



1 The APSIM Barley Model

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

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

List of Plant Model Components.

Component Name	Component Type
Arbitrator	Models.PMF.OrganArbitrator
Phenology	Models.PMF.Phen.Phenology
Structure	Models.PMF.Struct.Structure
Grain	Models.PMF.Organs.ReproductiveOrgan
Root	Models.PMF.Organs.Root
Leaf	Models.PMF.Organs.Leaf
Spike	Models.PMF.Organs.GenericOrgan
Stem	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.

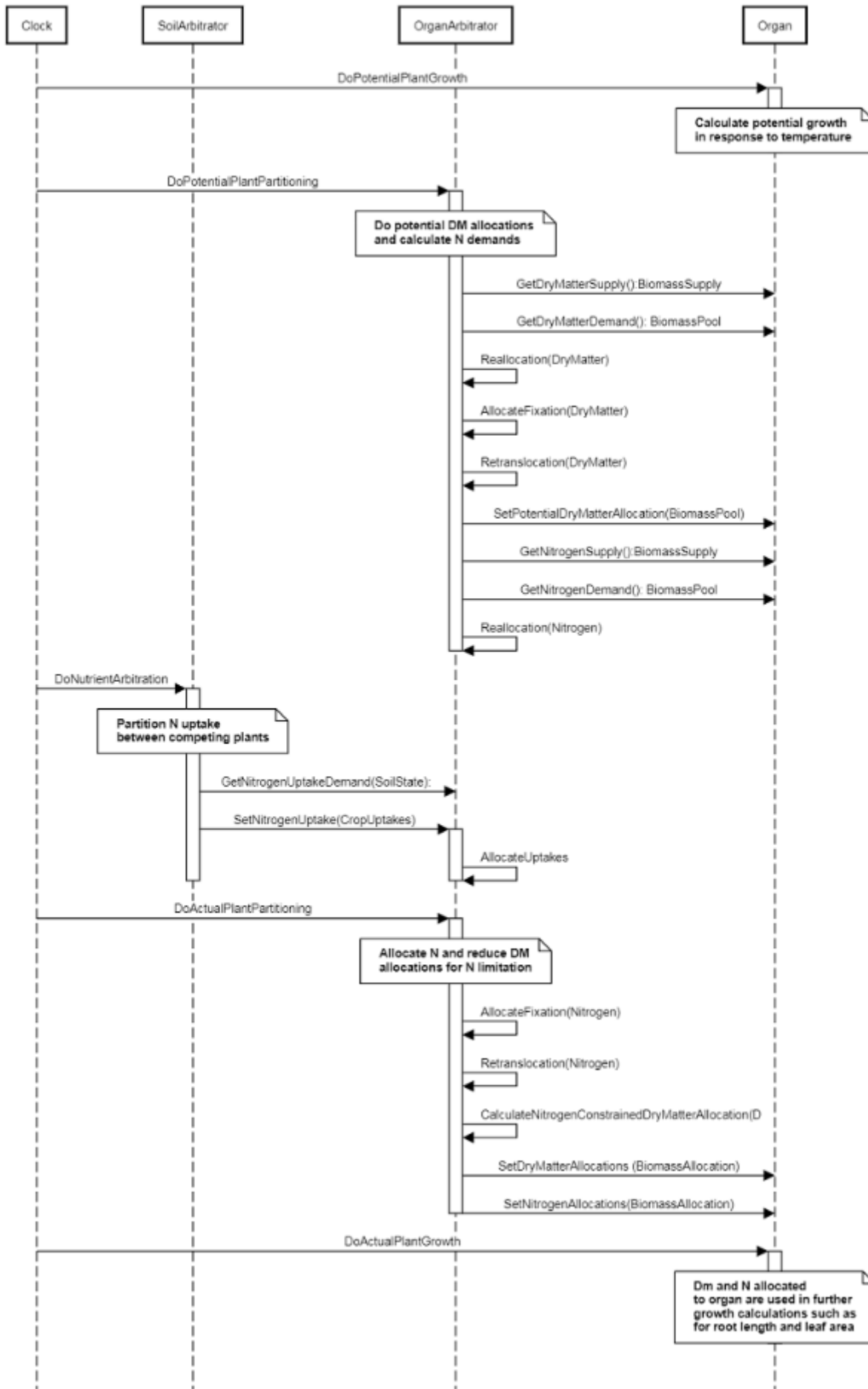


Figure 1: Schematic showing the procedure for arbitration of biomass partitioning. Pink boxes represent events that occur every day and their numbering shows the order of calculations. Blue boxes represent the methods that are called when these events occur. Orange boxes contain properties that make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

Barley exhibits a range of developmental responses to environment and these are strongly influenced by genotype characteristics. Temperature affects development increasing development rates and decreasing phase durations as temperatures increase. These effects are captured by thermal time. However, Barley also exhibits vernalisation and photoperiod sensitivities in its Vegetative phase and further photoperiod sensitivity in the EarlyReproductivePhase. Photoperiod responses are seen as a reduction in the length of a phase for a photoperiod sensitive genotype in response to a longer 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.

This model draws 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 ([Jamieson et al., 1995](#)).

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

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

Where MinLeafNumber is the number of leaves that a barley 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.

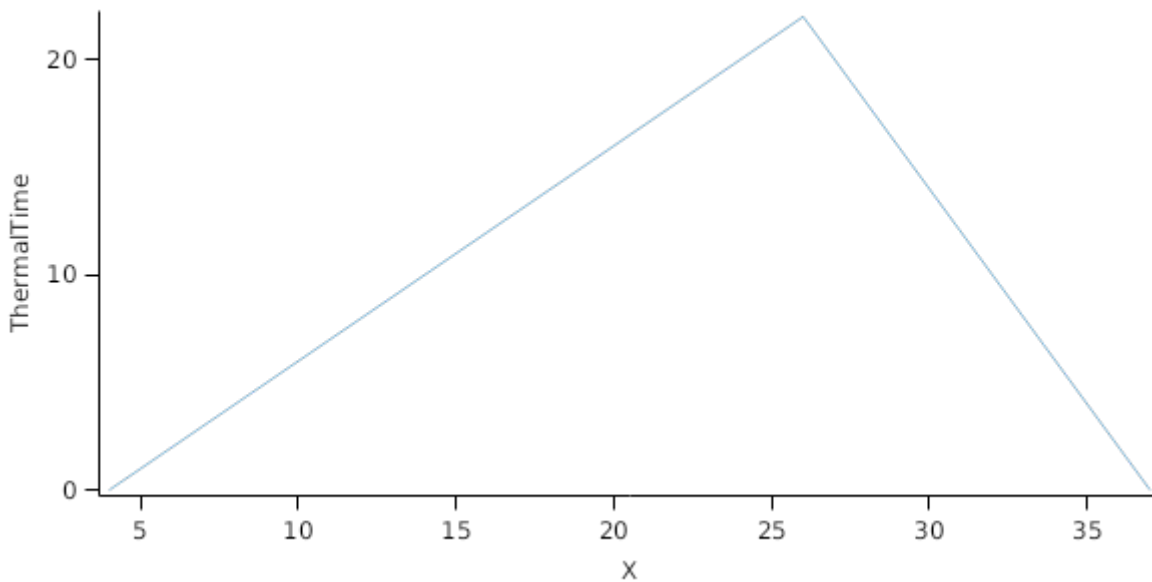
Thermal time determines the rate of developmental progress through many of the crop's phases and is used by organs to determine potential growth rates.

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
4.0	0.0
26.0	22.0
37.0	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:

$$\text{ShootRate} = 1 \text{ (deg day/mm)},$$

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

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:

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

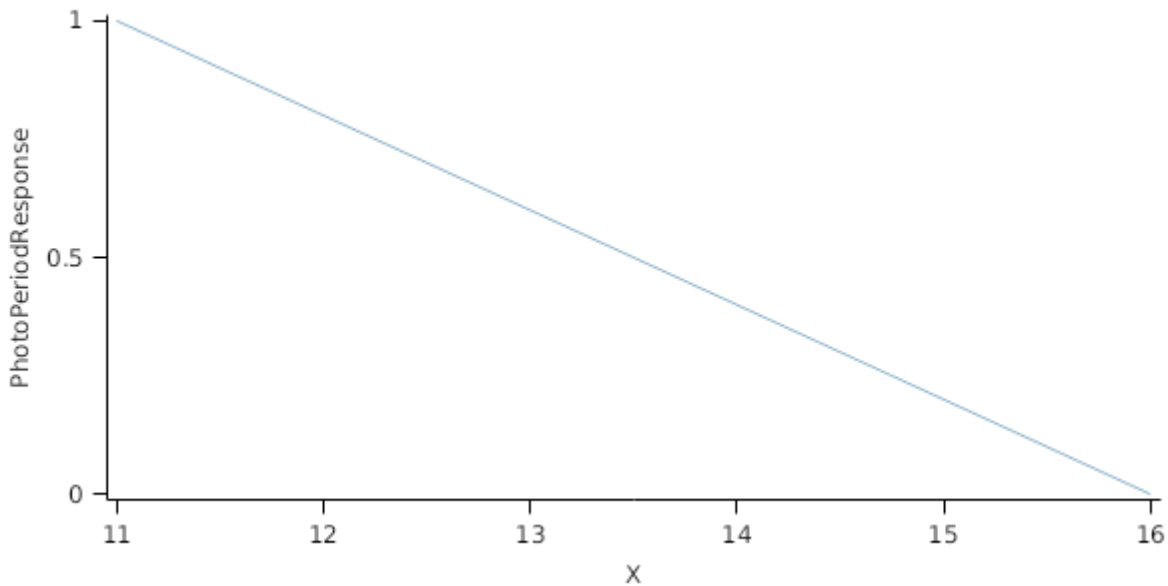
$$Phyllochrons = [Phenology].EarlyReproductiveLongDayBase + IncreaseDueToShortPhotoPeriod$$

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

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 = 50 (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 = 540 (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 = 35 (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 = 10 (oD)

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

$Progression = [Phenology].ThermalTime$

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

MinimumLeafNumber = 9 (Leaves)

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

VrnSensitivity = 0 (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

VernLag = 1 (Unitless)

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

PpSensitivity = 3 (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.

EarlyReproductivePpSensitivity = 0

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

EarlyReproductiveLongDayBase = 1

1.2.13 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 18°C.

$DailyVernalisation = [Structure].DeltaHaunStage \times TempResponseProfile$

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

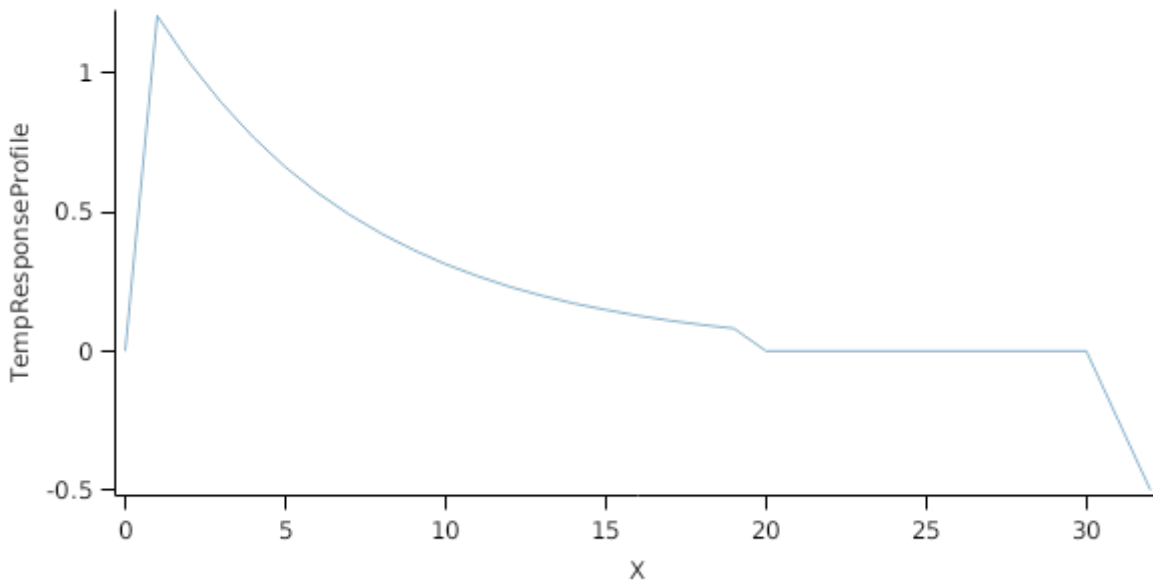
Firstly 3-hourly estimates of air temperature (Ta) are interpolated using the method of [Jones et al., 1986](#) which assumes a sinusoidal temperature. pattern between Tmax and Tmin.

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
3.0	0.9
4.0	0.8
5.0	0.7

X	TempResponseProfile
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



1.2.14 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)

1.2.15 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:

$$\text{Photoperiod} = 0 \text{ (h)}$$

ApexAboveGround has a value between Emergence and HarvestRipe calculated as:

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

1.2.16 Vrn1

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

$$\text{Vrn1} = \text{Min}(\text{Saturation}, \text{CurrentExpression})$$

Where:

$$\text{Saturation} = 1 \text{ (Relative Expression)}$$

CurrentExpression = Accumulated Vernalisation between germination and terminalspikelet

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

$$\text{Return_Zero} = 0$$

ELSE

$$\text{elseReturn_Vernalisation} = [\text{Phenology}].\text{DailyVernalisation}$$

1.2.17 Vrn4

$$\text{Vrn4} = \text{Min}(\text{MaxExpression}, \text{CurrentExpression})$$

Where:

$$\text{MaxExpression} = [\text{Phenology}].\text{VernLag}$$

CurrentExpression = Accumulated VernalisationConditioning between germination and terminalspikelet

$$\text{VernalisationConditioning} = [\text{Phenology}].\text{DailyVernalisation}$$

1.2.18 Zadok

1.2.18.1 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
	stage number using the following table.
Growth Stage	ZadokStage
3.9	30

Growth Stage	ZadokStage
4.9	33
5.0	39
6.0	65
7.0	71
8.0	87
9.0	90

1.2.19 EmergenceDAS

Before Emergence

PreEventValue = 0

On Emergence the value is set to:

PostEventValue = [Plant].DaysAfterSowing

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 Barley 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:

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

Where *DeltaTips* is calculated as:

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

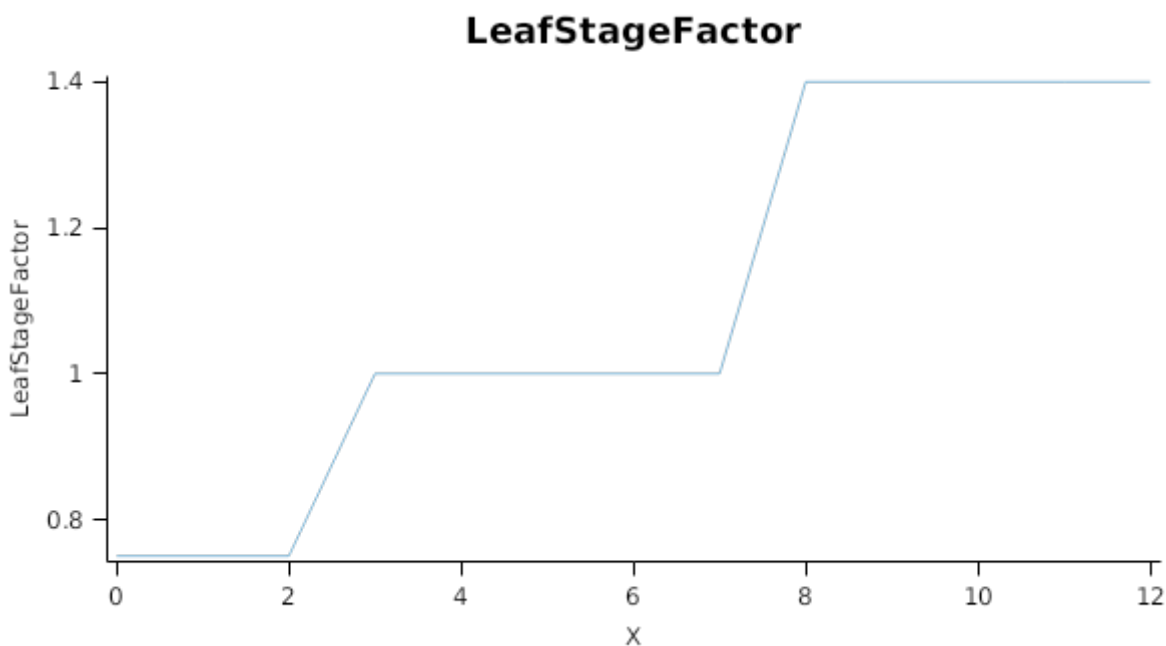
Where *Phyllochron* is the thermal time duration between the appearance of leaf tips given by:

This is the thermal time between the emergence of leaf tips where leaf appearance is 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 (Jamieson et al., 1998). There is also a photoperiod effect to give larger phyllochrons in shorter photoperiods (Miralles et al., 2000)

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

LeafStageFactor is calculated using linear interpolation

X	LeafStageFactor
0.0	0.8
2.0	0.8
3.0	1.0
7.0	1.0
8.0	1.4
11.0	1.4
12.0	1.4

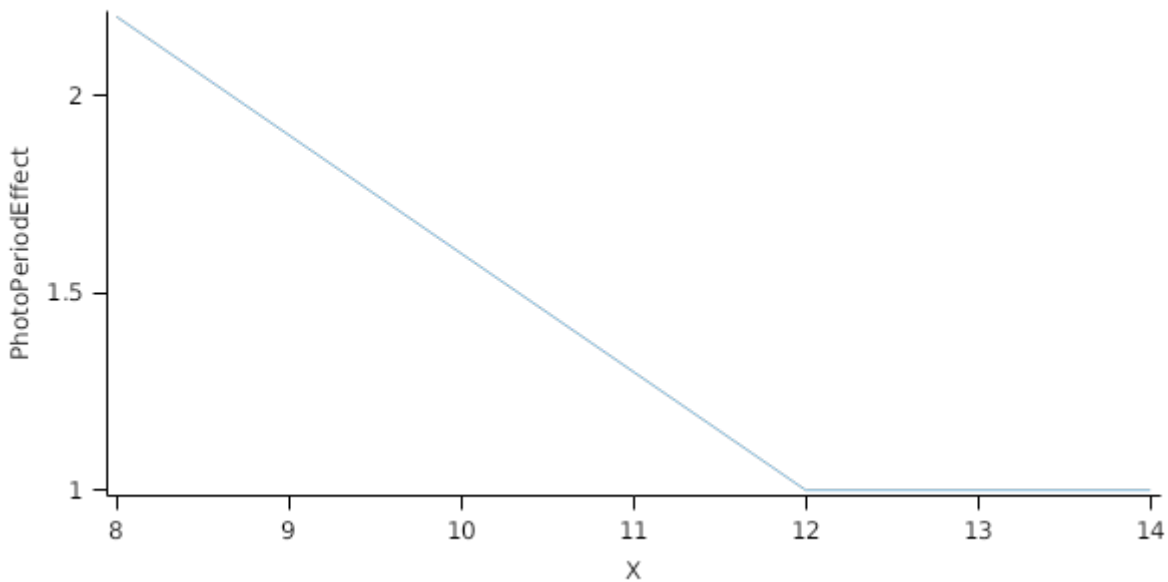


BasePhyllochron = 50 (oC.d)

PhotoPeriodEffect is calculated using linear interpolation

X	PhotoPeriodEffect
8.0	2.2
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:

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

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

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

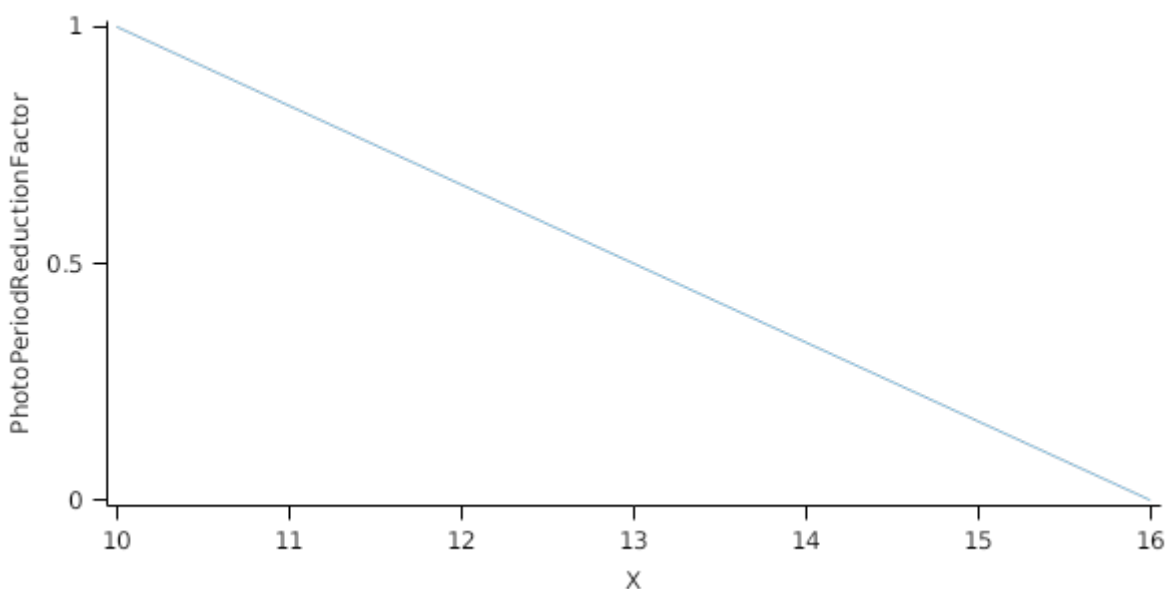
$$\text{VernalisationReductionFactor} = 1 - [\text{Phenology}].\text{Vrn1}$$

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

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:

$$TotalStemPopn = MainStemPopn + NewBranches - NewlyDeadBranches$$

Where:

$$NewBranches = MainStemPopn \times BranchingRate$$

BranchingRate is given by:

Potential branching rate is determined by the commonly observed pattern of tillering in Barley, 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.

$$BranchingRate = PotentialBranchingRate \times StressFactors$$

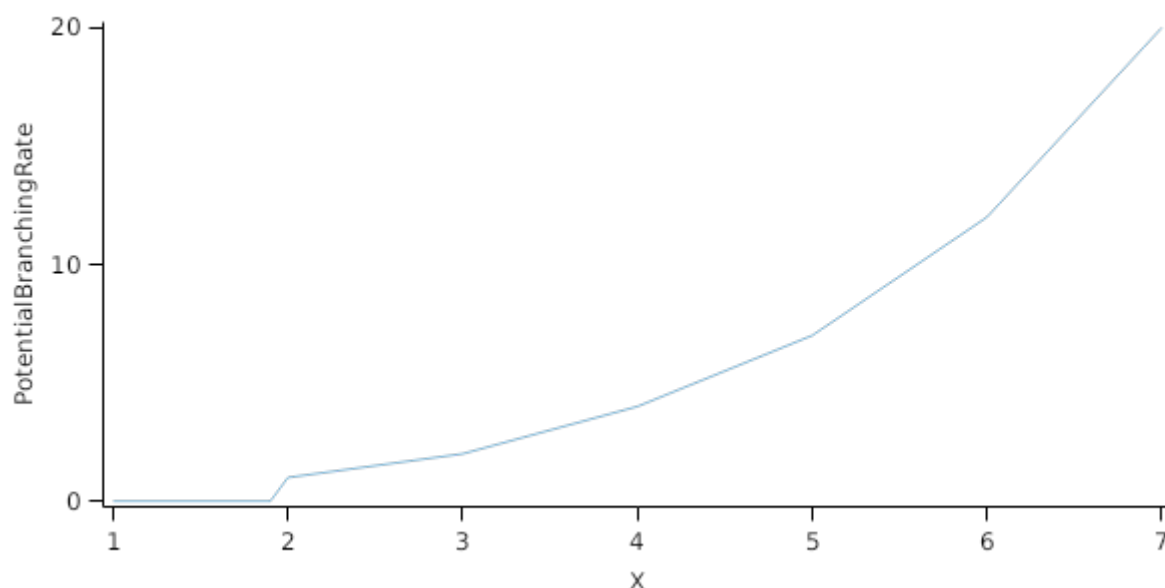
PotentialBranchingRate is calculated using specific values or functions for various growth phases. The function will use a value of zero for phases not specified below.

Vegetative has a value between Emergence and FlagLeaf calculated as:

PotentialBranchingRate is calculated using linear interpolation

X	PotentialBranchingRate
1.0	0.0
1.9	0.0
2.0	1.0
3.0	2.0
4.0	4.0
5.0	7.0
6.0	12.0
7.0	20.0

PotentialBranchingRate



Reproductive has a value between FlagLeaf and HarvestRipe calculated as:

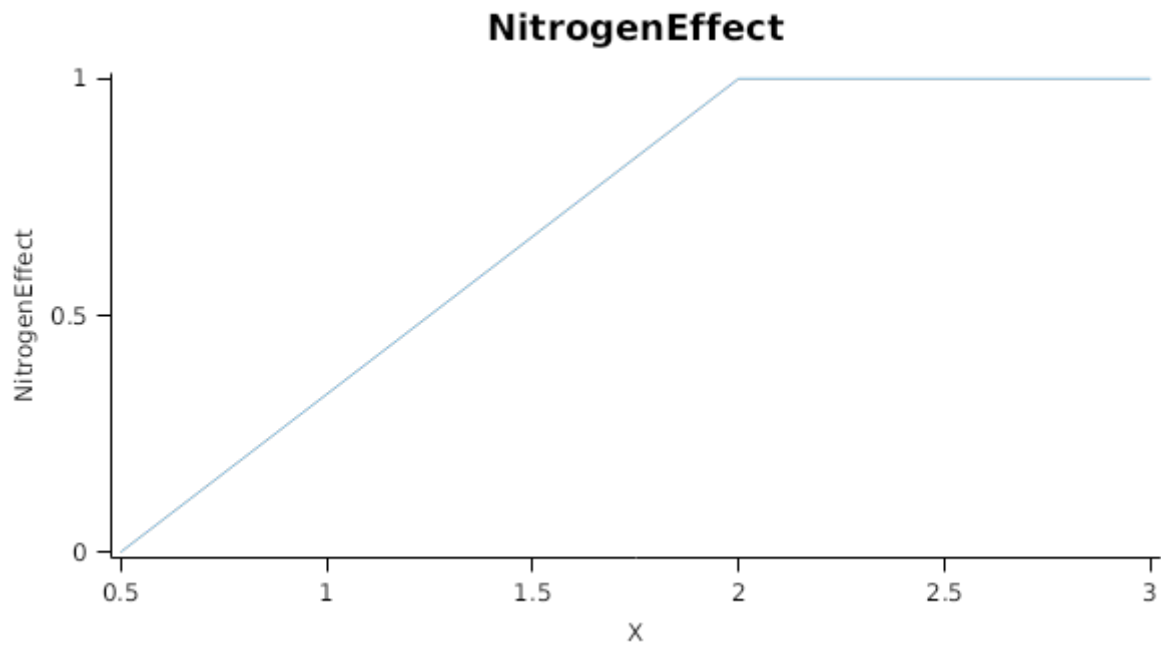
Zero = 0

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

Where:

NitrogenEffect is calculated using linear interpolation

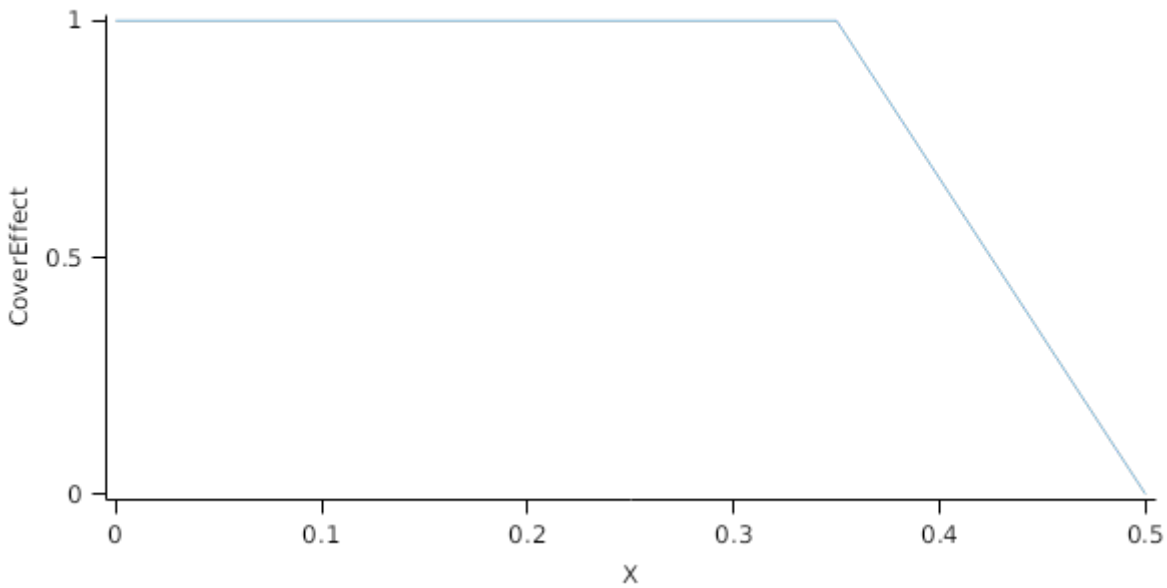
X	NitrogenEffect
0.5	0.0
2.0	1.0
3.0	1.0



CoverEffect is calculated using linear interpolation

X	CoverEffect
0.0	1.0
0.3	1.0
0.5	0.0

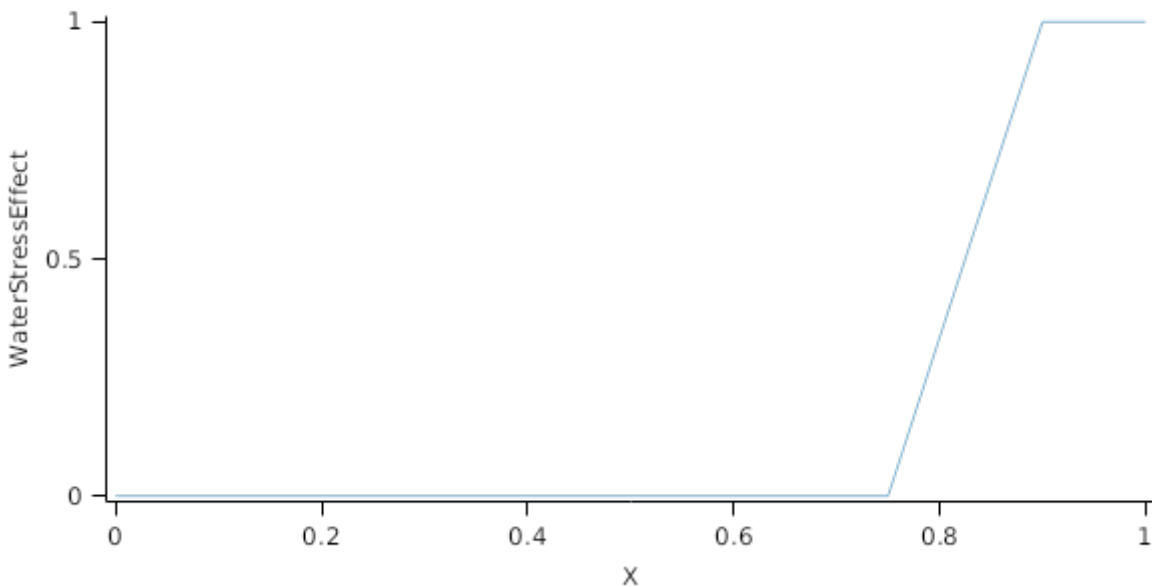
CoverEffect



WaterStressEffect is calculated using linear interpolation

X	WaterStressEffect
0.0	0.0
0.8	0.0
0.9	1.0
1.0	1.0

WaterStressEffect



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.

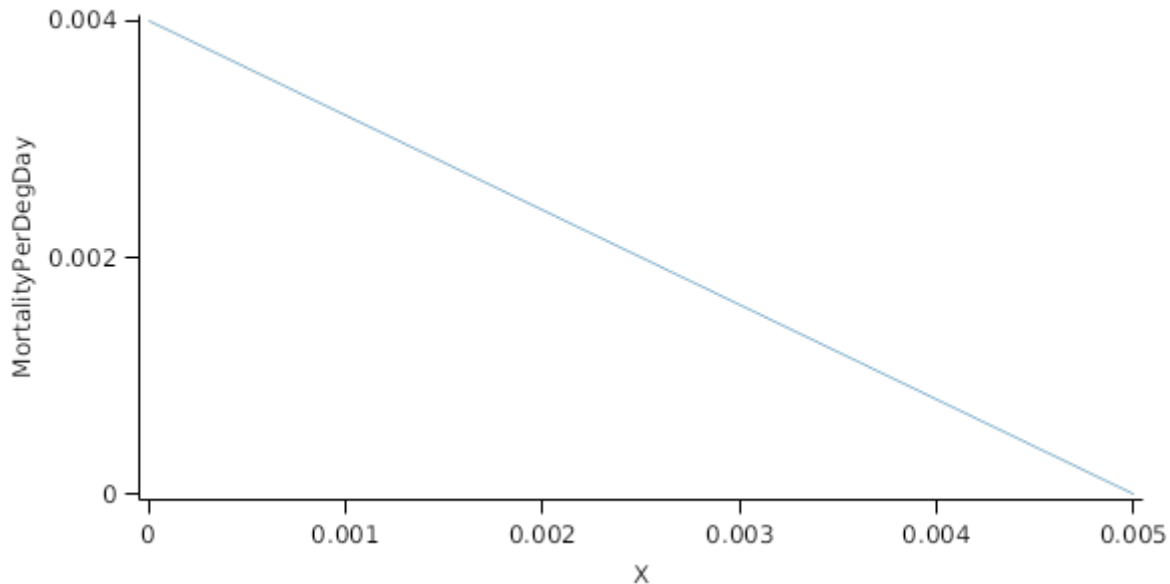
MortalityPhase has a value between *TerminalSpikelet* and *Flowering* calculated as:

$Mortality = MortalityPerDegDay \times [Phenology].ThermalTime$

$MortalityPerDegDay$ 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 = 0.05 (g)

MinimumNConc = 0.01

MaxNConcDailyGrowth = 0.02

MaximumNConc = 0.02

WaterContent = 0.12

DMConversionEfficiency = 1

RemobilisationCost = 0

CarbonConcentration = 0.4

1.4.2 NumberFunction

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

$GrainNumber = GrainsPerGramOfStem \times [StemPlusSpike].Wt$

GrainsPerGramOfStem = 35 (grains)

1.4.3 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.

$NumberFunction = [Grain].NumberFunction$

$FillingDuration = [Phenology].GrainDevelopment.Target$

$ThermalTime = [Phenology].ThermalTime$

$PotentialSizeIncrement = [Grain].InitialGrainProportion \times [Grain].MaximumPotentialGrainSize$

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.

$NumberFunction = [Grain].NumberFunction$

$FillingDuration = [Phenology].GrainFilling.Target$

$ThermalTime = [Phenology].ThermalTime$

$PotentialSizeIncrement = ProportionLinearPhase \times [Grain].MaximumPotentialGrainSize$

$ProportionLinearPhase = 1 - [Grain].InitialGrainProportion$

1.4.4 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 Flowering and EndGrainFill calculated as:

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

$NumberFunction = [Grain].NumberFunction$

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

$ThermalTime = [Phenology].ThermalTime$

$PotentialSizeIncrement = [Grain].MaximumPotentialGrainSize \times [Grain].MaximumNConc$

1.4.5 AccumThermalTime

$AccumThermalTime = Accumulated DailyThermalTimeValue$ between flowering and maturity

$DailyThermalTimeValue = [Phenology].ThermalTime$

1.4.6 Protein

$Protein = ([Grain].Live.N + [Grain].Dead.N) / ([Grain].Live.Wt + [Grain].Dead.Wt) \times 100 \times 5.71$

1.4.7 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	0	0	0
Cut	100	0	0	0
Prune	0	0	80	0
Graze	60	0	20	0
Thin	0	0	5	0

1.4.8 DM Demand Priority Factors

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

Structural = 1

Metabolic = 1

Storage = 1

1.4.9 N 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 Root

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

1.5.1 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.

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

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

Root depth is also constrained by a maximum root depth.

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

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

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

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

1.5.2 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.

1.5.3 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.

1.5.4 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. $NO_3 \text{ uptake} = NO_3 \times kNO_3 \times NO_{3ppm,i} \times NUptakeSWFactor$ $NH_4 \text{ uptake} = NH_4 \times kNH_4 \times NH_{4ppm,i} \times NUptakeSWFactor$ As can be seen from the above equations, the values of kNO3 and kNH4 equate to the potential fraction of each mineral N pool which can be taken up per day for wet soil when that pool has a concentration of 1 ppm. Nitrogen uptake demand is limited to the maximum daily potential uptake (MaxDailyNUptake) and the plant's N demand. The former provides a means to constrain N uptake to a maximum value observed in the field for the crop as a whole. The demand for soil N is then passed to the soil arbitrator which determines how much of the N uptake demand each plant instance will be allowed to take up.

1.5.5 Water Uptake

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

1.5.6 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

1.5.7 RootShape

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

1.5.8 NitrogenDemandSwitch

NitrogenDemandSwitch has a value between Germination and Maturity calculated as:

Constant = 1

1.5.9 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	20	0
Cut	0	0	30	0
Prune	0	0	10	0
Graze	0	0	15	0
Thin	0	0	5	0

1.5.10 RootFrontVelocity

$$\text{RootFrontVelocity} = \text{PotentialRootFrontVelocity} \times \text{TemperatureFactor} \times \text{WaterFactor}$$

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)

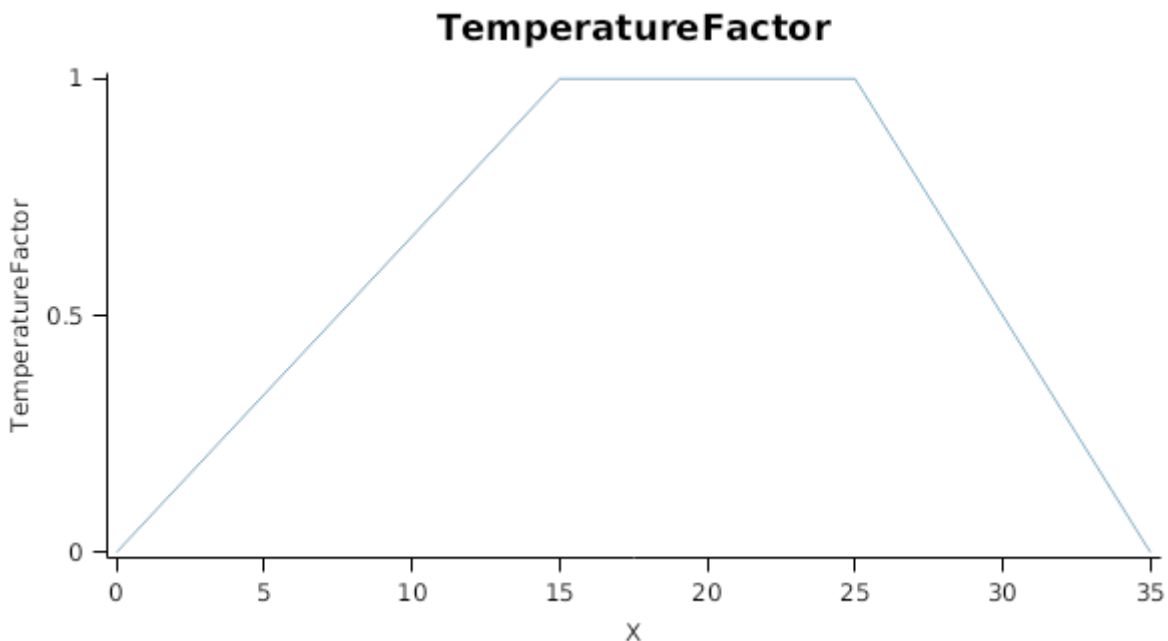
PostEmergence has a value between Emergence and Maturity calculated as:

Value = 20 (mm/d)

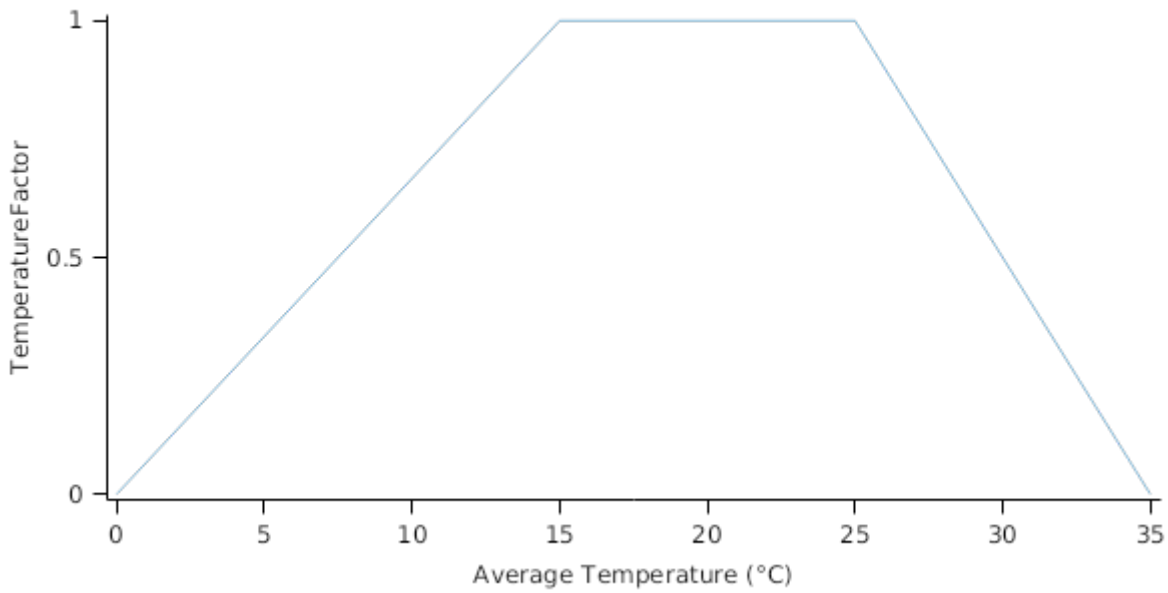
TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

$$\text{MaximumTemperatureWeighting} = 0.5$$

X	TemperatureFactor
0.0	0.0
15.0	1.0
25.0	1.0
35.0	0.0



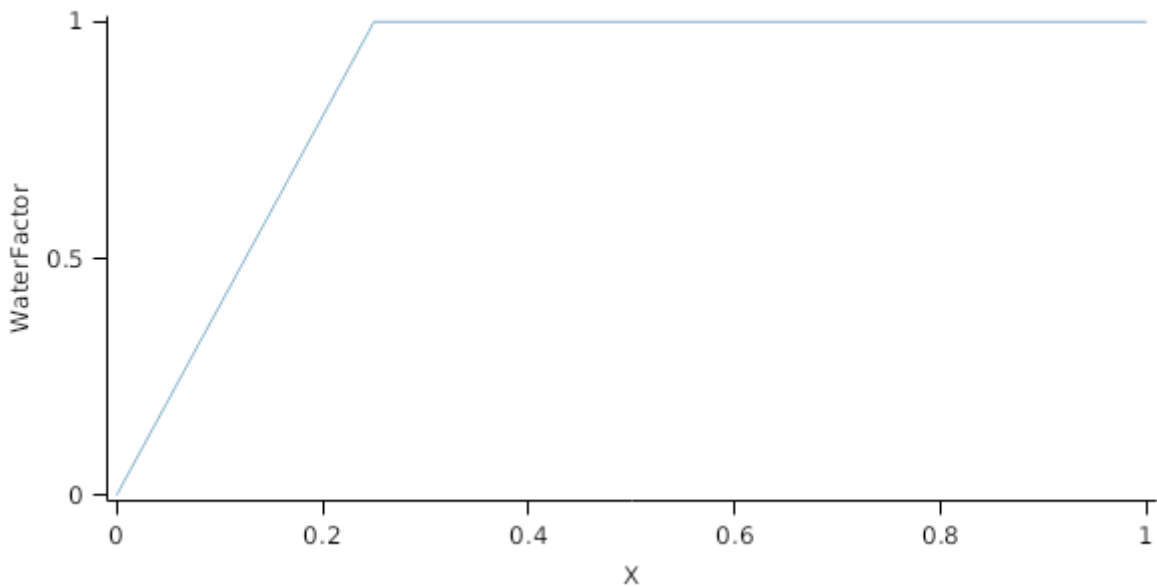
TemperatureFactor



WaterFactor is calculated using linear interpolation

X	WaterFactor
0.0	0.0
0.2	1.0
1.0	1.0

WaterFactor

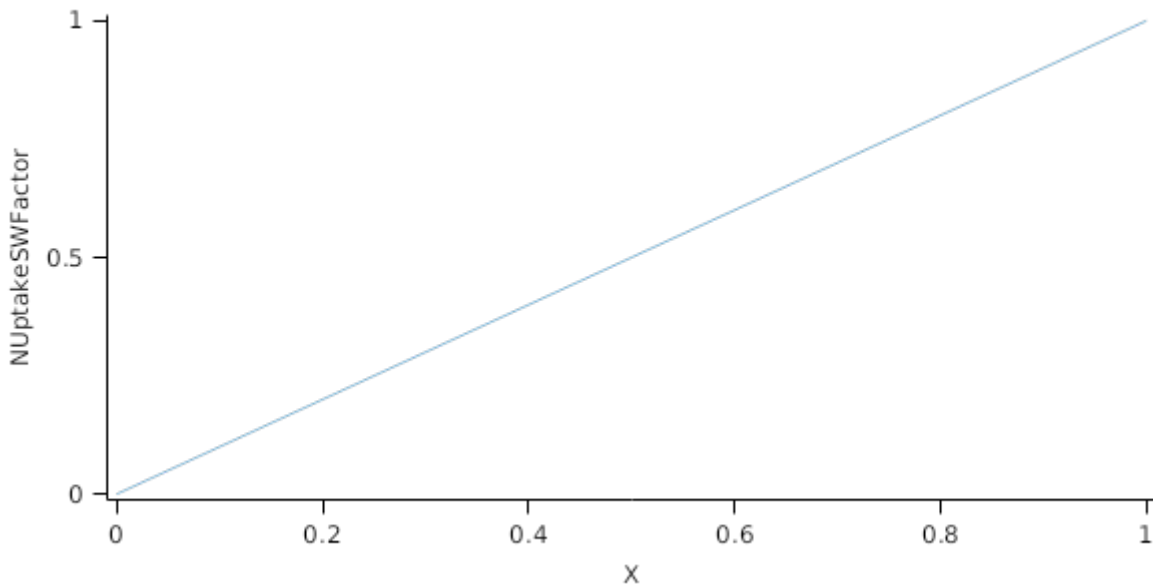


1.5.11 NUptakeSWFactor

NUptakeSWFactor is calculated using linear interpolation

X	NUptakeSWFactor
0.0	0.0
1.0	1.0

NUptakeSWFactor



1.5.12 DMDemands

1.5.12.1 DMDemands

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

Structural = DMDemandFunction x StructuralFraction

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

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction is calculated using 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:

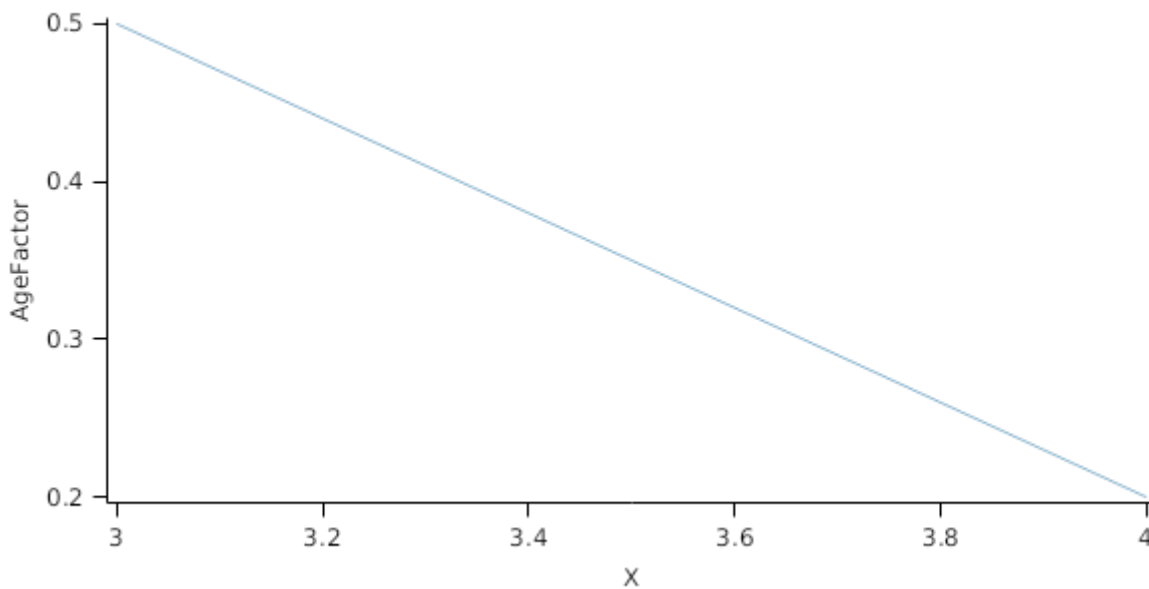
Value = 0

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.

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.5.13 NDemands

1.5.13.1 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

1.5.14 CriticalNConc

CriticalNConc = *[Root].MinimumNConc*

1.5.15 InitialWt

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

Structural = 0.005 (g/plant)

Metabolic = 0

Storage = 0

1.6 Leaf

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

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

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

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

1.6.1 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:

ExtinctionCoeff = 0.6

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

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

The potential photosynthesis calculated using RUE is then adjusted according to stress factors, these account for plant nutrition (FN), air temperature (FT), vapour pressure deficit (FVPD), water supply (FW) and atmospheric CO₂ concentration (FCO₂).

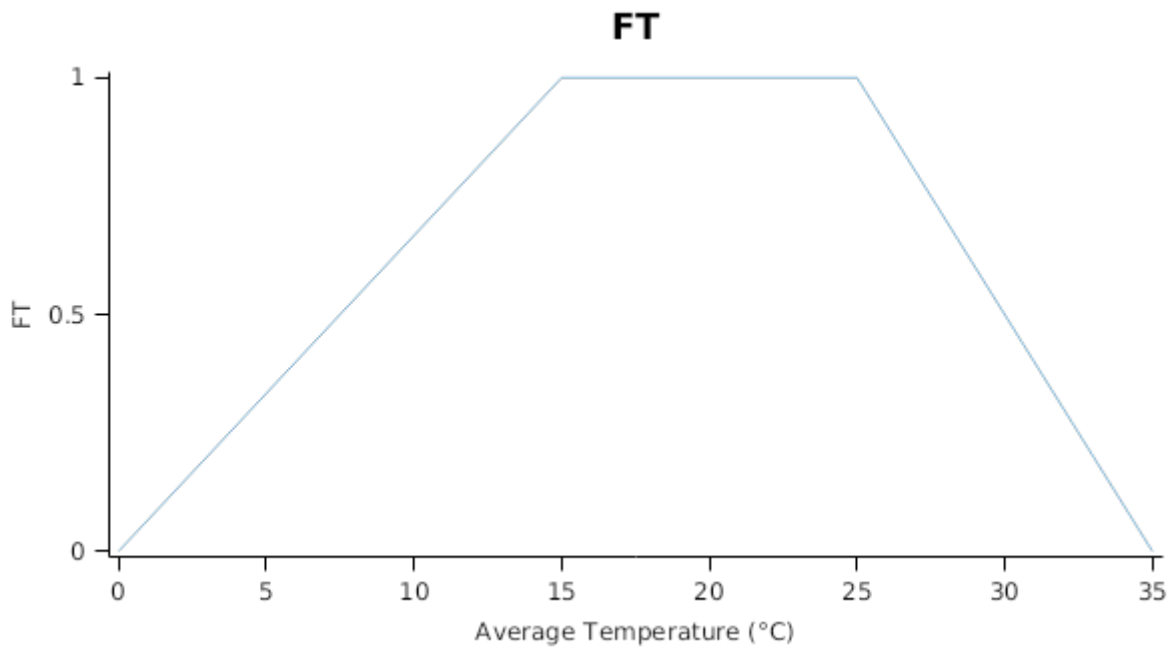
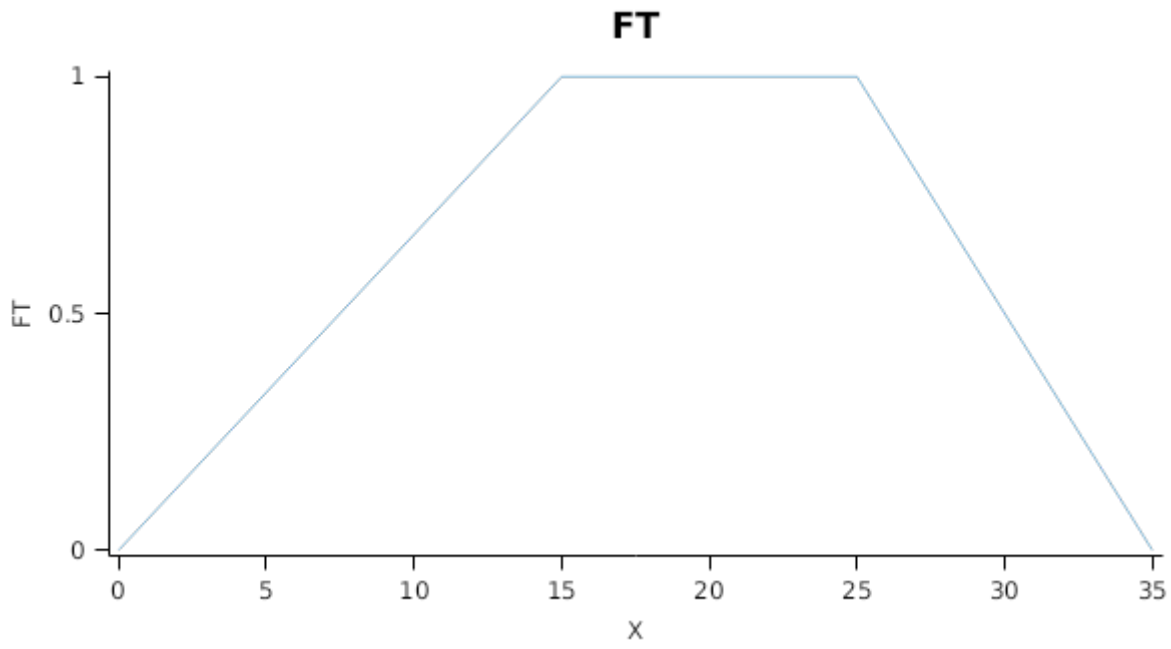
NOTE: RUE in this model is expressed as g/MJ for a whole plant basis, including both above and below ground growth.

RUE = 1.5

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

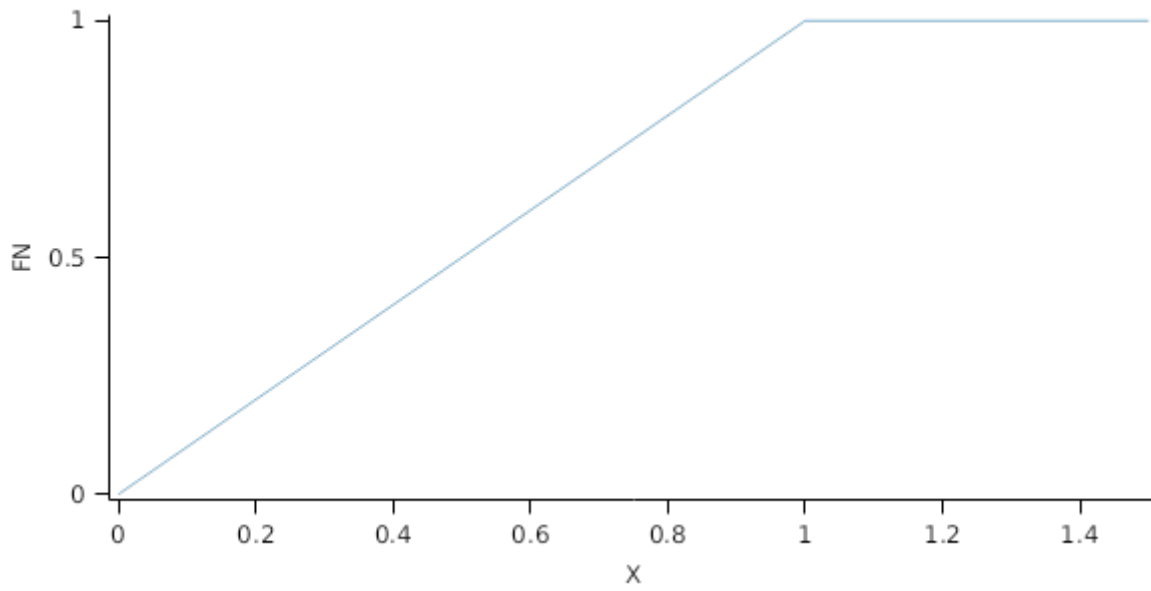
X	FT
0.0	0.0
15.0	1.0
25.0	1.0
35.0	0.0



FN is calculated using linear interpolation

X	FN
0.0	0.0
1.0	1.0
1.5	1.0

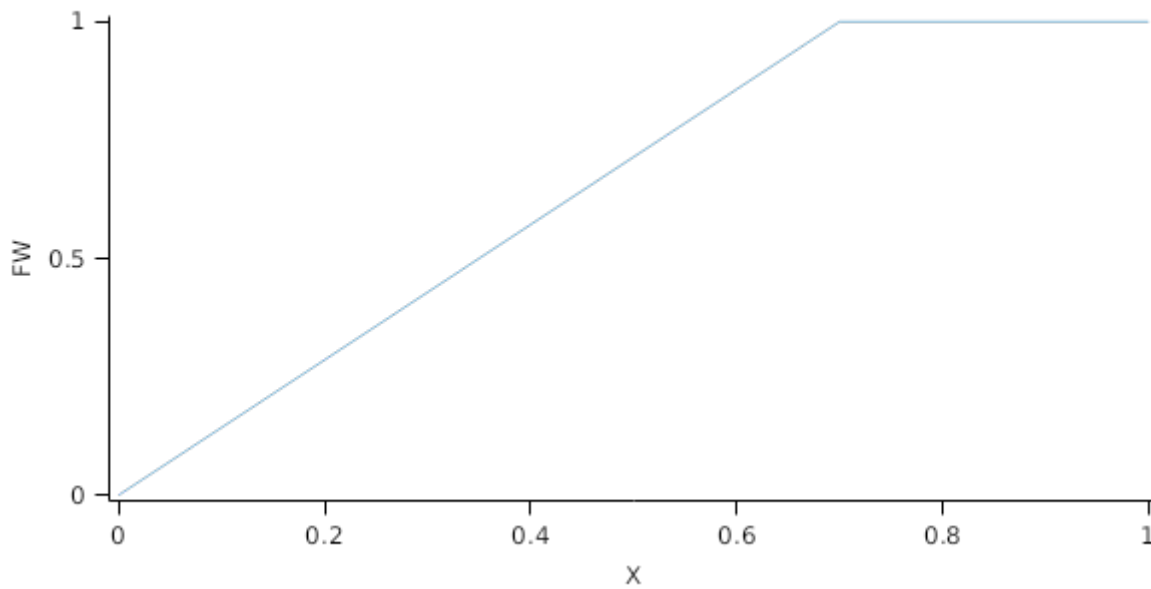
FN



FW is calculated using linear interpolation

X	FW
0.0	0.0
0.7	1.0
1.0	1.0

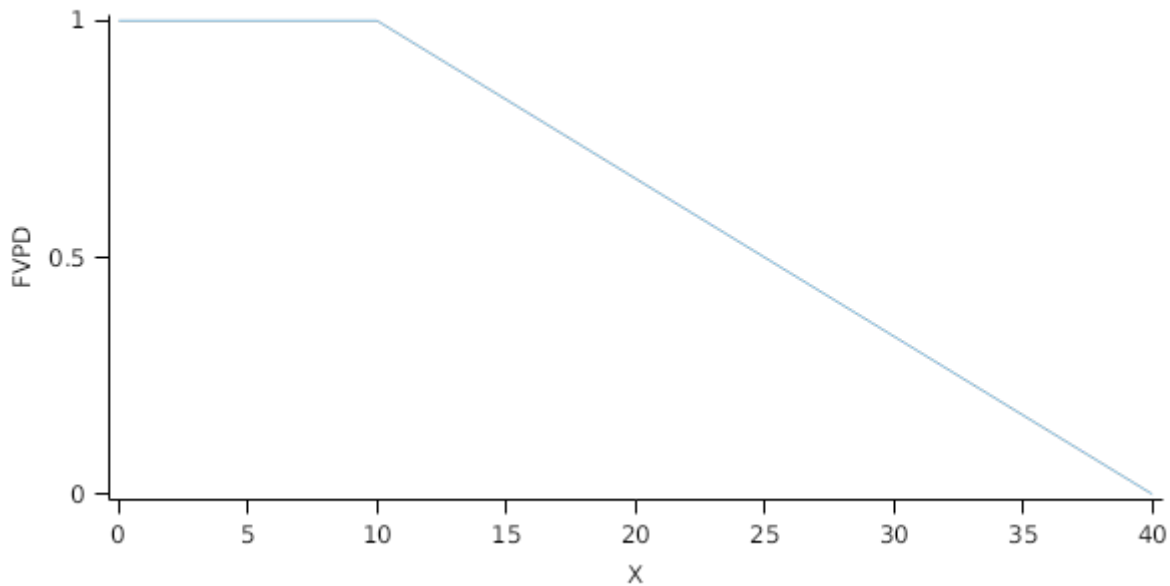
FW



FVPD is calculated using linear interpolation

X	FVPD
0.0	1.0
10.0	1.0
40.0	0.0

FVPD



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

For C3 plants,

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

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

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

For C4 plants,

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

$$RadnInt = [Leaf].RadiationIntercepted$$

1.6.2 Constants

FrostFraction = 0

ExtinctionCoeff = 0.6

StructuralFraction = 0.5

DMConversionEfficiency = 1

RemobilisationCost = 0

CarbonConcentration = 0.4

StomatalConductanceCO2Modifier = 1

WidthFunction = 0

1.6.3 InitialLeaves[1]

Area = 200

1.6.4 InitialLeaves[2]

Area = 0

1.6.5 CohortParameters

1.6.5.1 Potential Leaf Area index

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

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

$$Multiplier = 1.3$$

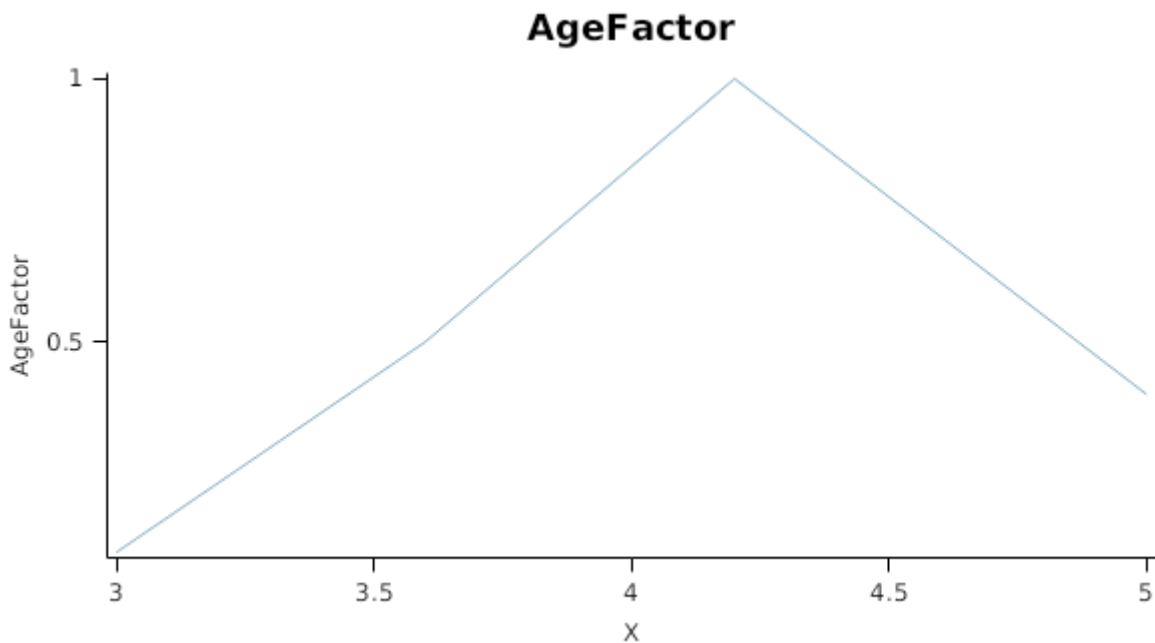
If no stress occurs the leaves will reach a Maximum area (*MaxArea*) at the end of the *GrowthDuration*. The *MaxArea* is defined by:

$$MaxArea = AreaLargestLeaves \times AgeFactor$$

$$AreaLargestLeaves = 2000 \text{ (mm}^2\text{)}$$

AgeFactor is calculated using linear interpolation

X	AgeFactor
3.0	0.1
3.6	0.5
4.2	1.0
5.0	0.4



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*

$$LagDuration = LastLeafDuration \times AgeFactor$$

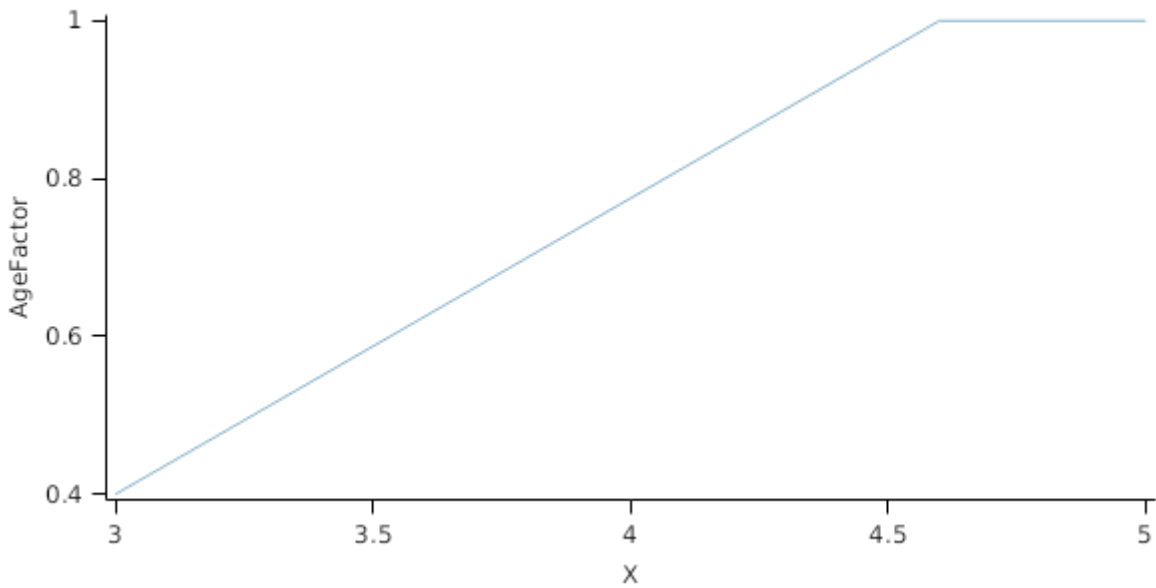
$$LastLeafDuration = ThermalTimeToRipe - [Leaf].CohortParameters.SenescenceDuration$$

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

AgeFactor is calculated using linear interpolation

X	AgeFactor
3.0	0.4
4.6	1.0
5.0	1.0

AgeFactor



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

Multiplier = 2

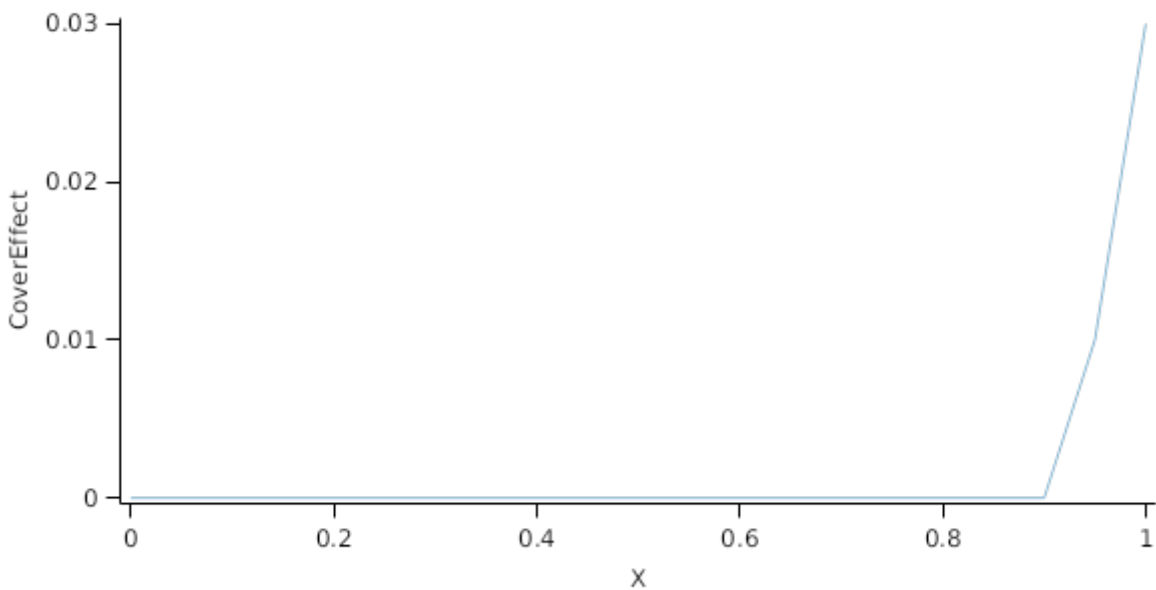
Mutual shading can cause premature senescence of cohorts if the leaf area above them becomes too great. Each cohort models the proportion of its area that is lost to shade induced senescence each day as:

$$\text{ShadeInducedSenescenceRate} = \text{CoverEffect} \times [\text{Phenology}].\text{ThermalTime}$$

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



1.6.5.2 Stress effects on Leaf Area Index

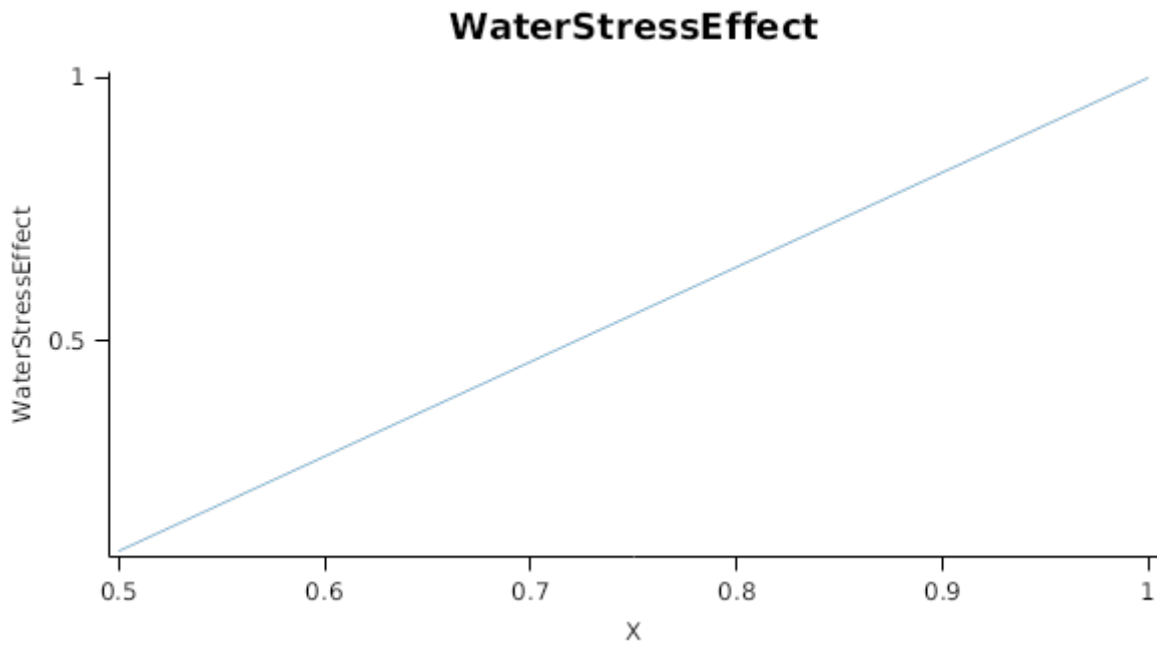
Stress reduces leaf area in a number of ways. Firstly, stress occurring prior to the appearance of the cohort can reduce cell division, so reducing the maximum leaf size. Leaf captures this by multiplying the *MaxSize* of each cohort by a *CellDivisionStress* factor which is calculated as:

$$\text{CellDivisionStress} = \text{Min}(\text{WaterStressEffect}, \text{NitrogenStressEffect})$$

Where:

WaterStressEffect is calculated using linear interpolation

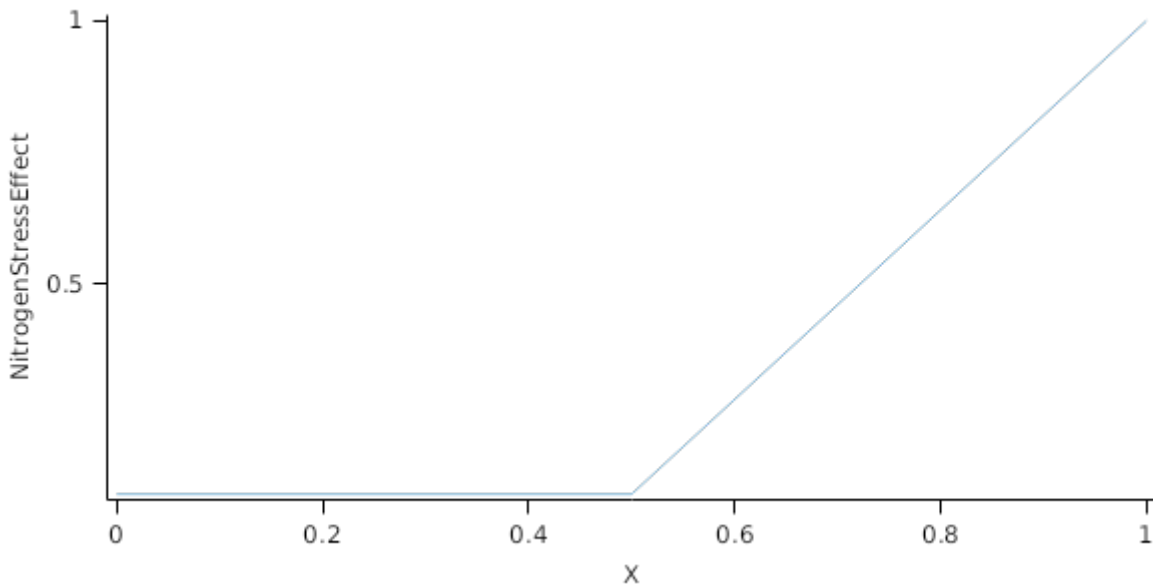
X	WaterStressEffect
0.5	0.1
1.0	1.0



NitrogenStressEffect is calculated using linear interpolation

X	NitrogenStressEffect
0.0	0.1
0.5	0.1
1.0	1.0

NitrogenStressEffect



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

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

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

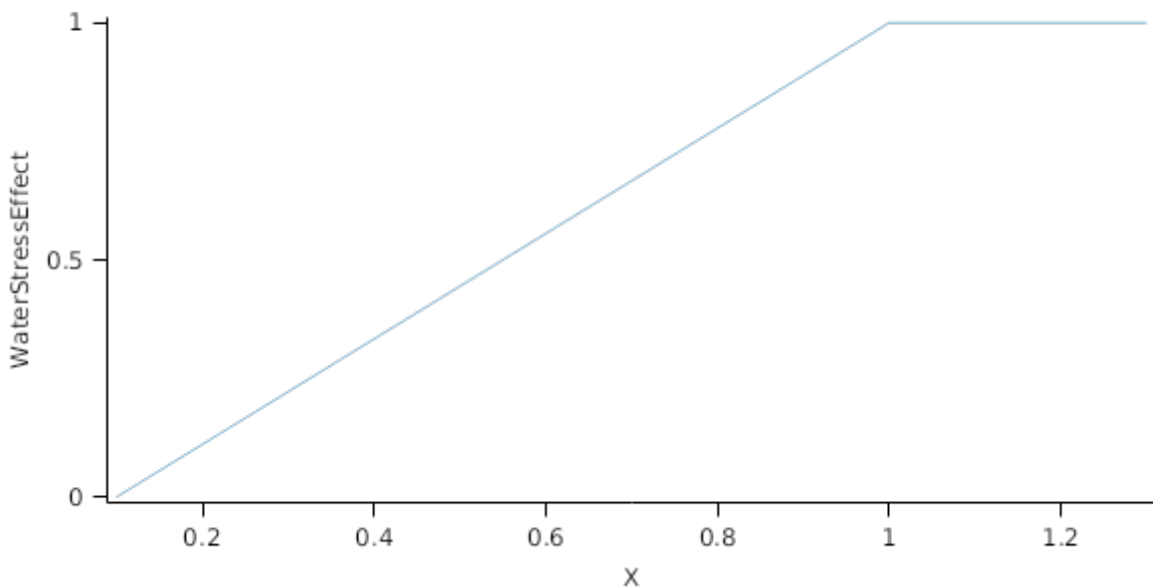
$$ExpansionStress = \text{Min}(WaterStressEffect, NitrogenStressEffect)$$

Where:

$WaterStressEffect$ is calculated using linear interpolation

X	WaterStressEffect
0.1	0.0
1.0	1.0
1.3	1.0

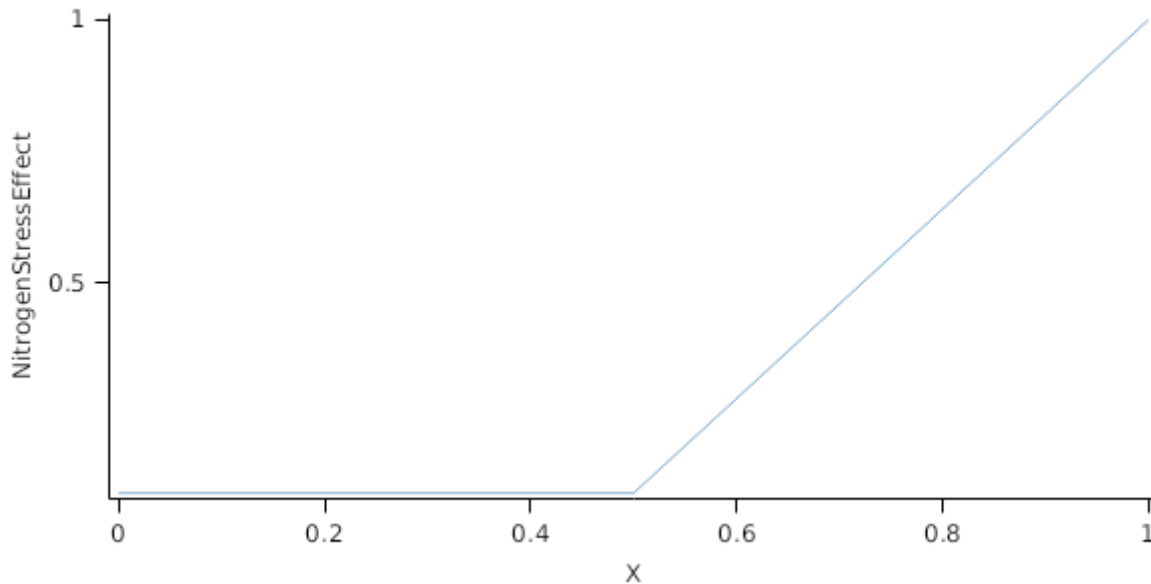
WaterStressEffect



NitrogenStressEffect is calculated using linear interpolation

X	NitrogenStressEffect
0.0	0.1
0.5	0.1
1.0	1.0

NitrogenStressEffect



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.

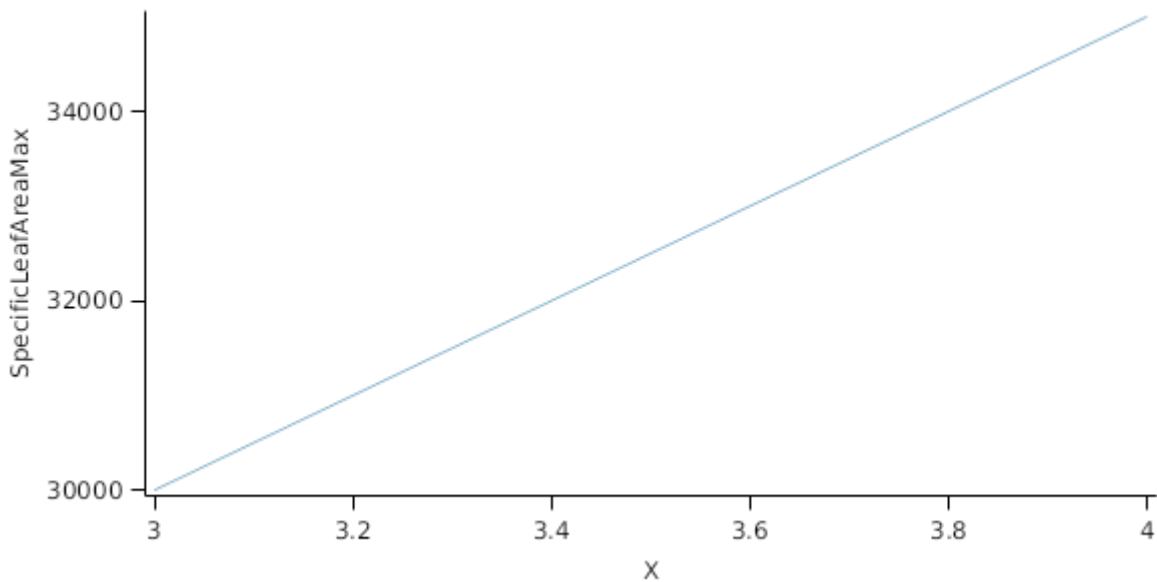
1.6.5.3 Dry matter Demand

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

SpecificLeafAreaMax is calculated using linear interpolation

X	SpecificLeafAreaMax
3.0	30000.0
4.0	35000.0

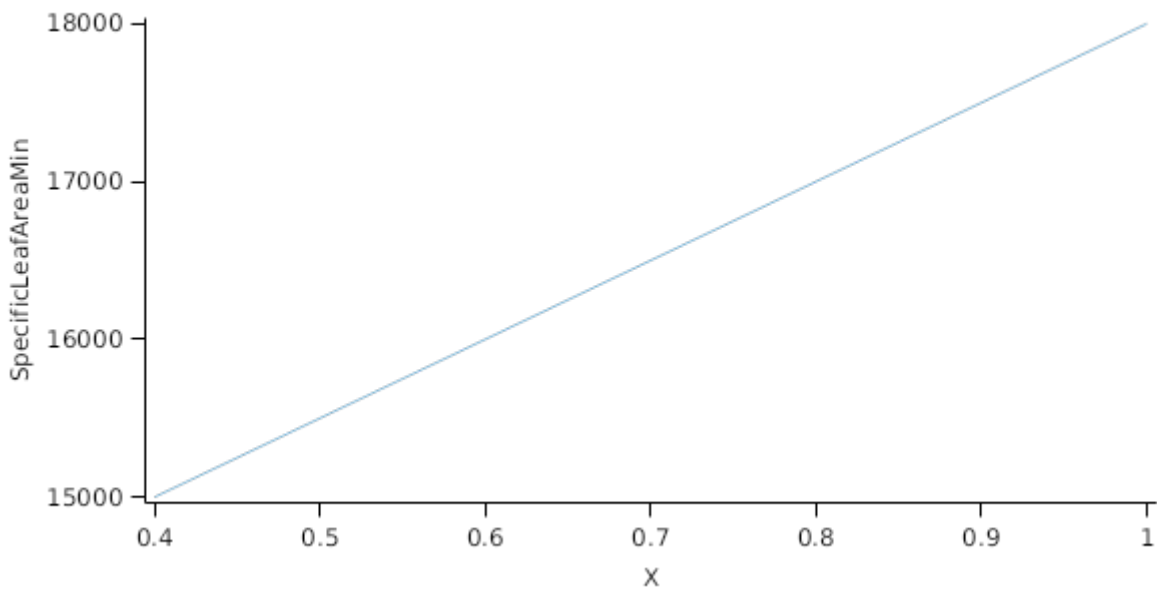
SpecificLeafAreaMax



SpecificLeafAreaMin is calculated using linear interpolation

X	SpecificLeafAreaMin
0.4	15000.0
1.0	18000.0

SpecificLeafAreaMin



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

$StructuralFraction = 0.1$

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

1.6.5.4 Nitrogen Demand

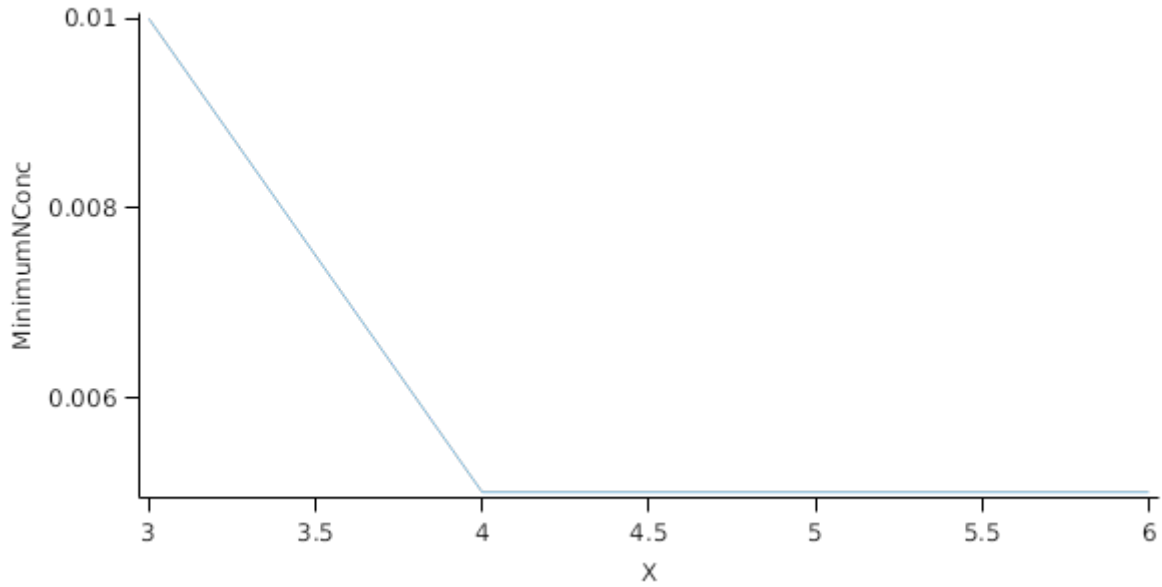
Leaf calculates the N demand from each cohort as a function of the potential DM increment and N concentration bounds.

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



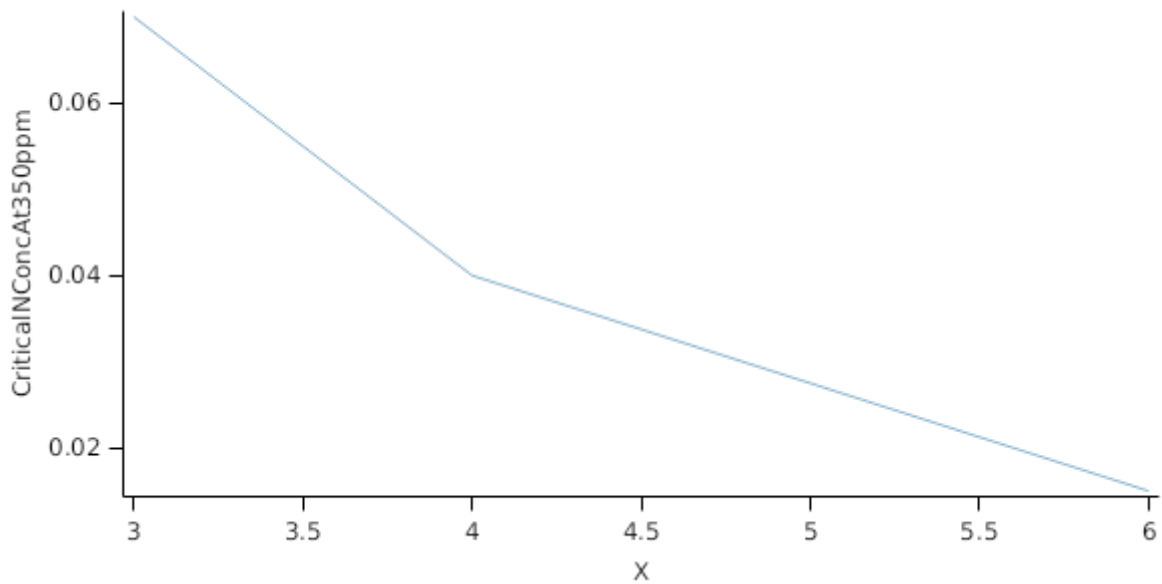
Metabolic N demand is calculated as $PotentialMetabolicDMAAllocation * (CriticalNConc - MinimumNConc)$ where:

$CriticalNConc = CriticalNConcAt350ppm * CO2Factor$

$CriticalNConcAt350ppm$ is calculated using linear interpolation

X	CriticalNConcAt350ppm
3.0	0.1
4.0	0.0
6.0	0.0

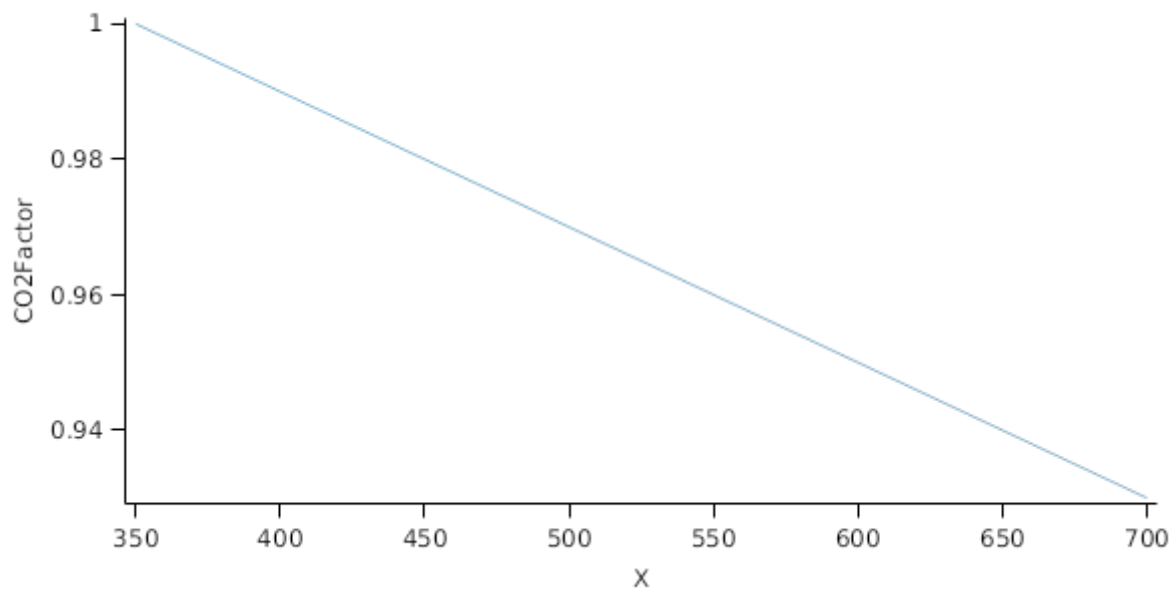
CriticalNConcAt350ppm



CO2Factor is calculated using linear interpolation

X	CO2Factor
350.0	1.0
700.0	0.9

CO2Factor

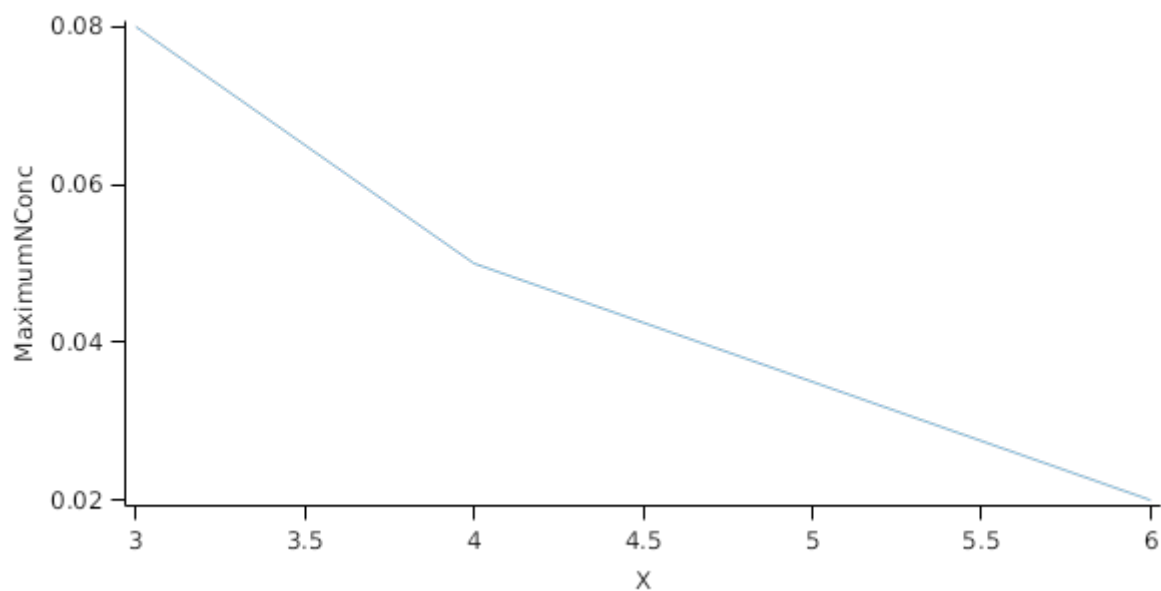


Storage N demand is calculated as the sum of metabolic and structural wt (including today's demands) multiplied by *LuxaryNconc* ($MaximumNConc - CriticalNConc$) less the amount of storage N already present. *MaximumNConc* is given by:

MaximumNConc is calculated using linear interpolation

X	MaximumNConc
3.0	0.1
4.0	0.1
6.0	0.0

MaximumNConc



1.6.5.5 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 :

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

1.6.5.6 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 :

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

1.6.5.7 Constants

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

$\text{MaintenanceRespirationFunction} = 0$

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

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

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

$\text{DetachmentLagDuration} = 1000000$

$\text{DetachmentDuration} = 1000000$

$\text{RelativeBranchLeafSize} = 1$

$\text{InitialNConc} = 0$

$\text{StructuralFraction} = 0.1$

$\text{StorageFraction} = 0$

$\text{LeafSizeShapeParameter} = 0.3$

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

$\text{RemobilisationCost} = 0$

$\text{CarbonConcentration} = 0.4$

1.6.6 ThermalTime

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

1.6.7 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:

$$RUE_FN = [Leaf].Photosynthesis.FN$$

$$RUE_FVPD = [Leaf].Photosynthesis.FVPD$$

1.6.8 BiomassRemovalDefaults

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

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	30	30
Cut	80	80	0	0
Prune	0	0	60	60
Graze	60	60	10	10
Thin	0	0	5	5

1.6.9 StomatalConductanceCO2Modifier1

$$StomatalConductanceCO2Modifier1 = [Leaf].Photosynthesis.FCO2 / RelativeCO2Gradient$$

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

1.6.10 CO2internal

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

1.6.11 DepthFunction

$$DepthFunction = [Leaf].Height$$

1.6.12 DMDemandPriorityFactors

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

$$\text{Structural} = 1$$

$$\text{Metabolic} = 1$$

$$\text{Storage} = 1$$

1.6.13 NDemandPriorityFactors

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

$$\text{Structural} = 1$$

$$\text{Metabolic} = 1$$

$$\text{Storage} = 1$$

1.7 Spike

1.7.1 Spike

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.

1.7.2 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.

1.7.2.1 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 = 1

$OrganPopulation = [Spike].HeadNumber$

StartStage = 5

MaximumOrganWt = 0.25

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

StructuralFraction = 0.9

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.7.3 Nitrogen Demand

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

1.7.3.1 NDemands

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

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

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

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

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

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

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

$NitrogenDemandSwitch = [Spike].nitrogenDemandSwitch$

$MaxNconc = [Spike].maximumNconc$

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.7.4 N Concentration Thresholds

MinimumNConc = 0.004

$CriticalNConc = [Spike].MinimumNConc$

MaximumNConc = 0.015

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

1.7.5 Dry Matter Supply

Spike 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

1.7.6 Nitrogen Supply

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

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

1.7.7 Senescence and Detachment

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

Spike 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	50	0	10	0
Cut	80	0	0	0
Prune	0	0	60	0
Graze	60	0	20	0
Thin	0	0	5	0

1.8 Stem

1.8.1 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.

1.8.2 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.

$Structural = DM_{DemandFunction} \times StructuralFraction$

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.

PreStemElongation has a value between Emergence and TerminalSpikelet calculated as:

StemFraction = 0.2

StemElongation has a value between TerminalSpikelet and StartGrainFill calculated as:

StemFraction = 0.7

EarEmergence has a value between StartGrainFill and Maturity calculated as:

StemFraction = 0.6

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 FlagLeaf calculated as:

Fraction = 0.7

ReproductiveGrowth has a value between FlagLeaf and HarvestRipe calculated as:

Fraction = 0.05

Metabolic = 0

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

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

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.

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

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

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

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

1.8.4 N Concentration Thresholds

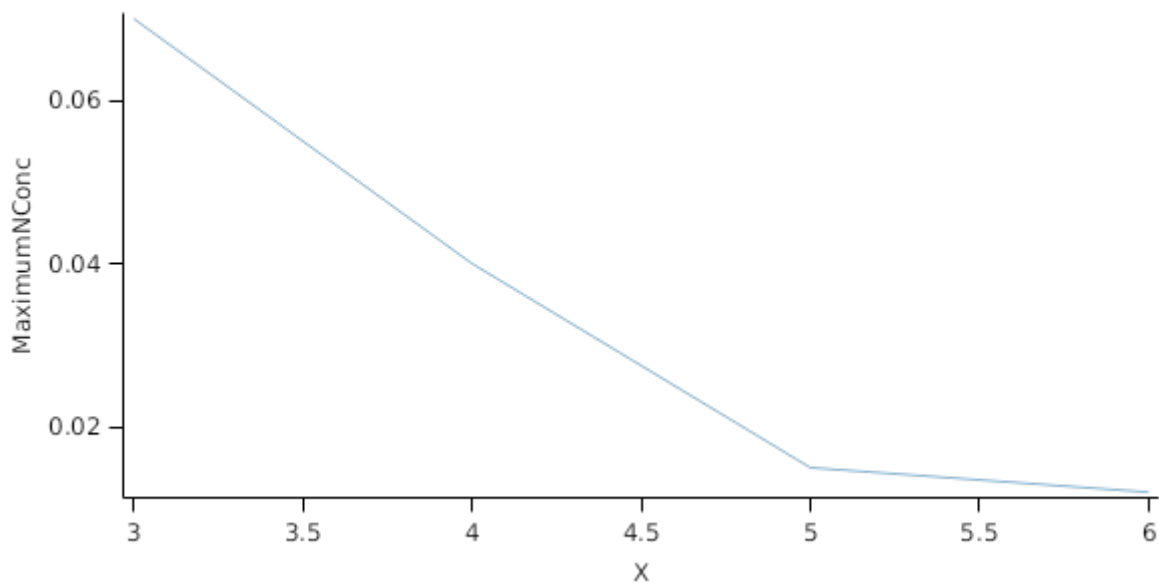
MinimumNConc = 0.0025

CriticalNConc = [Stem].MinimumNConc

MaximumNConc is calculated using linear interpolation

X	MaximumNConc
3.0	0.1
4.0	0.0
5.0	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

1.8.5 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 = 0.05

1.8.6 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

1.8.7 Senescence and Detachment

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

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	50	0	10	0
Cut	80	0	0	0
Prune	0	0	60	0
Graze	60	0	20	0
Thin	0	0	5	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
- * Spike
- * 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
- * Spike
- * 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
- * Spike
- * 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
- * Spike
- * 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
- * Spike
- * 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
- * Spike
- * 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:

- * Spike
- * Grain

1.17 StemPlusSpike

1.17.1 StemPlusSpike

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

StemPlusSpike summarises the following biomass objects:

- * Stem
- * Spike

1.18 Cultivars

1.18.1 NewZealand

1.18.1.1 Booma

Booma overrides the following properties:

1.18.1.2 Bumpa

Bumpa overrides the following properties:

1.18.1.3 Boss

Boss overrides the following properties:

[Phenology].PpSensitivity.FixedValue = 5

1.18.1.4 Cellar

Cellar overrides the following properties:

1.18.1.5 County

County overrides the following properties:

1.18.1.6 Dash

Dash overrides the following properties:

[Leaf].ExtinctionCoeff.FixedValue = 0.5

[Root].RootFrontVelocity.PotentialRootFrontVelocity.PostEmergence.Value.FixedValue = 20

1.18.1.7 Doyen

Doyen overrides the following properties:

1.18.1.8 Hooded

Hooded overrides the following properties:

1.18.1.9 Omaka

Omaka overrides the following properties:

[Root].RootFrontVelocity.PotentialRootFrontVelocity.PostEmergence.Value.FixedValue = 30

1.18.1.10 Omaka1

Omaka1 overrides the following properties:

[Leaf].ExtinctionCoeff.FixedValue = 0.5

[Leaf].CohortParameters.MaxArea.AreaLargestLeaves.FixedValue = 2000

[Root].RootFrontVelocity.PotentialRootFrontVelocity.PostEmergence.Value.FixedValue = 30

1.18.1.11 Optic

Optic overrides the following properties:

1.18.1.12 Pyramid

Pyramid overrides the following properties:

1.18.1.13 Quench

Quench overrides the following properties:

1.18.1.14 Retriever

Retriever overrides the following properties:

[Phenology].PpSensitivity.FixedValue = 5

1.18.1.15 Sherwood

Sherwood overrides the following properties:

1.18.1.16 Tavern

Tavern overrides the following properties:

1.18.1.17 Triumph

Triumph overrides the following properties:

[Phenology].PpSensitivity.FixedValue = 10

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.1.18 Valetta

Valetta overrides the following properties:

[Phenology].PpSensitivity.FixedValue = 3

1.18.1.19 Vortex

Vortex overrides the following properties:

1.18.2 Australia

1.18.2.1 Alestar

Alestar overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 0.33

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.2 Banks

Banks overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8

[Phenology].PpSensitivity.FixedValue = 0.5

[Phenology].VrnSensitivity.FixedValue = 1.33

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.3 Baudin

Baudin overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 3

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.4 Bass

Bass overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8.33

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 2

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.5 Biere

Biere overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8.33

[Phenology].PpSensitivity.FixedValue = 0

[Phenology].VrnSensitivity.FixedValue = 2.66

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.6 Buloke

Buloke overrides the following properties:

[Phenology].PpSensitivity.FixedValue = 4

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.7 Cassiopee

Cassiopee overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 11.33

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 0.33

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.8 Capstan

Capstan overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 4

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.9 Commander

Commander overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 3

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.10 Compass

Compass overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 1.33

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.11 CSIROB1

CSIROB1 overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 7.33

[Phenology].PpSensitivity.FixedValue = 1.66

[Phenology].VrnSensitivity.FixedValue = 2.66

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.12 CSIROB3

CSIROB3 overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 6

[Phenology].PpSensitivity.FixedValue = 2

[Phenology].VrnSensitivity.FixedValue = 0.66

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.13 Dash

Dash overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 10.66

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 2.33

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.14 Fathom

Fathom overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 6

[Phenology].PpSensitivity.FixedValue = 3

[Phenology].VrnSensitivity.FixedValue = 3

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.15 Fleet

Fleet overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 4

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.16 Flinders

Flinders overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8.33

[Phenology].PpSensitivity.FixedValue = 0.66

[Phenology].VrnSensitivity.FixedValue = 1.16

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.17 Franklin

Franklin overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 10

[Phenology].PpSensitivity.FixedValue = 0.5

[Phenology].VrnSensitivity.FixedValue = 1

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.18 Gairdner

Gairdner overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 10

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 2

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.19 Granger

Granger overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 2.5

[Phenology].VrnSensitivity.FixedValue = 1

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.20 Grimmatt

Grimmett overrides the following properties:

[Phenology].PpSensitivity.FixedValue = 5

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

[Grain].NumberFunction.GrainNumber.GrainsPerGramOfStem.FixedValue = 25

1.18.2.21 Grout

Grout overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 7.33

[Phenology].PpSensitivity.FixedValue = 1.66

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.22 Hindmarsh

Hindmarsh overrides the following properties:

[Phenology].PpSensitivity.FixedValue = 4

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.23 Keel

Keel overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 2

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.24 Lockyer

Lockyer overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 6.66

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 1

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.25 Mudah

Mudah overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.26 Navigator

Navigator overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8

[Phenology].PpSensitivity.FixedValue = 2

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.27 Oxford

Oxford overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 4

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.28 RGT_Planet

RGT_Planet overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 0.5

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.29 Rosalind

Rosalind overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 2

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.30 Schooner

Schooner overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8

[Phenology].PpSensitivity.FixedValue = 0

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.31 Scope

Scope overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 2

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.32 Shepherd

Shepherd overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 0

[Phenology].VrnSensitivity.FixedValue = 0.33

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.33 Spartacus_CL

Spartacus_CL overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 6

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 1.33

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.34 Stirling

Stirling overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 8

[Phenology].PpSensitivity.FixedValue = 1

[Phenology].VrnSensitivity.FixedValue = 0

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.35 Unicorn

Unicorn overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 7

[Phenology].PpSensitivity.FixedValue = 3

[Phenology].VrnSensitivity.FixedValue = 0.66

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.36 Urambie

Urambie overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9.66

[Phenology].PpSensitivity.FixedValue = 0.33

[Phenology].VrnSensitivity.FixedValue = 8

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.37 Westminster

Westminster overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 9

[Phenology].PpSensitivity.FixedValue = 0.5

[Phenology].VrnSensitivity.FixedValue = 0.33

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.18.2.38 Yagan

Yagan overrides the following properties:

[Phenology].MinimumLeafNumber.FixedValue = 7

[Phenology].PpSensitivity.FixedValue = 2

[Phenology].VrnSensitivity.FixedValue = 1.33

[Phenology].EarlyReproductivePpSensitivity.FixedValue = 2

[Structure].BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay.XYPairs.Y = 0.001,0

1.19 MortalityRate

MortalityRate = 0

2 Validation

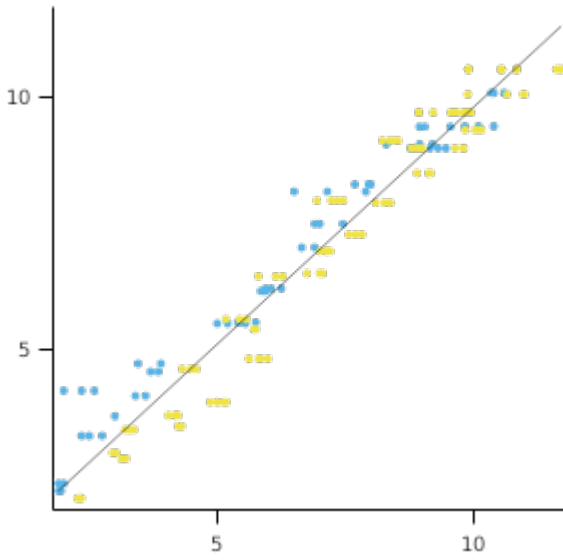
A test dataset has been developed to test the APSIM barley model for a range of environmental (soil and climate) conditions, management options (sowing dates, populations, nitrogen rates, irrigation) and genetic backgrounds (different regions, cultivar types). These tests have been grouped into various 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.

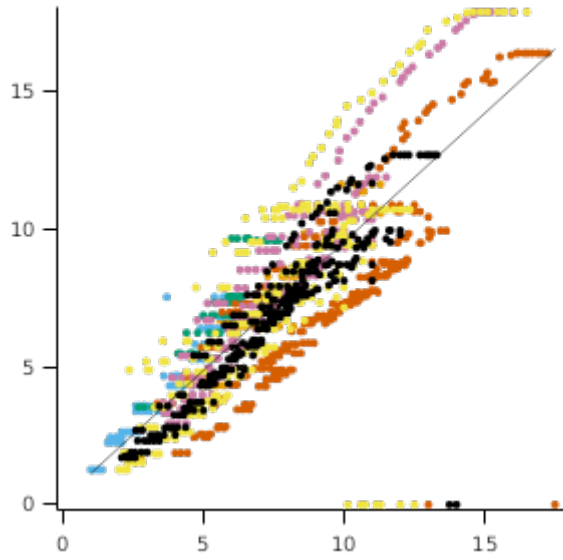


2.1 Combined Results

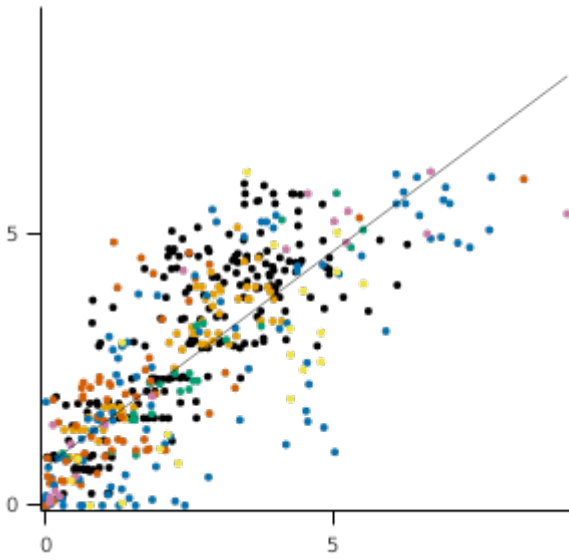
AppearedLeafTips



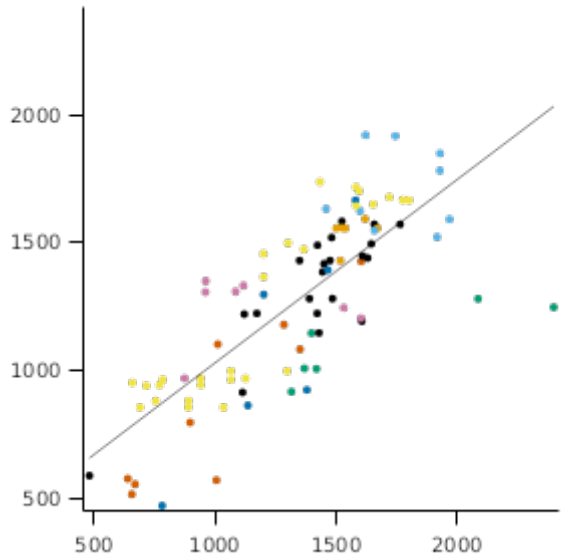
HaunStage



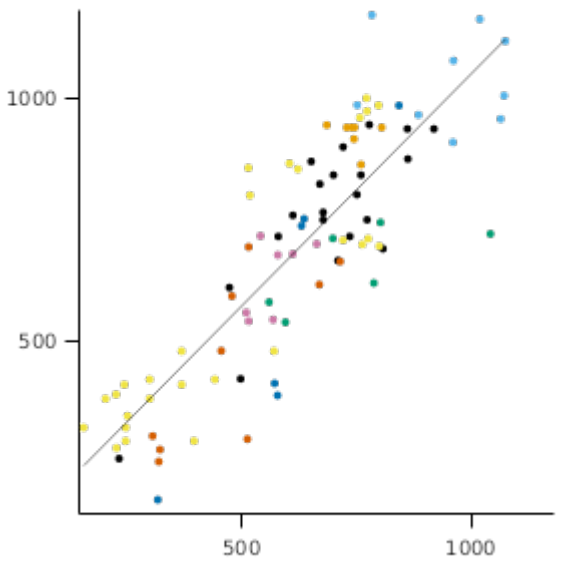
Leaf Area Index



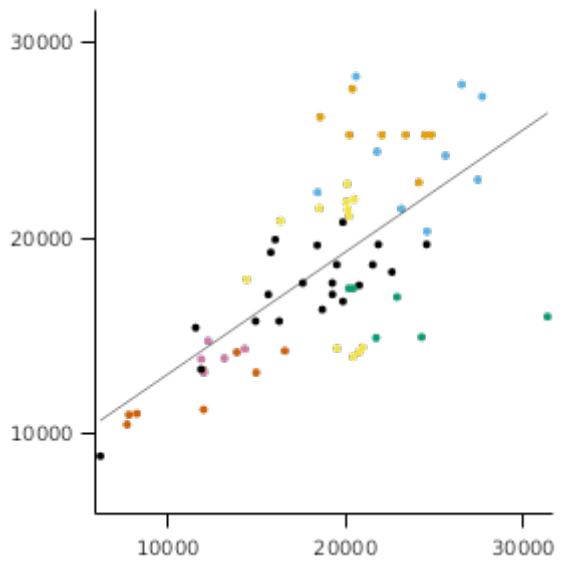
Harvest Biomass

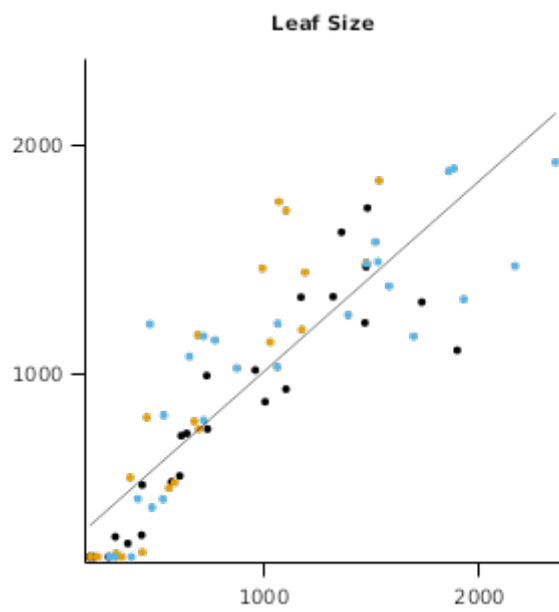
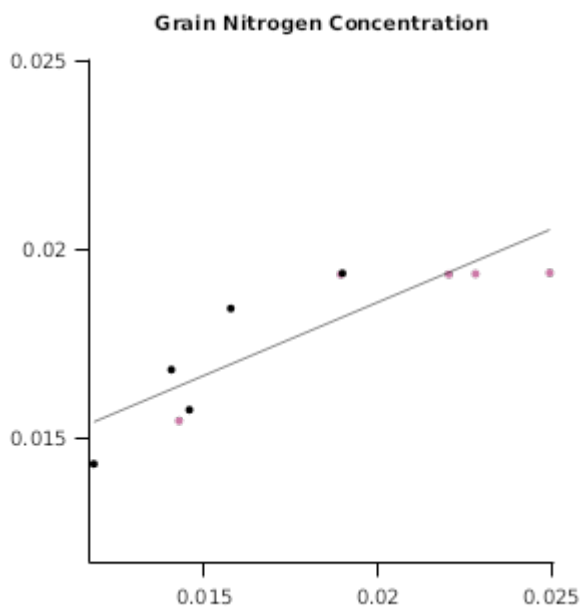
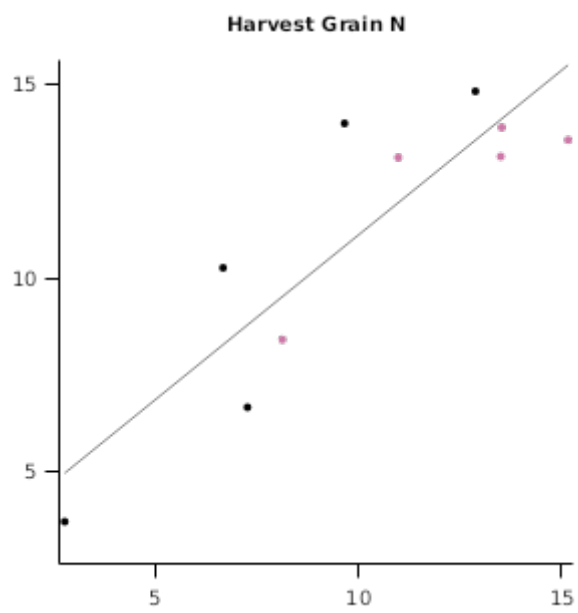
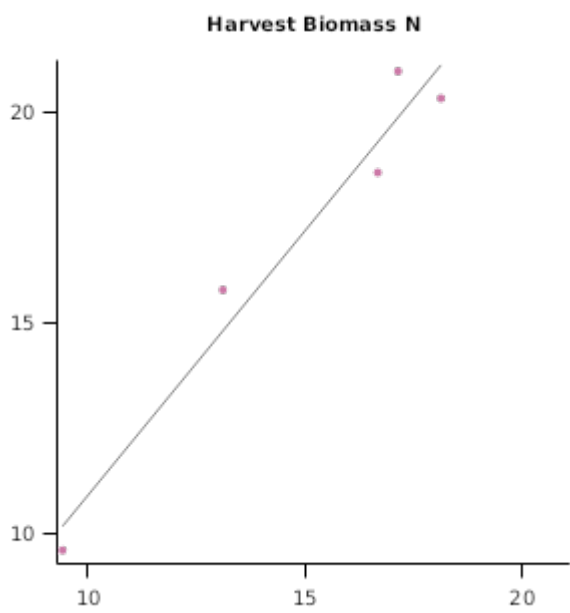
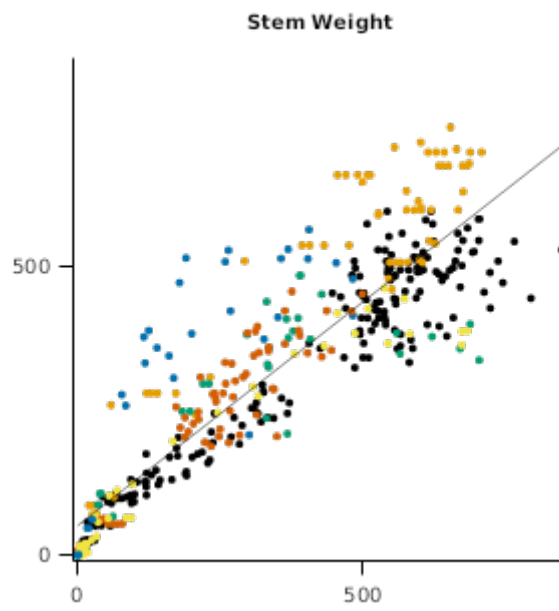
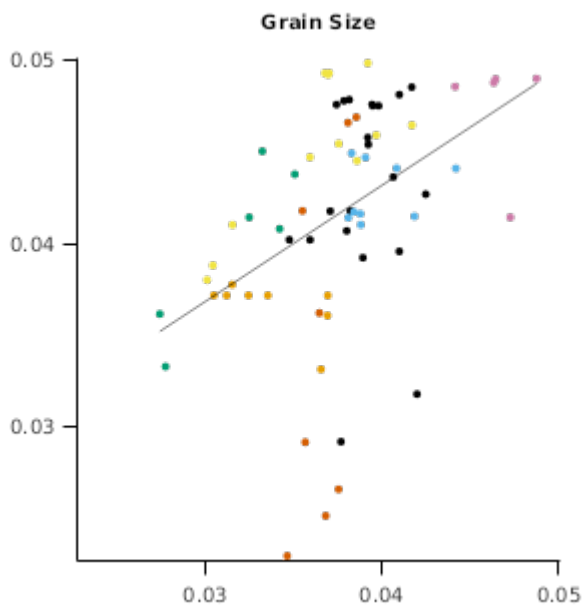


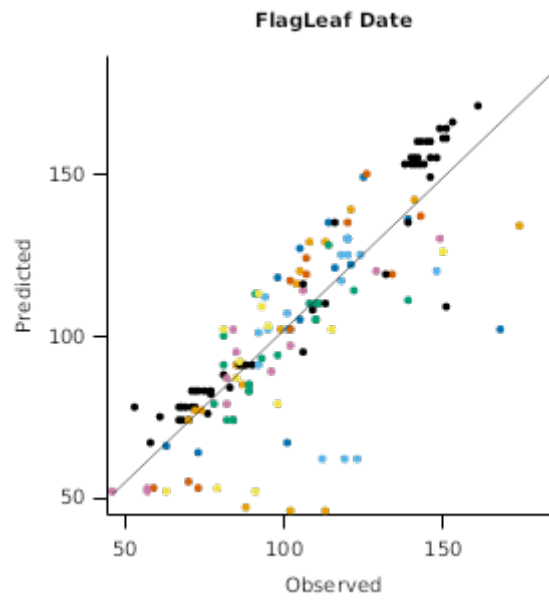
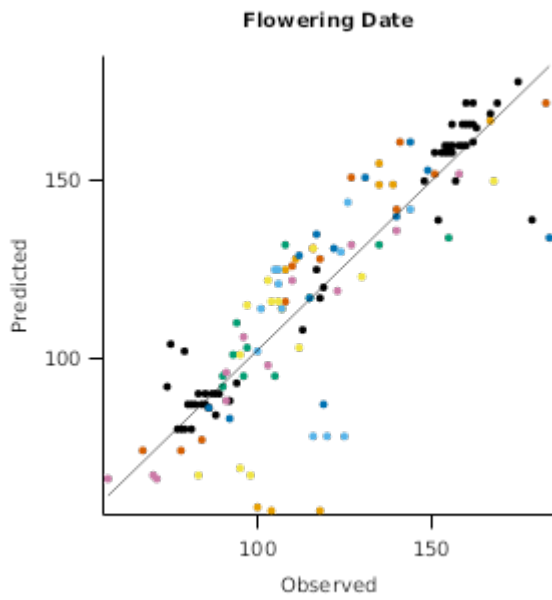
Harvest Yield



Grain Number





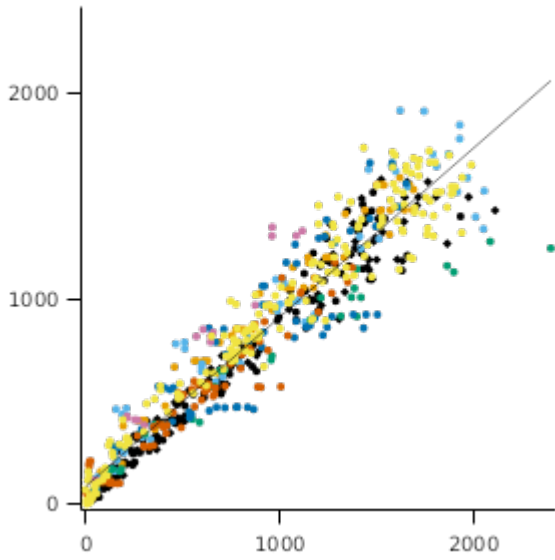


2.2 NewZealand

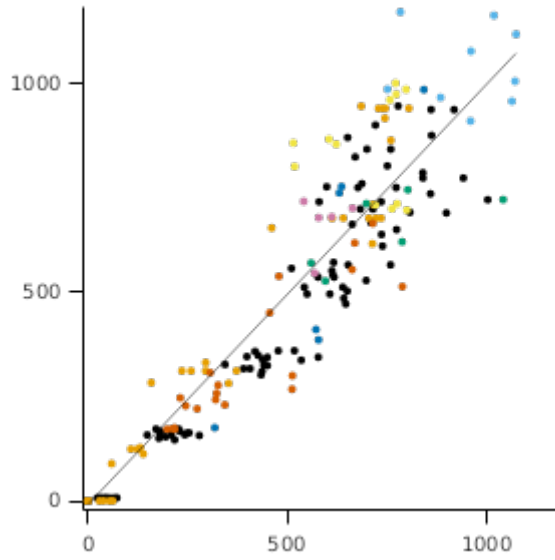
List of experiments.

Experiment Name	Design (Number of Treatments)
MCPD09_10	Cult x Nit x Irr (16)
MCPD10_11	Cult (8)
MCPD11_12	Cult x SD (9)
RS2014_15	Cult x Irr (6)
RS1988_89	Irr (6)
RS1995_96	Water x N (8)
LUDF2015_16	NProp (5)
ABlock99_00	Sow x Pop (12)

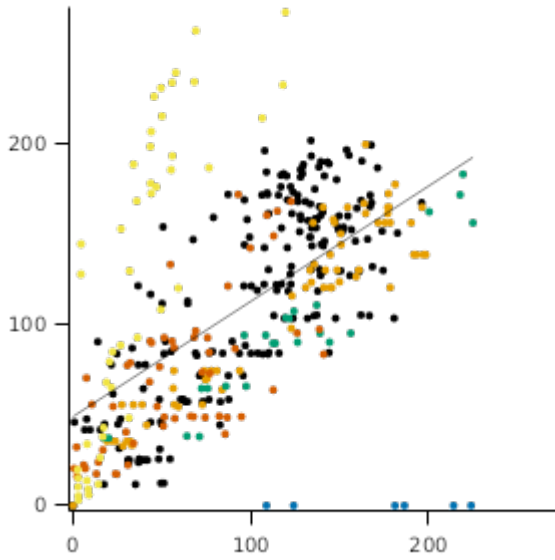
TotalWt



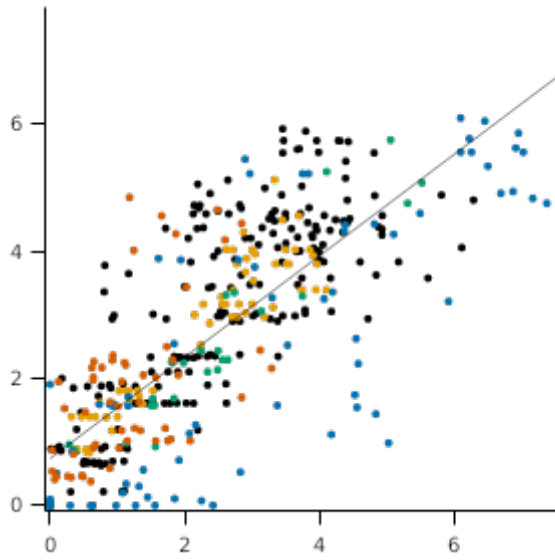
GrainWt



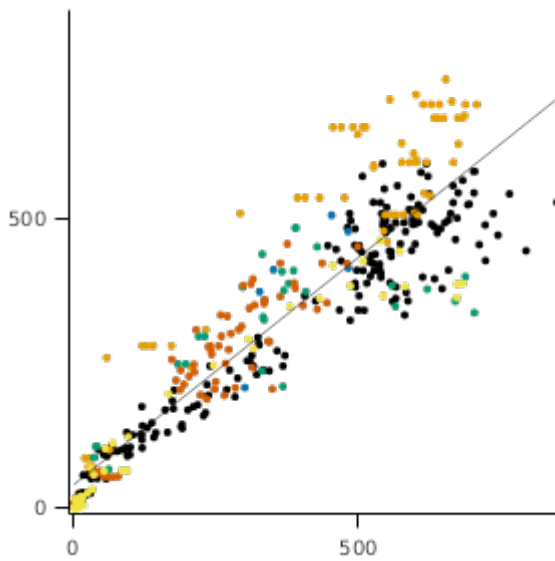
LeafWt



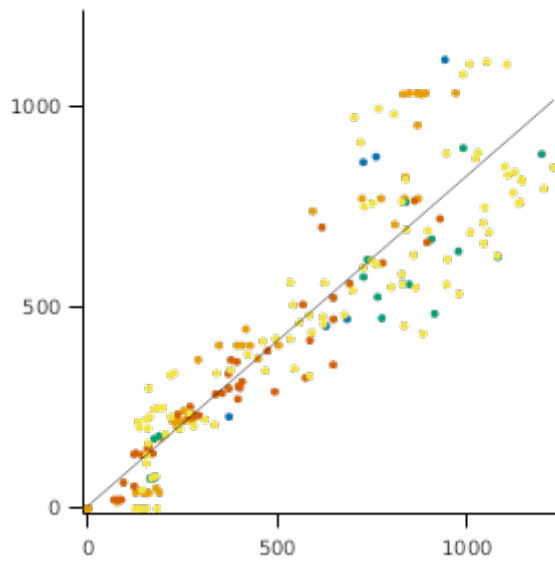
LAI



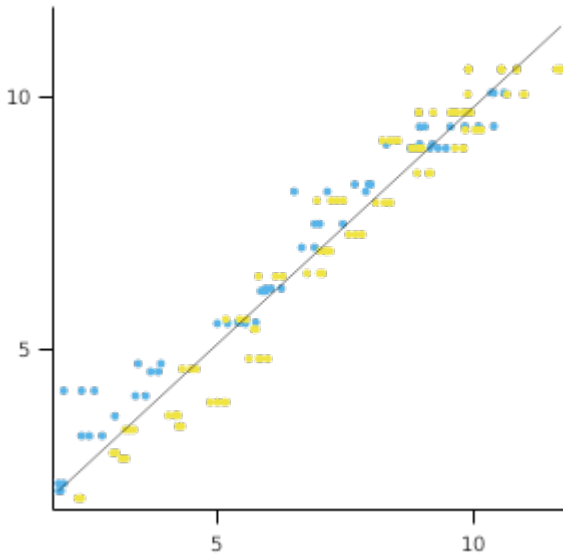
StemWt



EarWt



AppearedLeaves



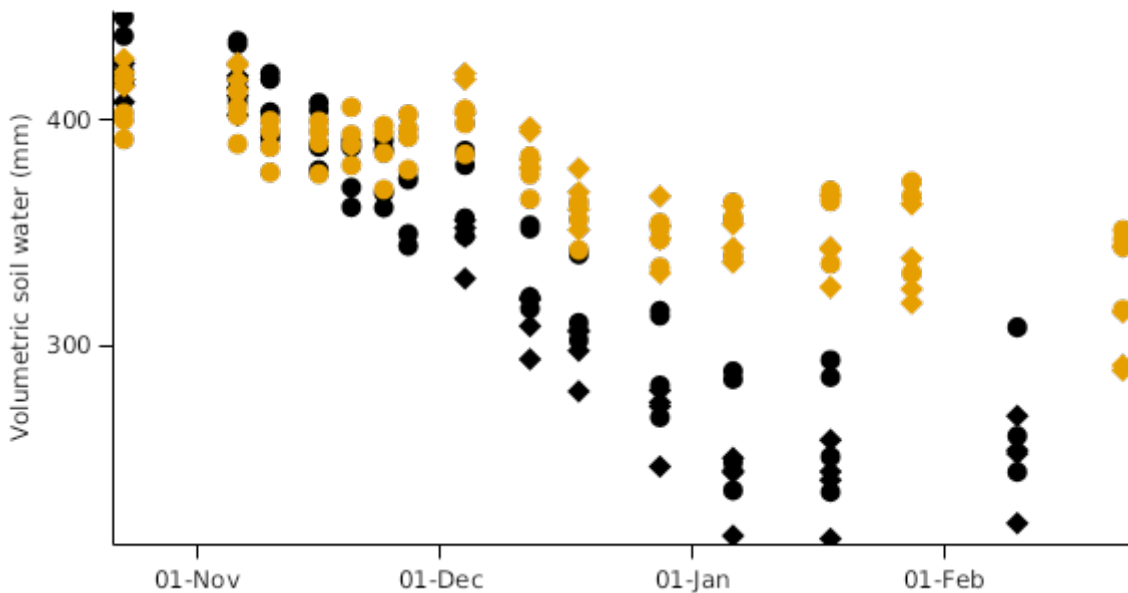
2.2.1 MCPD09_10

This experiment was conducted in A Block near Lincoln, New Zealand to determine if there were any differences in the water use efficiency of different commercial varieties of barley. The results are un-published to date.

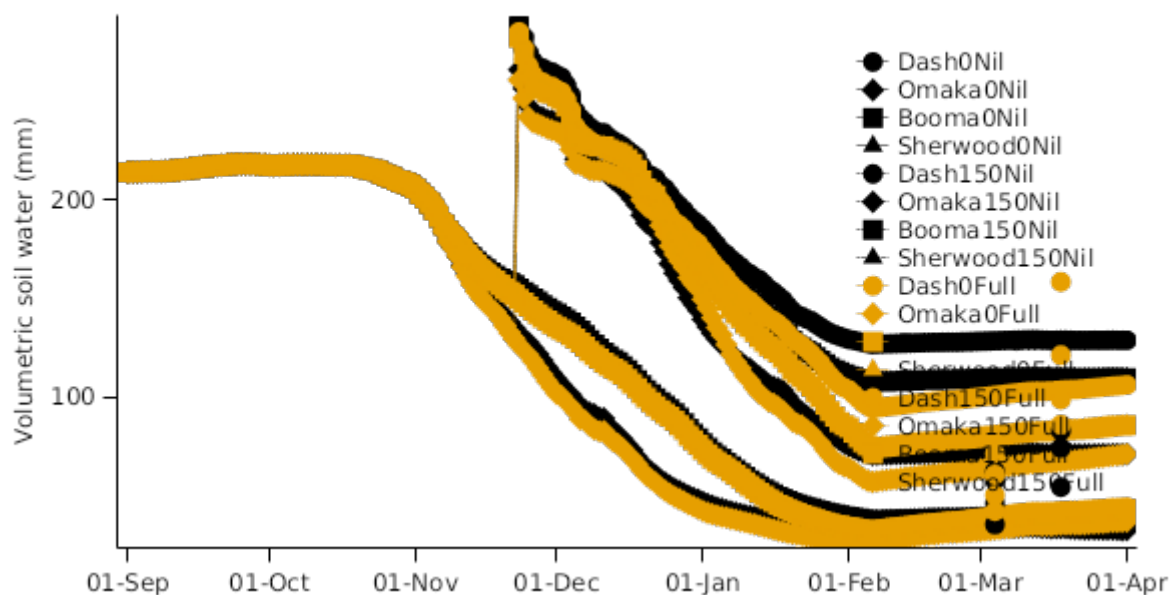
Four cultivars of Barley ('Omaka', 'Dash', 'Sherwood' and 'Booma') were sown on the 1st of October 2009 in a randomised complete block design with 4 replicates and two other factors, Irrigation and Nitrogen. The irrigation treatments consisted of full irrigation (to replace measured evapotranspiration) or nil irrigation (receiving only rainfall). The nitrogen treatments were 150 kg N broadcast in the early vegetative stage or nil fertiliser.

Biomass accumulation, organ N content, Leaf area index, radiation interception and soil water content were measured at regular frequencies throughout the experiment.

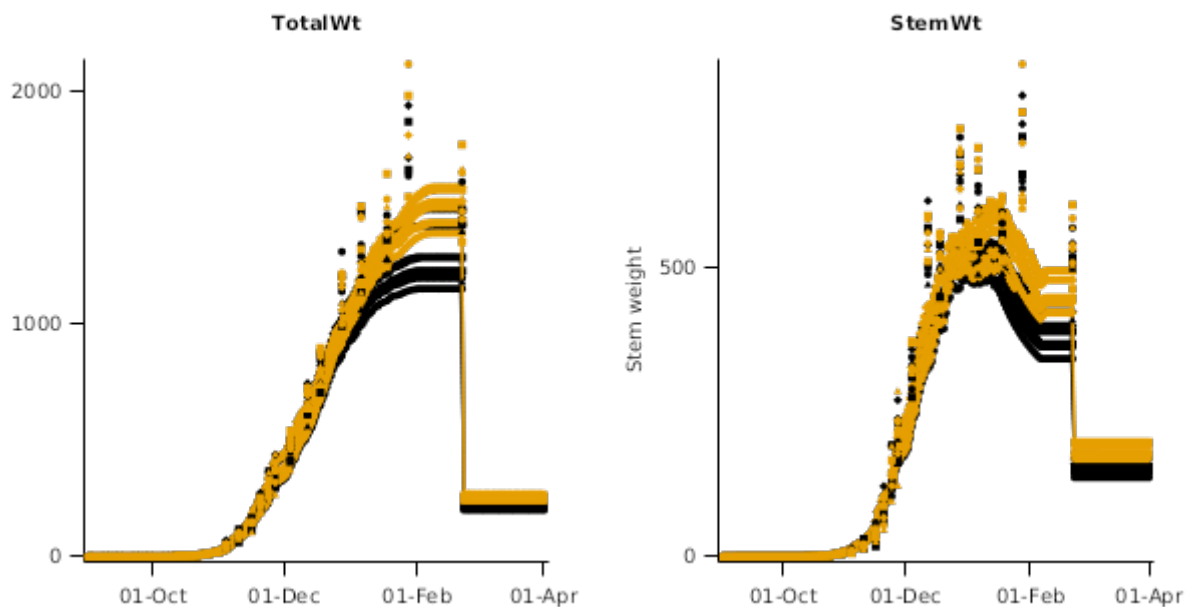
SoilWaterProfile

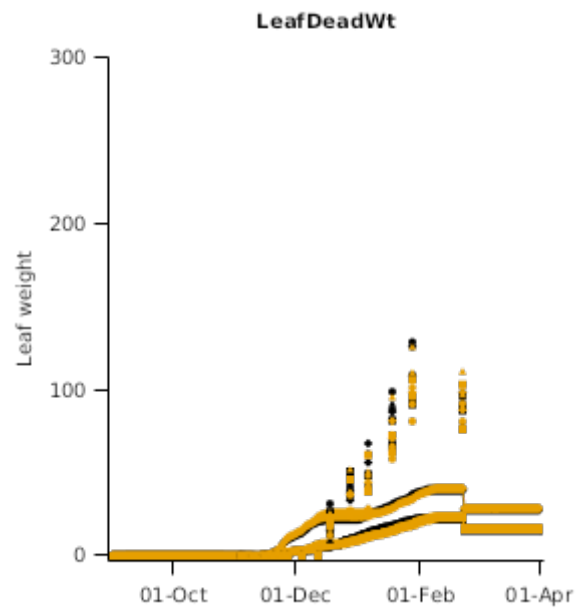
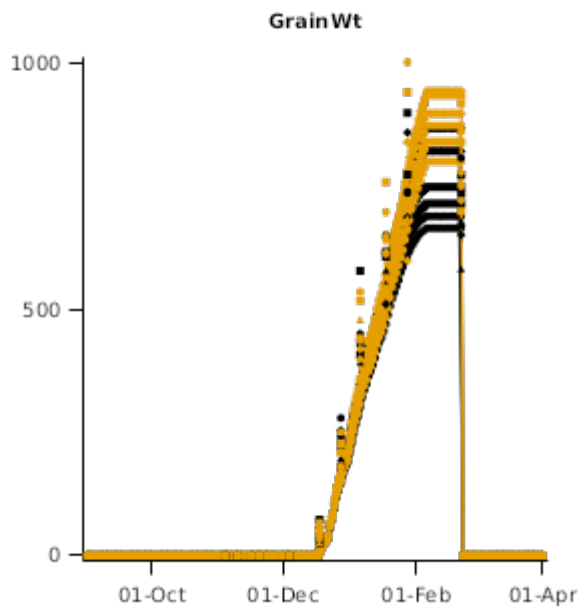
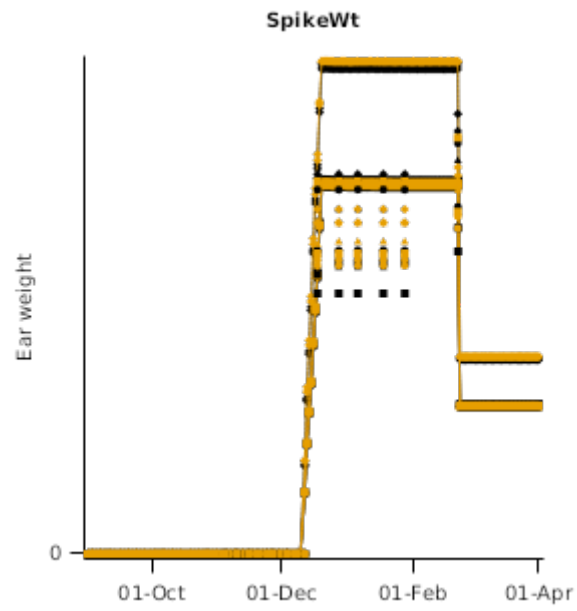
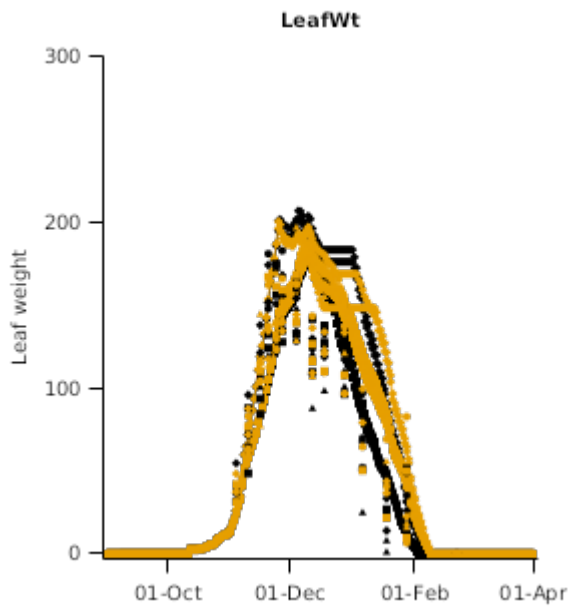


SoilNProfile

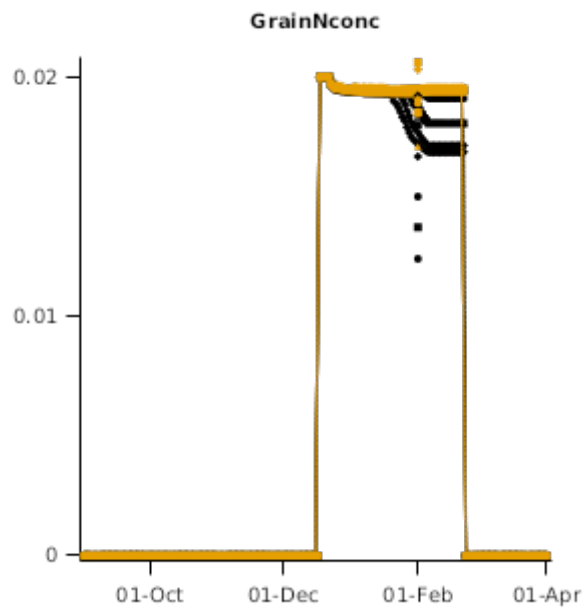
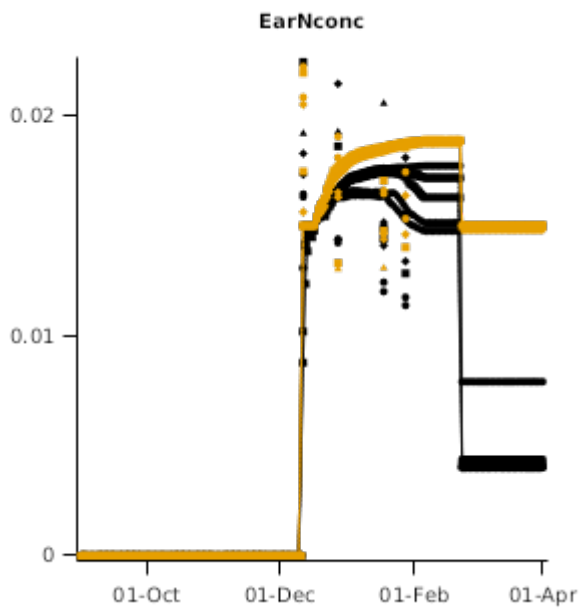
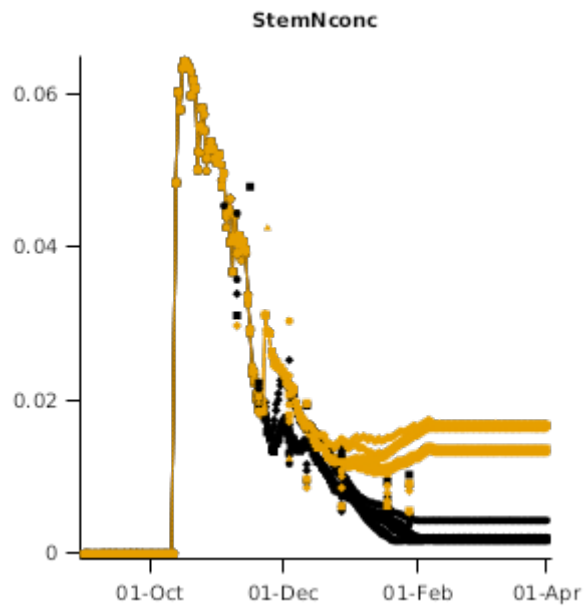
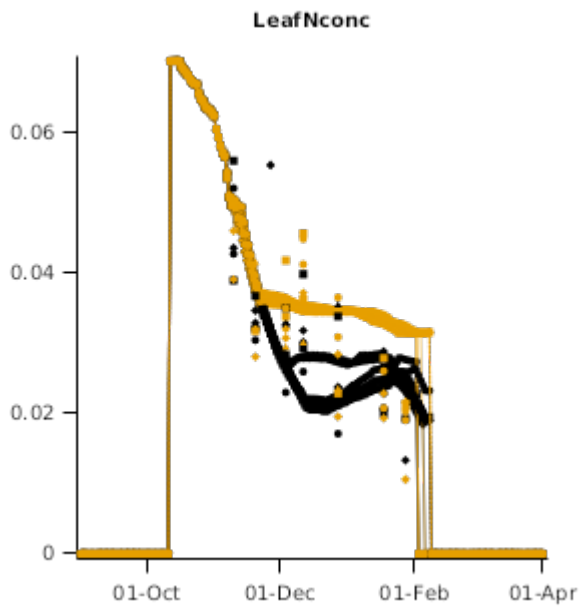


2.2.1.1 Biomass

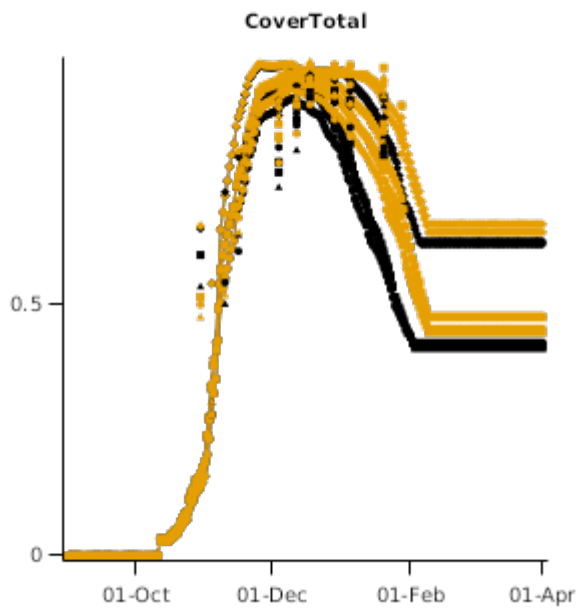
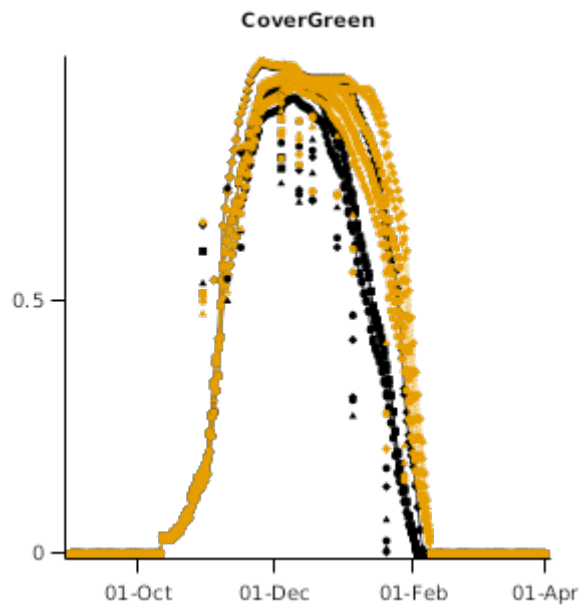
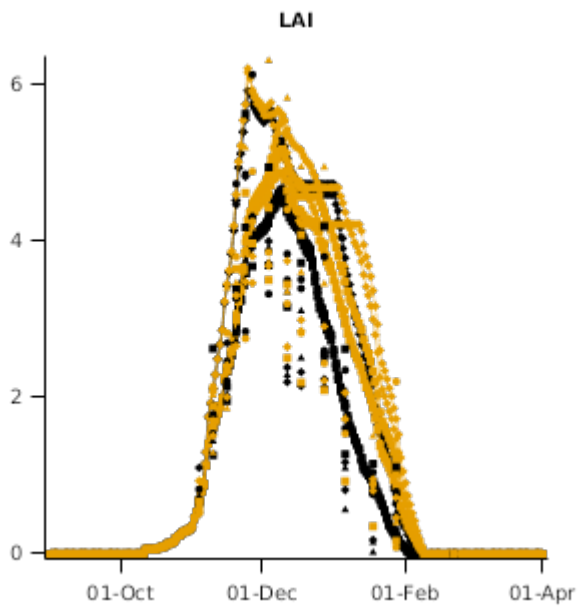




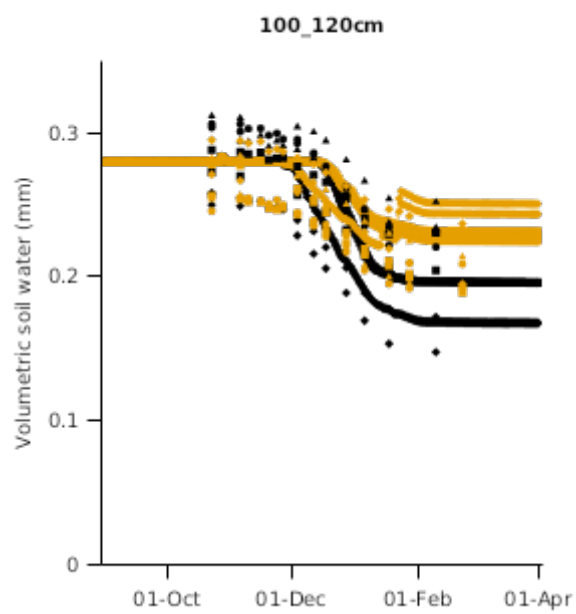
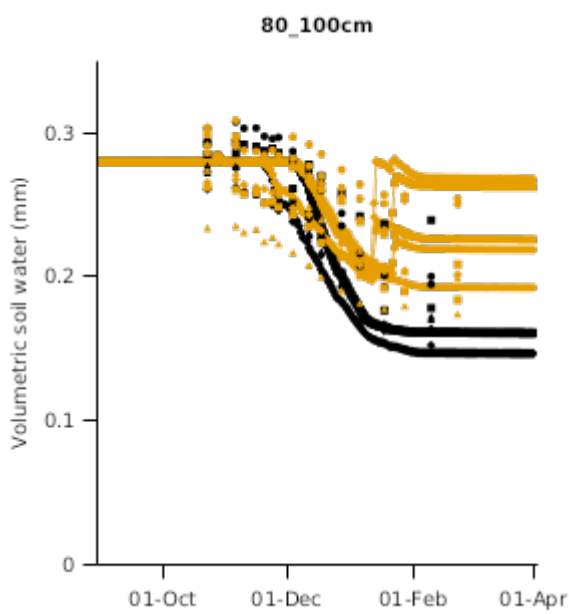
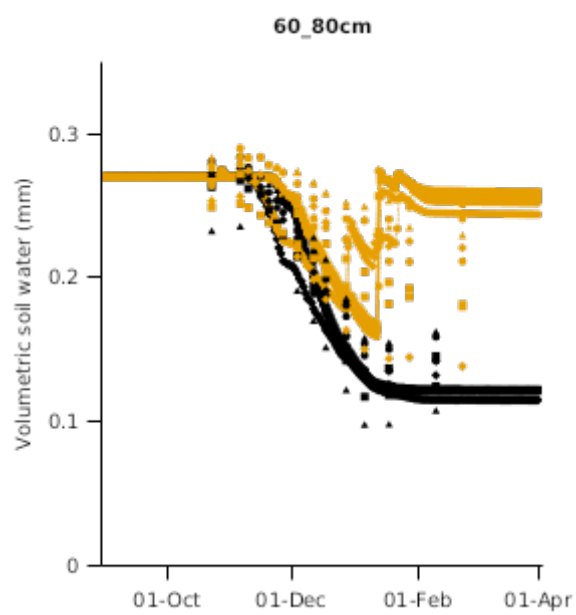
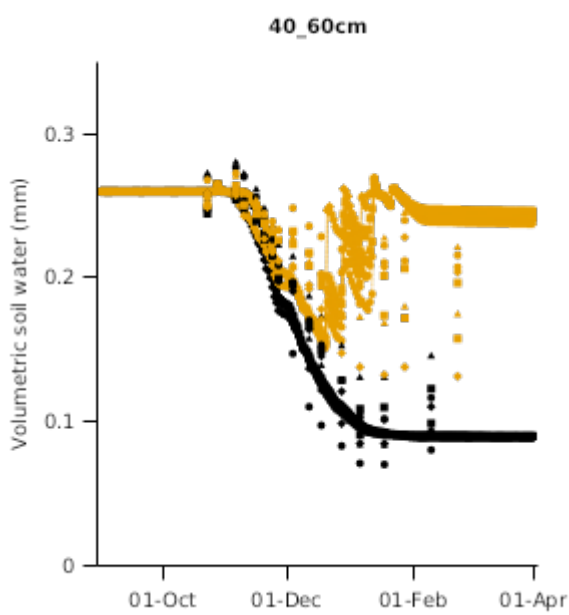
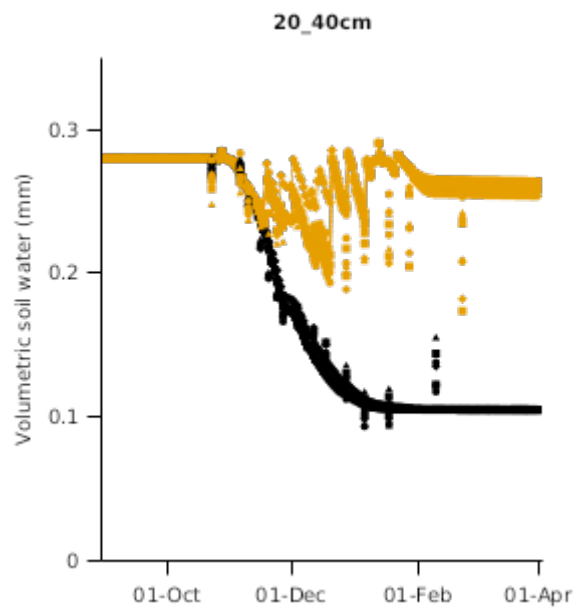
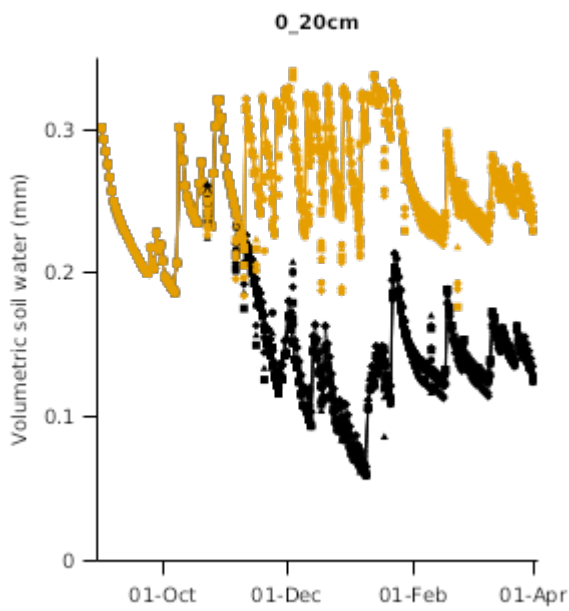
2.2.1.2 Nitrogen

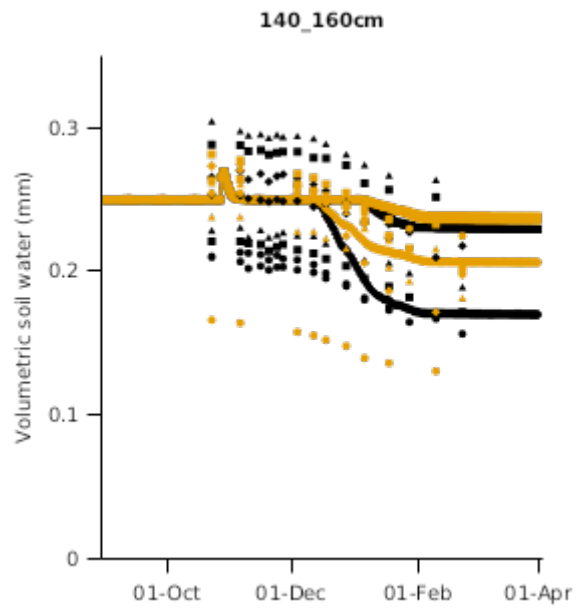
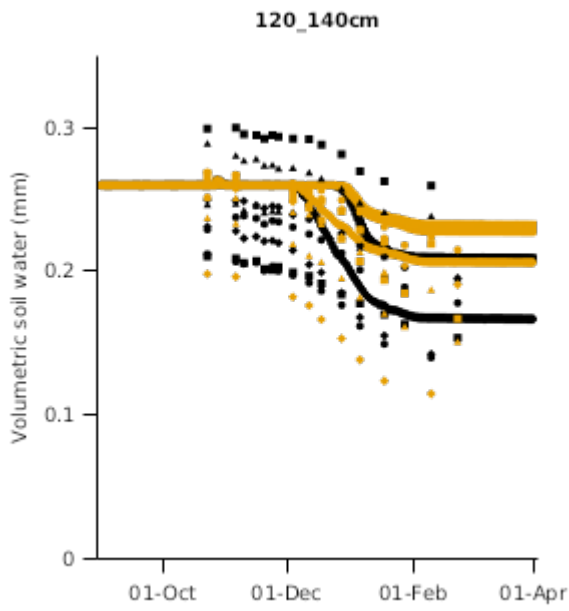


2.2.1.3 Canopy

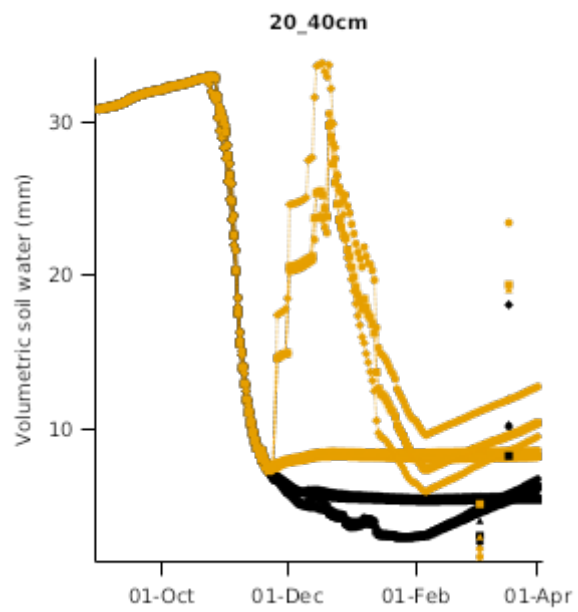
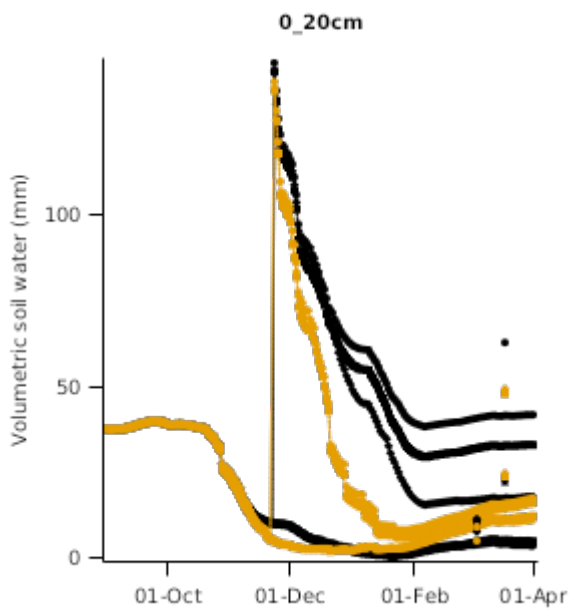


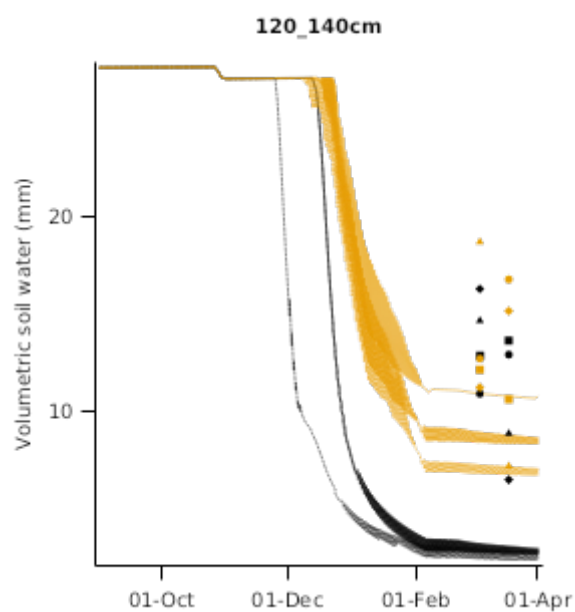
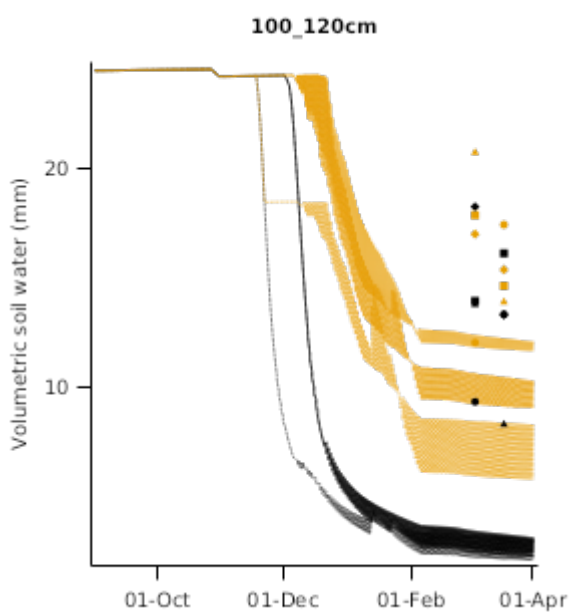
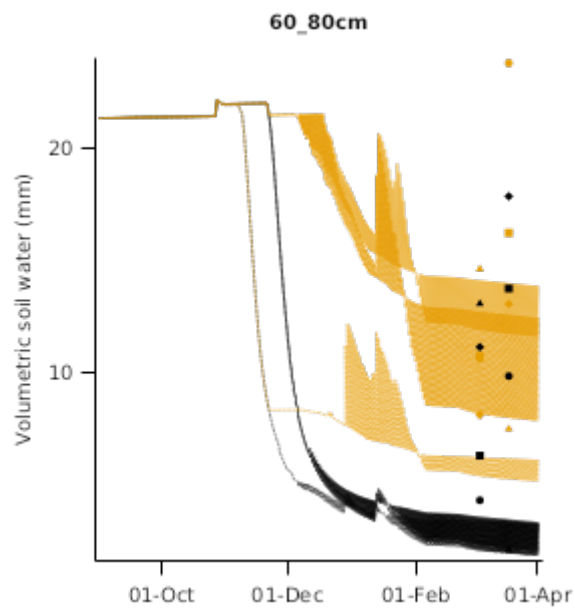
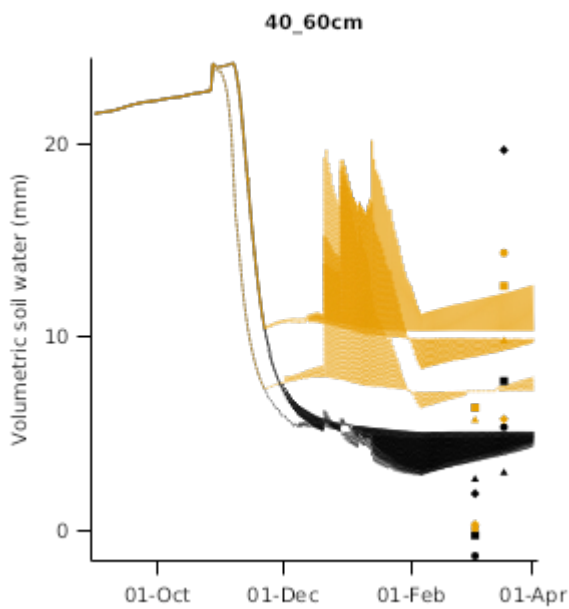
2.2.1.4 SoilWater





2.2.1.5 SoilN





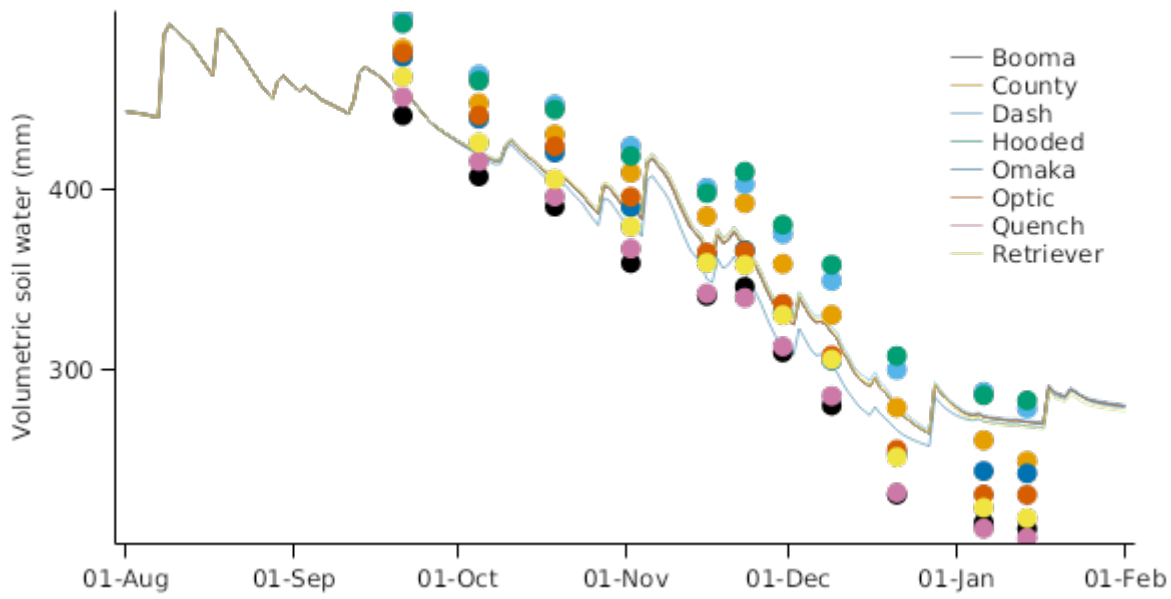
2.2.2 MCPD10_11

Following on from MCPD09_10, this experiment was conducted in A Block near Lincoln, New Zealand to test a wider range of barley genotypes for differences in water use efficiency. The results are un-published to date.

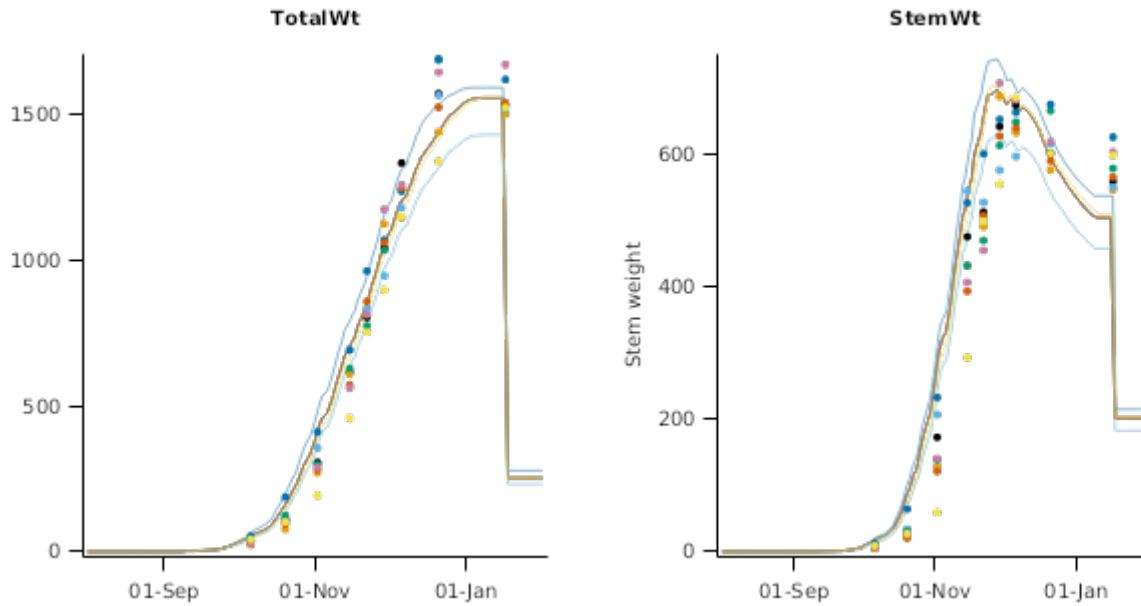
Treatments were simply 8 commercially available varieties of barley ('Booma', 'County', 'Dash', 'Hooded', 'Omaka', 'Optic', 'Quench' and 'Retriever')

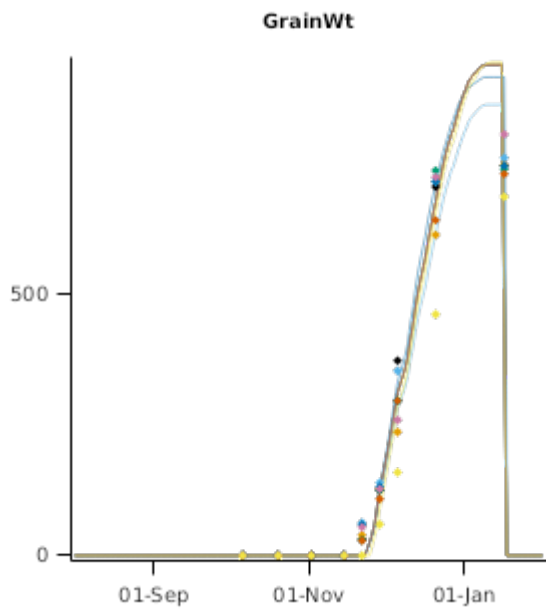
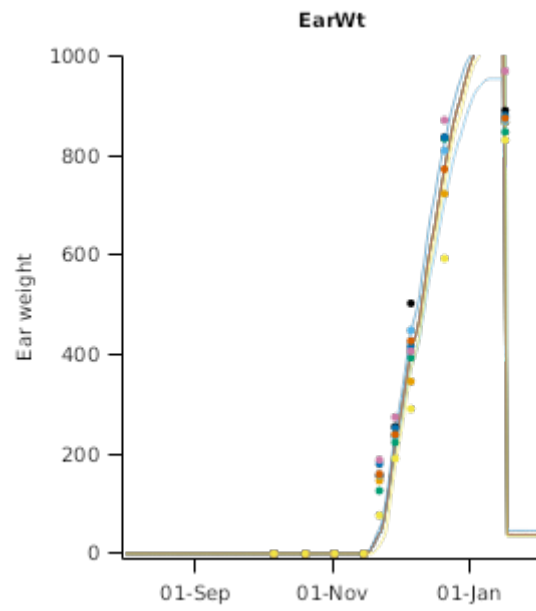
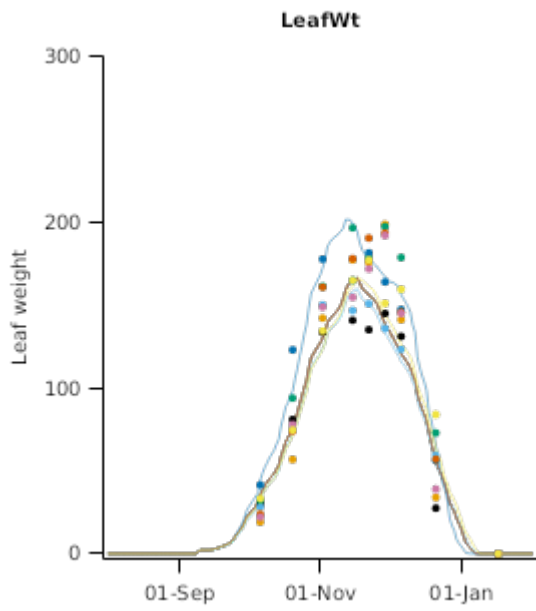
Biomass accumulation, Leaf area index, radiation interception and soil water content were measured at regular frequencies throughout the experiment.

SoilWaterProfile

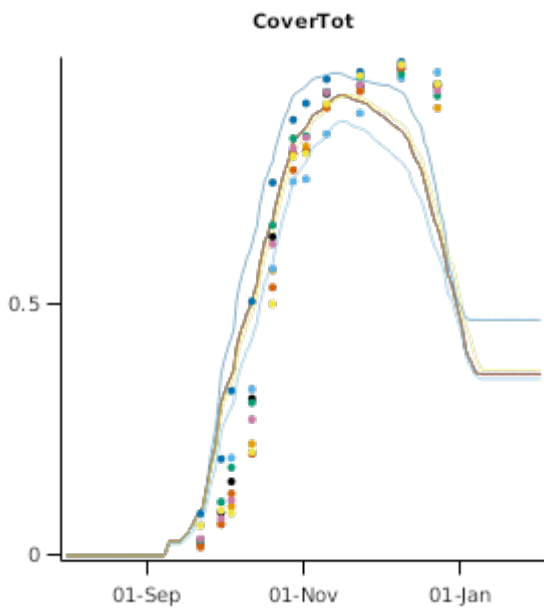
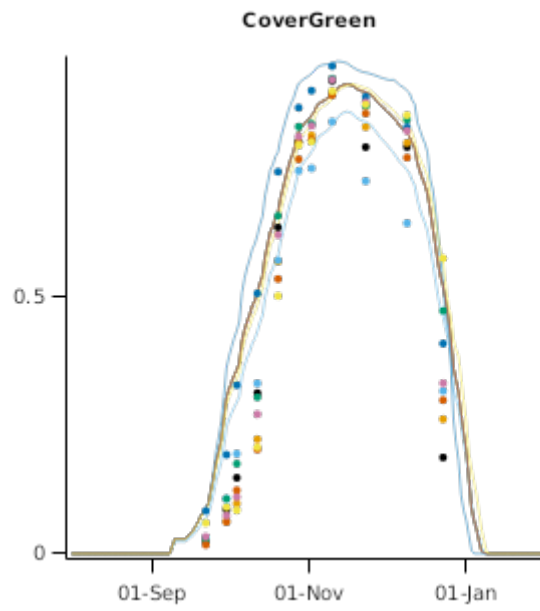
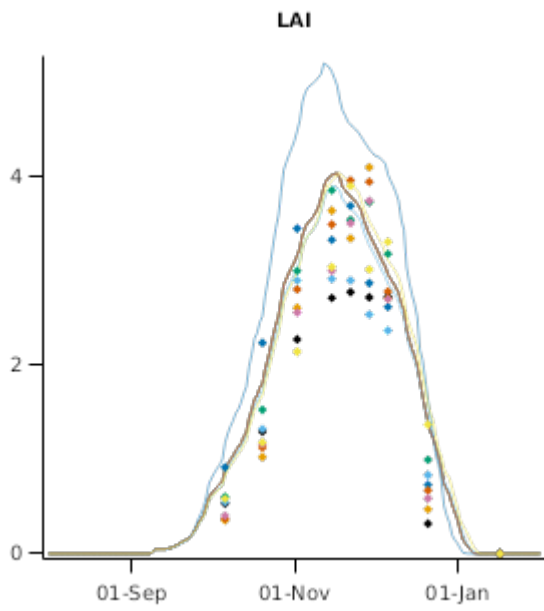


2.2.2.1 Biomass

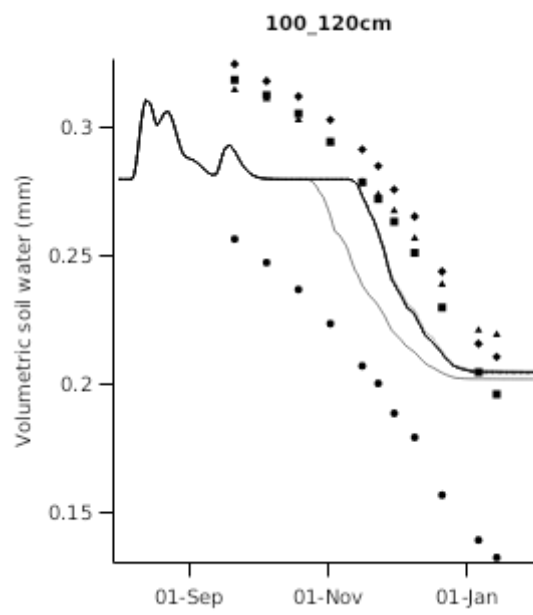
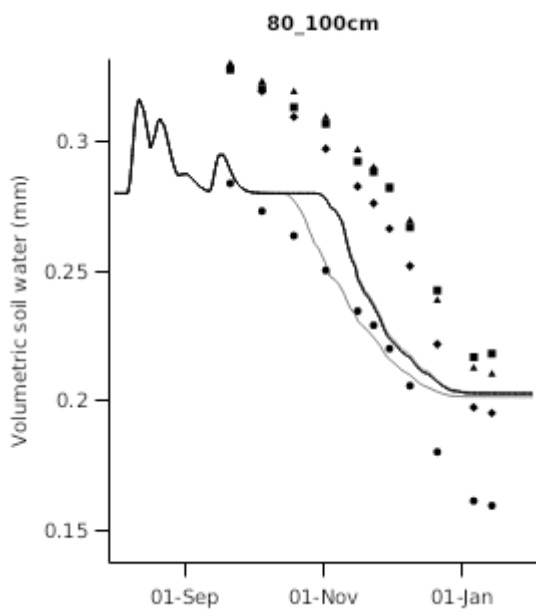
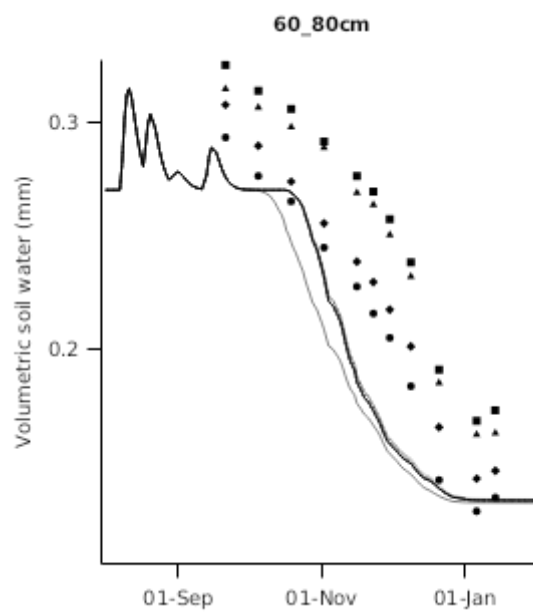
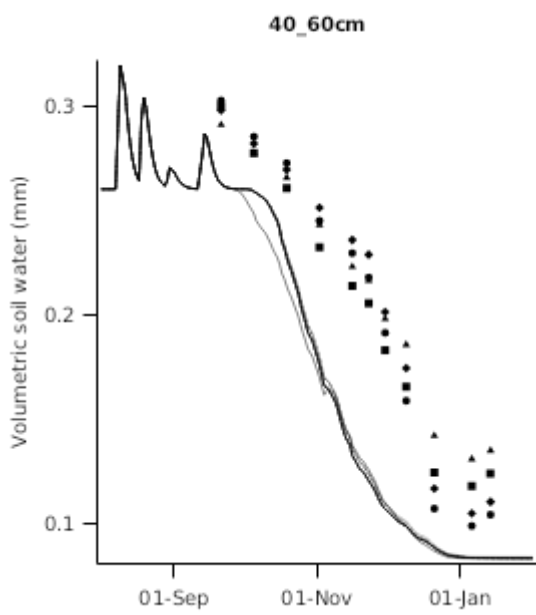
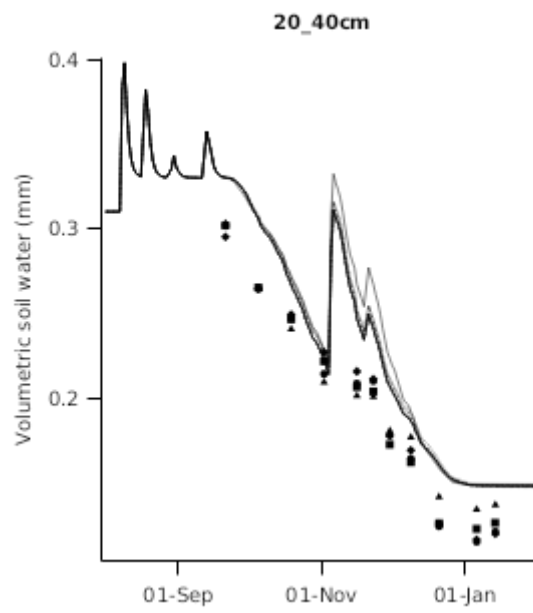
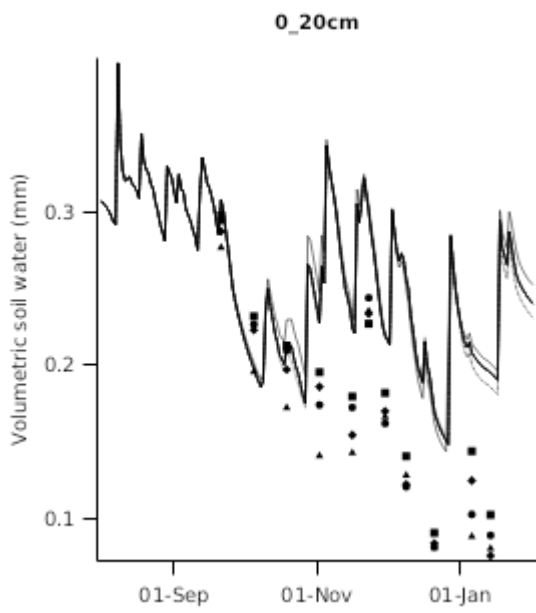


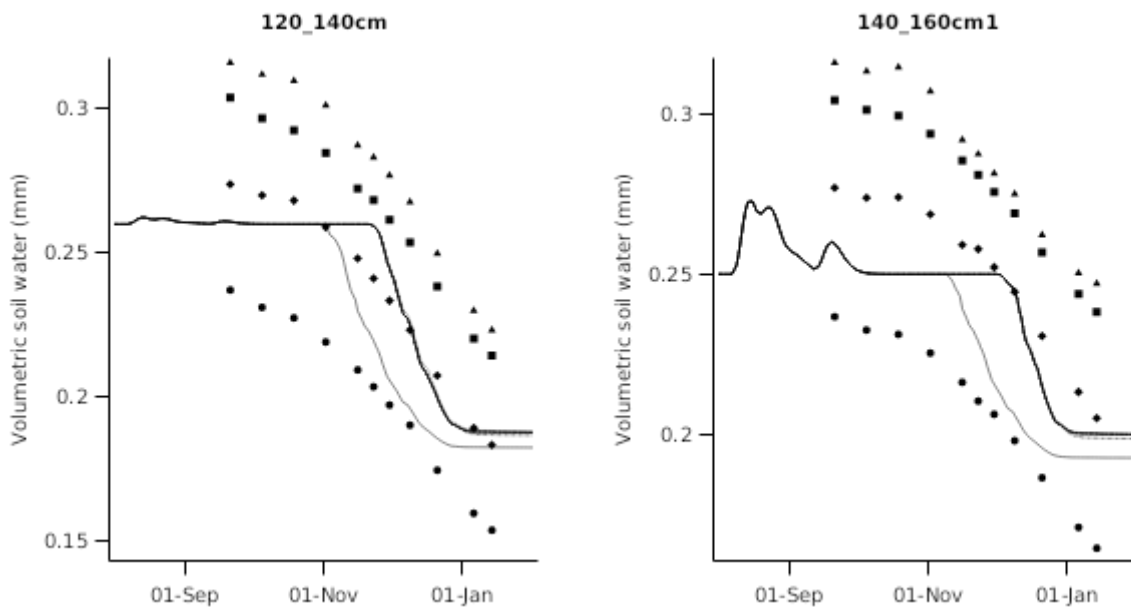


2.2.2.2 Canopy



2.2.2.3 SoilWater



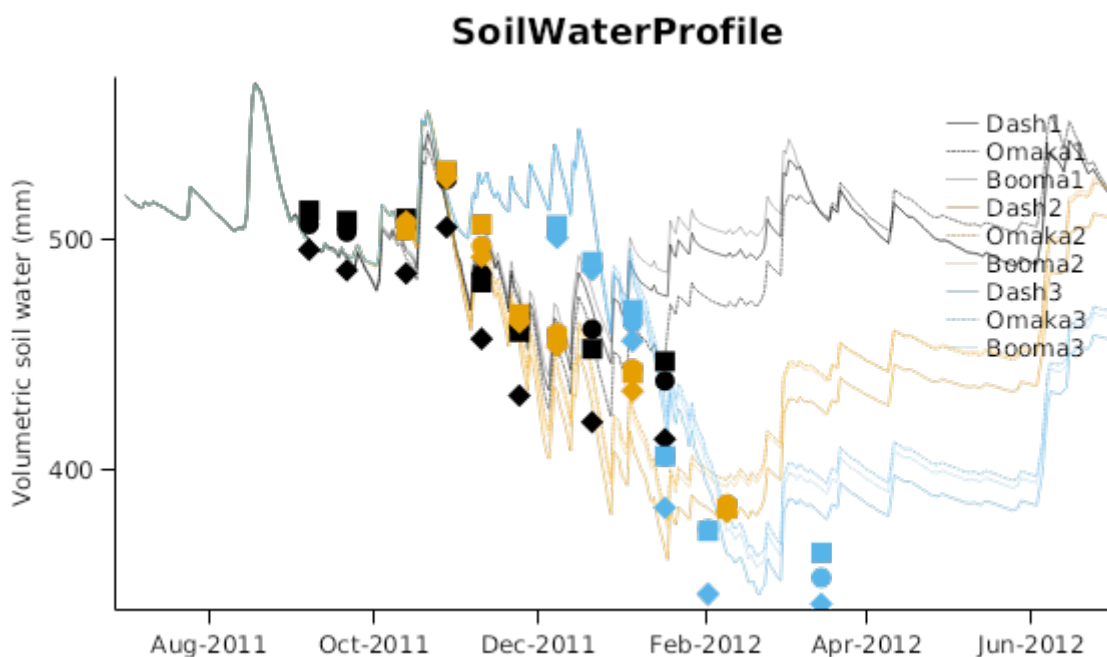


2.2.3 MCPD11_12

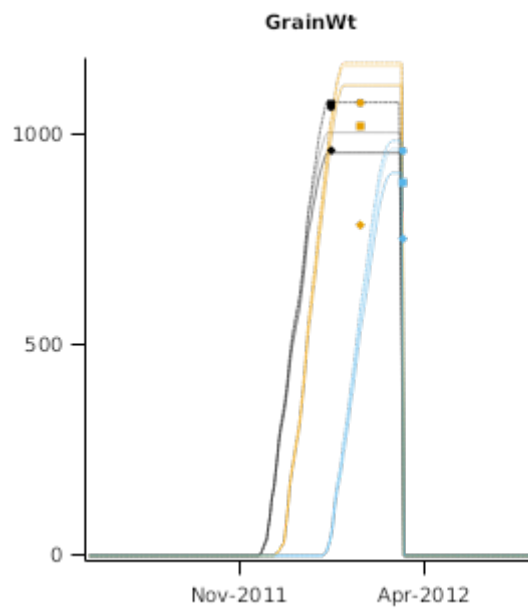
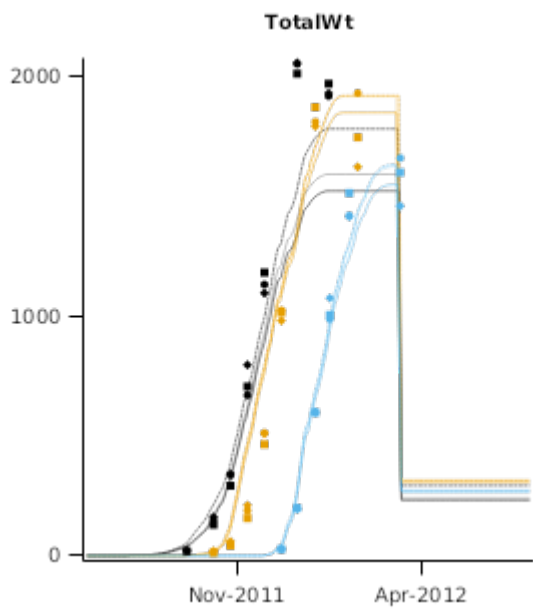
Following on from MCPD10_11, this experiment was conducted in A Block near Lincoln, New Zealand to test the effects of sowing time on apparent water use efficiency of three varieties of Barley. The results are un-published to date.

Treatments were simply 3 commercially available varieties of barley ('Booma', 'Dash' and 'Omaka') sown on three different sowing dates (13 Aug, 9 Sep and 15 Nov).

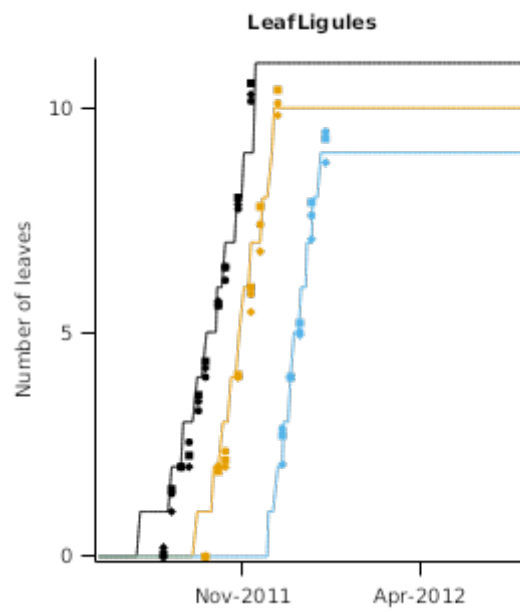
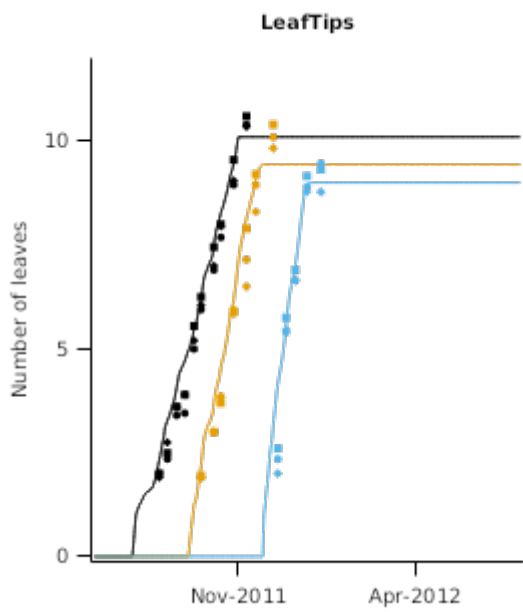
Biomass accumulation, Leaf appearance, leaf size, radiation interception and soil water content were measured at regular frequencies throughout the experiment.

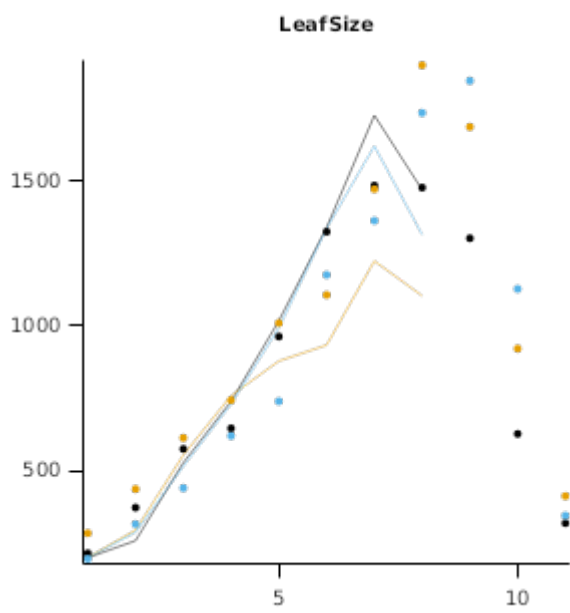
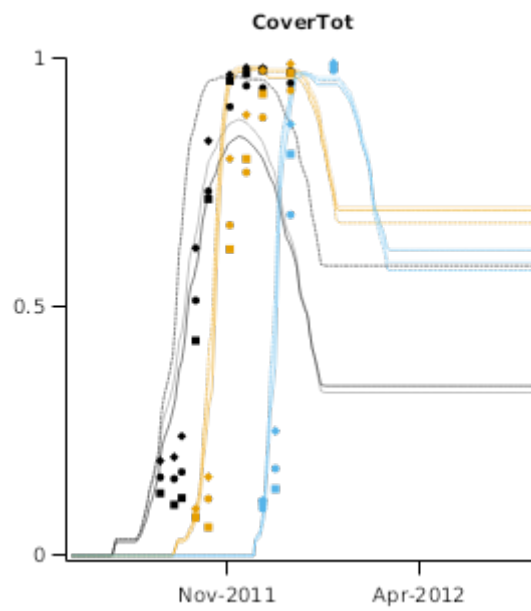
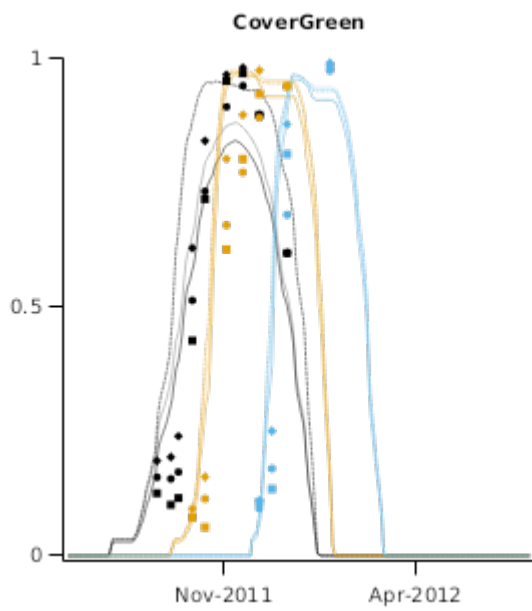


2.2.3.1 Biomass

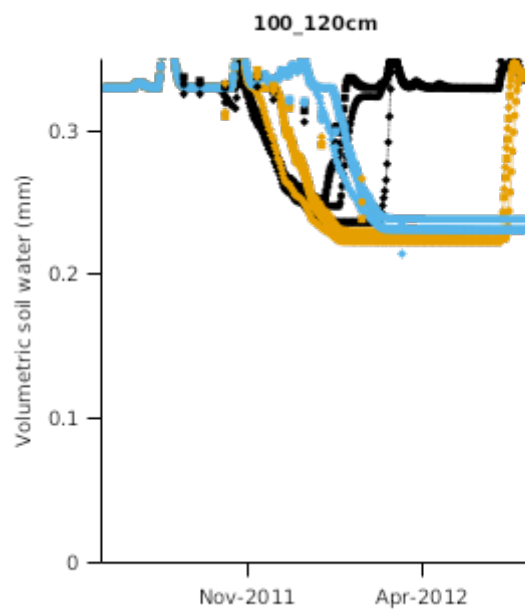
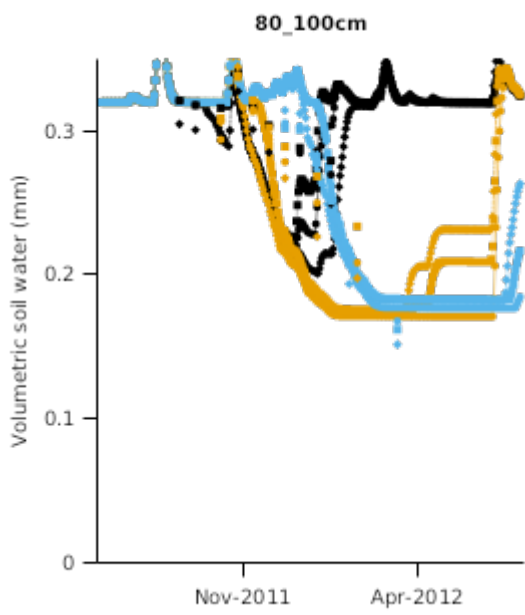
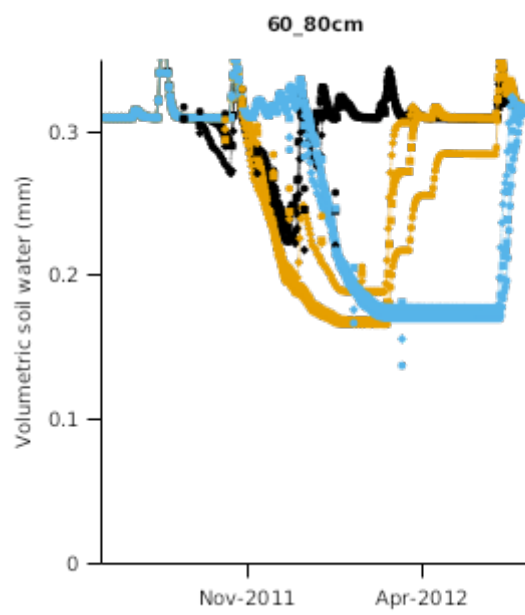
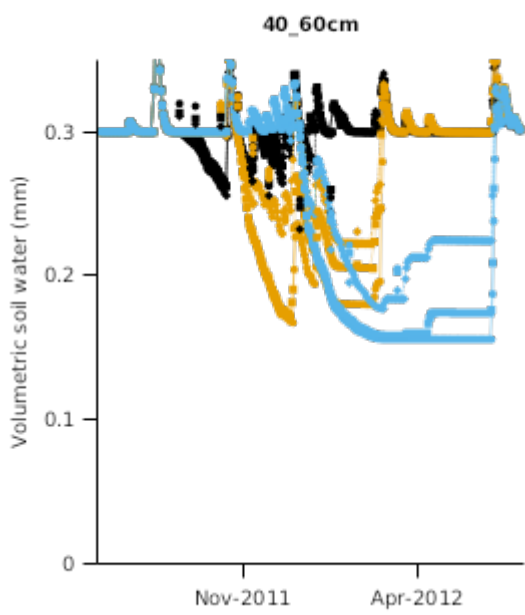
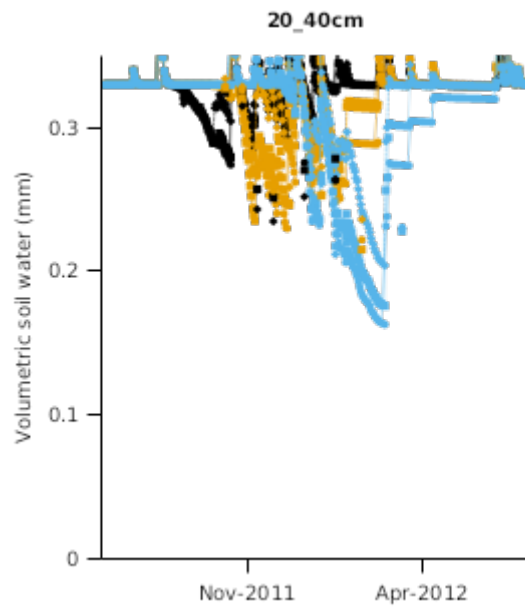
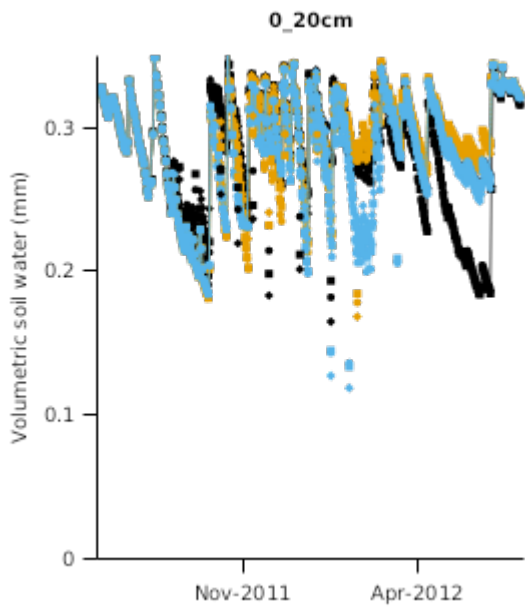


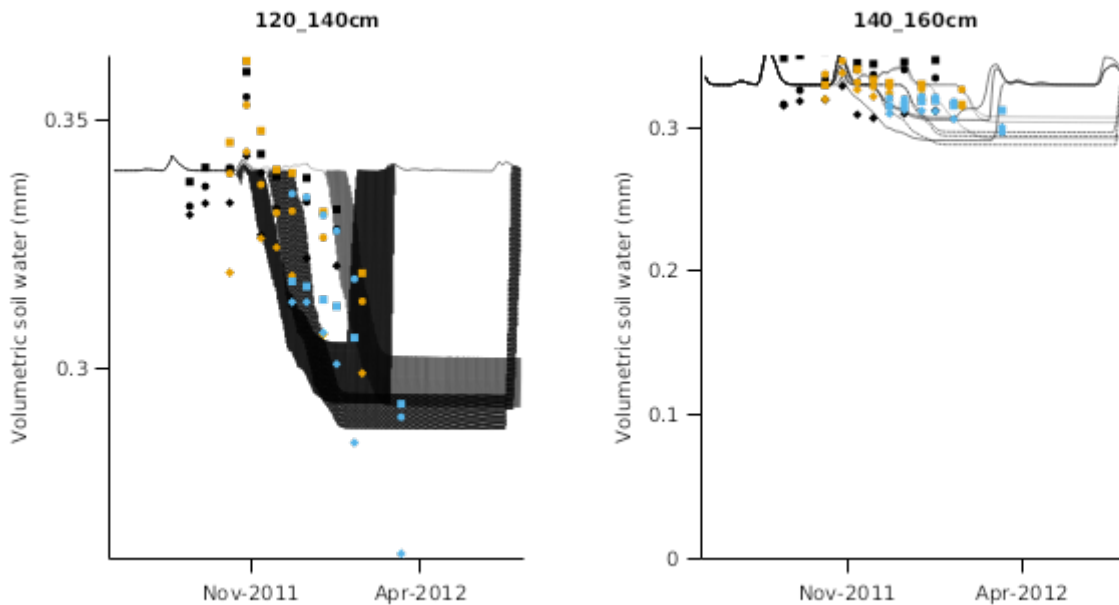
2.2.3.2 Canopy





2.2.3.3 SoilWater





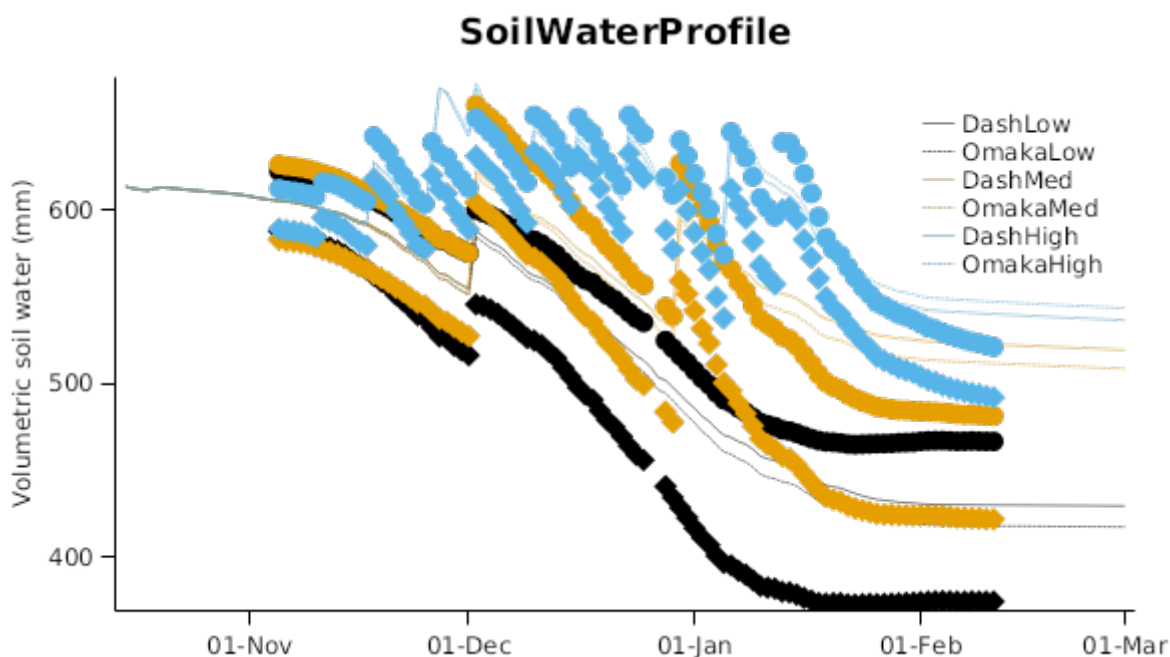
2.2.4 RS2014_15

This was a field experiment established at the New Zealand Institute for Plant & Food Research Limited rain-out shelter in October 2014. Barley cultivars cv Dash and cv Omaka, differing canopy characteristics and water extraction capabilities were established with a range of irrigation treatments aimed at producing a range of soil moisture deficits.

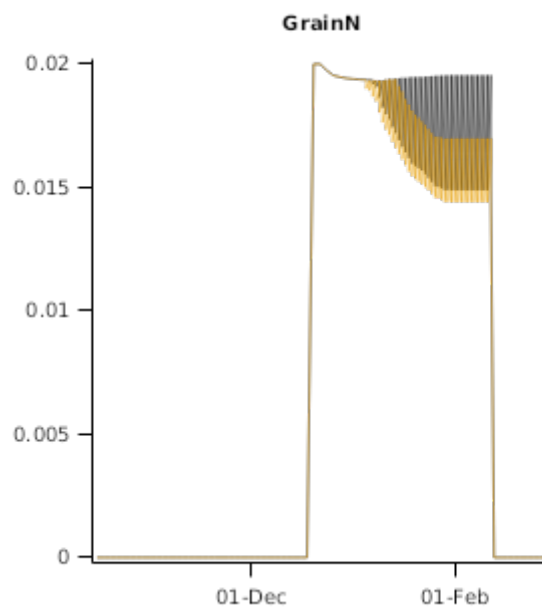
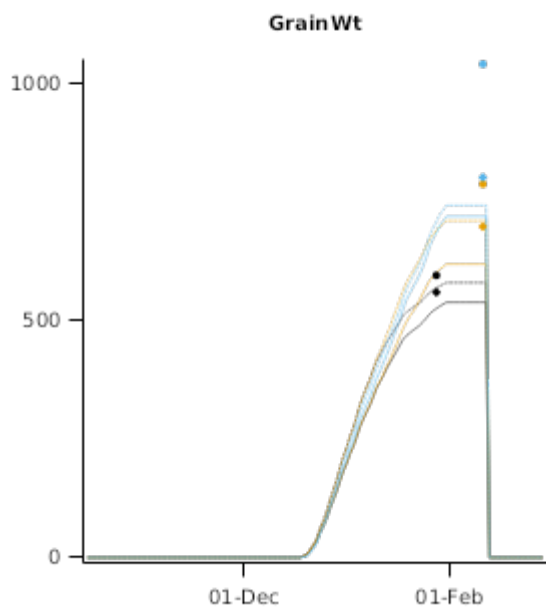
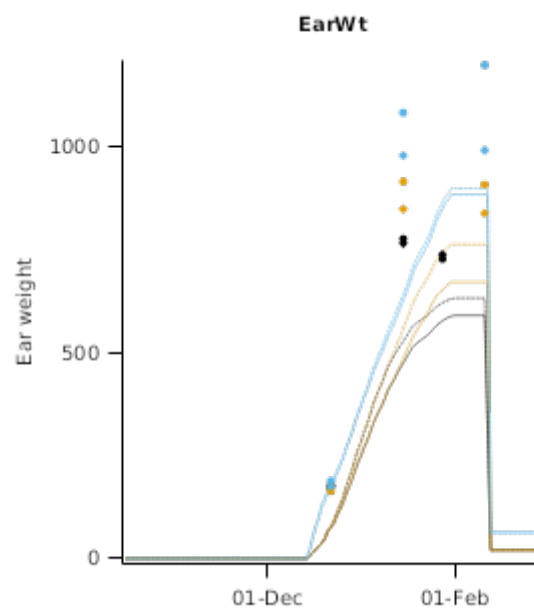
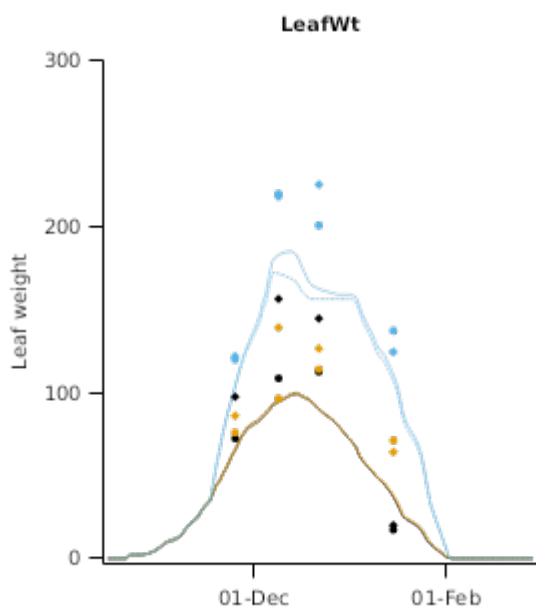
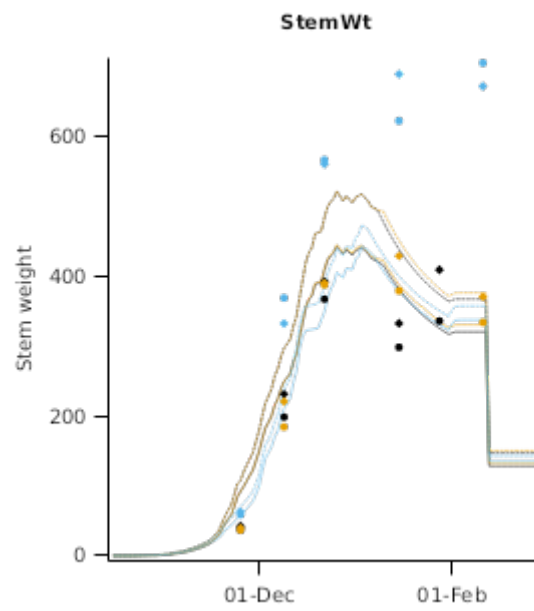
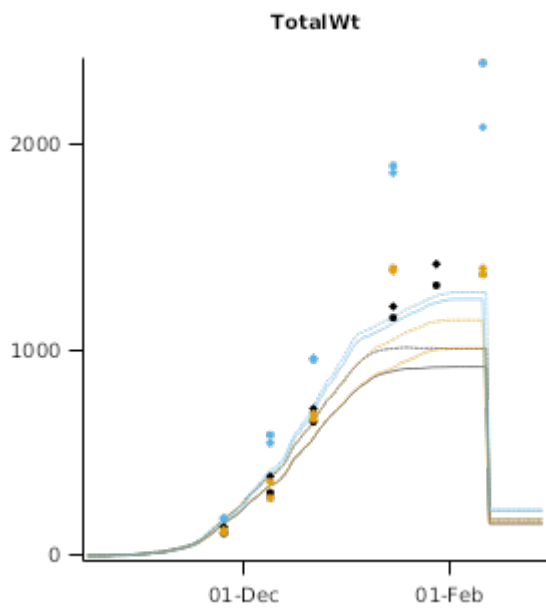
- High =Full replacement irrigation: replace weekly, measured crop water use;
- Mid =Intermediate replacement with reduced frequency and higher volume e.g. monthly application of ½ measured crop water use;
- Low =Nil (or near nil) irrigation, e.g. irrigated once at anthesis.

The treatments were monitored for:

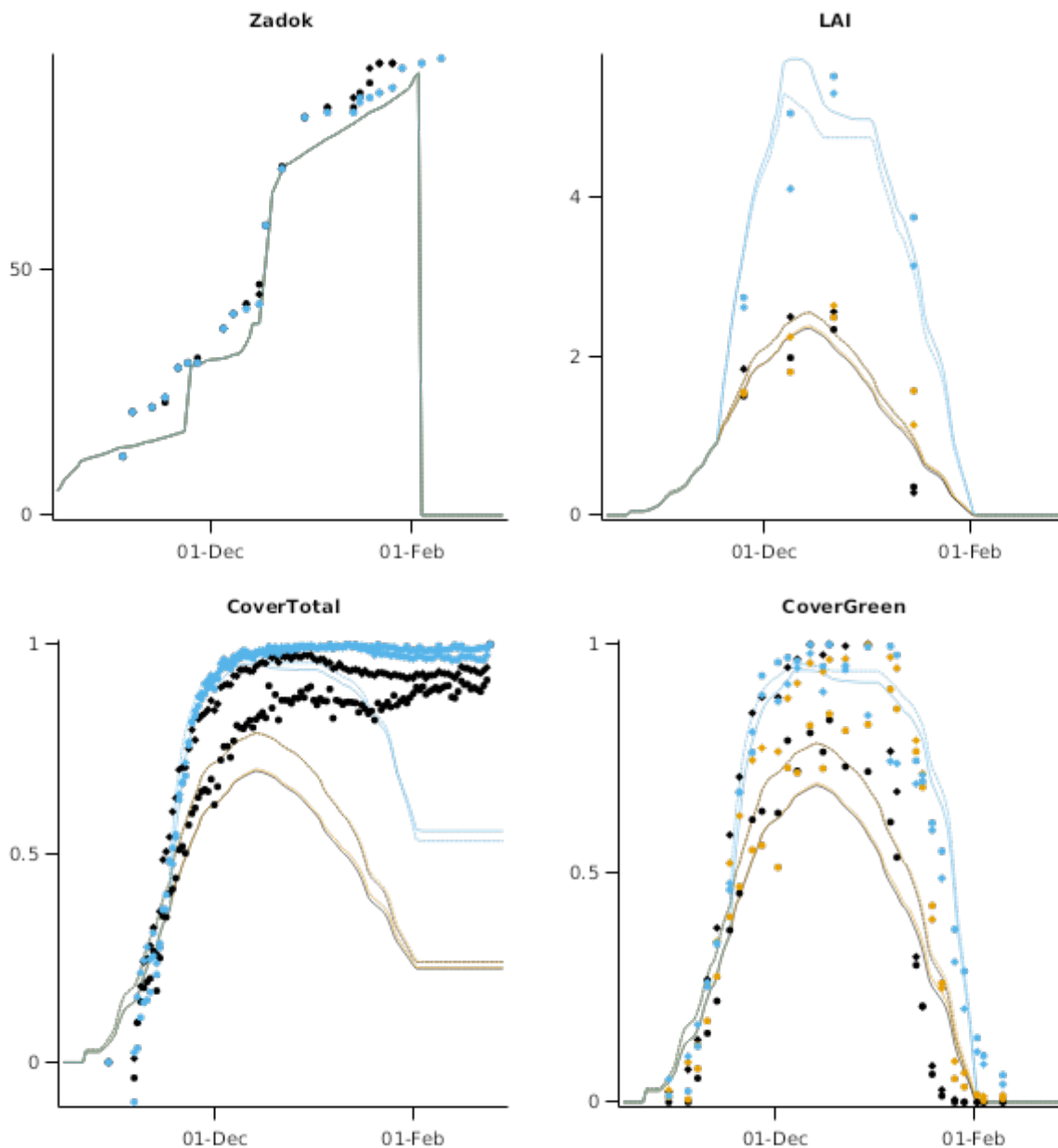
- Soil water - this was measured continuously using auto logging TDR and weekly using a neutron probe;
- Canopy light interception;
- Biomass - quantified four times during crop growth and at final harvest
- Leaf area index



2.2.4.1 Biomass



2.2.4.2 Canopy

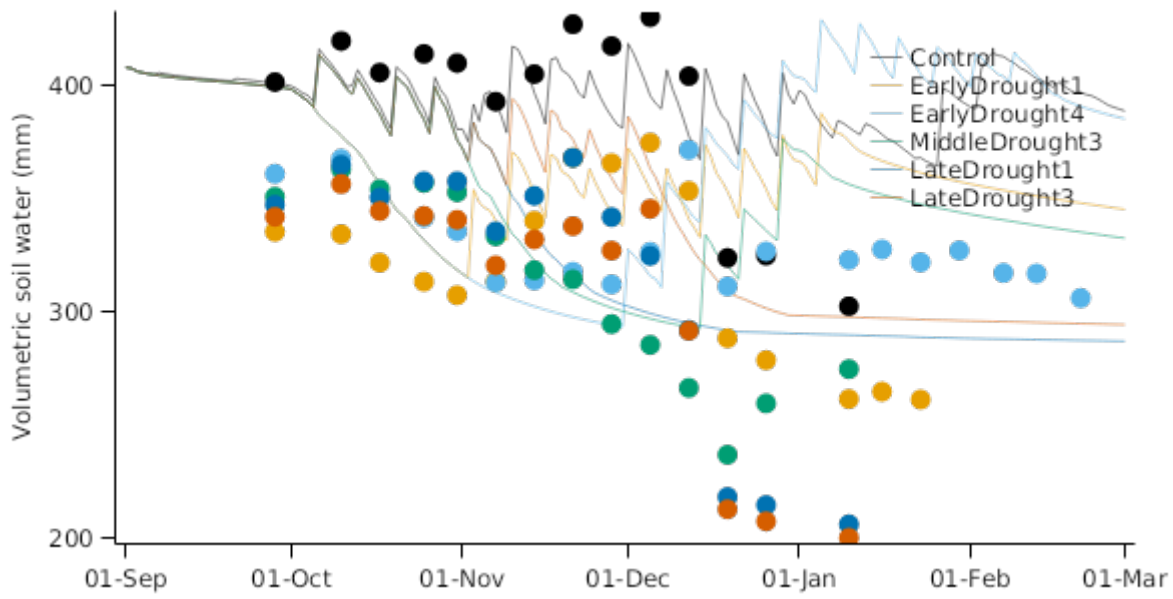


2.2.5 RS1988_89

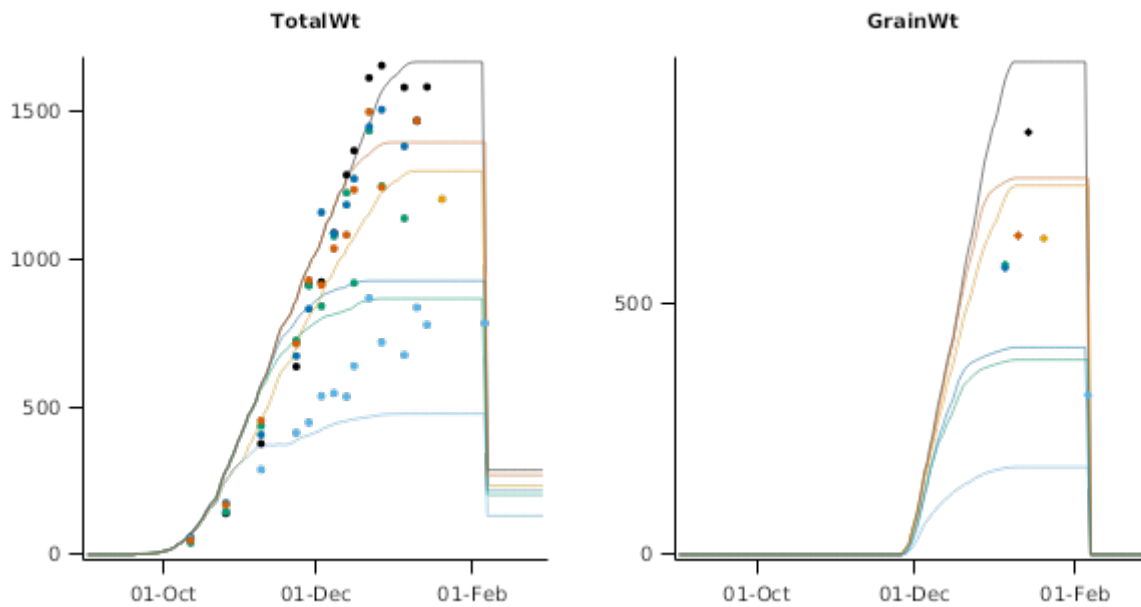
This experiment was conducted in the rainshelter at Plant and Food Research in Lincoln, New Zealand. The objective was to evaluate the effect of drought on the yield of barley crops. The experiment is fully described by Jamieson et al. (1995). Briefly, 'Triumph' barley was sown at 188kg/ha on 07 September 1988. This sowing rate resulted in a population of 291 ± 6 plants/m². Plants were evaluated for their response to drought of varying duration. The treatments were:

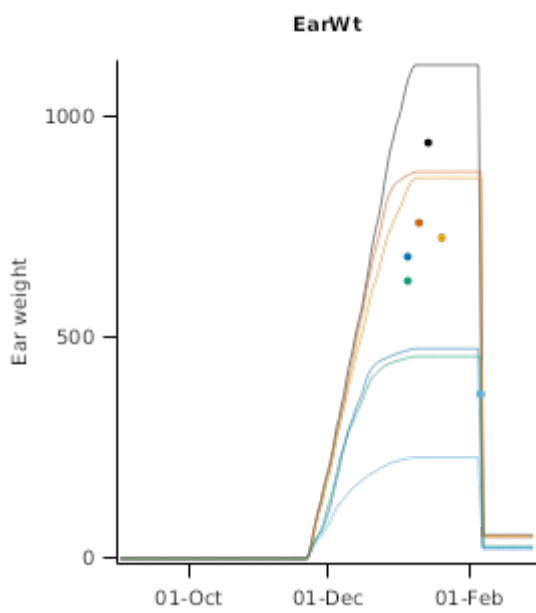
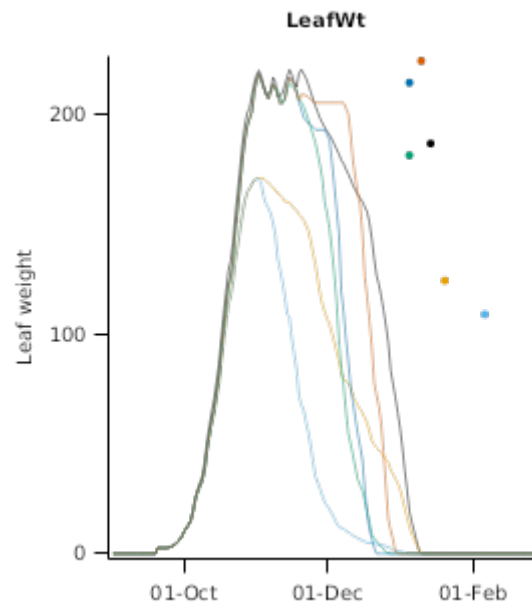
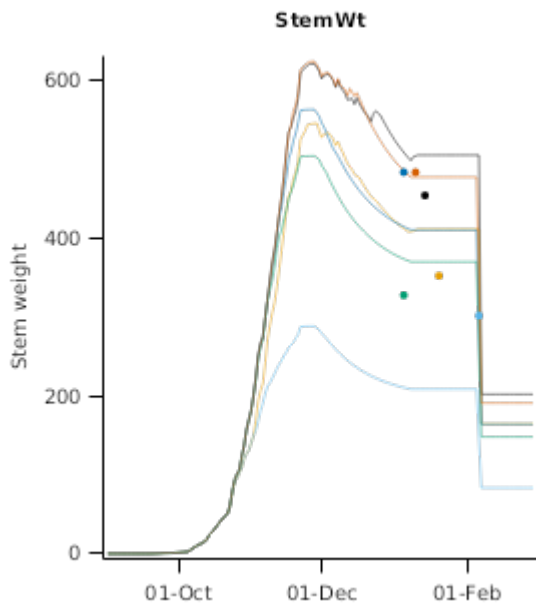
- Full irrigation – measured ET replaced weekly (06 October to 29 December)
- Early Drought 1 – irrigated from 03 November to 05 January
- Early Drought 2 – irrigated from 17 November to 19 January
- Early Drought 3 – irrigated from 24 November to 19 January
- Early Drought 3 – irrigated from 01 December to 09 February
- Middle Drought 1 – irrigated (06/10/1988 to 03/11/1988) and (24/11/1988 to 29/12/1989)
- Middle Drought 2 – irrigated (06/10/1988 to 03/11/1988) and (01/12/1988 to 29/12/1989)
- Middle Drought 3 – irrigated (06/10/1988 to 03/11/1988) and (15/12/1988 to 29/12/1989)
- Middle Drought 3 – irrigated (06/10/1988 to 03/11/1988)
- Late Drought 1 – irrigated (06/10/1988 to 17/11/1988)
- Late Drought 2 – irrigated (06/10/1988 to 24/11/1988)
- Late Drought 3 – irrigated (06/10/1988 to 01/12/1989)

SoilWaterProfile

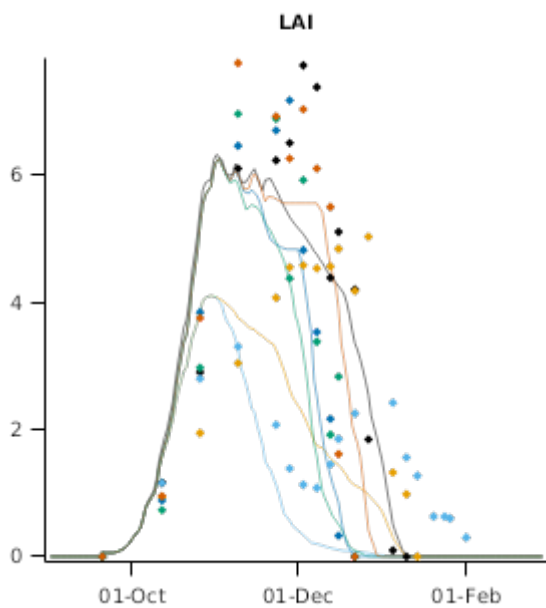


2.2.5.1 Biomass

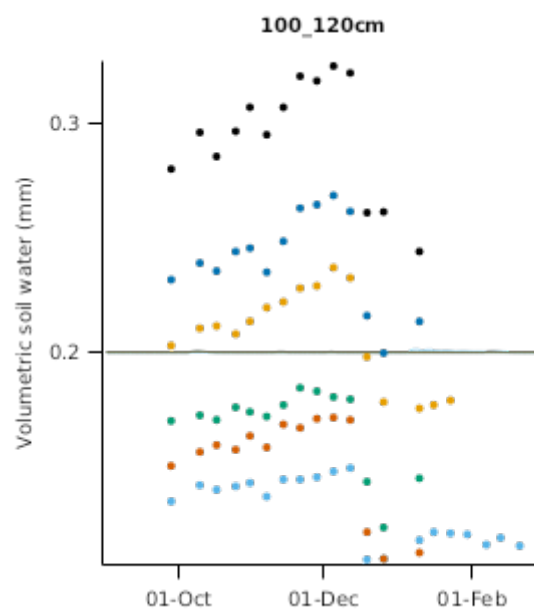
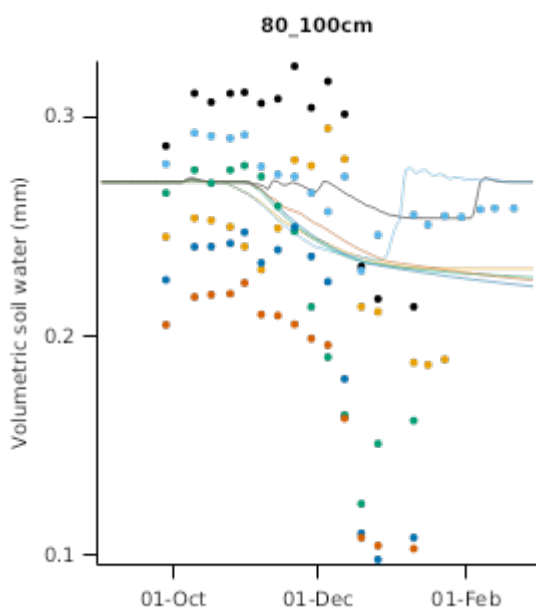
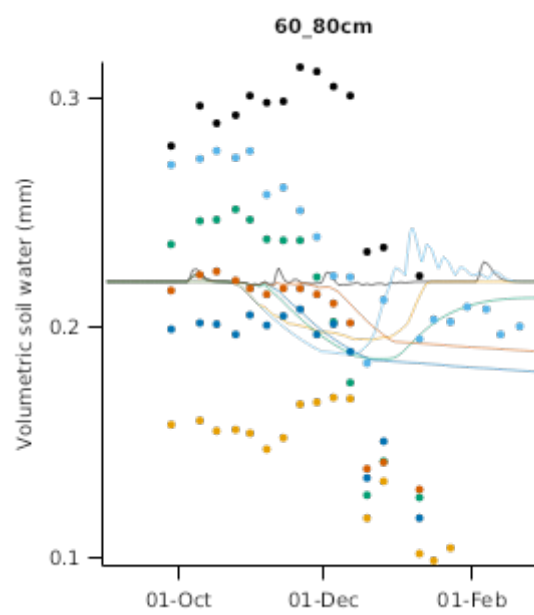
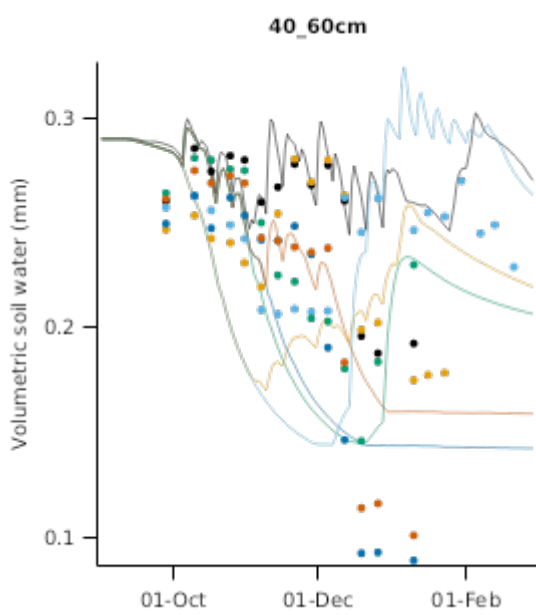
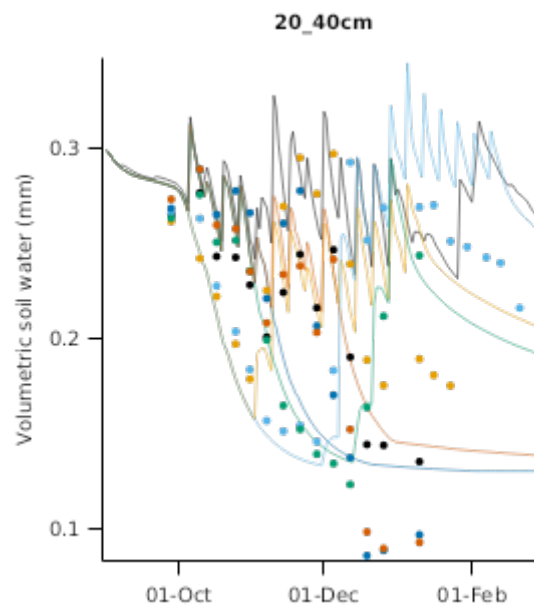
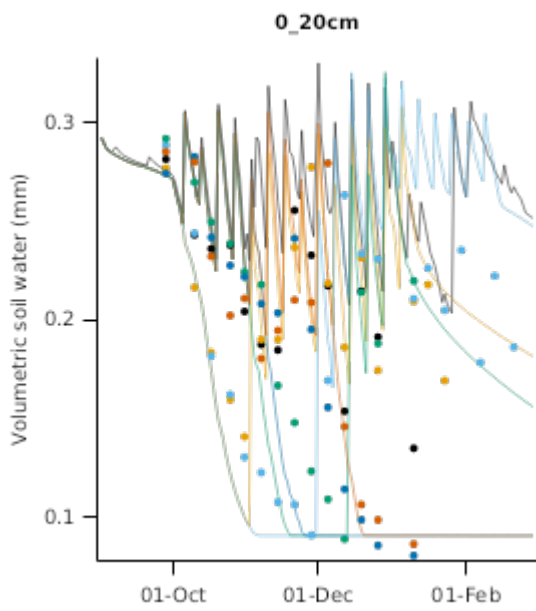


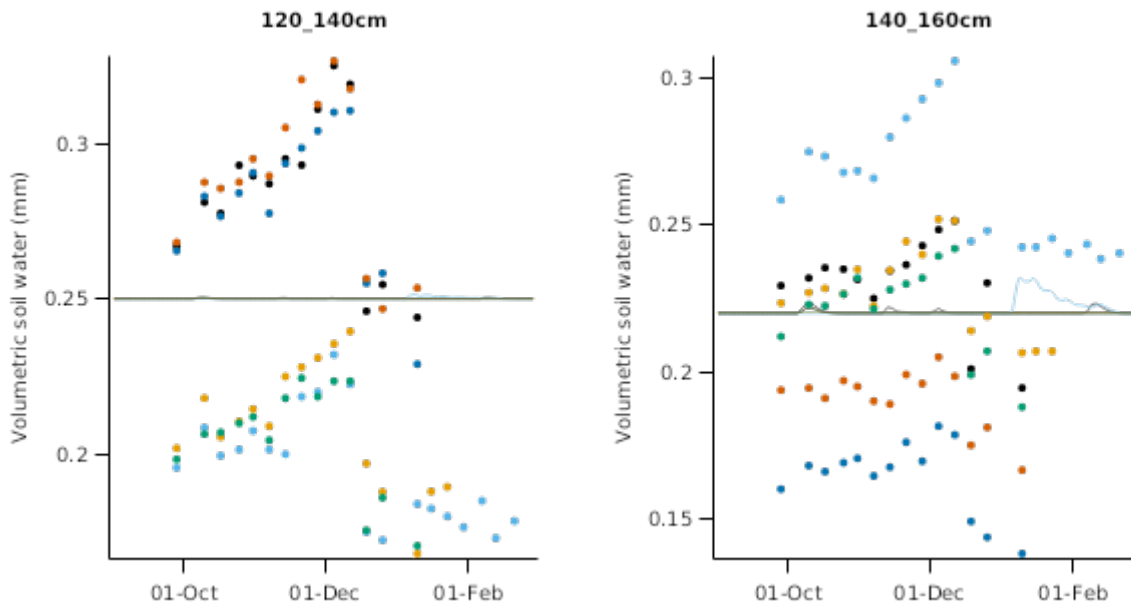


2.2.5.2 Canopy



2.2.5.3 SoilWater



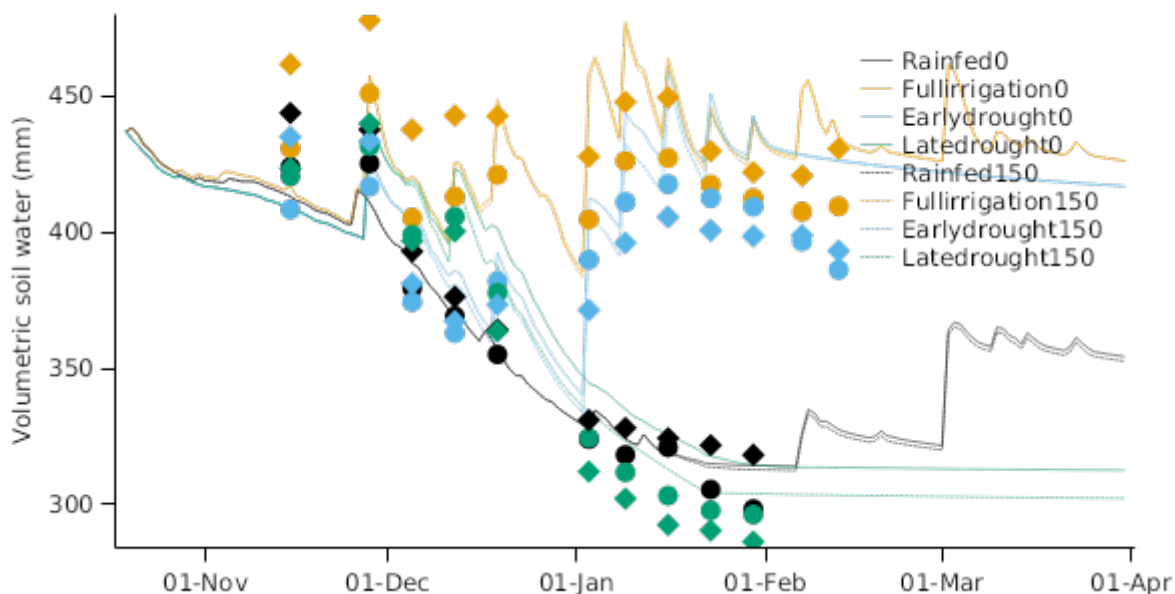


2.2.6 RS1995_96

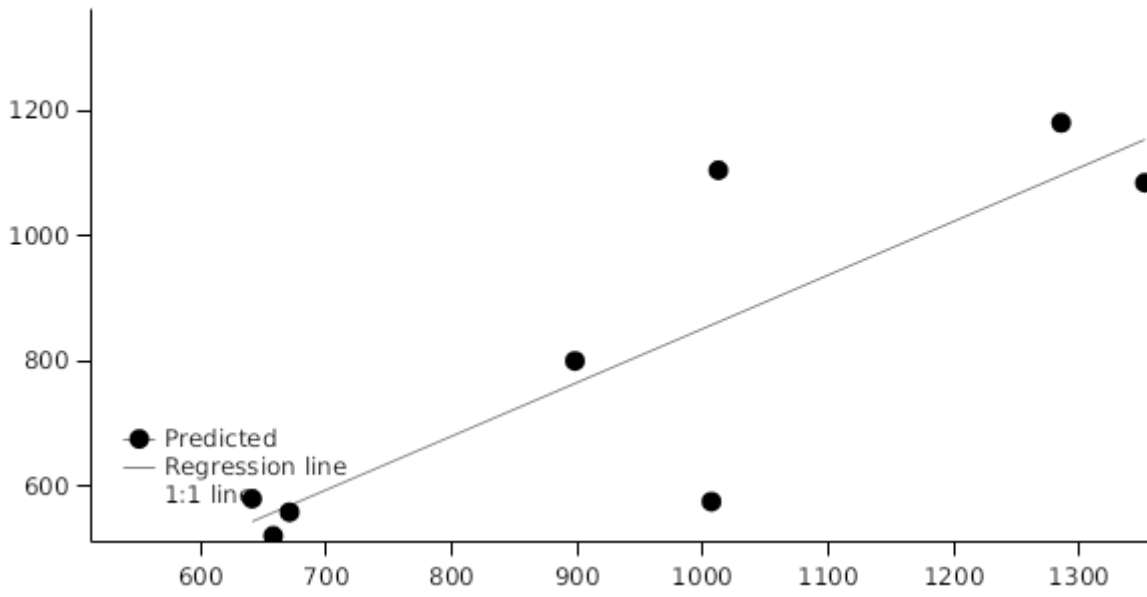
This is a water response trial conducted inside and outside the rain shelter at the New Zealand Institute for Plant & Food Research in Lincoln and described in De Ruiter et al (1999). Briefly, a vernalisation insensitive barley, variety "Valetta", was sown at 280 plant/m² on 20 October 1995 and subjected to five water treatments as follows:

- Full drought (in rain shelter) – was not irrigated except for 17 mm rainfall as a result of shelter failure 42 days after sowing;
- Early drought (in rain shelter) – also receive 17 mm rainfall and the drought was fully relieved at the onset stem elongation;
- Late drought (in rain shelter) – fully irrigated (i.e. net crop water use + soil water evaporation) up to stem elongation and nil irrigation thereafter;
- Rain-fed (outside the rain shelter) – received all the rain but no irrigation;
- Full irrigation (located outside the rain shelter) – received all the rain and irrigation to replace ET.

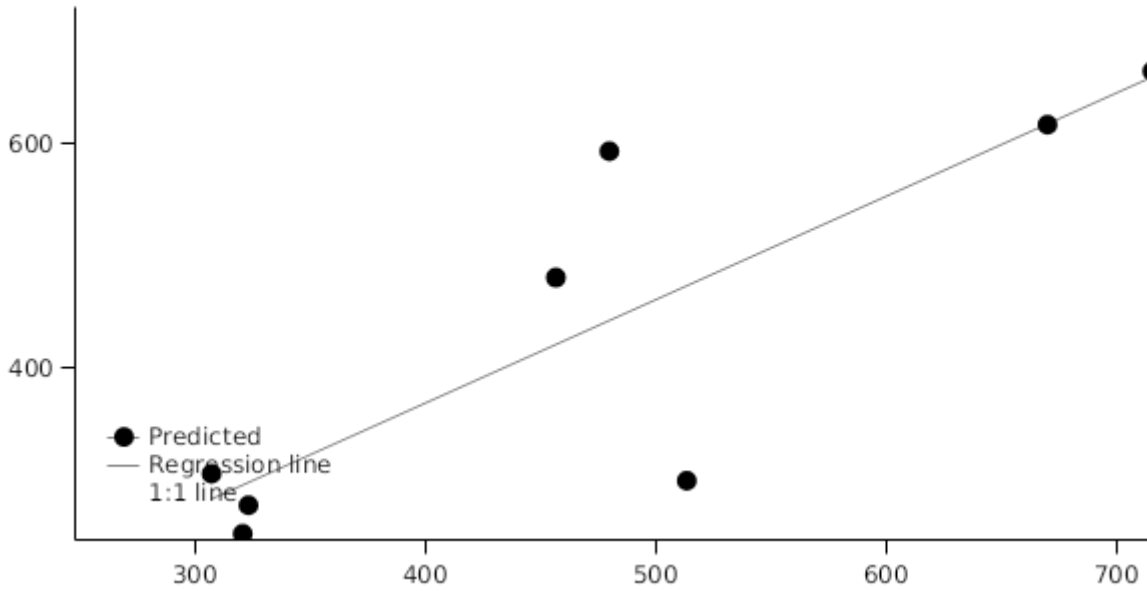
SoilWaterProfile



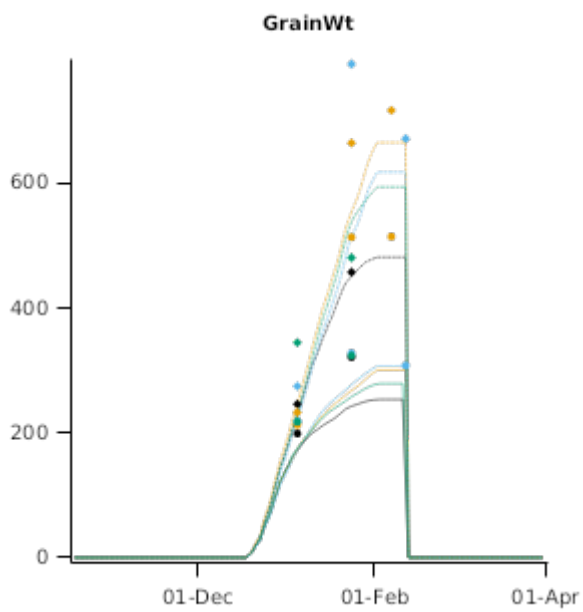
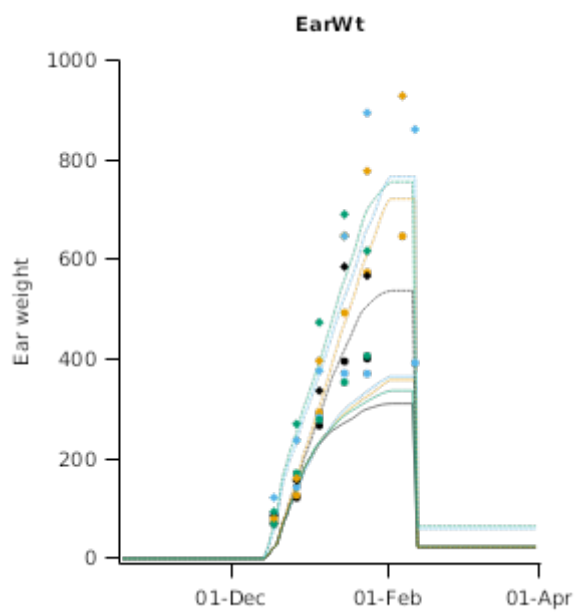
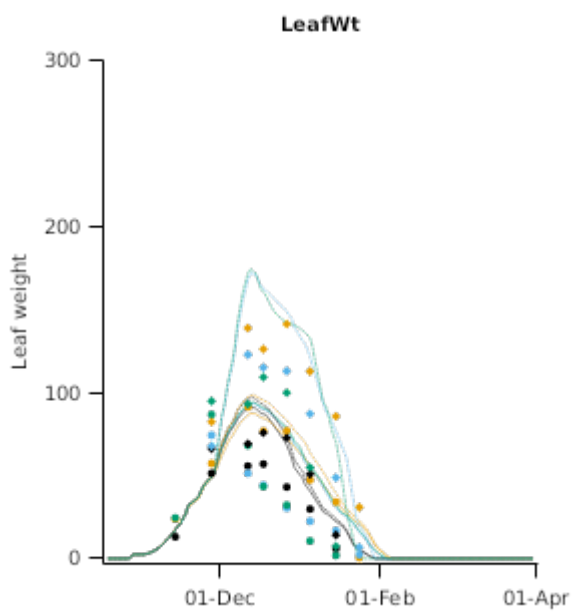
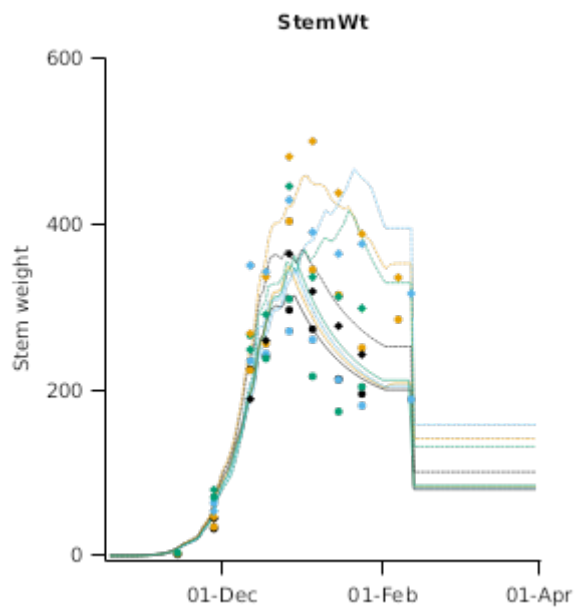
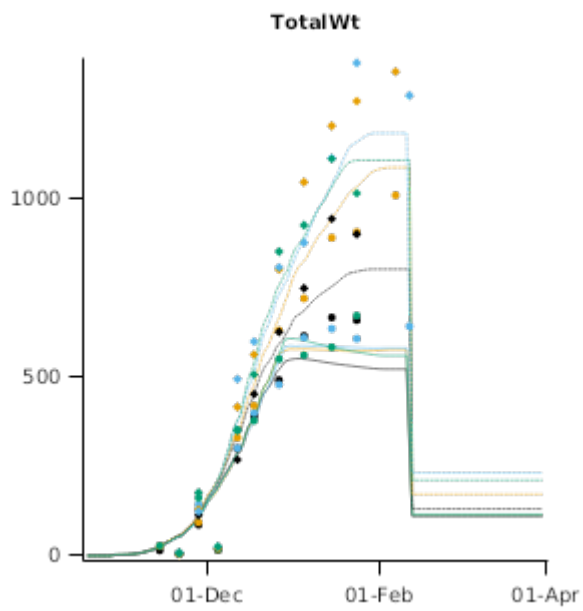
Harvest Biomass



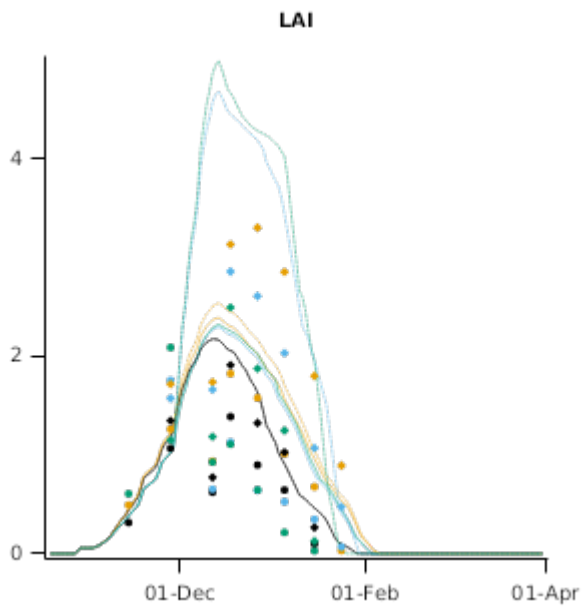
Harvest Yield



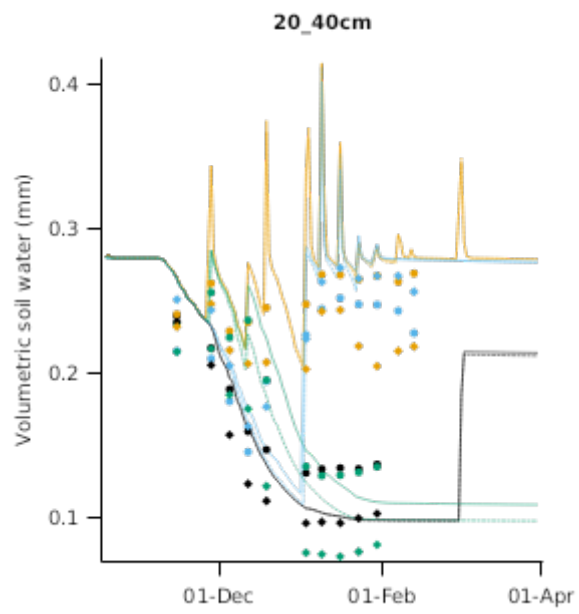
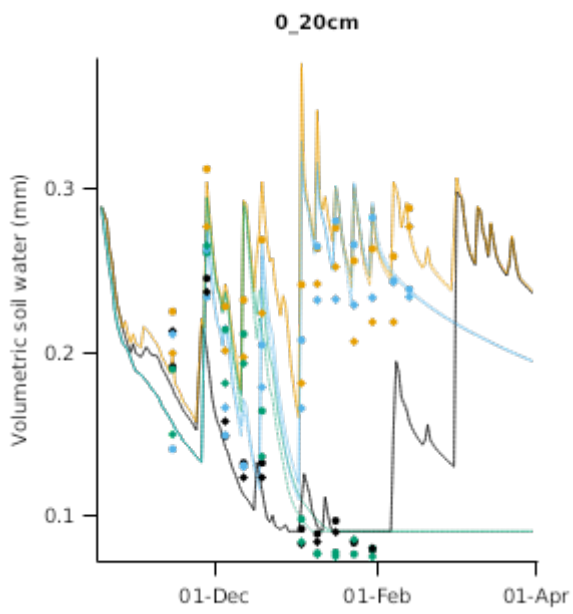
2.2.6.1 Biomass

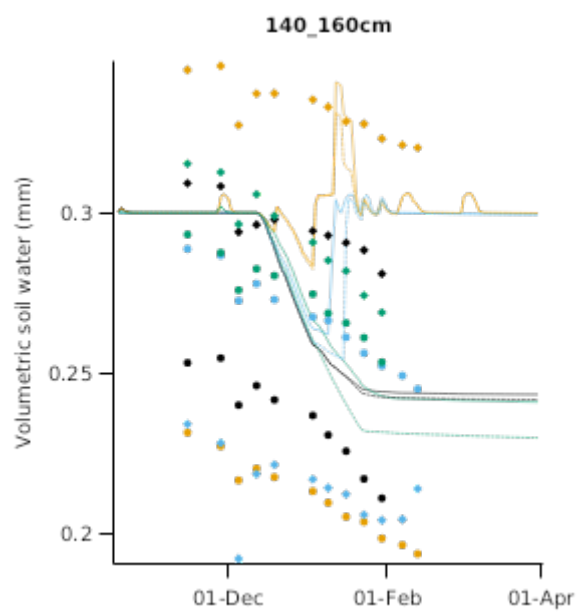
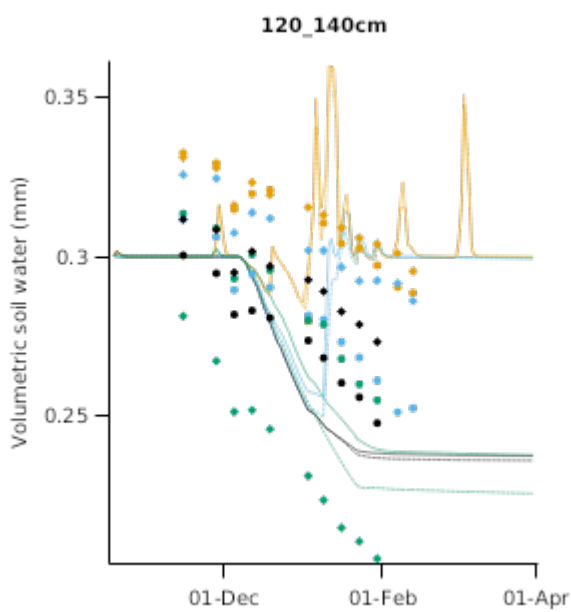
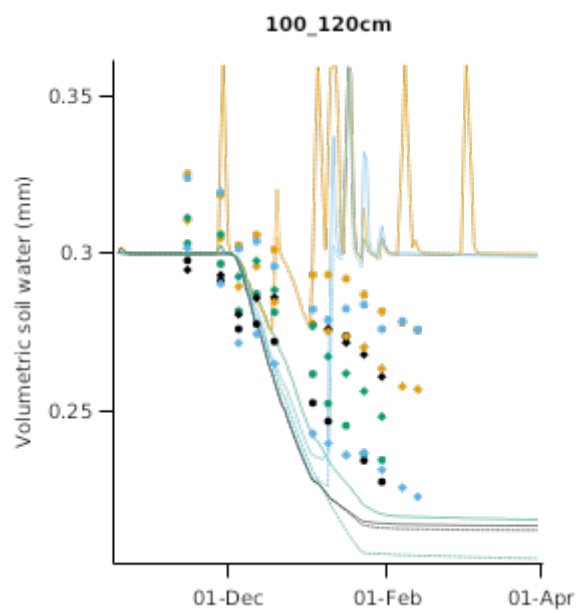
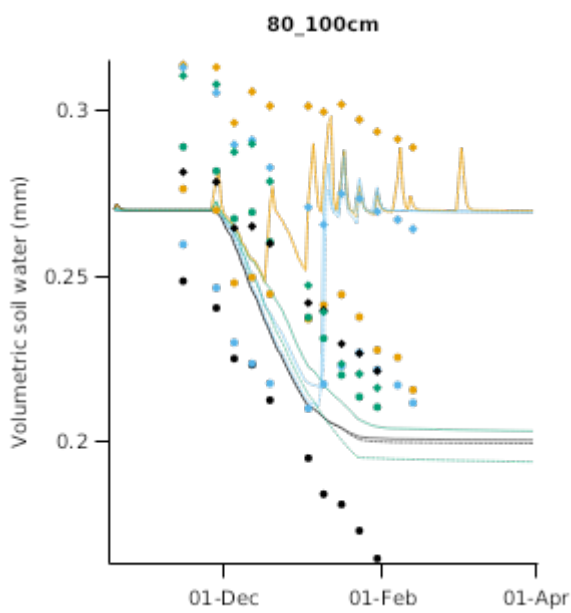
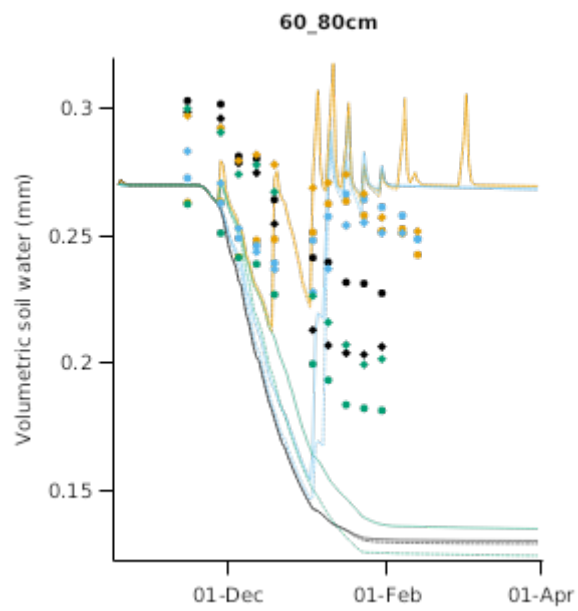
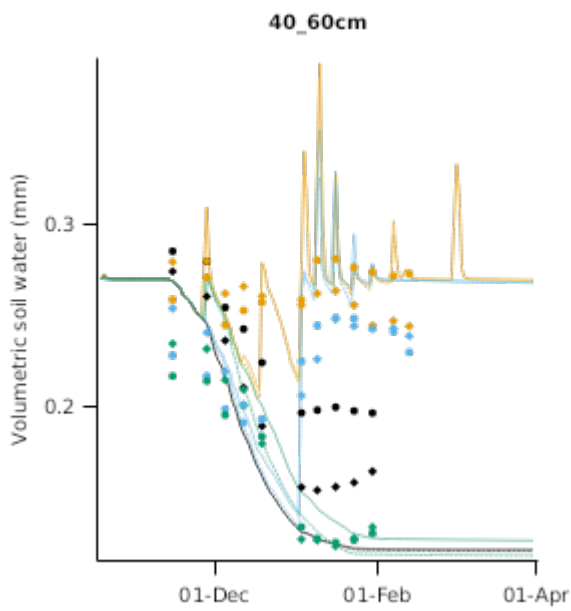


2.2.6.2 Canopy



2.2.6.3 SoilWater



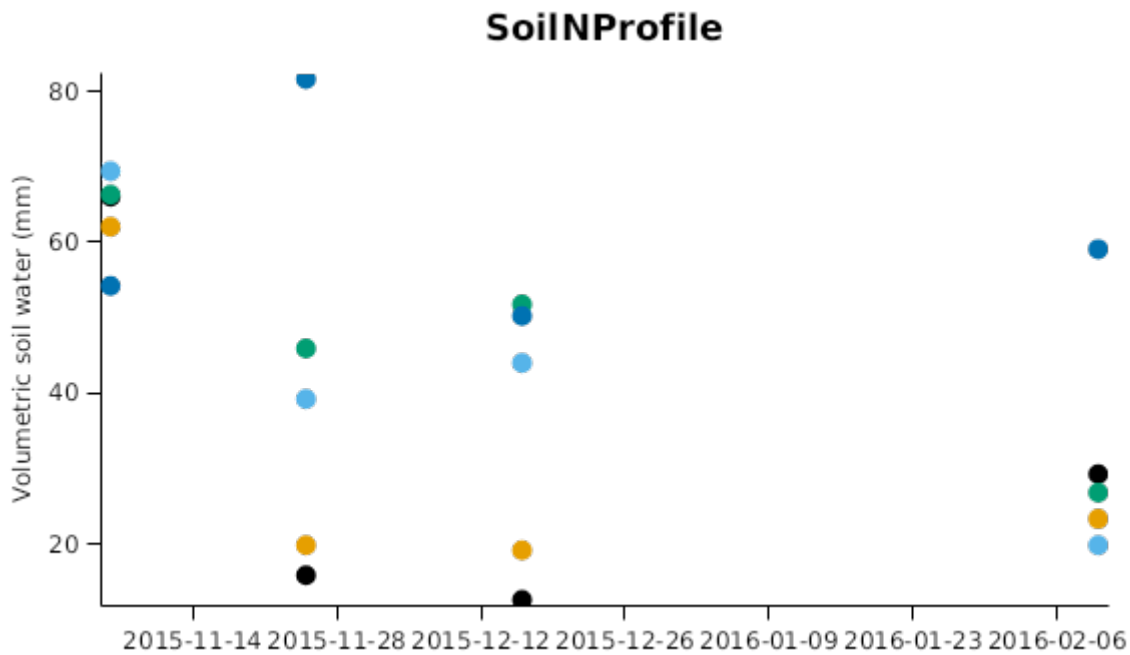


2.2.7 LUDF2015_16

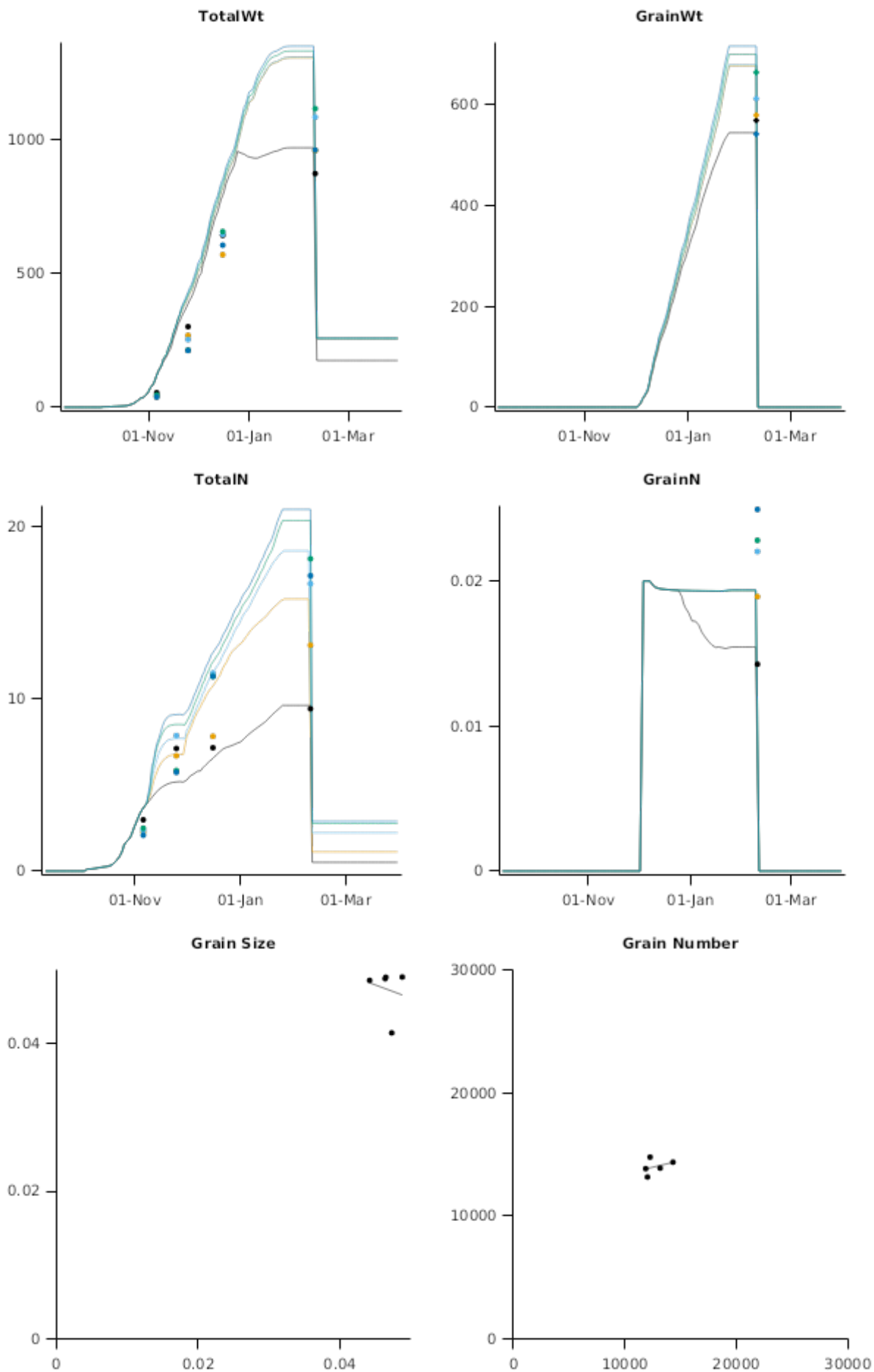
This is the mineral nitrogen (N) validation trial conducted by the New Zealand Institute for Plant & Food Research from

September 2015 to February 2016. The experiment was established at the Lincoln University Dairy Farm on a deep well-drained Templeton silt loam soil. Five N fertiliser treatments were evaluated:

- Nil (0%) N - the crop did not get any fertiliser N
- 50% N - the crop received 50% of the required fertiliser N
- 75% N - the crop received 75% of the required fertiliser N
- 100% N - the crop received the required fertiliser N as estimated by the fertiliser calculator
- 125% N - the crop received 25% fertiliser N above the requirement.



2.2.7.1 Biomass

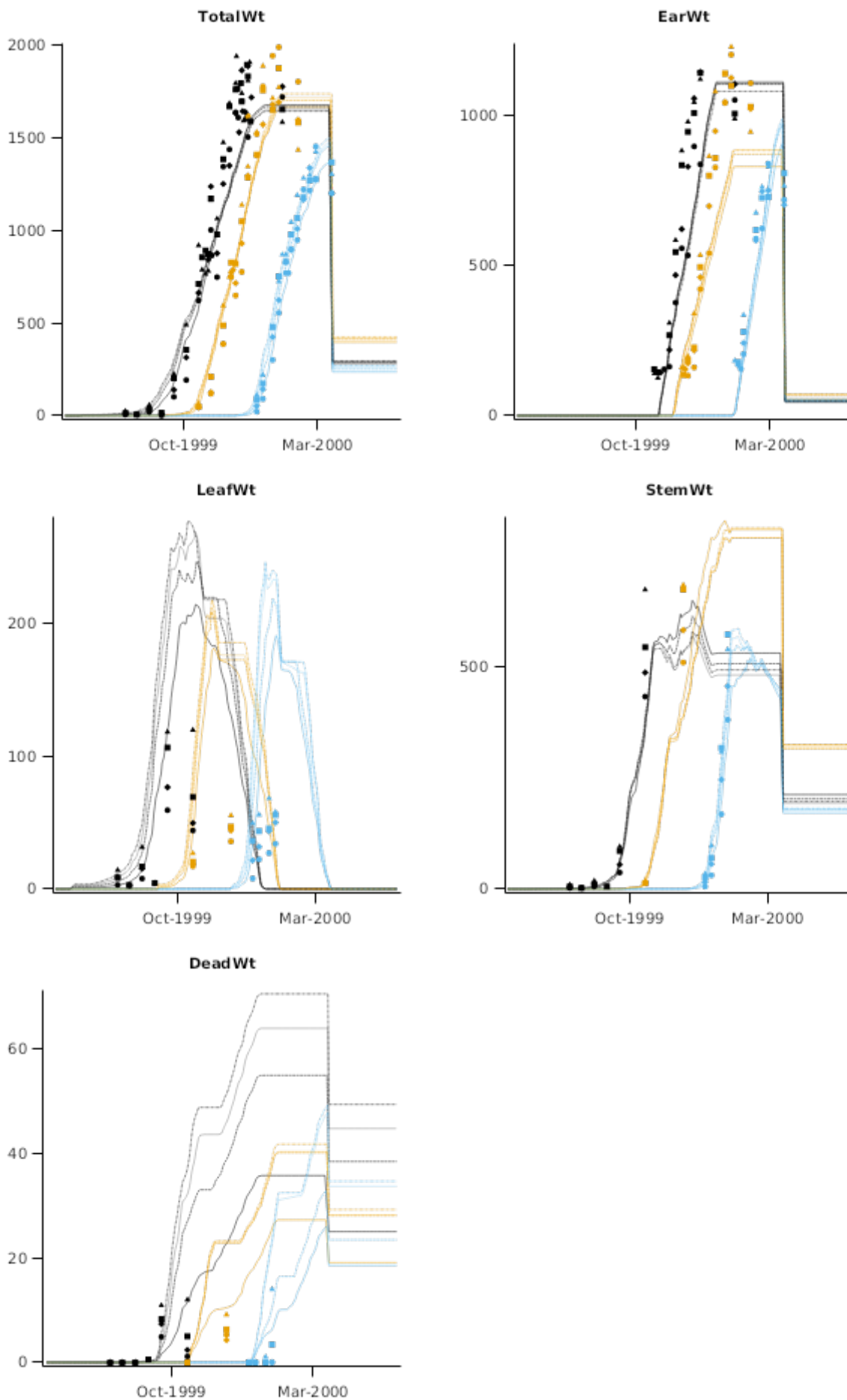


2.2.8 ABlock99_00

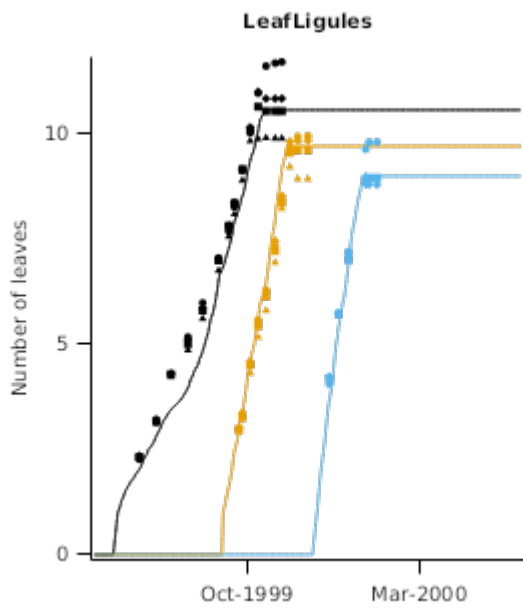
This was a sowing date by irrigation trial conducted at Lincoln. The following were evaluated:

- Two water treatments; Rainfed (nil irrigation) and irrigated (310 mm)
- Two fertiliser N treatments; 0N (no fertiliser) and 150N (150 kg N/ha)

2.2.8.1 Biomass



2.2.8.2 Canopy

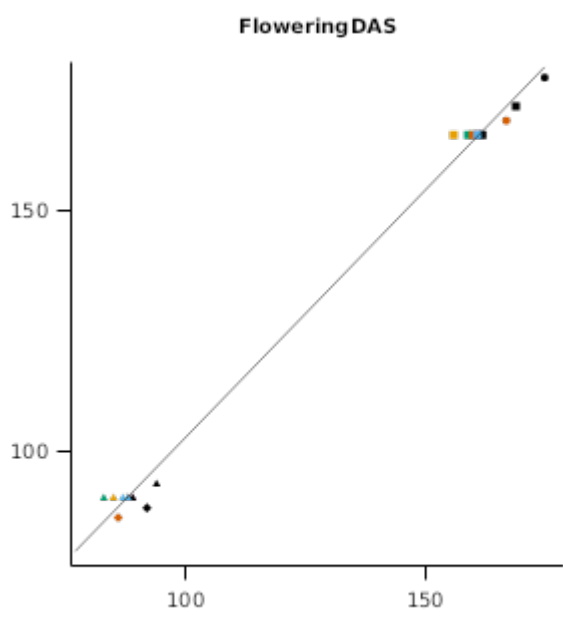
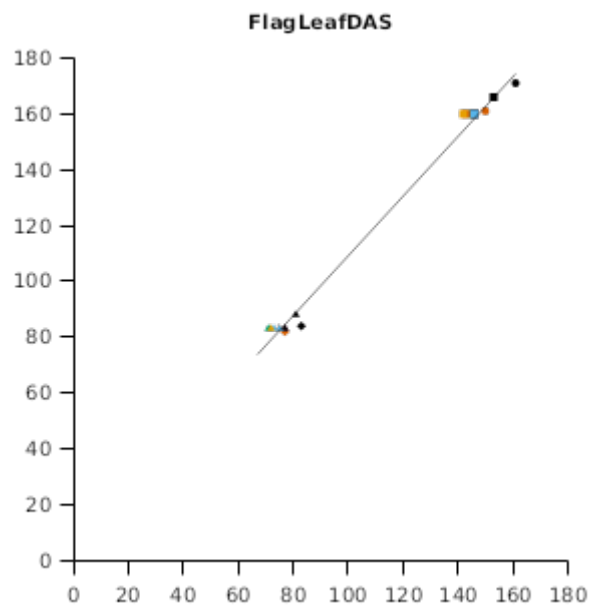
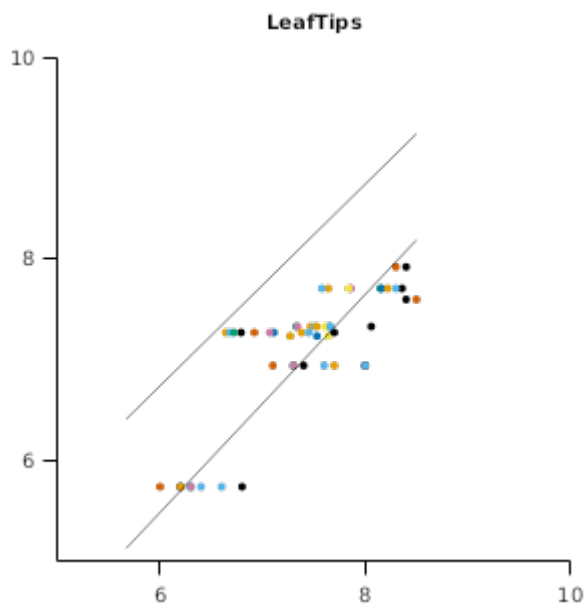


2.2.9 CPT

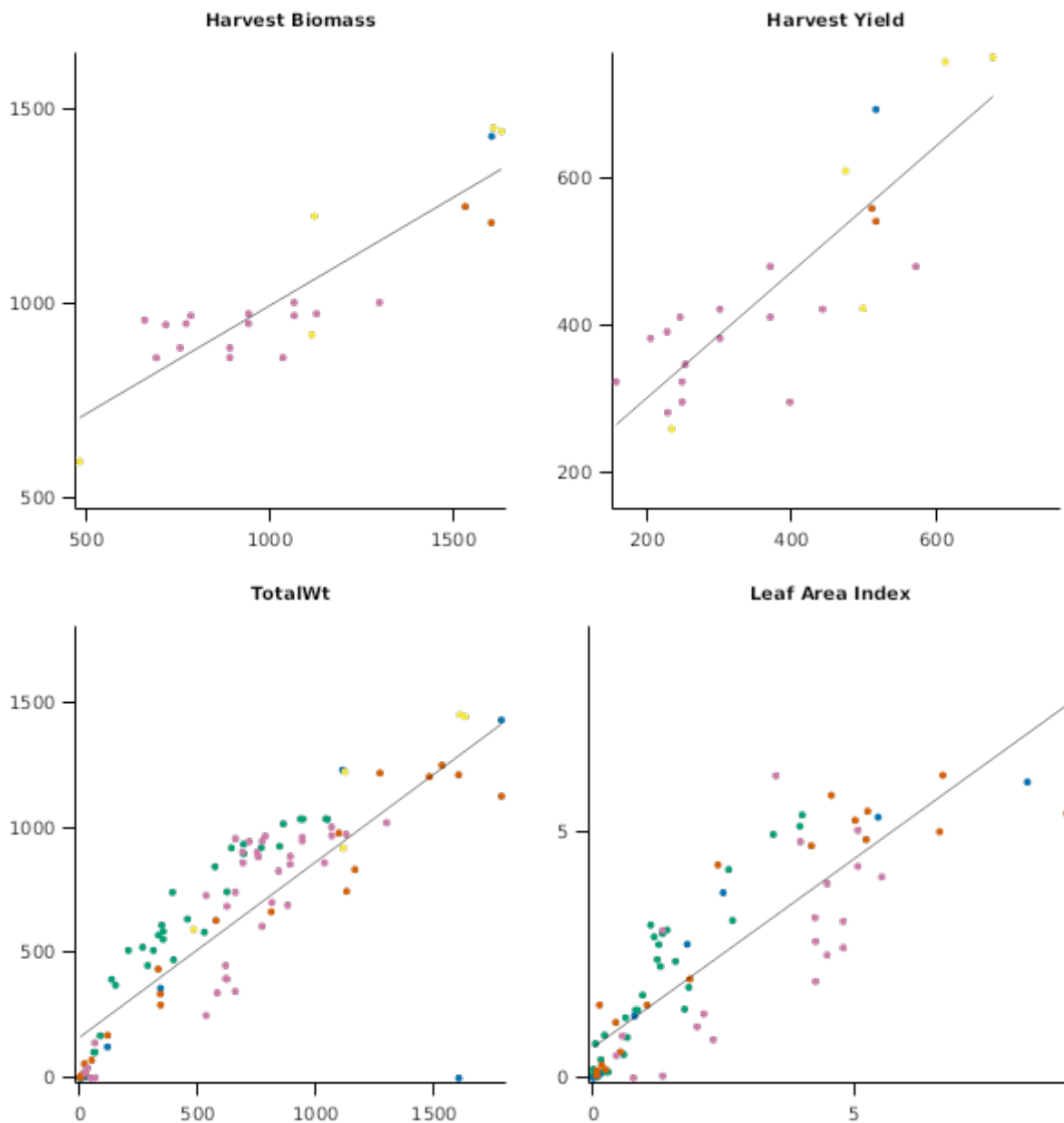
This was a cultivar evaluation trial conducted in Lincoln New Zealand between 2003 and 2006. Crops were sown in either May or September. Observations made were of (i) DAS to flag leaf appearance and (ii) DAS to flowering.

List of experiments.

Experiment Name	Design (Number of Treatments)
CPT	Cult x SD (110)



2.3 Australia

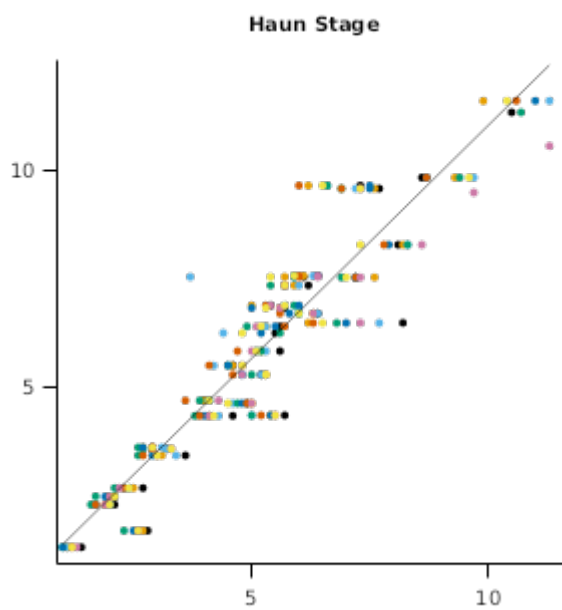
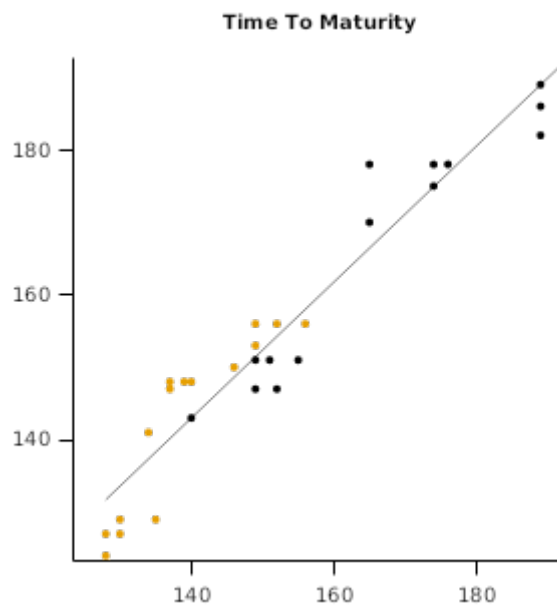
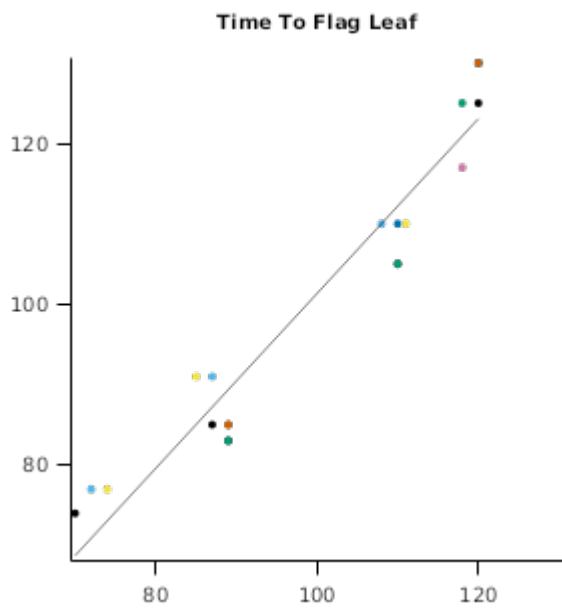


2.3.1 MCVP

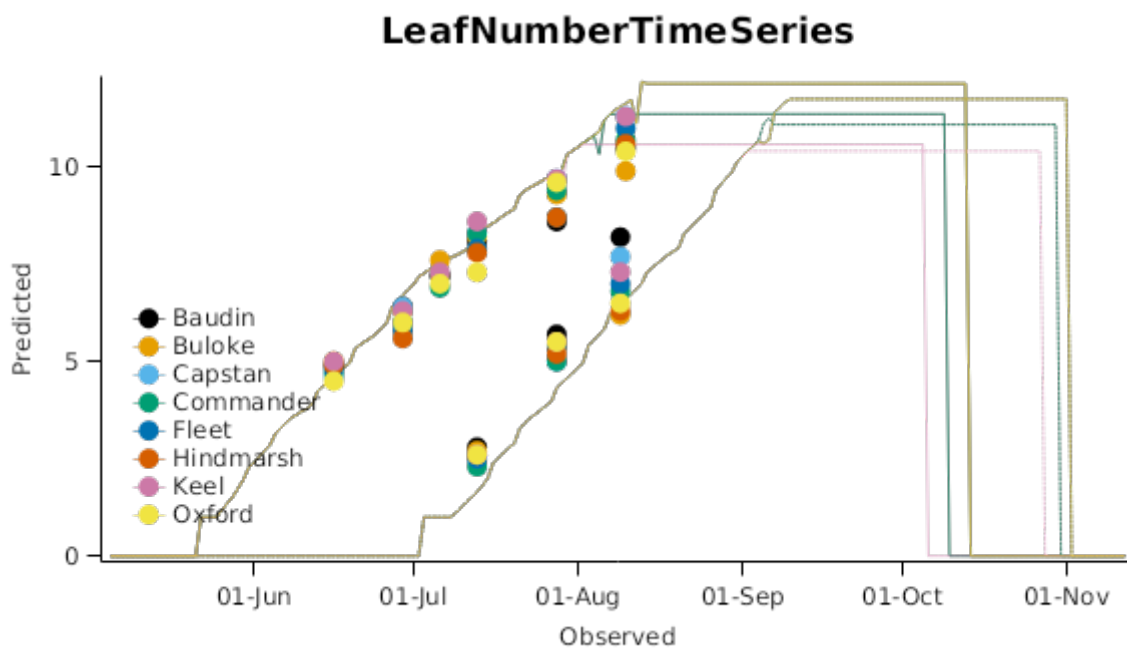
This experiment was funded as part of the Australian Managing Climate Variability Program. Barley cultivars were sown at two planting dates at three sites for the purpose of improving APSIM predictions of the phenology of commercial cultivars. The locations included Gatton in Queensland (subtropical location), Birchip in Victoria (temperate inland location) and Tarlee in South Australia (temperate location).

List of experiments.

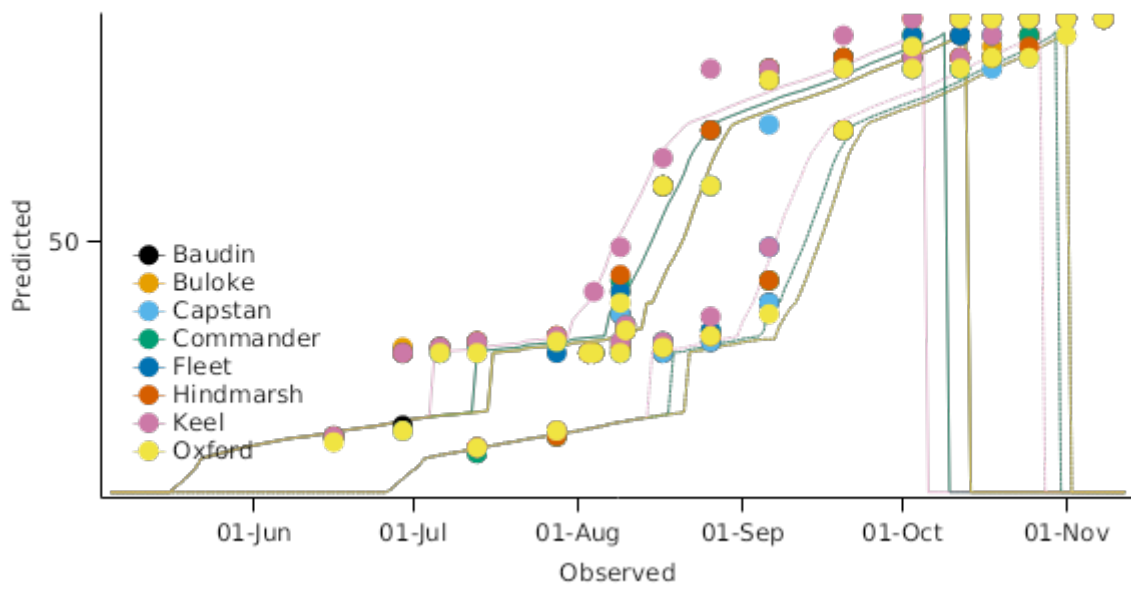
Experiment Name	Design (Number of Treatments)
Gatton2011	TOS x Cv (16)
Birchip2011	TOS x Cv (16)
Tarlee2011	TOS x Cv (16)



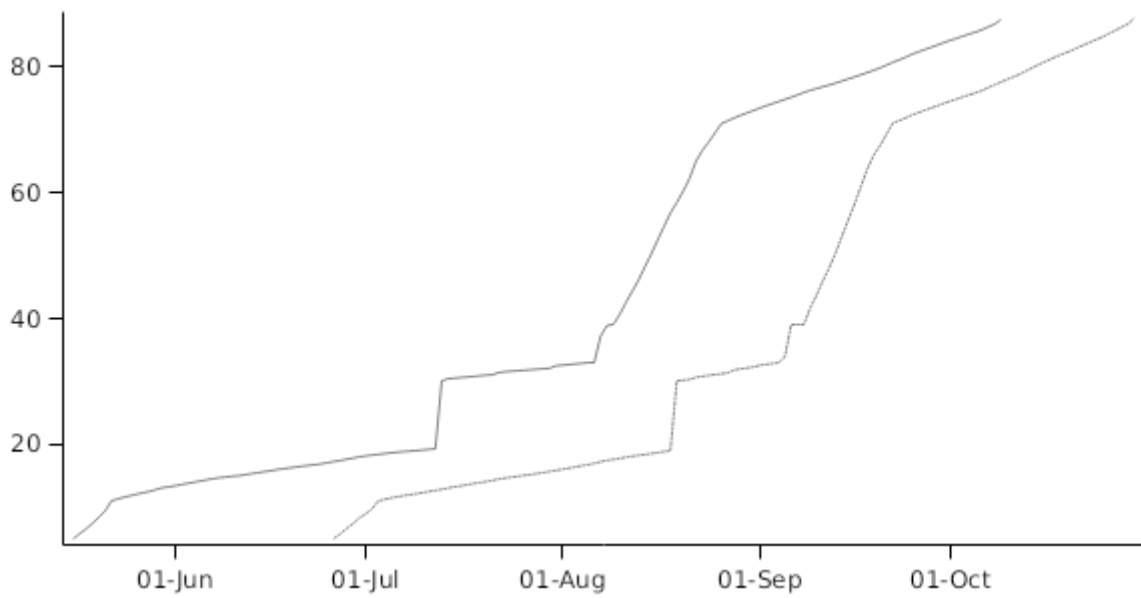
2.3.1.1 Gatton2011



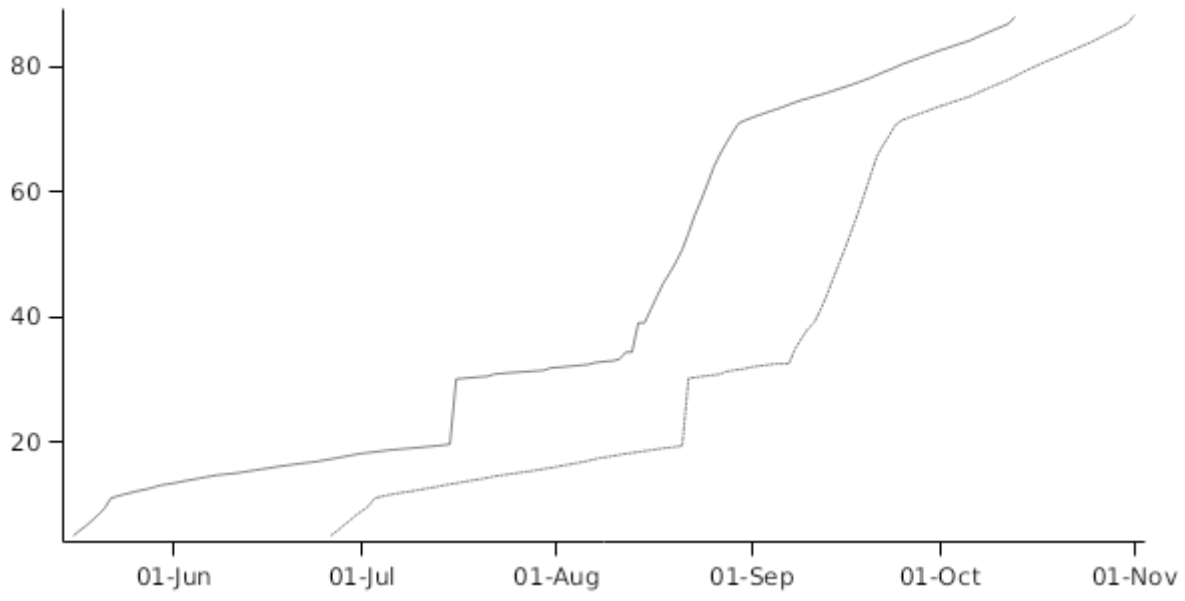
ZadokTimeSeries



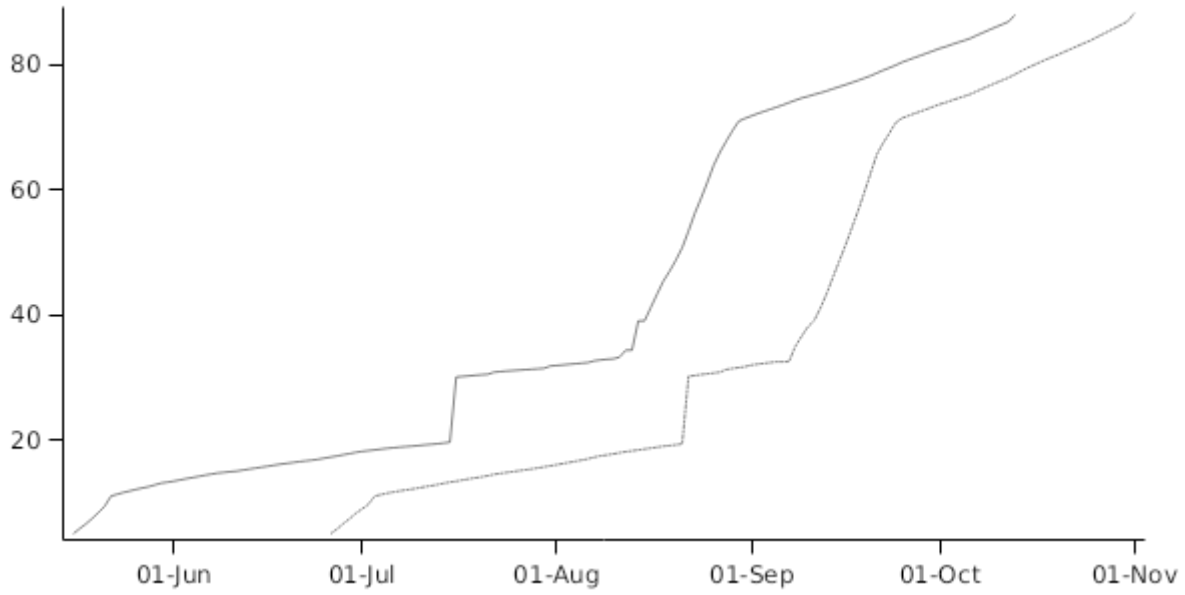
Baudin



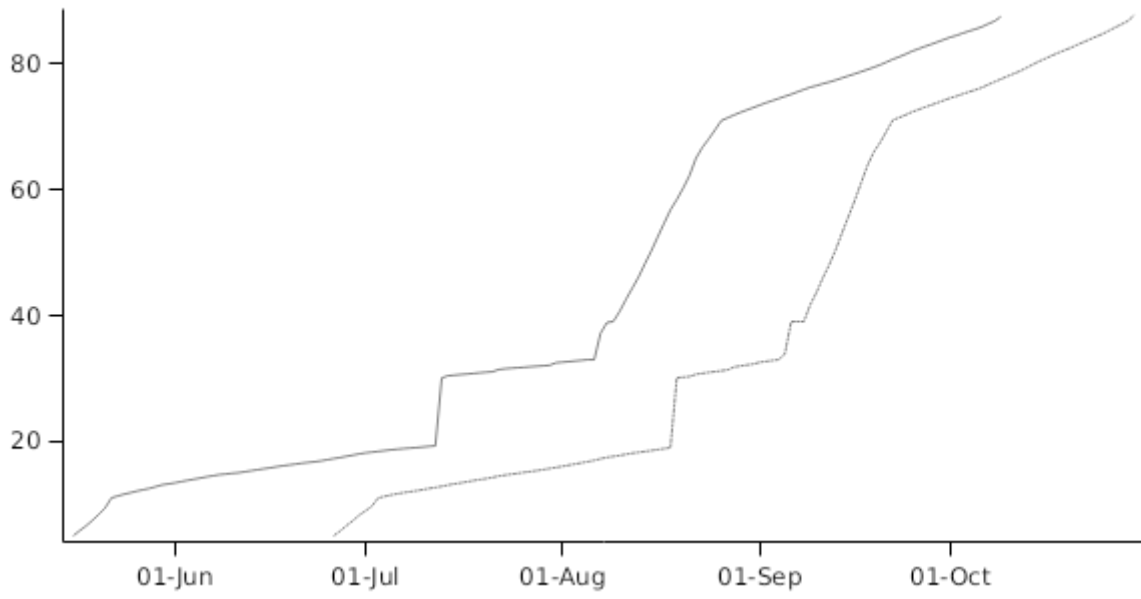
Buloke



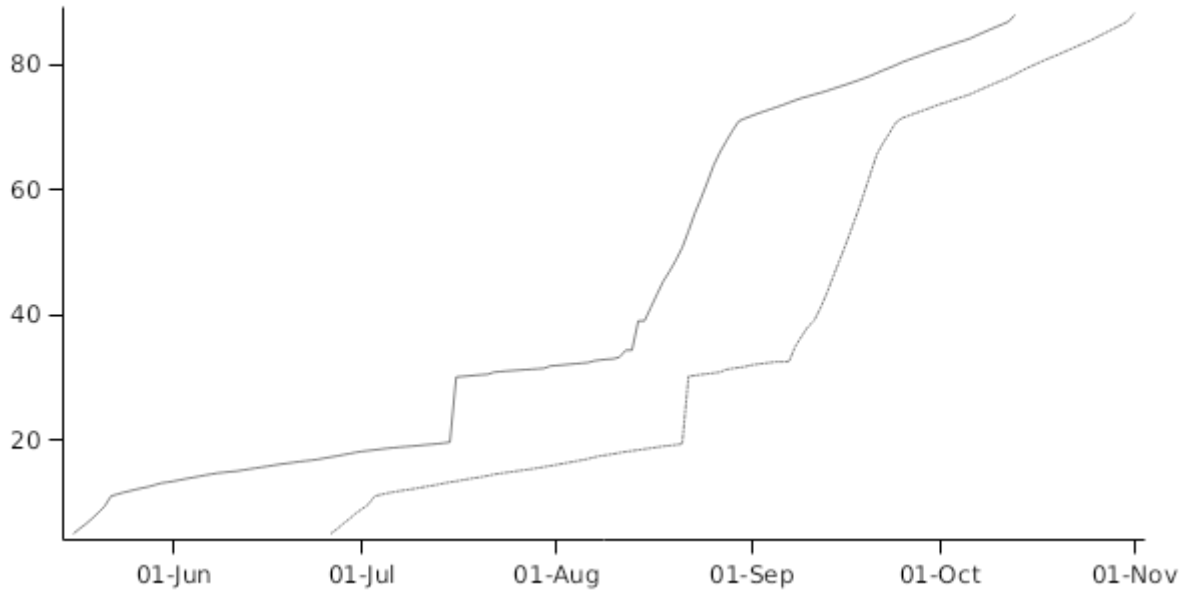
Capstan



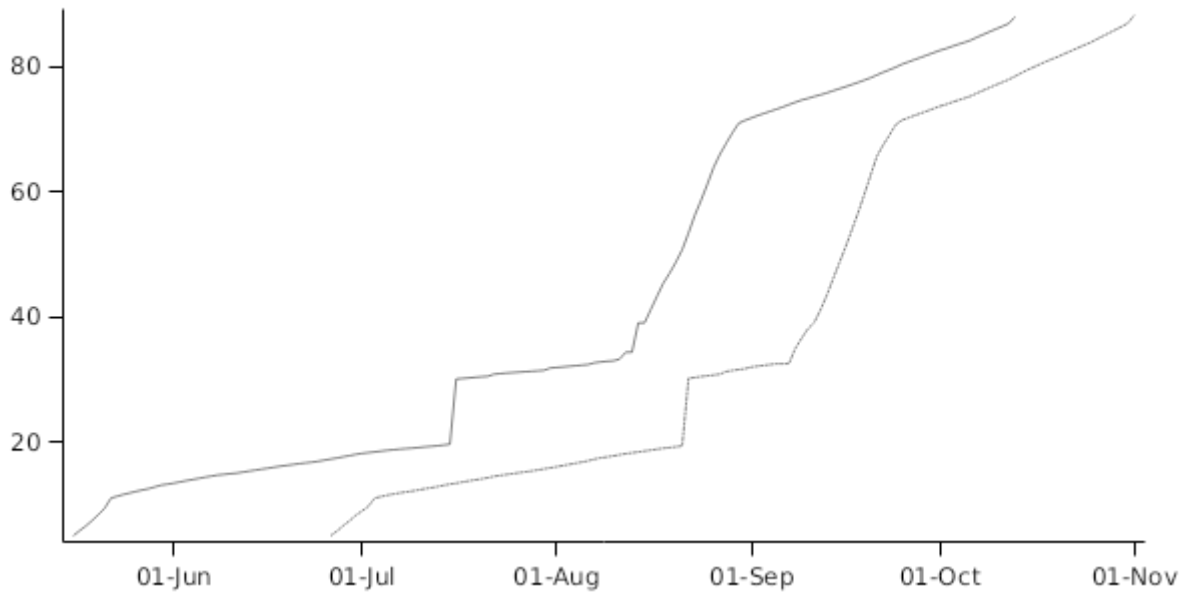
Commander



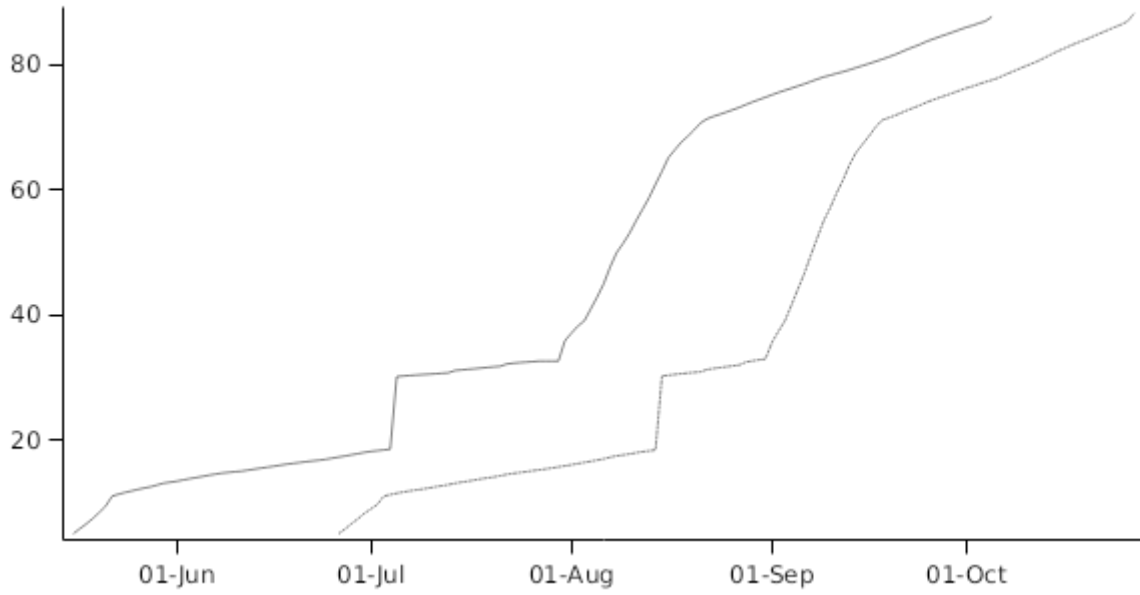
Fleet



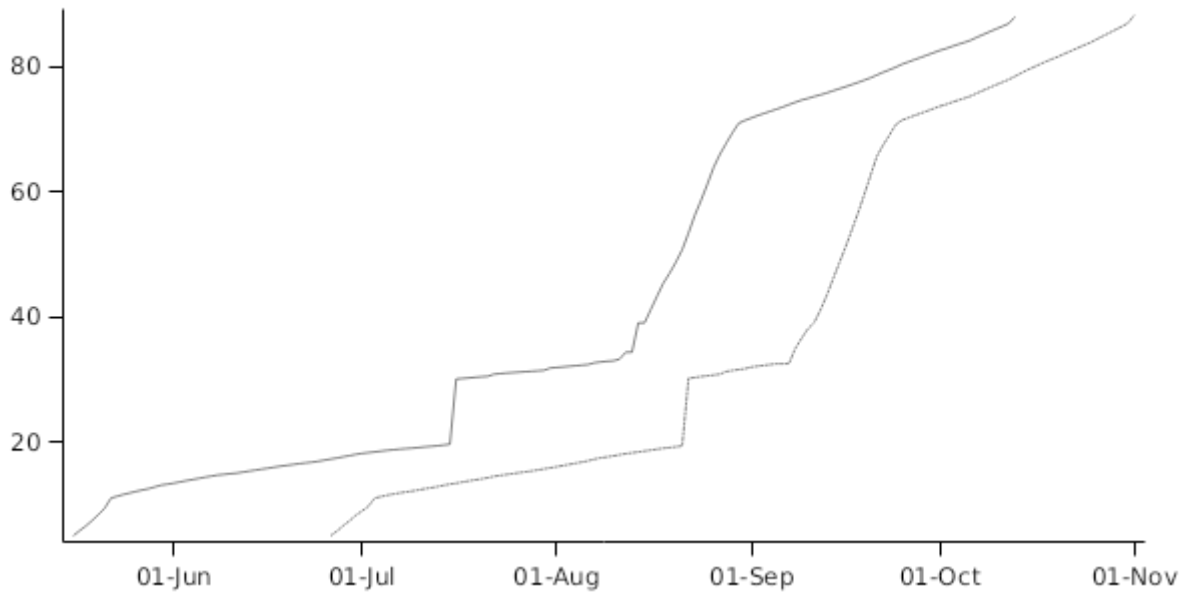
Hindmarsh



Keel

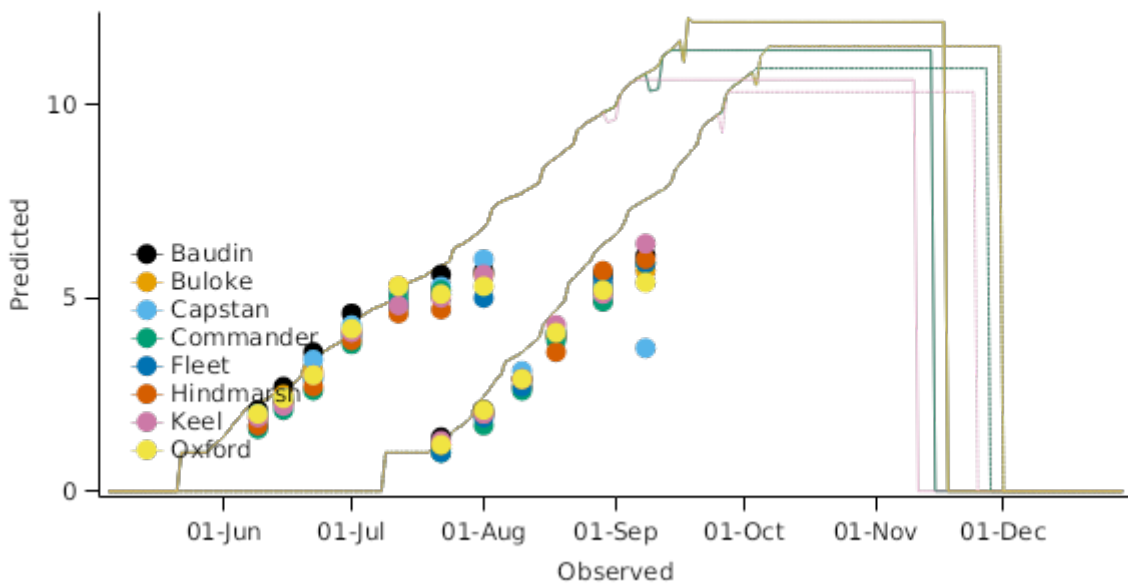


Oxford

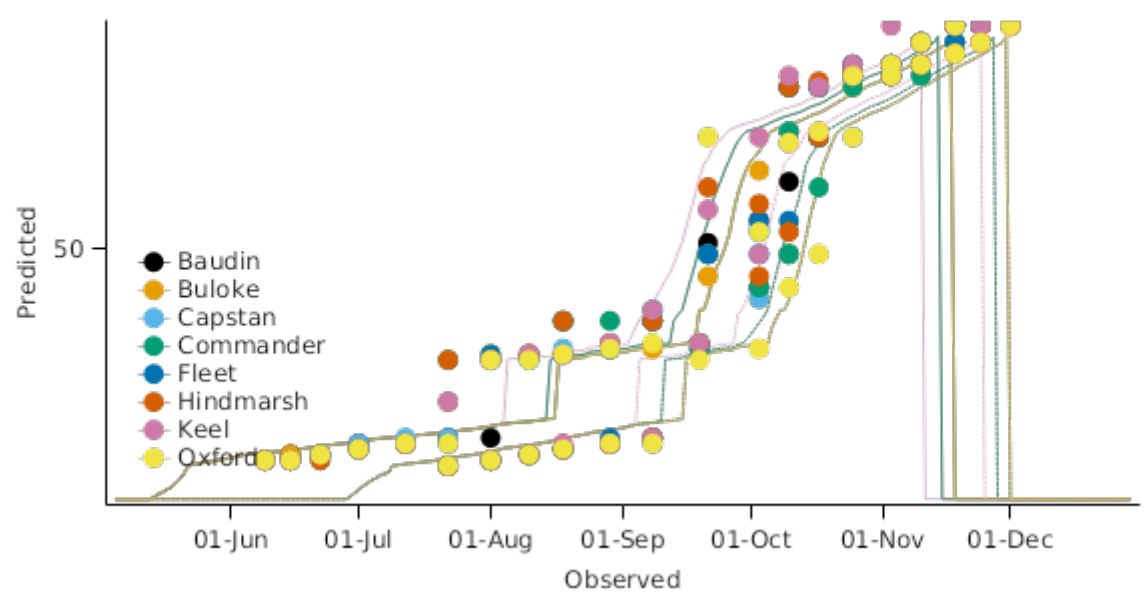


2.3.1.2 Birchip2011

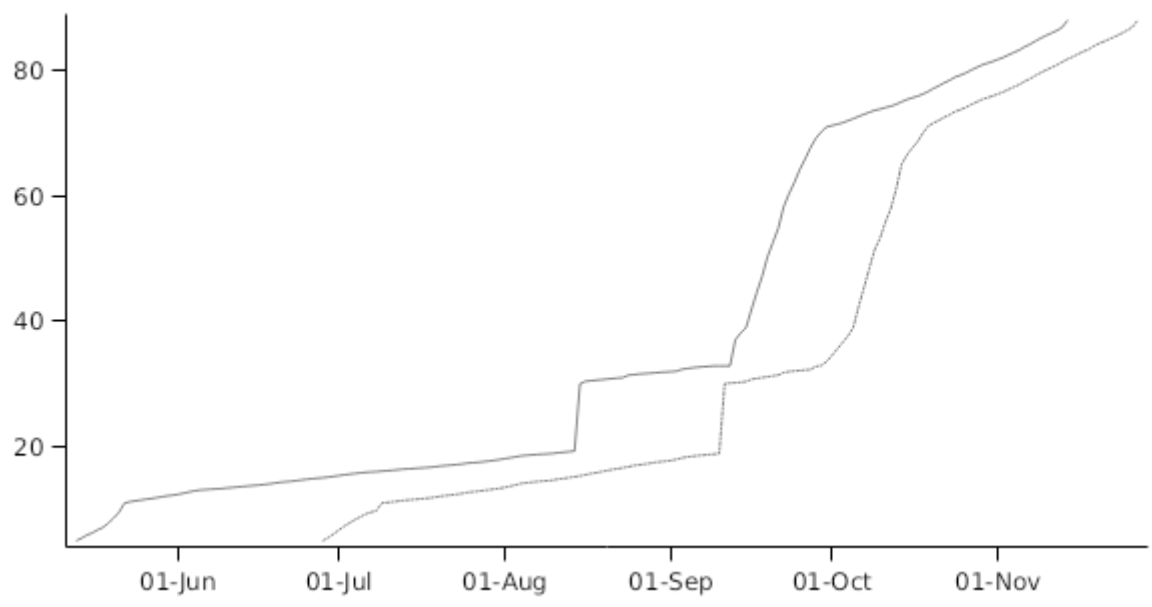
LeafNumberTimeSeries



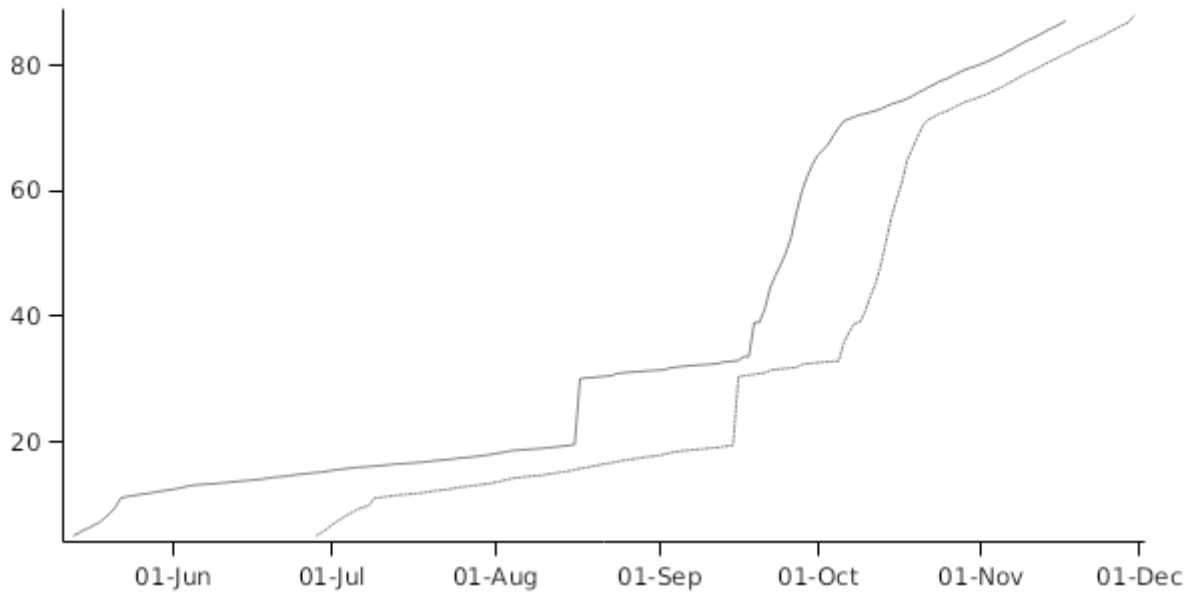
ZadokTimeSeries



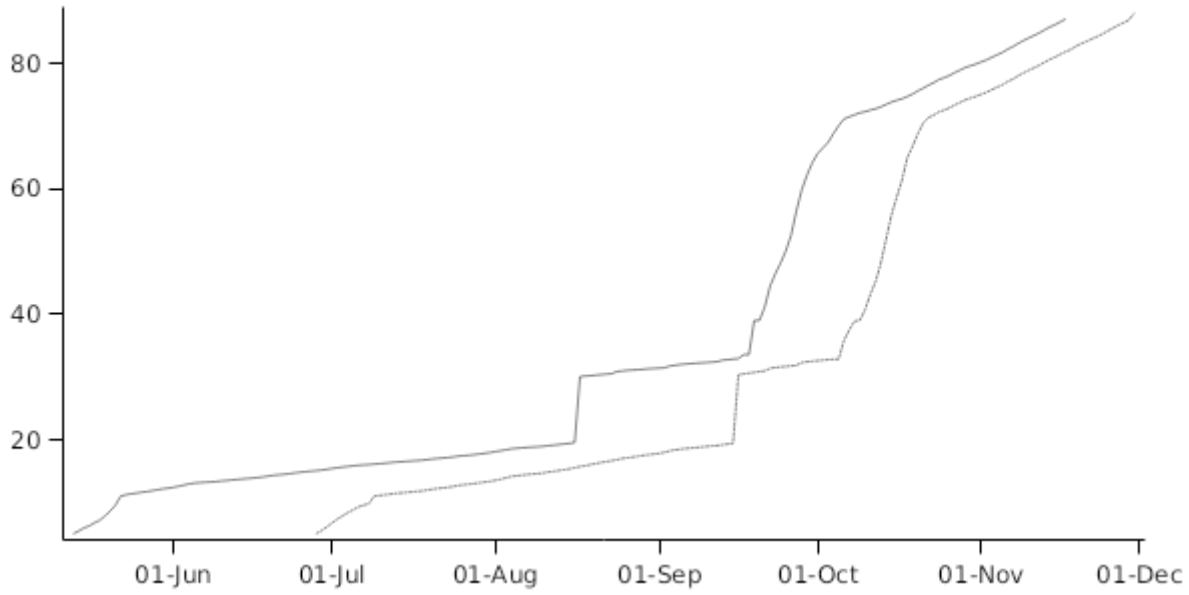
Baudin



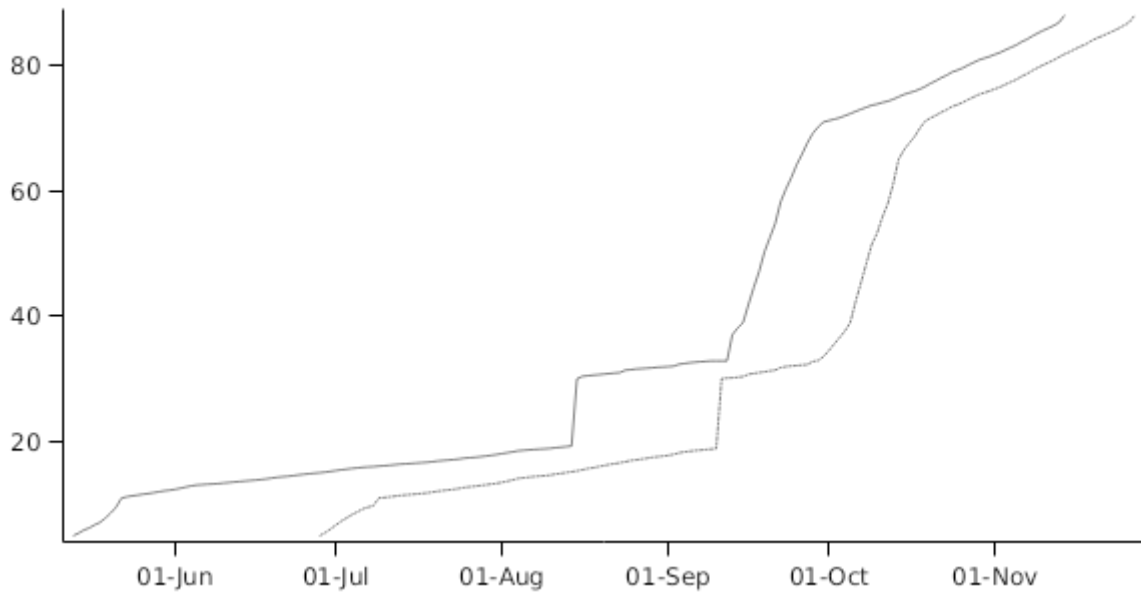
Buloke



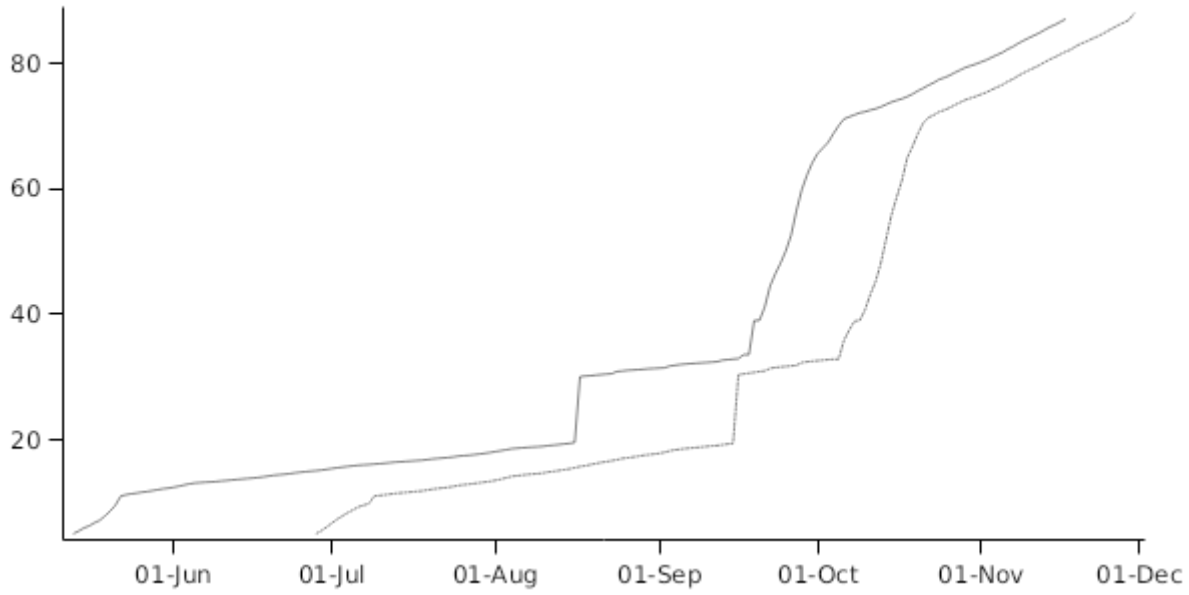
Capstan



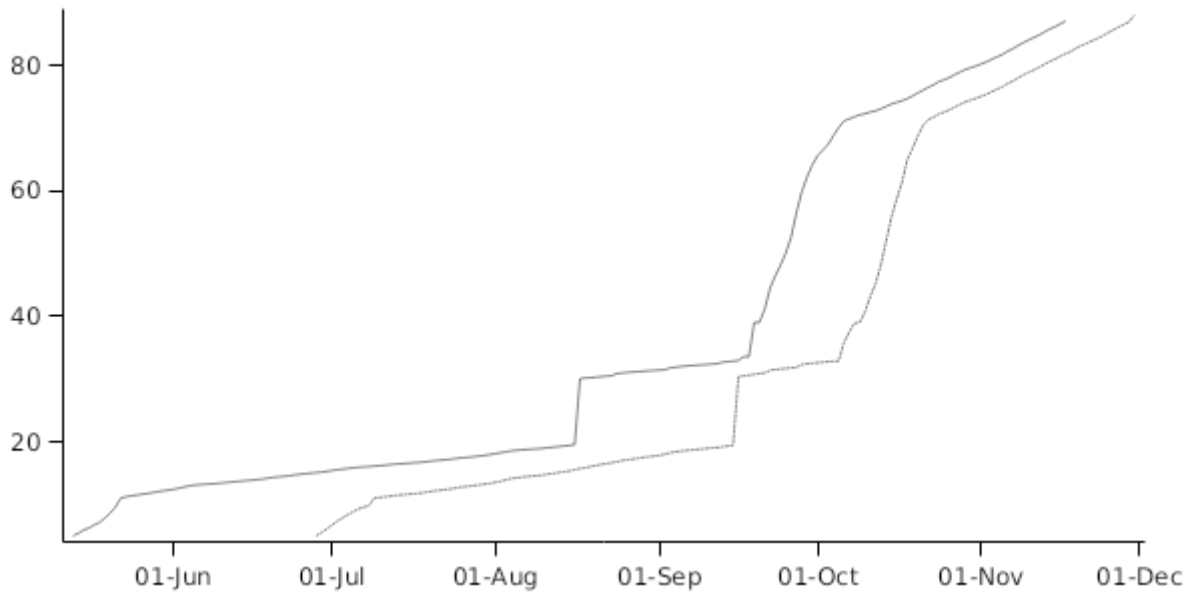
Commander



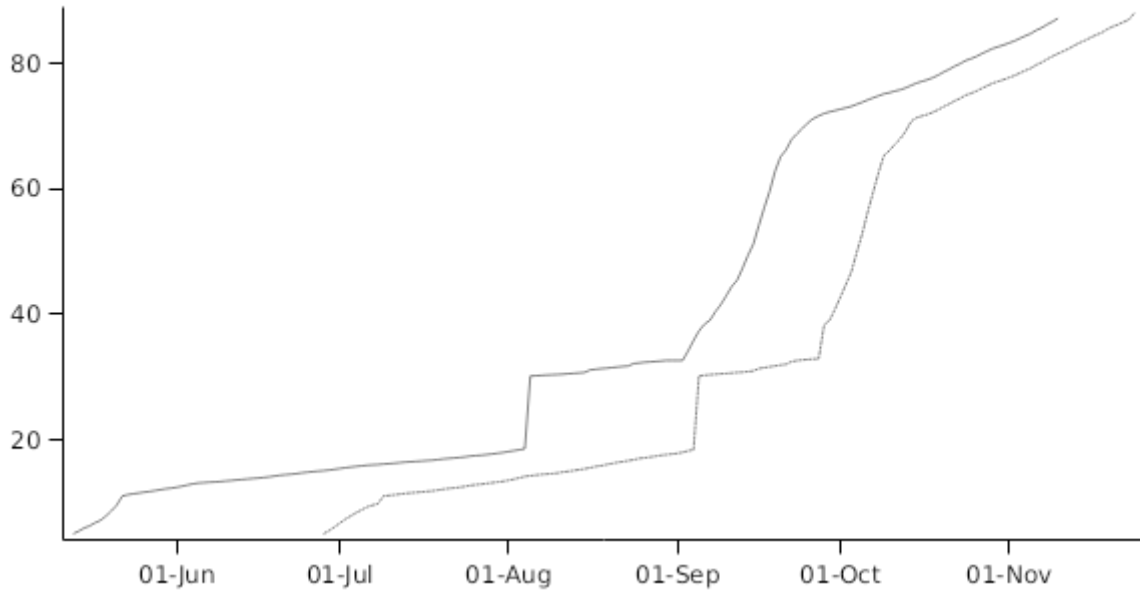
Fleet



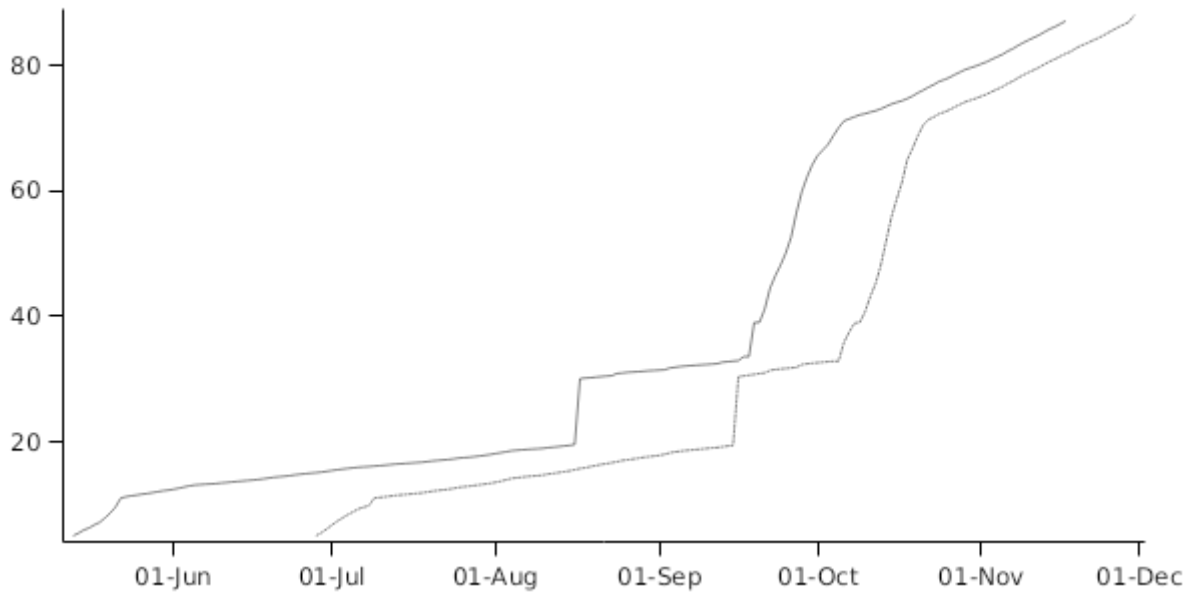
Hindmarsh



Keel

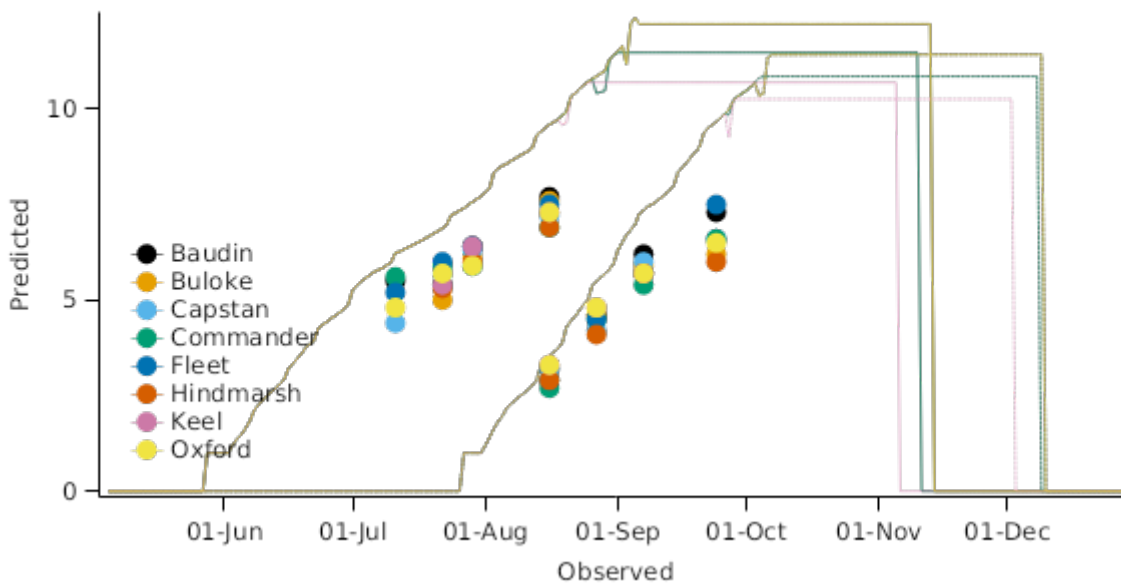


Oxford

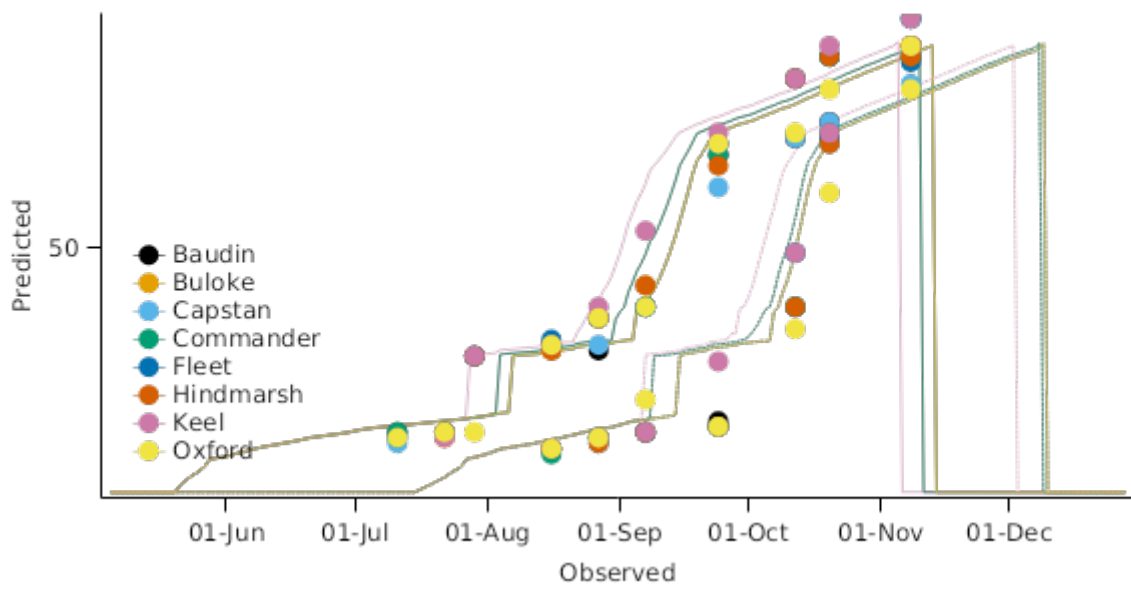


2.3.1.3 Tarlee2011

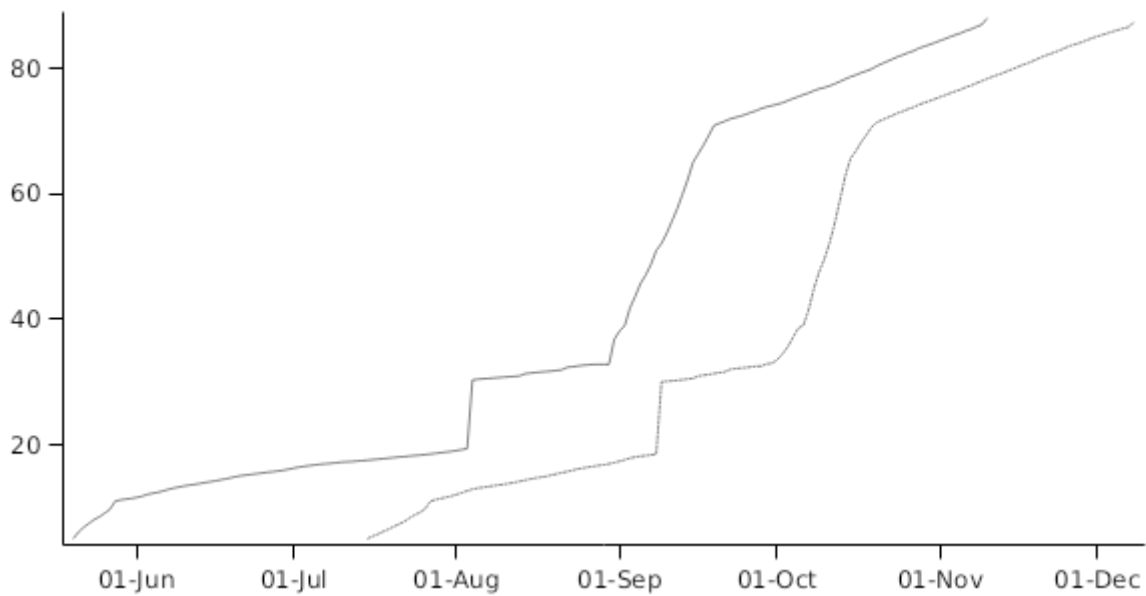
LeafNumberTimeSeries



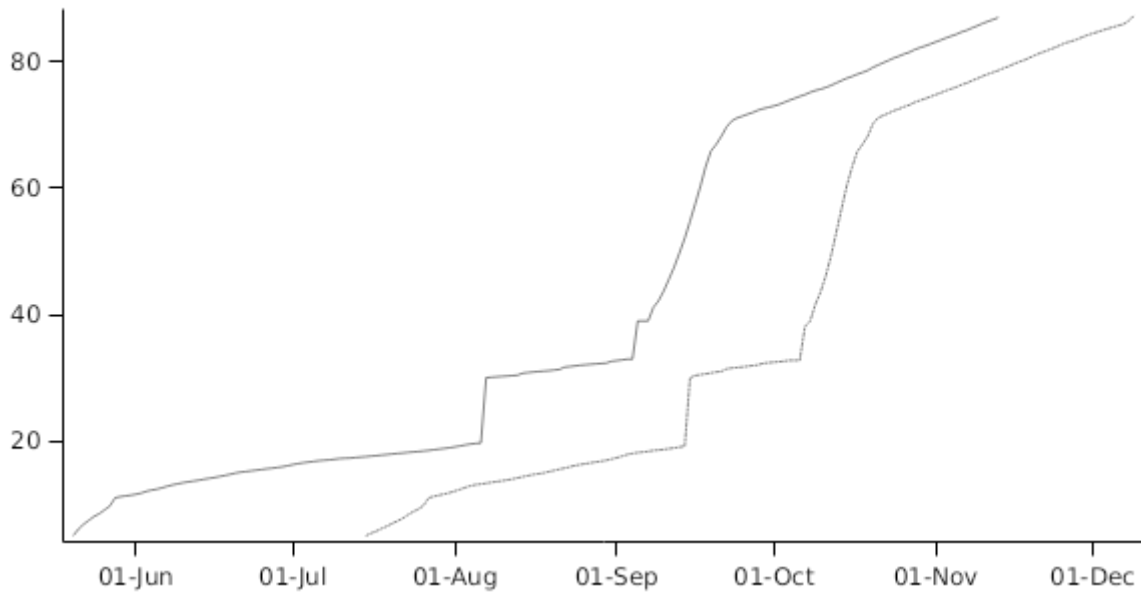
ZadokTimeSeries



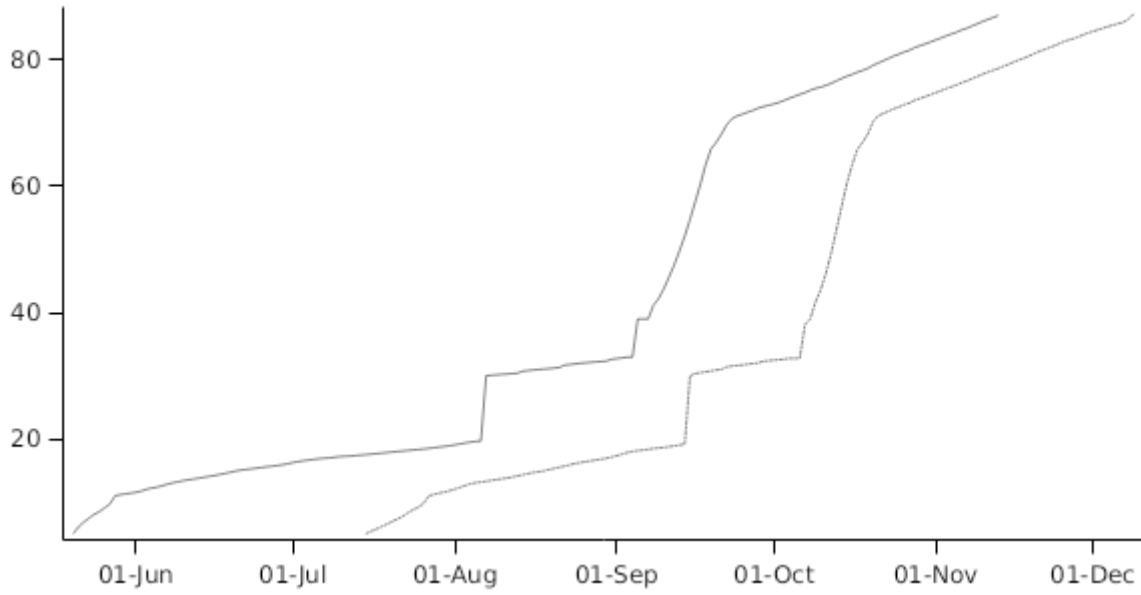
Baudin



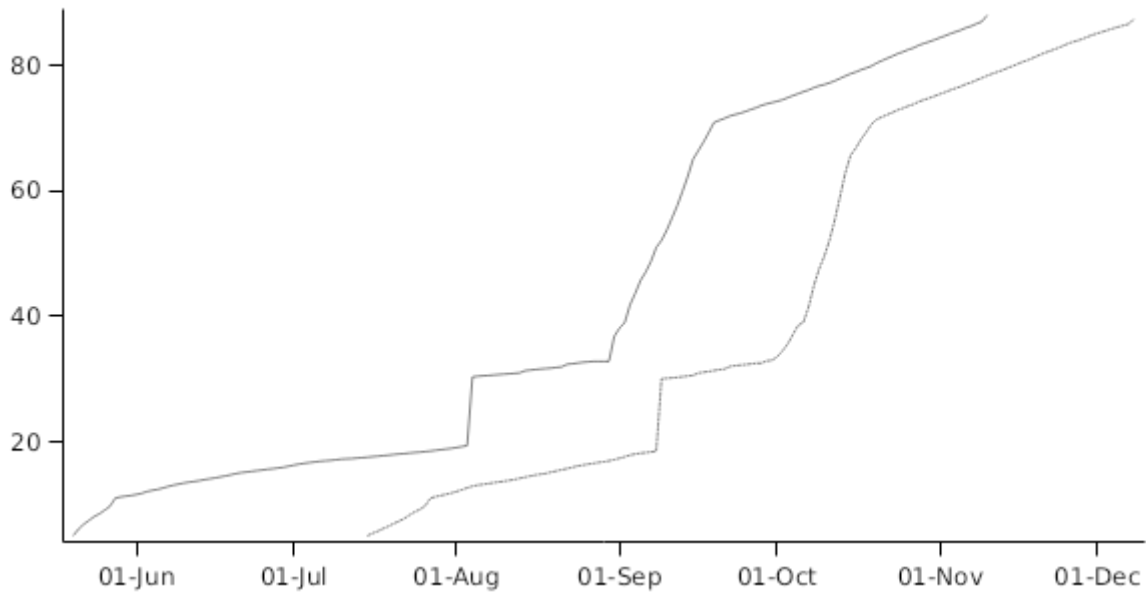
Buloke



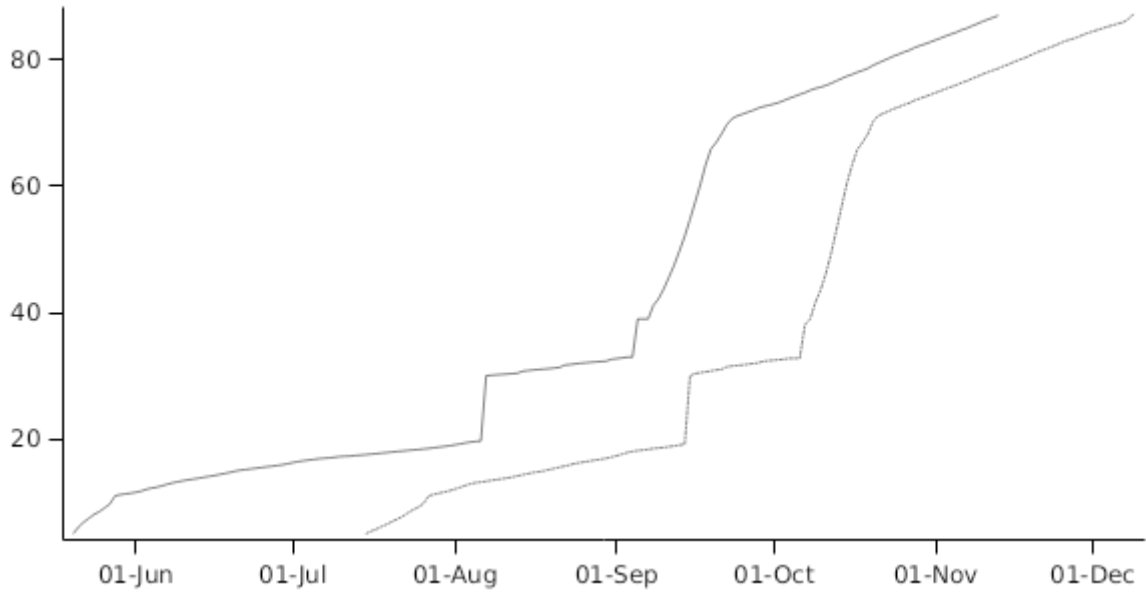
Capstan



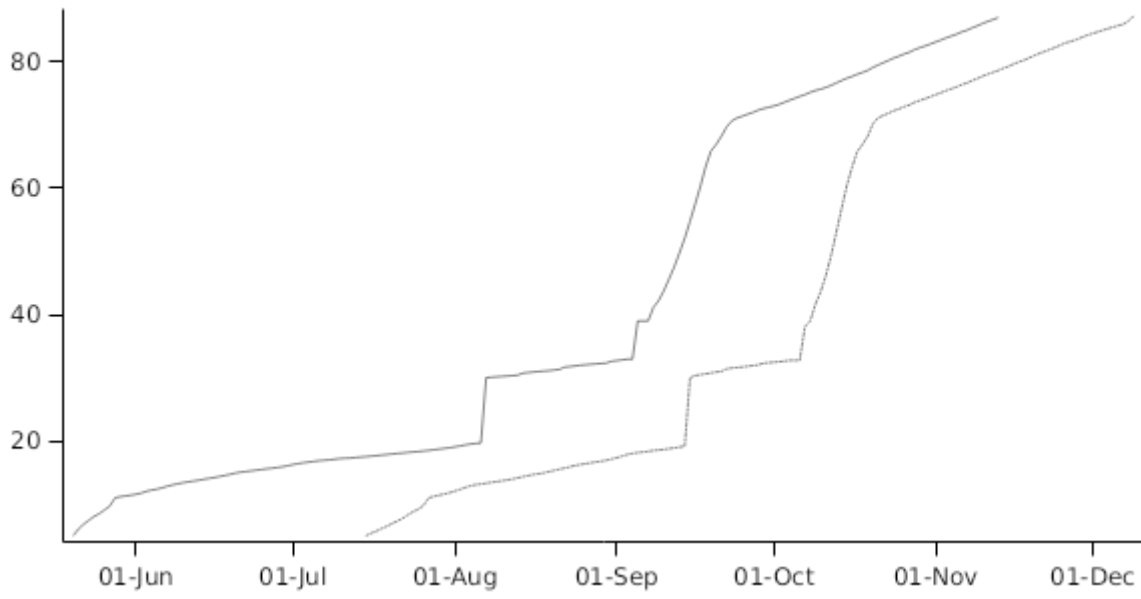
Commander



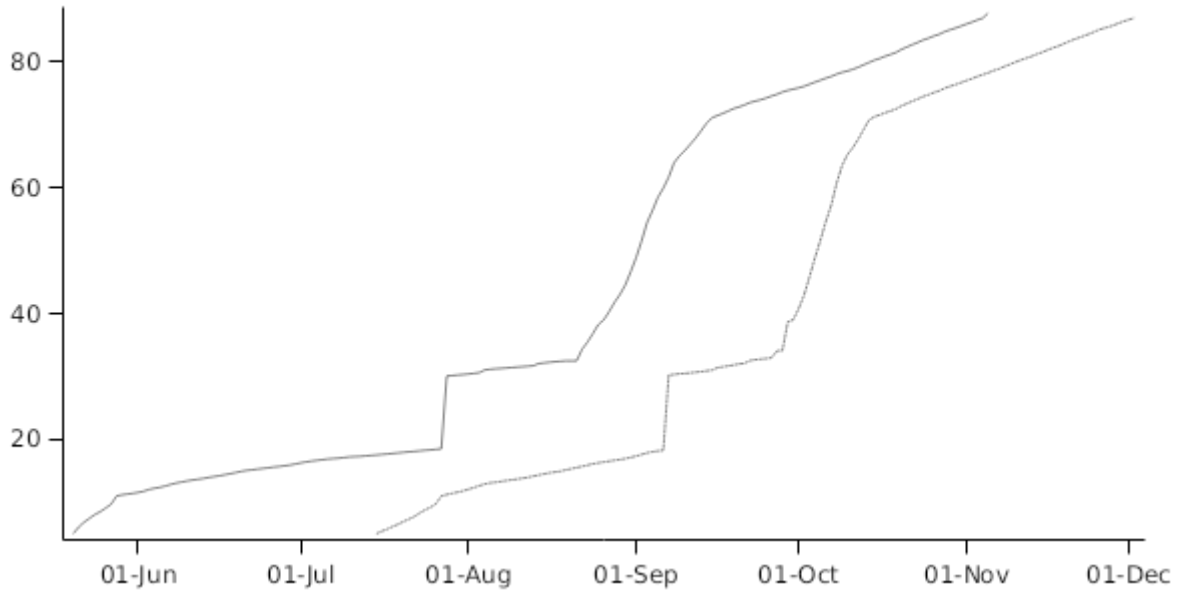
Fleet



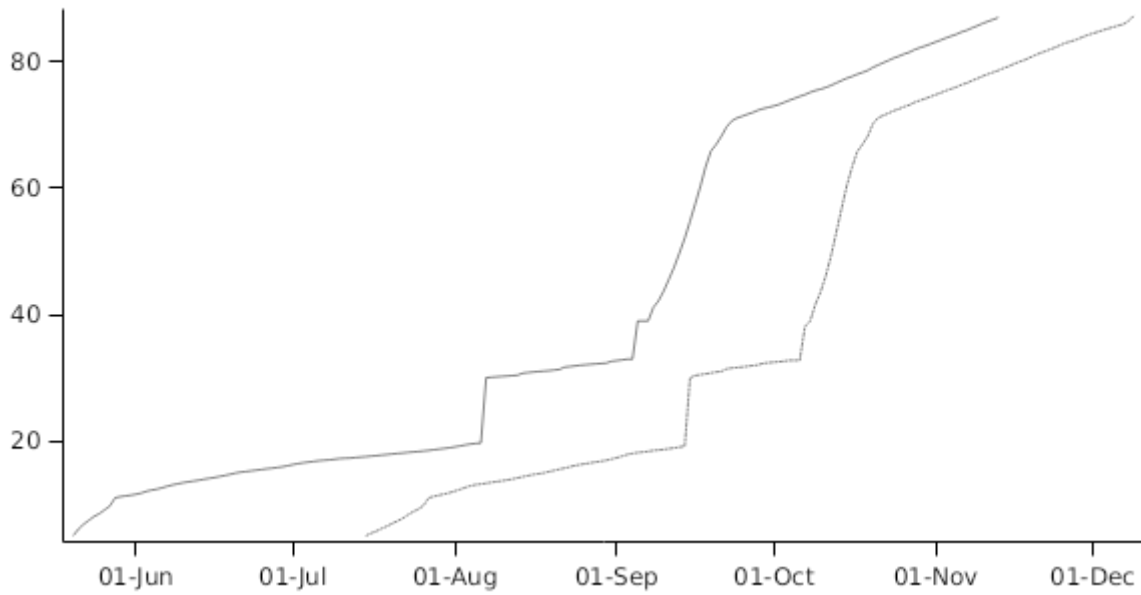
Hindmarsh



Keel



Oxford



2.3.2 HermitageRS

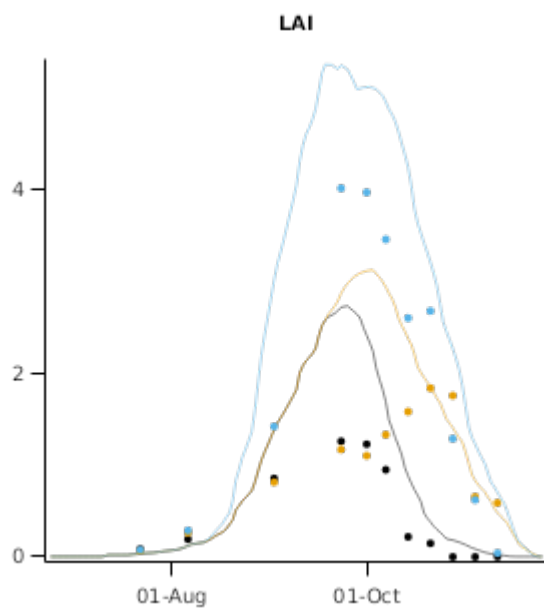
This rain-out shelter experiment was undertaken at the Hermitage Research Station near Warwick, Queensland. Treatments included 3 irrigation experiments to provide combinations of early and later water stress. The experiment was described by [Goyne et al., 1996](#).

List of experiments.

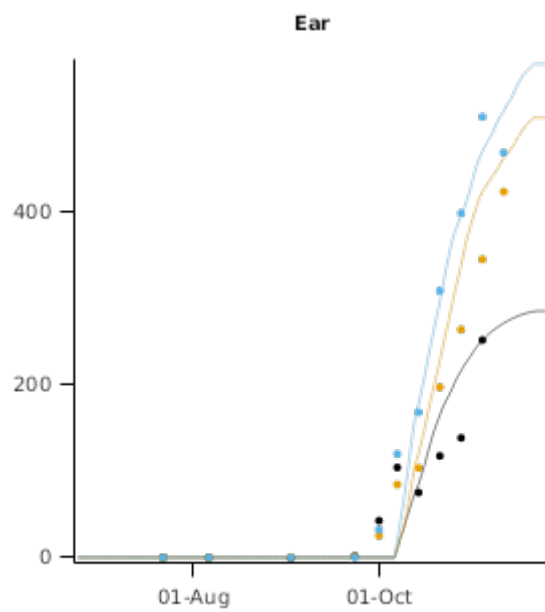
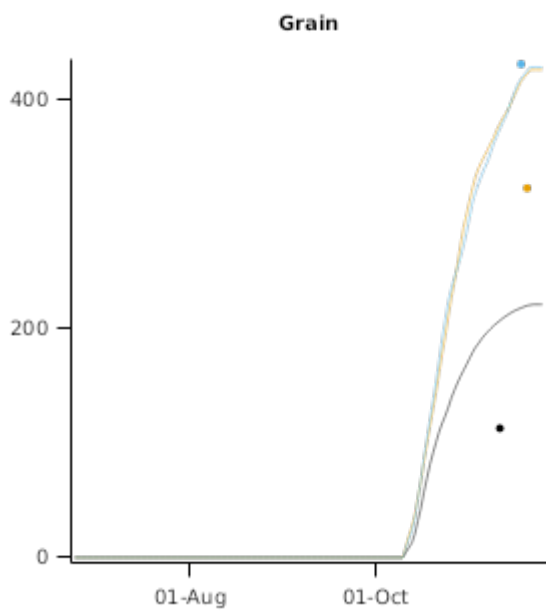
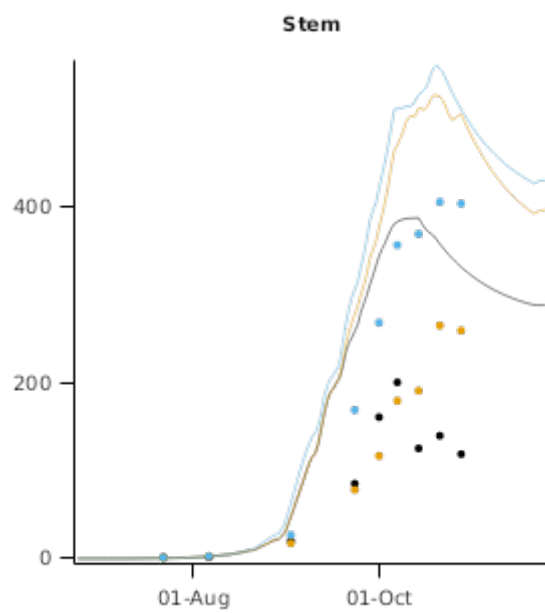
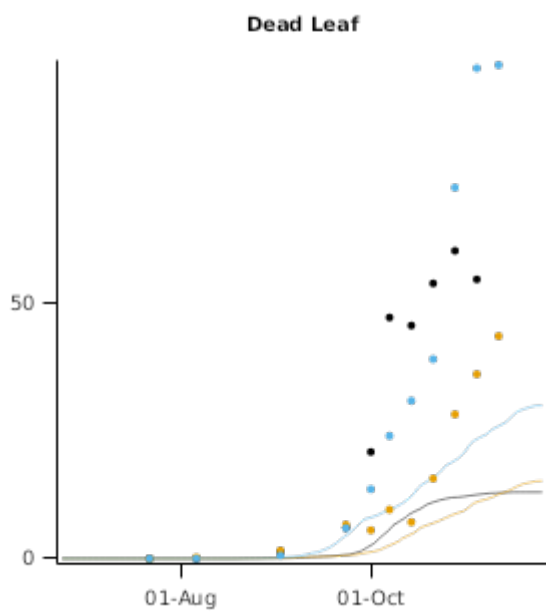
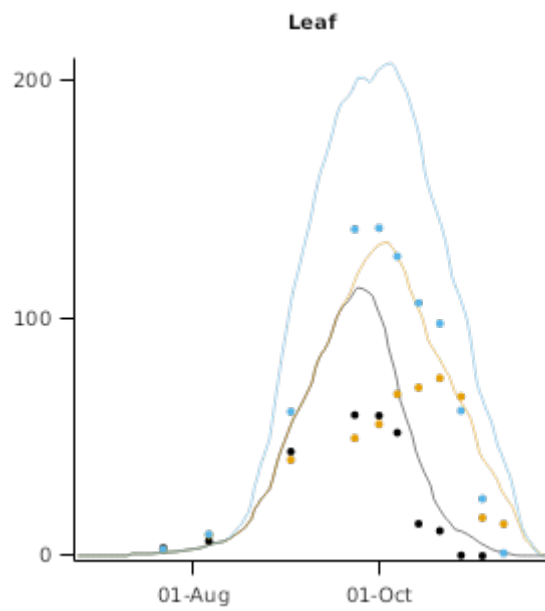
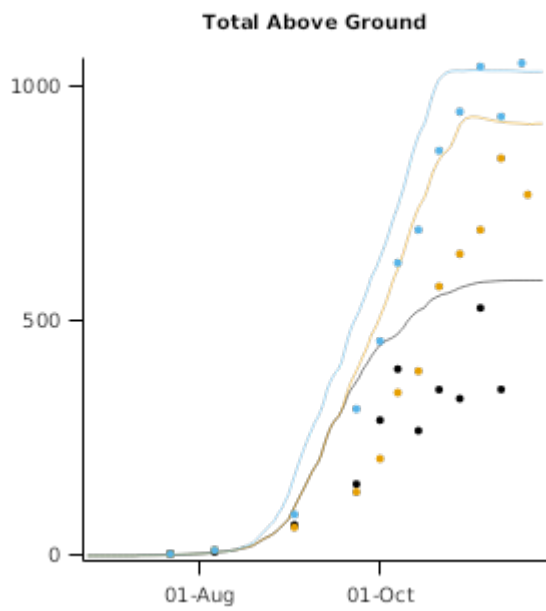
Experiment Name	Design (Number of Treatments)
HermitageRS	Irr (3)

2.3.2.1 HermitageRS

2.3.2.1.1 Canopy

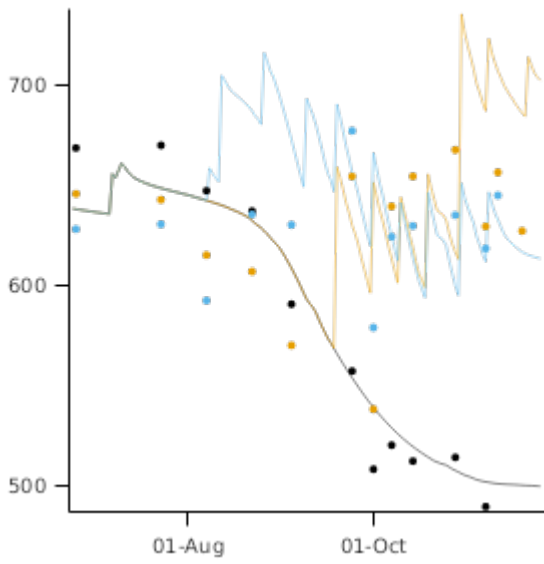


2.3.2.1.2 Biomass

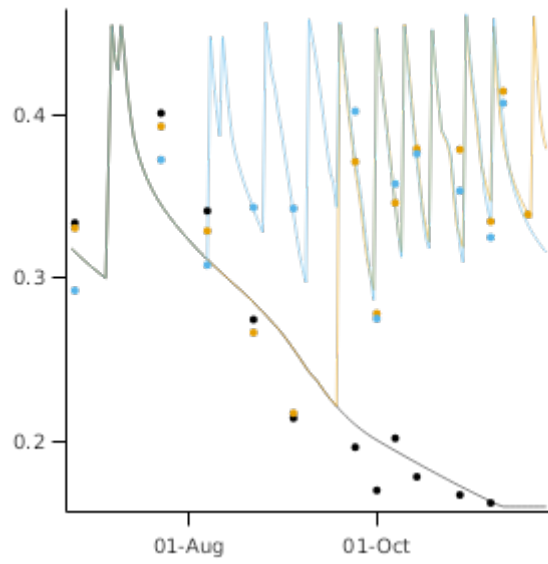


2.3.2.1.3 Soil Water

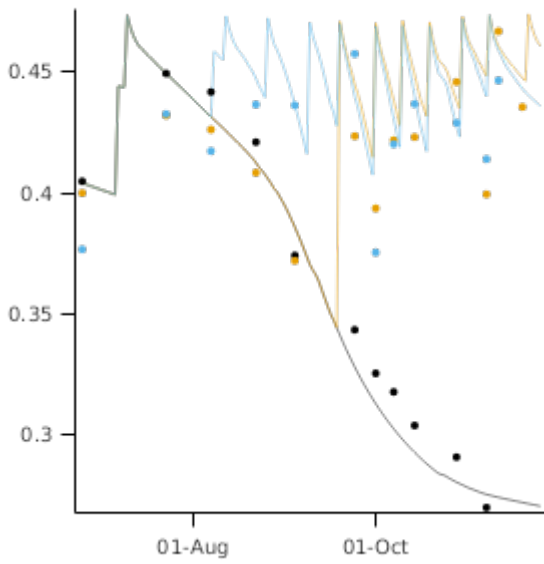
Total Soil Water



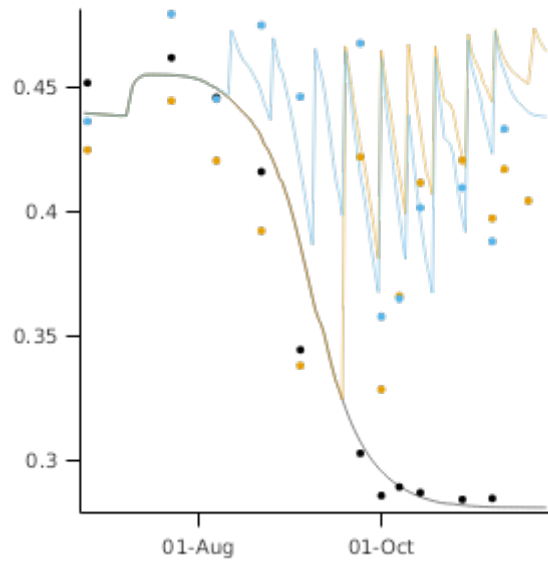
SW 0_10cm



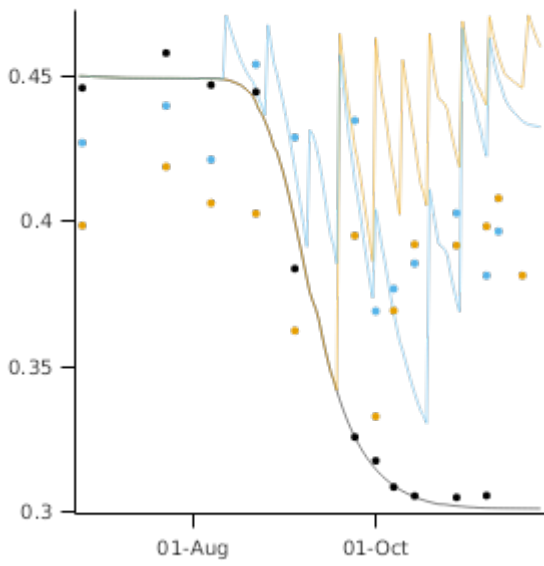
SW 10_20cm



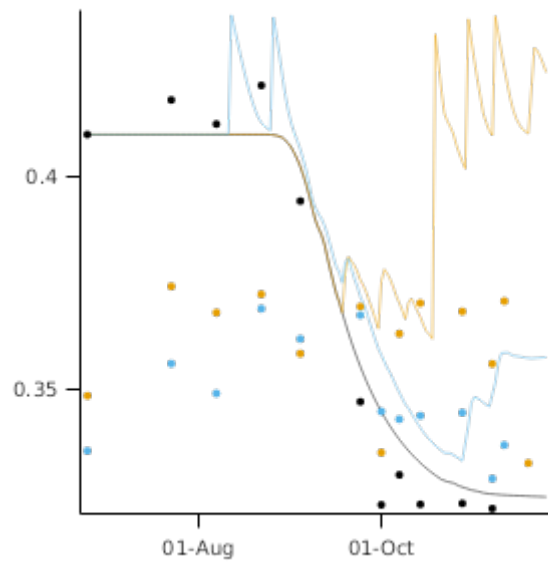
SW 20_40cm

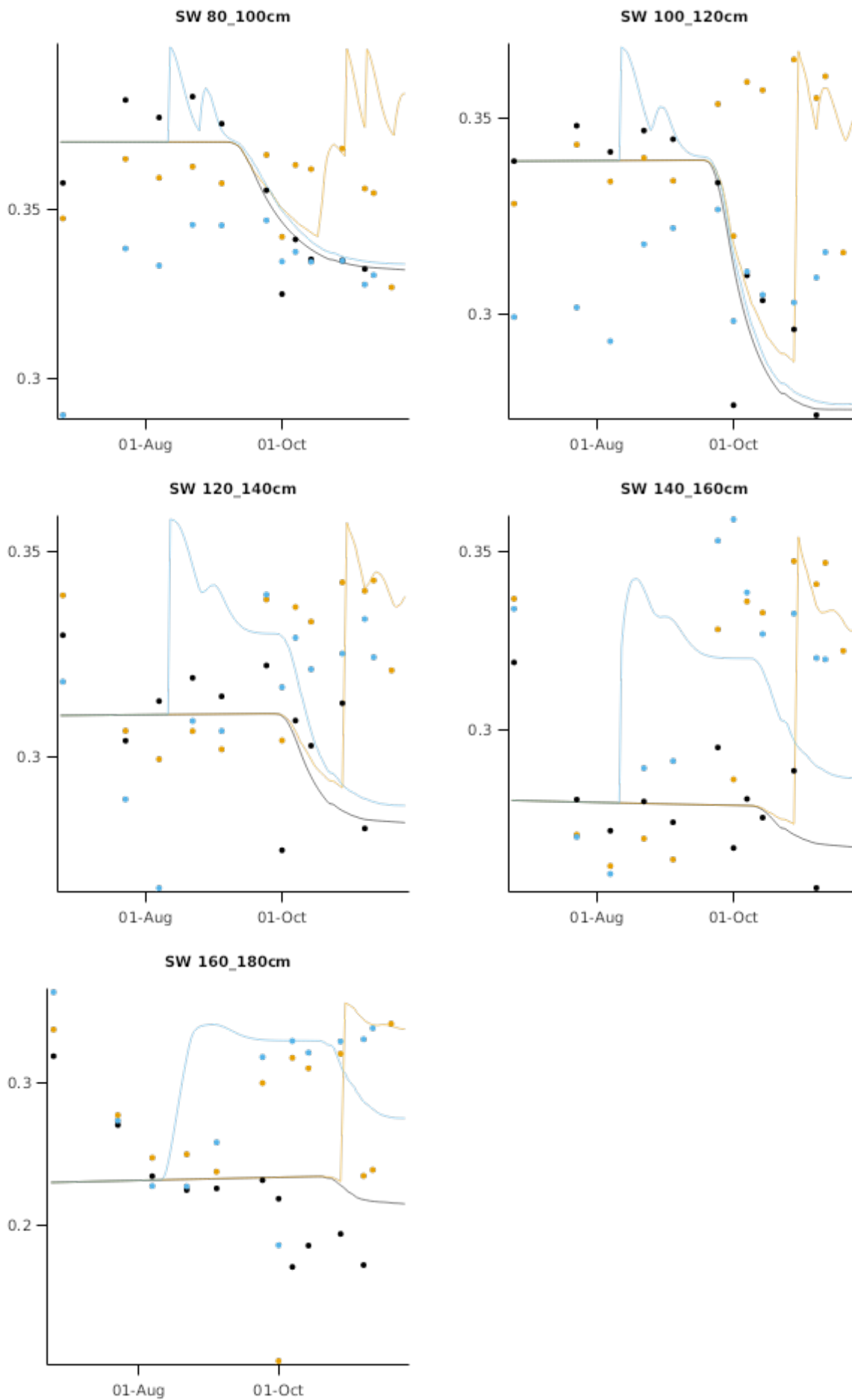


SW 40_60cm



SW 60_80cm





2.3.3 Wellcamp

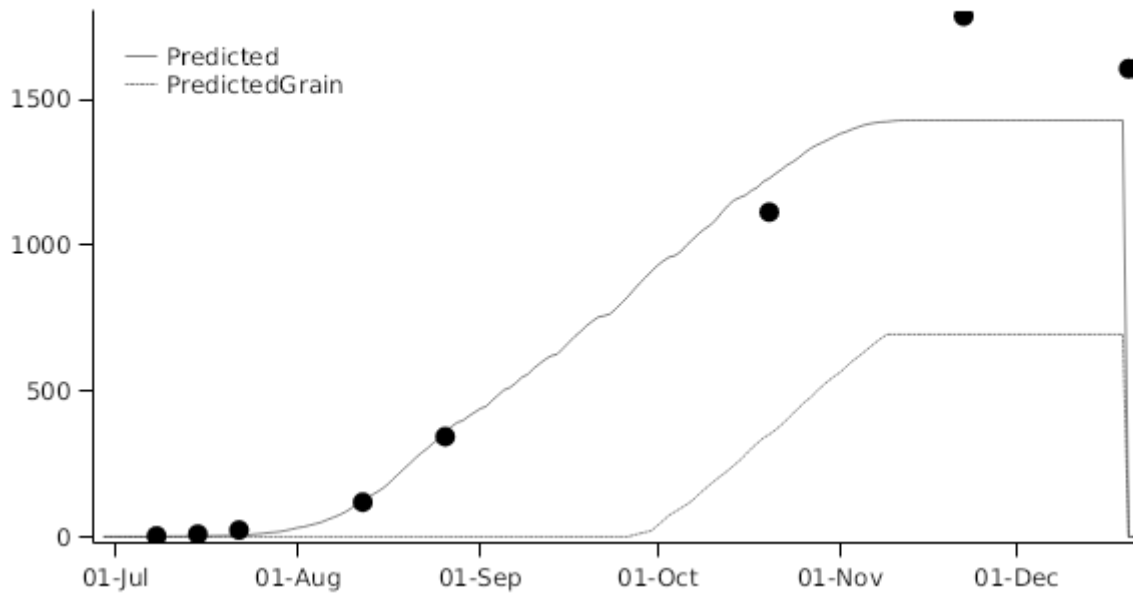
This experiment provides information on biomass accumulation, canopy development and final yield for Barley sown on the eastern Darling Downs. The experiment is explained in [Goyné et al., 1996](#).

List of experiments.

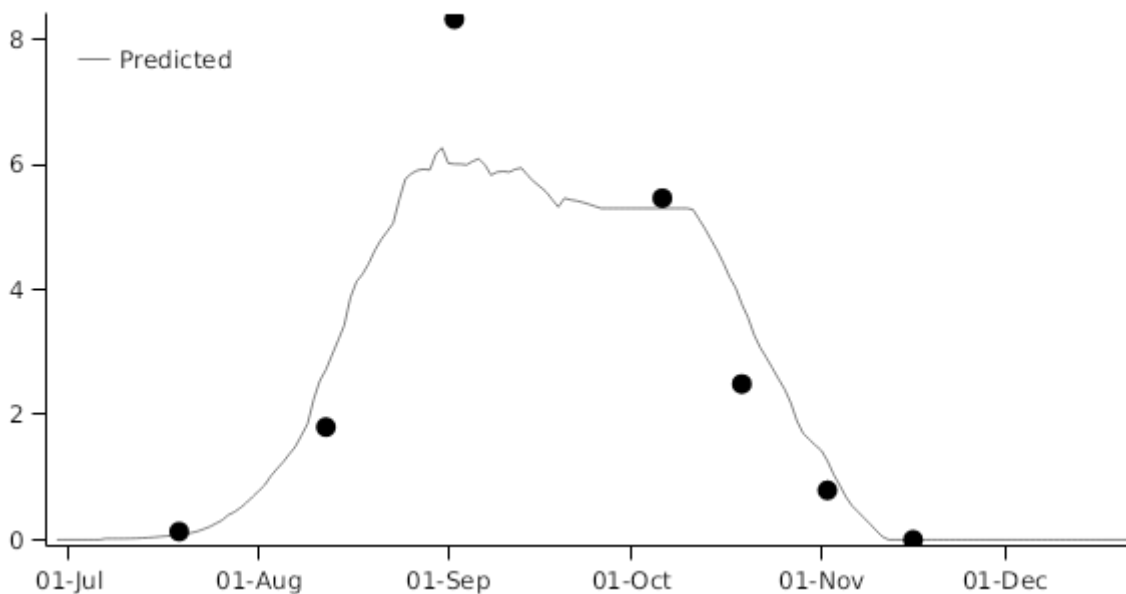
Experiment Name	Design (Number of Treatments)
Wellcamp	1993 (1)

2.3.3.1 Wellcamp

Biomass and Yield



LAI



2.3.4 Hermitage1990

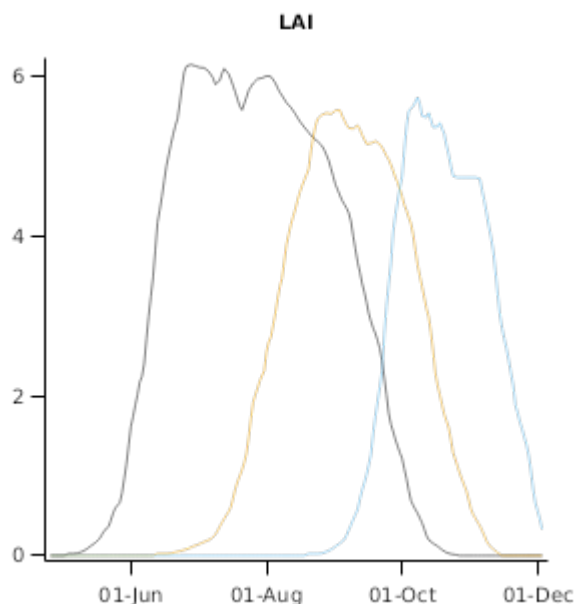
This experiment was conducted at Hermitage Research Station near Warwick, Queensland. Three sowing dates were used to study changes in phenology, biomass accumulation and canopy development. The experiment is explained in [Goyne et al., 1993](#).

List of experiments.

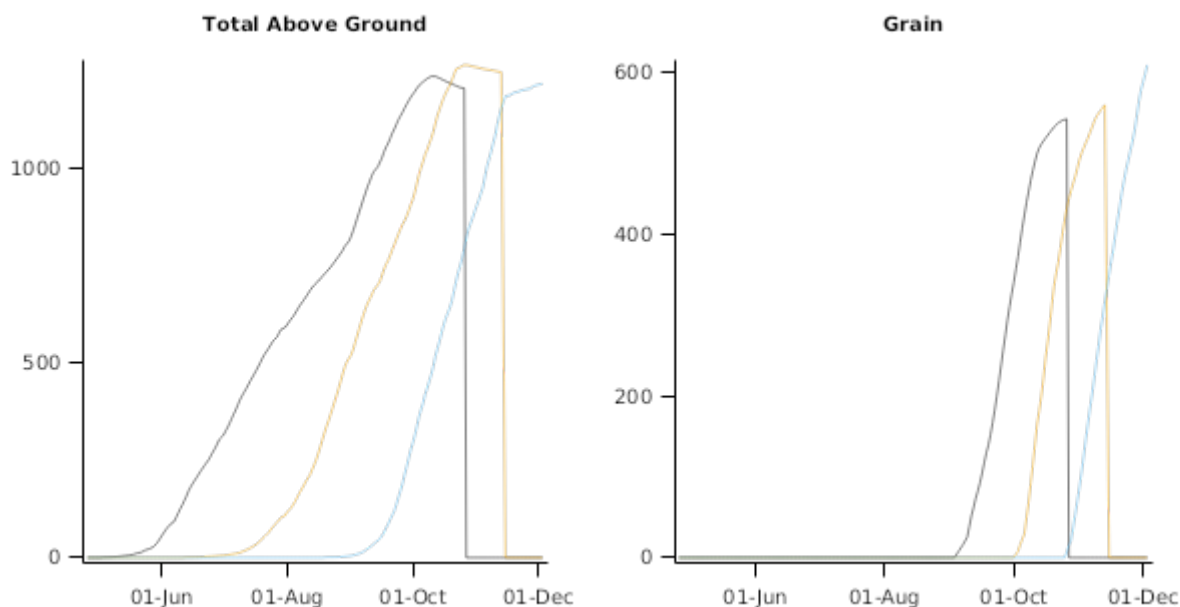
Experiment Name	Design (Number of Treatments)
Hermitage1990	TOS (3)

2.3.4.1 Hermitage1990

2.3.4.1.1 Canopy



2.3.4.1.2 Biomass



2.3.5 Roma1988

This sowing date x plant population experiment was undertaken near Roma, Queensland. Measurements include biomass accumulation, leaf area development and final grain yield. The experiment is explained in [Gojne et al., 1996](#).

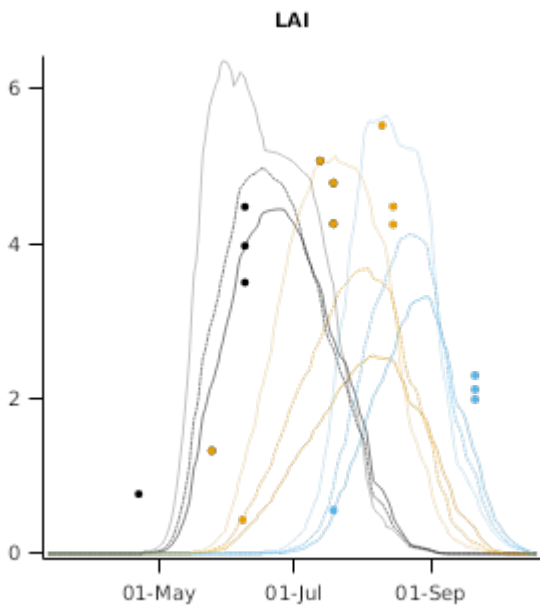
List of experiments.

Experiment Name	Design (Number of Treatments)
Roma1988	Sow x Pop (9)

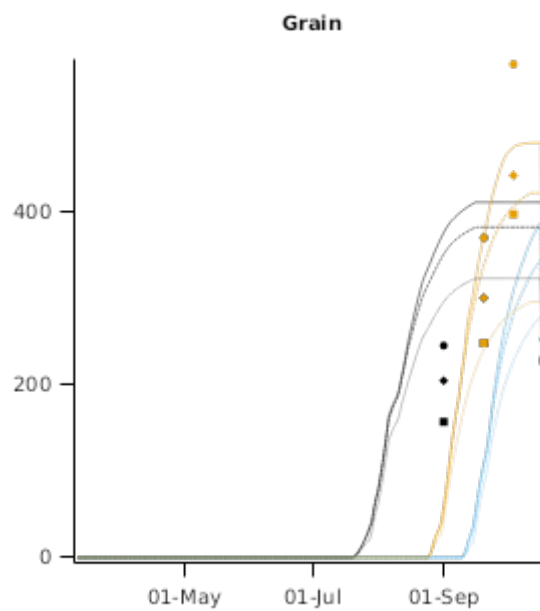
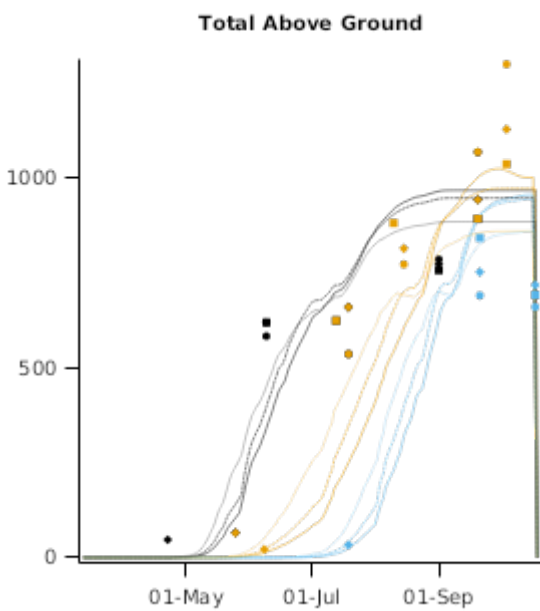
2.3.5.1 Roma1988

NOTE: Sowing was 12-Mar but simulations are sown on 30 March to capture delayed germination until following rainfall event

2.3.5.1.1 Canopy



2.3.5.1.2 Biomass



2.3.6 Gatton1984

This nitrogen rate (0 to 200 kg N/ha) experiment was conducted in 1984 at Gatton, Queensland. The experiment is explained in [Birch et al., 1990](#).

List of experiments.

Experiment Name	Design (Number of Treatments)
Gatton1984	NRate (5)

2.3.6.1 Gatton1984

NOTE: High N treatment lodged. Final grain sizes were less than expected.

2.3.7 NPIField2019

List of experiments.

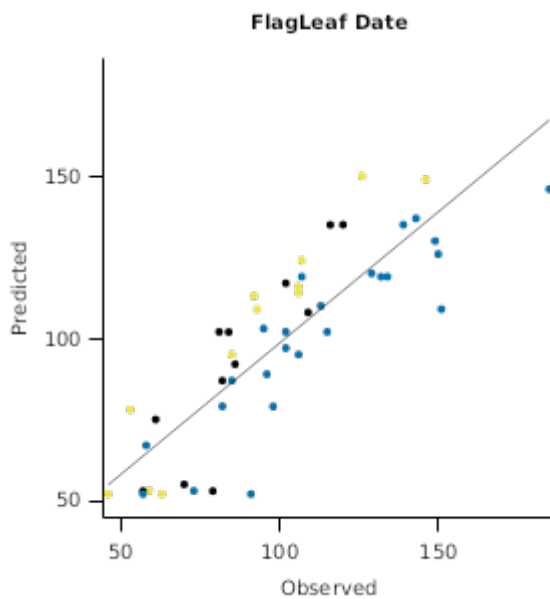
Experiment Name	Design (Number of Treatments)
WaggaWagga2019	TOS x Cv (240)

Experiment Name	Design (Number of Treatments)
Callington2019	TOS x Cv (240)
Dale2019	TOS x Cv (240)
YanYean2019	TOS x Cv (240)

2.3.8 NPIField2020

List of experiments.

Experiment Name	Design (Number of Treatments)
WaggaWagga2020	TOS x Cv (240)
Urrbrae2020	TOS x Cv (240)
Dale2020	TOS x Cv (240)
YanYean2020	TOS x Cv (210)



2.3.9 ControlledEnvironment

List of experiments.

Experiment Name	Design (Number of Treatments)
LaTrobeCE	Treat x Cv x Durat (140)

3 Sensibility tests

List of experiments.

Experiment Name	Design (Number of Treatments)
WaterByNFactorial	Irrigation x Nitrogen (10)

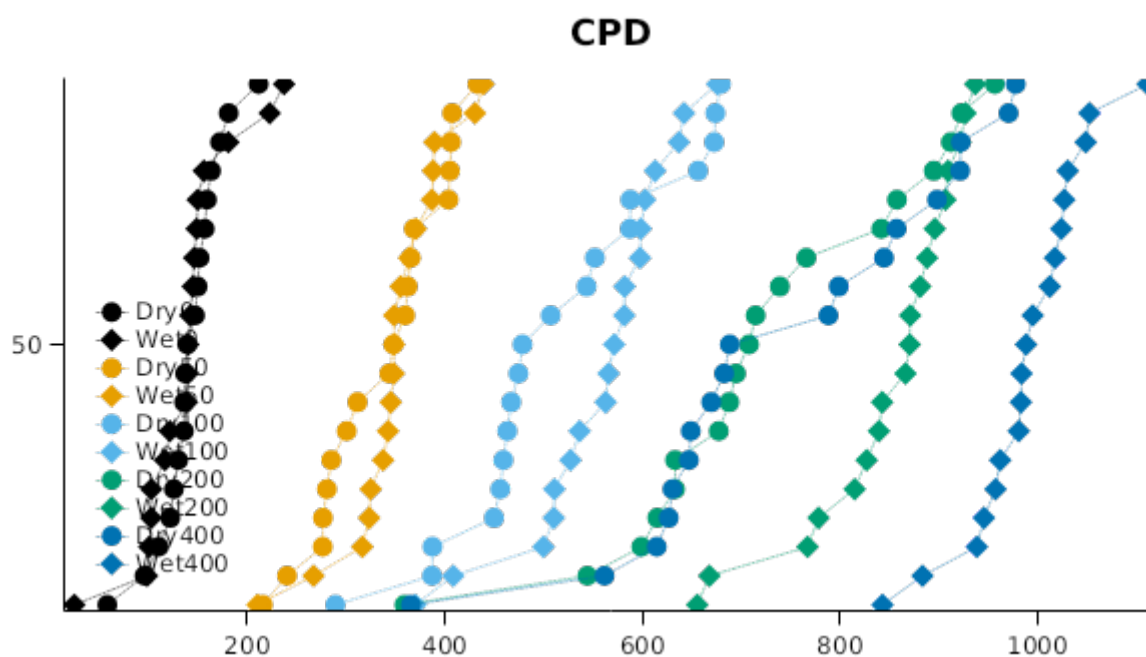
3.1 WaterByNFactorial

This is a hypothetical experiment with Barley sown on the 15th of October every year for 20 years at Lincoln, New Zealand. The treatments applied are as follows:

- Two water treatments; Dry (nil irrigation) and Wet, with irrigation applied when soil water deficit reaches 60% to return water content to 100% of capacity.

- five fertiliser N treatments; 0, 50, 100, 200 and 400 kg N/ha with half of the N applied at sowing and the other half applied at growth stage 32.

The results for irrigated, High N treatments the range of yields are inline with expectations for the location of the simulations. There is no sensitivity to irrigation with zero nitrogen as N supply is the factor limiting production. As N inputs increase the crop becomes increasingly sensitive to water application and the crop is more responsive to nitrogen with irrigation. These results show the model is giving sensible predictions



4 References

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