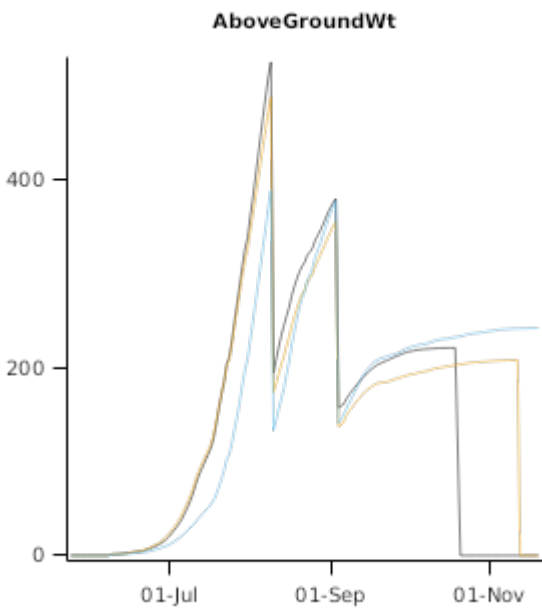
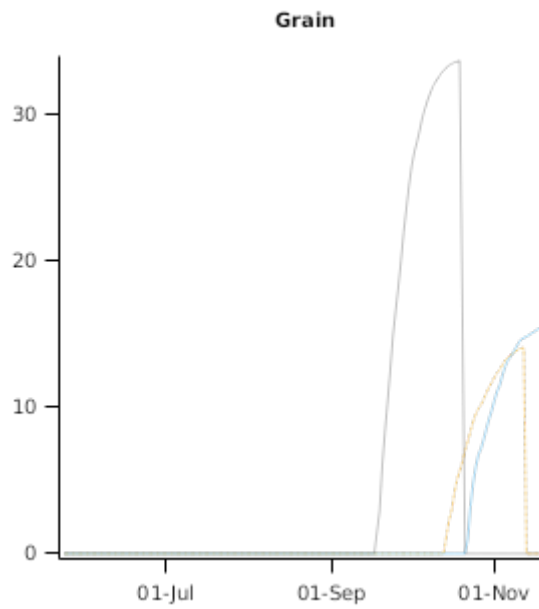
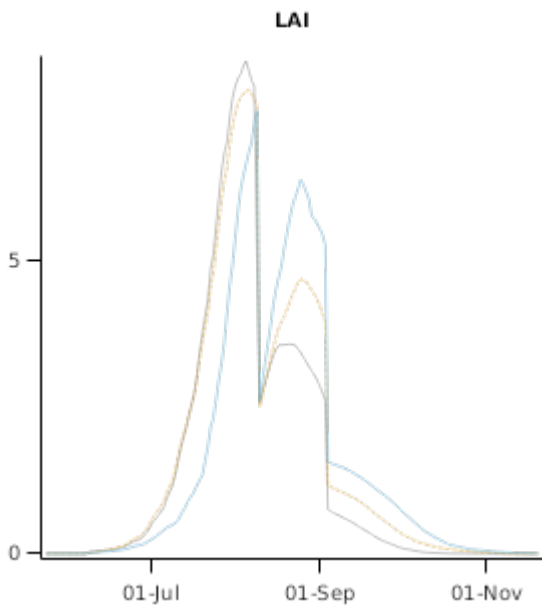
**TillerNo****SLA****LiveLeafWt****StemWt****GrowthStage****WaterStress**



**2.3.3.4 TwoCutGraphs**



**TillerNo****SLA****LiveLeafWt****StemWt****GrowthStage****WaterStress**

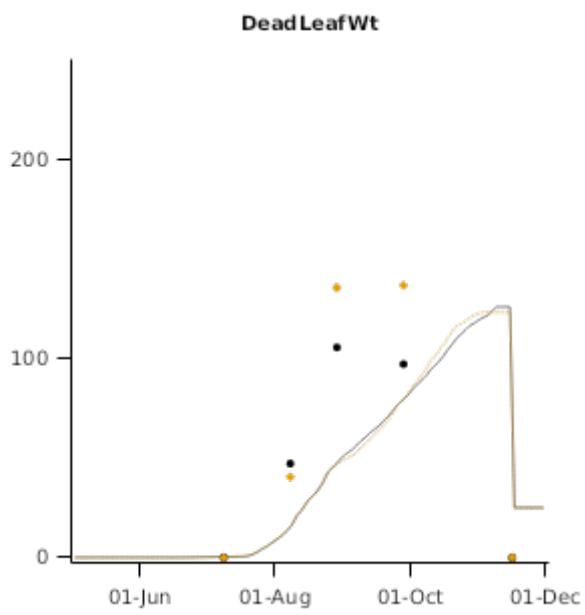
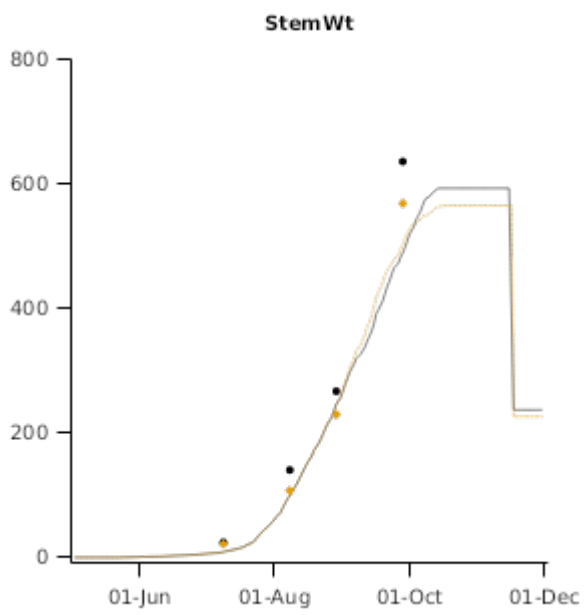
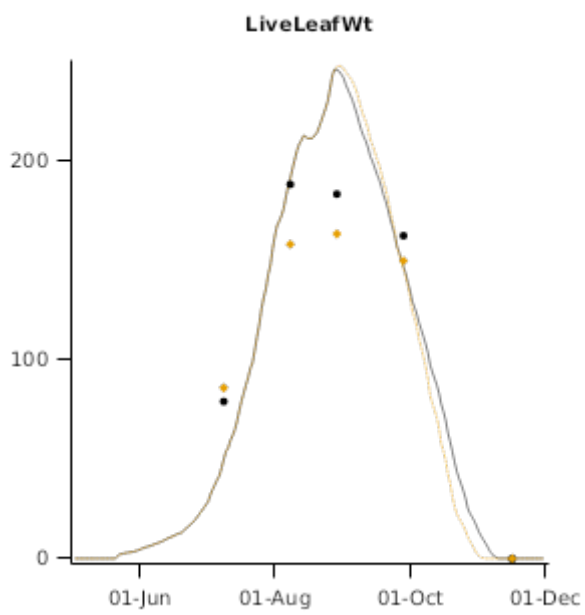
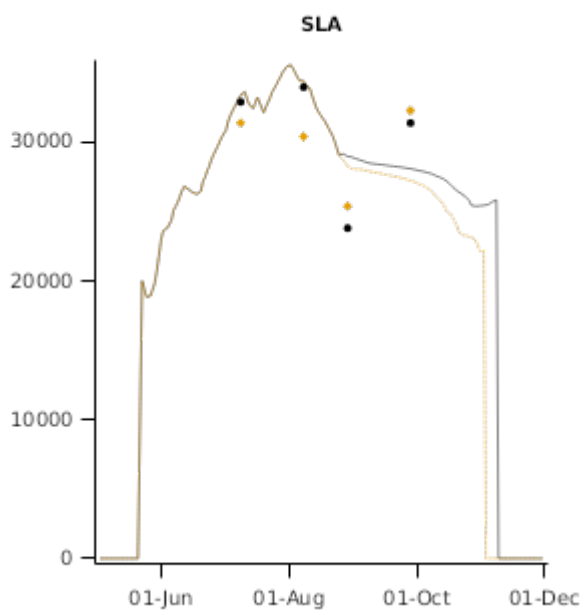
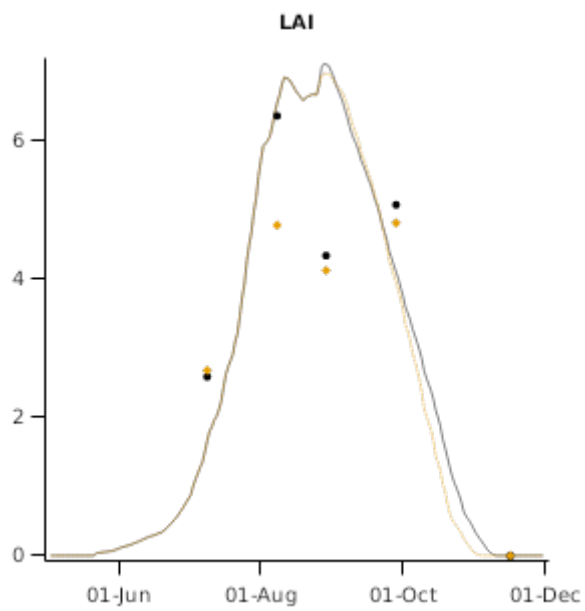
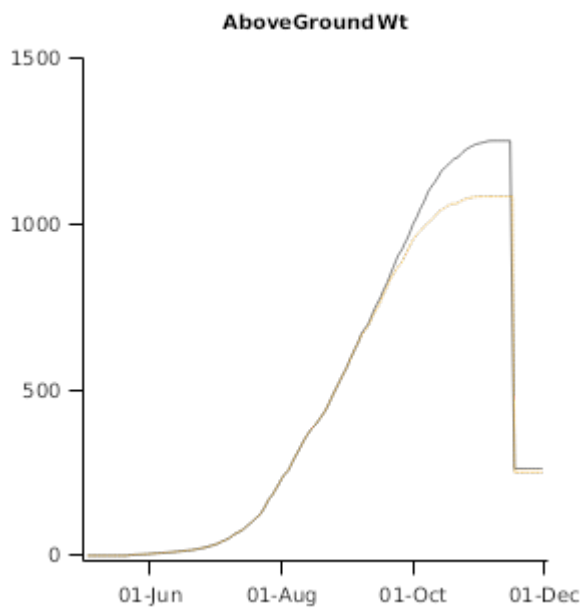


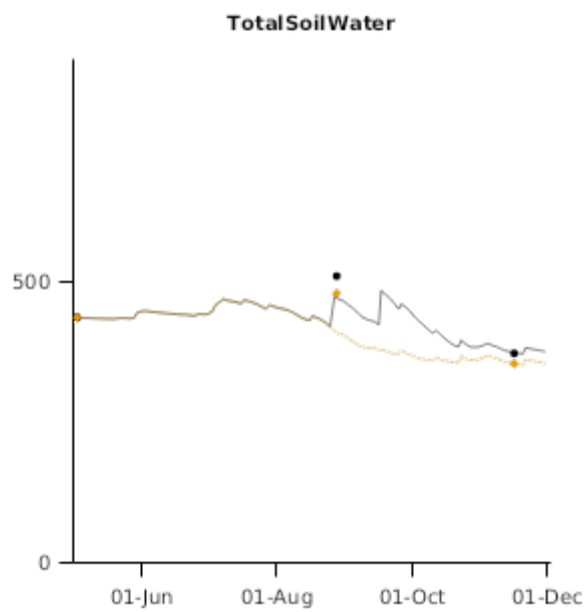
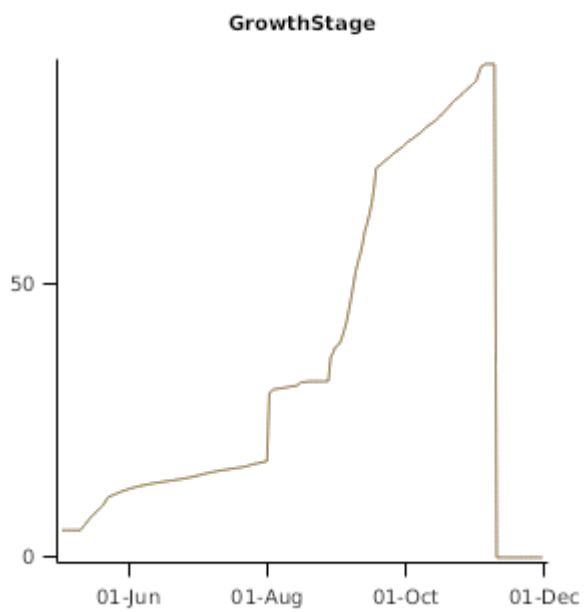
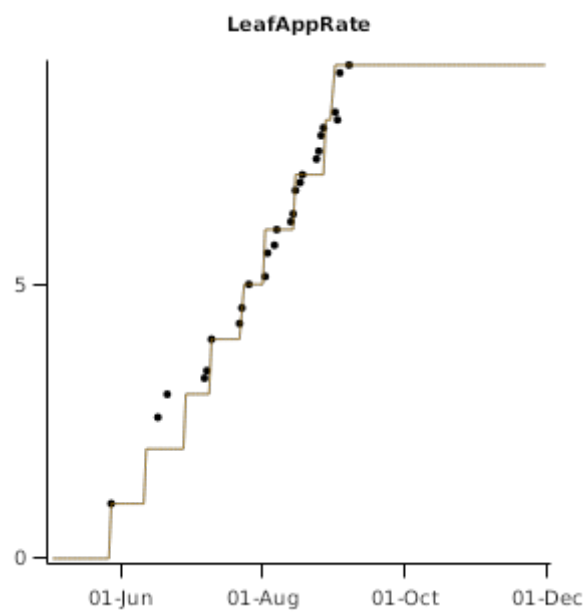
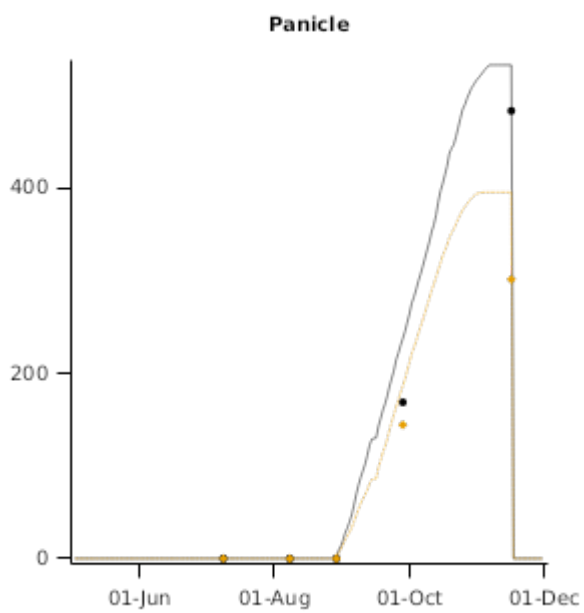
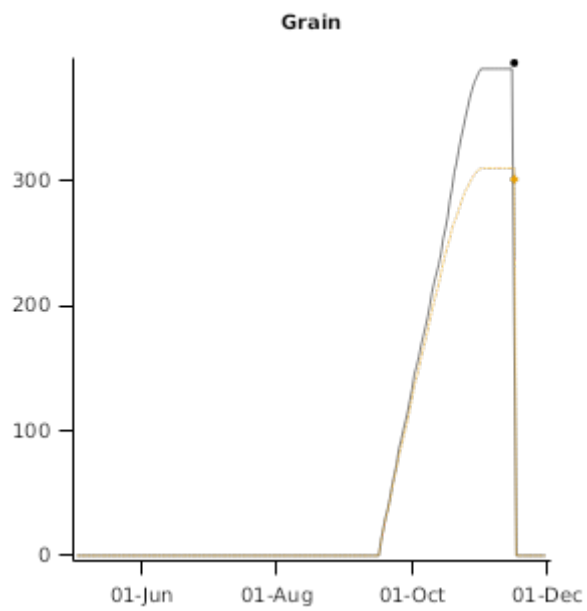
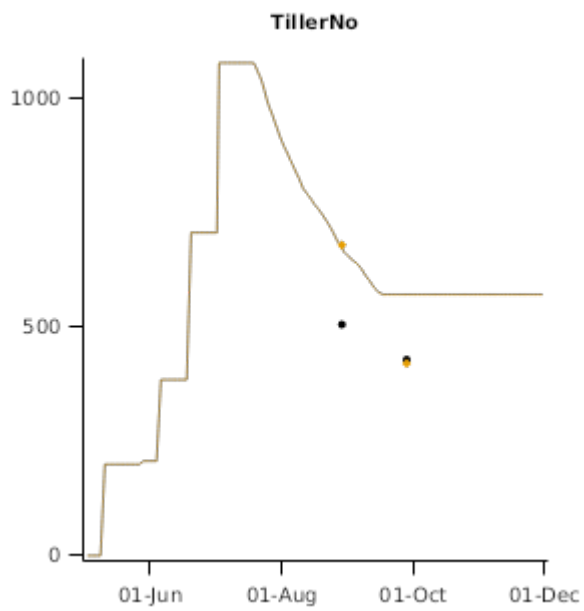
### 2.3.4 Tarlee2007

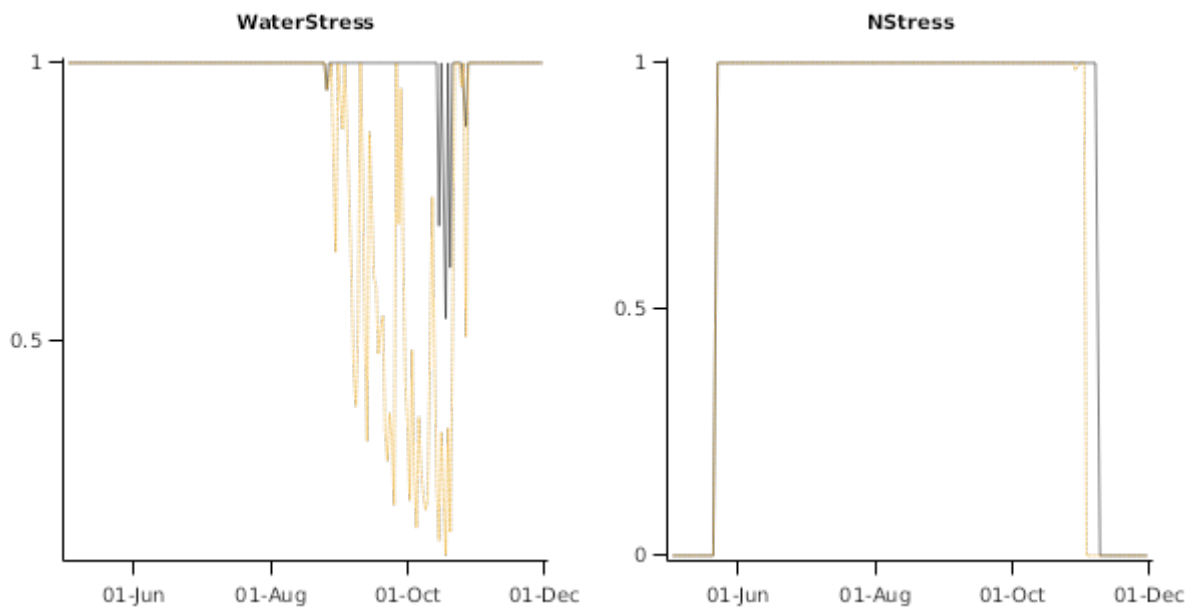
This experiment was run at Tarlee, South Australia, in 2007. Leaf disease (probably yellow spot) was observed to take hold in the latter stages of the experiment that may explain differences between observed and simulated LAI, leaf biomass and dead leaf biomass toward the end of the experiment.

#### List of experiments.

Experiment Name	Design (Number of Treatments)
Tarlee2007	AgRegime (2)







### 2.3.5 LRCphenology

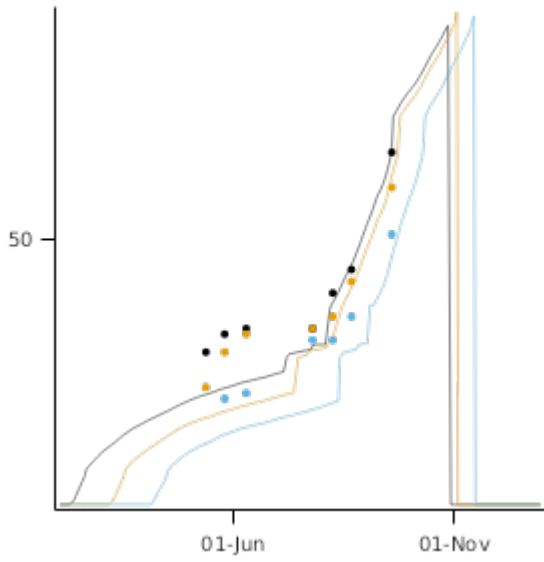
These simulations were used to develop phenology parameters for a range of cultivars used in northern Australia. Observed data was kindly supplied by Bruce Winter (Oats Breeder) and Richard Uebergang from experiments conducted at DAFQ Leslie Research Centre, Holberton St Toowoomba. SILO weather data from the nearby Toowoomba Airport was used. Approximated irrigation data and fertiliser regime was provided by LRC staff who managed the phenology screening trials to be non-water and N limiting.

#### List of experiments.

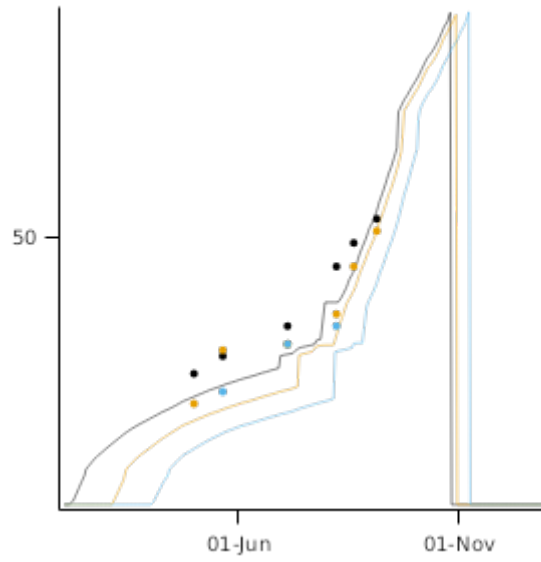
Experiment Name	Design (Number of Treatments)
LRC2011	Cv x Management (12)
LRC2012	Cv x Management (15)
LRC2014	Cv x Management (14)
LRC2015	Cv x Management (21)
LRC2016	Cv x Management (21)
LRC2017	Cv x Management (21)

#### 2.3.5.1 Algerian

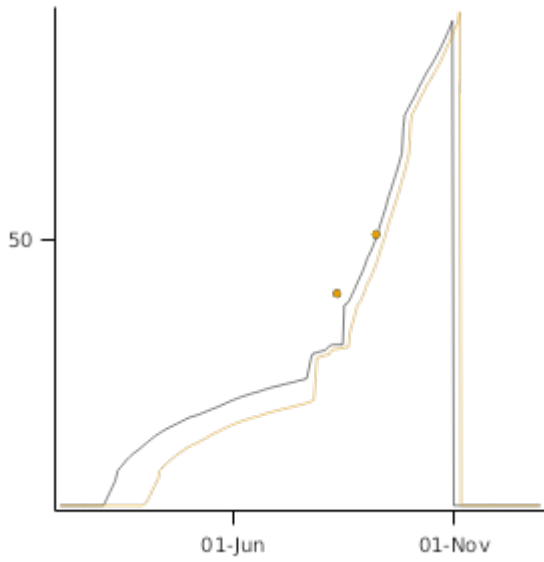
**Algerian2011**



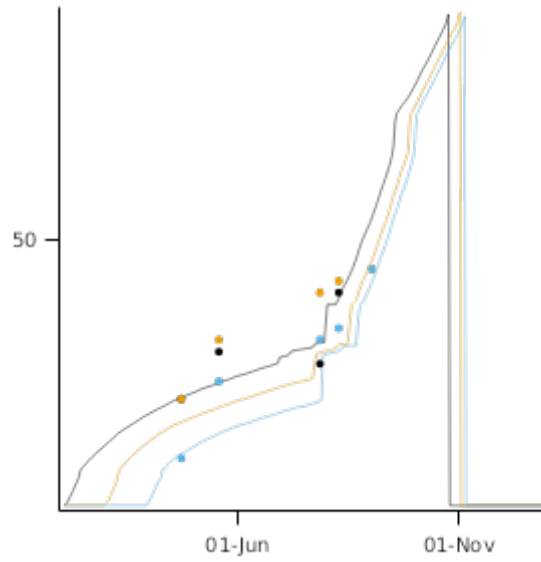
**Algerian2012**



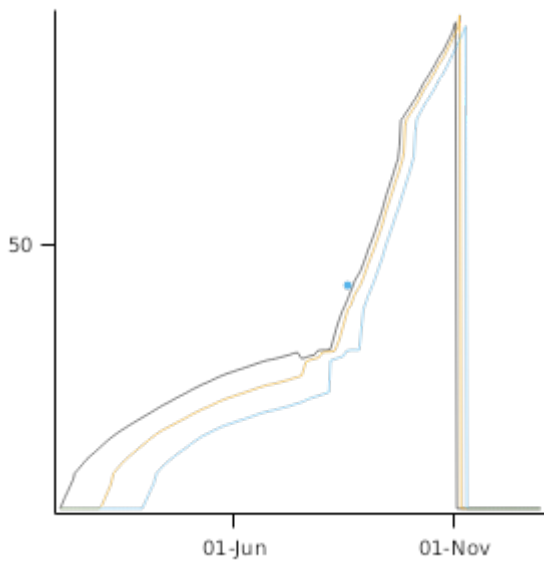
**Algerian2014**



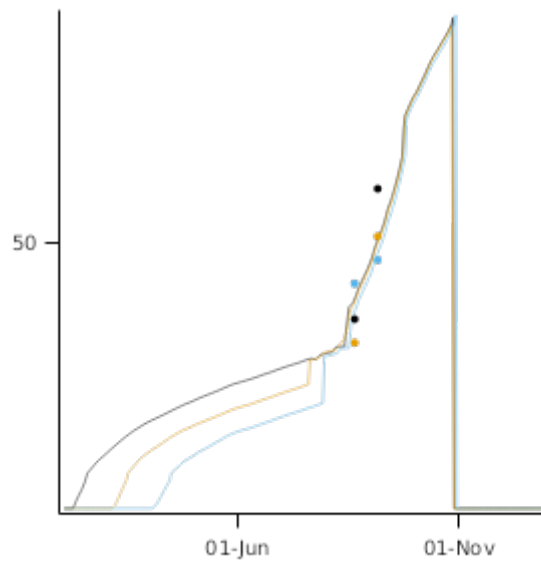
**Algerian2015**



**Algerian2016**

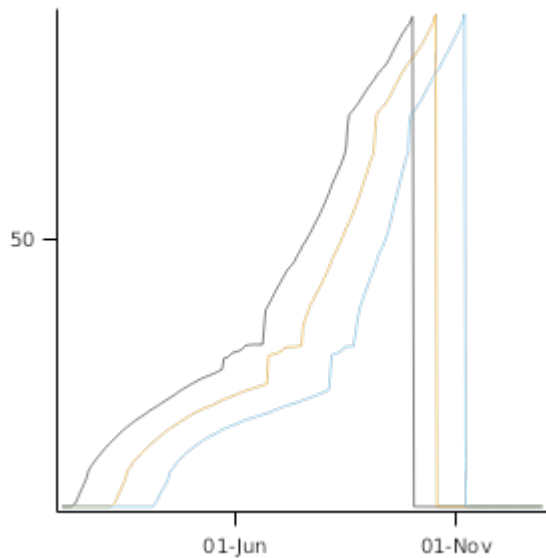


**Algerian2017**

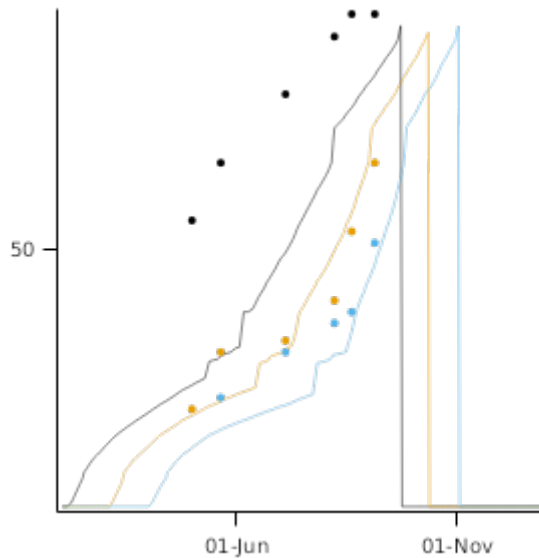


**2.3.5.2 Drover**

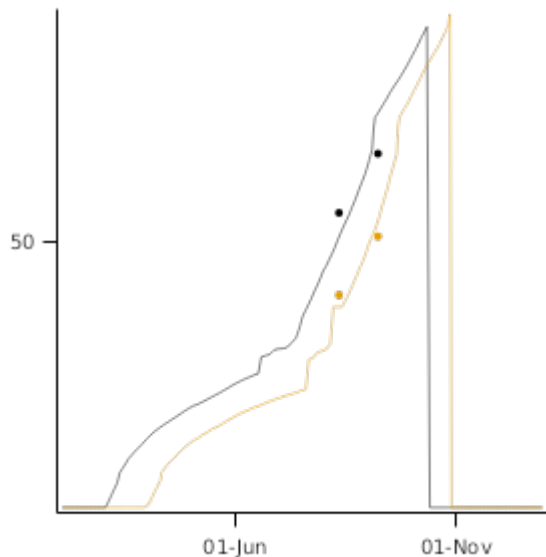
**Drover2011**



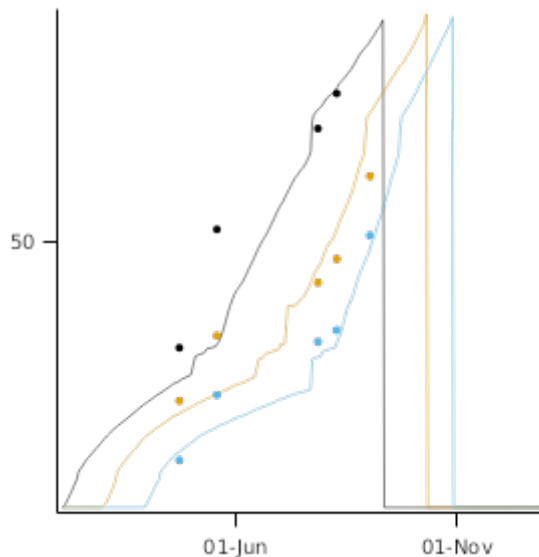
**Drover2012**



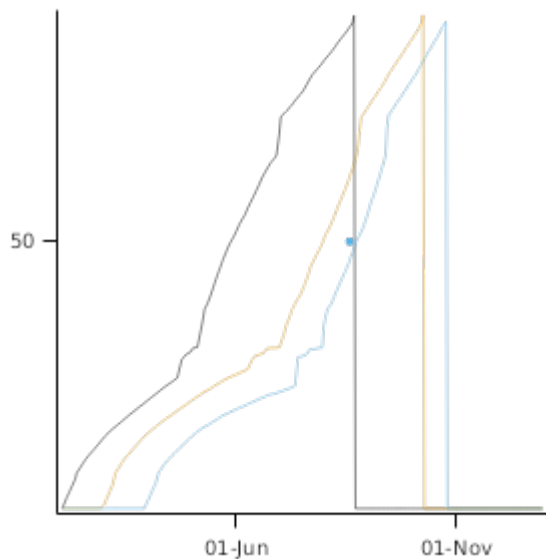
**Drover2014**



**Drover2015**

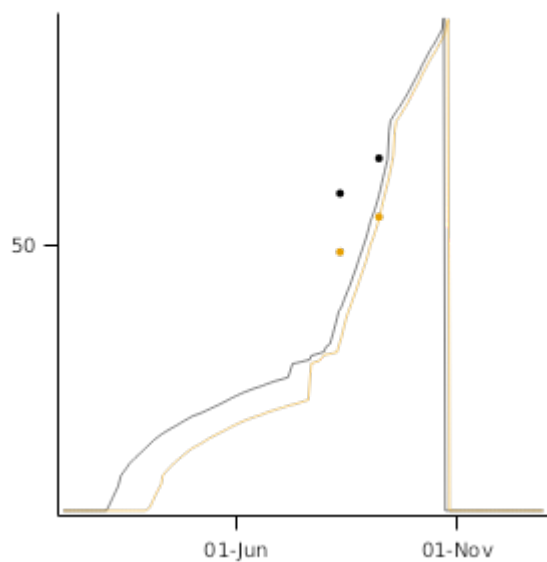


**Drover2016**

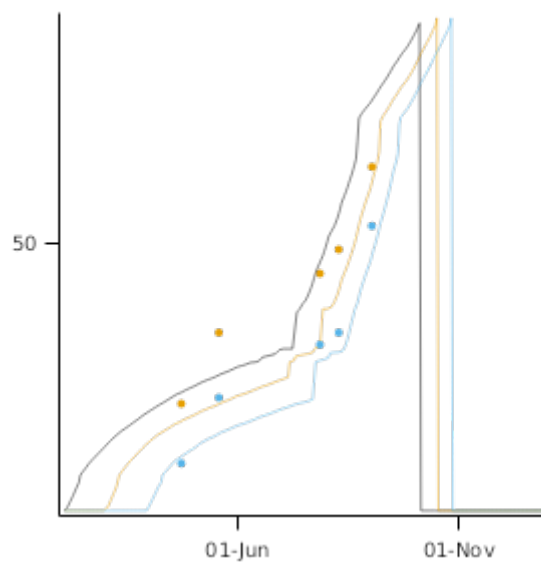


**2.3.5.3 Taipan**

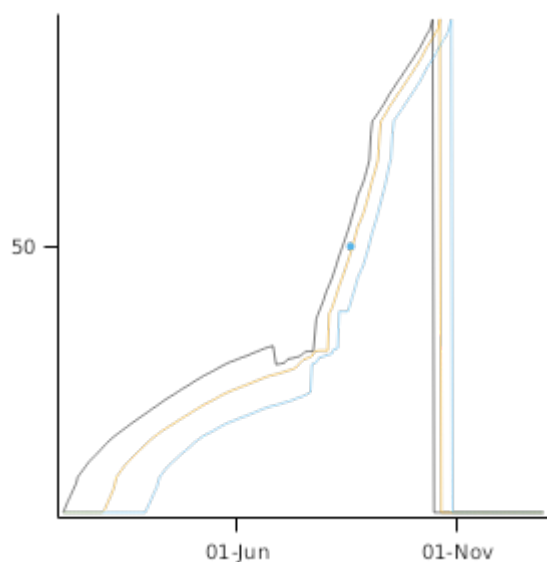
**Taipan2014**



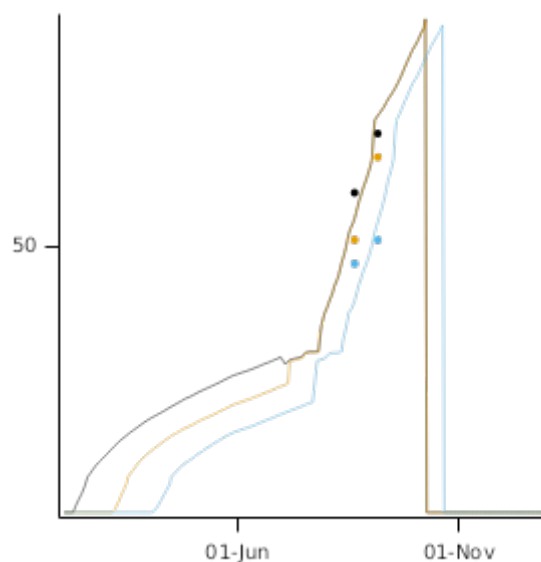
**Taipan2015**



**Taipan2016**

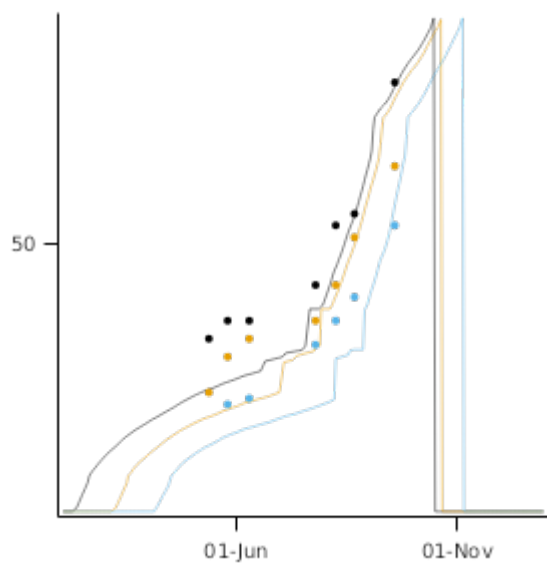


**Taipan2017**

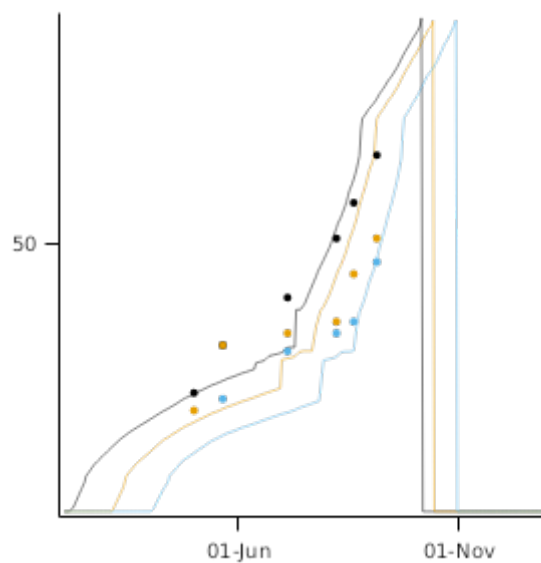


#### 2.3.5.4 Nugene

**Nugene2011**

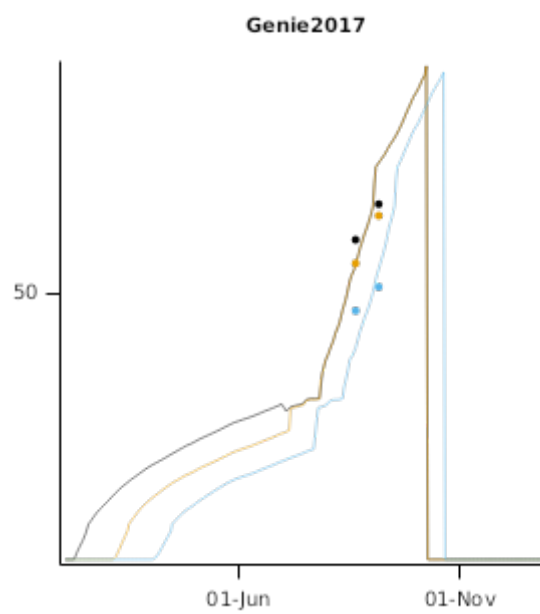
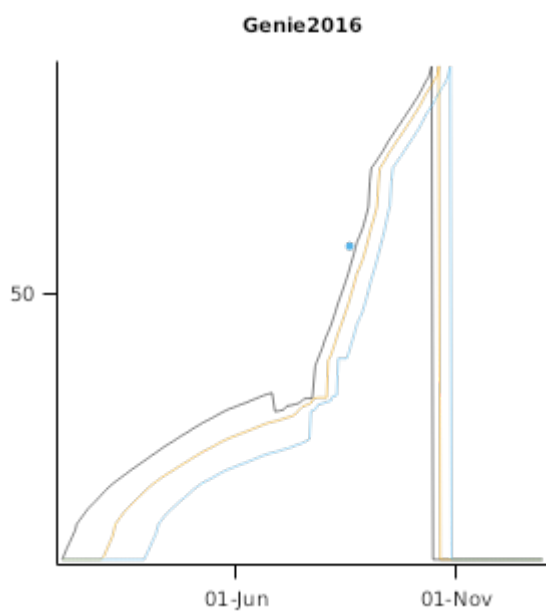
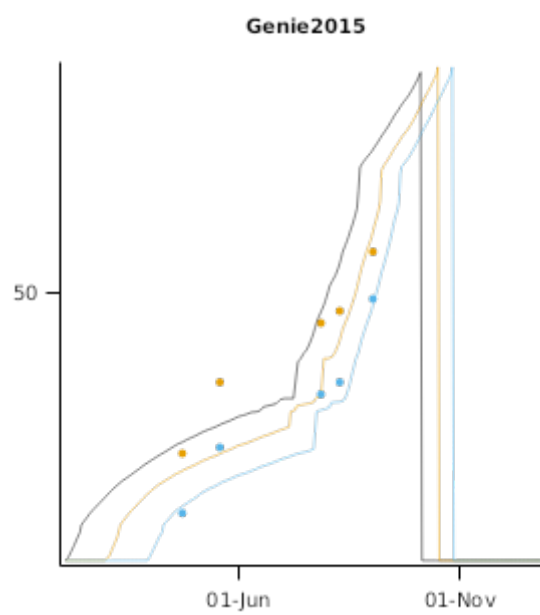
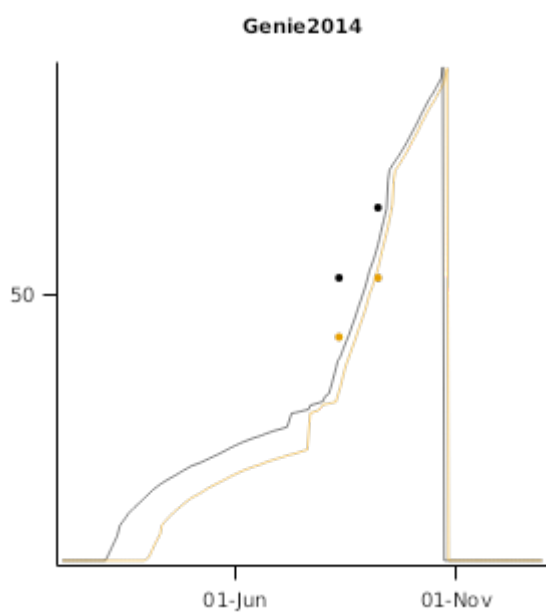
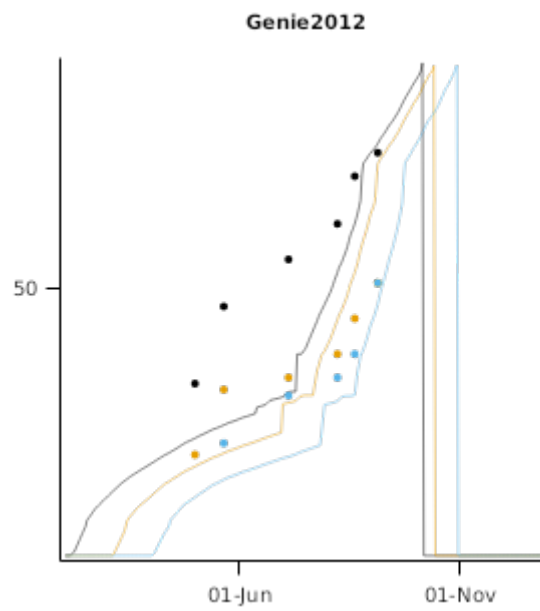
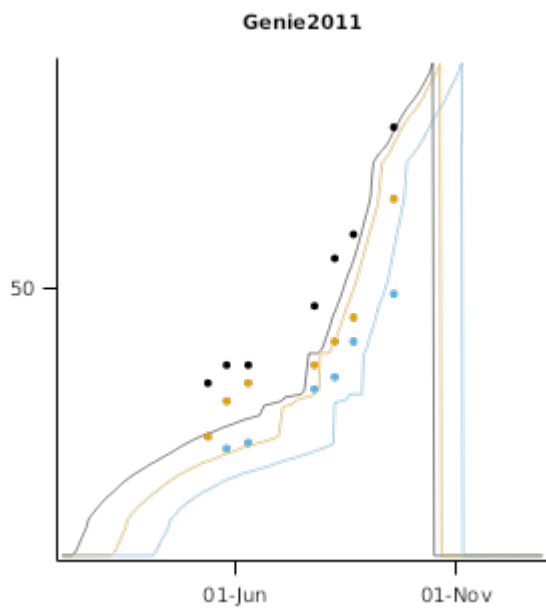


**Nugene2012**



#### 2.3.5.5 Genie

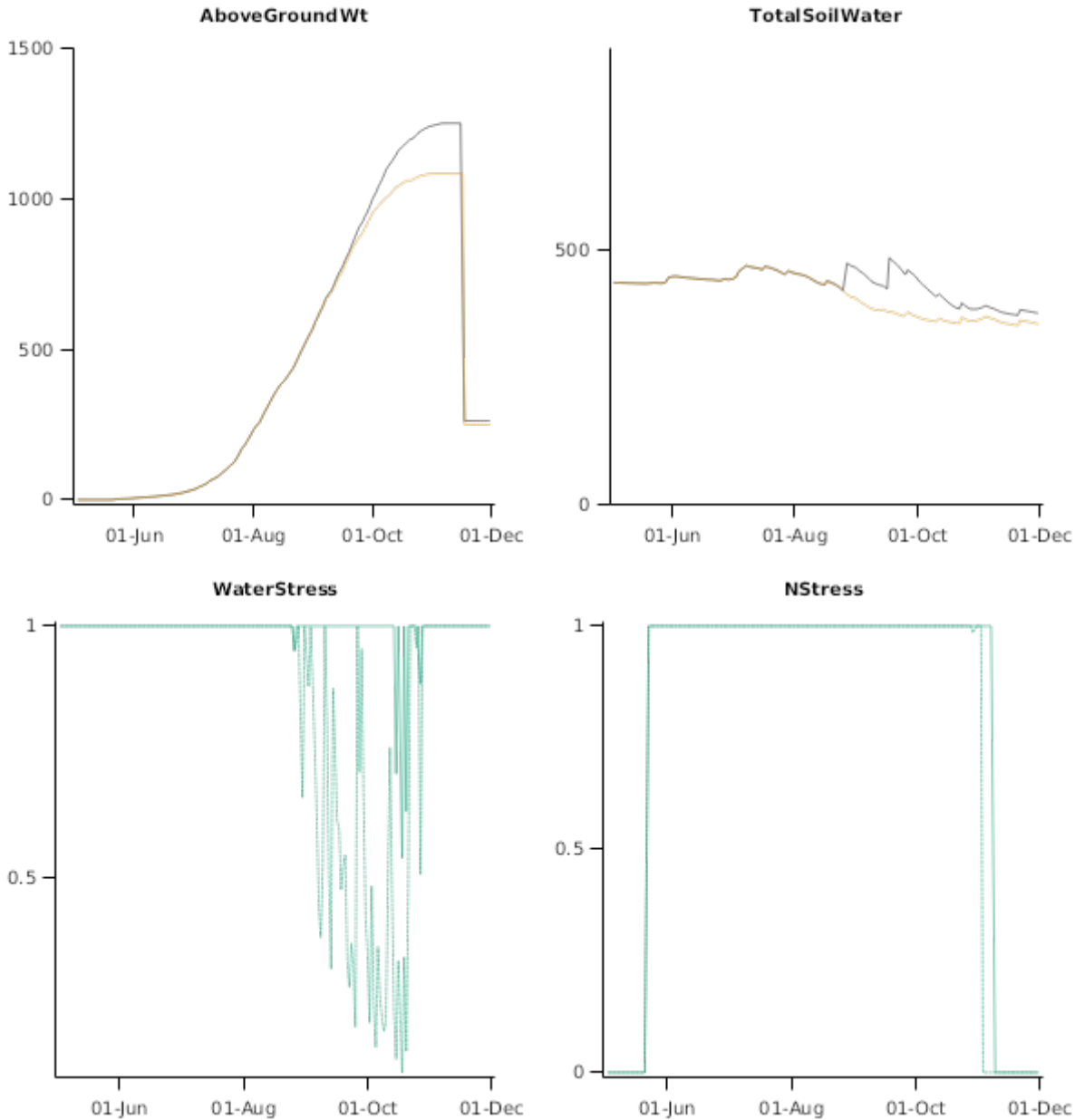




### 3 Sensibility

List of experiments.

Experiment Name	Design (Number of Treatments)
OatsExampleTarlee2007	AgRegime (2)



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