



1 The APSIM Chickpea Model

The APSIM Chickpea model has been developed from the original APSIM Chickpea model described by [Robertson et al., 2002](#) using the Plant Modelling Framework of [Brown et al., 2014](#).

Note to users: Desi and Kabuli chickpea are two subspecies of chickpea. The variety set includes both types. As indicated by [Peake et al., 2021 \(GRDC Updates\)](#), there was less confidence in predicting

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
Shell	Models.PMF.Organs.GenericOrgan
Leaf	Models.PMF.Organs.Leaf
Stem	Models.PMF.Organs.GenericOrgan
Nodule	Models.PMF.Organs.Nodule
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.

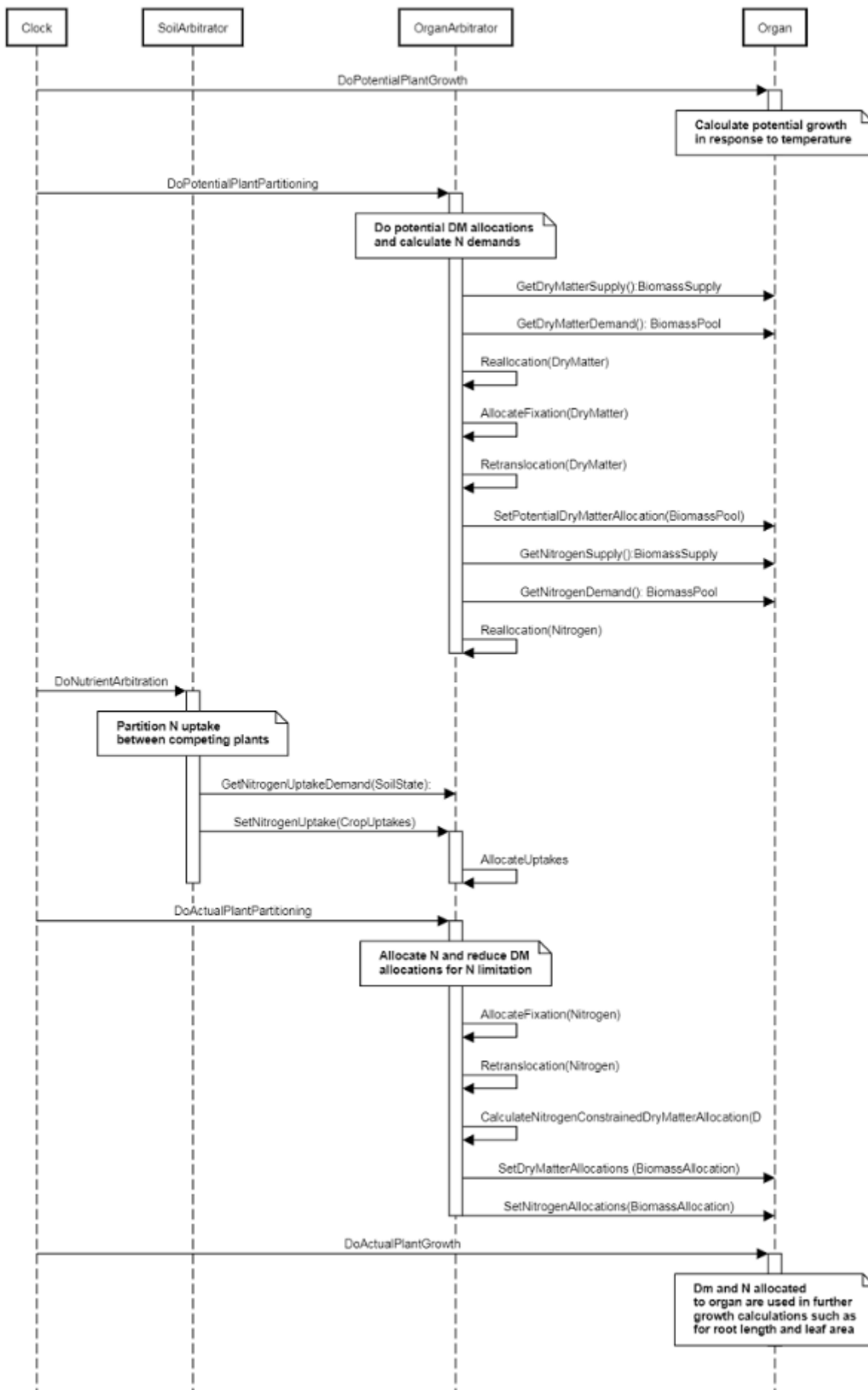


Figure 1: Schematic showing the procedure for arbitration of biomass partitioning. Pink boxes represent events that occur every day and their numbering shows the order of calculations. Blue boxes represent the methods that are called when these events occur. Orange boxes contain properties that make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

1.2.1 ThermalTime

ThermalTime 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:

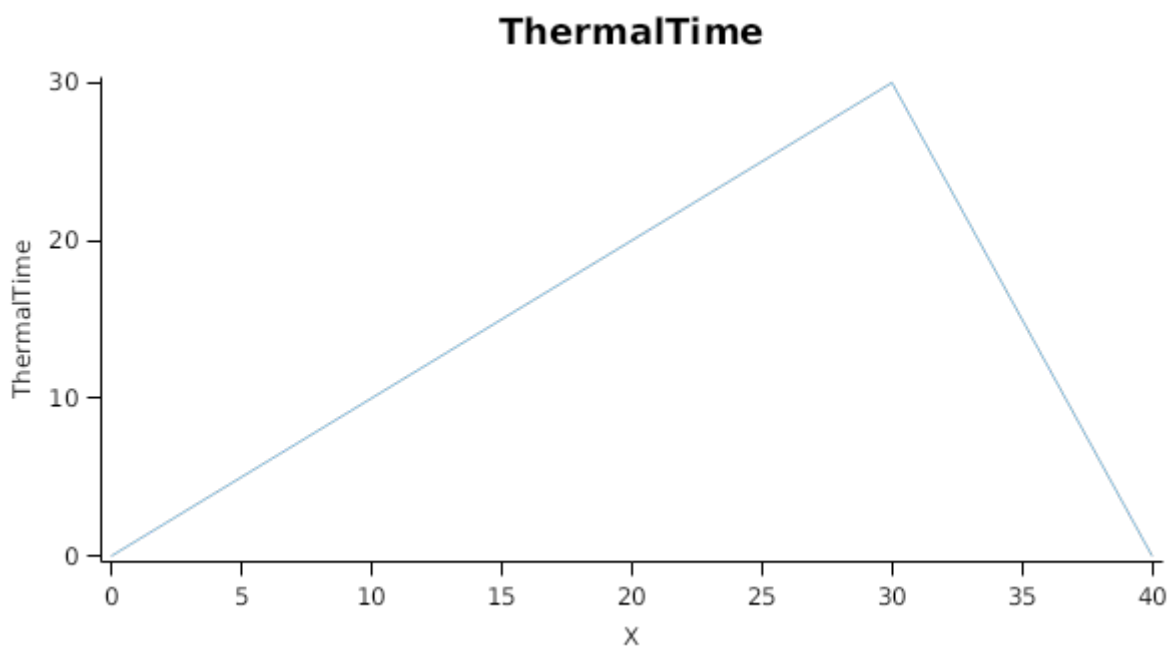
ThermalTime is the average of sub-daily values from a XYPairs.

The cardinal temperatures for calculating thermal time have been taken from [Piara Singh et al., 1996](#) as used by [Robertson et al., 2002](#).

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

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

X	ThermalTime
0.0	0.0
30.0	30.0
40.0	0.0



Emerge_to_EndFlower has a value between Emergence and HarvestRipe calculated as:

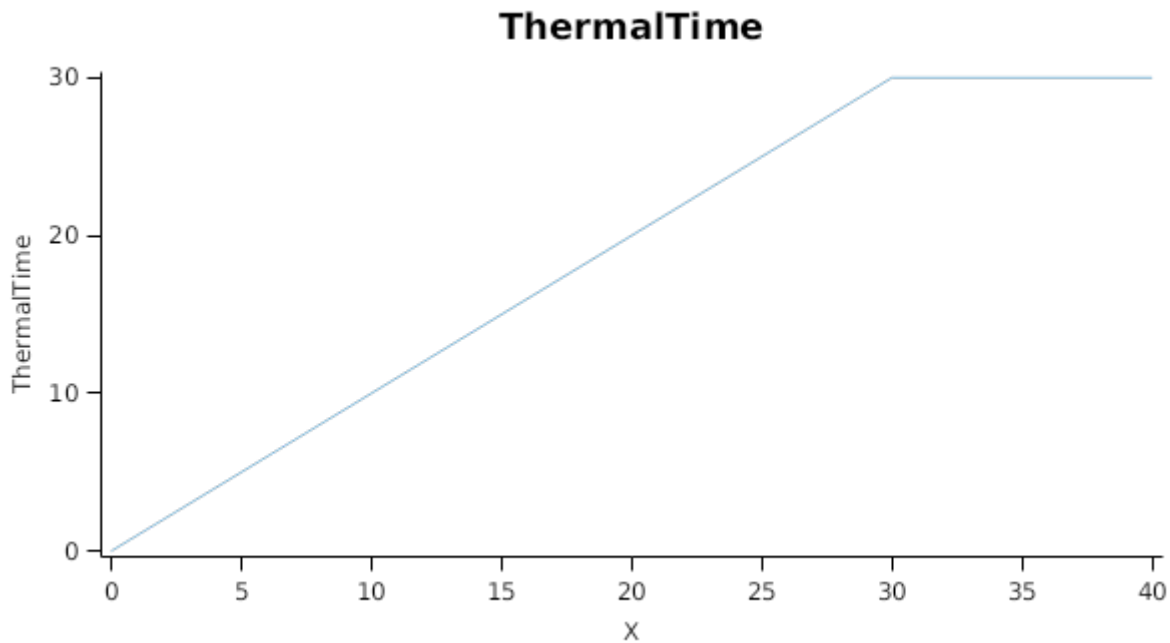
ThermalTime is the average of sub-daily values from a XYPairs.

The cardinal temperatures for calculating thermal time have been taken from [Piara Singh et al., 1996](#) as used by [Robertson et al., 2002](#).

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

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

X	ThermalTime
0.0	0.0
30.0	30.0
40.0	30.0



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	EndJuvenile
4	FloralInitiation	EndJuvenile	StartBudding
5	Budding	StartBudding	StartFlowering
6	Flowering	StartFlowering	EndFlowering
7	PodInitiation	EndFlowering	EndPodInitiation
8	EarlyGrainFilling	EndPodInitiation	MidGrainFilling
9	MidGrainFilling	MidGrainFilling	LateGrainFilling
10	LateGrainFilling	LateGrainFilling	EndGrainFill
11	Maturing	EndGrainFill	Maturity
12	Ripening	Maturity	HarvestRipe
13	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:

$$\text{ShootRate} = 0.7 \text{ (deg day/mm),}$$

$$\text{ShootLag} = 120 \text{ (deg day),}$$

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

Shoot lag = constant

Shoot rate = multiplier on sowing depth (mm)

Note could be beneficial to set differently for large-seeded kabuli cultivars, which anecdotally seem to be slower emerging.

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 endjuvenile.

The *Target* for completion is calculated as:

$$\text{Target} = 400 \text{ (Degree Days)}$$

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

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

1.2.5 FlorallInitiation

This phase goes from endjuvenile to startbudding.

This phase simulates the time between end of the Non-inductive phase of [Robertson et al., 2002](#) (515 TT) and the appearance of visible buds on petioles

The *Target* for completion is calculated as:

$$\text{Target} = 250 \text{ (thermal time)}$$

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

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

1.2.6 Budding

This phase goes from startbudding to startflowering.

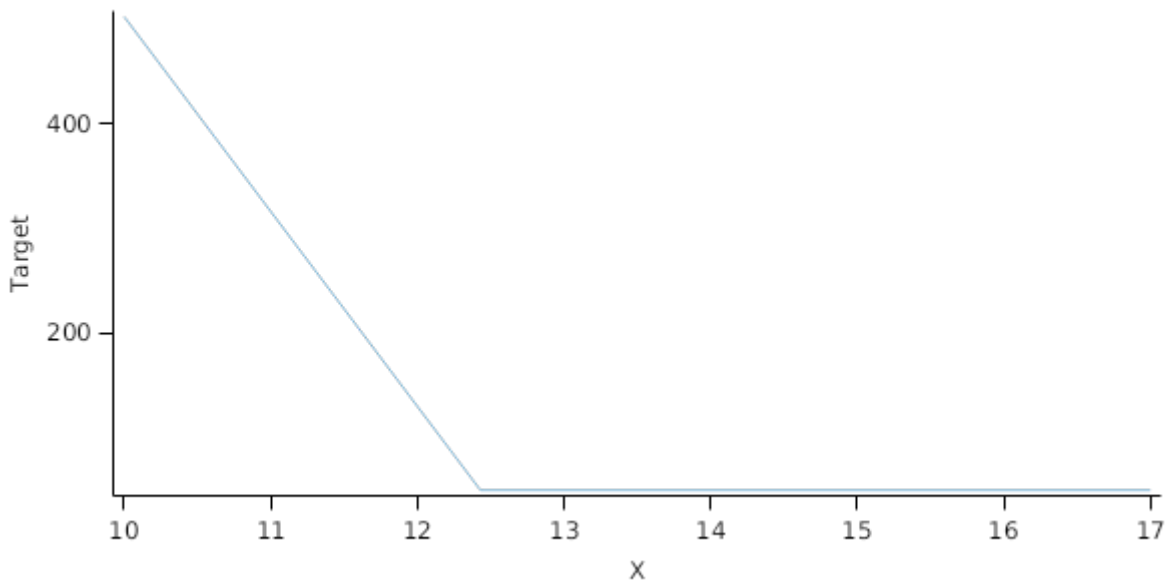
This phase encompasses the budding phase. All photoperiod response is currently contained here although in reality probably carries across LateVeg as well as this one

The *Target* for completion is calculated as:

Target is calculated using linear interpolation

X	Target
10.0	501.6
12.4	50.0
17.0	50.0

Target



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

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

1.2.7 Flowering

This phase goes from startflowering to endflowering.

Minimum thermal time target for duration of flowers prior to pod initiation.

The *Target* for completion is calculated as:

$$\text{Target} = 100 \text{ (oD)}$$

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

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

1.2.8 PodInitiation

This phase goes from endflowering to endpodinitiation.

Requires 5 days of temp above 16 degrees (or ten days at 15 degrees) before 1cm pods are visible, due to sensitivity of pod initiation to mean daily temperature (see Srinivasan et al. 1998; Clarke and Siddique, 2004). These days may accumulate anytime after flowering begins (i.e. during previous growth stage as well as during the current one). so the 'EndFloweringPodStartTT' is subtracted from the 5 days target

The *Target* for completion is calculated as:

$$\text{Target} = \text{Total} - [\text{Phenology}].\text{EndFloweringPodStartTT}$$

$$\text{Total} = 5$$

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

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

1.2.9 EarlyGrainFilling

This phase goes from endpodinitiation to midgrainfilling.

Function shortens the available TT for grainfilling when there is a big gap between beginning of flowering and beginning of pod initiation

Can't be less than zero for obvious reasons

The *Target* for completion is calculated as:

$Target = \text{Max}(\text{Reducer}, \text{constant_zero})$

Where:

$Reducer = \text{Max} - Adjust$

Max = 300

$Adjust = [\text{Phenology}].\text{TotalPodInitTT} / \text{Total}$

Total = 2

constant_zero = 0

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

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

1.2.10 MidGrainFilling

This phase goes from midgrainfilling to lategrainfilling.

The *Target* for completion is calculated as:

Target = 250 (oD)

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

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

1.2.11 LateGrainFilling

This phase goes from lategrainfilling to endgrainfill.

The *Target* for completion is calculated as:

Target = 250 (oD)

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

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

1.2.12 Maturing

This phase goes from endgrainfill to maturity.

The duration of the Maturing phase has been taken from the model of [Robertson et al., 2002](#).

The *Target* for completion is calculated as:

Target = 60 (oD)

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

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

1.2.13 Ripening

This phase goes from maturity to harvestripe.

The *Target* for completion is calculated as:

Target = 60 (oD)

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

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

1.2.14 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

1.2.15 Photoperiod

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

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

Twilight = -6 (degrees)

1.2.16 BuddingDAS

Before StartBudding

PreEventValue = 0

On StartBudding the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.17 FloweringDAS

Before StartFlowering

PreEventValue = 0

On StartFlowering the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.18 MaturityDAS

Before Maturity

PreEventValue = 0

On Maturity the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.19 EmergenceDAS

Before Emergence

PreEventValue = 0

On Emergence the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.20 EndBuddingMSLeafNo

Before EndBudding

PreEventValue = 0

On EndBudding the value is set to:

PostEventValue = [Structure].LeafTipsAppeared

1.2.21 EndFloweringMSLeafNo

Before EndFlowering

PreEventValue = 0

On EndFlowering the value is set to:

PostEventValue = [Structure].LeafTipsAppeared

1.2.22 MeanTemp

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

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

1.2.23 RadDegDays

RadDegDays = Accumulated *RDD* between emergence and endgrainfill

$$\text{RDD} = [\text{Weather}].\text{Radn} / [\text{Phenology}].\text{ThermalTime}$$

1.2.24 StartBudSoiIT

Before StartBudding

$$\text{PreEventValue} = 0$$

On StartBudding the value is set to:

$$\text{PostEventValue} = [\text{Soil}].\text{Temperature.Value}[1]$$

1.2.25 StartBudding_PhotoPeriod

Before StartBudding

$$\text{PreEventValue} = 15$$

On StartBudding the value is set to:

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

1.2.26 PoddingDAS

Before EndPodInitiation

$$\text{PreEventValue} = 0$$

On EndPodInitiation the value is set to:

$$\text{PostEventValue} = [\text{Plant}].\text{DaysAfterSowing}$$

1.2.27 EndJuv_PhotoPeriod

Before EndJuvenile

$$\text{PreEventValue} = 12$$

On EndJuvenile the value is set to:

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

1.2.28 PodStartTT

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

PreFlower has a value between Germination and StartFlowering calculated as:

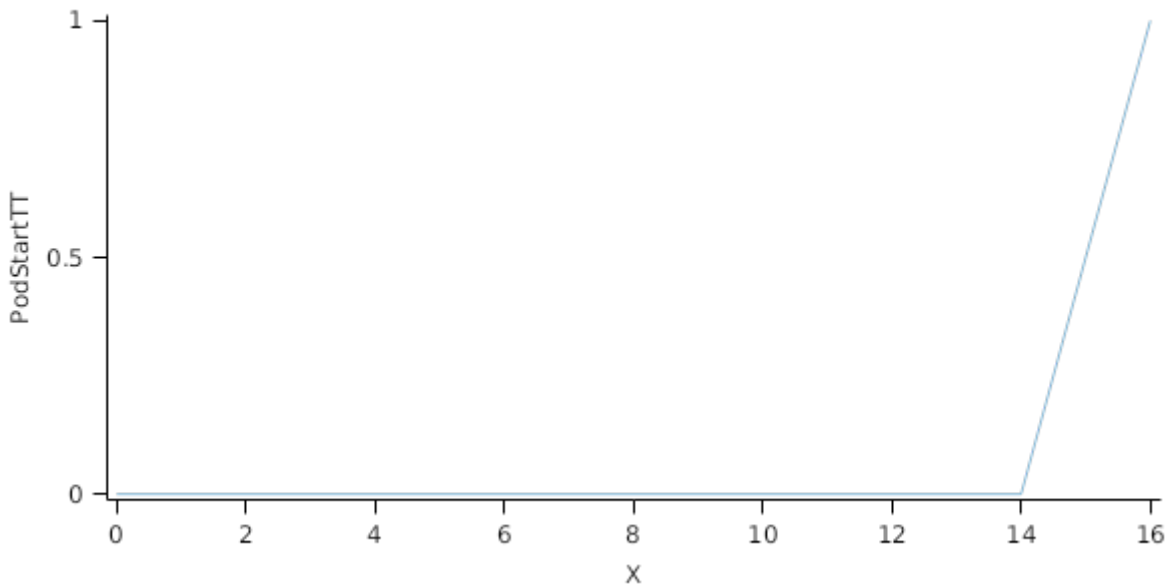
$$\text{PodStartTT} = 0$$

PostFlower has a value between StartFlowering and HarvestRipe calculated as:

PodStartTT is calculated using linear interpolation

X	PodStartTT
0.0	0.0
14.0	0.0
16.0	1.0

PodStartTT



1.2.29 AccumPodStartTT

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

PreFlowering has a value between Germination and StartFlowering calculated as:

PodStartTT = 0

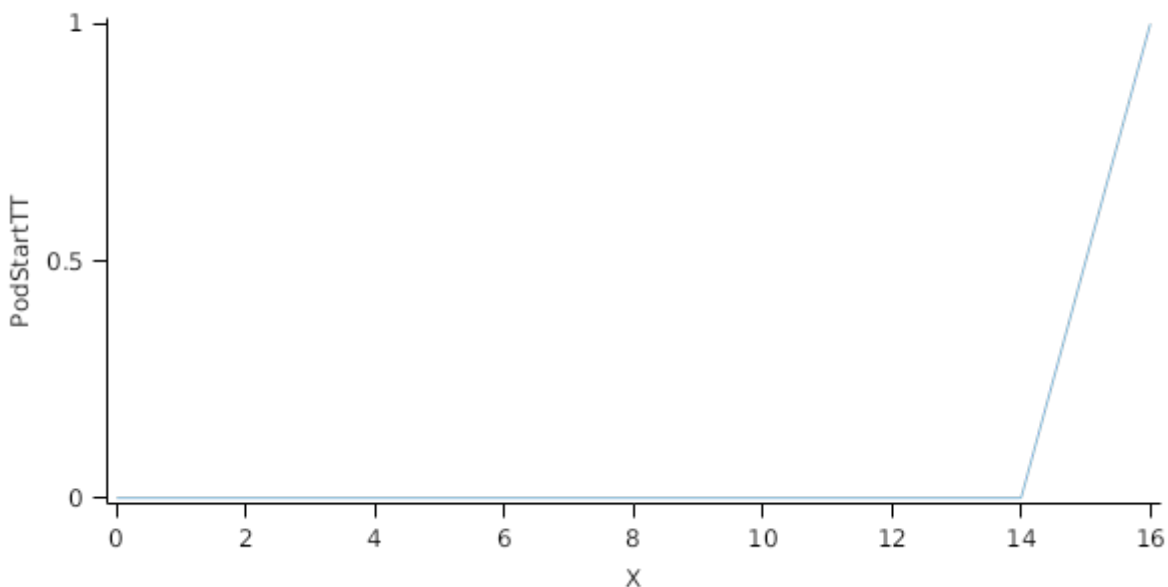
FloweringtoMaturity has a value between StartFlowering and HarvestRipe calculated as:

PodStartTTsum = Accumulated *PodStartTT* between startflowering and maturity

PodStartTT is calculated using linear interpolation

X	PodStartTT
0.0	0.0
14.0	0.0
16.0	1.0

PodStartTT



1.2.30 StartPodInitTT

Before EndFlowering

PreEventValue = 0

On EndFlowering the value is set to:

PostEventValue = [Phenology].AccumulatedTT

1.2.31 EndPodInitTT

Before EndPodInitiation

PreEventValue = 0

On EndPodInitiation the value is set to:

PostEventValue = [Phenology].AccumulatedTT

1.2.32 StartFloweringPodStartTT

Before StartFlowering

PreEventValue = 0

On StartFlowering the value is set to:

PostEventValue = [Phenology].AccumPodStartTT

1.2.33 EndFloweringPodStartTT

Before EndFlowering

PreEventValue = 0

On EndFlowering the value is set to:

PostEventValue = [Phenology].AccumPodStartTT

1.2.34 TotalPodInitTT

Shortens TT for grainfilling when there is a big gap between beginning of flowering and beginning of pod initiation

TotalPodInitTT = [Phenology].EndPodInitTT - [Phenology].StartPodInitTT

1.2.35 EndFloweringNodeLeafArea

Before EndFlowering

PreEventValue = 1

On EndFlowering the value is set to:

PostEventValue = [Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea

1.2.36 PostFloweringMSLeafNo

Shortens TT for grainfilling when there is a big gap between beginning of flowering and beginning of pod initiation

PostFloweringMSLeafNo = [Structure].LeafTipsAppeared - [Phenology].EndFloweringMSLeafNo

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 Chickpea is calculated as:

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

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

1.3.2 Main-Stem leaf appearance

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

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

Where *DeltaTips* is calculated as:

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

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

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

Water stress impacts on phyllochron during grainfilling as per Peake et al. 2020. May impact on earlier growth stages so other stages made available for modification in future.

PreEmergence has a value between Germination and Emergence calculated as:

$$\text{Function} = 0$$

CanopyDevelopment has a value between Emergence and EndFlowering calculated as:

$$\text{NodeAppearanceRate} = [\text{Structure}].\text{NodeAppearanceRate}$$

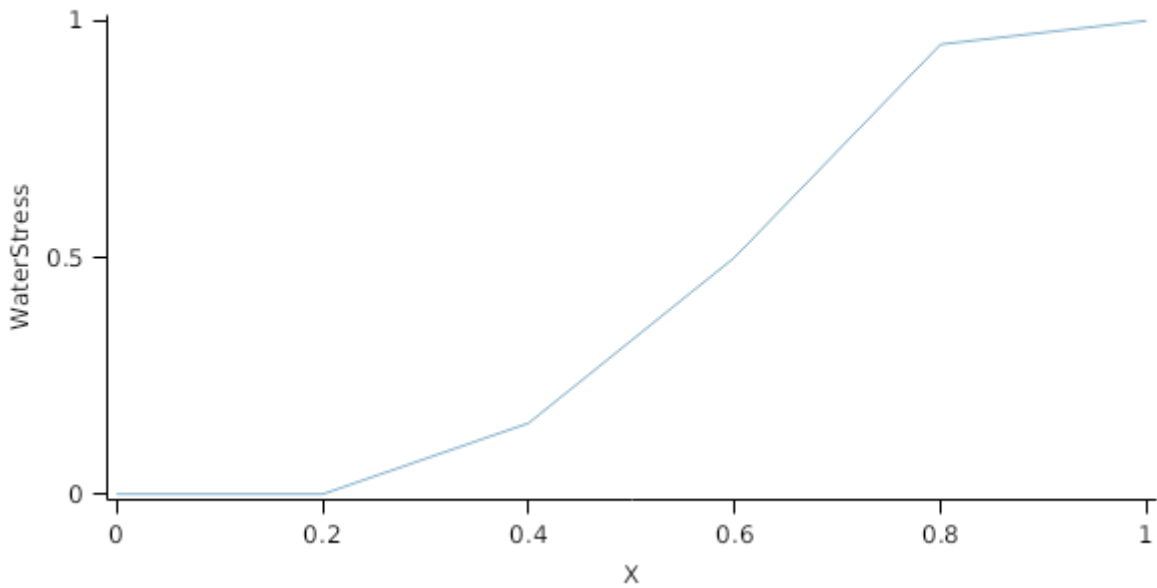
EarlyGrainfilling has a value between EndFlowering and MidGrainFilling calculated as:

$$\text{DivideFunction} = [\text{Structure}].\text{NodeAppearanceRate} / \text{WaterStress}$$

WaterStress is calculated using linear interpolation

X	WaterStress
0.0	0.0
0.2	0.0
0.4	0.1
0.6	0.5
0.8	0.9
1.0	1.0

WaterStress



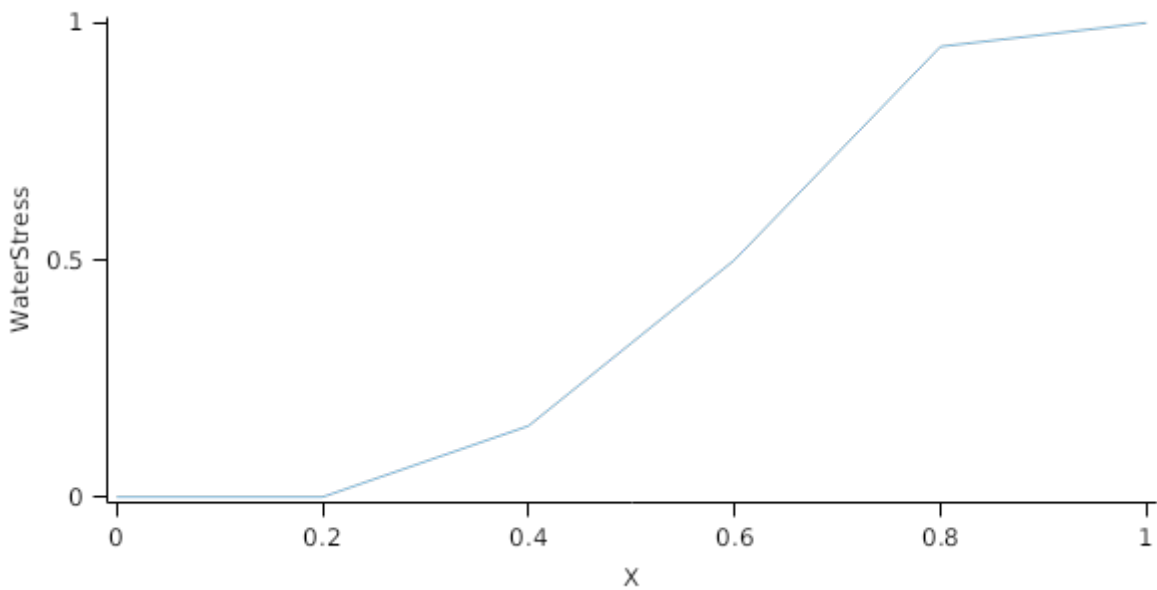
MidGrainfilling has a value between MidGrainFilling and LateGrainFilling calculated as:

$$\text{DivideFunction} = [\text{Structure}].\text{NodeAppearanceRate} / \text{WaterStress}$$

WaterStress is calculated using linear interpolation

X	WaterStress
0.0	0.0
0.2	0.0
0.4	0.1
0.6	0.5
0.8	0.9
1.0	1.0

WaterStress

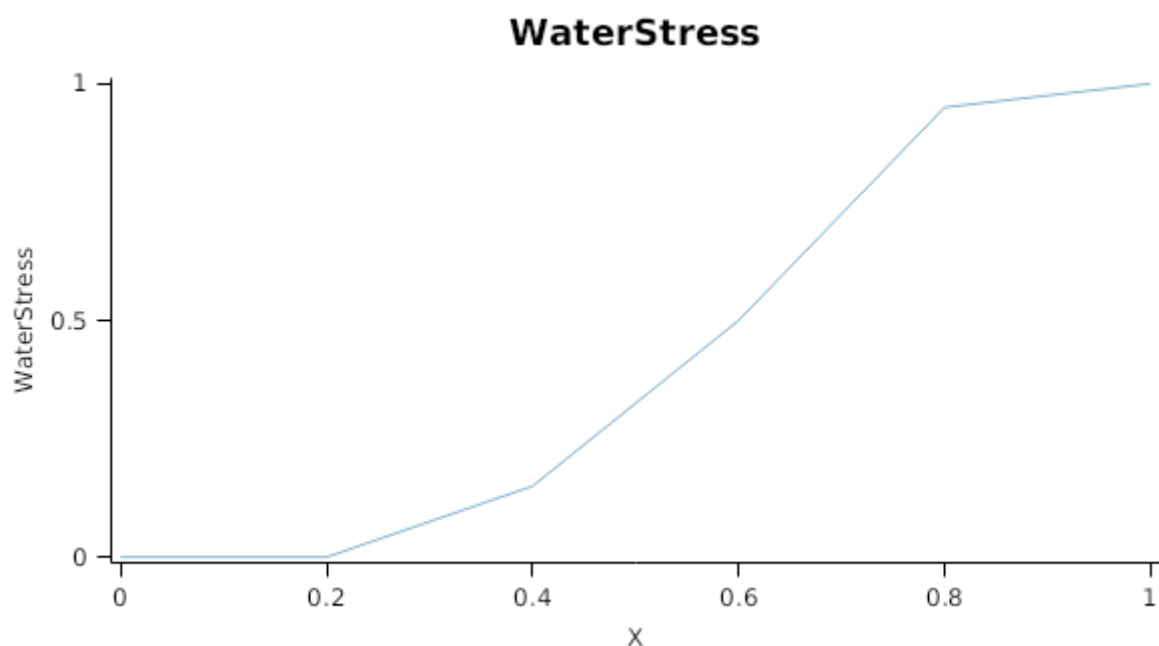


LateGrainfilling has a value between LateGrainFilling and EndGrainFill calculated as:

$DivideFunction = [Structure].NodeAppearanceRate / WaterStress$

$WaterStress$ is calculated using linear interpolation

X	WaterStress
0.0	0.0
0.2	0.0
0.4	0.1
0.6	0.5
0.8	0.9
1.0	1.0



$ThermalTime$ is given by

$ThermalTime = [Phenology].ThermalTime$

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

$FinalLeafNumber = 40$

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:

Cover response as per soybean

$BranchingRate = Potential_Branching_Rate \times BranchModifier$

$Potential_Branching_Rate$ 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:

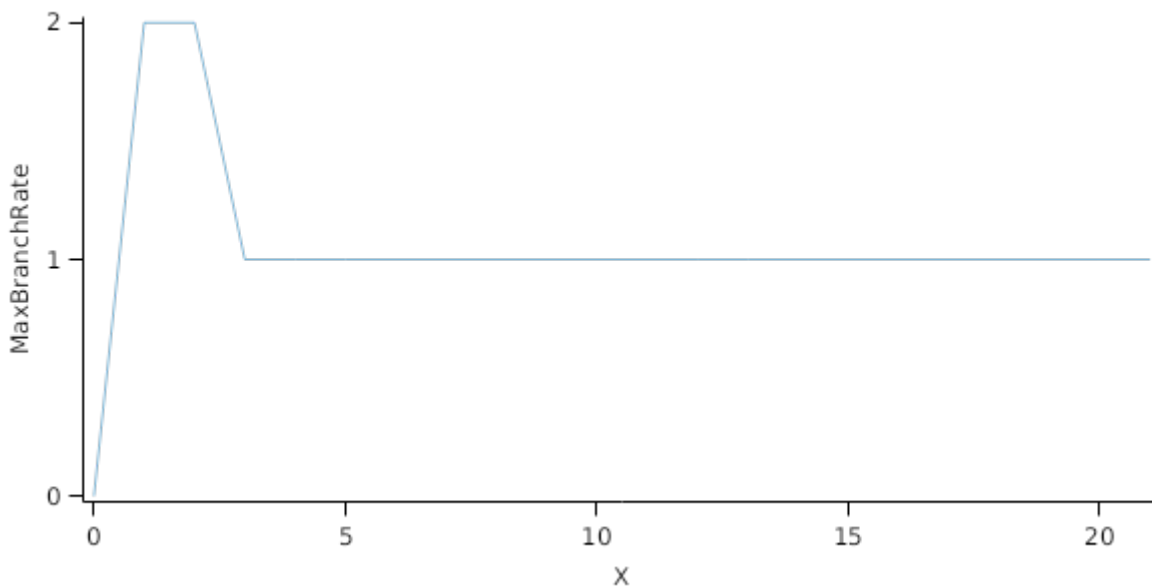
Function = 0

Vegetative has a value between Emergence and EndPodInitiation calculated as:

MaxBranchRate is calculated using linear interpolation

X	MaxBranchRate
0.0	0.0
1.0	2.0
2.0	2.0
3.0	1.0
4.0	1.0
5.0	1.0
12.0	1.0
13.0	1.0
20.0	1.0
21.0	1.0

MaxBranchRate



PostFlowering has a value between EndPodInitiation and Maturity calculated as:

Function = 0

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

EarlyVegetative has a value between Emergence and StartBudding calculated as:

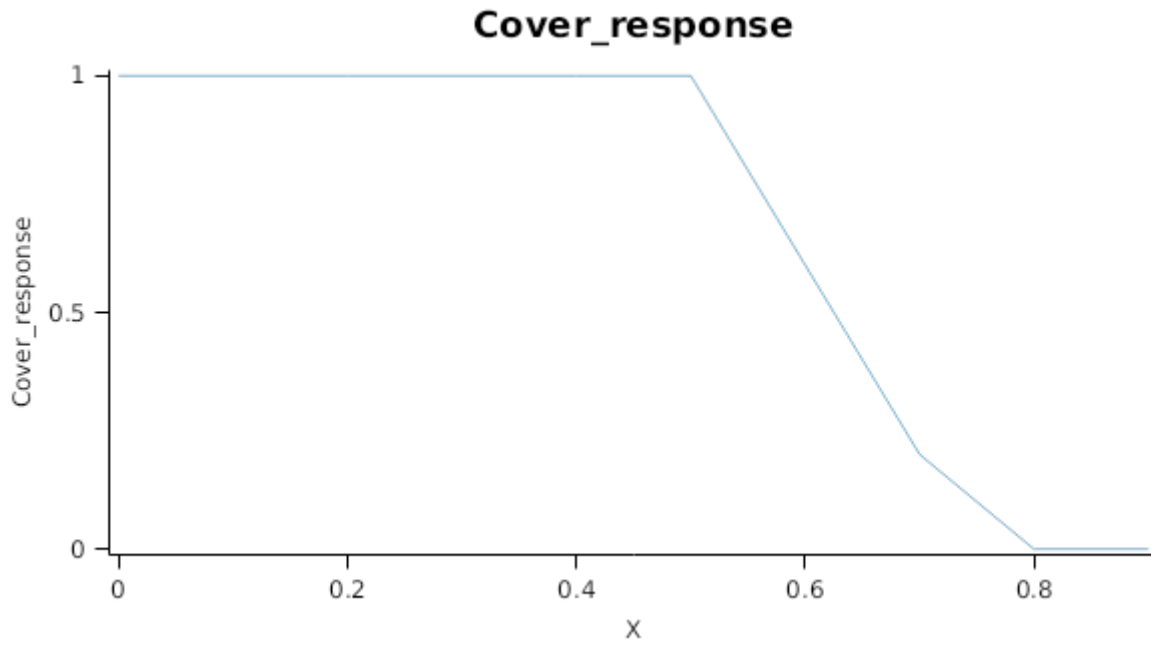
$$EarlyVeg = \text{Min}(Cover_response, WaterStress, TempResponse)$$

Where:

Cover_response is calculated using linear interpolation

X	Cover_response
0.0	1.0

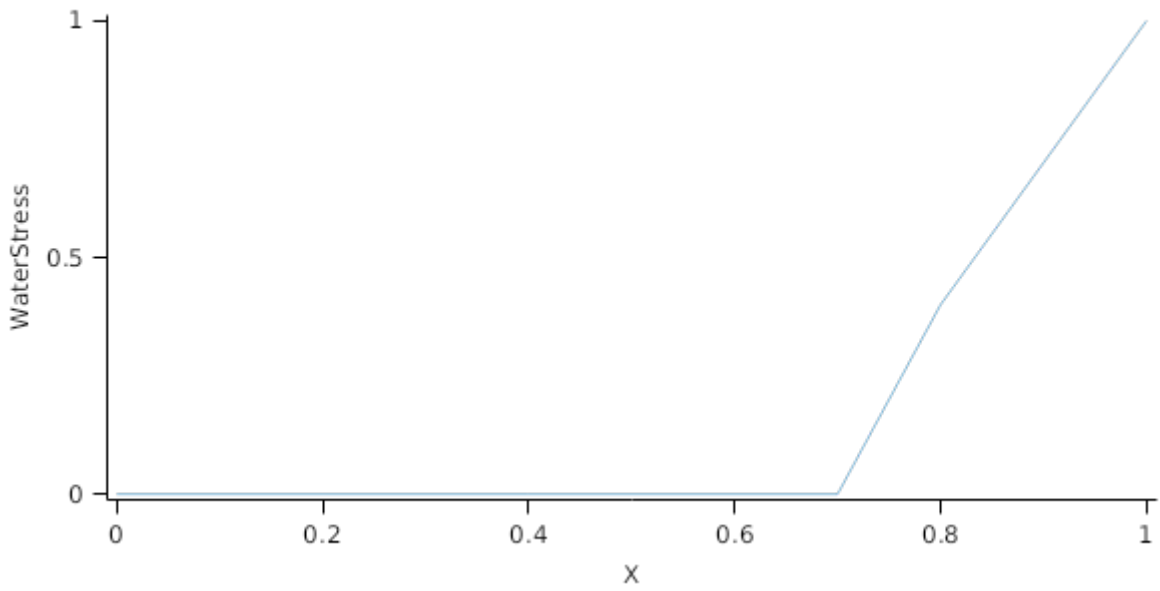
X	Cover_response
0.2	1.0
0.4	1.0
0.5	1.0
0.7	0.2
0.8	0.0
0.9	0.0



WaterStress is calculated using linear interpolation

X	WaterStress
0.0	0.0
0.2	0.0
0.4	0.0
0.7	0.0
0.8	0.4
1.0	1.0

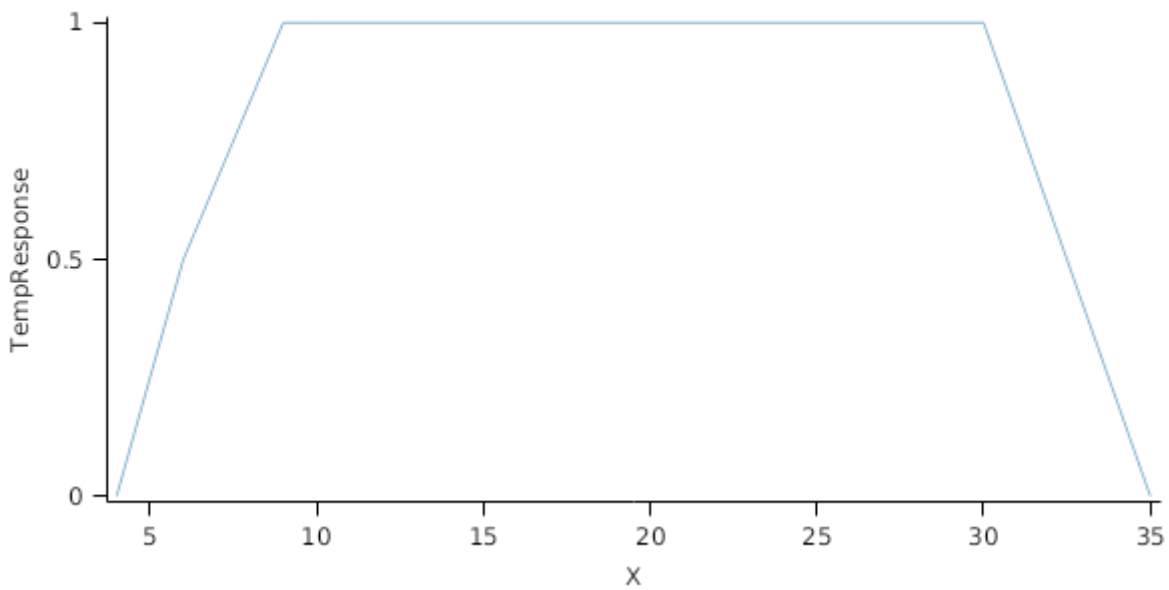
WaterStress



TempResponse is calculated using linear interpolation

X	TempResponse
4.0	0.0
6.0	0.5
9.0	1.0
10.0	1.0
30.0	1.0
35.0	0.0

TempResponse



FloralInitiation has a value between StartBudding and StartFlowering calculated as:

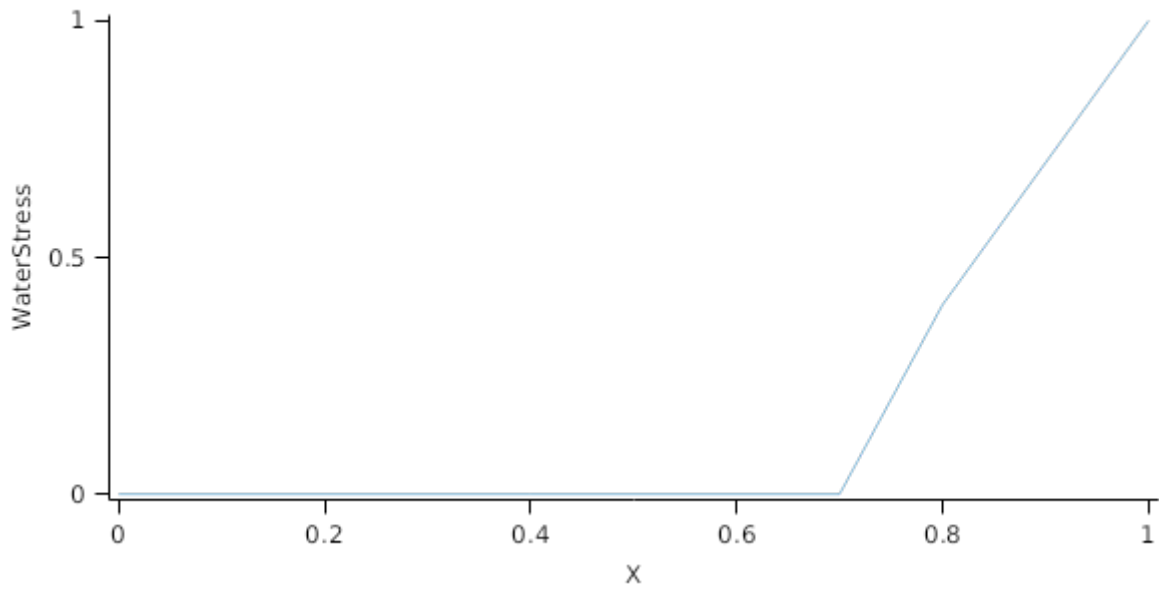
$$\text{LateVeg} = \text{Min}(\text{WaterStress}, \text{TempResponse})$$

Where:

WaterStress is calculated using linear interpolation

X	WaterStress
0.0	0.0
0.2	0.0
0.4	0.0
0.7	0.0
0.8	0.4
1.0	1.0

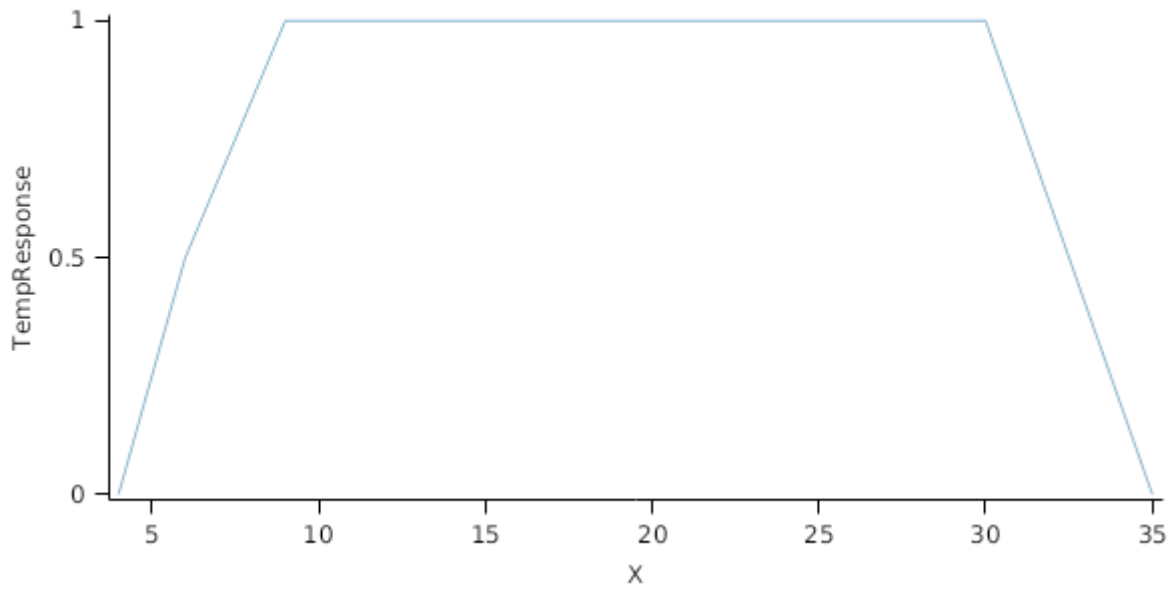
WaterStress



TempResponse is calculated using linear interpolation

X	TempResponse
4.0	0.0
6.0	0.5
9.0	1.0
10.0	1.0
30.0	1.0
35.0	0.0

TempResponse



Flowering has a value between StartFlowering and EndPodInitiation calculated as:

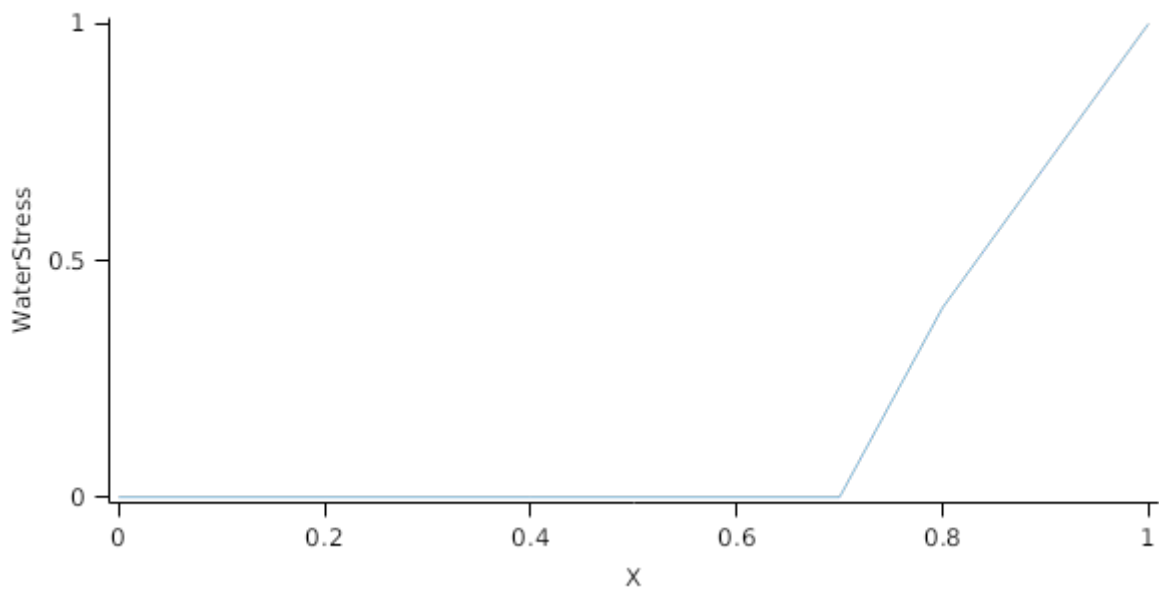
$$FlowerResponse = \text{Min}(WaterStress, TempResponse)$$

Where:

WaterStress is calculated using linear interpolation

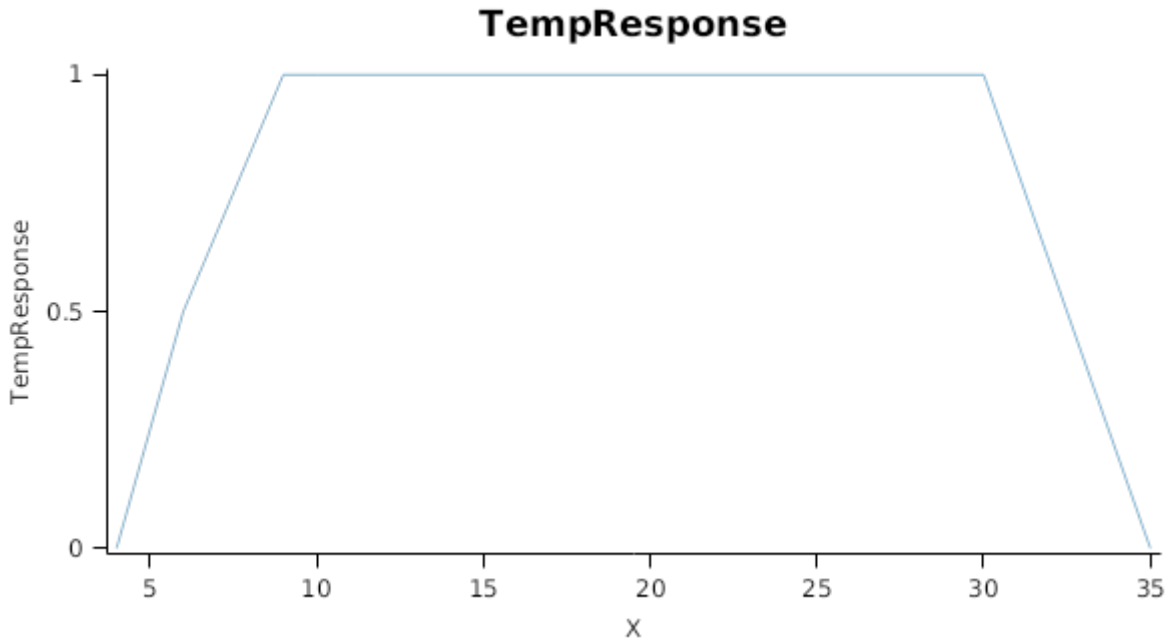
X	WaterStress
0.0	0.0
0.2	0.0
0.4	0.0
0.7	0.0
0.8	0.4
1.0	1.0

WaterStress



TempResponse is calculated using linear interpolation

X	TempResponse
4.0	0.0
6.0	0.5
9.0	1.0
10.0	1.0
30.0	1.0
35.0	0.0



EarlyGrainfilling has a value between EndPodInitiation and MidGrainFilling calculated as:

Fraction = 0

MidGrainfilling has a value between MidGrainFilling and LateGrainFilling calculated as:

Fraction = 0

LateGrainfilling has a value between LateGrainFilling and EndGrainFill calculated as:

Fraction = 0

NewlyDeadBranches is calculated as:

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

where *BranchMortality* is given by:

BranchMortality = 0

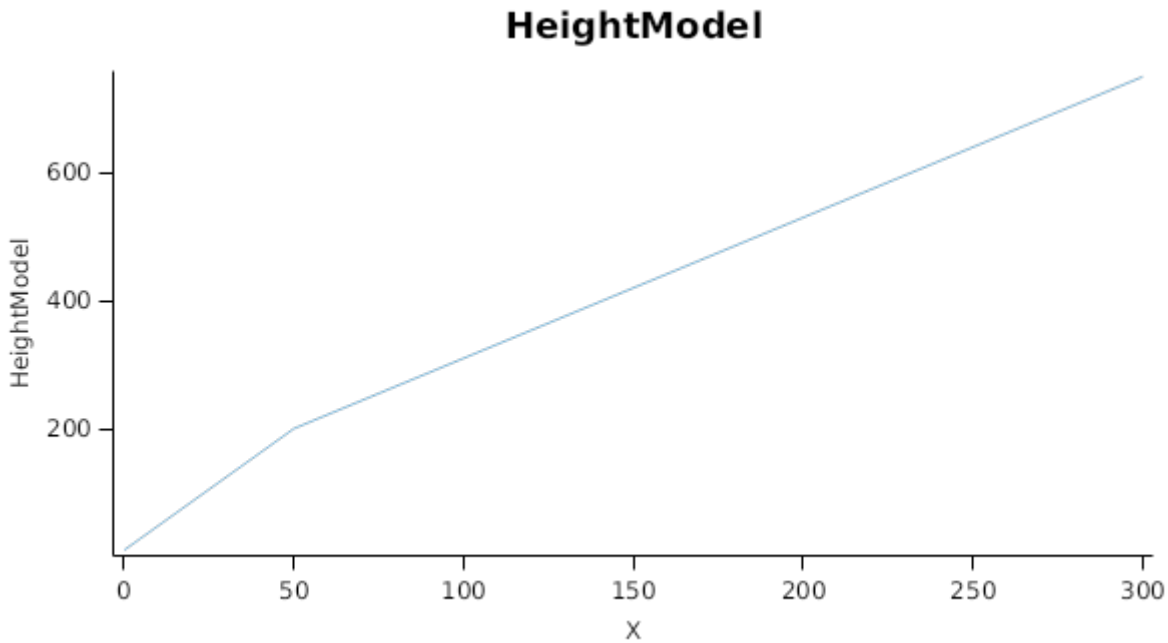
1.3.4 Height

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

HeightModel is calculated using linear interpolation

X	HeightModel
0.0	10.0

X	HeightModel
50.0	200.0
300.0	750.0



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

PotentialHarvestIndex = 0.5

MaximumPotentialGrainSize = 0.25

MinimumNConc = 0.02

MaximumNConc = 0.04

WaterContent = 0.12

DMConversionEfficiency = 0.89

RemobilisationCost = 0

CarbonConcentration = 0.4

1.4.2 FillingDuration

$FillingDuration = [Phenology].EarlyGrainFilling.Target + [Phenology].MidGrainFilling.Target + [Phenology].LateGrainFilling.Target$

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.

GrainFilling has a value between EndPodInitiation and HarvestRipe calculated as:

$HIGrainDemand = [AboveGround].Wt \times HarvestIndexIncrease \times [Phenology].ThermalTime$

$HarvestIndexIncrease = [Grain].PotentialHarvestIndex / [Grain].FillingDuration$

1.4.4 NumberFunction

$$\text{NumberFunction} = \text{PeasPerPod} \times [\text{Shell}].\text{PodNumber}$$

$$\text{PeasPerPod} = 1$$

1.4.5 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

1.4.6 NFillingRate

$$\text{NFillingRate} = [\text{Grain}].\text{MaximumNConc} \times [\text{Grain}].\text{DMDemandFunction} \times [\text{Grain}].\text{DMConversionEfficiency}$$

1.4.7 HarvestIndex

$$\text{HarvestIndex} = [\text{Grain}].\text{Wt} / [\text{AboveGround}].\text{Wt}$$

1.4.8 AboveGroundWt

$$\text{AboveGroundWt} = [\text{AboveGround}].\text{Wt}$$

1.4.9 DMDemandPriorityFactors

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

$$\text{Structural} = 1$$

$$\text{Metabolic} = 1$$

$$\text{Storage} = 1$$

1.4.10 NDemandPriorityFactors

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

$$\text{Structural} = 1$$

$$\text{Metabolic} = 1$$

$$\text{Storage} = 1$$

1.5 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.

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

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

Root depth is also constrained by a maximum root depth.

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

$$RAw_i = -WaterUptake_i / LiveRootWt_i \times LayerThickness_i \times ProportionThroughLayer$$

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

$$DMAAllocated_i = TotalDMAAllocated \times RAw_i / TotalRAw$$

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

MaxDailyNUptake = 6

SenescenceRate = 0.005

MaximumRootDepth = 1000000

MaximumNConc = 0.01

MinimumNConc = 0.005

KNO3 = 0.02

KNH4 = 0

SpecificRootLength = 40 (m/g)

DMConversionEfficiency = 1

MaintenanceRespirationFunction = 1

RemobilisationCost = 0

CarbonConcentration = 0.4

RootDepthStressFactor = 1

1.5.7 Memo

Minimal root biomass has been simulated. It appears to interfere with simulation of stem biomass (arbitrator).

1.5.8 RootShape

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

1.5.9 KLModifier

KLModifier 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:

Function = 0.1

PreCanopyDevelopment has a value between Emergence and EndFlowering calculated as:

$klTTfactor1 = [Root].klComboeffects$

Soil data at Kulai and ICRISAT suggests wider row spacing and late sowing can catch up with kl - so allow the function to continue post flowering

PostCanopyDevelopment has a value between EndFlowering and Maturity calculated as:

Soil data at Kulai and ICRISAT suggests wider row spacing and late sowing can catch up with kl - so allow the function to continue post flowering

$klTTfactor1 = [Root].klComboeffects$

1.5.10 RootFrontVelocity

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

PreEmergence has a value between Germination and Emergence calculated as:

Function = 3

early has a value between Emergence and StartFlowering calculated as:

Function = 15

late has a value between StartFlowering and Maturity calculated as:

Function = 17

1.5.11 NitrogenDemandSwitch

NitrogenDemandSwitch has a value between Emergence and EndGrainFill calculated as:

Constant = 1

1.5.12 BiomassRemovalDefaults

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

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	20	0
Cut	0	0	30	0

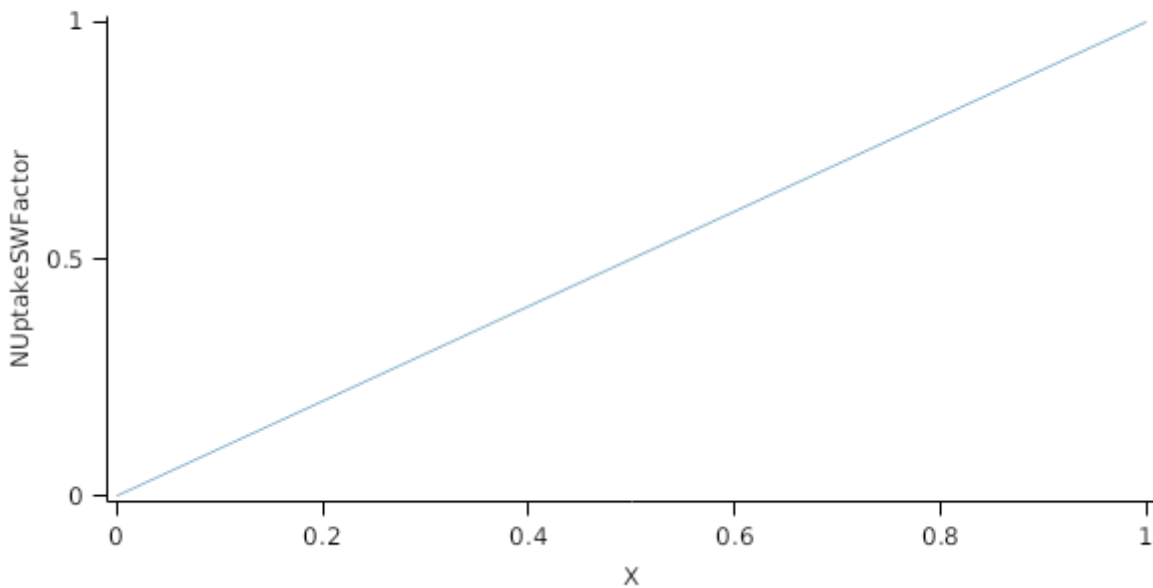
Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Prune	0	0	10	0
Graze	0	0	15	0

1.5.13 NUptakeSWFactor

NUptakeSWFactor is calculated using linear interpolation

X	NUptakeSWFactor
0.0	0.0
1.0	1.0

NUptakeSWFactor



1.5.14 DMDemands

1.5.14.1 DMDemands

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

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

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

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

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.

Early has a value between Emergence and StartFlowering calculated as:

$$\text{Function} = 0.2$$

Middle has a value between StartBudding and StartFlowering calculated as:

$$\text{Function} = 0.2$$

Late has a value between StartFlowering and Maturity calculated as:

$$\text{Function} = 0$$

$$\text{StructuralFraction} = 1$$

$$\text{Metabolic} = 0$$

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

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

$$\text{QStructuralPriority} = 1$$

$$\text{QMetabolicPriority} = 1$$

$$\text{QStoragePriority} = 1$$

1.5.15 NDemands

1.5.15.1 NDemands

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

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

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

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

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

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

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

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

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

$$\text{QStructuralPriority} = 1$$

$$\text{QMetabolicPriority} = 1$$

$$\text{QStoragePriority} = 1$$

1.5.16 SurfaceWaterAvailability

$$\text{SurfaceWaterAvailability} = [\text{Soil}].\text{SoilWater}.\text{PAWmm}[1] / [\text{Soil}].\text{Physical}.\text{PAWCmm}[1]$$

1.5.17 WithinRowSpaceFactor

$$\text{WithinRowSpaceFactor} = 1000 / [\text{Chickpea}].\text{SowingData}.\text{RowSpacing} / [\text{Chickpea}].\text{SowingData}.\text{Population} / \text{Constant1}$$

$$\text{Constant1} = 0.001$$

1.5.18 KLComboeffects

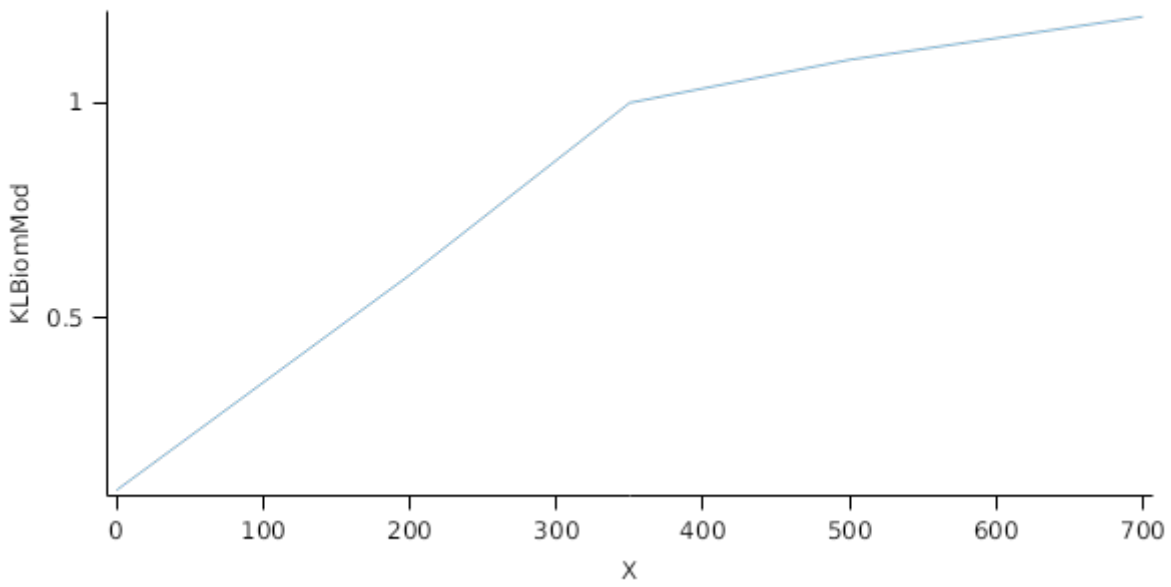
$$\text{KLComboeffects} = [\text{Root}].\text{KLBiomMod} \times [\text{Root}].\text{klPopMultiplier} \times [\text{Root}].\text{klRowSpaceMultiplier}$$

1.5.19 KLBiomMod

KLBiomMod is calculated using linear interpolation

X	KLBiomMod
0.0	0.1
200.0	0.6
350.0	1.0
500.0	1.1
700.0	1.2

KL BiomMod

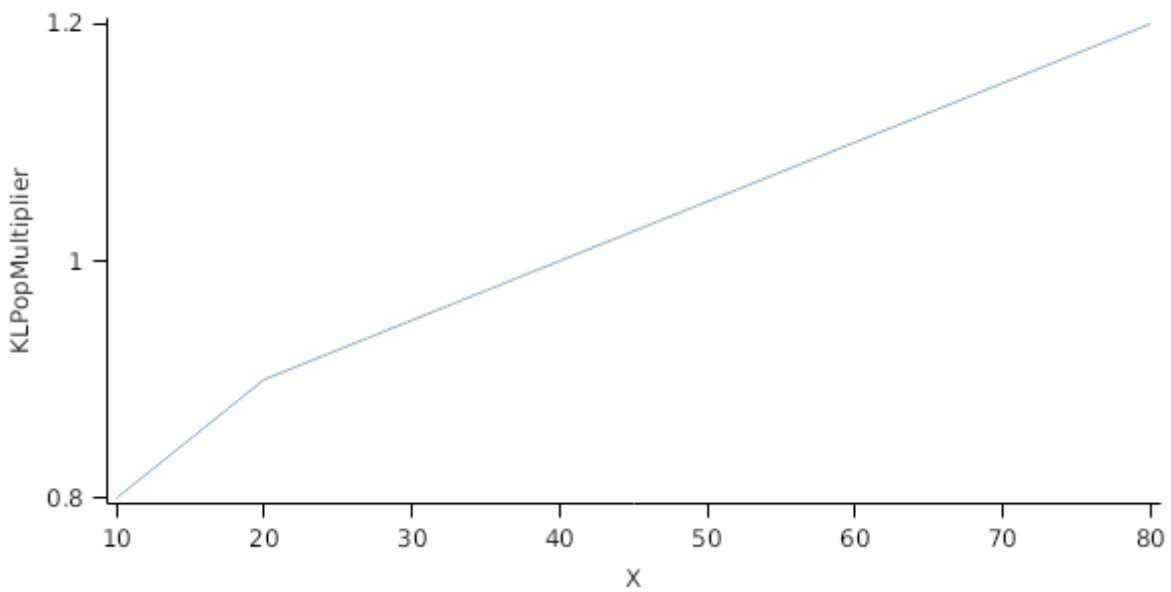


1.5.20 KL PopMultiplier

KL PopMultiplier is calculated using linear interpolation

X	KL PopMultiplier
10.0	0.8
20.0	0.9
40.0	1.0
60.0	1.1
80.0	1.2

KL PopMultiplier

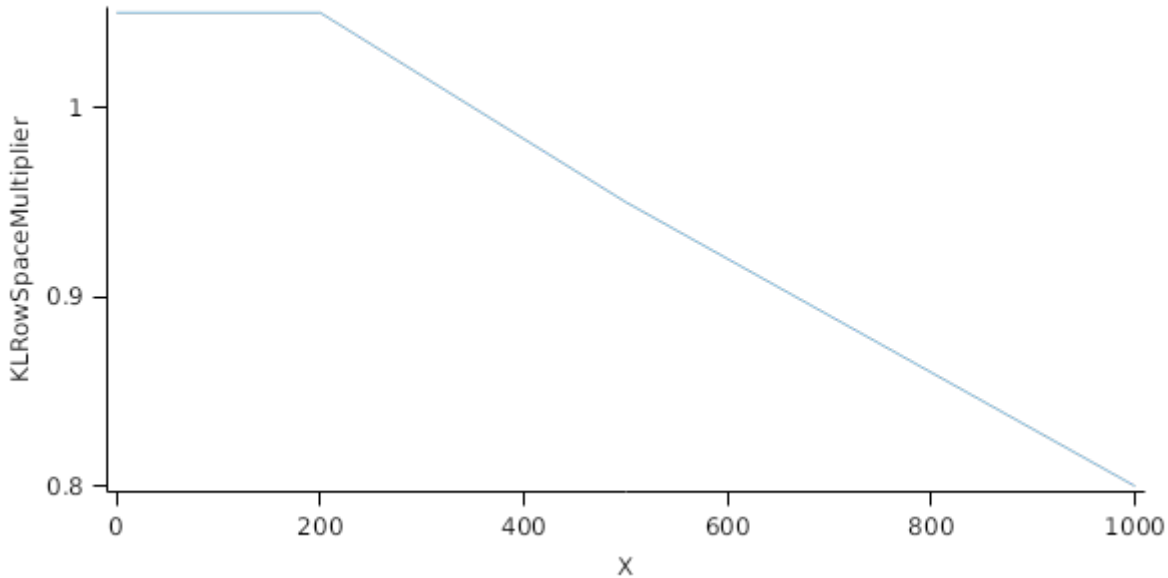


1.5.21 KL RowSpaceMultiplier

KL RowSpaceMultiplier is calculated using linear interpolation

X	KLRowSpaceMultiplier
0.0	1.1
200.0	1.1
350.0	1.0
500.0	0.9
1000.0	0.8

KLRowSpaceMultiplier



1.5.22 CriticalNConc

$CriticalNConc = [Root].MinimumNConc$

1.5.23 InitialWt

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

Structural = 0.2 (g/plant)

Metabolic = 0

Storage = 0

1.6 Shell

1.6.1 Shell

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

1.6.2 Dry Matter Demand

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

1.6.2.1 DMDemands

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

$Structural = DMDemandFunction \times StructuralFraction$

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

PodDevelopment has a value between EndPodInitiation and MidGrainFilling calculated as:

$HIPodDemand = [AboveGround].Wt \times HarvestIndexIncrease \times [Phenology].ThermalTime$

$HarvestIndexIncrease = [Shell].PotentialHarvestIndex / [Shell].FillingDuration$

StructuralFraction = 1 (g/g)

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.6.3 Nitrogen Demand

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

1.6.3.1 NDemands

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

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

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

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

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

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

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

$NitrogenDemandSwitch = [Shell].nitrogenDemandSwitch$

$MaxNconc = [Shell].maximumNconc$

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.6.4 N Concentration Thresholds

MinimumNConc = 0.007

$CriticalNConc = [Shell].MinimumNConc$

MaximumNConc = 0.02

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

NitrogenDemandSwitch has a value between Germination and Maturity calculated as:

Constant = 1

1.6.5 Dry Matter Supply

Shell will reallocate 100% of DM that senesces each day.

Shell will retranslocate 50% of non-structural DM each day.

1.6.6 Nitrogen Supply

Shell can reallocate up to 100% of N that senesces each day if required by the plant arbitrator to meet N demands.

Shell can retranslocate up to 50% of non-structural N each day if required by the plant arbitrator to meet N demands.

1.6.7 Senescence and Detachment

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

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

ReproductivePhase has a value between *MidGrainFilling* and *Maturity* calculated as:

$$Rate = \text{Min}(Fraction, One)$$

Where:

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

$$One = 1$$

Shell 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

1.7 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.

1.7.1 Dry Matter Fixation

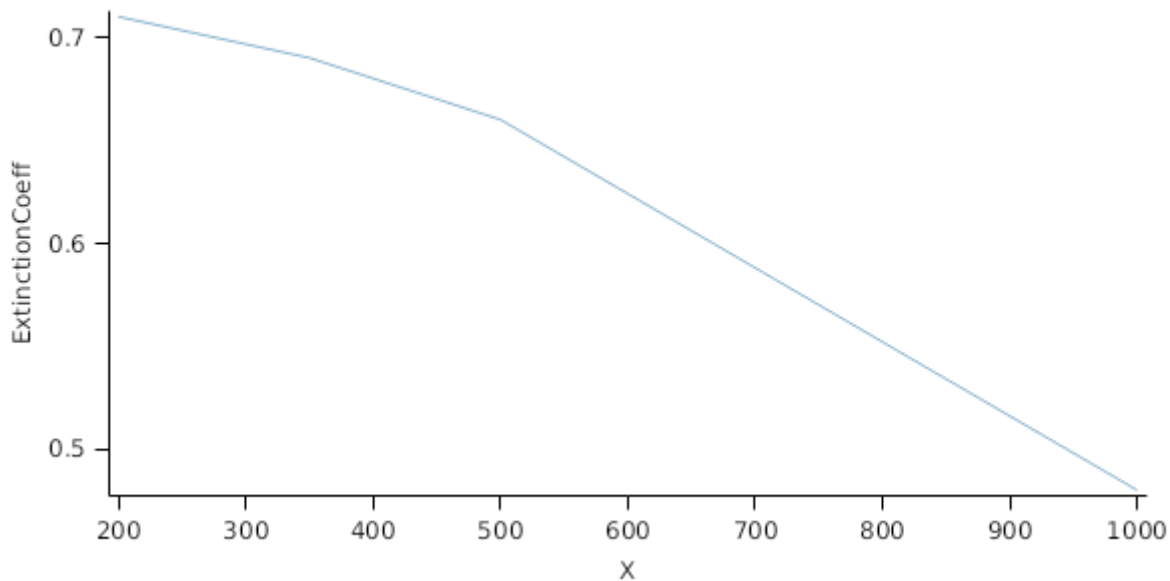
The most important DM supply from leaf is the photosynthetic fixation supply. Radiation interception is calculated from LAI using an extinction coefficient of:

ExtinctionCoeff is calculated using linear interpolation

X	ExtinctionCoeff
200.0	0.7
350.0	0.7
500.0	0.7

X	ExtinctionCoeff
750.0	0.6
1000.0	0.5

ExtinctionCoeff



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.

There is no specific TE parameter in NextGen. TE is an emergent property calculated separately from water use and biomass production

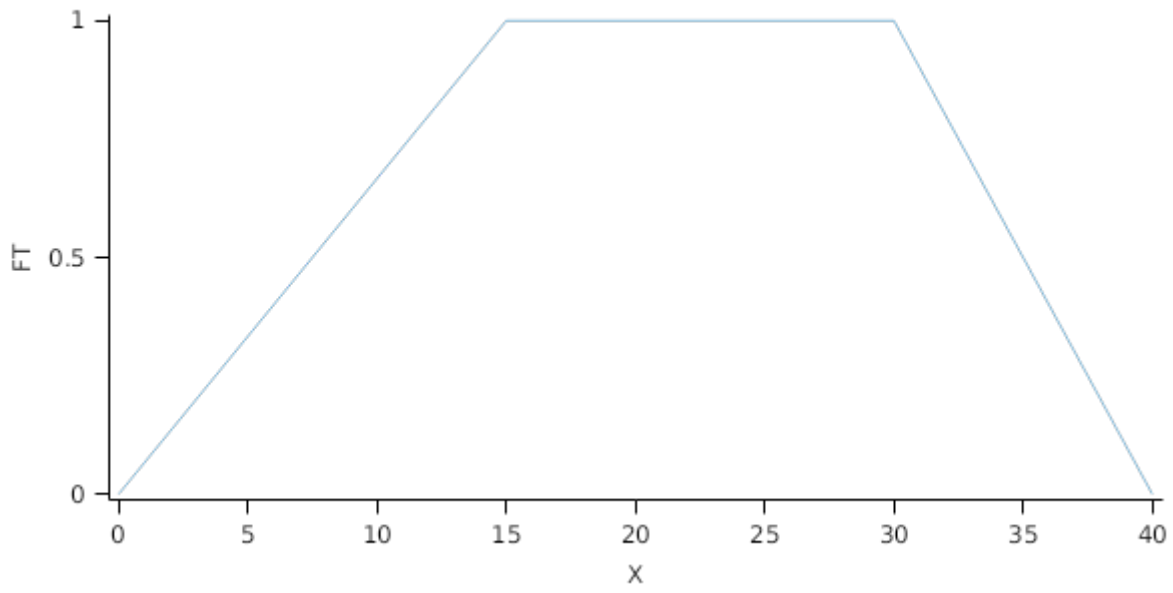
RUE = 1.25

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.

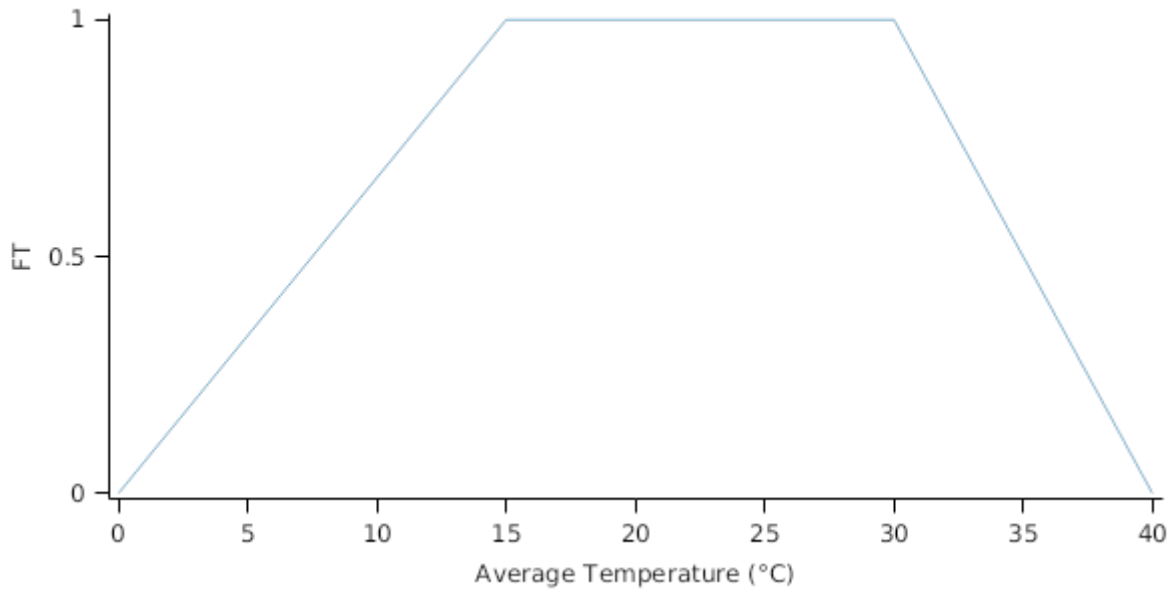
MaximumTemperatureWeighting = 0.75

X	FT
0.0	0.0
15.0	1.0
30.0	1.0
40.0	0.0

FT



FT

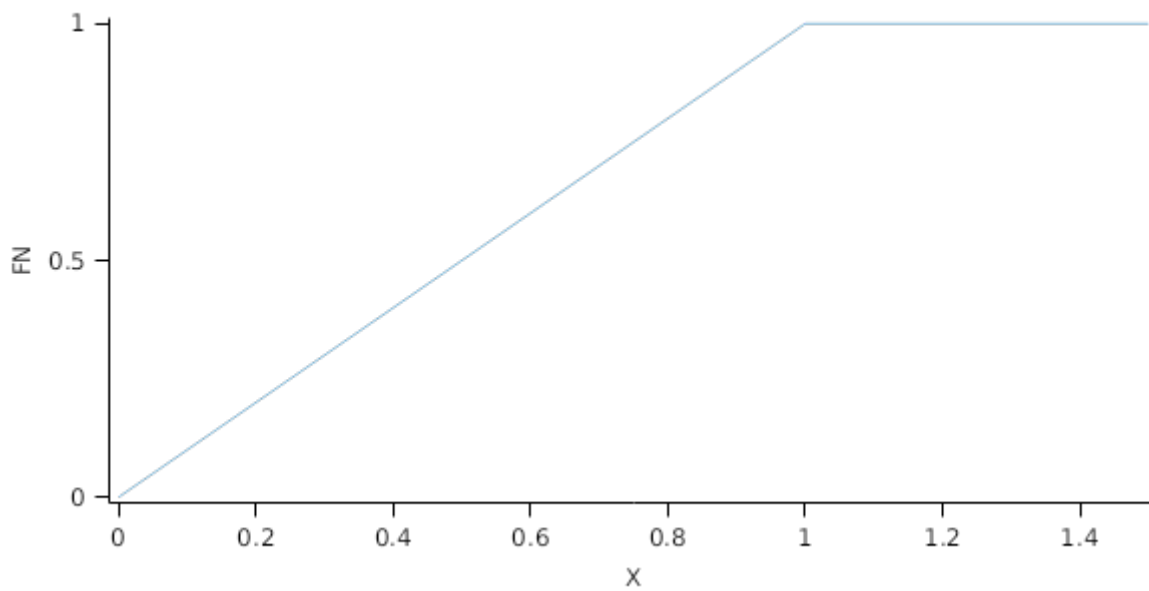


FVPD = 1

FN is calculated using linear interpolation

X	FN
0.0	0.0
1.0	1.0
1.5	1.0

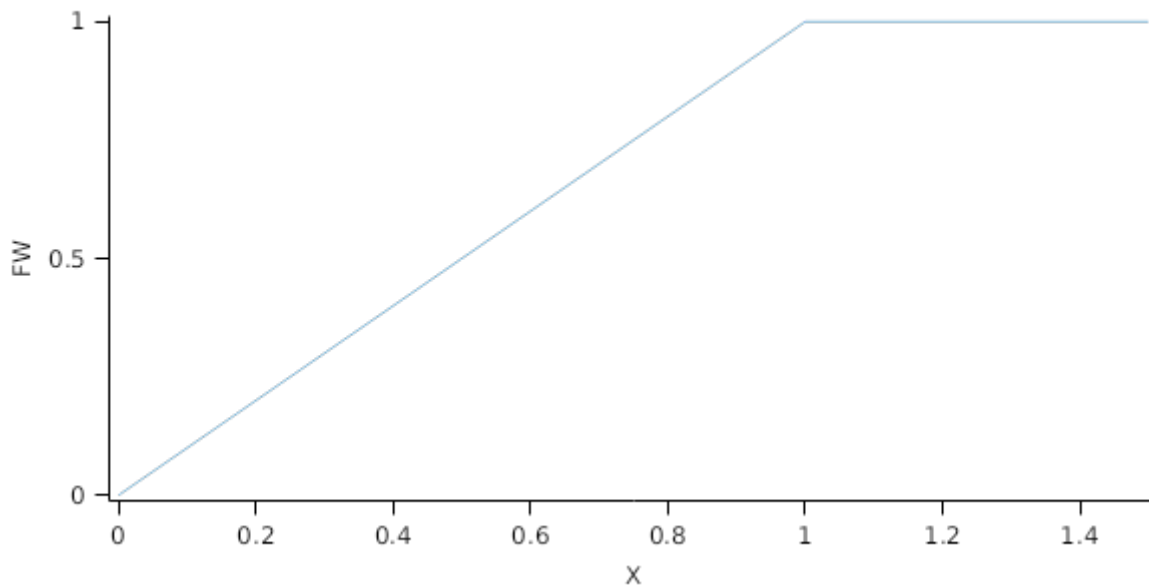
FN



FW is calculated using linear interpolation

X	FW
0.0	0.0
1.0	1.0
1.5	1.0

FW



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,

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

Ayaz eta 2004 presented a RUE of 1.6 g/MJ PAR during non-limiting temperature conditions for field pea. Halving this to make it total radiation gives 0.8 g/MJ and adding 20% to account for root and nodule production and N fixation costs gives 1.0 g/MJ

However Sincalir had data that presented RUE of 2.0 hence by the same calcs we have advanced RUE to 1.2

$$RadnInt = [Leaf].RadiationIntercepted$$

1.7.2 Constants

$$DMConversionEfficiency = 1$$

$$RemobilisationCost = 0$$

$$CarbonConcentration = 0.4$$

$$WidthFunction = 0$$

1.7.3 Memo

Dead leaf ext coeff - may need to be higher than 0.3 - chickpea holds its shape pretty well when dead

1.7.4 InitialLeaf1

$$Area = 50$$

1.7.5 InitialLeaf2

$$Area = 100$$

1.7.6 InitialLeaf3

$$Area = 150$$

1.7.7 LeafCohortParameters

1.7.7.1 Potential Leaf Area index

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

$$GrowthDuration = Multiplier * [Structure].Phyllochron$$

$$Multiplier = 4$$

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

MaxArea 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:

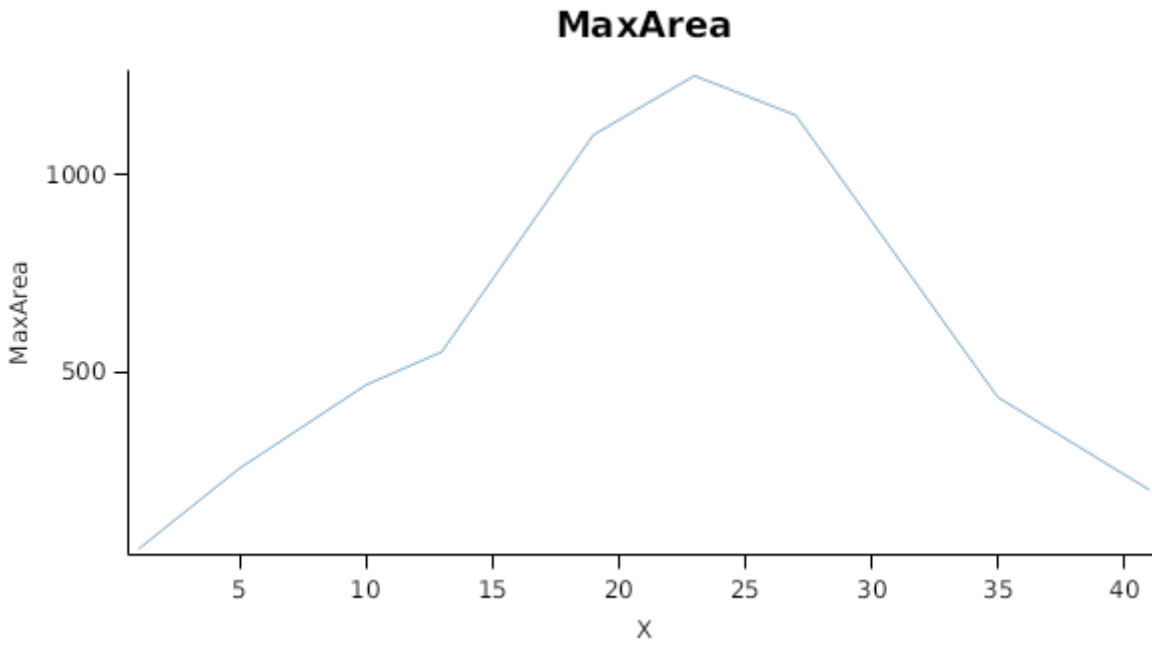
$$MaxArea = 0$$

Vegetative_to_Flowering has a value between Emergence and EndFlowering calculated as:

MaxArea is calculated using linear interpolation

X	MaxArea
1.0	50.0
5.0	255.0
10.0	466.0

X	MaxArea
13.0	550.0
19.0	1100.0
23.0	1250.0
27.0	1150.0
35.0	435.0
41.0	200.0



Flowering_to_Maturity has a value between EndFlowering and Maturity calculated as:

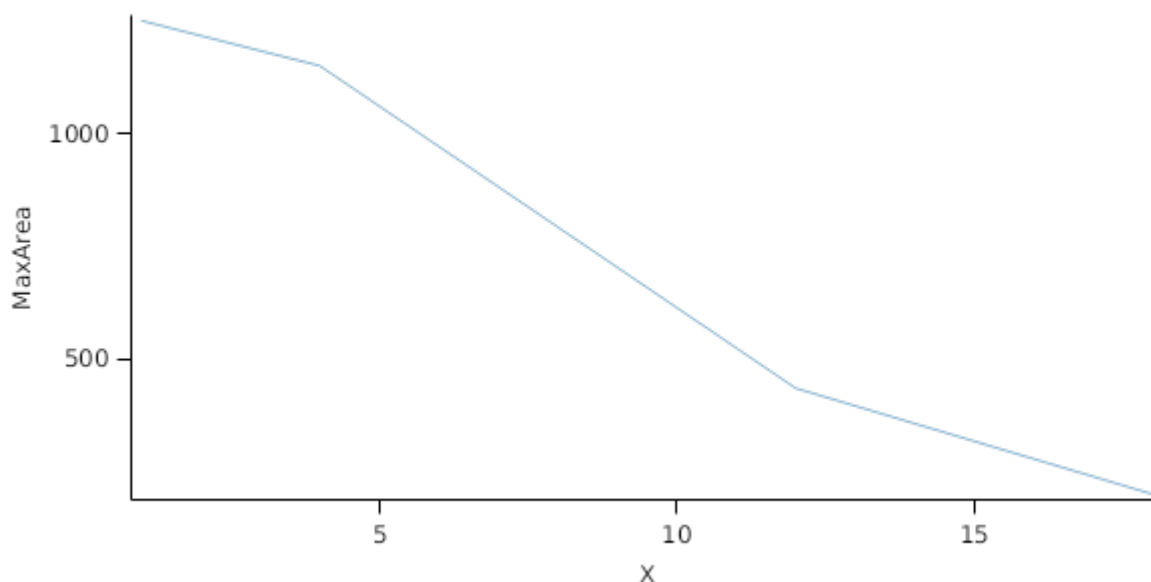
$$\text{MinimumFunction} = \text{Min}(\text{MaxArea}, \text{PreFlowerMaxLA})$$

Where:

MaxArea is calculated using linear interpolation

X	MaxArea
1.0	1250.0
4.0	1150.0
12.0	435.0
18.0	200.0

MaxArea



$$PreFlowerMaxLA = [Phenology].EndFloweringNodeLeafArea$$

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*

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

$$Multiplier = 18$$

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

$$Multiplier = 2$$

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:

$$ShadeInducedSenescenceRate = 0$$

1.7.7.2 Stress effects on Leaf Area Index

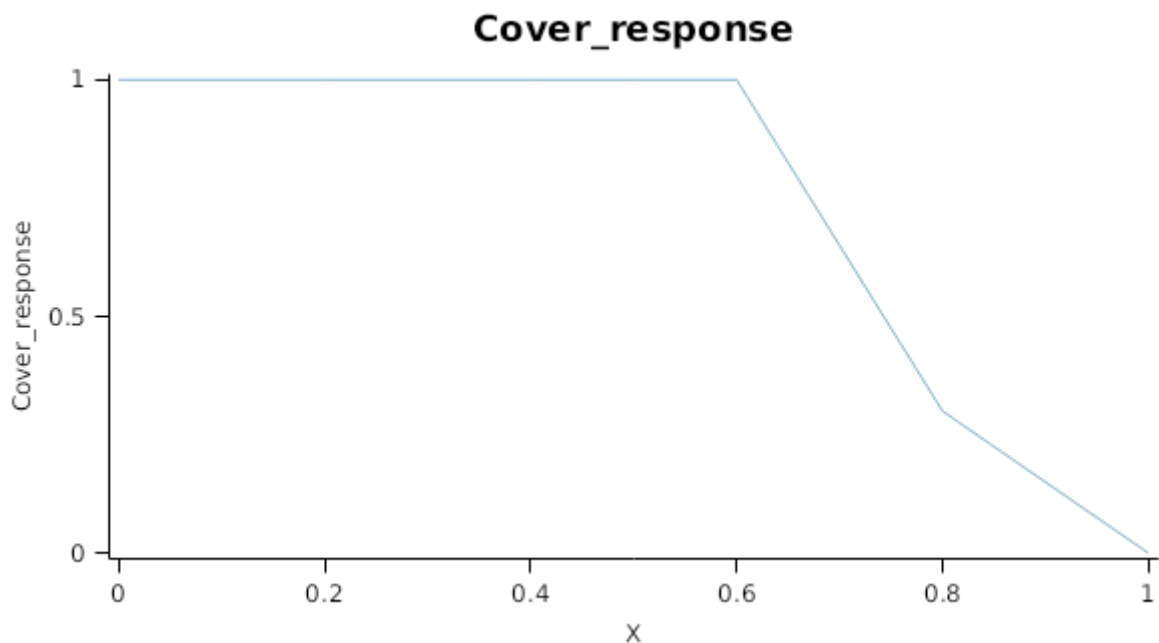
Stress reduces leaf area in a number of ways. Firstly, stress occurring prior to the appearance of the cohort can reduce cell division, so reducing the maximum leaf size. Leaf captures this by multiplying the *MaxSize* of each cohort by a *CellDivisionStress* factor which is calculated as:

$$CellDivisionStress = \text{Min}(Cover_response, WaterStress)$$

Where:

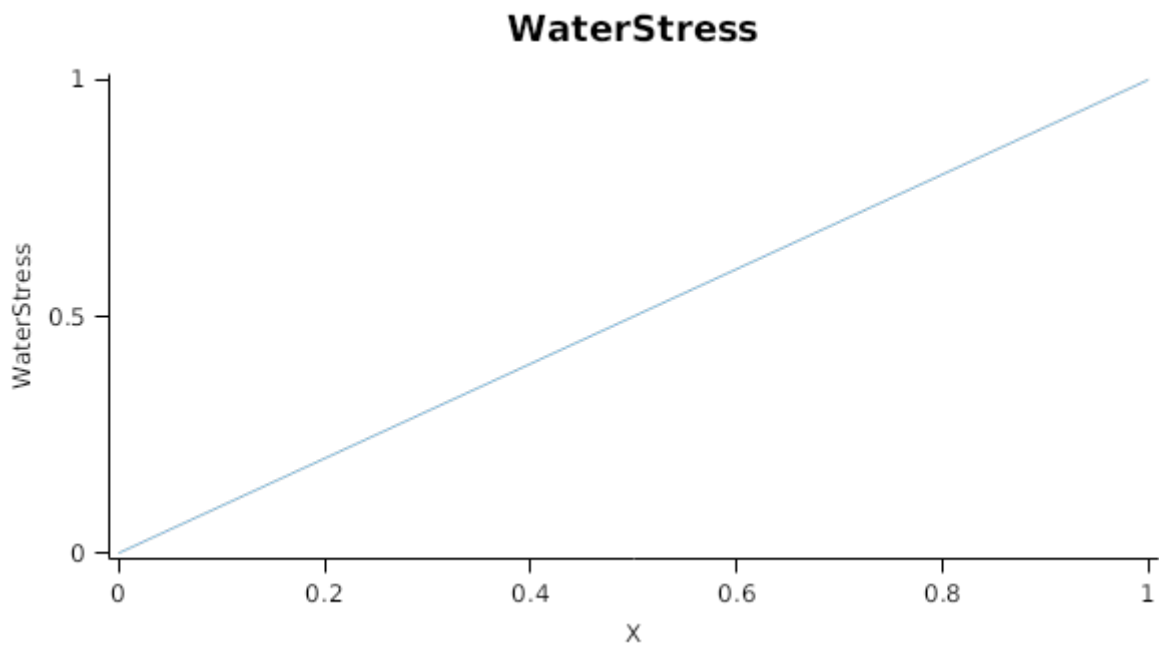
Cover_response is calculated using linear interpolation

X	Cover_response
0.0	1.0
0.2	1.0
0.4	1.0
0.5	1.0
0.6	1.0
0.8	0.3
1.0	0.0



WaterStress is calculated using linear interpolation

X	WaterStress
0.0	0.0
1.0	1.0



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

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

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

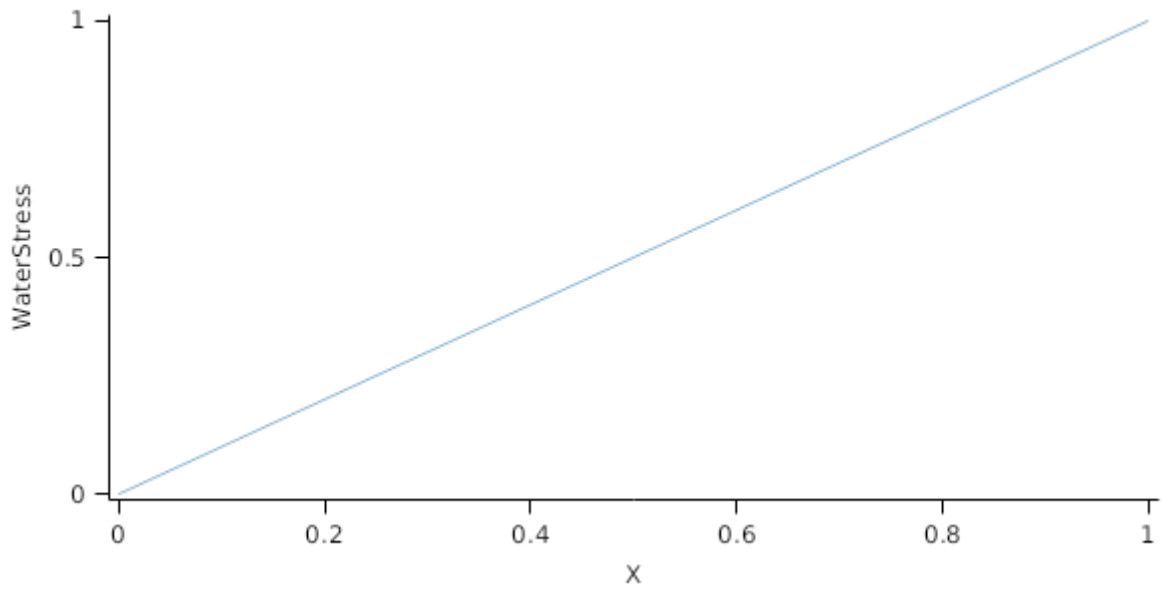
$$ExpansionStress = \text{Min}(WaterStress, TemperatureEffect, Cover_response)$$

Where:

WaterStress is calculated using linear interpolation

X	WaterStress
0.0	0.0
1.0	1.0

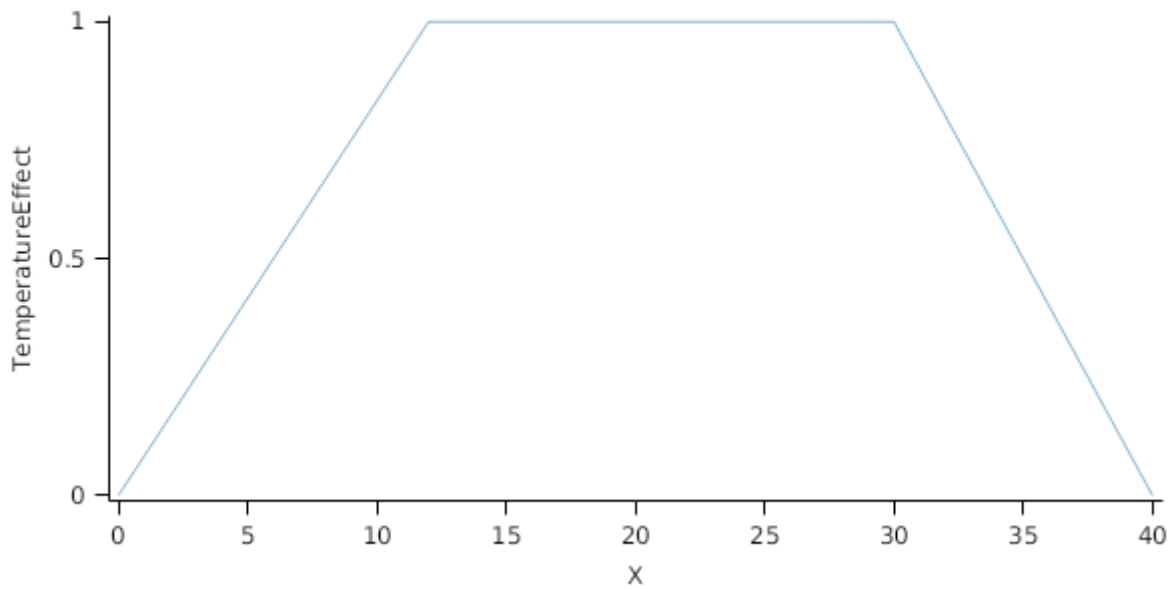
WaterStress



TemperatureEffect is calculated using linear interpolation

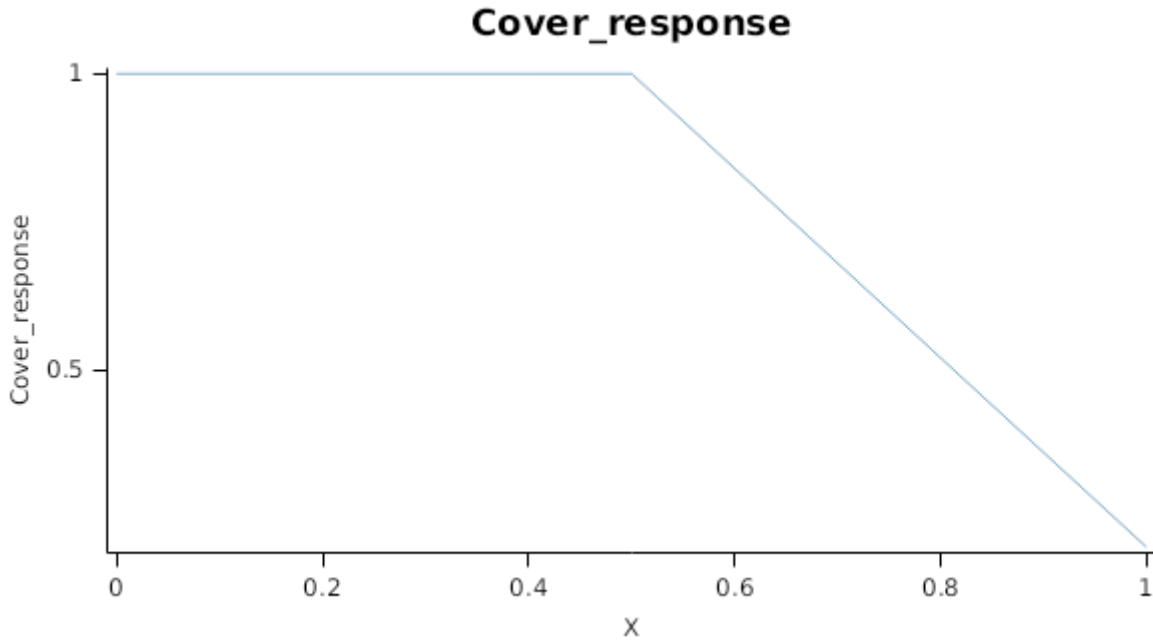
X	TemperatureEffect
0.0	0.0
12.0	1.0
14.0	1.0
25.0	1.0
30.0	1.0
40.0	0.0

TemperatureEffect



Cover_response is calculated using linear interpolation

X	Cover_response
0.0	1.0
0.4	1.0
0.5	1.0
1.0	0.2



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.

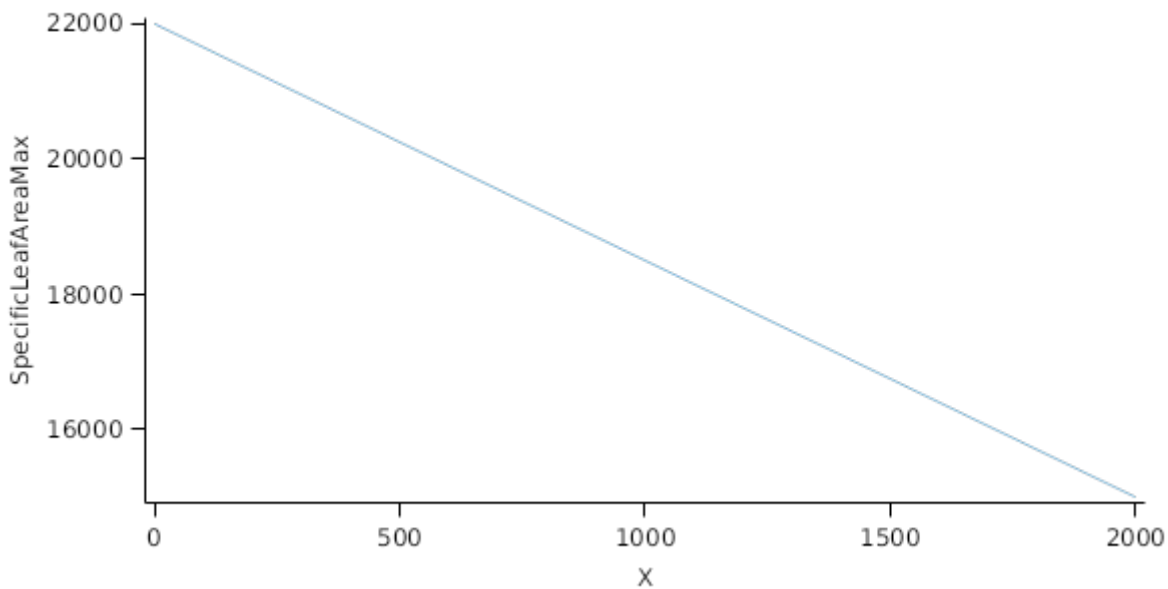
1.7.7.3 Dry matter Demand

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
0.0	22000.0
2000.0	15000.0

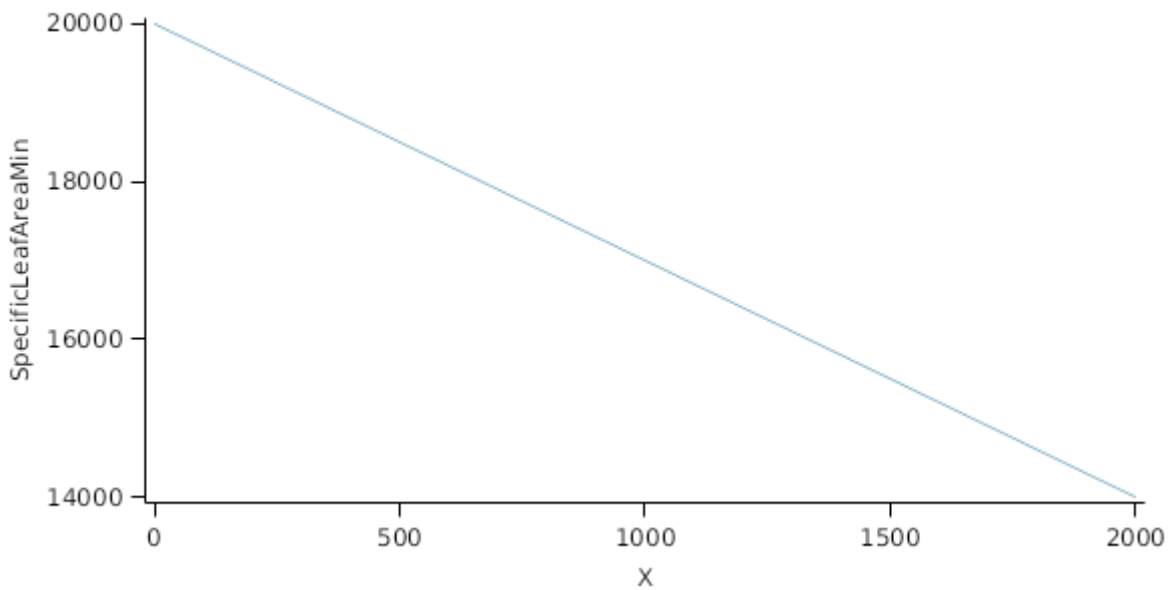
SpecificLeafAreaMax



SpecificLeafAreaMin is calculated using linear interpolation

X	SpecificLeafAreaMin
0.0	20000.0
2000.0	14000.0

SpecificLeafAreaMin



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

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.

Vegetative_to_Flowering has a value between Emergence and StartFlowering calculated as:

Fraction = 0.99

Flowering has a value between StartFlowering and EndPodInitiation calculated as:

Fraction = 0.99

Grainfilling has a value between EndPodInitiation and EndGrainFill calculated as:

Fraction = 0.99

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

1.7.7.4 Nitrogen Demand

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

Structural N demand = *PotentialStructuralDMAAllocation* * *MinimumNConc* where:

MinimumNConc = 0.02

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

CriticalNConc = 0.05

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

MaximumNConc = 0.08

1.7.7.5 Drymatter supply

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

Reallocation = from senesced organs, fraction that can be moved per day

DMReallocationFactor = 1

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

Retranslocation = movement of reserves out of live organs, what proportion can be moved each day

DMRetranslocationFactor = 0.3

1.7.7.6 Nitrogen supply

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

NReallocationFactor = 0.3

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

Retranslocation = movement of reserves out of live organs. Reallocation = from senesced organs

Storage fraction decides how much is available to be moved, while these decide what proportion can be moved each day

NRetranslocationFactor = 0.1

1.7.7.7 Constants

SenescingLeafRelativeSize = 1 (0-1)

DetachmentLagDuration = 1000000

DetachmentDuration = 46

MinimumNConc = 0.02

CriticalNConc = 0.05

MaximumNConc = 0.08

NReallocationFactor = 0.3

Retranslocation = movement of reserves out of live organs. Reallocation = from senesced organs

Storage fraction decides how much is available to be moved, while these decide what proportion can be moved each day

NRetranslocationFactor = 0.1

Reallocation = from senesced organs, fraction that can be moved per day

DMReallocationFactor = 1

Retranslocation = movement of reserves out of live organs, what proportion can be moved each day

DMRetranslocationFactor = 0.3

ShadeInducedSenescenceRate = 0

InitialNConc = 0.08

LeafSizeShapeParameter = 0.01

MaintenanceRespirationFunction = 0

LagAcceleration = 1

SenescenceAcceleration = 1

ArchiveCellDivisionStress = 1 (0-1)

RemobilisationCost = 0

CarbonConcentration = 0.4

1.7.8 ThermalTime

ThermalTime = [Phenology].ThermalTime

1.7.9 FrostFraction

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

Also includes high T and water stress effect end of season

PreEmergence has a value between Germination and Emergence calculated as:

NA = 1

Vegetative_to_Flowering has a value between Emergence and StartFlowering calculated as:

FrostFraction = 0

Flowering has a value between StartFlowering and EndPodInitiation calculated as:

FrostFraction = 0

EarlyGrainfilling has a value between EndPodInitiation and MidGrainFilling calculated as:

FrostFraction = 0

MidGrainfilling has a value between MidGrainFilling and LateGrainFilling calculated as:

FrostFraction = 0

LateGrainfilling has a value between LateGrainFilling and EndGrainFill calculated as:

MaximumFunction = Max(*FrostFraction*, *HighTemp*, *WaterStress*)

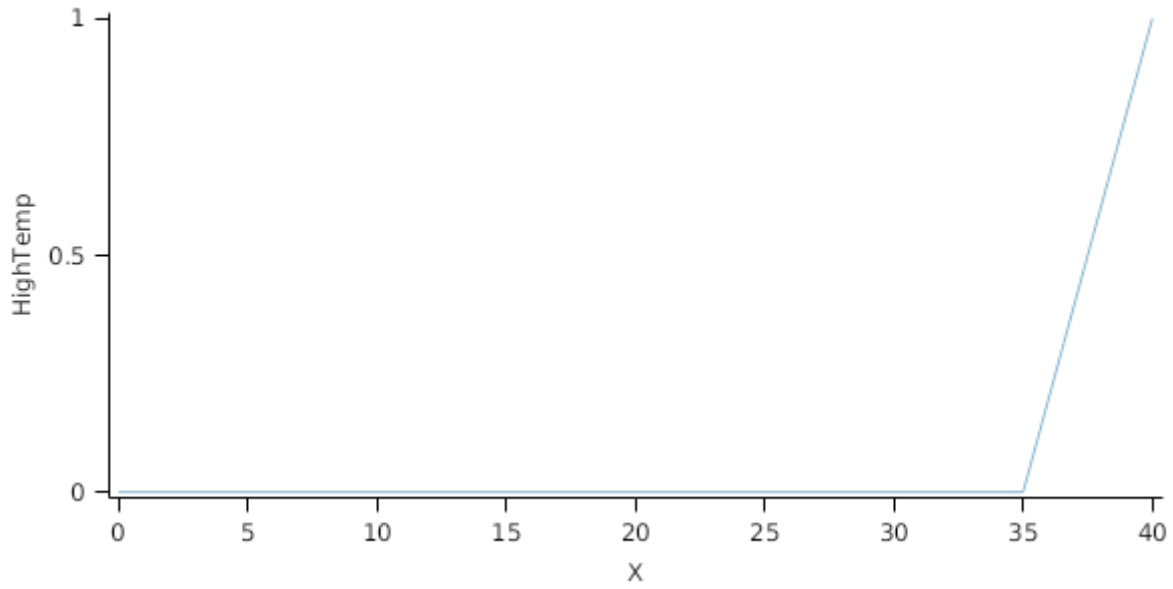
Where:

FrostFraction = 0

HighTemp is calculated using linear interpolation

X	HighTemp
0.0	0.0
35.0	0.0
40.0	1.0

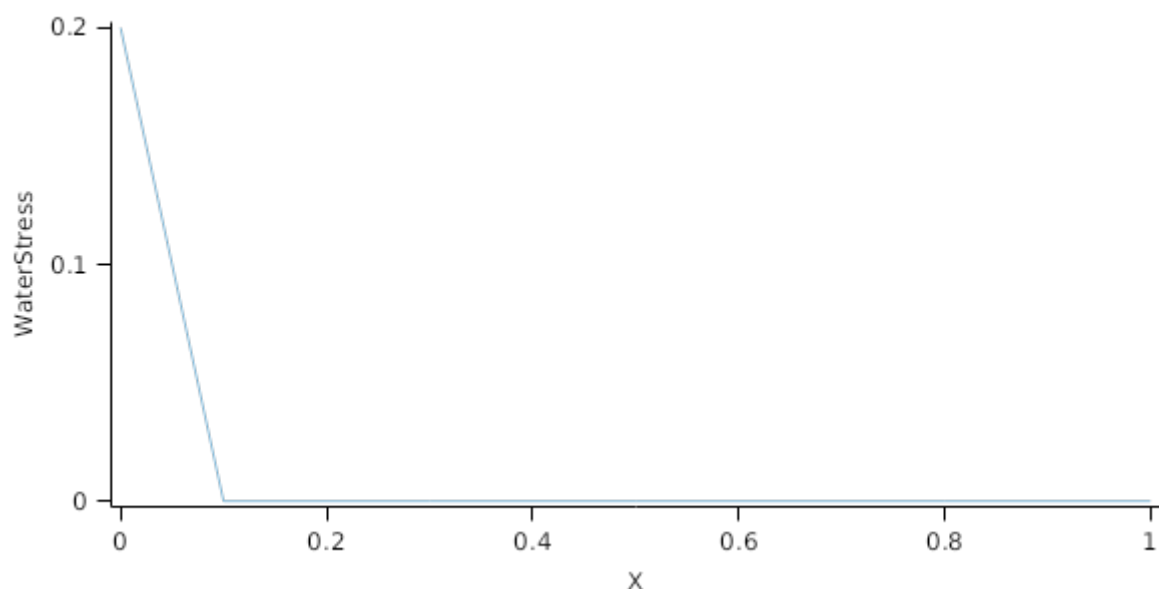
HighTemp



WaterStress is calculated using linear interpolation

X	WaterStress
0.0	0.2
0.1	0.0
0.2	0.0
0.3	0.0
0.5	0.0
0.8	0.0
1.0	0.0

WaterStress



1.7.10 FRGRFunction

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

Where:

$$RUE_FT = [Leaf].Photosynthesis.FT$$

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

Where:

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

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

1.7.11 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	0
Cut	80	0	0	0
Prune	0	0	60	0
Graze	60	0	10	0

1.7.12 DepthFunction

$$DepthFunction = [Leaf].Height$$

1.7.13 StomatalConductanceCO2Modifier

This model calculates the CO₂ impact on stomatal conductance using the approach of [Elli et al., 2020](#).

$$StomatalConductanceCO2Modifier = PhotosynthesisCO2Modifier \times (350 - CP)/(CO_2 - CP)$$

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

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

$$PhotosynthesisCO2Modifier = [Leaf].Photosynthesis.FCO2$$

1.7.14 StructuralFraction

$$StructuralFraction = [Leaf].LeafCohortParameters.StructuralFraction$$

1.7.15 DMDemandPriorityFactors

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

Structural = 1

Metabolic = 1

Storage = 1

1.7.16 NDemandPriorityFactors

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

Structural = 1

Metabolic = 1

Storage = 1

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.

$$Structural = Fraction \times [Stem].PotentialGrowth$$

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

EarlyVegetative has a value between Emergence and StartBudding calculated as:

Fraction = 0.5

FloralInitiation has a value between StartBudding and StartFlowering calculated as:

Fraction = 0.5

Flowering has a value between StartFlowering and EndPodInitiation calculated as:

Fraction = 0.3

EarlyGrainfilling has a value between EndPodInitiation and MidGrainFilling calculated as:

Fraction = 0.2

MidGrainfilling has a value between MidGrainFilling and LateGrainFilling calculated as:

Fraction = 0.1

LateGrainfilling has a value between LateGrainFilling and EndGrainFill calculated as:

Fraction = 0

Metabolic = 0

$Storage = [Stem].PotentialGrowth \times StorageFraction$

$StorageFraction = 1 - [Stem].DMDemands.Structural.Fraction$

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 = 0.007

$CriticalNConc = [Stem].MinimumNConc$

MaximumNConc = 0.02

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

NitrogenDemandSwitch has a value between Emergence and EndGrainFill calculated as:

Constant = 1

1.8.5 Dry Matter Supply

Stem will reallocate 100% of DM that senesces each day.

Stem will retranslocate 50% of non-structural DM each day.

1.8.6 Nitrogen Supply

Stem can reallocate up to 100% of N that senesces each day if required by the plant arbitrator to meet N demands.

Stem can retranslocate up to 50% of non-structural N each day if required by the plant arbitrator to meet N demands.

1.8.7 Senescence and Detachment

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

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

PostCanopyPhase has a value between MidGrainFilling and Maturity calculated as:

$$Rate = \text{Min}(Fraction, One)$$

Where:

$$Fraction = [Phenology].ThermalTime / TTRemaining$$

$$TTRemaining = PostCanopyTT - PostCanopyTTComplete$$

$$PostCanopyTT = [Phenology].MidGrainFilling.Target + [Phenology].LateGrainFilling.Target$$

$$PostCanopyTTComplete = [Phenology].MidGrainFilling.ProgressThroughPhase + [Phenology].LateGrainFilling.ProgressThroughPhase$$

$$One = 1$$

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

1.9 Nodule

This organ simulates the root structure associate with symbiotic N-fixing bacteria. It provides the core functions of determining N fixation supply and related costs. It also calculates the growth, senescence and detachment of nodules.

1.9.1 Dry Matter Demand

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

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

$$Structural = DMDemandFunction \times StructuralFraction$$

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

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

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

Early has a value between Emergence and StartFlowering calculated as:

$$Function = 0$$

Middle has a value between StartFlowering and EndFlowering calculated as:

$$Function = 0$$

Late has a value between EndFlowering and Maturity calculated as:

Function = 0

StructuralFraction = 1 (g/g)

Metabolic = 0

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

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

1.9.2 Nitrogen Demand

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

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

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

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

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

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

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

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

$NitrogenDemandSwitch = [Nodule].nitrogenDemandSwitch$

$MaxNconc = [Nodule].maximumNconc$

MinimumNConc = 0.01

$CriticalNConc = [Nodule].MinimumNConc$

MaximumNConc = 0.02

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

NitrogenDemandSwitch has a value between Emergence and EndGrainFill calculated as:

Constant = 1

1.9.3 Dry Matter Supply

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

Nodule does not retranslocate non-structural DM.

1.9.4 Nitrogen Supply

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

Nodule does not retranslocate non-structural N.

FixationRate = 10000 (g/m²/d)

1.9.5 Senescence and Detachment

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

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

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

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	0	0
Cut	0	0	0	0
Prune	0	0	0	0
Graze	0	0	0	0

1.10 AboveGround

1.10.1 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
- * Grain
- * Shell

1.11 BelowGround

1.11.1 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
- * Nodule

1.12 Total

1.12.1 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
- * Grain
- * Shell
- * Root
- * Nodule

1.13 TotalLive

1.13.1 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
- * Grain
- * Shell
- * Root
- * Nodule

1.14 TotalDead

1.14.1 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
- * Grain
- * Shell
- * Root
- * Nodule

1.15 Pod

1.15.1 Pod

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

Pod summarises the following biomass objects:

- * Shell
- * Grain

1.16 MortalityRate

MortalityRate = 0

1.17 Cultivars

1.17.1 Australian cvv

1.17.1.1 Amethyst

Amethyst overrides the following properties:

1.17.1.2 Almaz

Almaz overrides the following properties:

[Phenology].Emerging.ShootLag = 140

[Phenology].Vegetative.Target.FixedValue = 500

[Phenology].FloralInitiation.Target.FixedValue = 100

[Phenology].Budding.Target.XYPairs.X = 10, 13.17, 17

[Phenology].Budding.Target.XYPairs.Y = 665, 50, 50

1.17.1.3 Boundary

Boundary overrides the following properties:

1.17.1.4 CICA1521

CICA1521 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 600

[Phenology].FloralInitiation.Target.FixedValue = 100

[Phenology].Budding.Target.XYPairs.X = 10, 12.54, 17

[Phenology].Budding.Target.XYPairs.Y = 453, 50, 50

1.17.1.5 Drummond

Drummond overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 600

[Phenology].FloralInitiation.Target.FixedValue = 100

[Phenology].Budding.Target.XYPairs.X = 10, 12.54, 17

[Phenology].Budding.Target.XYPairs.Y = 453, 50, 50

[Phenology].Flowering.Target.FixedValue = 200

[Phenology].PodInitiation.Target.Total.FixedValue = 8

1.17.1.6 Genesis90

Genesis90 overrides the following properties:

[Phenology].Emerging.ShootLag = 140

[Phenology].Vegetative.Target.FixedValue = 600

[Phenology].FloralInitiation.Target.FixedValue = 0

[Phenology].Budding.Target.XYPairs.X = 10, 15.62, 17

[Phenology].Budding.Target.XYPairs.Y = 300, 300, 300

[Phenology].Flowering.Target.FixedValue = 200

[Phenology].PodInitiation.Target.Total.FixedValue = 8

1.17.1.7 HatTrick

HatTrick overrides the following properties:

1.17.1.8 Kalkee

Kalkee overrides the following properties:

[Phenology].Emerging.ShootLag = 140

[Phenology].Vegetative.Target.FixedValue = 600

[Phenology].FloralInitiation.Target.FixedValue = 0

[Phenology].Budding.Target.XYPairs.X = 10, 14.31, 17

[Phenology].Budding.Target.XYPairs.Y = 633, 50, 50

[Phenology].Flowering.Target.FixedValue = 200

1.17.1.9 Kyabra

Kyabra overrides the following properties:

[Phenology].FloralInitiation.Target.FixedValue = 200

[Phenology].Budding.Target.XYPairs.X = 10, 12.51, 17

[Phenology].Budding.Target.XYPairs.Y = 466, 50, 50

[Phenology].Flowering.Target.FixedValue = 250

[Phenology].PodInitiation.Target.Total.FixedValue = 8

1.17.1.10 Monarch

Monarch overrides the following properties:

[Phenology].Emerging.ShootLag = 140

[Phenology].Vegetative.Target.FixedValue = 600

[Phenology].FloralInitiation.Target.FixedValue = 0

[Phenology].Budding.Target.XYPairs.X = 10, 13.45, 17

[Phenology].Budding.Target.XYPairs.Y = 621, 50, 50

[Phenology].Flowering.Target.FixedValue = 200

[Phenology].PodInitiation.Target.Total.FixedValue = 8

1.17.1.11 Pistol

Pistol overrides the following properties:

[Phenology].FloralInitiation.Target.FixedValue = 200

[Phenology].Budding.Target.XYPairs.X = 10, 12.51, 17

[Phenology].Budding.Target.XYPairs.Y = 466, 50, 50

[Phenology].Flowering.Target.FixedValue = 200

1.17.1.12 QuickKabuli

QuickKabuli overrides the following properties:

[Phenology].Emerging.ShootLag = 140

[Phenology].Vegetative.Target.FixedValue = 600

[Phenology].FloralInitiation.Target.FixedValue = 0

[Phenology].Budding.Target.XYPairs.X = 10, 13.45, 17

[Phenology].Budding.Target.XYPairs.Y = 621, 50, 50

[Phenology].Flowering.Target.FixedValue = 150

1.17.1.13 Seamer

Seamer overrides the following properties:

[Phenology].FloralInitiation.Target.FixedValue = 200

[Phenology].Budding.Target.XYPairs.X = 10, 12.51, 17

[Phenology].Budding.Target.XYPairs.Y = 466, 50, 50

[Phenology].Flowering.Target.FixedValue = 200

[Phenology].PodInitiation.Target.Total.FixedValue = 5

1.17.1.14 Slasher

Slasher overrides the following properties:

[Phenology].FloralInitiation.Target.FixedValue = 200

[Phenology].Budding.Target.XYPairs.X = 10, 12.51, 17

[Phenology].Budding.Target.XYPairs.Y = 466, 50, 50

[Phenology].Flowering.Target.FixedValue = 100

[Phenology].PodInitiation.Target.Total.FixedValue = 5

1.17.1.15 SlowDesi

SlowDesi overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 600

[Phenology].FloralInitiation.Target.FixedValue = 100

[Phenology].Budding.Target.XYPairs.X = 10, 12.54, 17

[Phenology].Budding.Target.XYPairs.Y = 453, 50, 50

1.17.1.16 Striker

Striker overrides the following properties:

[Phenology].FloralInitiation.Target.FixedValue = 200

[Phenology].Budding.Target.XYPairs.X = 10, 12.51, 17

[Phenology].Budding.Target.XYPairs.Y = 466, 50, 50

[Phenology].Flowering.Target.FixedValue = 200

[Phenology].PodInitiation.Target.Total.FixedValue = 5

1.17.1.17 Genesis90_archivePPsensitive

Genesis90_archivePPsensitive overrides the following properties:

[Phenology].Emerging.ShootLag = 140

[Phenology].Vegetative.Target.FixedValue = 600

[Phenology].FloralInitiation.Target.FixedValue = 0

[Phenology].Budding.Target.XYPairs.X = 10, 15.62, 17

[Phenology].Budding.Target.XYPairs.Y = 478, 50, 50

[Phenology].Flowering.Target.FixedValue = 200

[Phenology].PodInitiation.Target.Total.FixedValue = 8

1.17.2 ICRISAT cvv

1.17.2.1 JAKI

JAKI overrides the following properties:

[Phenology].Emerging.ShootLag = 140

[Phenology].Vegetative.Target.FixedValue = 550

[Phenology].FloralInitiation.Target.FixedValue = 0

[Phenology].Budding.Target.XYPairs.X = 10, 15.62, 17

[Phenology].Budding.Target.XYPairs.Y = 478, 50, 50

[Phenology].Flowering.Target.FixedValue = 200

[Phenology].PodInitiation.Target.Total.FixedValue = 8

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 9, 19, 23, 30, 38

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 200, 400, 1000, 1000, 400, 0

[Leaf].LeafCohortParameters.MaxArea.Flowering_to_Maturity.MinimumFunction.MaxArea.XYPairs.X = 1, 7, 15

[Leaf].LeafCohortParameters.MaxArea.Flowering_to_Maturity.MinimumFunction.MaxArea.XYPairs.Y = 1000, 400, 10

[Leaf].LeafCohortParameters.SpecificLeafAreaMax.XYPairs.X = 0, 1800

[Leaf].LeafCohortParameters.SpecificLeafAreaMax.XYPairs.Y = 32000, 2000

[Leaf].LeafCohortParameters.SpecificLeafAreaMin.XYPairs.X = 0, 1800

[Leaf].LeafCohortParameters.SpecificLeafAreaMin.XYPairs.Y = 30000, 1000

[Root].KLBiomMod.XYPairs.X = 0, 200, 350, 500, 700

[Root].KLBiomMod.XYPairs.Y = 0.3, 0.8, 1.0, 1.2, 1.4

[Structure].FinalLeafNumber.FixedValue = 26

1.17.2.2 ICCV2

ICCV2 overrides the following properties:

[Phenology].Emerging.ShootLag = 140

[Phenology].FloralInitiation.Target.FixedValue = 100

[Phenology].Budding.Target.XYPairs.X = 10, 12.51, 17

[Phenology].Budding.Target.XYPairs.Y = 466, 50, 50

[Phenology].Flowering.Target.FixedValue = 150

[Phenology].PodInitiation.Target.Total.FixedValue = 5

[Phenology].MidGrainFilling.Target.FixedValue = 350

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 8, 21, 25, 40

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 200, 700, 1000, 200, 100

[Leaf].LeafCohortParameters.MaxArea.Flowering_to_Maturity.MinimumFunction.MaxArea.XYPairs.X = 1, 5, 20

[Leaf].LeafCohortParameters.MaxArea.Flowering_to_Maturity.MinimumFunction.MaxArea.XYPairs.Y = 1000, 200, 100

[Leaf].LeafCohortParameters.SpecificLeafAreaMax.XYPairs.X = 0, 1800

[Leaf].LeafCohortParameters.SpecificLeafAreaMax.XYPairs.Y = 32000, 2000

[Leaf].LeafCohortParameters.SpecificLeafAreaMin.XYPairs.X = 0, 1800

[Leaf].LeafCohortParameters.SpecificLeafAreaMin.XYPairs.Y = 30000, 1000

[Root].KLBiomMod.XYPairs.X = 0, 200, 350, 500, 700

[Root].KLBiomMod.XYPairs.Y = 0.3, 0.8, 1.0, 1.2, 1.4

[Structure].FinalLeafNumber.FixedValue = 24

1.17.2.3 NBeG47

NBeG47 overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 9, 16, 21, 31, 39

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 270, 670, 1250, 1250, 670, 0

[Leaf].LeafCohortParameters.MaxArea.Flowering_to_Maturity.MinimumFunction.MaxArea.XYPairs.X = 1, 11, 19

[Leaf].LeafCohortParameters.MaxArea.Flowering_to_Maturity.MinimumFunction.MaxArea.XYPairs.Y = 1250, 670, 10

[Leaf].ExtinctionCoeff.XYPairs.X = 200, 350, 500, 750, 1000

[Leaf].ExtinctionCoeff.XYPairs.Y = 0.51, 0.49, 0.46, 0.43, 0.35

[Leaf].LeafCohortParameters.SpecificLeafAreaMax.XYPairs.X = 0, 1800

[Leaf].LeafCohortParameters.SpecificLeafAreaMax.XYPairs.Y = 32000, 2000

[Leaf].LeafCohortParameters.SpecificLeafAreaMin.XYPairs.X = 0, 1800

[Leaf].LeafCohortParameters.SpecificLeafAreaMin.XYPairs.Y = 30000, 1000

[Root].KLBiomMod.XYPairs.X = 0, 200, 350, 500, 700

[Root].KLBiomMod.XYPairs.Y = 0.3, 0.8, 1.0, 1.2, 1.4

[Phenology].MidGrainFilling.Target.FixedValue = 350

[Structure].FinalLeafNumber.FixedValue = 30

1.17.2.4 NBeG119

NBeG119 overrides the following properties:

[Phenology].Emerging.ShootLag = 140

[Phenology].FloralInitiation.Target.FixedValue = 100

[Phenology].Budding.Target.XYPairs.X = 10, 12.51, 17

[Phenology].Budding.Target.XYPairs.Y = 466, 50, 50

[Phenology].Flowering.Target.FixedValue = 150

[Phenology].PodInitiation.Target.Total.FixedValue = 5

[Phenology].MidGrainFilling.Target.FixedValue = 350

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 10, 22, 30, 40

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 200, 900, 900, 300, 100

[Leaf].LeafCohortParameters.MaxArea.Flowering_to_Maturity.MinimumFunction.MaxArea.XYPairs.X = 1, 8, 18

[Leaf].LeafCohortParameters.MaxArea.Flowering_to_Maturity.MinimumFunction.MaxArea.XYPairs.Y = 900, 300, 100

[Leaf].ExtinctionCoeff.XYPairs.X = 200, 350, 500, 750, 1000

[Leaf].ExtinctionCoeff.XYPairs.Y = 0.76, 0.74, 0.71, 0.60, 0.51

[Leaf].LeafCohortParameters.SpecificLeafAreaMax.XYPairs.X = 0, 1800

[Leaf].LeafCohortParameters.SpecificLeafAreaMax.XYPairs.Y = 32000, 2000

[Leaf].LeafCohortParameters.SpecificLeafAreaMin.XYPairs.X = 0, 1800

[Leaf].LeafCohortParameters.SpecificLeafAreaMin.XYPairs.Y = 30000, 1000

[Root].KLBiomMod.XYPairs.X = 0, 200, 350, 500, 700

[Root].KLBiomMod.XYPairs.Y = 0.3, 0.8, 1.0, 1.2, 1.4

[Structure].FinalLeafNumber.FixedValue = 28

1.17.3 Other cvv

1.17.3.1 Anwar

Anwar overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 490

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.17.3.2 Ayaz

Ayaz overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 550

1.17.3.3 Hashem

Hashem overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 610

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.3

1.18 Archived Cultivars

1.18.1 99_73C

99_73C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 440

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.2 99_66C

99_66C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 410

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.3 99_34C

99_34C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 420

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.4 98_79C

98_79C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 410

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.5 98_55C

98_55C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 410

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.6 98_16C

98_16C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 430

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10

1.18.7 98_107C

98_107C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 410

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.8 98_106C

98_106C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 400

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.9 97_219C

97_219C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 430

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.10 97_120C

97_120C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 400

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.11 97_118C

97_118C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 420

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.12 97_116C

97_116C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 405

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.13 02_35C

02_35C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 505

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.14 02_30C

02_30C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 400

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.15 02_23C

02_23C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 400

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 11

1.18.16 02_10C

02_10C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 500

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.17 02_03C

02_03C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 500

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.18 01_7C

01_7C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 485

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.19 01_61C

01_61C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 500

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.20 01_36C

01_36C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 600

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10

1.18.21 00_40C

00_40C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 430

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10

1.18.22 00_21C

00_21C overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 500

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.23 Ghab4

Ghab4 overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 500

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.24 Ghab5

Ghab5 overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 500

[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

1.18.25 Ghab3

Ghab3 overrides the following properties:

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.X = 1, 5, 10, 21

[Leaf].LeafCohortParameters.MaxArea.Vegetative_to_Flowering.MaxArea.XYPairs.Y = 224, 224, 489, 1080

[Phenology].Vegetative.Target.FixedValue = 510

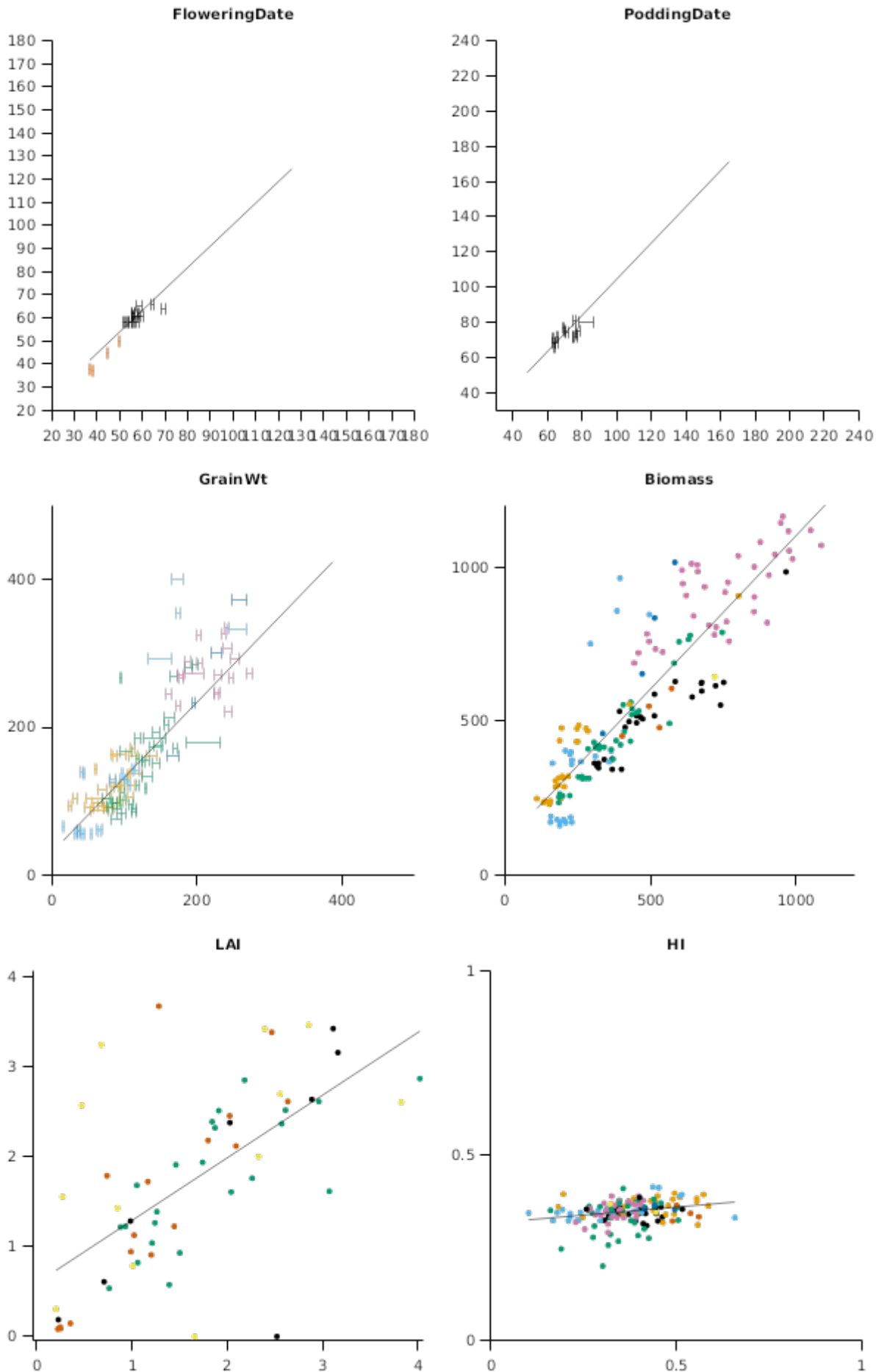
[Phenology].Vegetative.Progression.PhotoperiodModifier.CriticalPhotoperiod = 10.5

2 Validation



2.1 Combined Results

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



2.2 2019_PulseAdaptation

Data from the one year GRDC funded 'Pulse Adaptation' project led by Allan Peake, CSIRO team members included Fernanda Dreccer, Jeremy Whish, Tony Swan.

Refer to project final report Peake et al (2020): <https://doi.org/10.25919/5f1f2438cd4e4>

List of experiments.

Experiment Name	Design (Number of Treatments)
Emerald19_	TOS x Cv (27)
Mildura19_	TOS x Cv (27)
Walgett19_	TOS x Cv x Pop (36)
Greenethorpe_2019_	TOS x Cv x Irr (36)
GreenethorpePhen19_	TOS x Cv (20)
GT_HatTrick_WU_2019_	TOS (6)
Narrabri19_	TOS x Cv x Irr (36)

2.2.1 Emerald19_

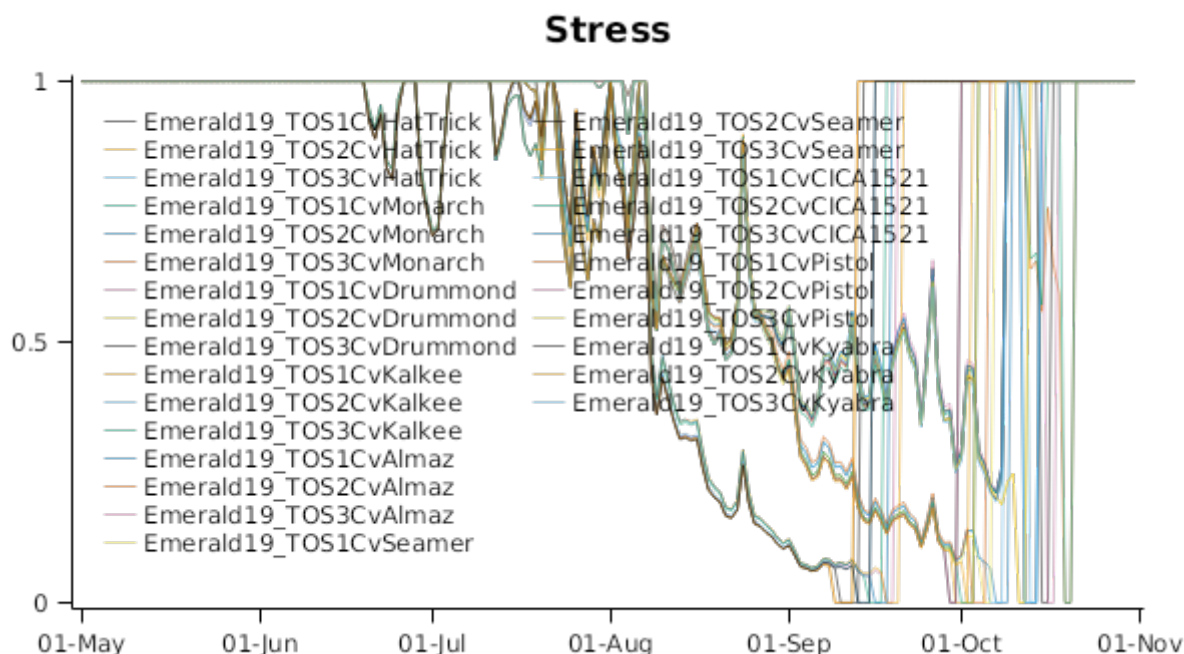
The experiment investigated chickpea for three times of sowing for nine cultivars at Emerald, Queensland, Australia. The soil was a light textured vertosol. Emerald Site run by DAFQ, site leader was Doug Sands, assisted by Peter Agius. Definitely no irrigation applied after 14th May, all trials were dryland. Measurements were undertaken for biomass accumulation during the crop, and grain yield at crop maturity.

May 10 chickpeas emerged about 19/5

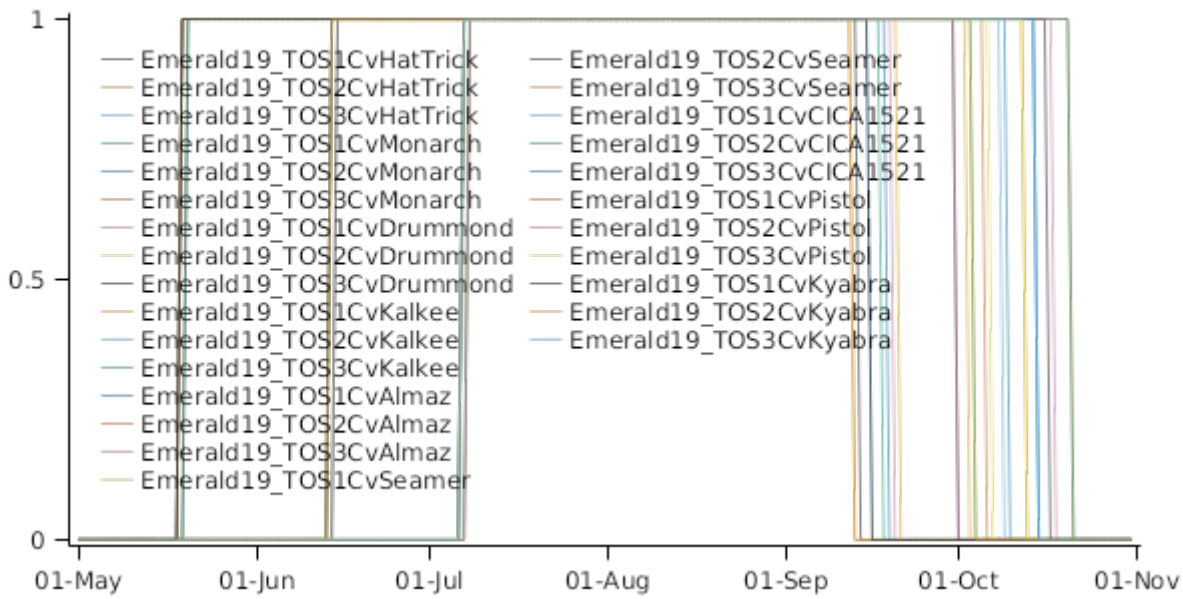
June 3 chickpeas emerged about 15/6

June 27 chickpeas emerged 9-10/7

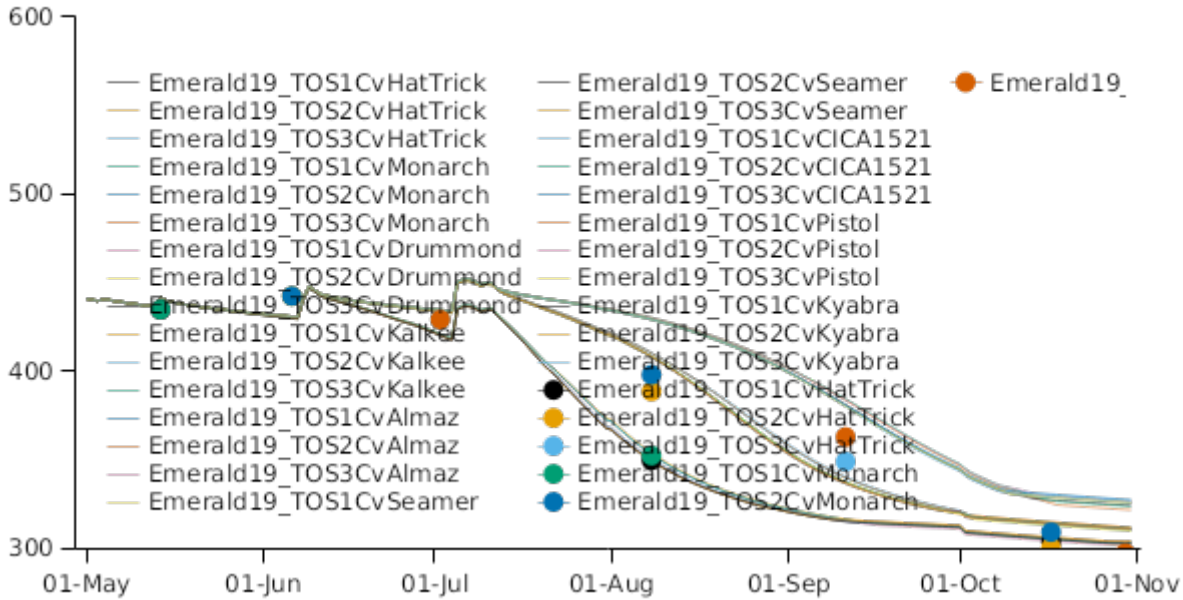
Note: soil monitoring was only as deep as 120cm. A small amount of water in the 120-150cm layer may have been available to the crop that might improve simulation of TOS1 which slightly underpredicted biomass and yield of some cultivars.



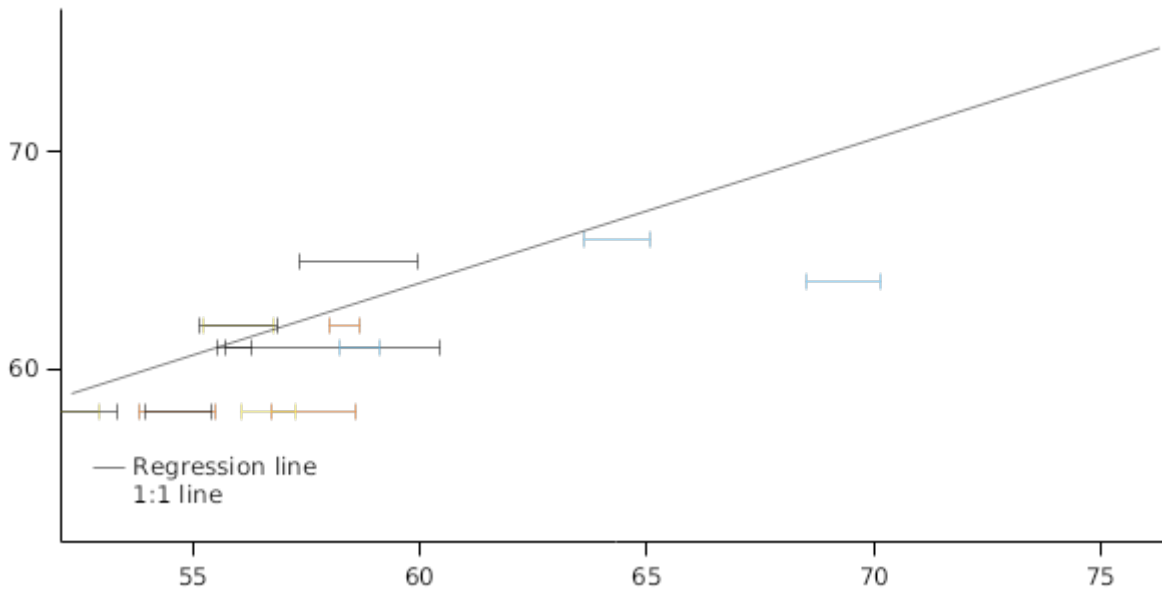
NStress



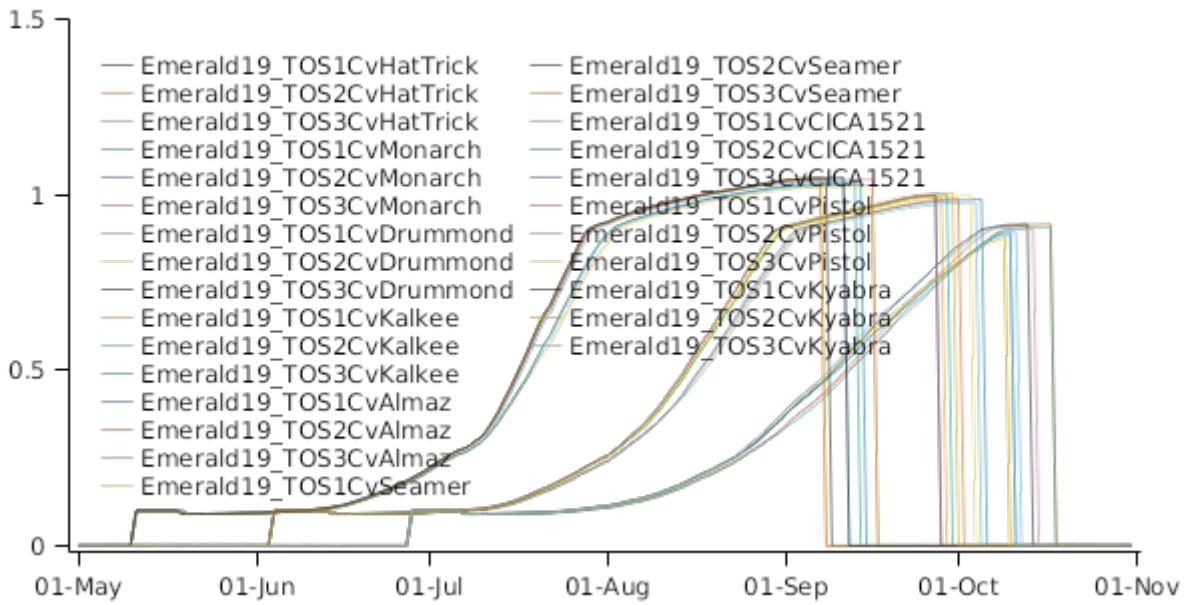
ProfileWater_5layers



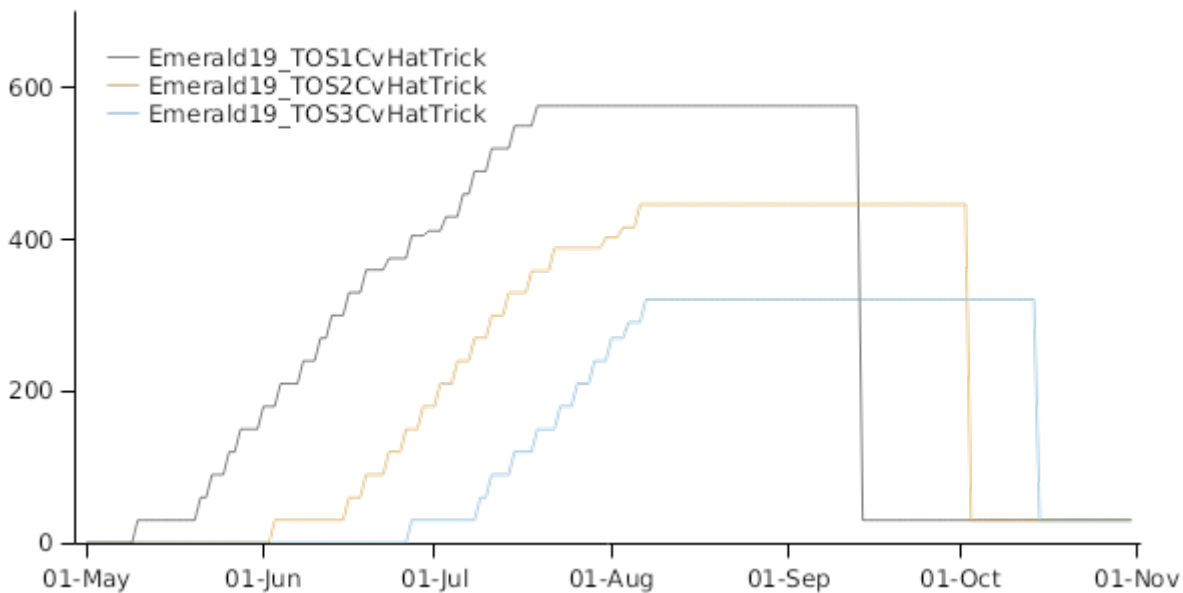
FloweringDate



klreport



Branches_vs_time



2.2.2 Mildura19_

Trial conducted by Michael Moodie (Frontier Farming Systems) on behalf of pulse adaptaton project led by Allan Peake. Soil = red kandosol

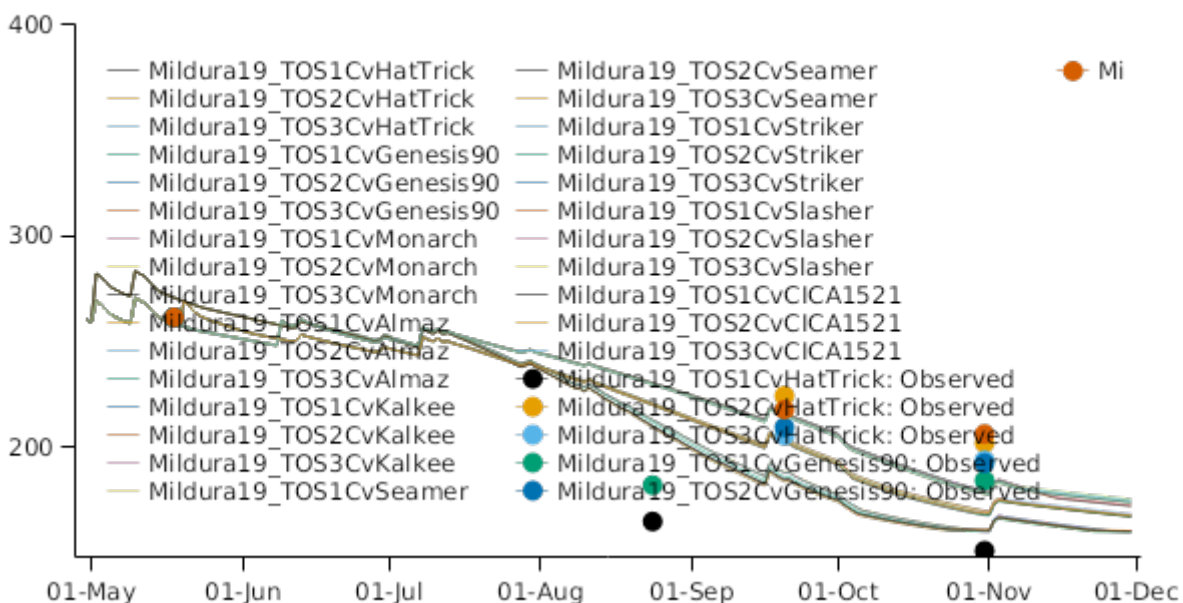
Time of sowing x cultivar trial

Emergence observed approx 11 days after sowing for lentils, 14 days for Desi chickpea and 16 days Kabuli chickpea. Sowing depth 6cm.

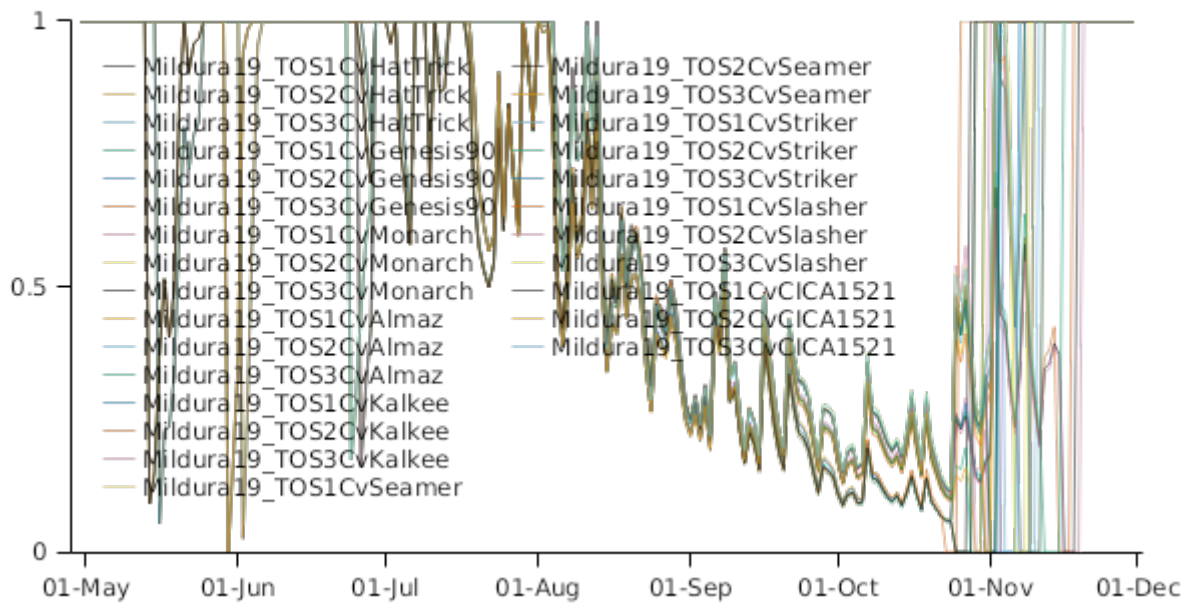
Trickle tape on the row was used to irrigated each sowing, so the irrigation was not evenly distributed. This concentration of water on the seed zone probably led to different growth patterns in the crop and makes the experiment more difficult to simulate.

Simulating way too much biomass. Possible or even likely that there are issues with the way APSIM simulates potential ET in an arid environment such as Mildura. Also possible that we need a dynamic CLL - later times of sowing don't extract as much water. Or it may be possible that biomass samples at maturity were collected too late and much of the leaf was on the ground.

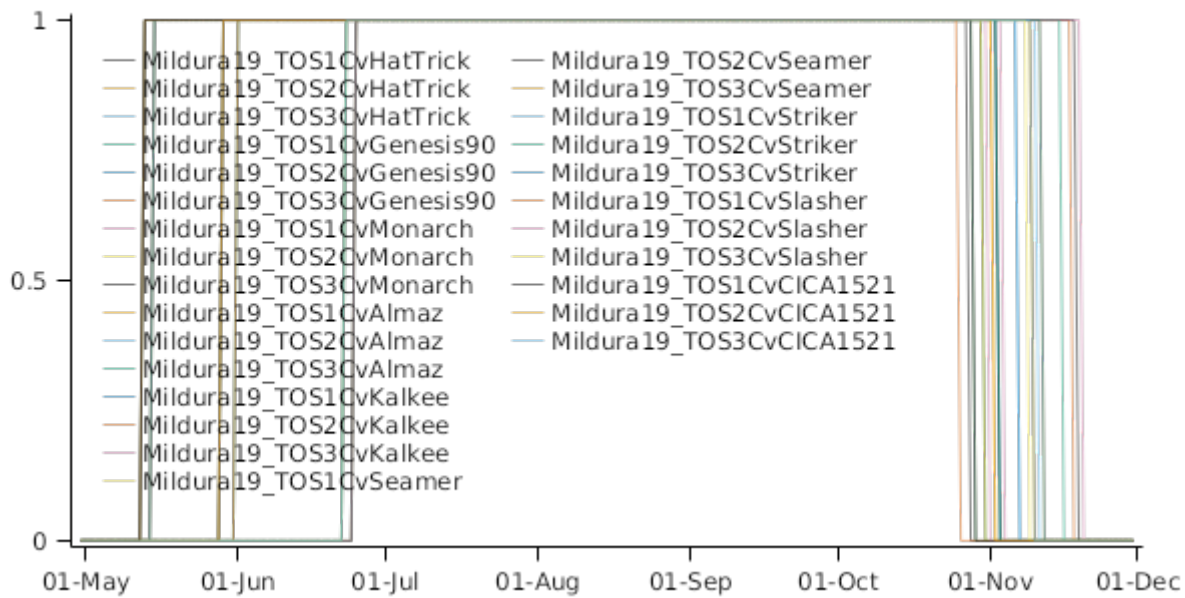
ProfileWater



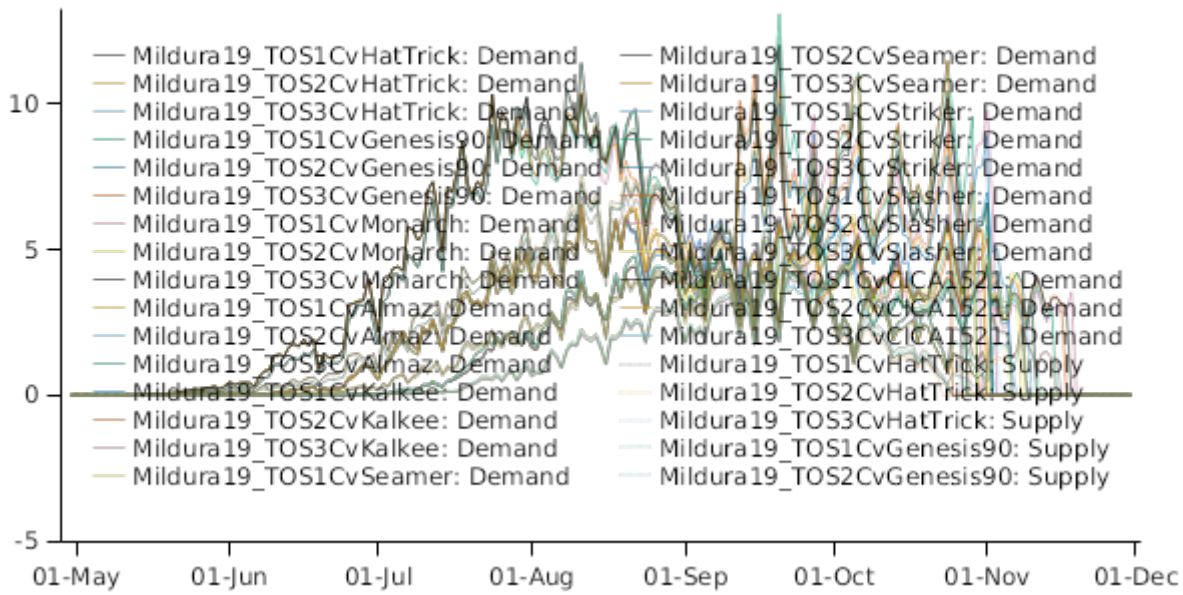
Stress



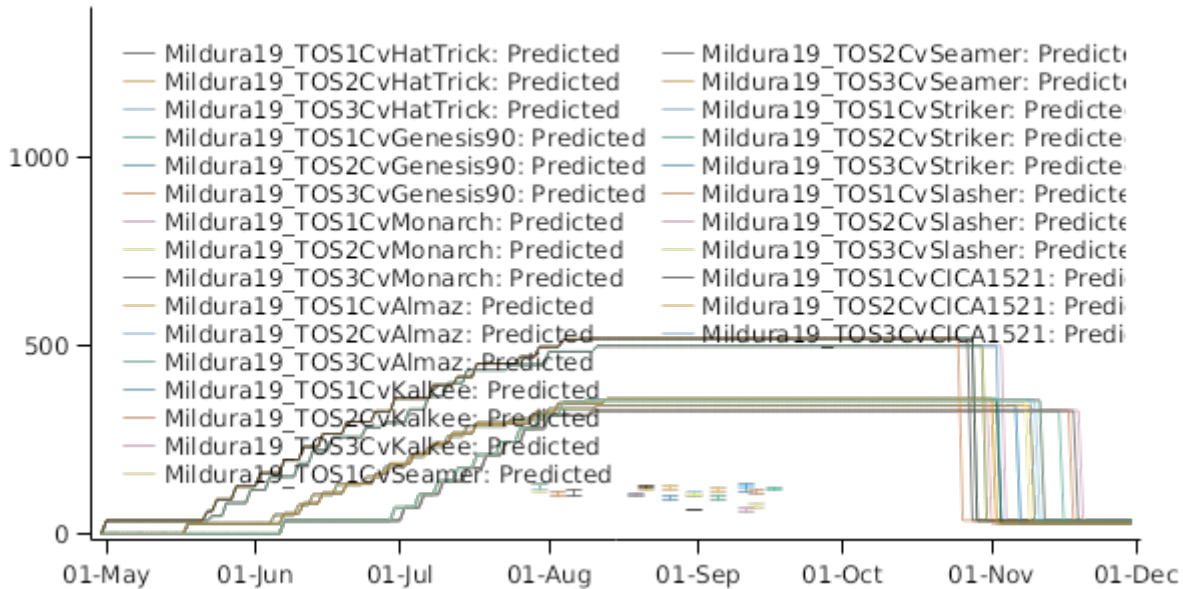
NStress



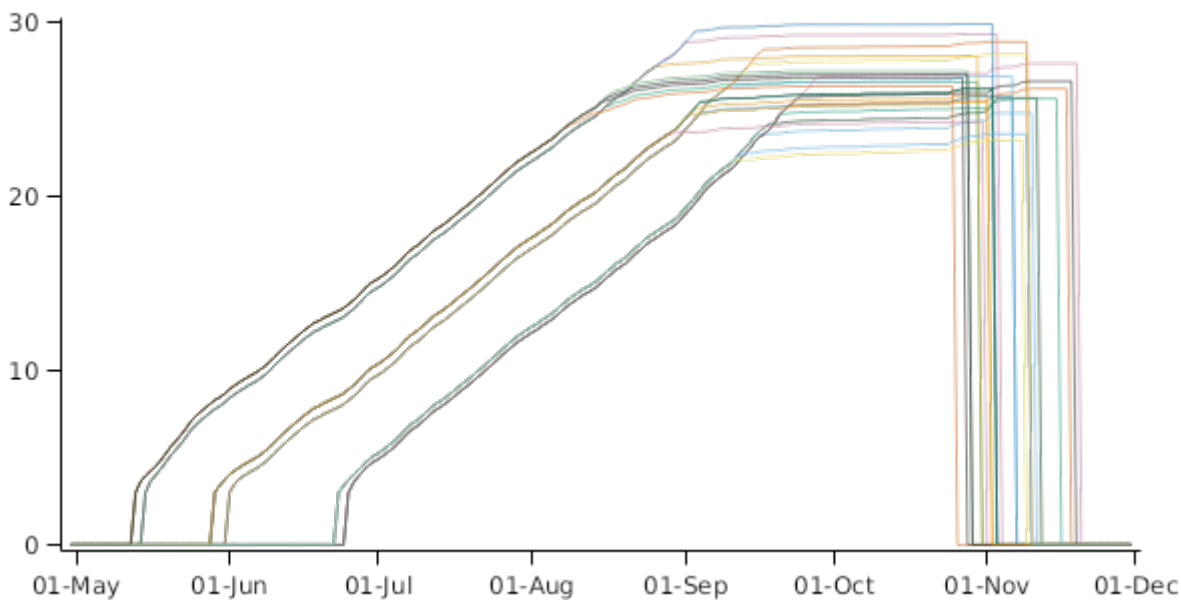
DMSupplyDemand



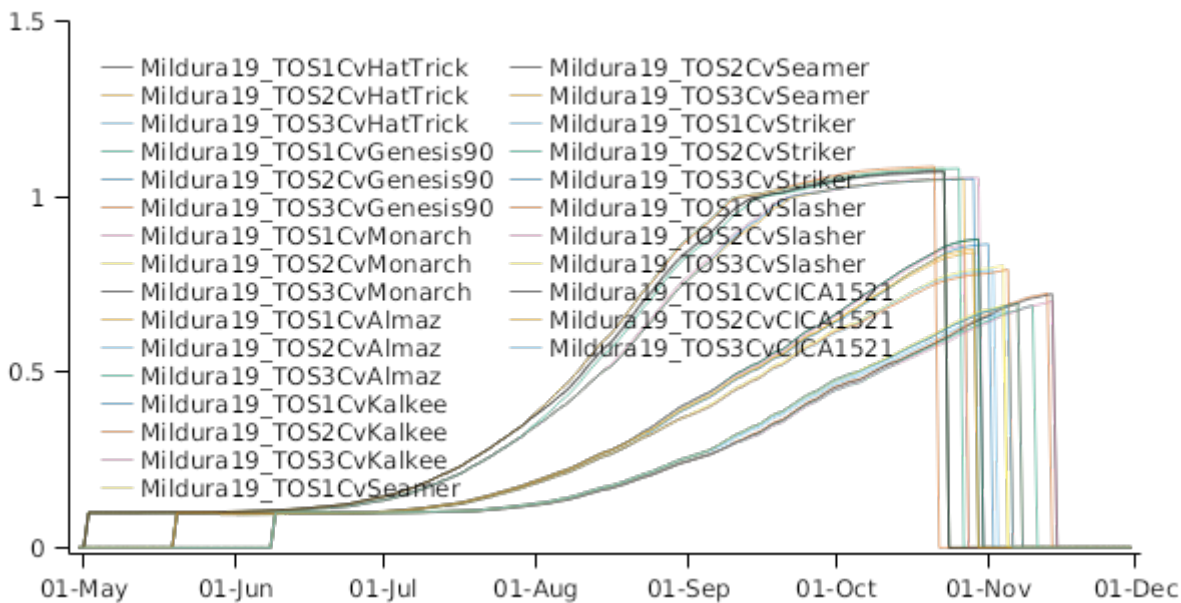
EarlyBranches



MSLeafNo



klreport



2.2.3 Walgett19_

Experiment conducted by AMPS research on behalf of Pulse Adaptation project. Soil = unusual, area of lighter loamy soil, not a kandosol but not a vertosol. Perhaps an extremely light textured vertosol. Retains water very well and yields well in a dry season, stores water deeper than a typical vertosol and loses less to evaporation as a result. Lower yield potential in a good season.

Time of sowing x cultivar experiment. Second TOS was lost for chickpea, seed uprooted overnight by wild pigs.

Plant population - initial population averaged at 23 plants/m²; used 30 plants/m² for the high population treatments.

Met file for Walgett - trial site located at -30.538537,148.614925 near Come By Chance. Several options in SILO:

* Bungle Gully, Come by Chance is approx 5 km from site

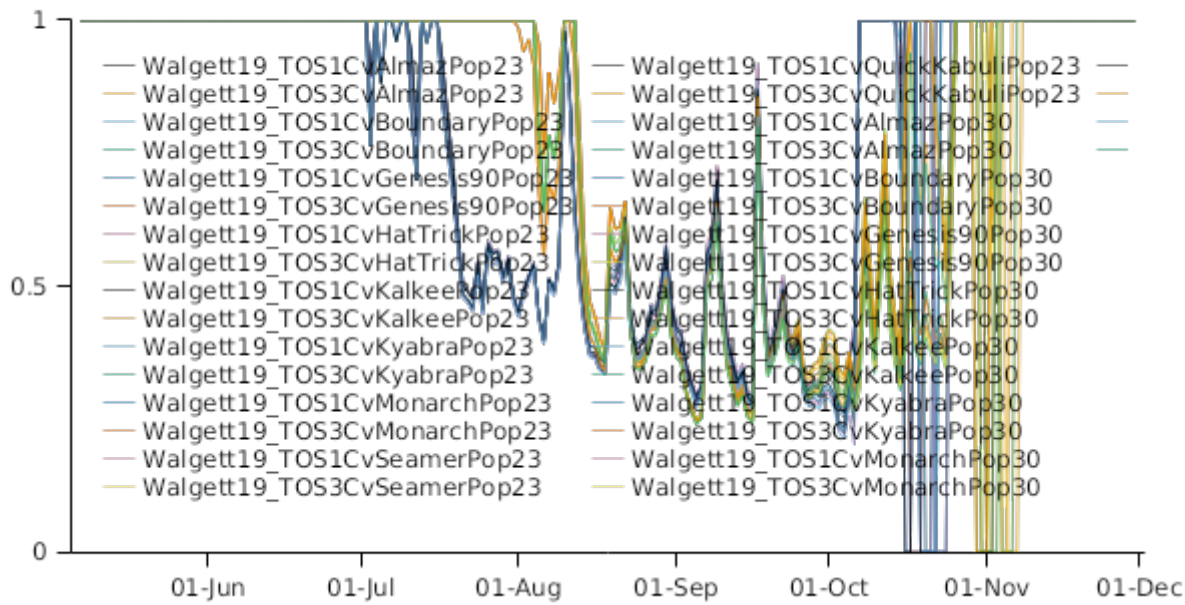
* Come by Chance store is approx 20 km from site

* Grid -30.55,148.60 is approx 2 km from site --> this met file was selected as is the closest. Combined with TTag data from site

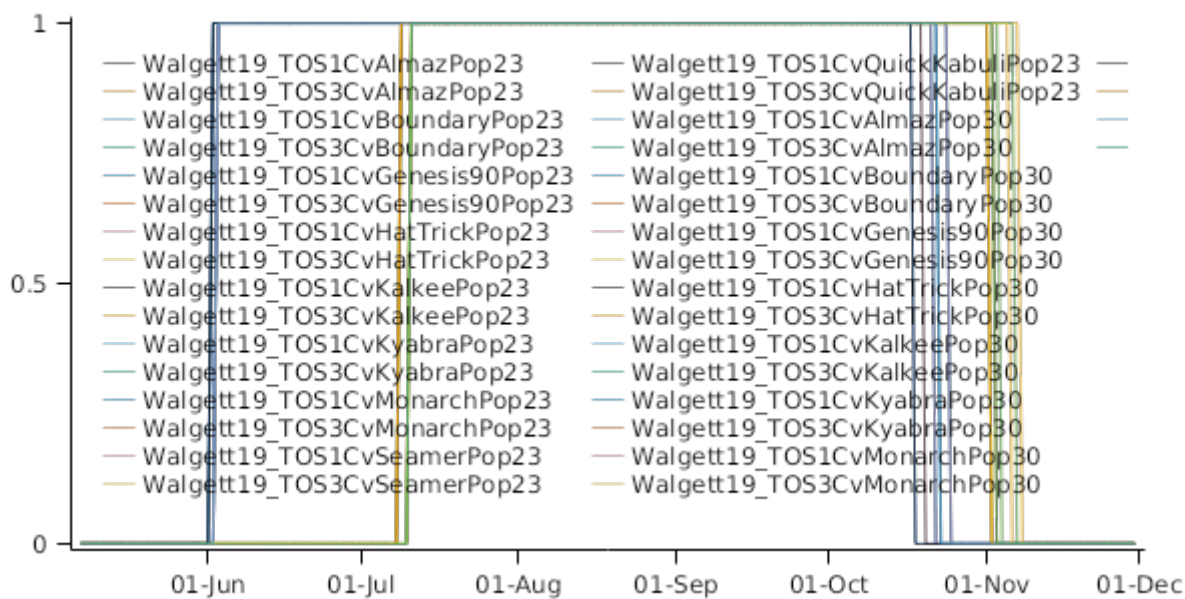
A difficult site to simulate. Felt that the 1st 2 biomass cuts may have been taken on 1/2 the stated area (which would explain why obs=2xpredicted). However trial cooperater is adamant that cut areas were correct, and says he felt the crop growth pattern was unusual, with extremely rapid growth after emergence. Possibly could have been a residual herbicide effect stimulating unusual plant hormone responses. Also potential for nutrient deficiency as we still ended up over-

simulating yield from TOS1 by a factor of 1.5 to 2, whereas TOS 2 was simulated accurately for yield when biomass was lower (i.e. less likely to experience nutrient deficiency). Field possibly short on K (but soil was unfortunately not tested for K).

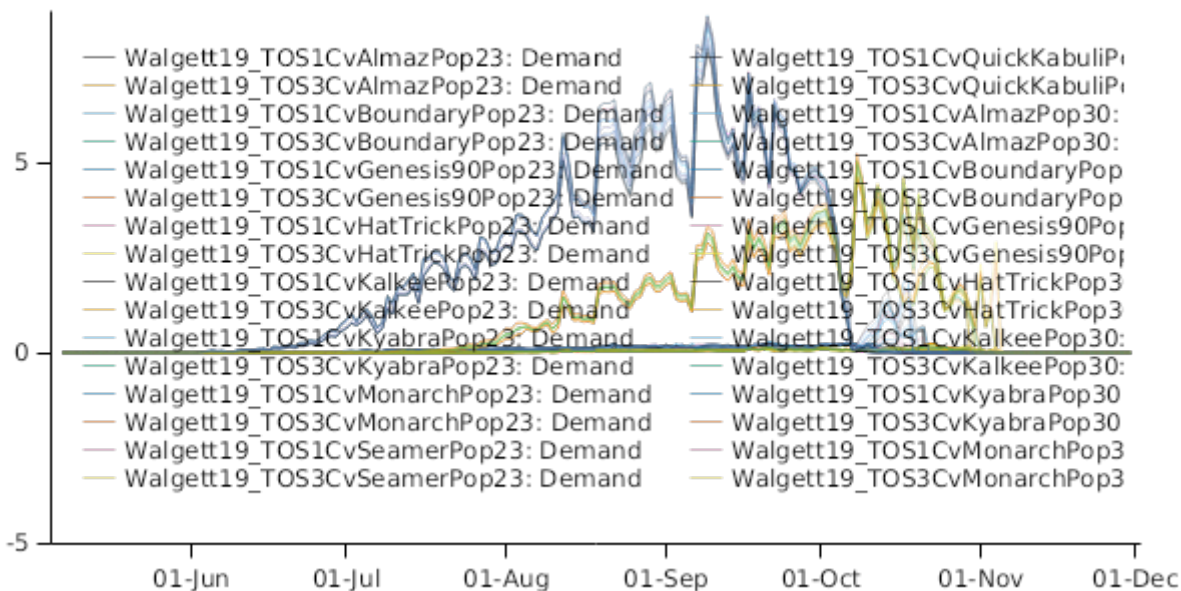
Stress



NStress



DMSupplyDemand



2.2.3.1 ProfileWater_Genesis90Only

Soil water measured only in HatTrick for Desi and Genesis90 for Kabuli Chickpeas.

2.2.3.2 ProfileWater_HatTrickOnly

Soil water measured only in HatTrick for Desi and Genesis90 for Kabuli Chickpeas.

2.2.4 Greenethorpe_2019_

Greenethorpe main trial 2019, Pulse Adaptation project. Irrigated and rainfed treatments, 2-3 cultivars per species (Desi/Kabuli/Lentils). Split plot design. Soil = red-brown earth.

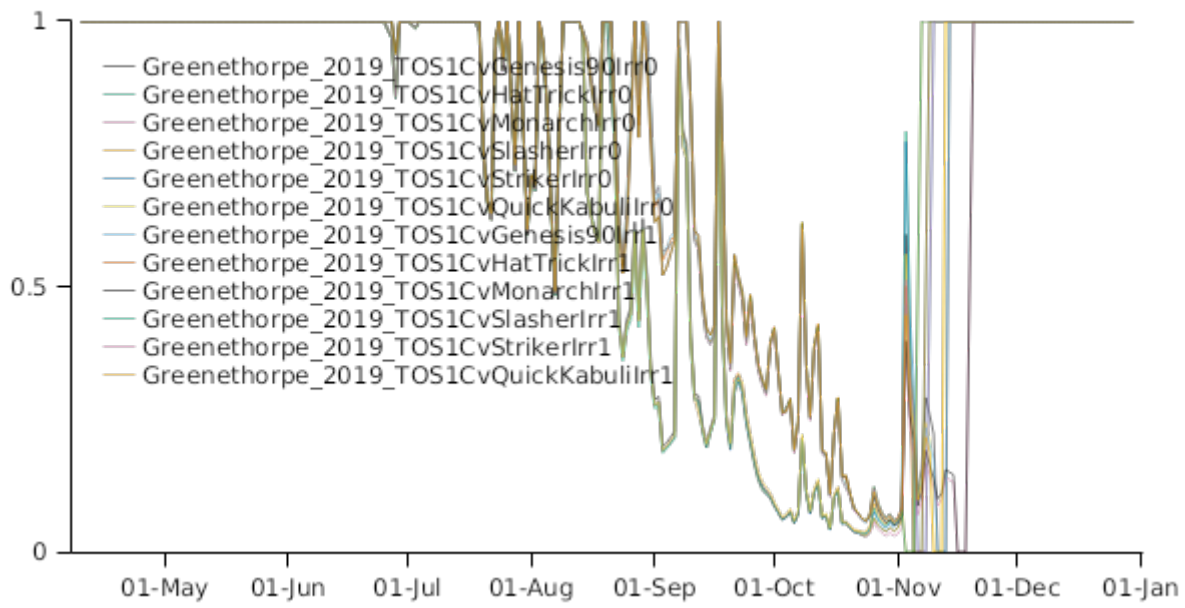
Irrigation system was a little uneven but was the best we could do with little preparation time (individual sprinklers along a long hand-shift hose line), but plant cuts were taken from mostly uniform areas.

Planting density information by TOS was available. It differed broadly by TOS and so average density for TOS used for all cvv.

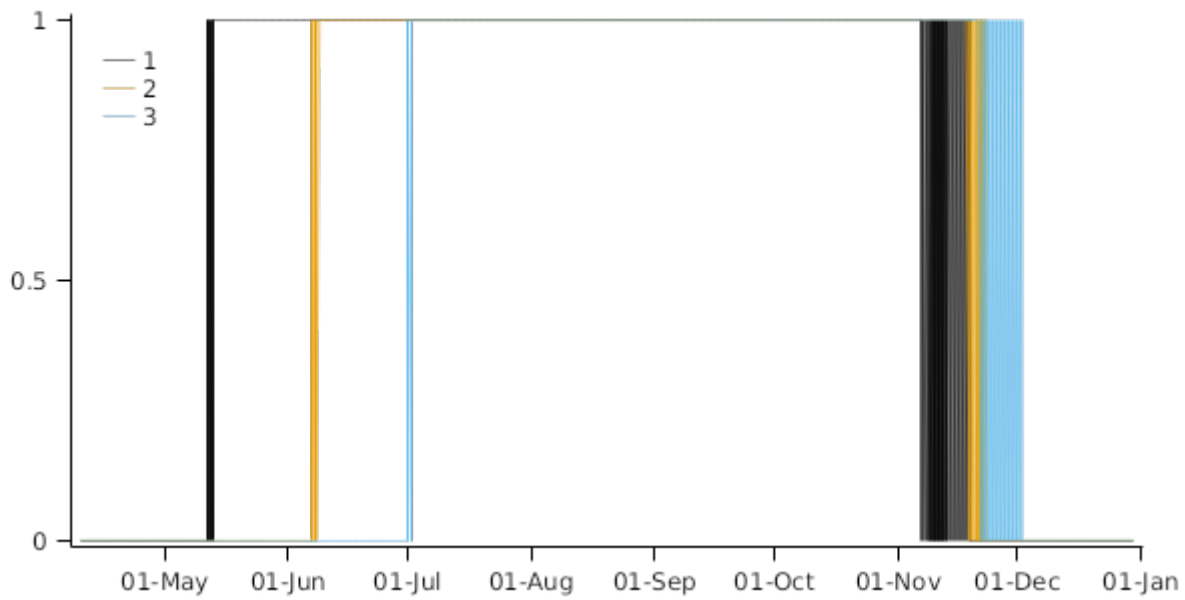
Initial SW across site is quite variable - questioned whether appropriate to model as factorial. Variability probably due to micro-environment variations at specific location for soil cores, so factorial design was retained. Would have been substantial variation in soil type up and down the steep slope. NMM calibration was from Farming systems site 5-6km away so not sure how trustworthy that data is.

Met file - based on SILO but used local TTag at trial for max/minT, because trial is at a different point in the landscape (north slope) to the SILO station (east slope)

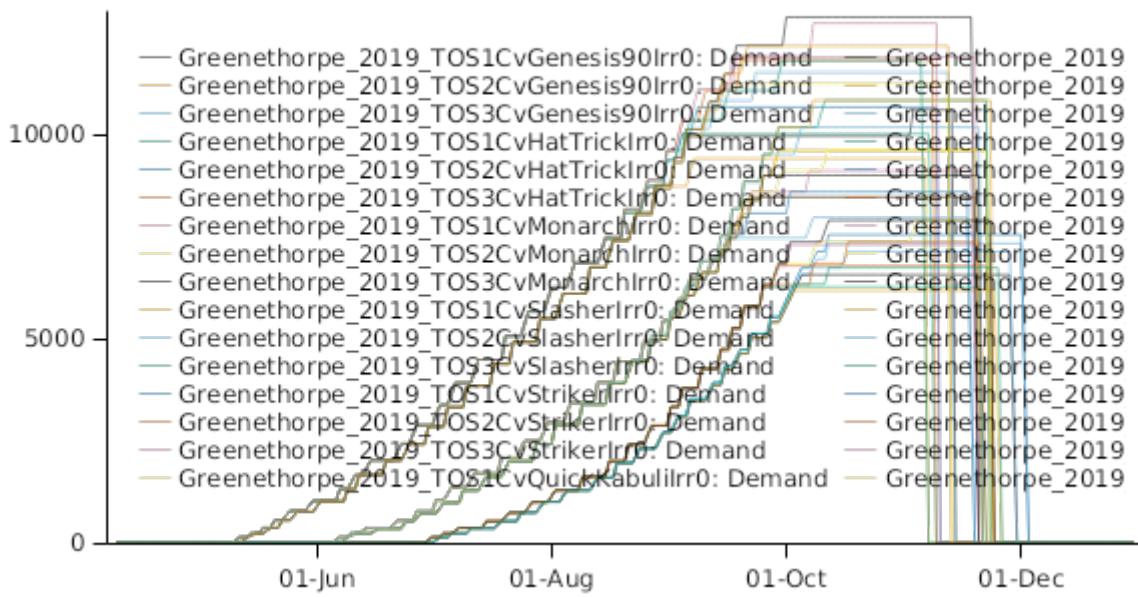
Stress



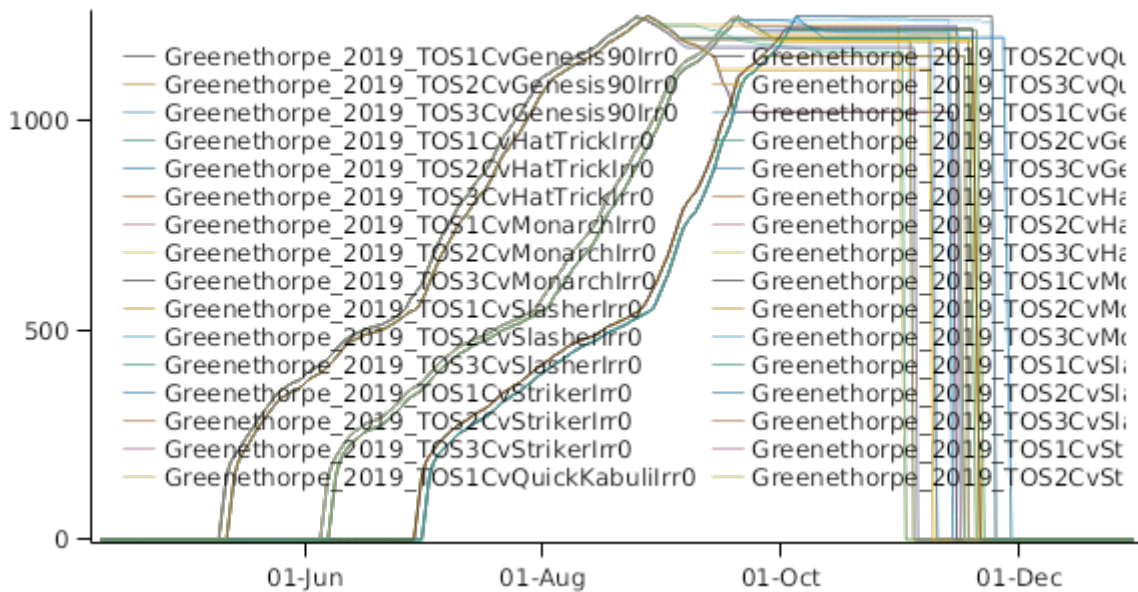
NStress



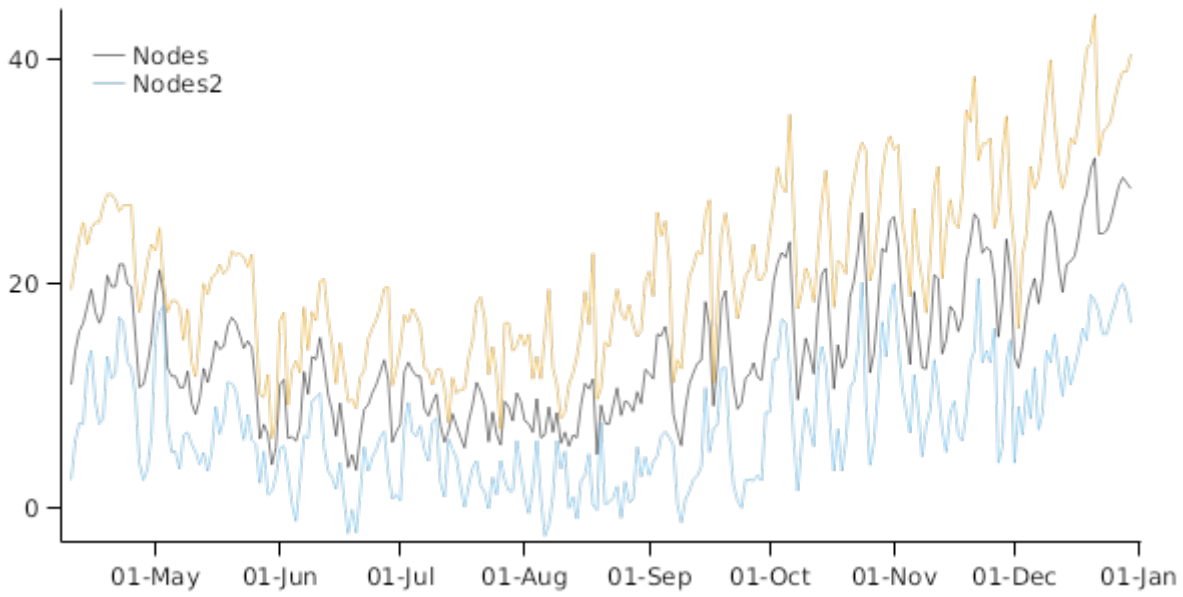
DMSupplyDemand



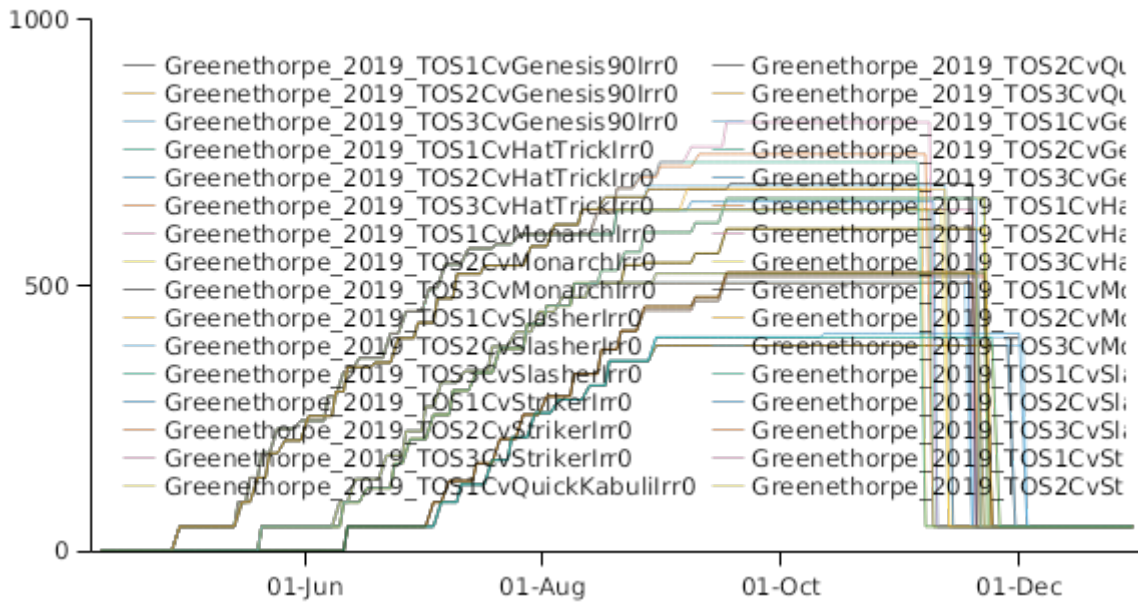
DMDemands



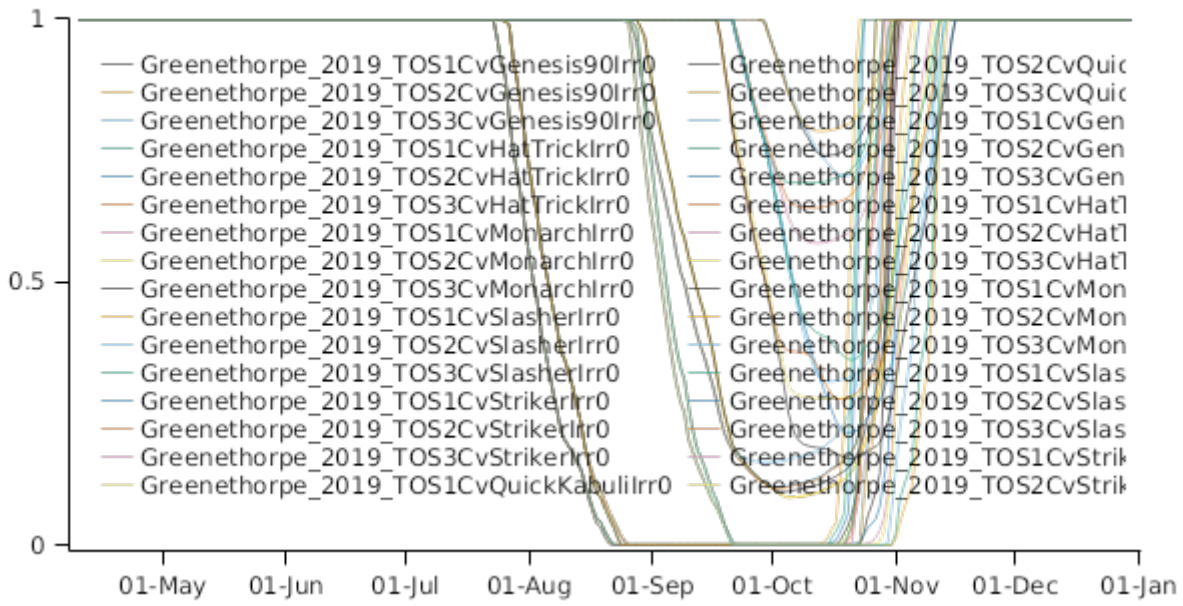
MeanT



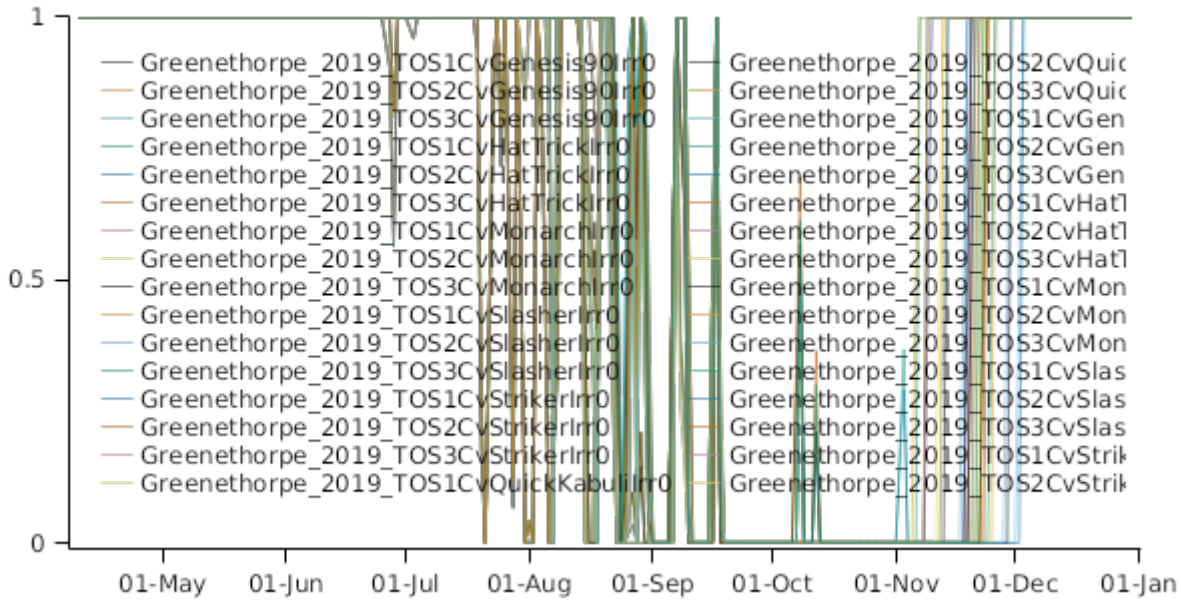
Branches_vs_time



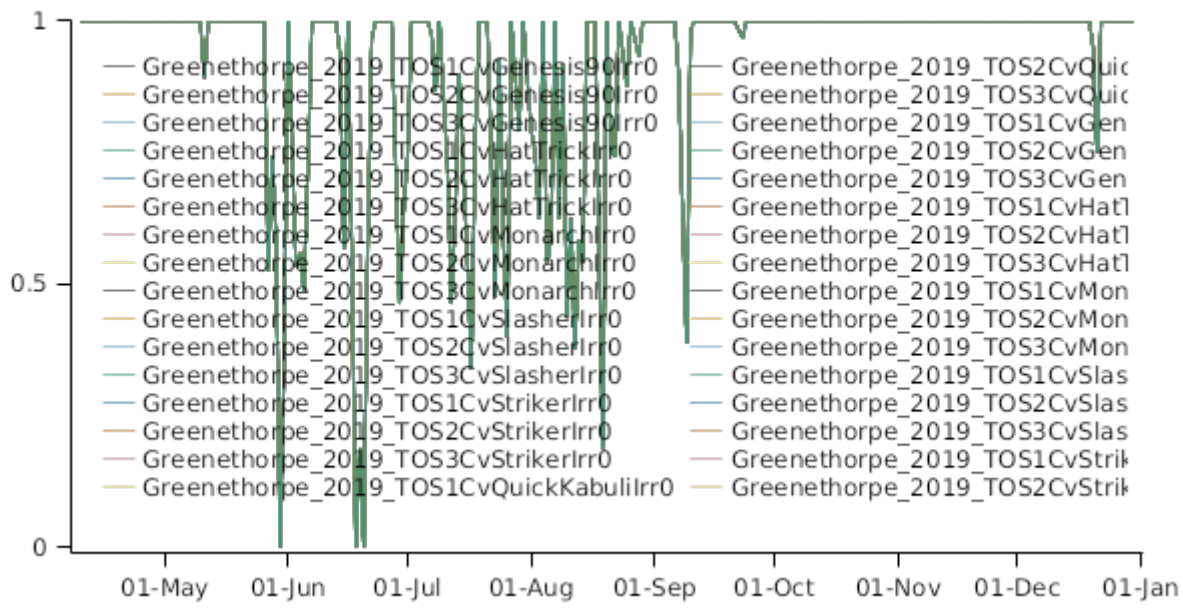
Fbranch



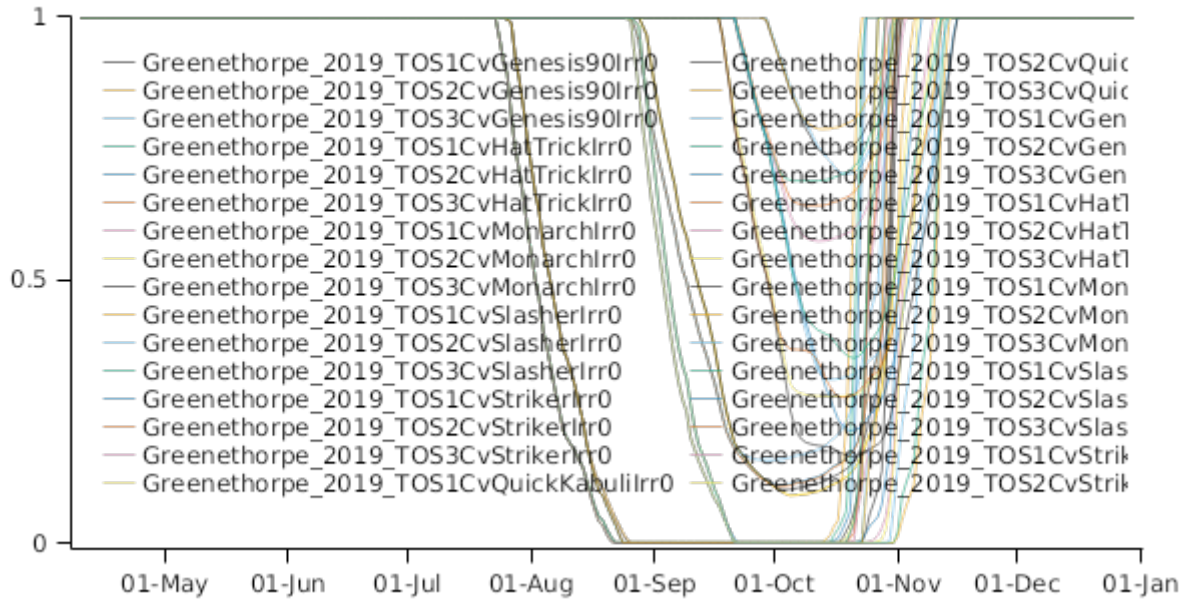
Fbranch1



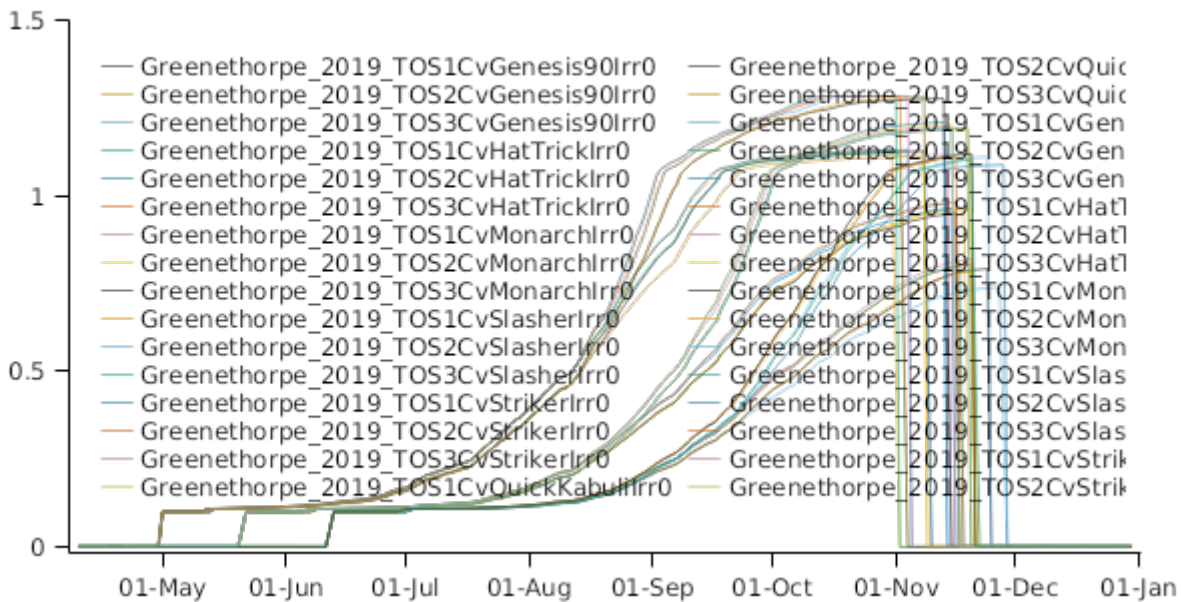
Fibranch11



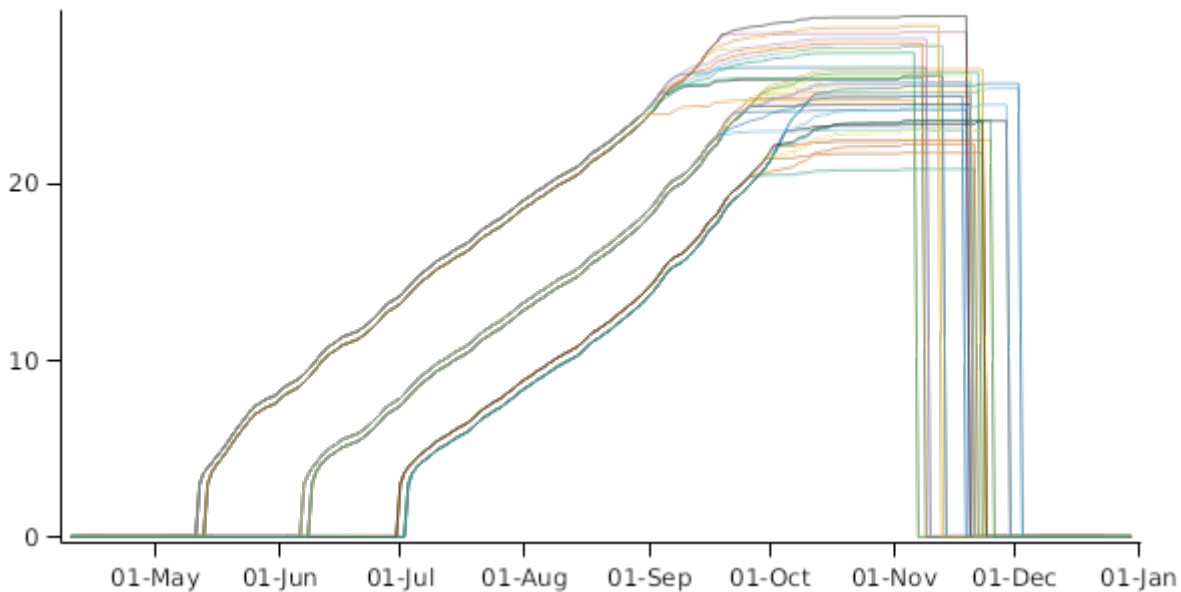
EarlyVEGbranch2



klreport



MSLeafNo



2.2.5 GreenethorpePhen19_

Greenethorpe phenology trial: sown as small 2m single row observation plots. Conducted at site 5-6km north of landra Castle farming systems site.

Trial was sown by hand, so sowing depth was variable and not recorded, establishment date also variable for the same reason. The important data for this trial is the rate of leaf appearance rather than the actual leaf number which is only simulated correctly where observed emergence date matches the simulation.

Some herbicide damage was observed on early sown plots and may have affected some data.

Experiment was situated at the bottom NW corner of the main trial, so temperature would not have been the same as the bulk of plots in the main trial (due to substantial slope). Experiment was on a north facing slope.

* all treatments are irrigated - "JW: For greenethorpe simulate unlimited. We tried to keep it unlimited but there would have been some stress no measure of water just applied when ever we were out there."

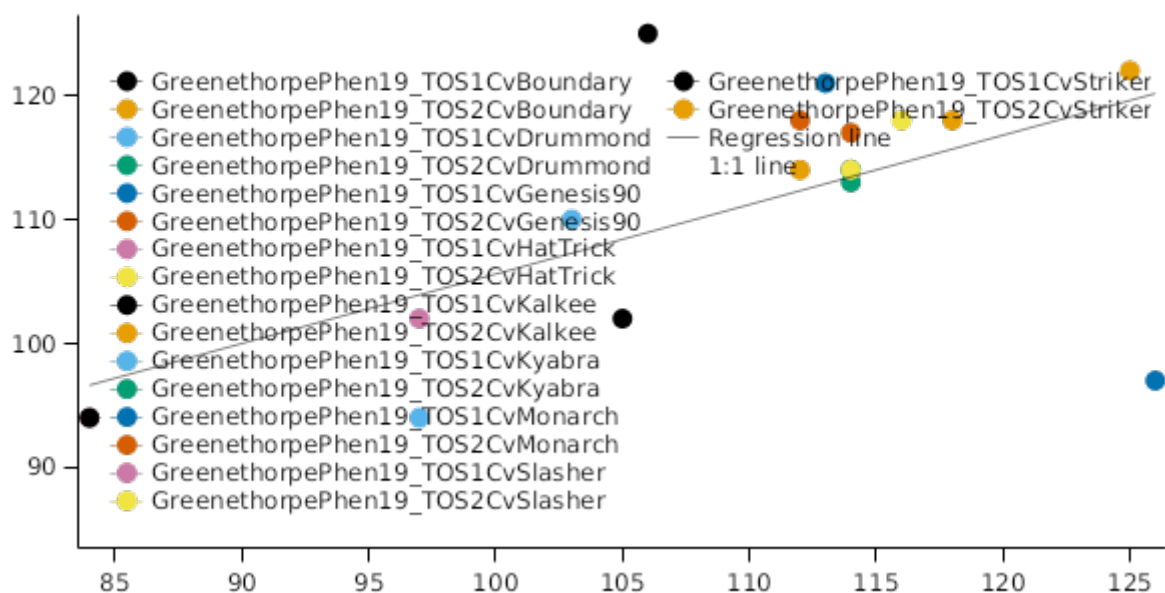
* this experiment used different sowing dates to the other Greenethorpe trial so is simulated separately

* there are only 2 sowing dates

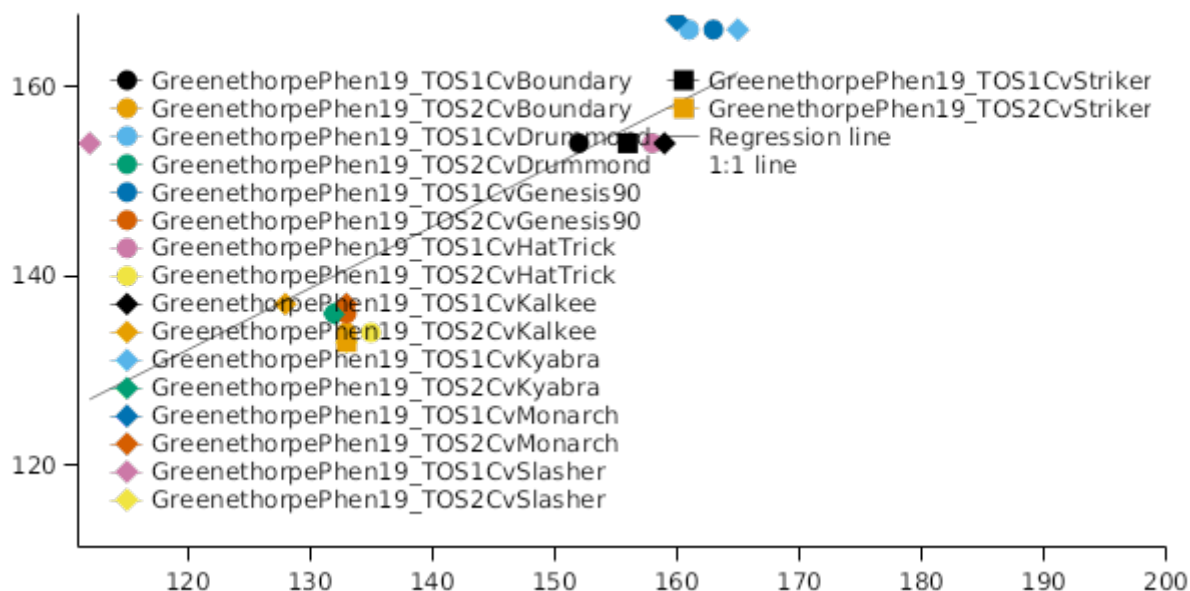
* only treatments without lights used (there were some artificially lit experiments at Gatton)

* phenology measurements are recorded only up until the time of flowering

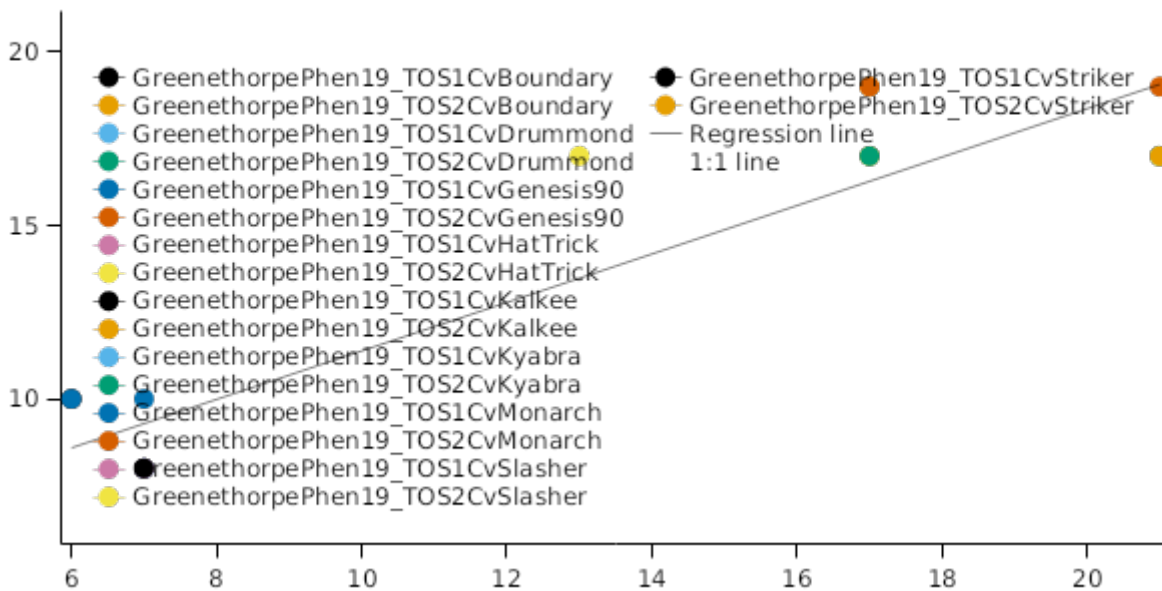
FloweringDAS



PoddingDate



EmergenceDAS



2.2.6 GT_HatTrick_WU_2019_

Greenethorpe main trial 2019, Pulse Adaptation project. Irrigated and rainfed treatments, 2-3 cultivars per species (Desi/Kabuli/Lentils). Split plot design. Soil = red-brown earth.

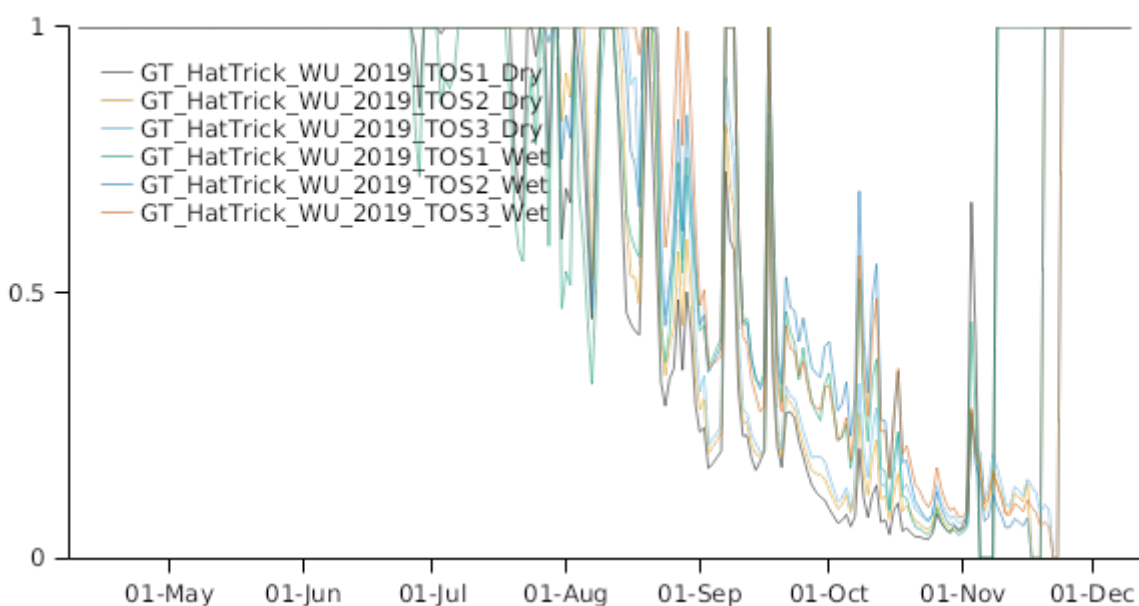
Irrigation system was a little uneven but was the best we could do with little preparation time (individual sprinklers along a long hand-shift hose line), but plant cuts were taken from mostly uniform areas.

**Water use was modelled separately to main trial so we could use individual SW data for each cultivar and treatment, hoping to get most accurate observed data by looking at individual NMM sites.

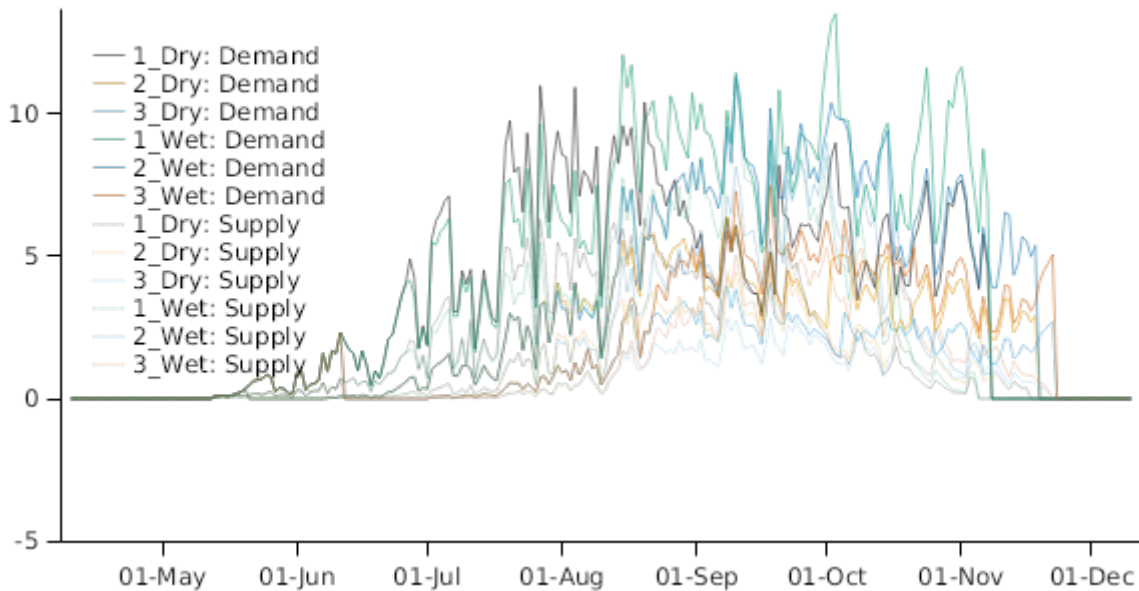
Would have been substantial variation in soil type up and down the steep slope. NMM calibration was from Farming systems site 5-6km away so not sure how trustworthy that data is. probably not great, unfortunately.

Met file - based on SILO but used local TTag at trial for max/minT, because trial is at a different point in the landscape (north slope) to the SILO station (east slope)

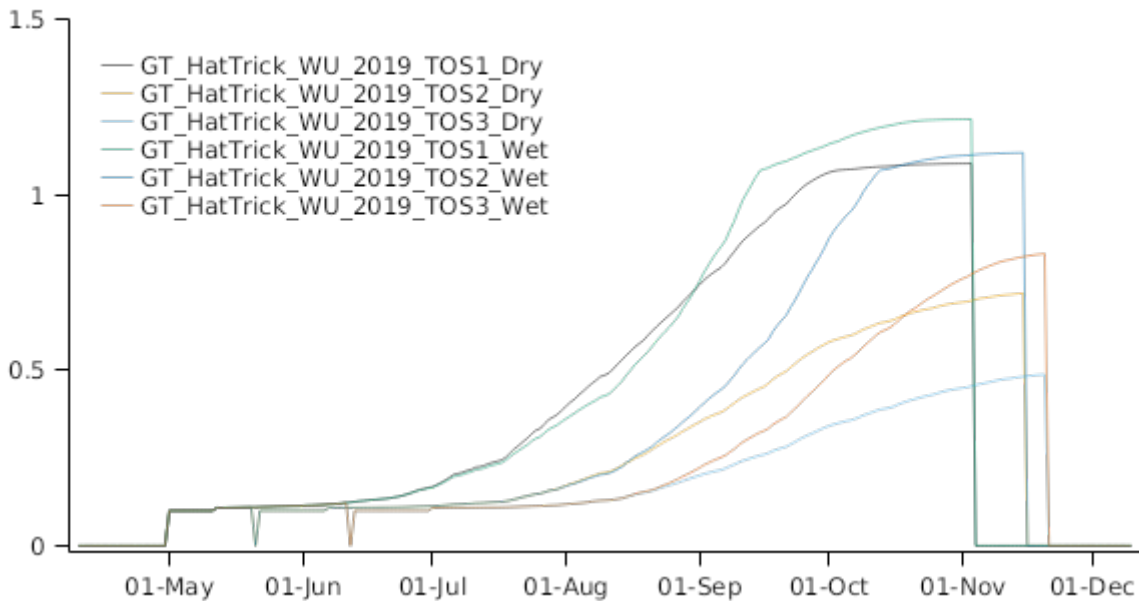
Stress



DMSupplyDemand



klreport



2.2.7 Narrabri19_

Experiment conducted at PBI Narrabri Research Station, by Helen Bramley from USYD on behalf of Pulse Adaptation project. Site was on the new section of the farm, over Killarney Gap Rd. Soil = Vertosol

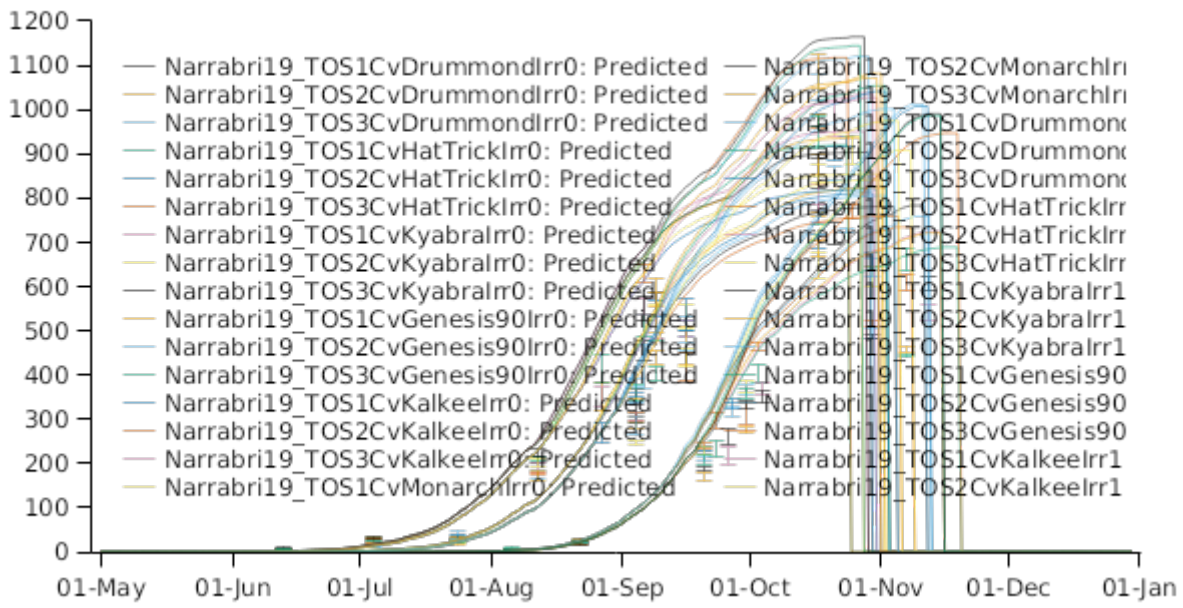
Met file - taken from SILO airport + field maxT, MinT and rain spliced in.

Irrigations from contractor -

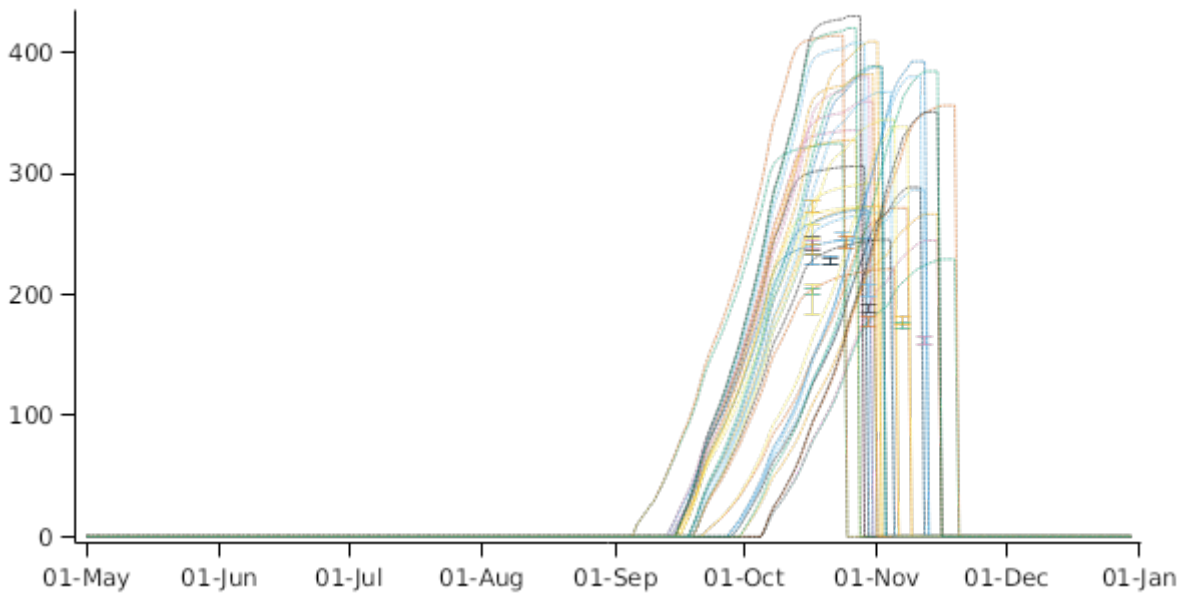
17/05 25 mm just after TOS 1 planted (accidentally typed 17/06 but you can see in excel entry is before and after other may entries) 17/06 30 mm - whole trial 06/08 irrigation 25 mm - whole trial 09/09 irrigation - 30mm irrigated part only 24/09 irrigated only 30 mm 25/10 irrigated only 30 mm

Soil water characterisation is a bit uncertain - cores weren't dried at 100 degrees. Still waiting on recalibrated soilwater data as of 7Aug20. This may explain consistent over-prediction at this site

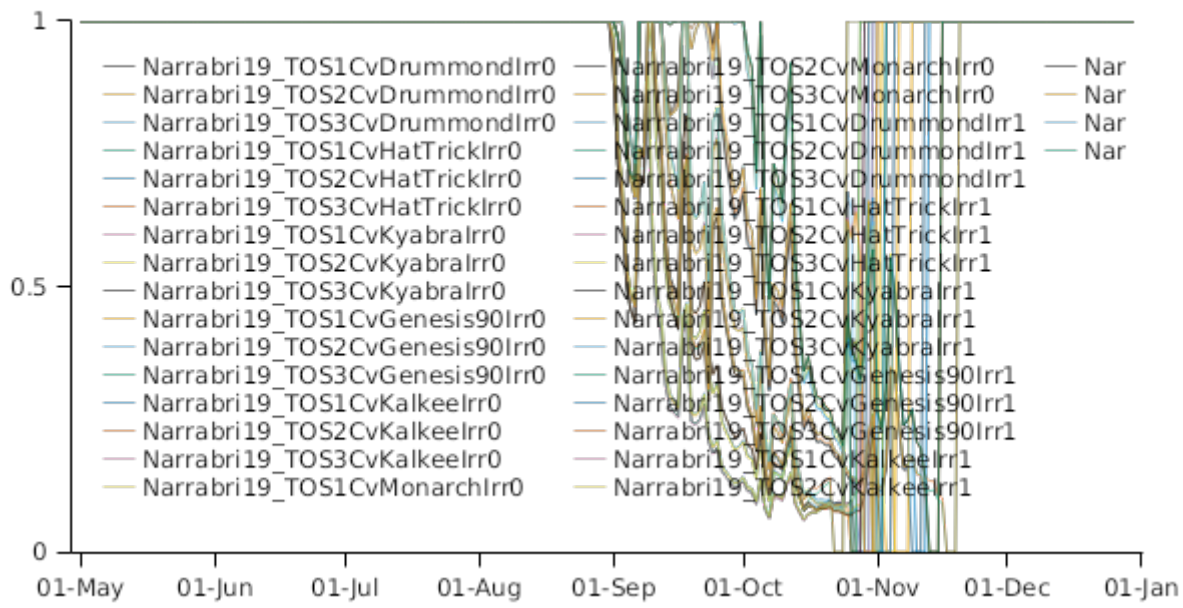
BiomassAllCvv



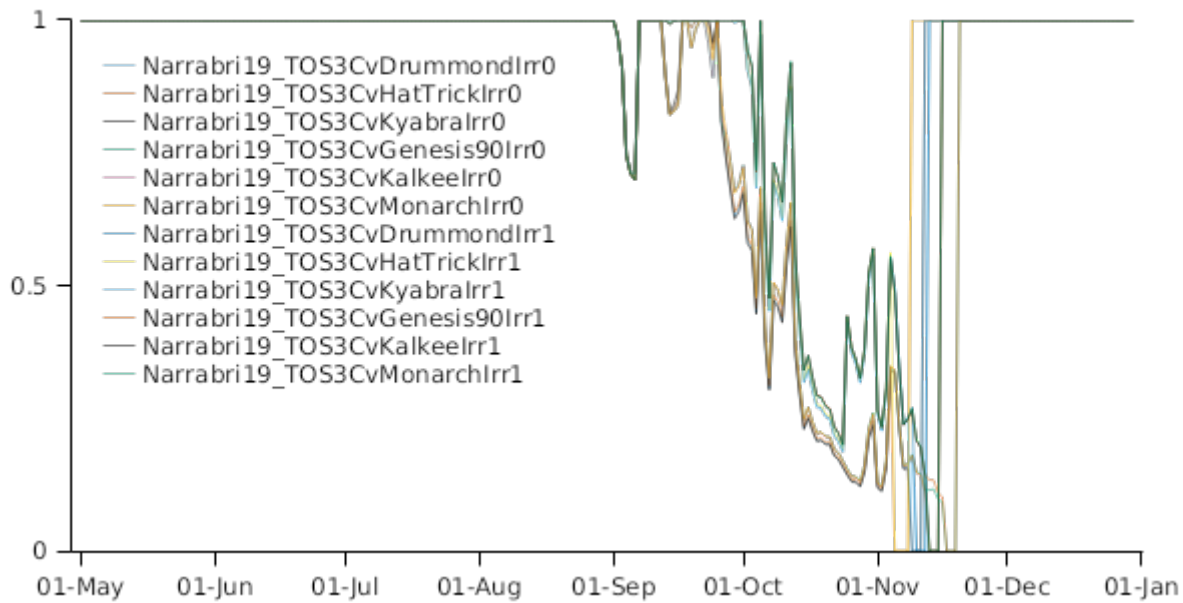
YieldAllCvv



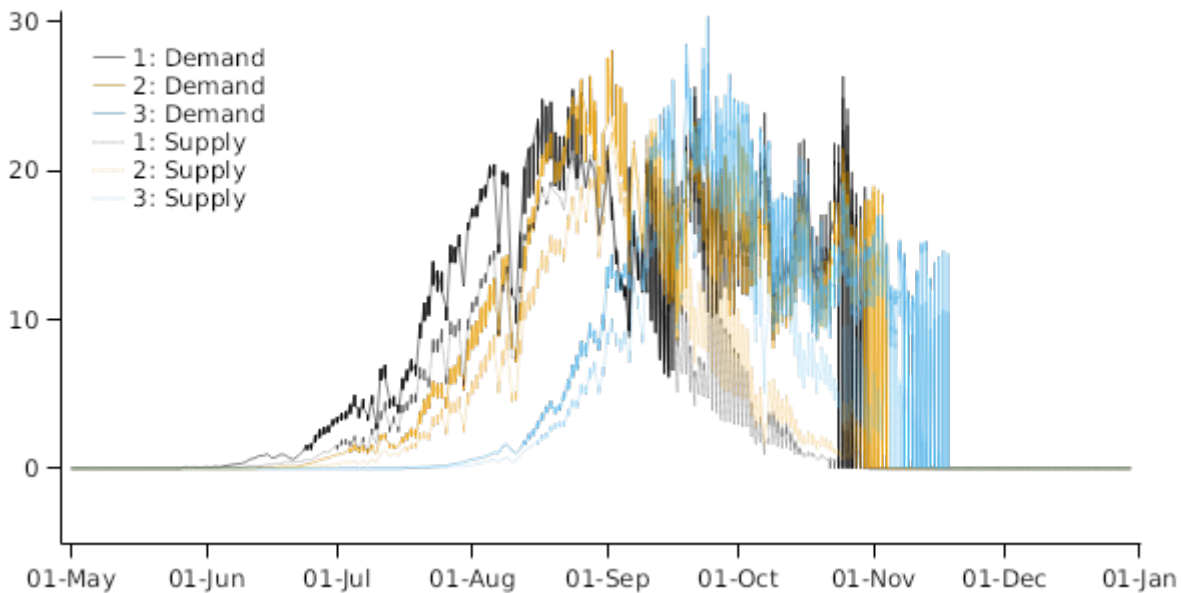
Stress



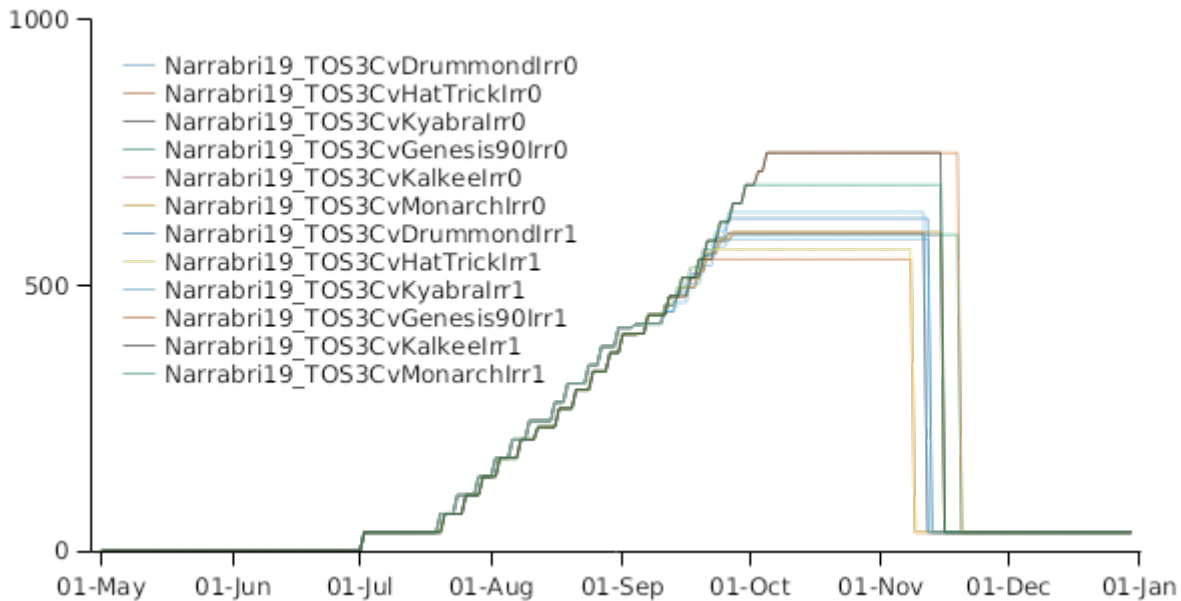
StressTOS3



DMSupplyDemand



Branches_vs_time



2.3 SE Queensland

List of experiments.

Experiment Name	Design (Number of Treatments)
Lawes1990	Sowing (2)
Lawes1991	Sowing (2)
Lawes1995	Trt (2)
Bremar_2003_	S (4)

2.3.1 Lawes1990

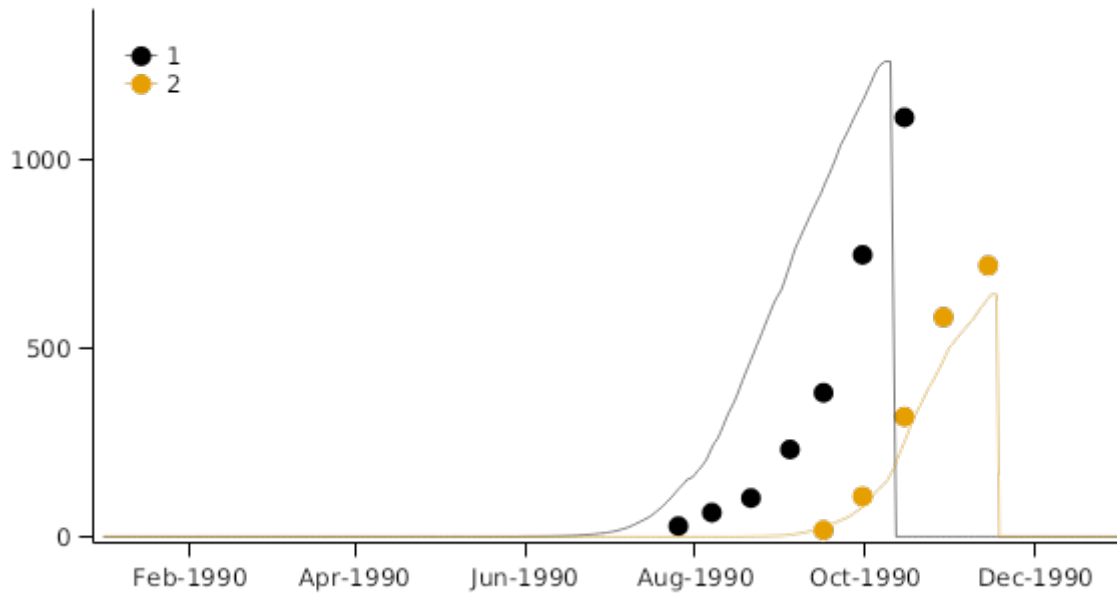
Peter Carberry data partially published in Brinsmead (1992). <http://www.regional.org.au/au/asa/1992/concurrent/cropping-systems/p-04.htm>

Experiment conducted at Gatton RS, 1990. One variety, two sowing dates. Creek bank soil is variable over short distances.

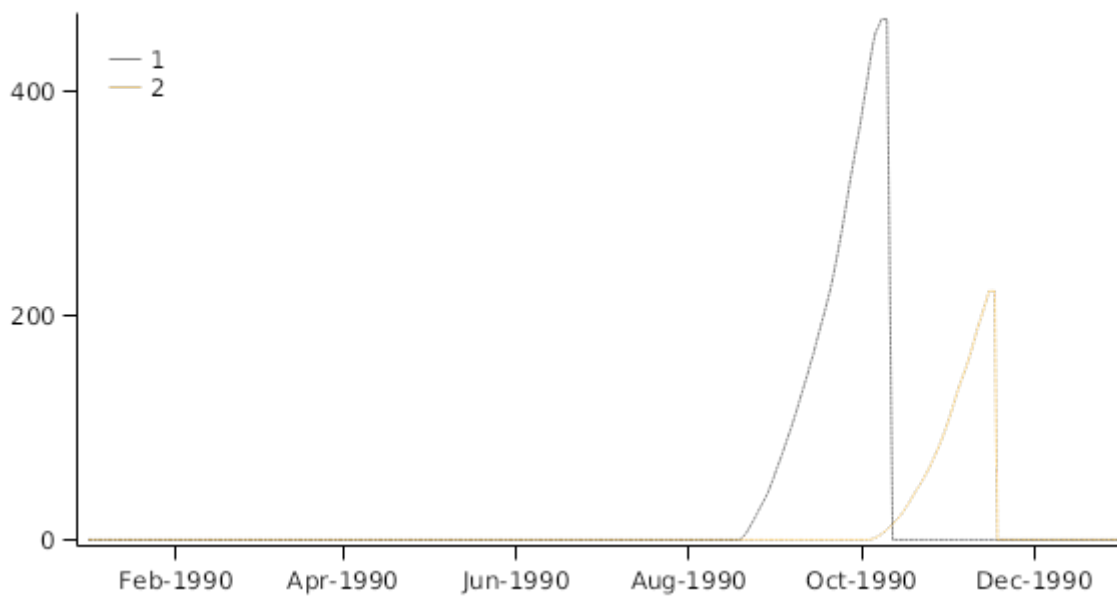
Note that Brinsmead paper says 1st sowing date was waterlogged soon after sowing, which would explain the delayed biomass growth curve in comparison to simulated.

Note - auto-irrigate function has been used as there is no record of actual irrigation, although in theory the experiment was fully irrigated. In practice, this usually means some low level water stress is experienced, as has been simulated with this experiment.

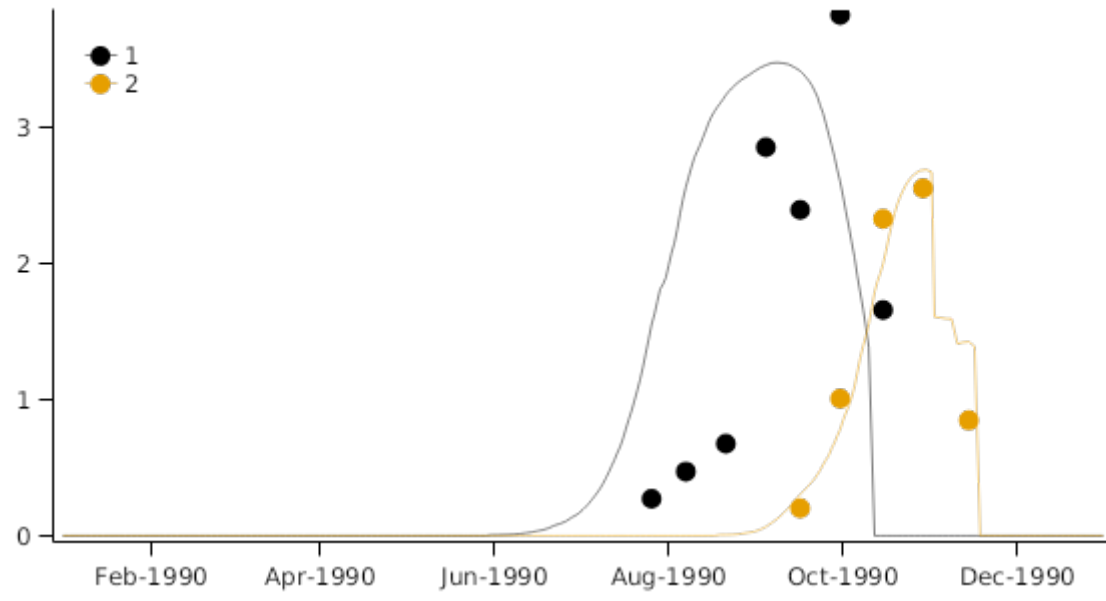
Biomass



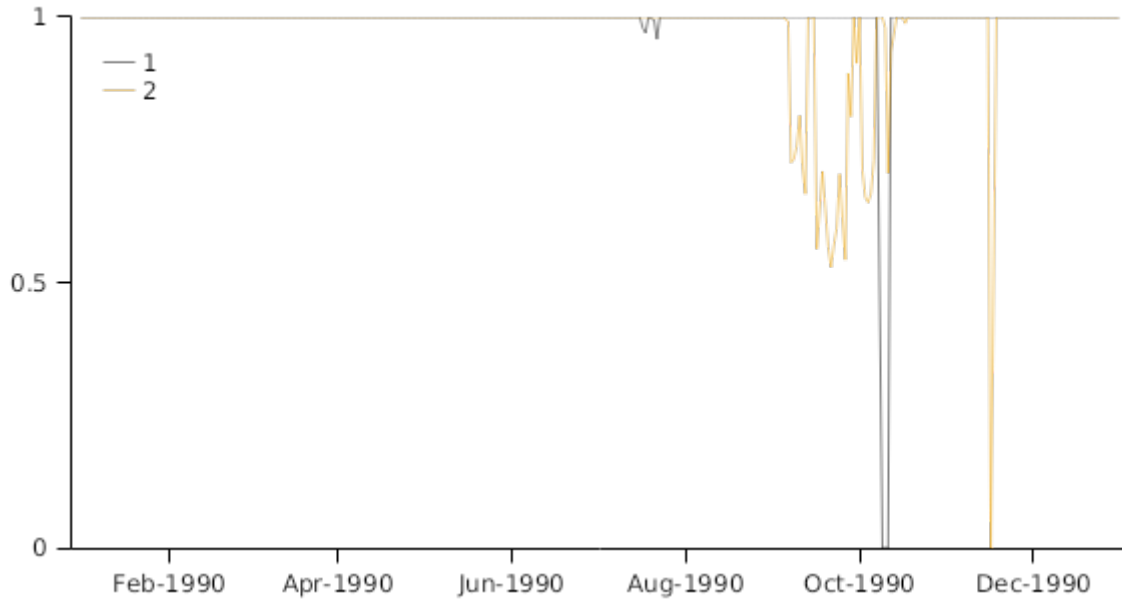
GrainWt



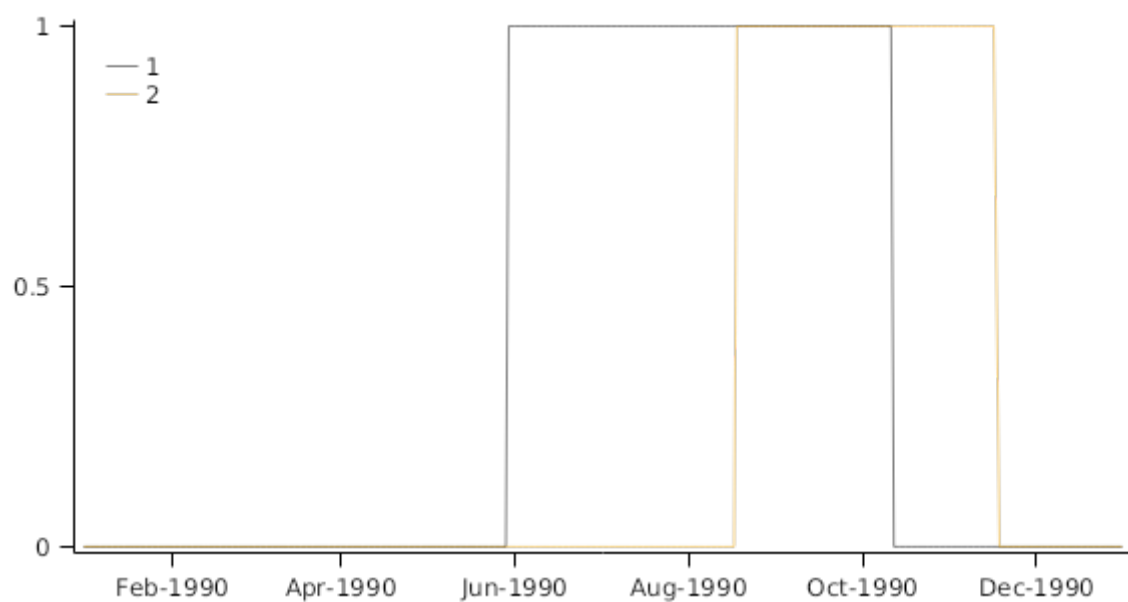
LAI



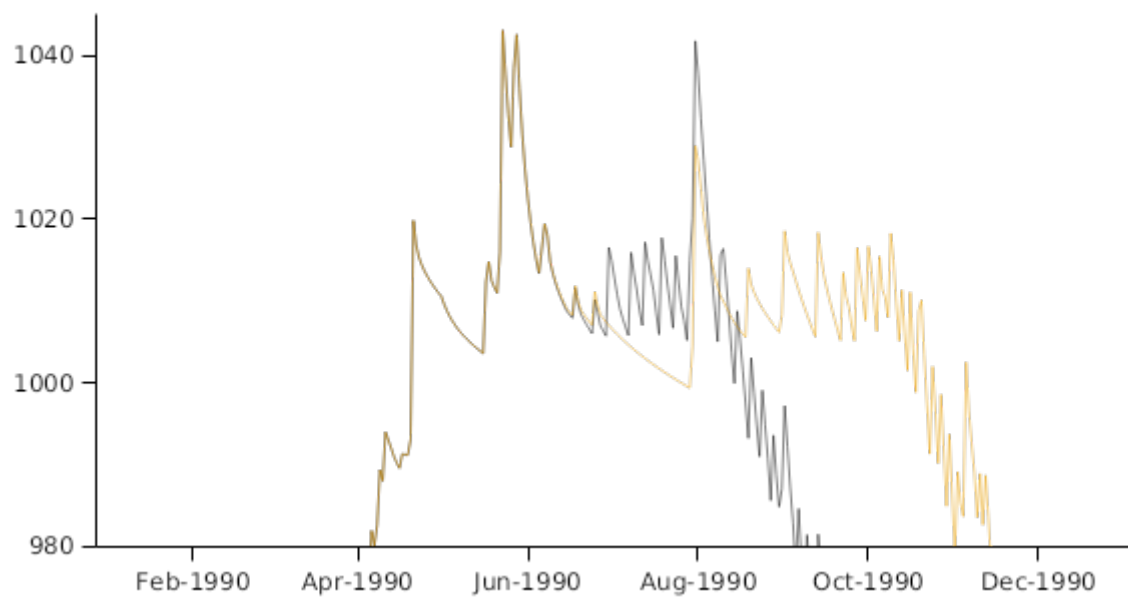
Stress



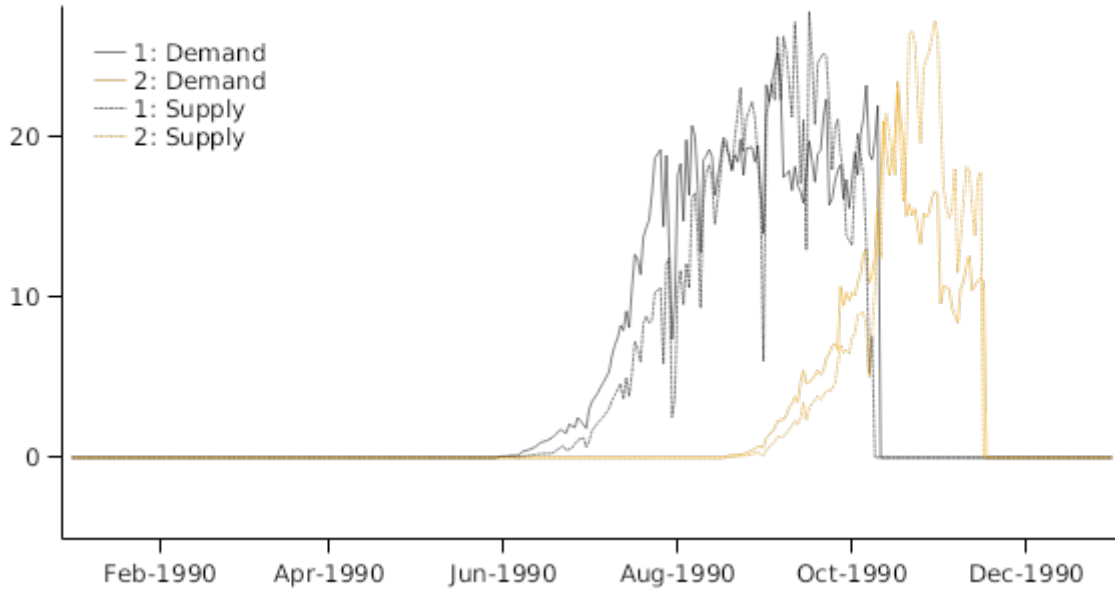
NStress



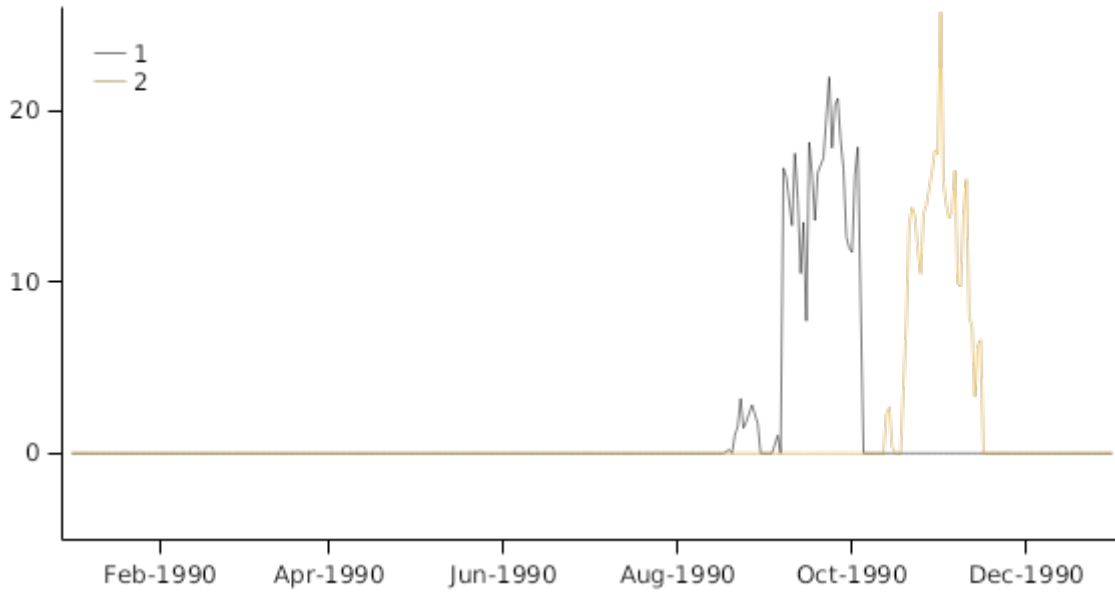
SoilWaterStatus



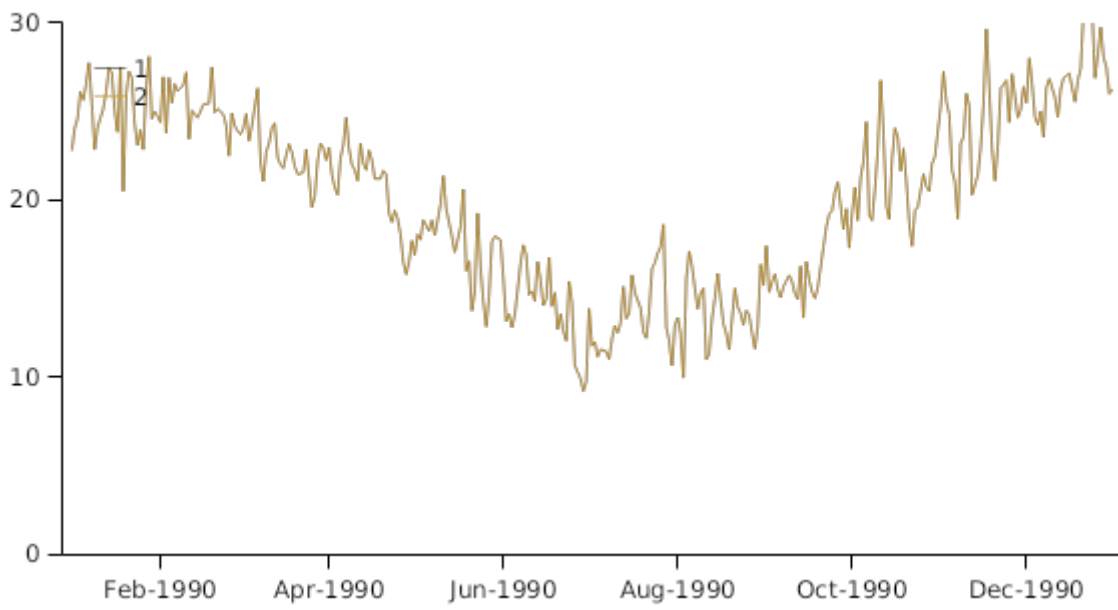
DMSupplyDemand



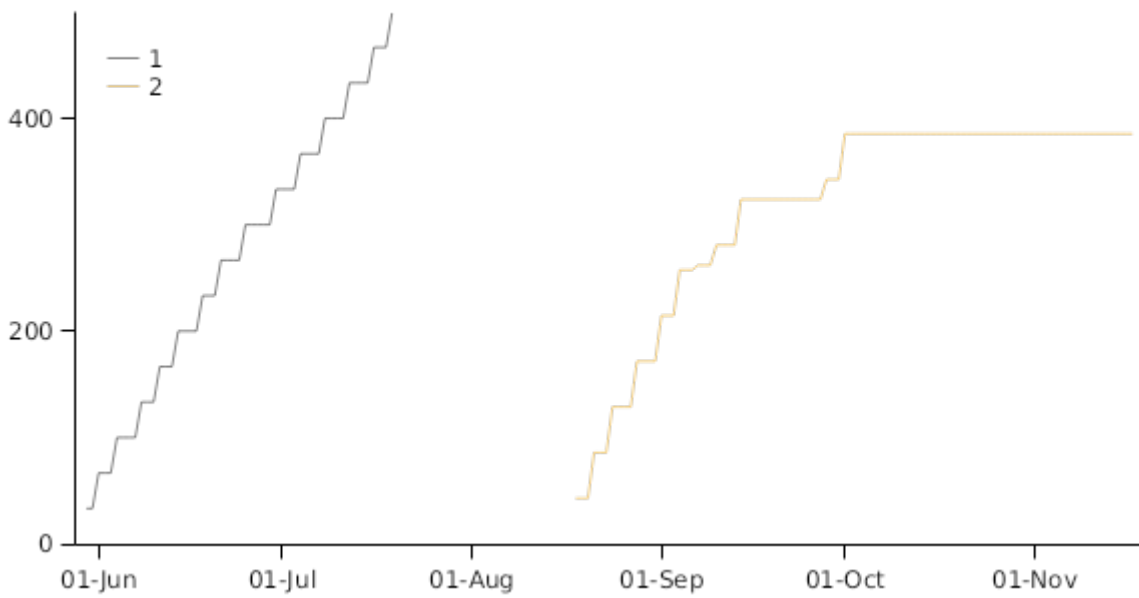
DMDemands



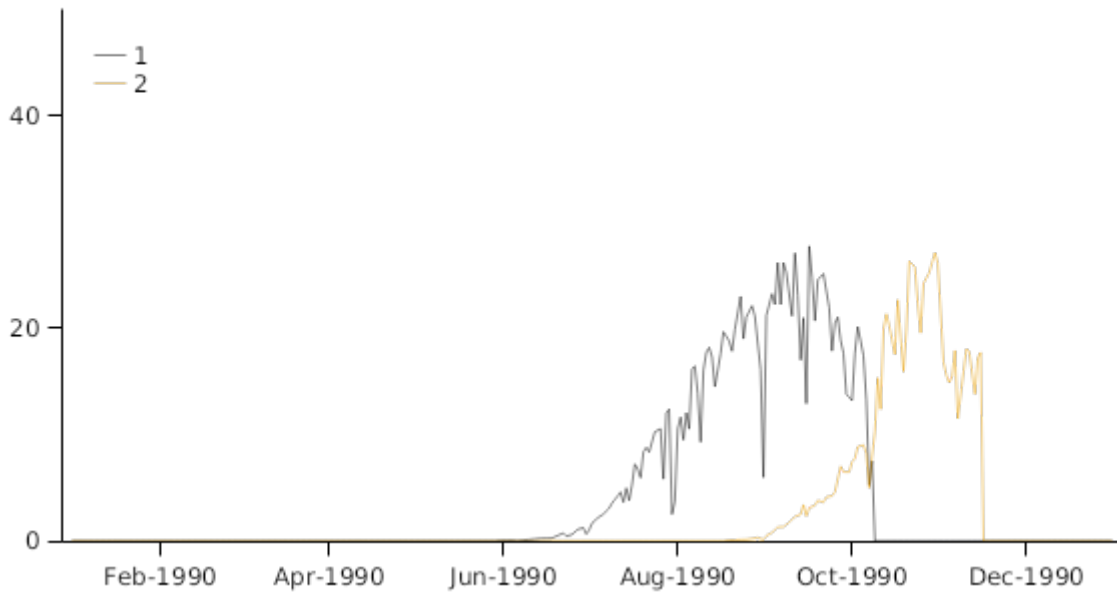
MeanT



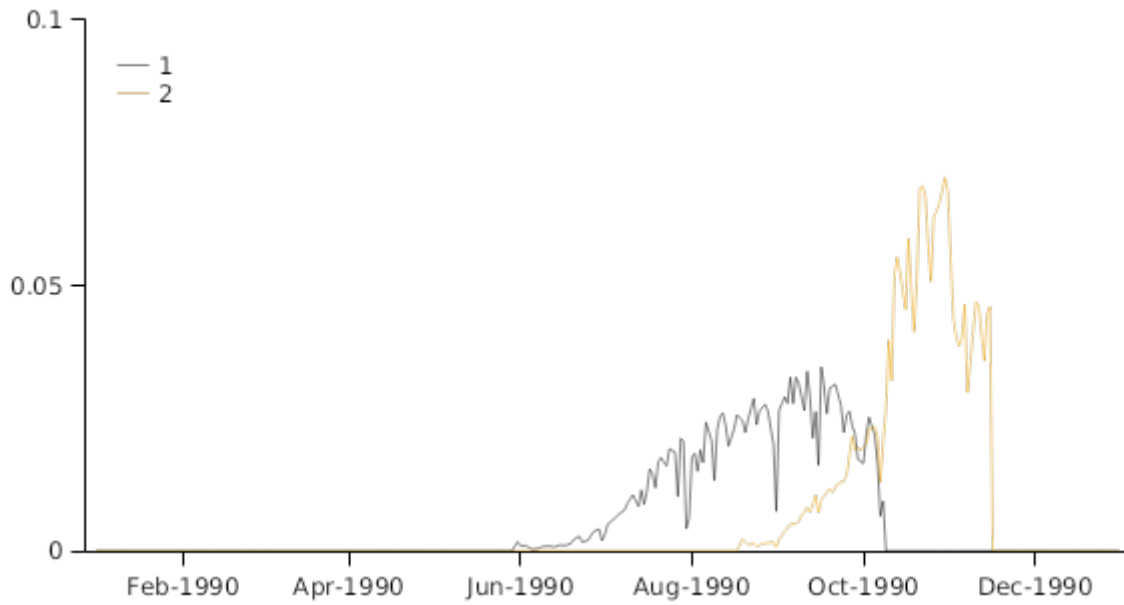
Branches_vs_time



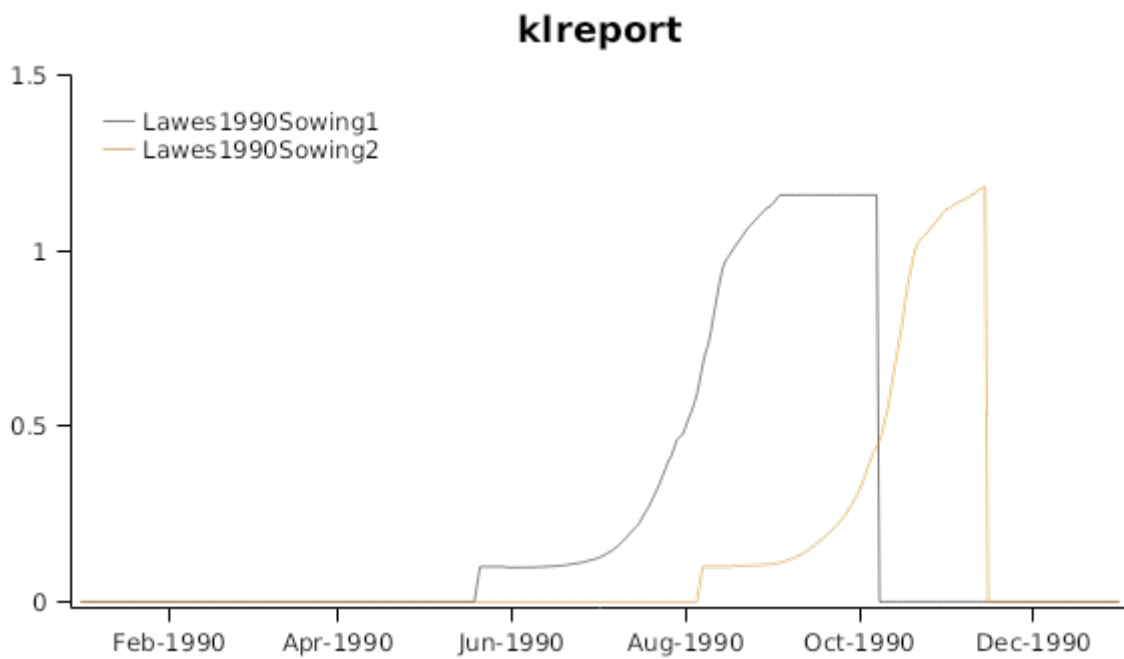
LeafPhotosynthesis



PhotoperBranch



BranchMod



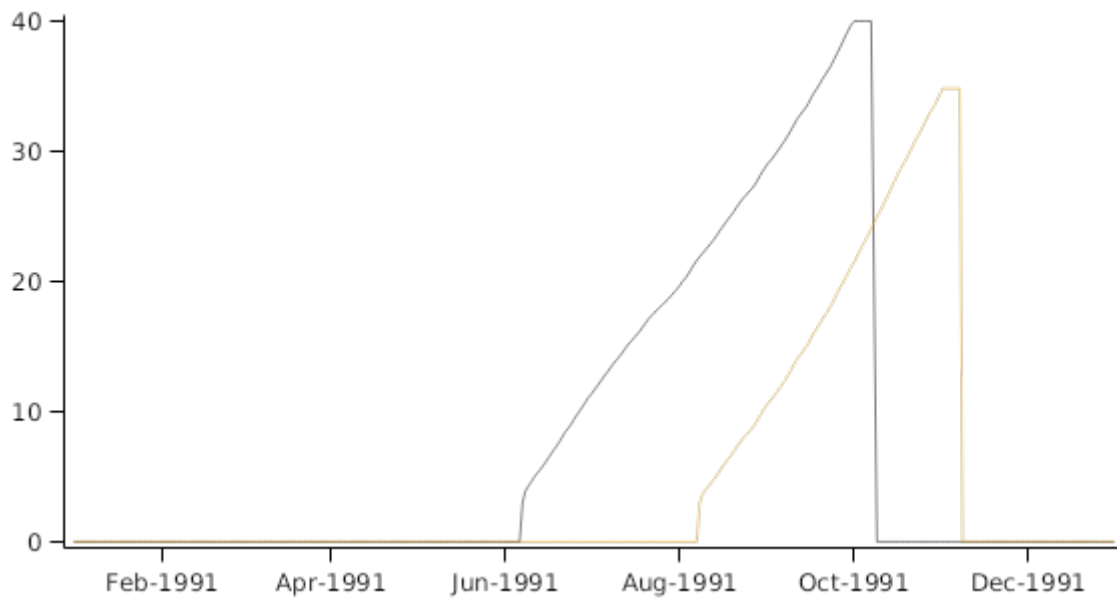
2.3.2 Lawes1991

Gatton RS 1991, 2 sowing date experiment. Creek bank soil is highly variable.

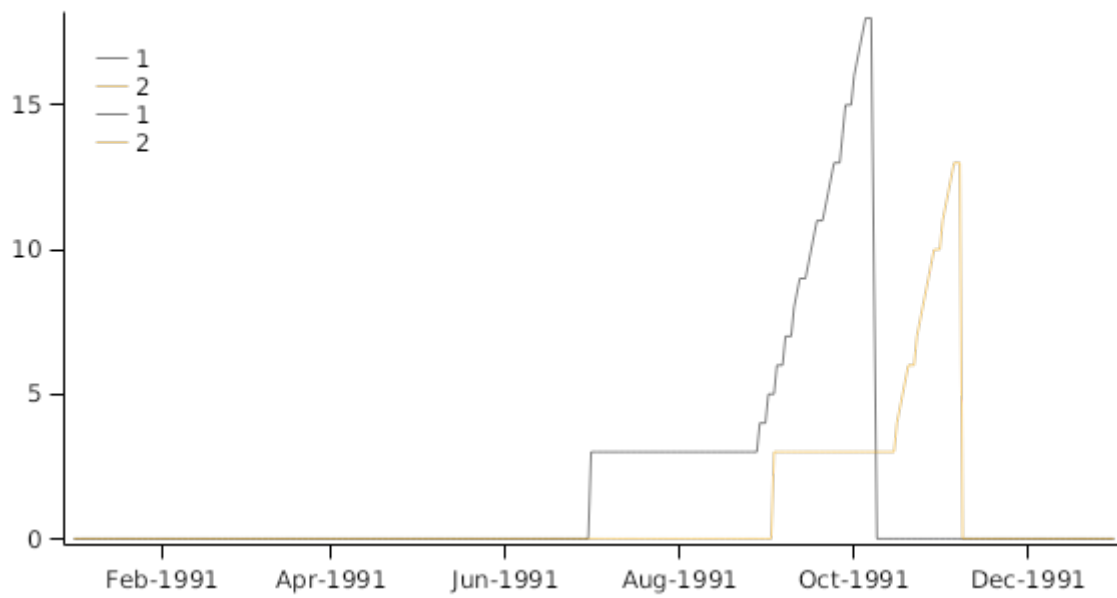
Peter Carberry unpublished data. Also known as APS2??

Current version of the model seems to be starting grainfill too early for this data. May have been a waterlogging stress that delayed flowering? Or do modern cultivars set seed faster than Amethyst?

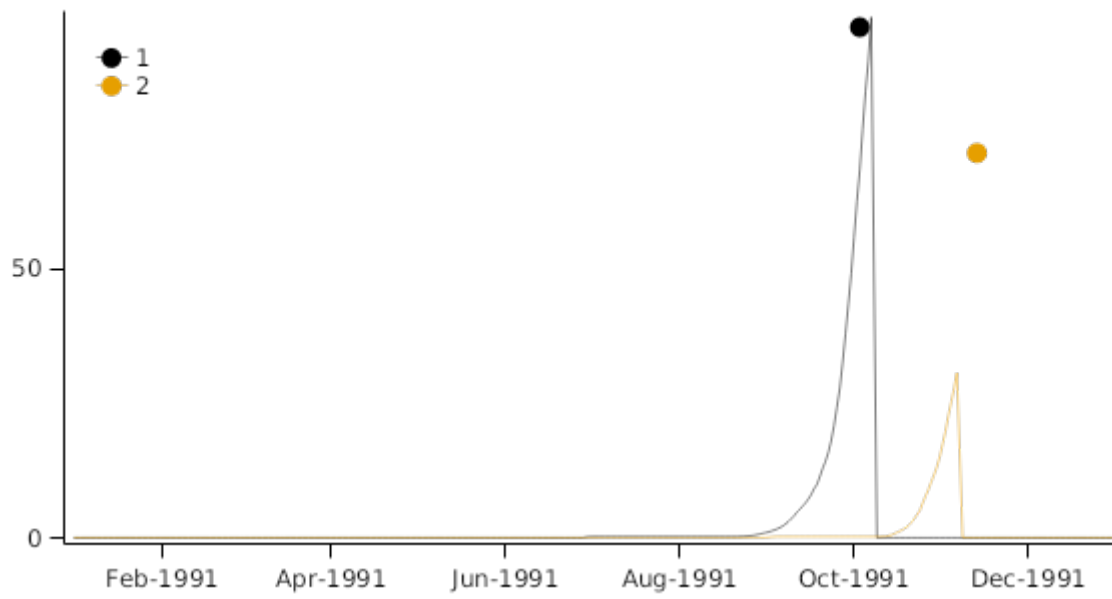
MSLeafNo



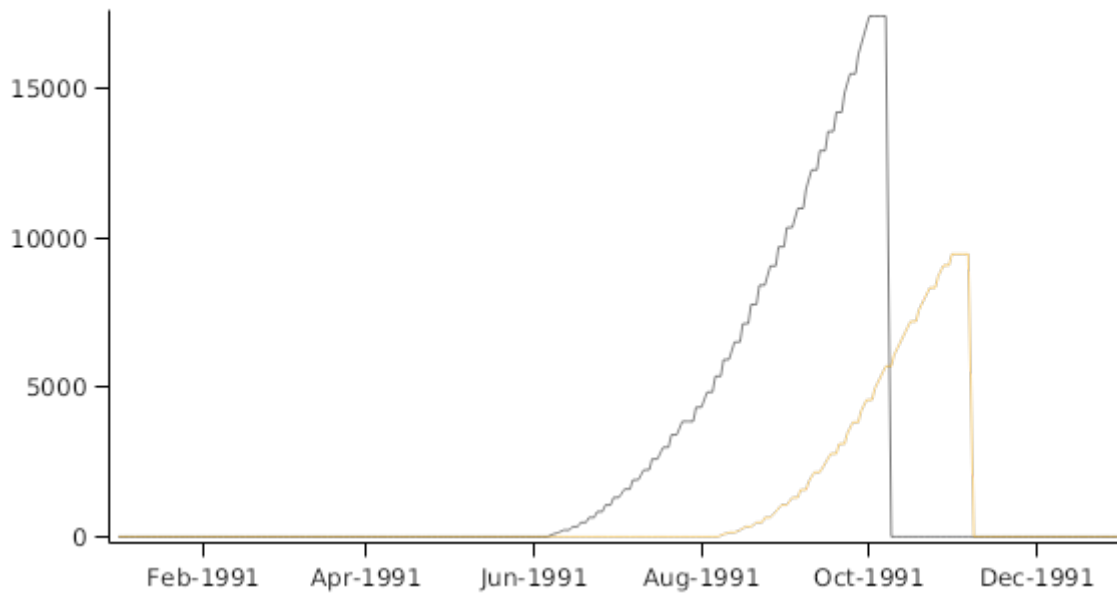
MSDeafLeafNo



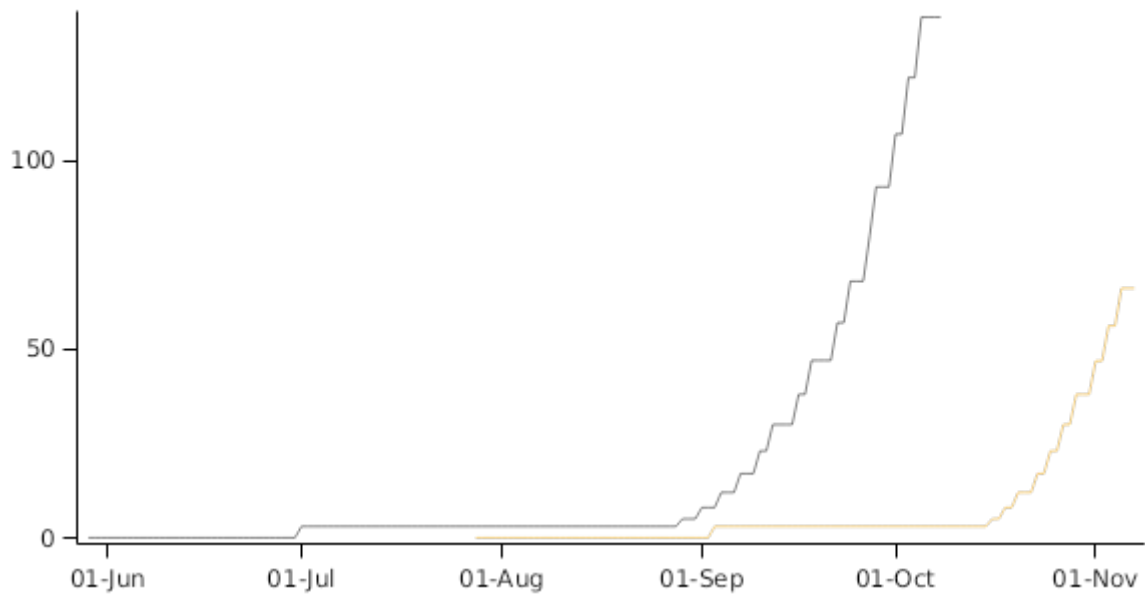
Dead Leaf Mass



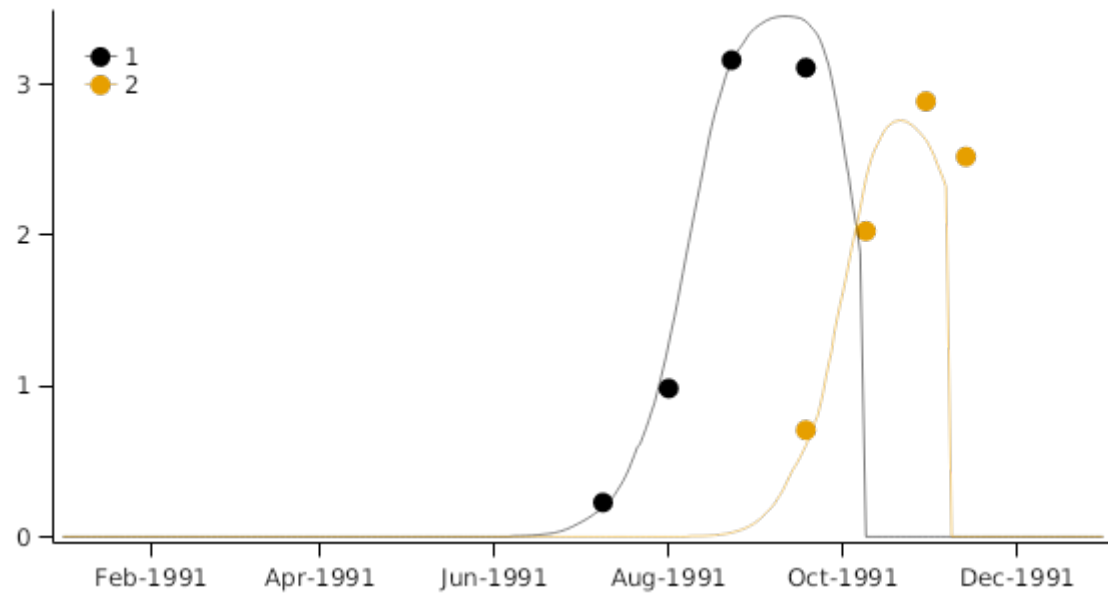
TotalLeaves



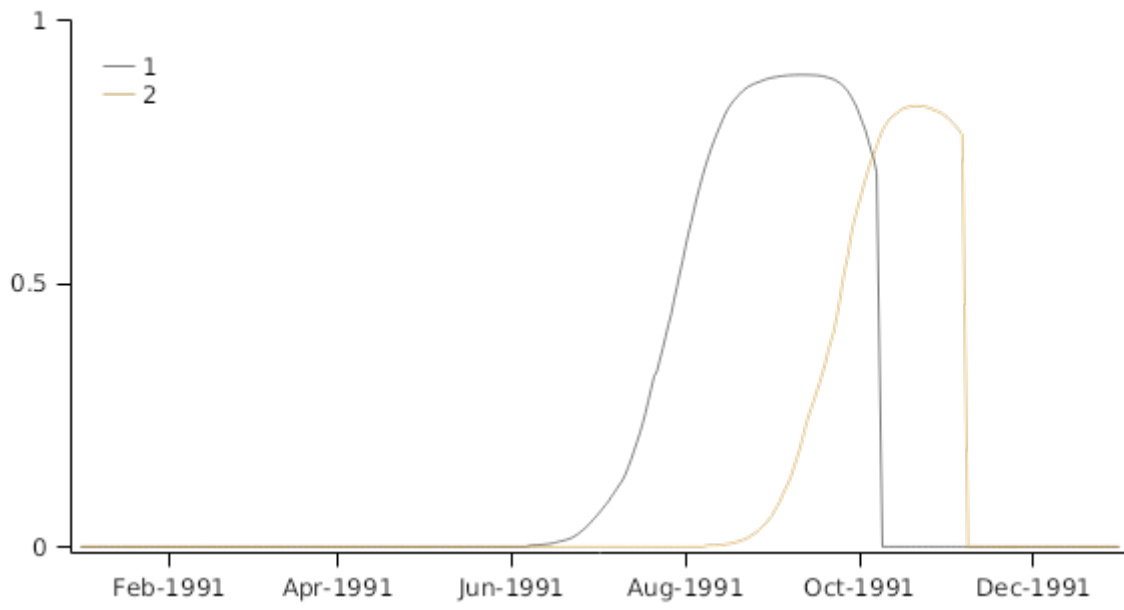
TotalSenescedLeaves



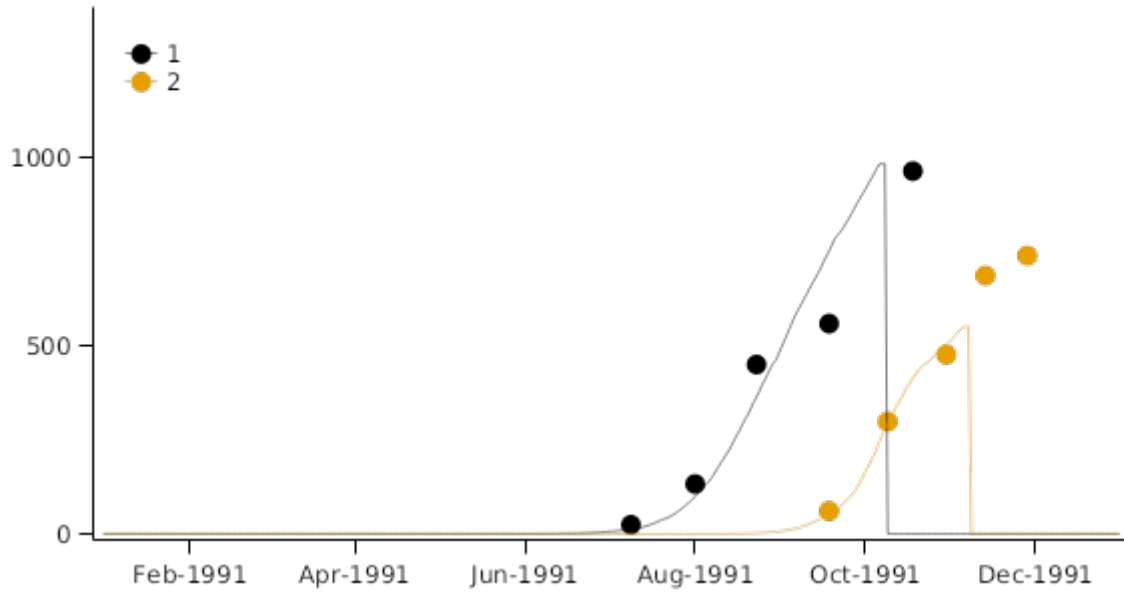
LAI



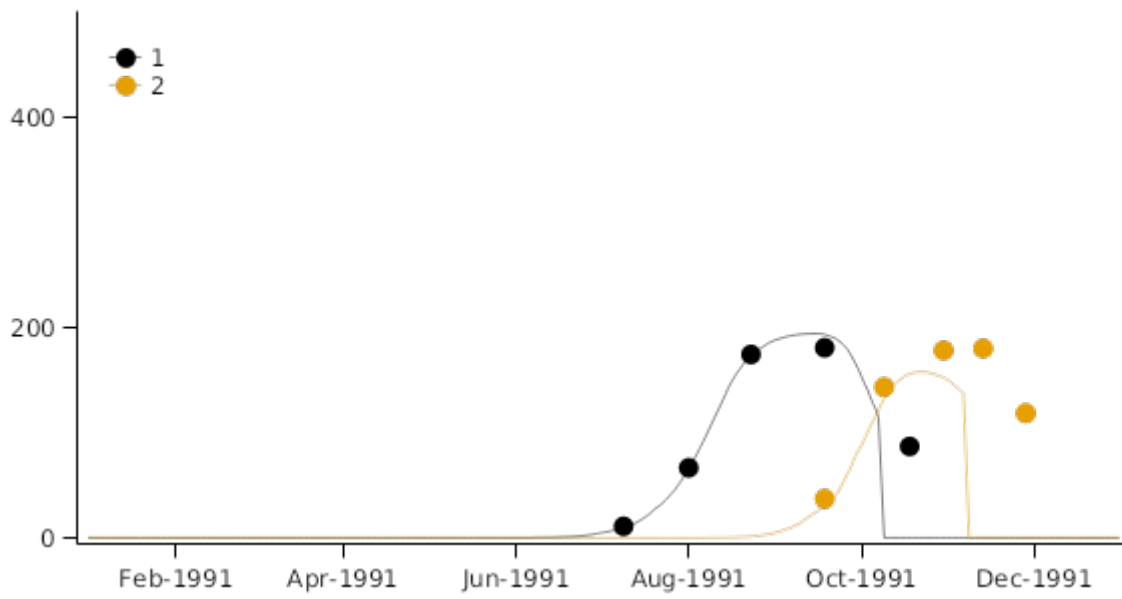
Cover



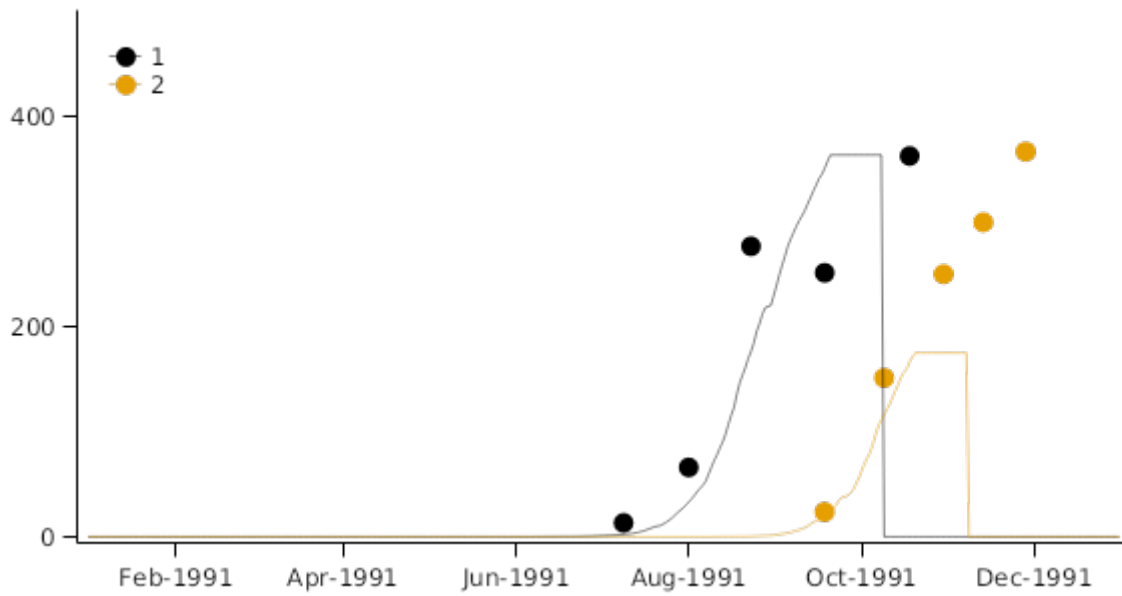
Biomass



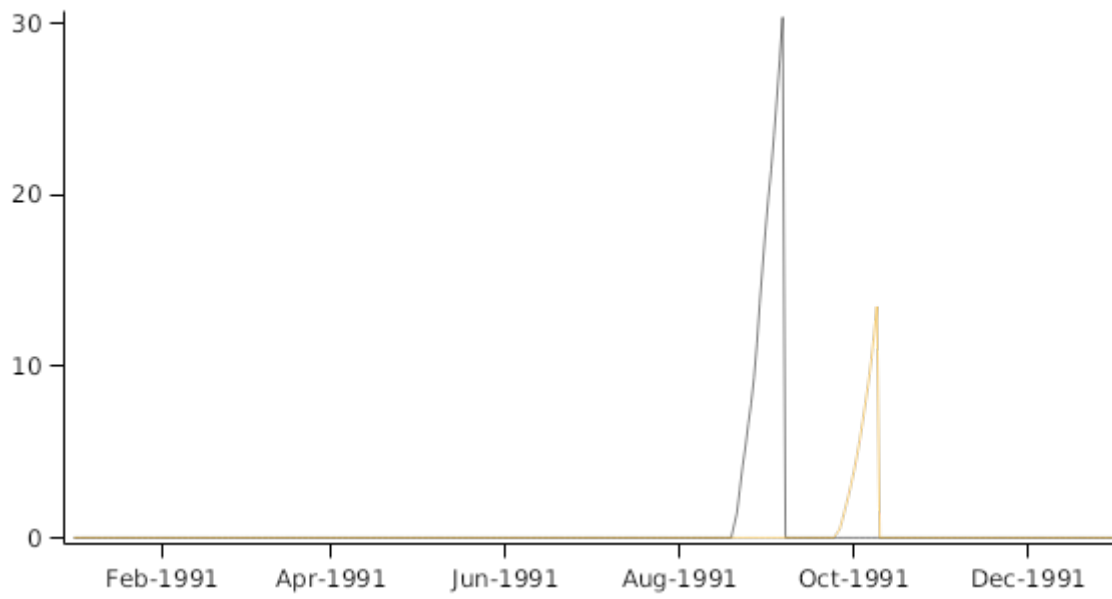
Leaf Mass



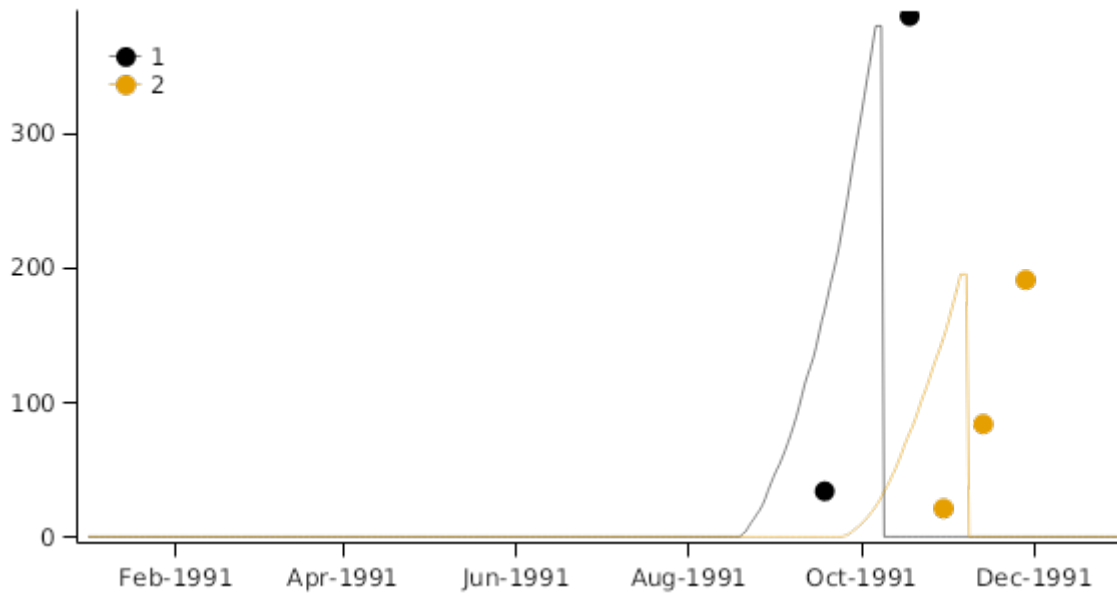
Stem Mass



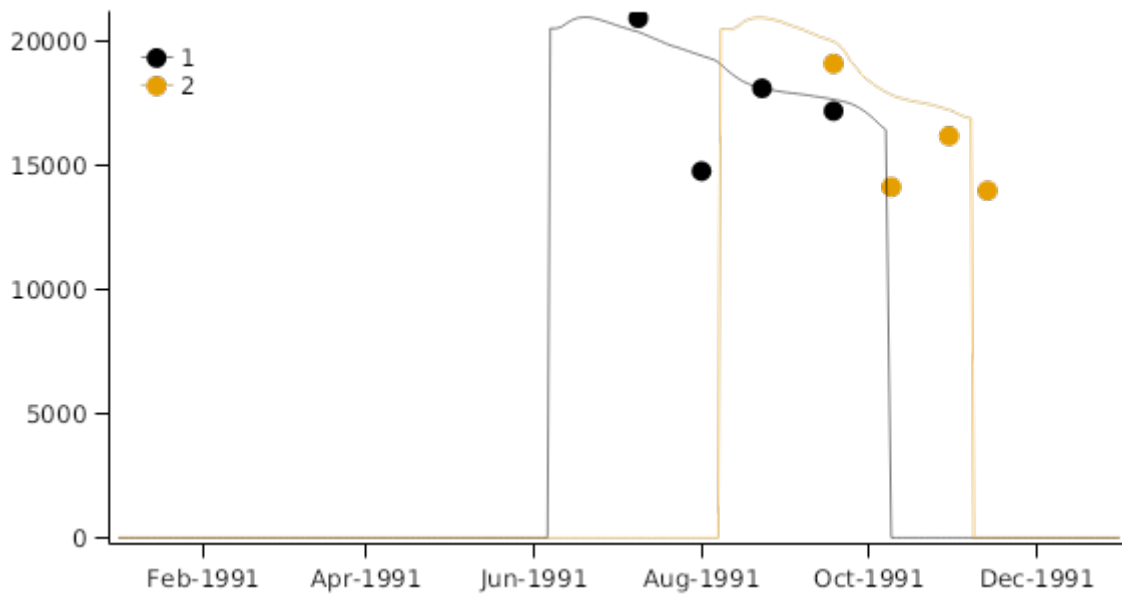
Shell Mass



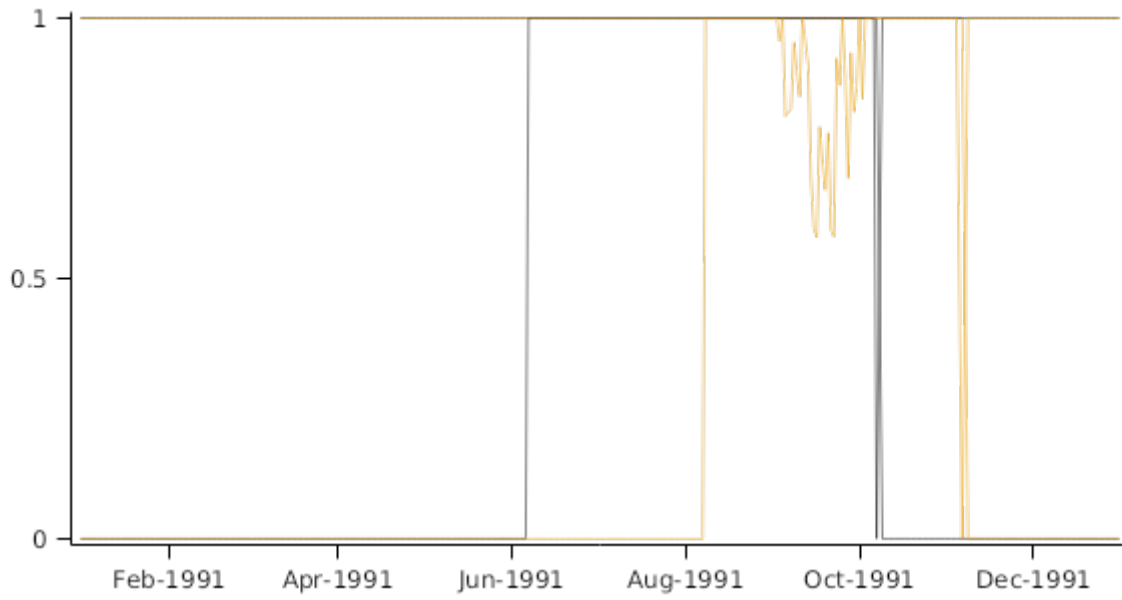
Grain Wt



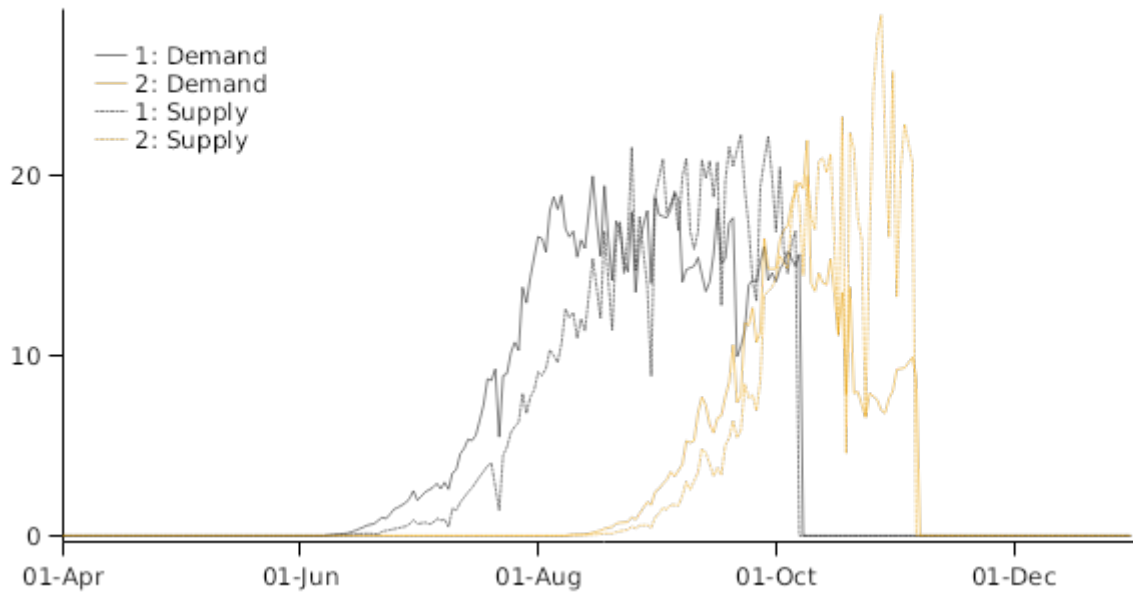
SpecificLeafArea



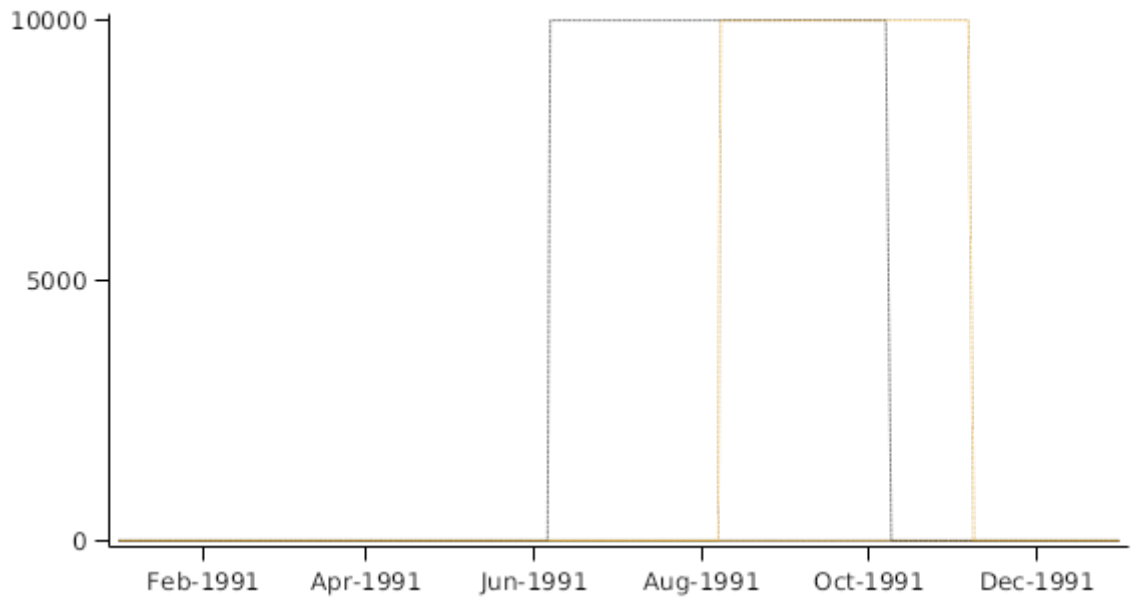
Stress



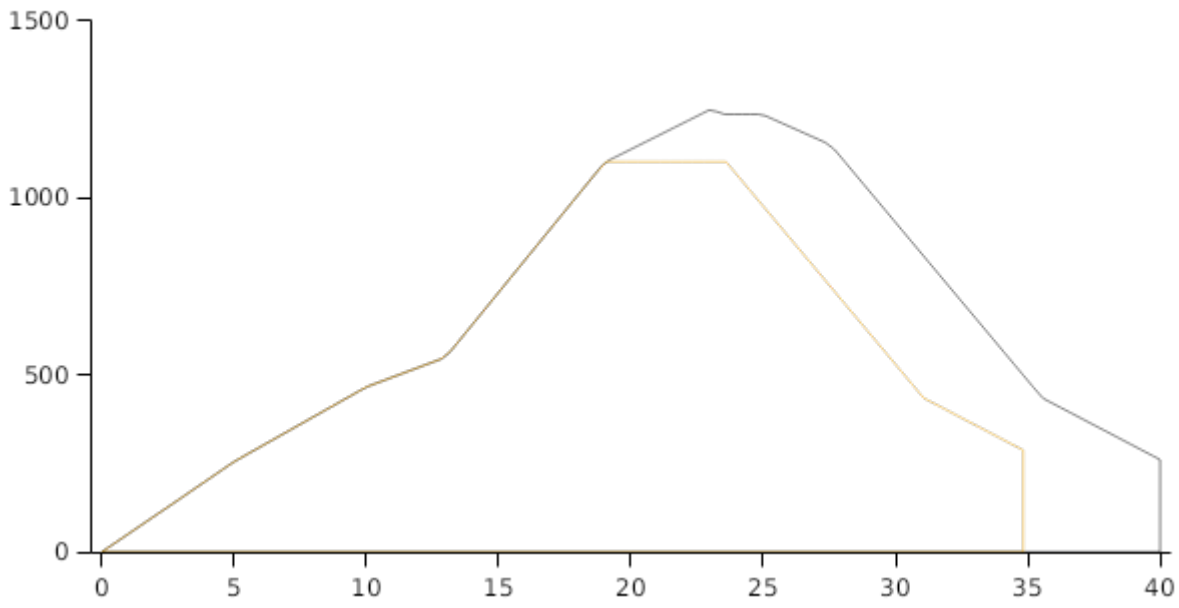
DMSupplyDemand



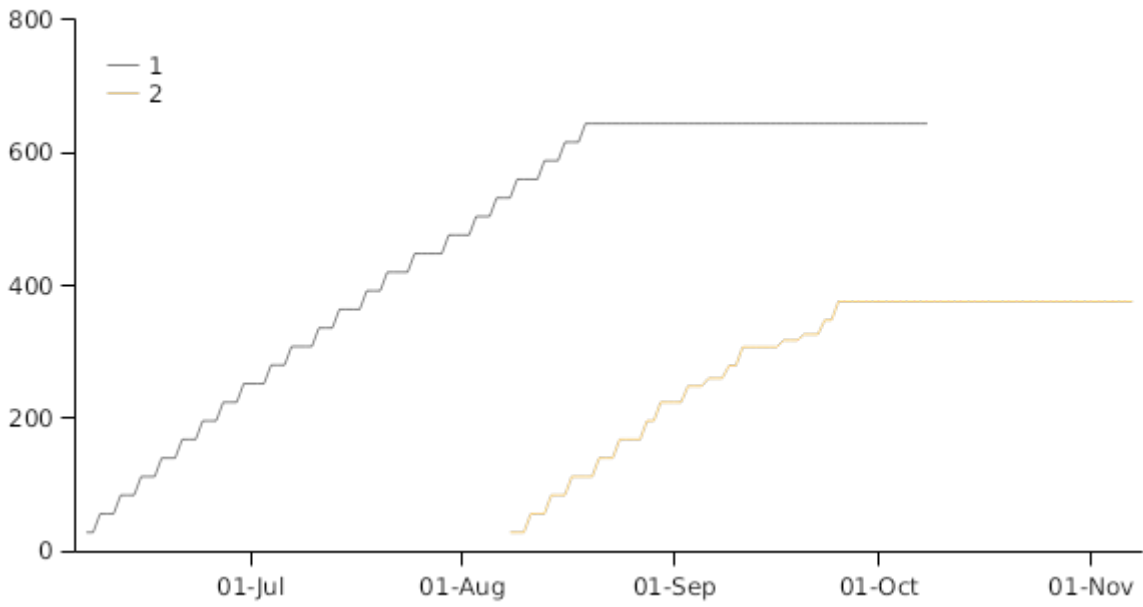
NSupplyDemand



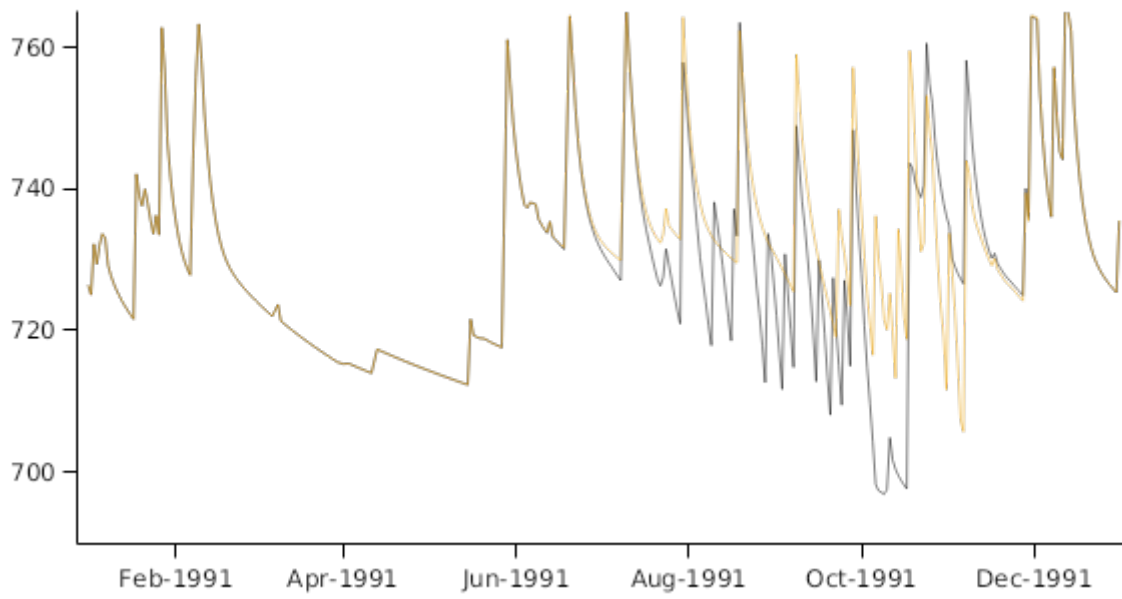
LeafSize



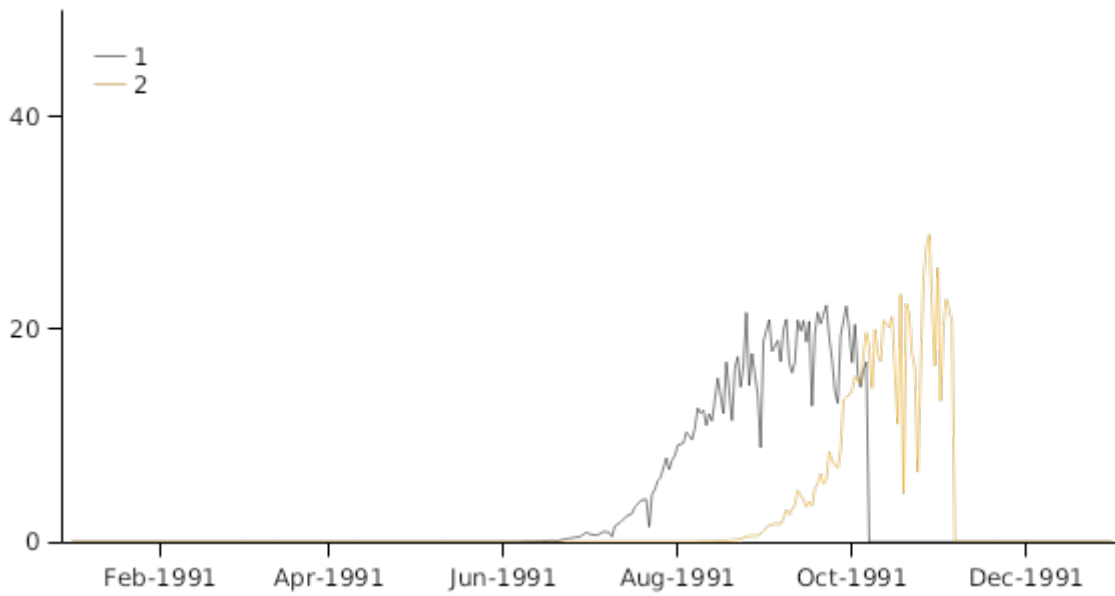
Branches_vs_time



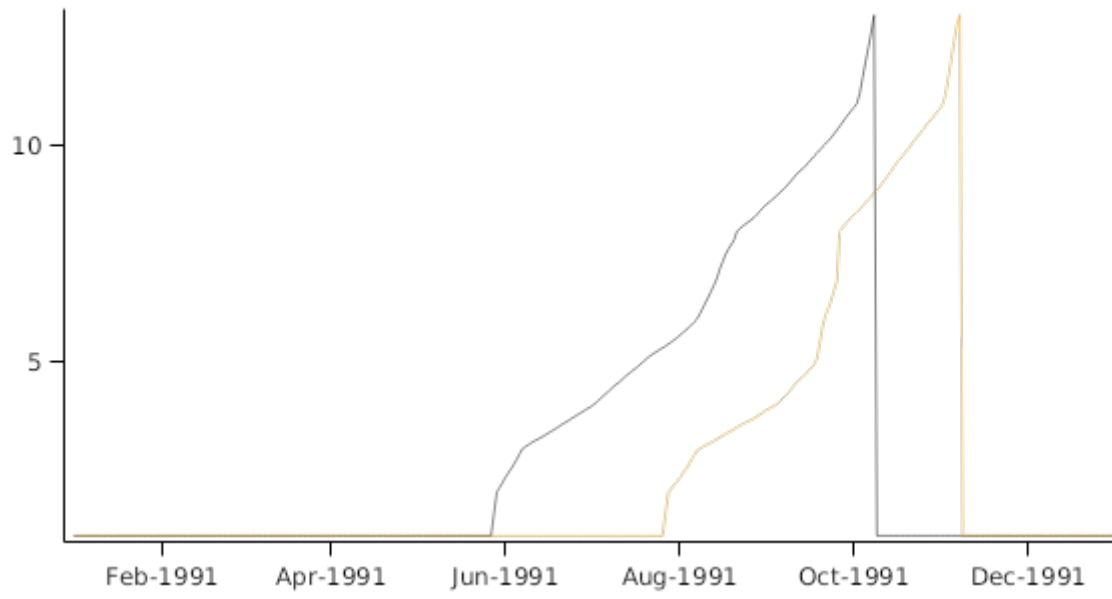
SoilWaterStatus



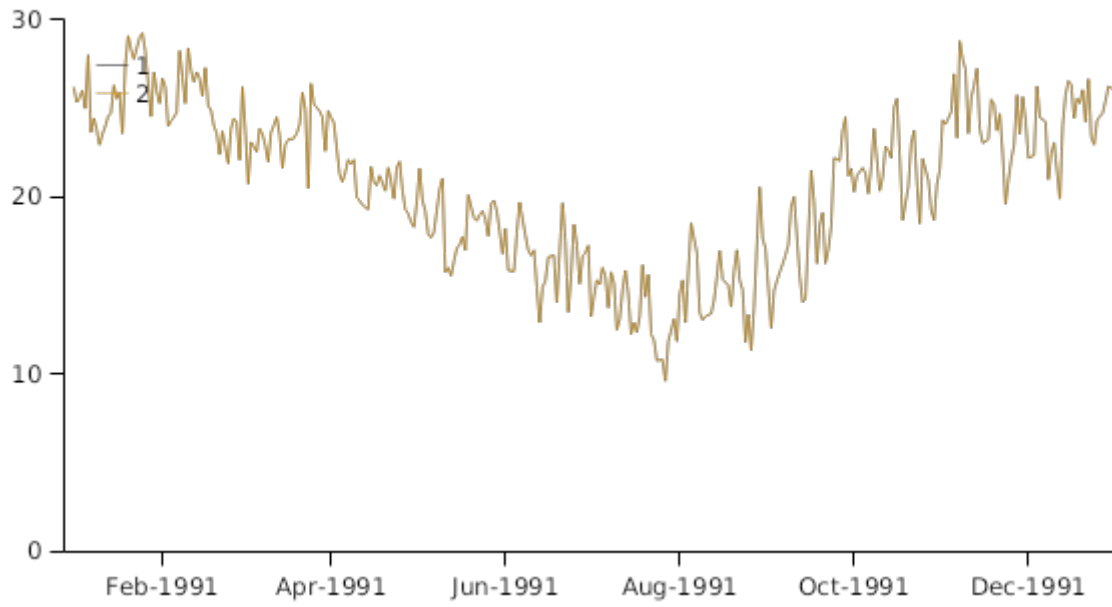
LeafPhotosynthesis



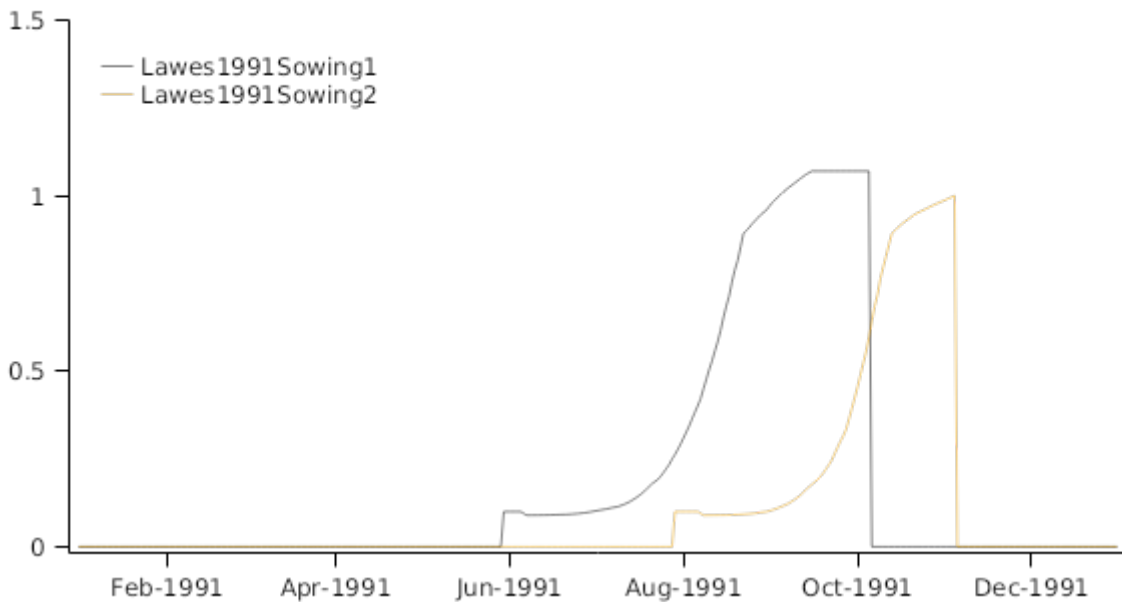
Stage



Meant



klreport



2.3.3 Lawes1995

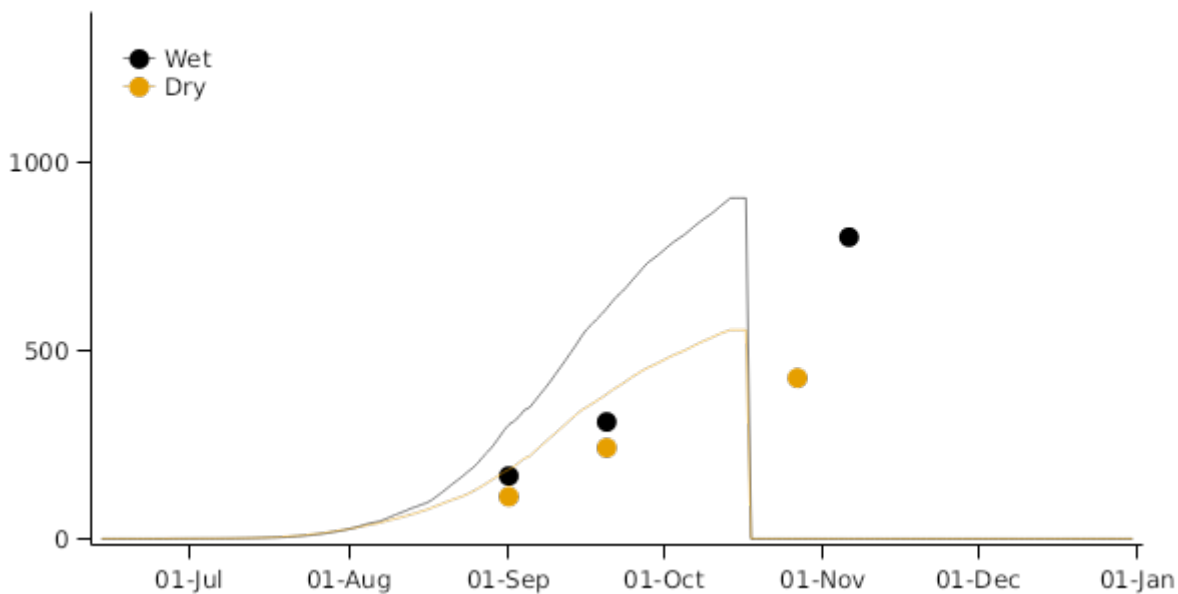
Experiment known as APS27. Irrigated vs rainfed treatments. Was sown adjacent to the APS26 wheat experiment and should theoretically have received the same irrigation. Creek bank soil is quite variable. There could be a problem with NMM calibration for this reason. WUE of APS26 wheat was not right, but their problem was too much biomass for the amount of water. This simulation has opposite problem of model getting away too fast. Doesn't seem possible to balance biomass development and water use for simulations of this experiment.

Published data from Yash Dang suggests there is little deep water extraction in Chickpea - at odds with this experiment. There may have been tree roots encroaching on the experimental area.

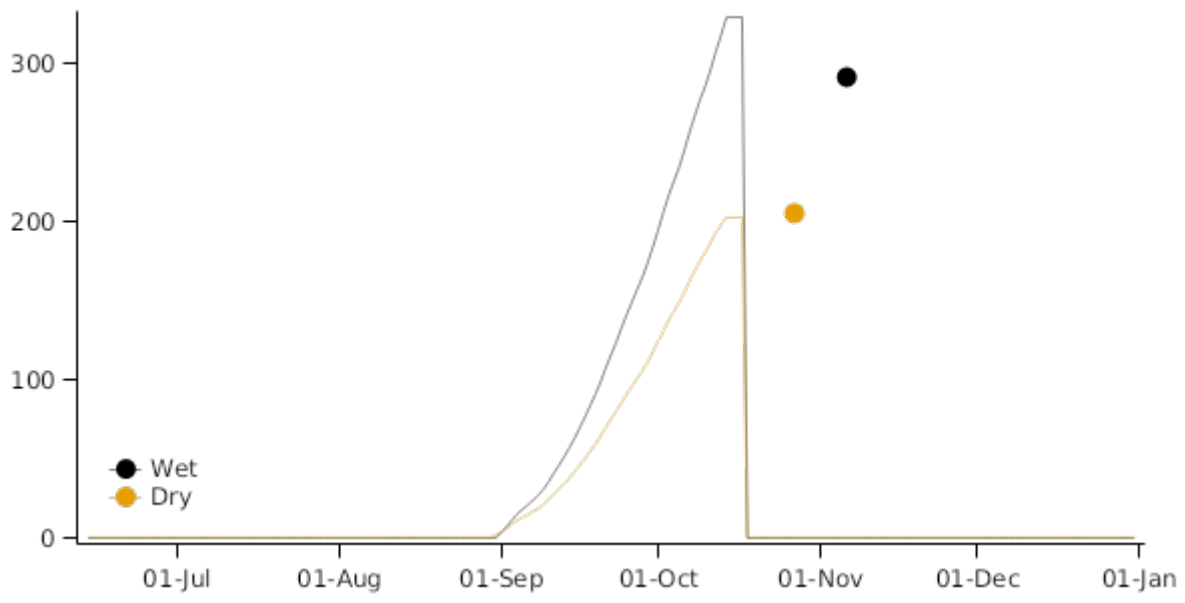
Possible that the wet treatment developed disease issues or N fixation issues due to over-watering which might explain overprediction of biomass.

Also possible that disease management in general was poor and/or undetected, although grain yield was predicted OK

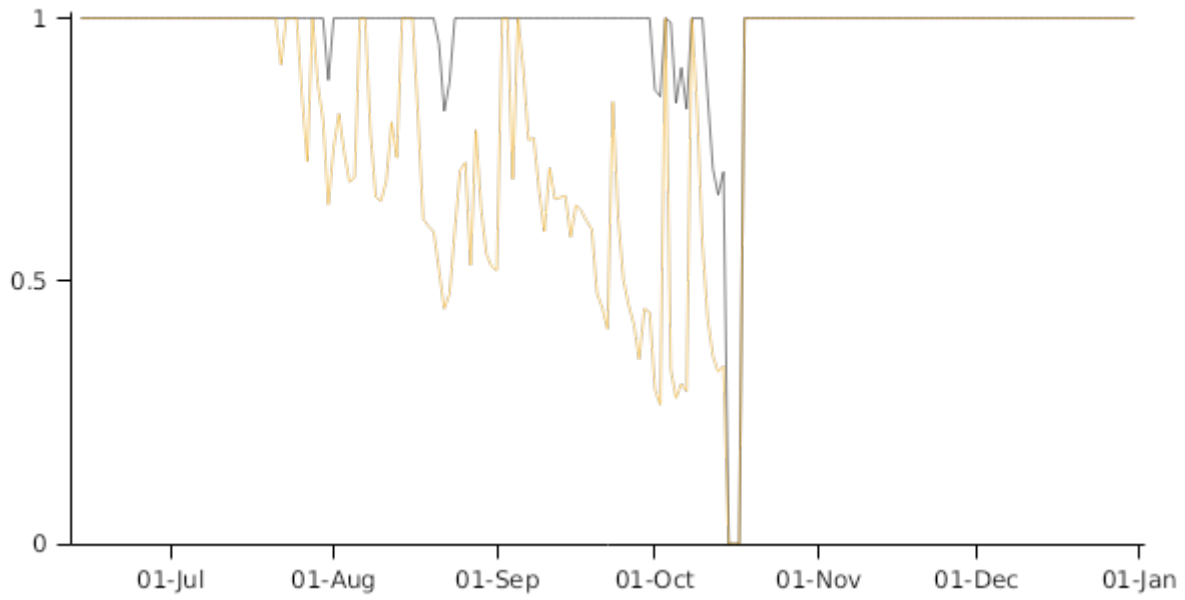
Biomass



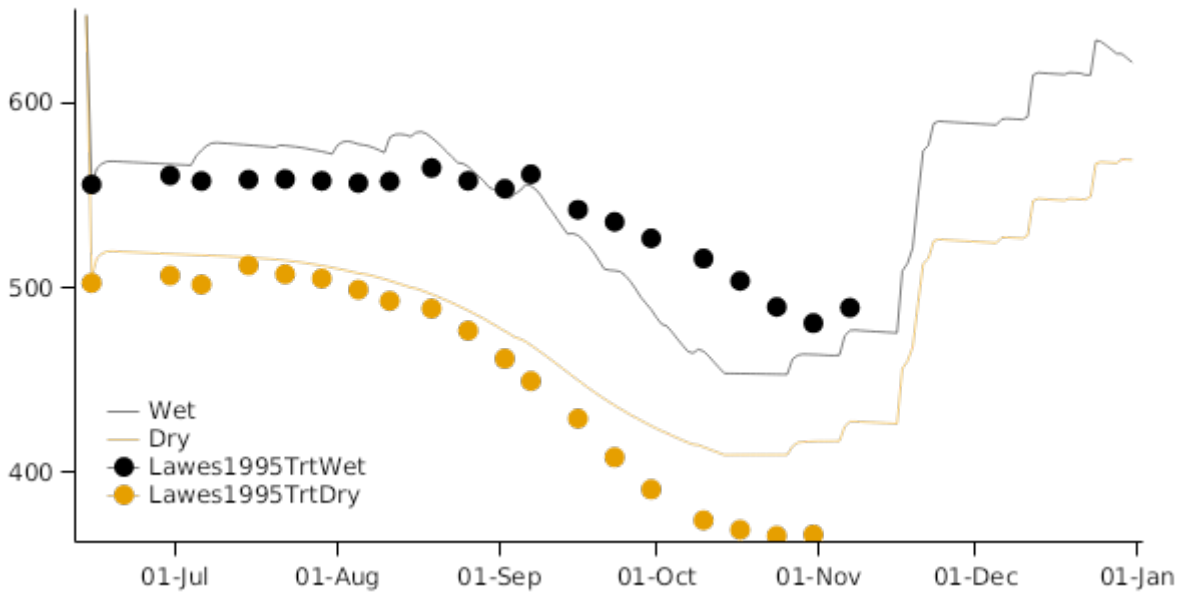
GrainWt



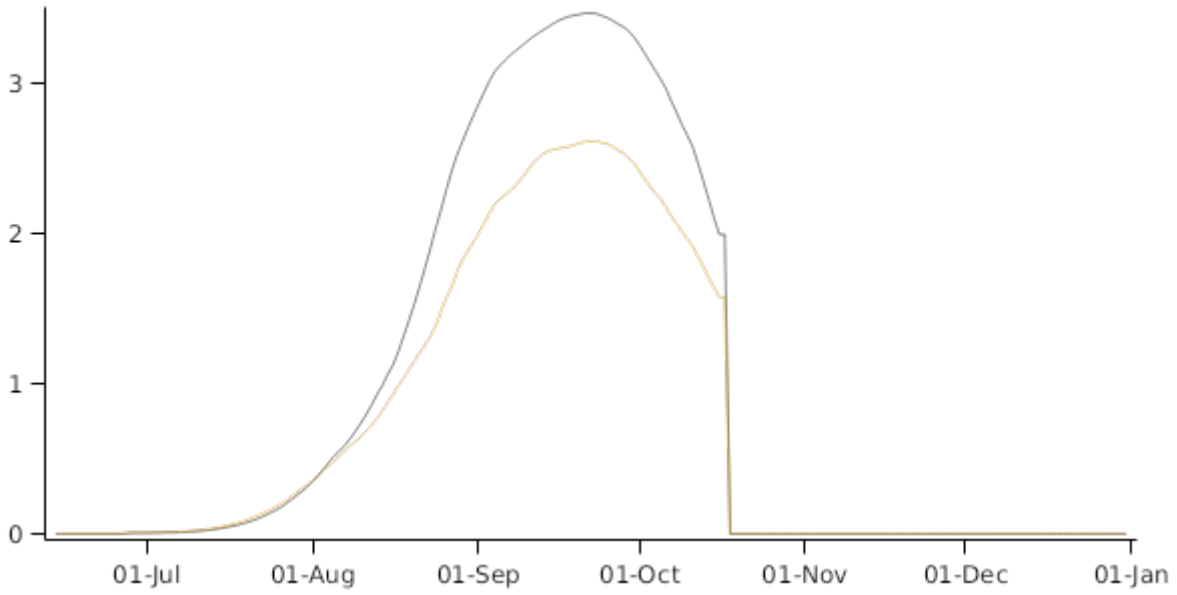
Stress



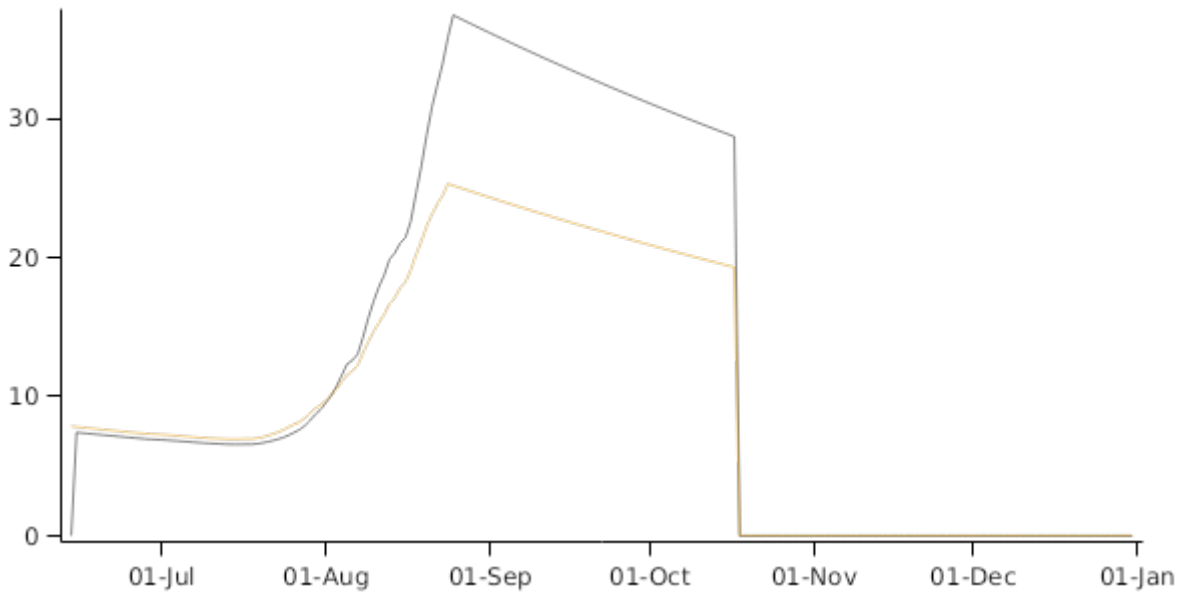
ProfileWater



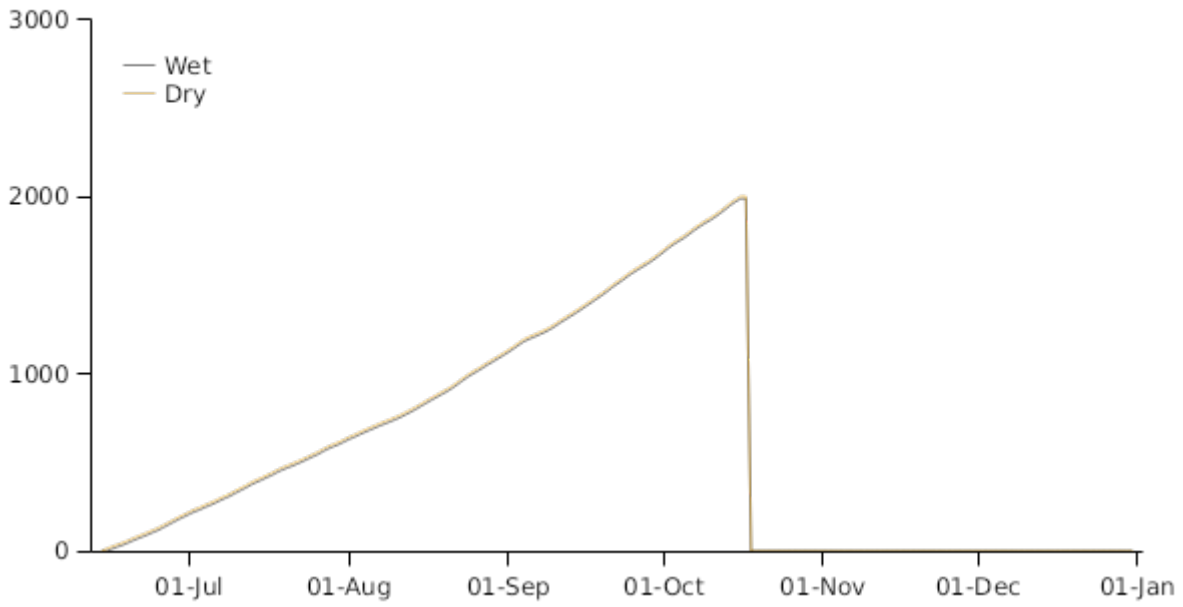
LAI



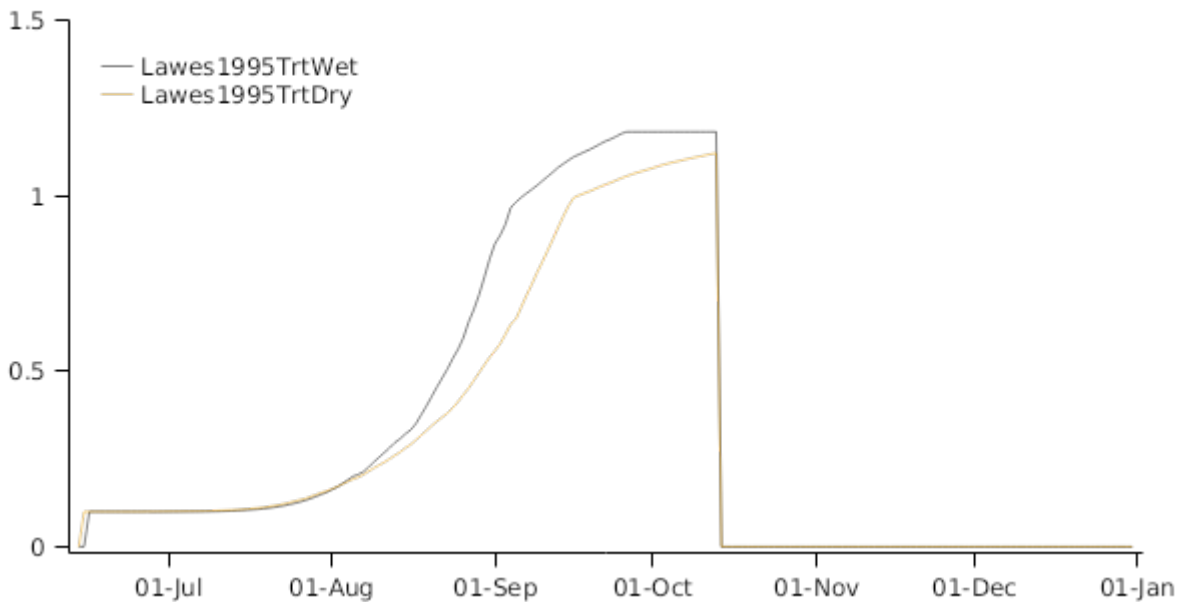
Root Mass



ThermalTime



klreport



2.3.4 Bremar_2003_

Experiment conducted by J Whish, near Meandarra. 2 time of sowing x 2 row spacing.

Some uncertainty about whether in-season soil cores were taken directly on the crop row, at the mid inter-row position.

Not great simulations but retained to show observed trends in relation to sowing date and row spacing. Some notes:

(1) site was quite a strong slope for southern QLD - may have simulated less runoff than actual.

(2) soil was highly variable, as per initial coring results from TOS1 and TOS2. The approach taken was to choose an average starting point that would go close to both TOS1 and TOS2, bearing in mind that increasing sowing soil water for TOS2 would increase overprediction.

(3) first biomass cut looks suspiciously similar to the second biomass cut. Areas may have been incorrectly reported either for first cut or subsequent cuts.

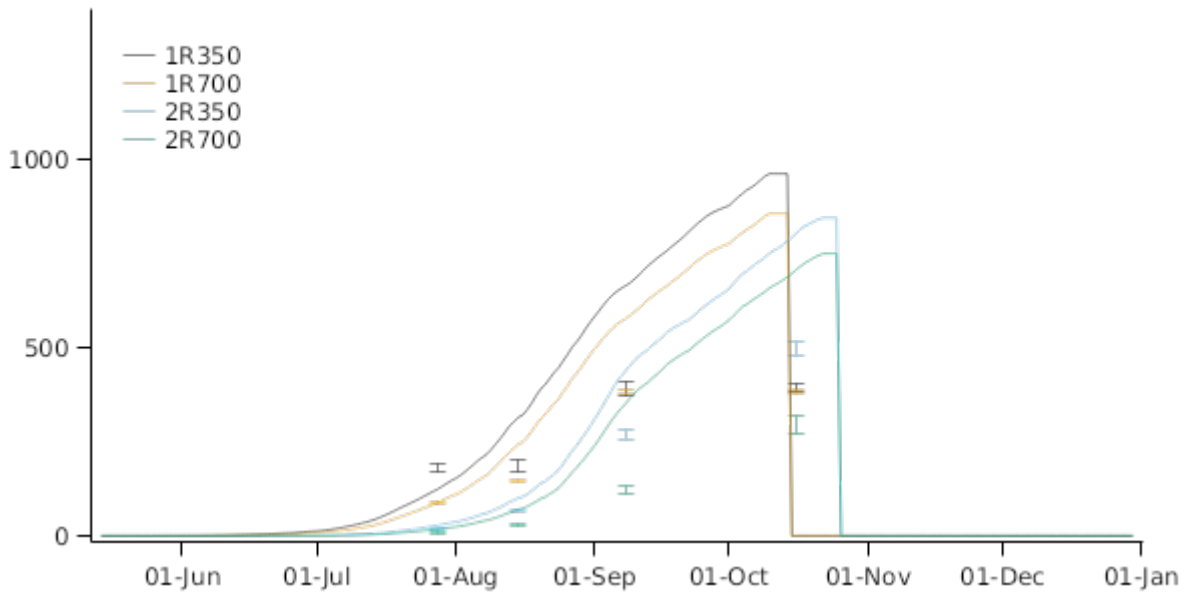
(4) It's quite possible that in 2003 undetected disease was limiting Chickpea growth and development

(5) the site was remote and biomass loss and shattering was likely during storms prior to harvest, and probably greater in TOS1 due to increased delay in obtaining final biomass.

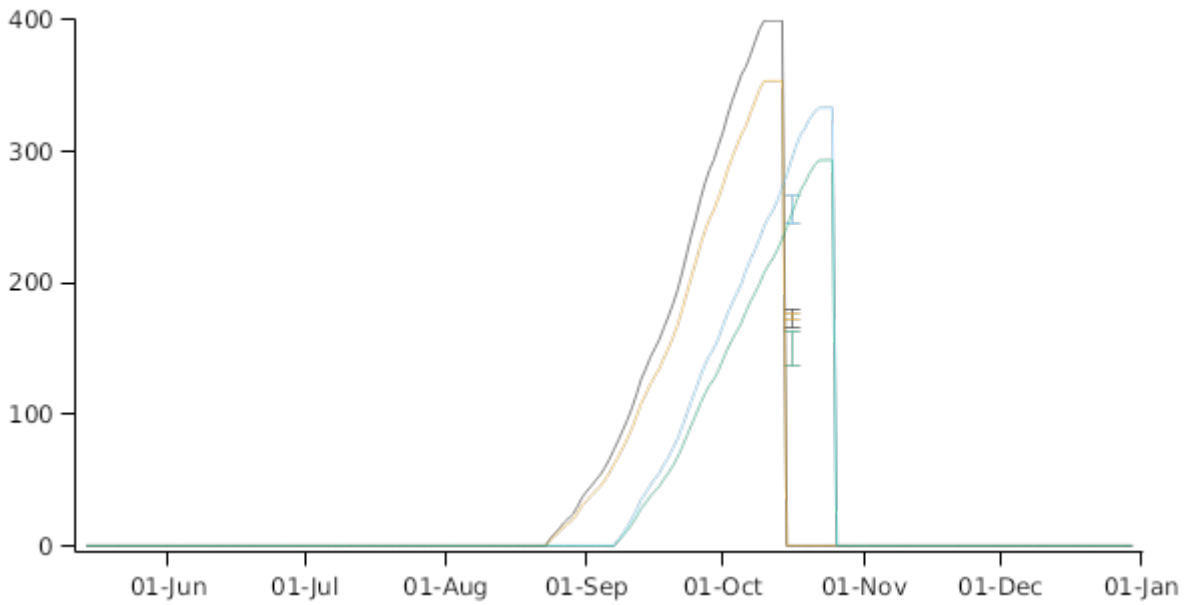
(6) some uncertainty around whether grower would actually have decreased plant pop for 35 cm row spacing, the plant pop for these treatments possibly may be double.

(7) Interesting note: the high population, narrow row spacing treatment was the highest yielding in the observed data - as per Kulai 2003. We haven't been able to simulate this. Possible that the narrow row spacing may have had double the plant population and this was not recorded correctly.

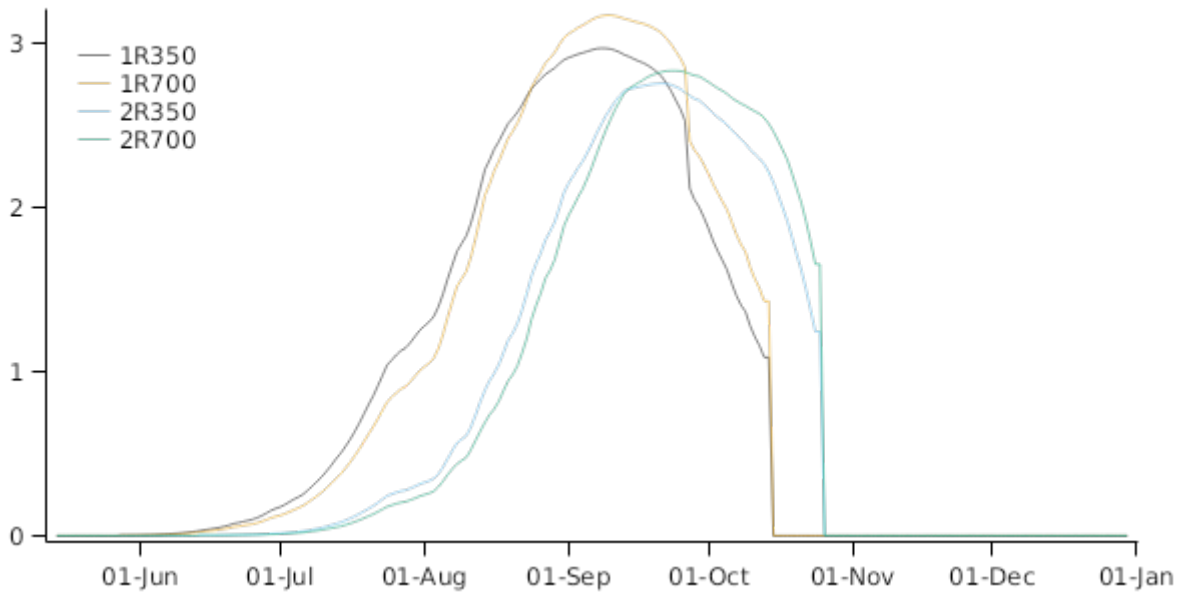
Biomass



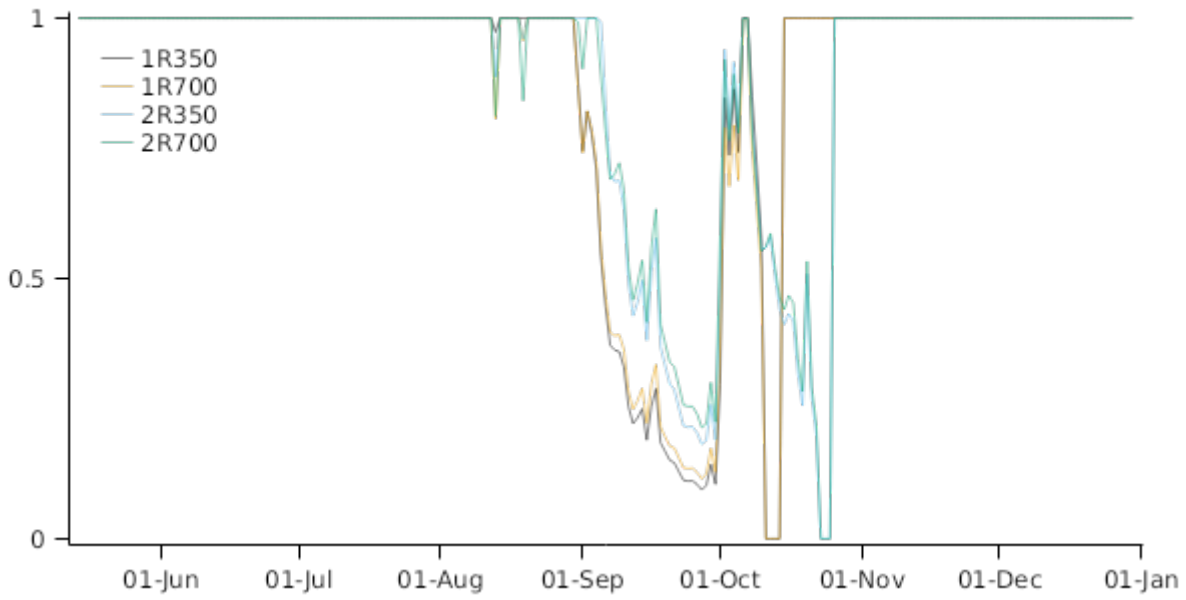
Grain Yield



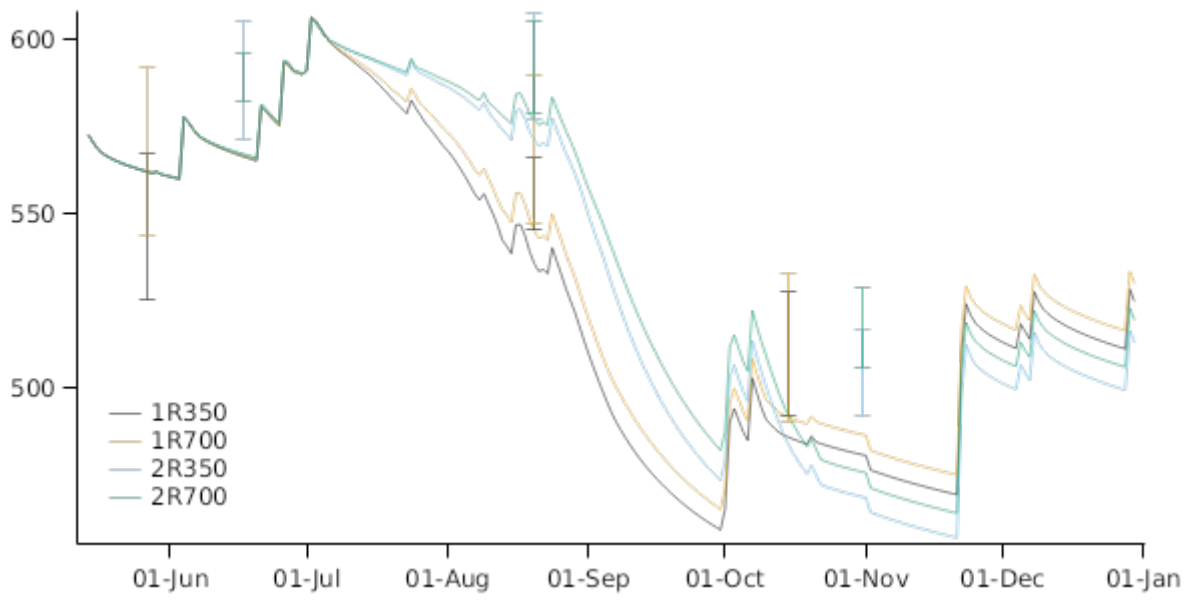
LAI



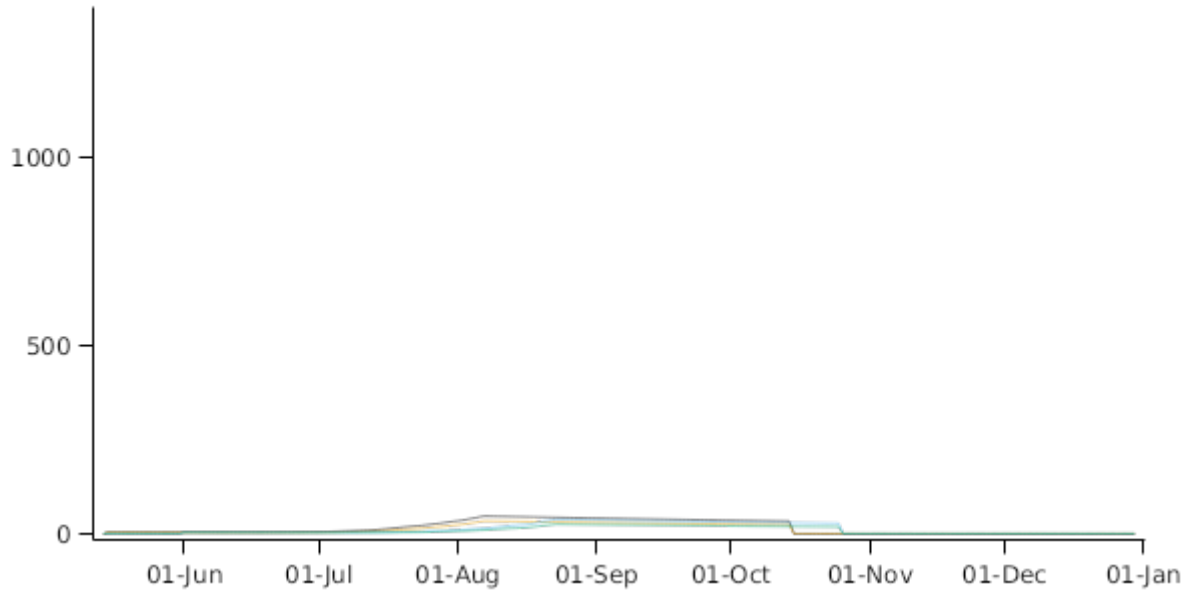
Stress



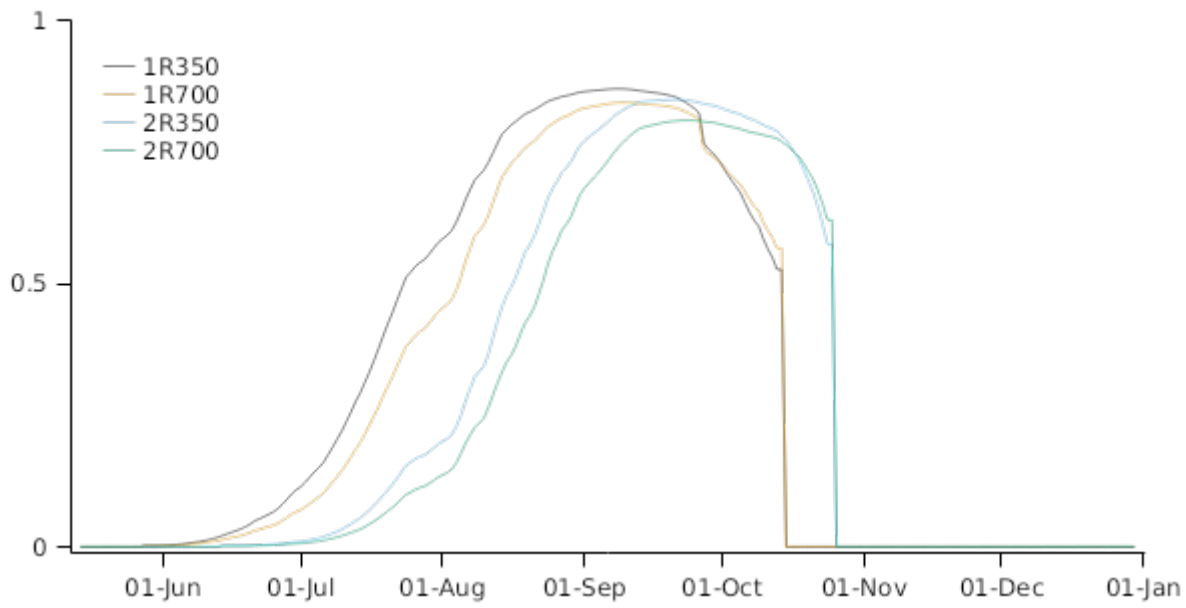
ProfileWater



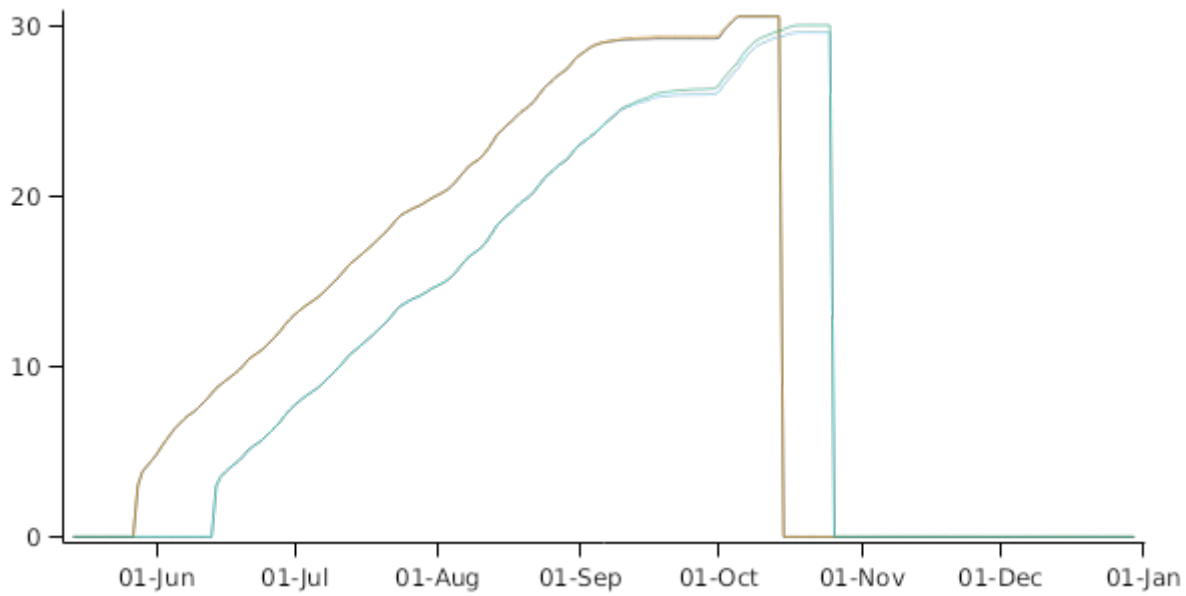
RootBiomass



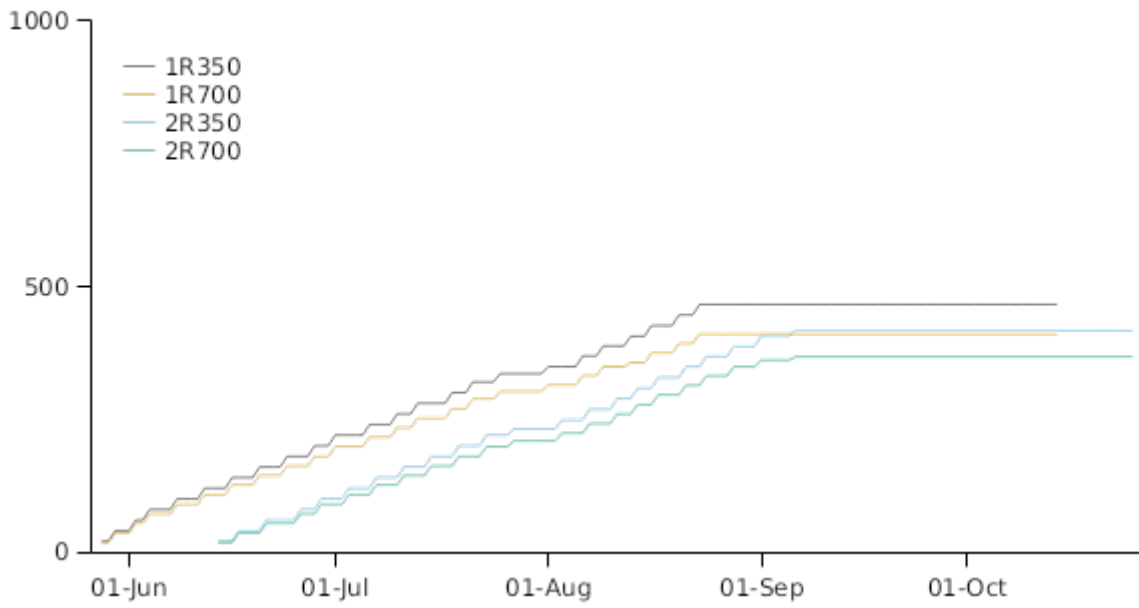
Cover



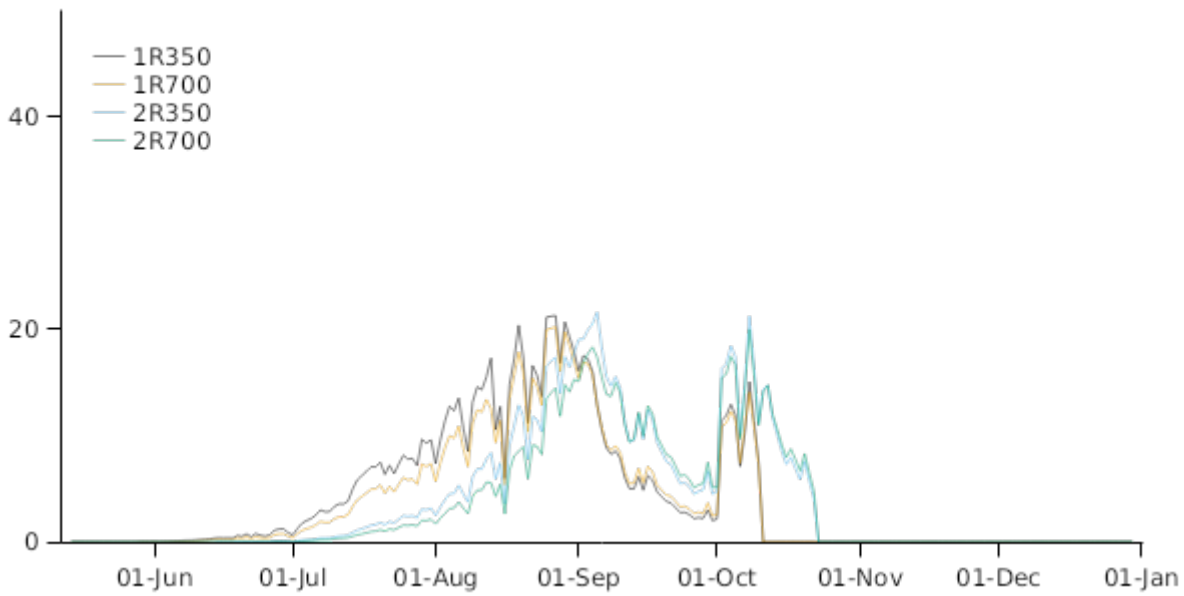
MSLeafNo



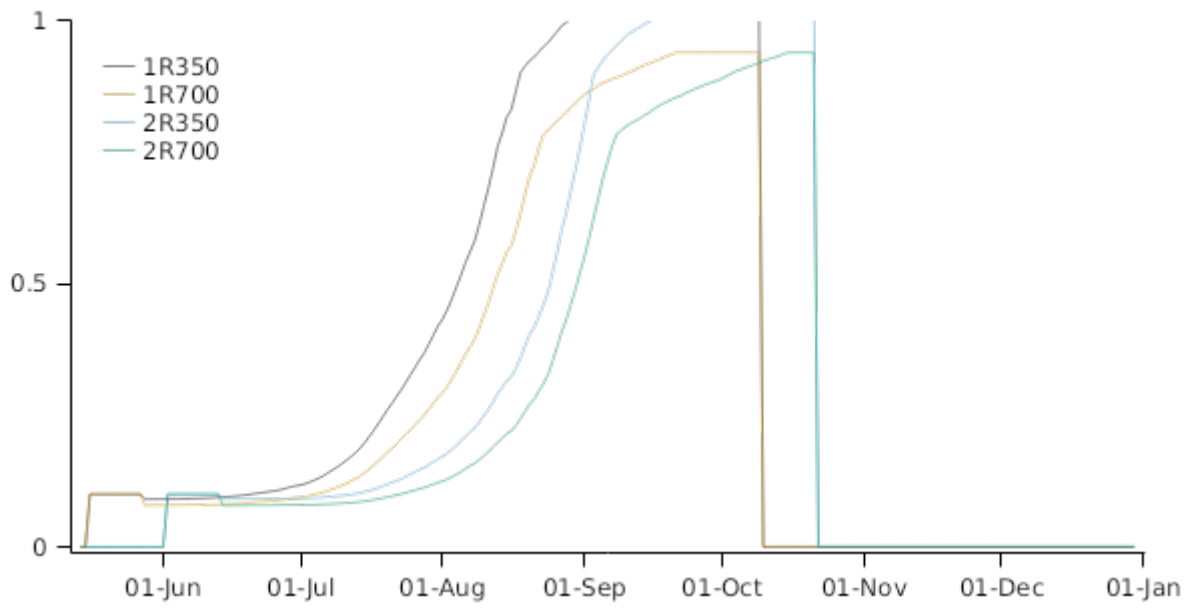
Branches_vs_time



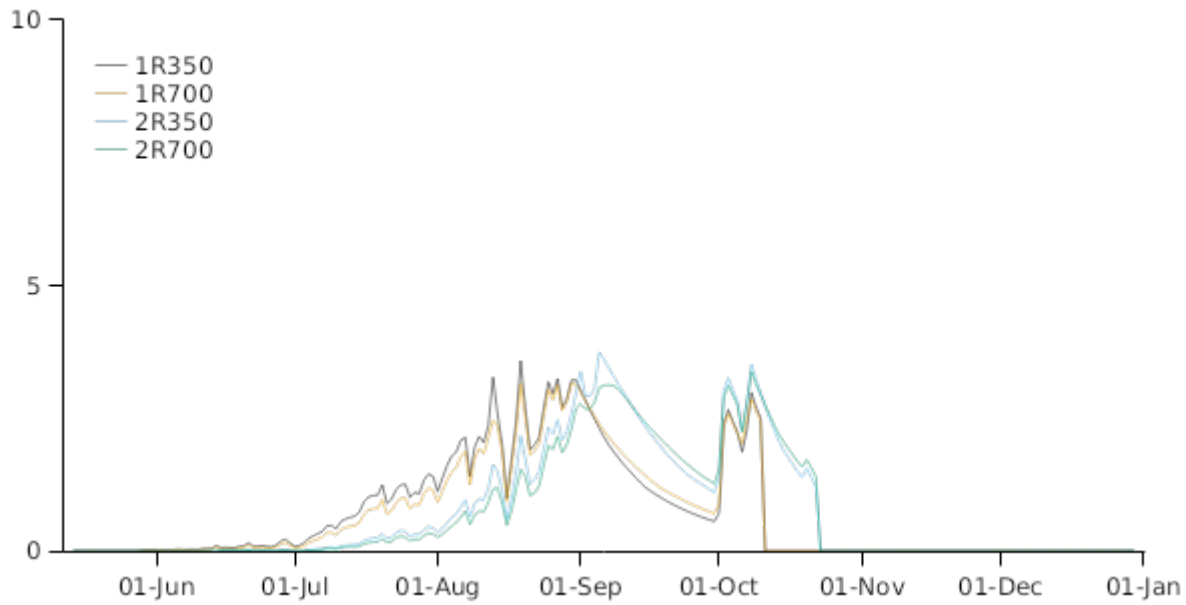
LeafPhotosynthesis



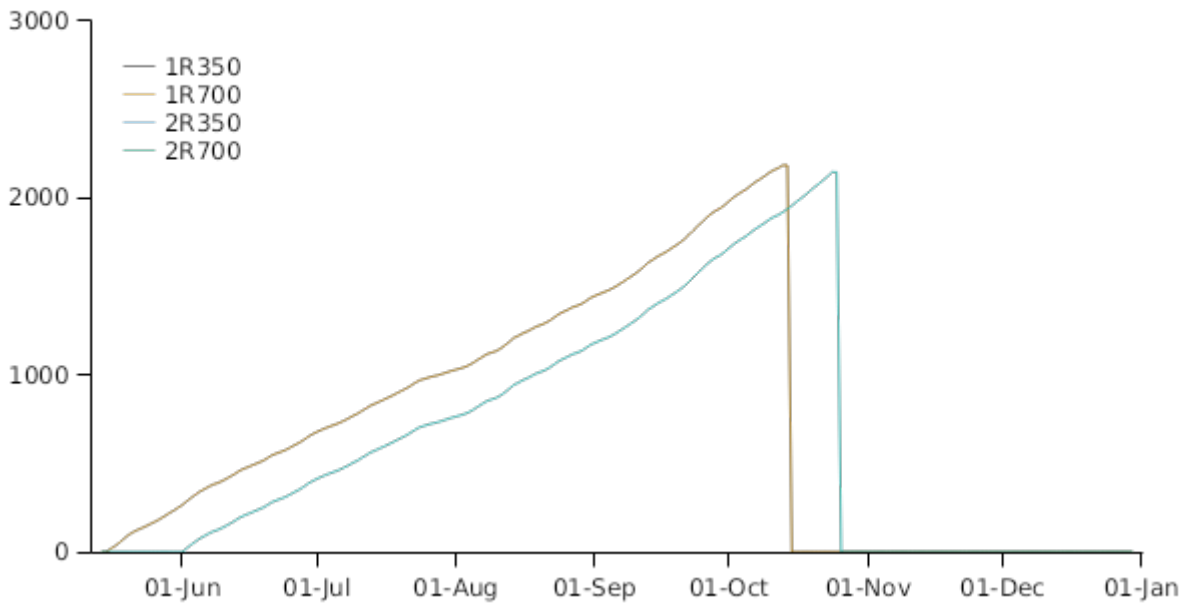
klreport



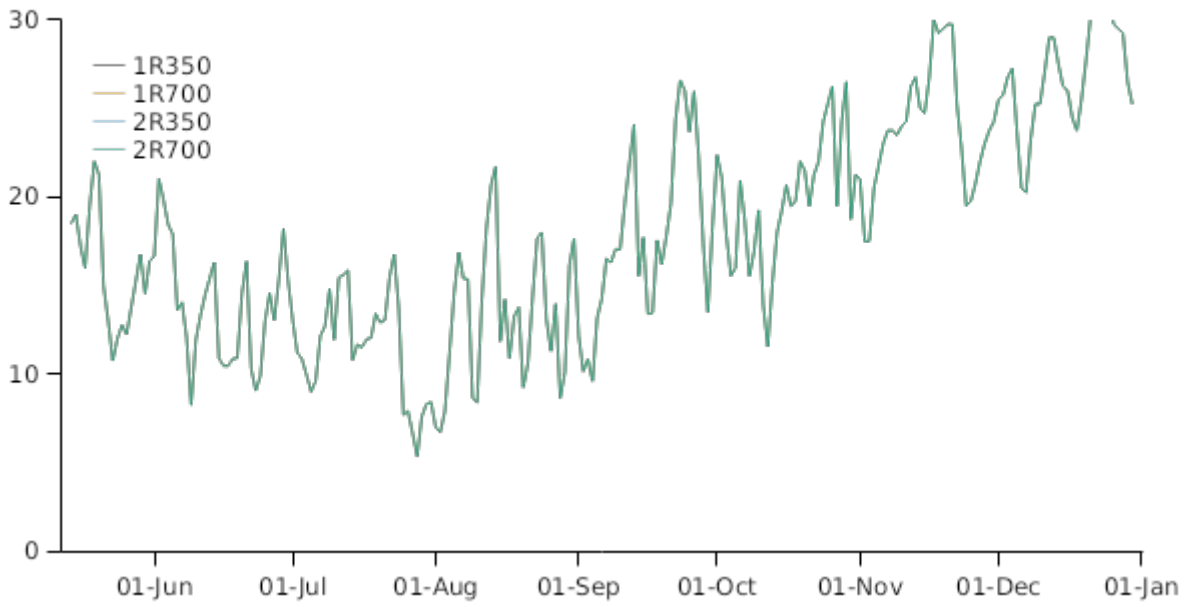
Transpiration



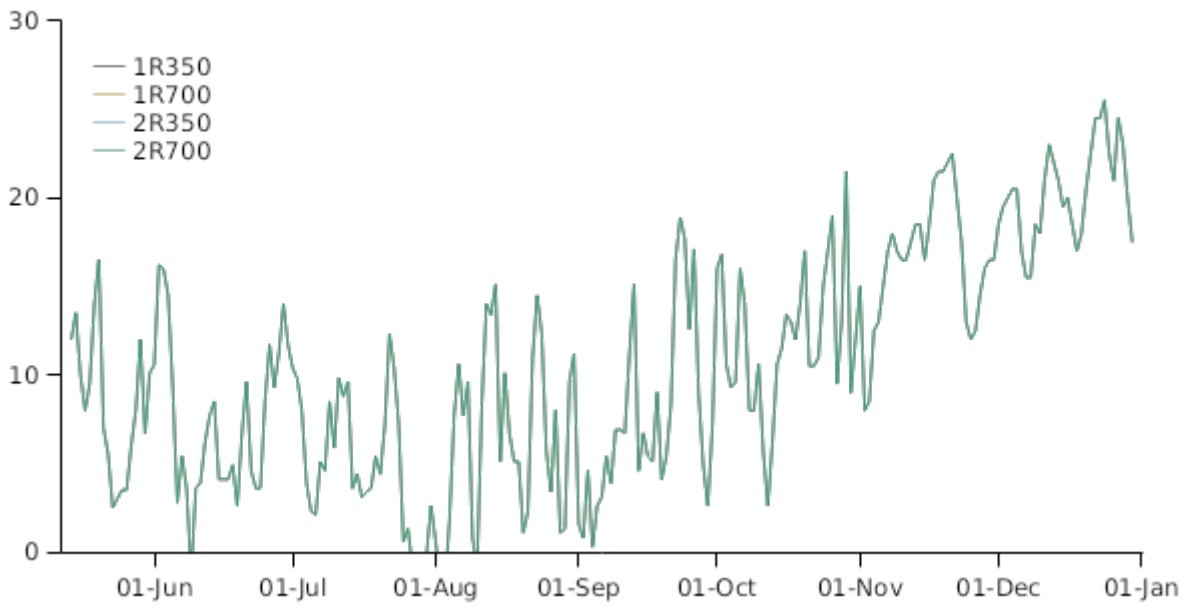
ThermalTime



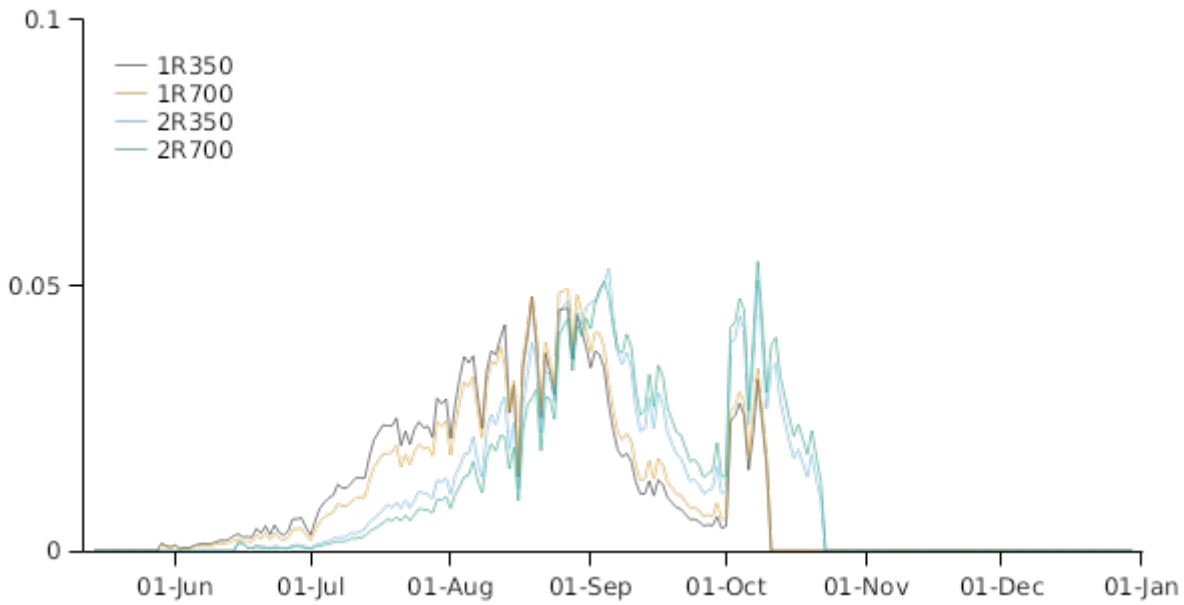
MeanT



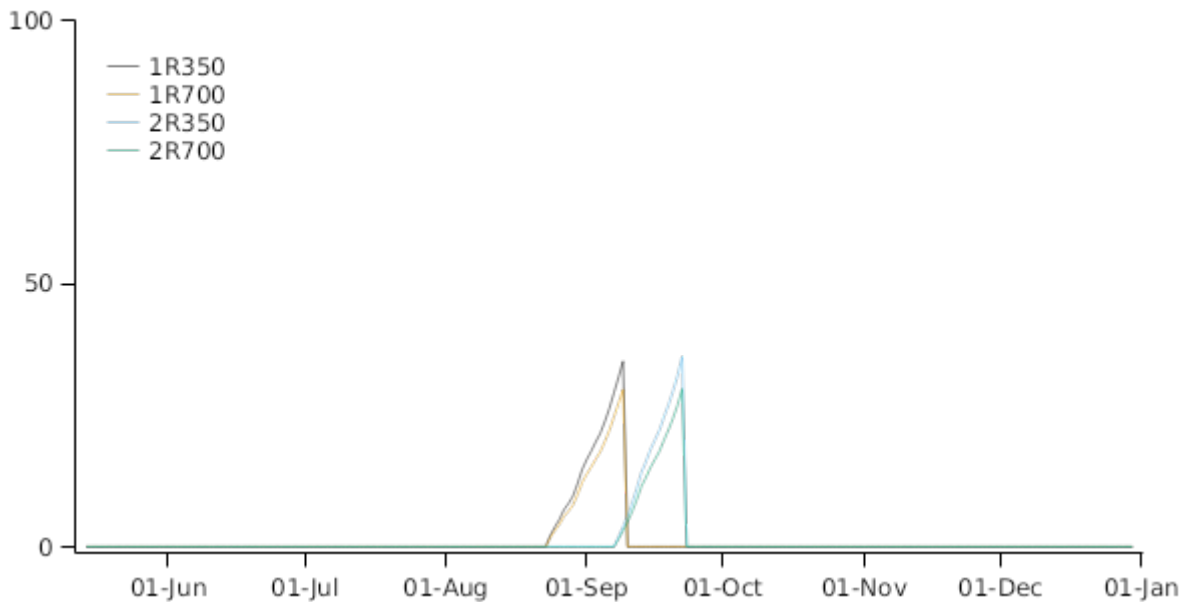
MinT



PhotoperBranch



ShellMass



2.4 NewSouthWales

List of experiments.

Experiment Name	Design (Number of Treatments)
Kulai_2003_	S (4)
Kulai_2004_	S (4)

2.4.1 Kulai_2003_

Experiment conducted by J Whish, near North Star on a red kandosol (there are a few paddocks with this soil in this district). 2 time of sowing x 2 row spacing.

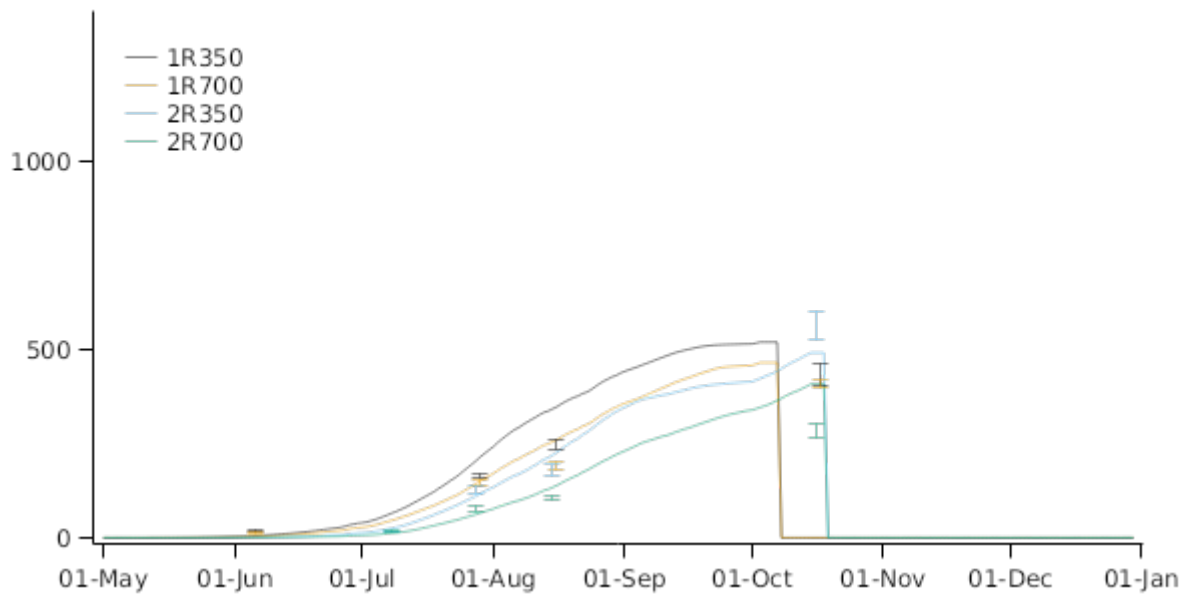
Some uncertainty about whether in-season soil cores were taken directly on the crop row, at the mid inter-row position.

Interesting note: the high population, narrow row spacing treatment was the highest yielding in the observed data - as per Bremar 2003. We haven't been able to simulate this. Possible that the narrow row spacing may have had double the plant population and this was not recorded correctly.

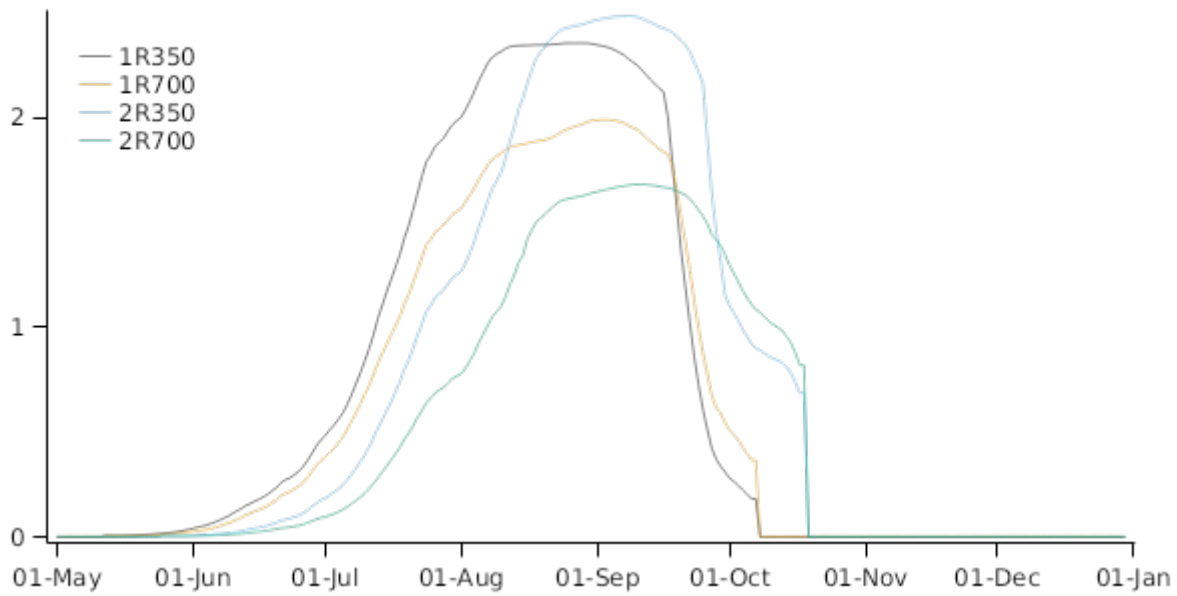
The site was remote and biomass loss and shattering was likely during storms prior to harvest, and probably greater in TOS1 due to increased delay in obtaining final biomass.

There is some uncertainty around whether grower would actually have decreased plant pop for 35 cm row spacing, the plant pop for these treatments possibly may be double.

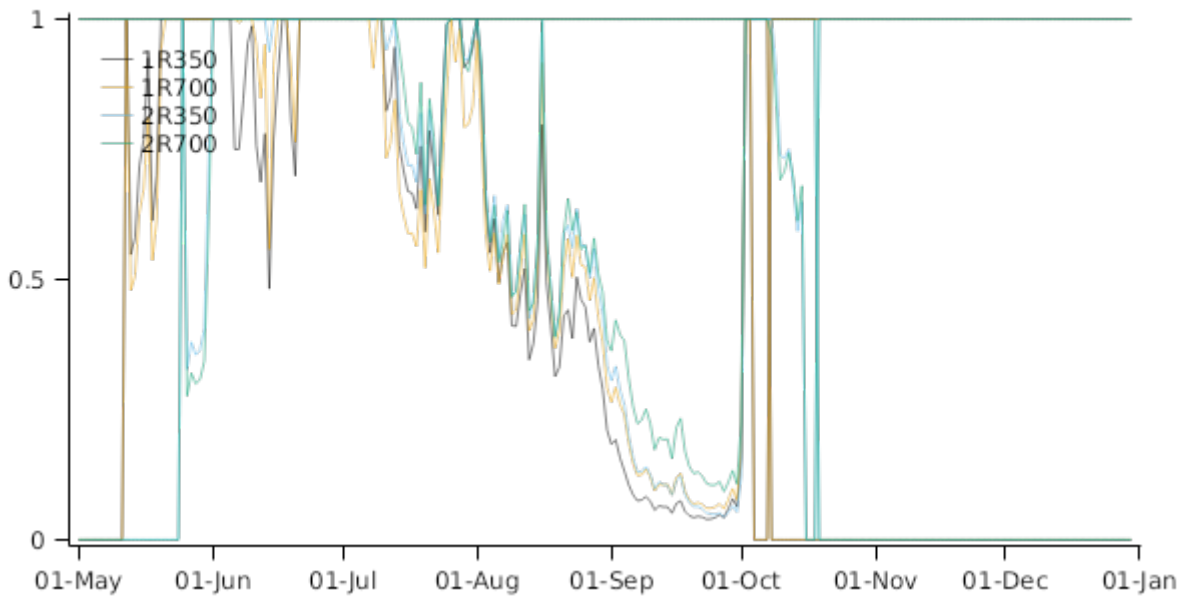
AboveGroundWt



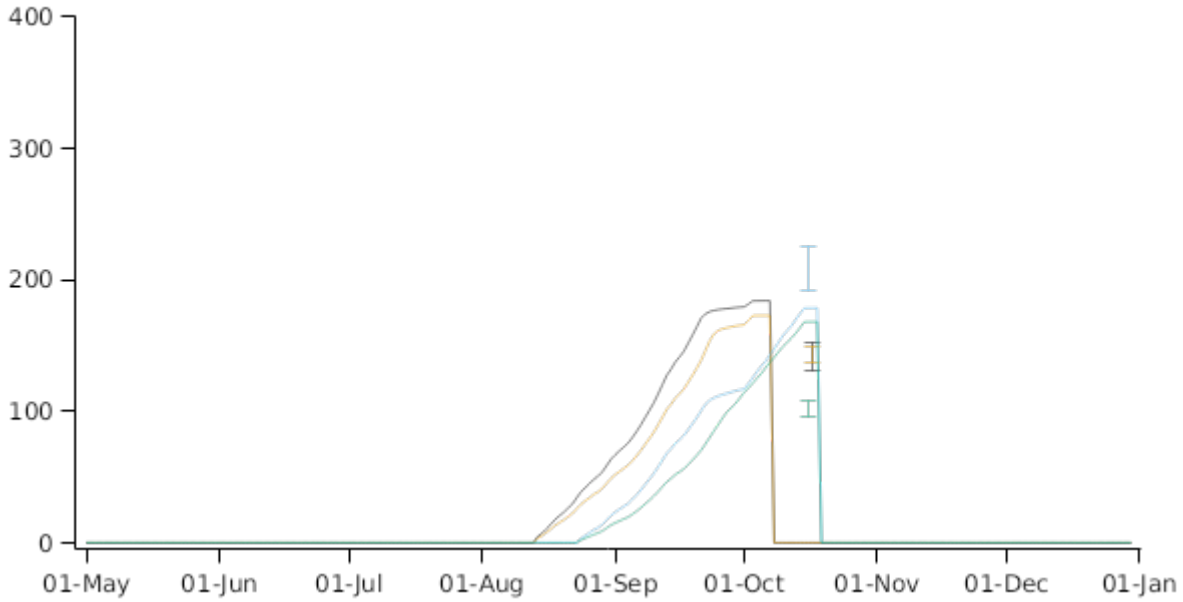
LAI



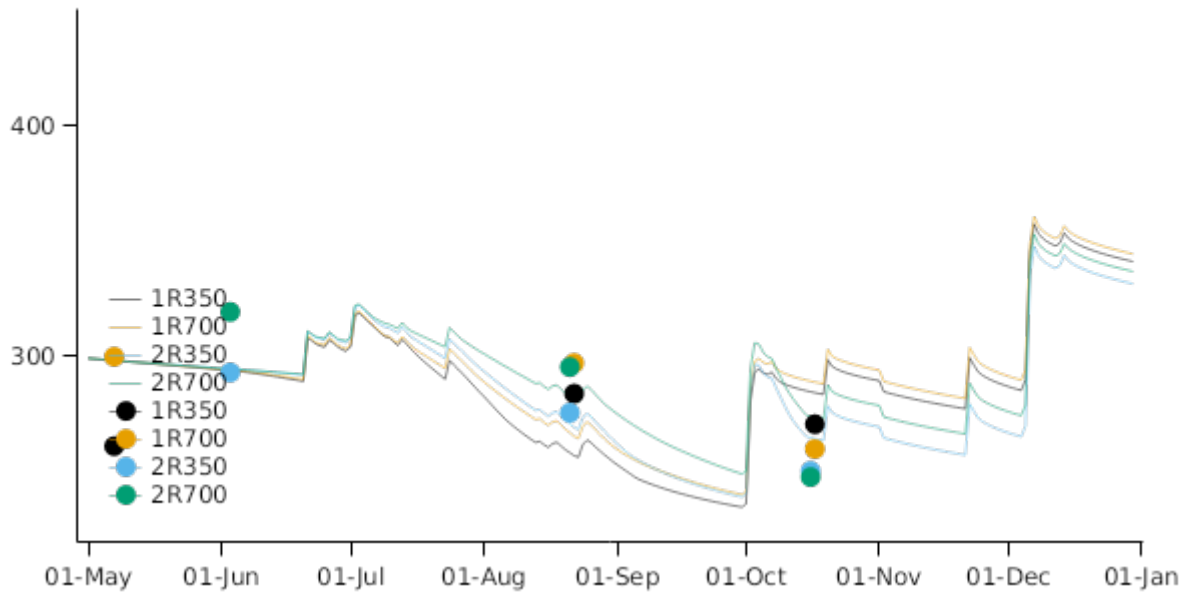
Stress



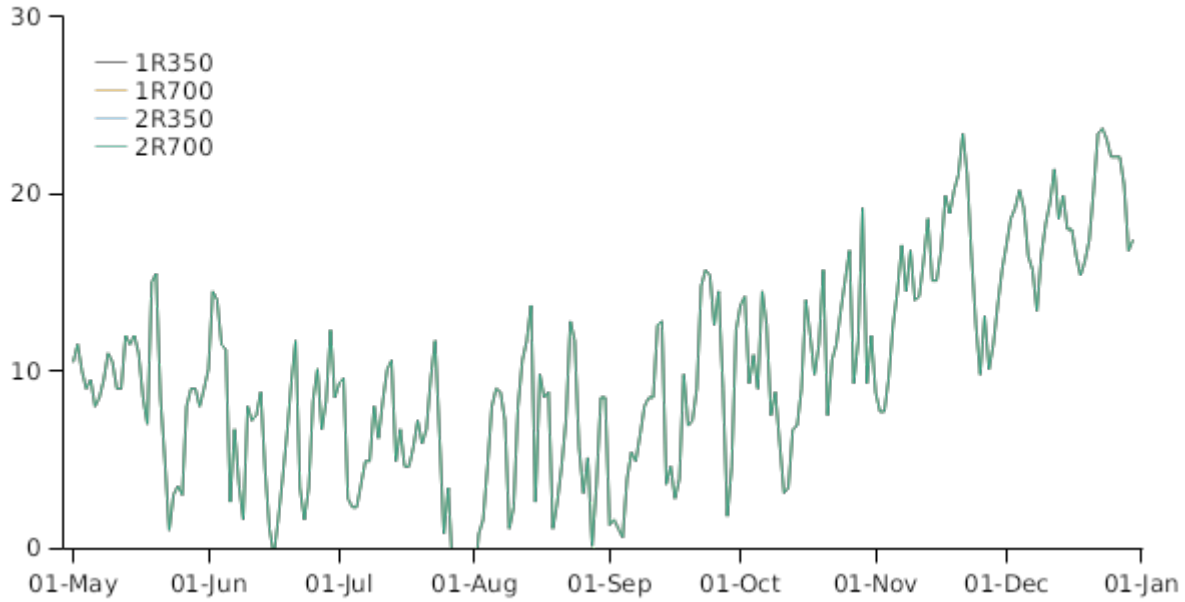
GrainWt



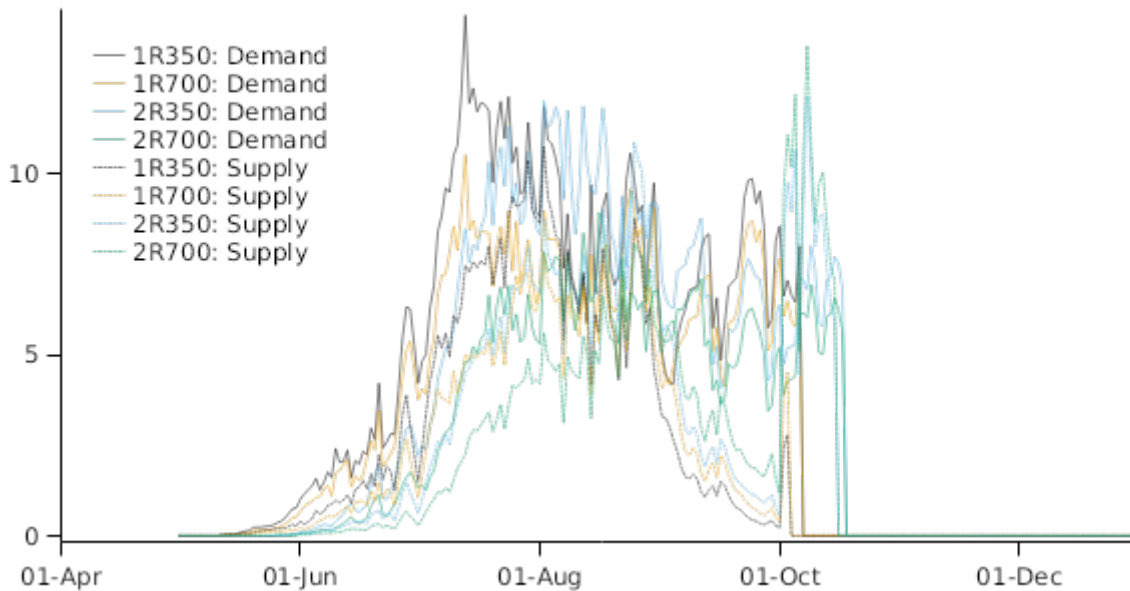
ProfileWater_5layers



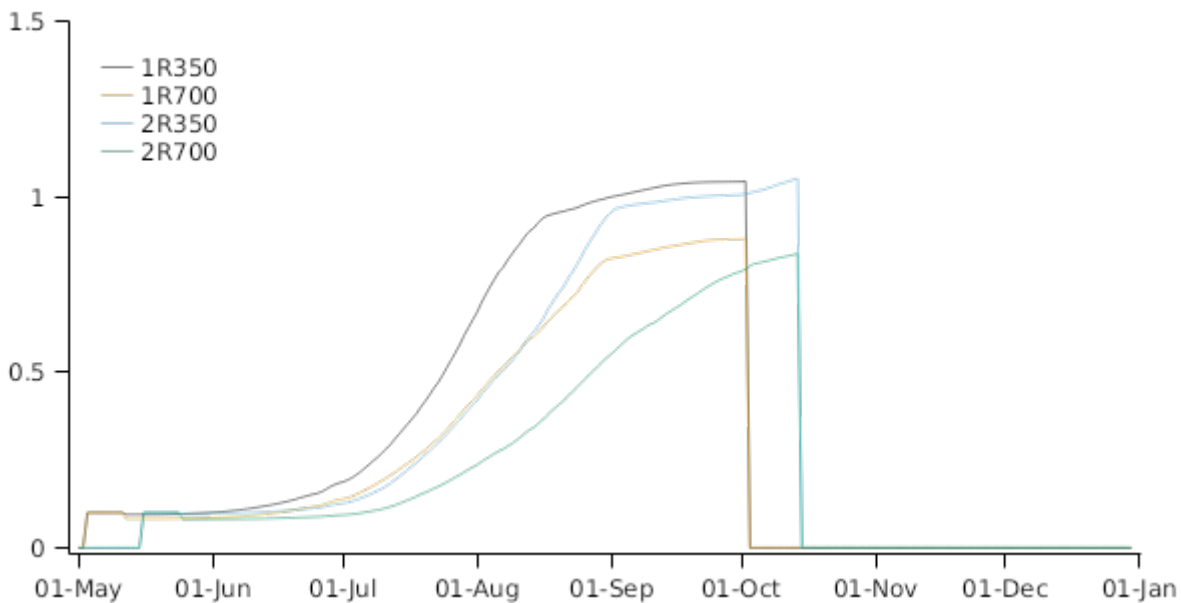
MinT



DMSupplyDemand



klreport



2.4.2 Kulai_2004_

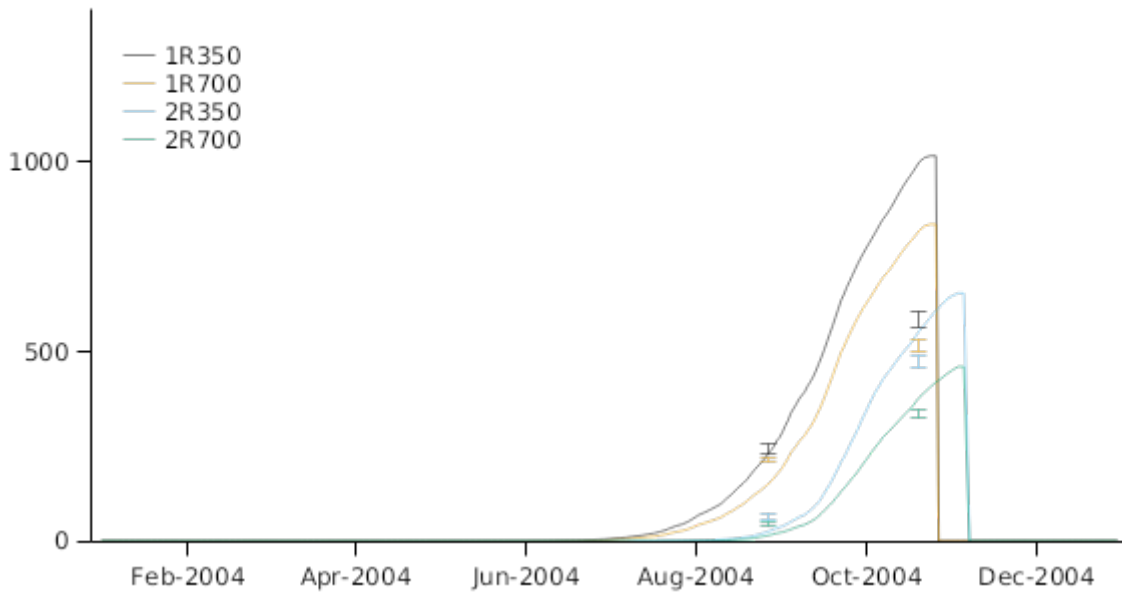
Experiment conducted by J Whish, near North Star. In this second year the experiment was conducted on a red-brown vertosol on the same farm as the year 1 experiment, which was on a red kandosol (there are a few paddocks with this soil in this district). 2 time of sowing x 2 row spacing.

Some uncertainty about whether in-season soil cores were taken directly on the crop row, at the mid inter-row position.

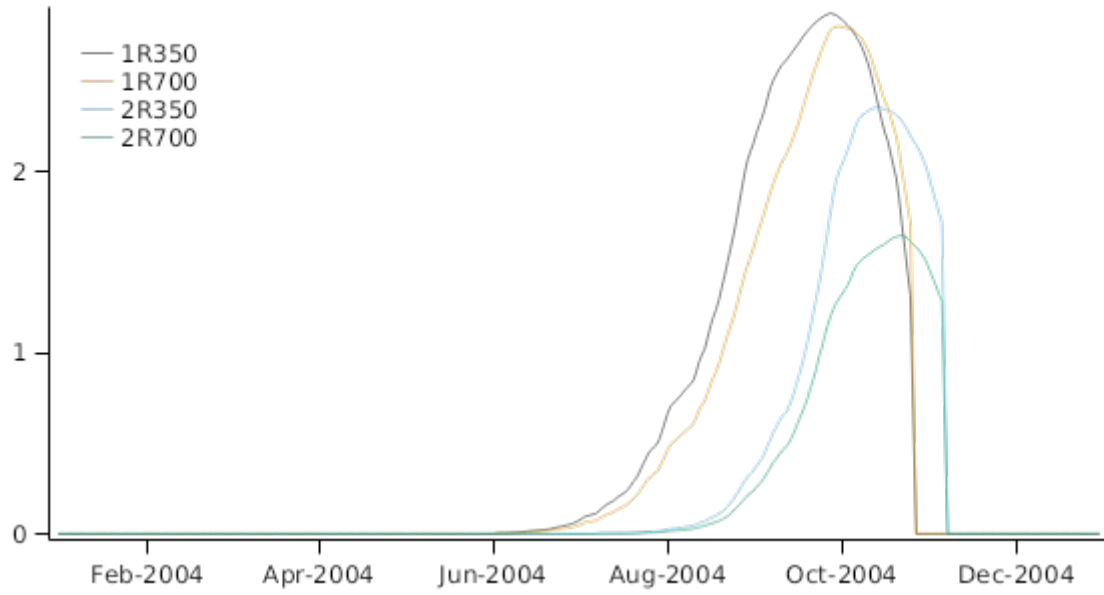
The site was remote and biomass loss and shattering was likely during storms prior to harvest, and probably greater in TOS1 due to increased delay in obtaining final biomass.

There is some uncertainty around whether grower would actually have decreased plant pop for 35 cm row spacing, the plant pop for these treatments possibly may be double.

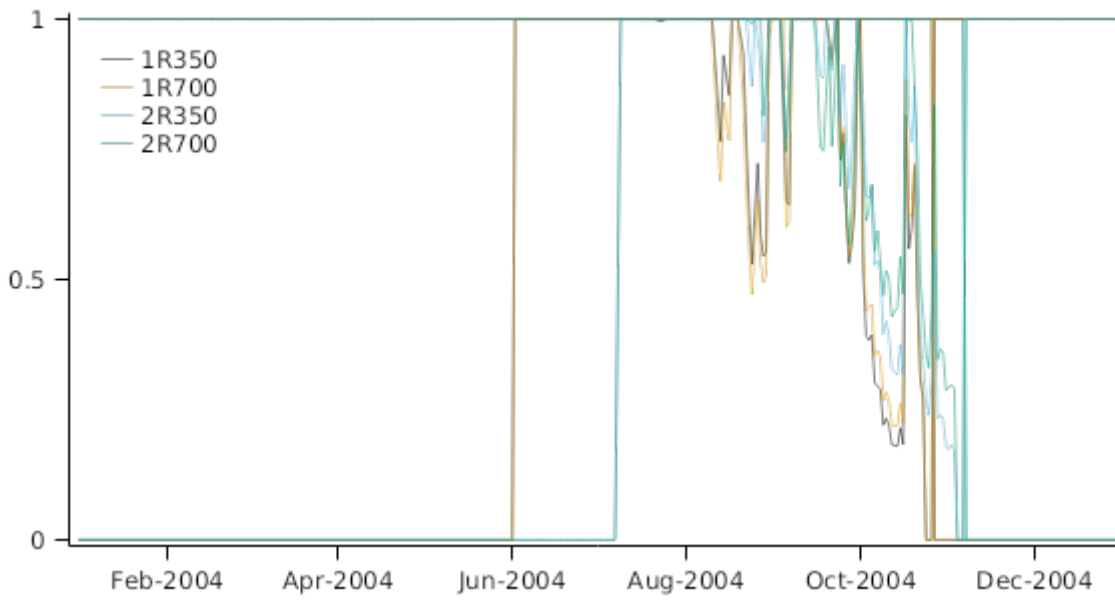
AboveGroundWt



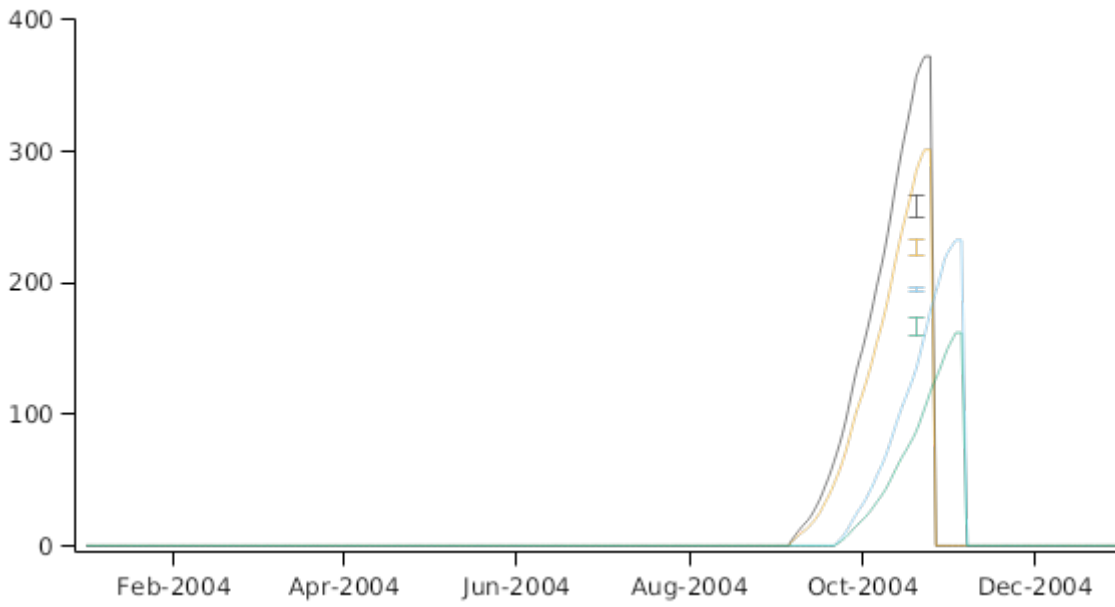
LAI



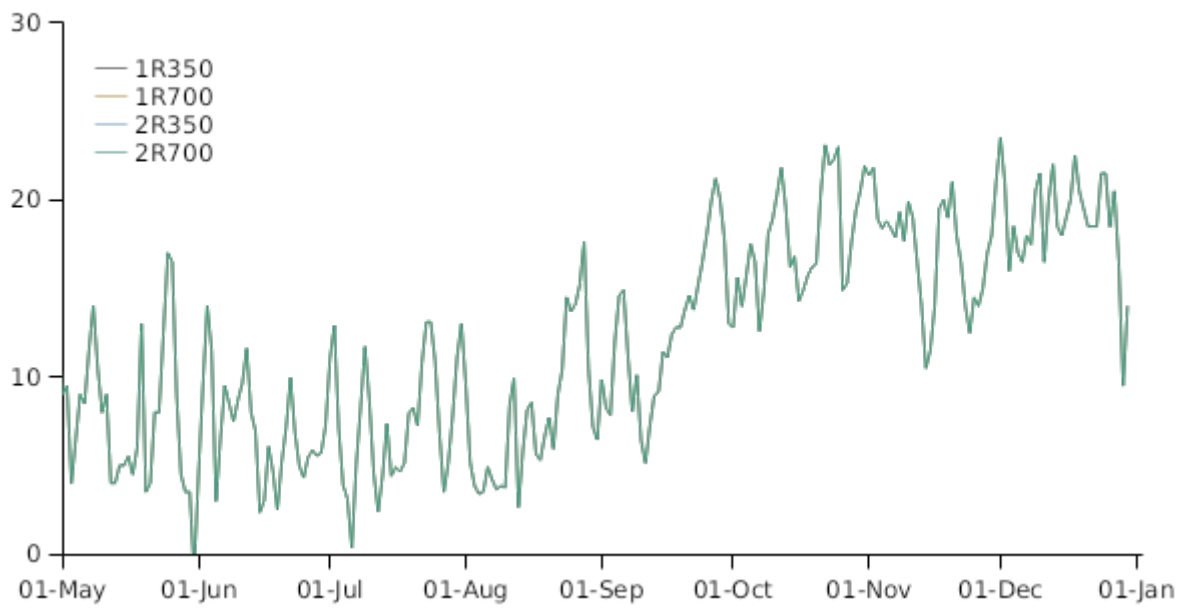
Stress



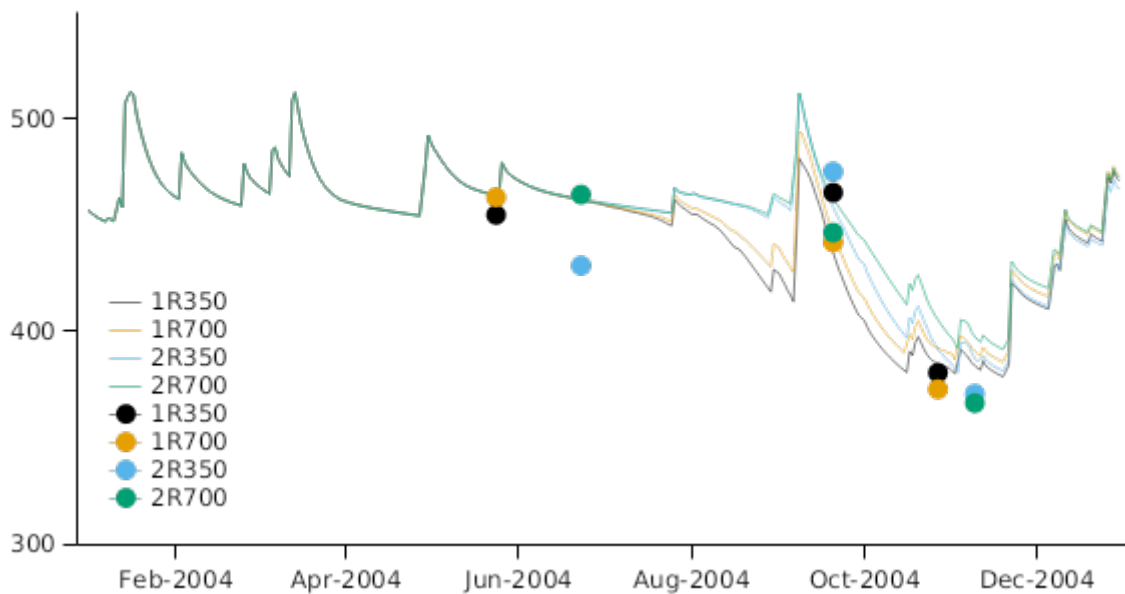
GrainWt



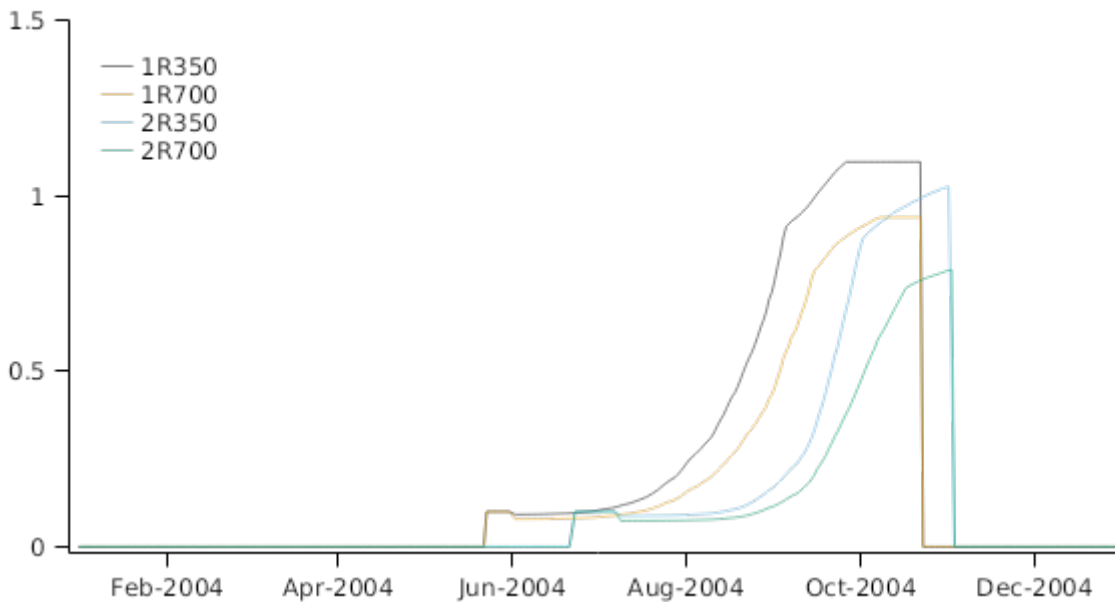
MinT



ProfileWater_5layers



klreport



2.5 ICRISAT

List of experiments.

Experiment Name	Design (Number of Treatments)
ICRISAT_18_19_BM8_	Cv_ (4)

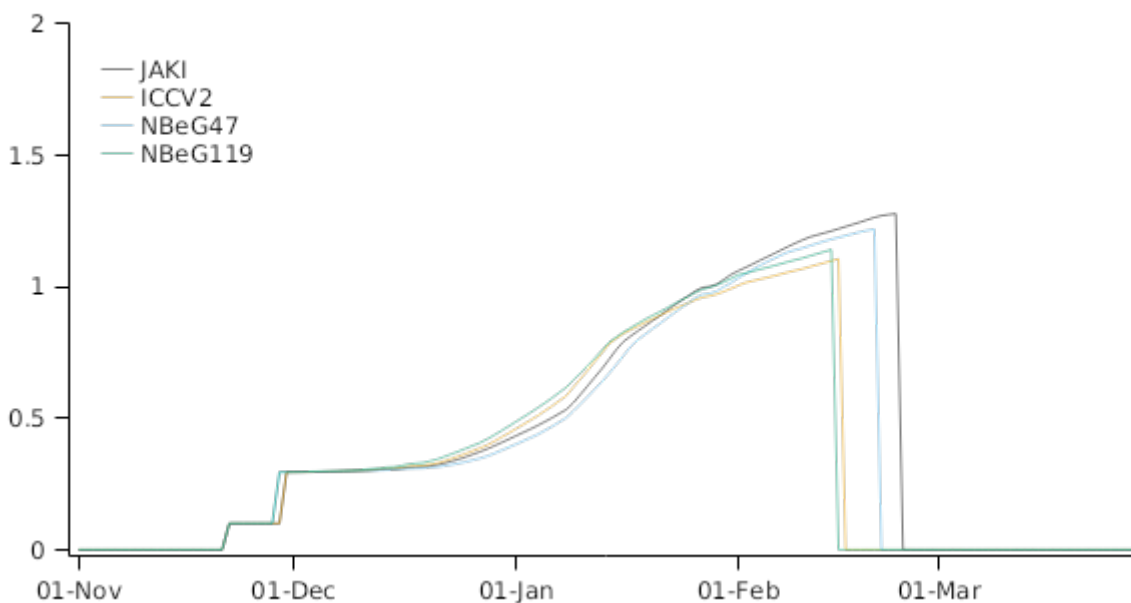
2.5.1 ICRISAT_18_19_BM8_

Experiment conducted at ICRISAT, Hyderabad in 2018/2019 by Amir Hajjapoor, postdoc working for Jana Kholova.

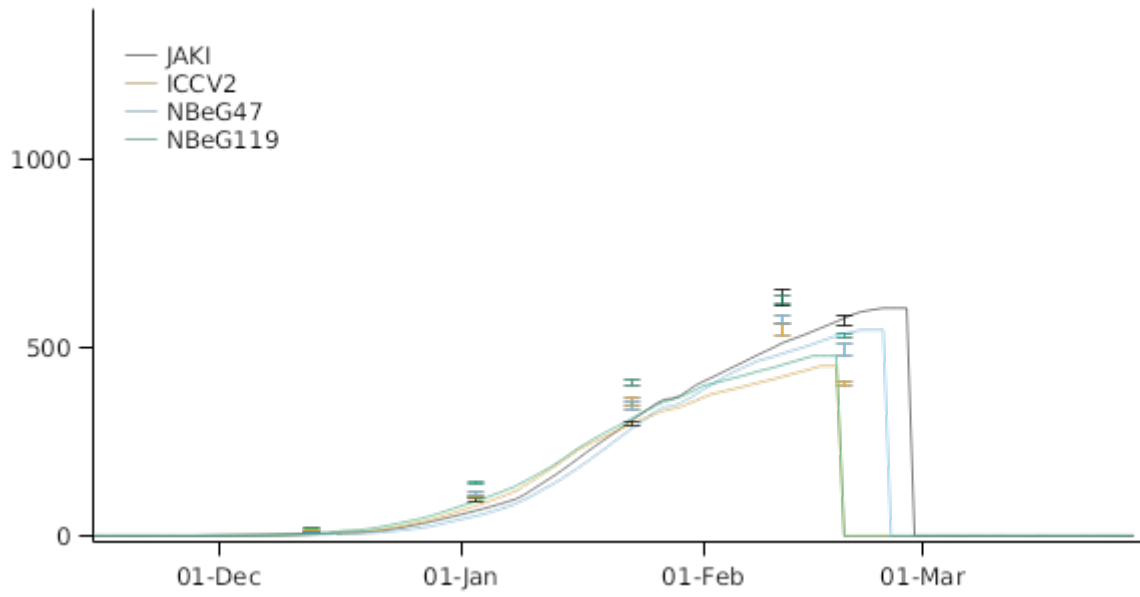
A number of experiments were conducted but there were many problems with emergence and pests (peacocks). This experiment was the best, 4 cultivars x one sowing date. Plant stand was uneven but OK.

Unsure why grain yield is not simulated well when biomass was. Pod + grain data indicates simulated grain development was behind the observed, perhaps in a warm environment pod initiation occurs sooner, or cultivars may have a different branching structure that allows them to set more grains faster once flowering begins. Also possible that flowering date was not correctly recorded and perhaps grainfilling began sooner.

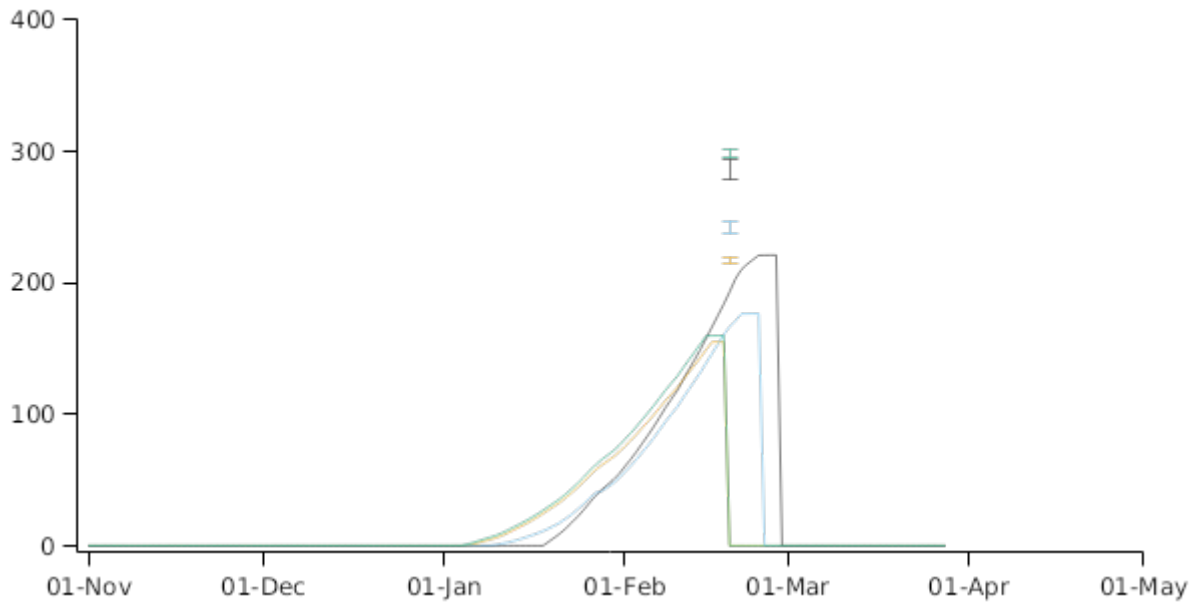
klreport



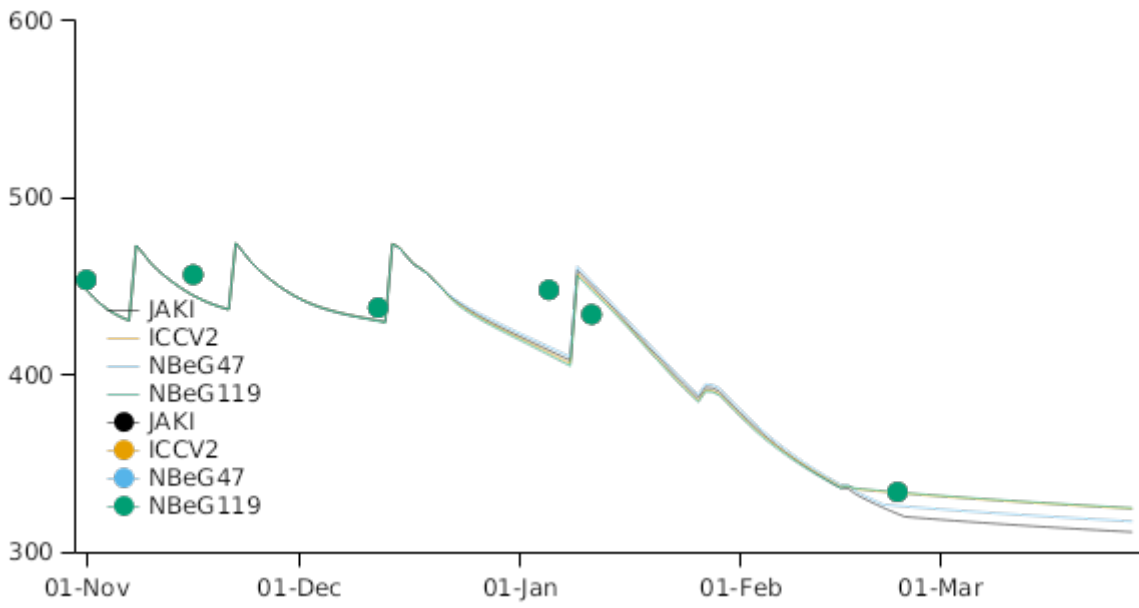
Biomass



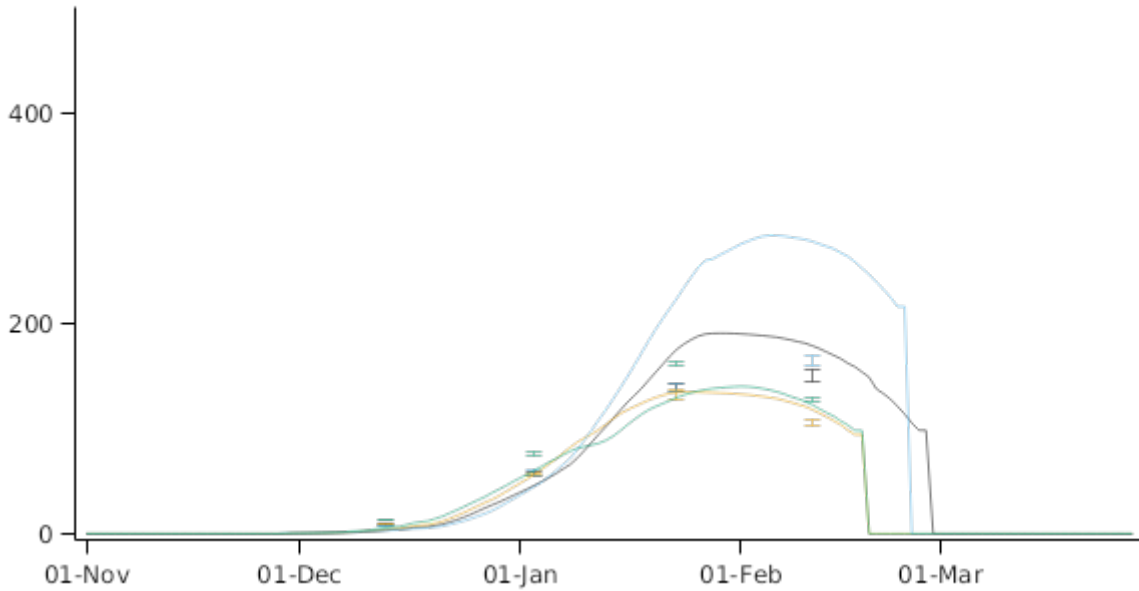
GrainWt



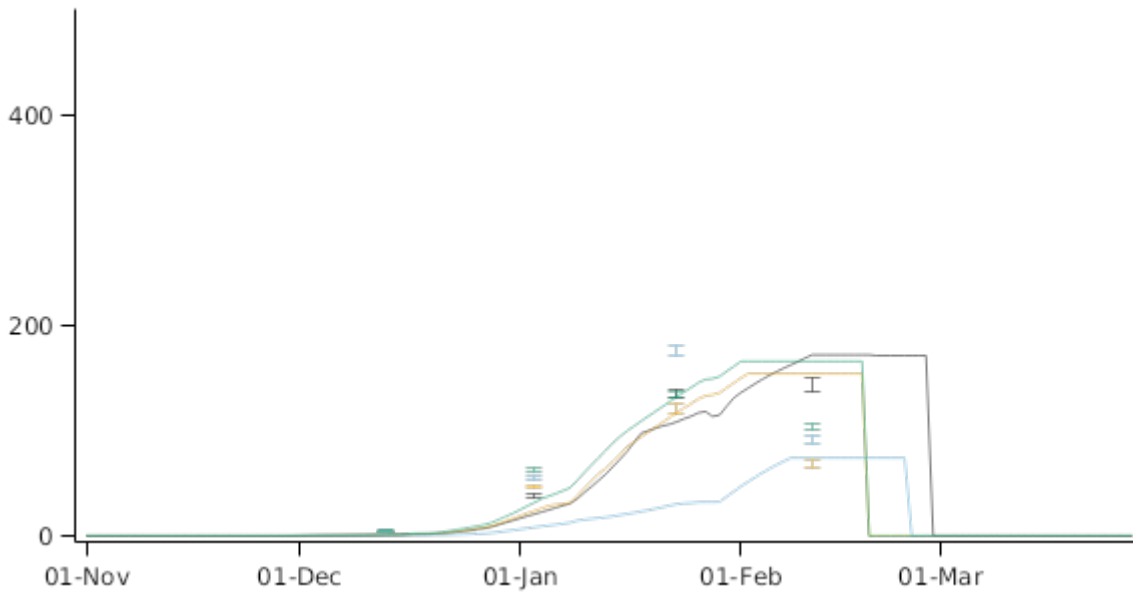
ProfileWater_5layers



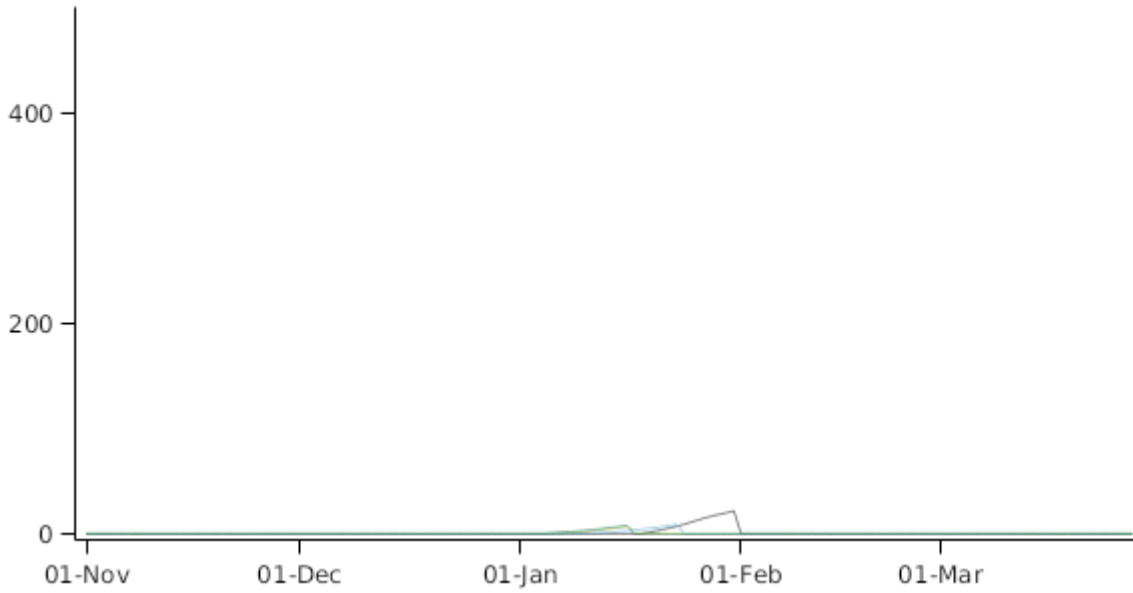
Leaf Mass



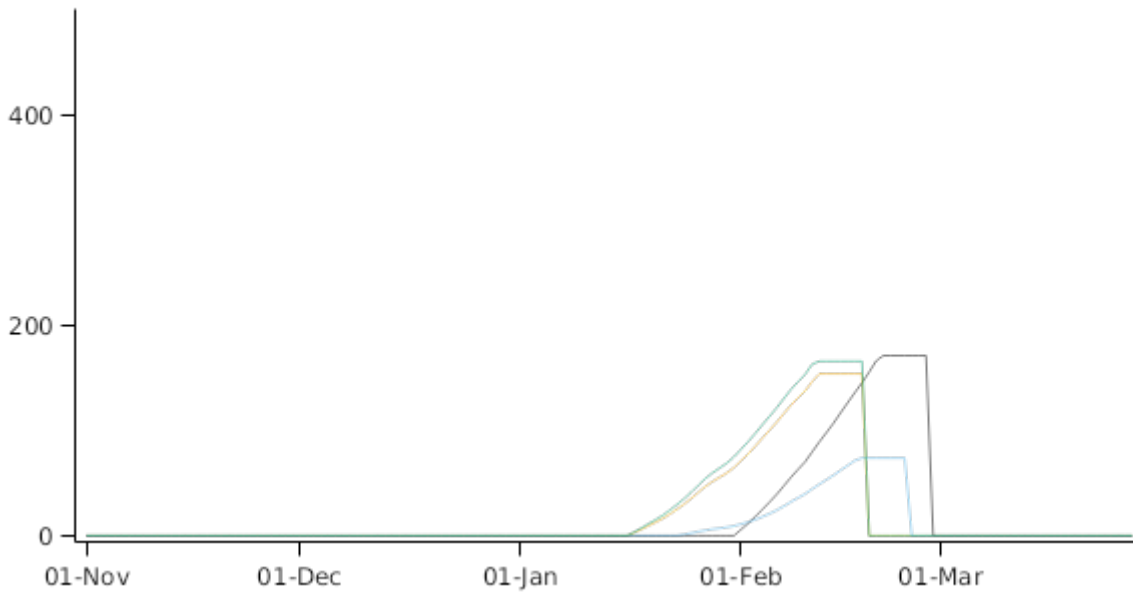
Stem Mass



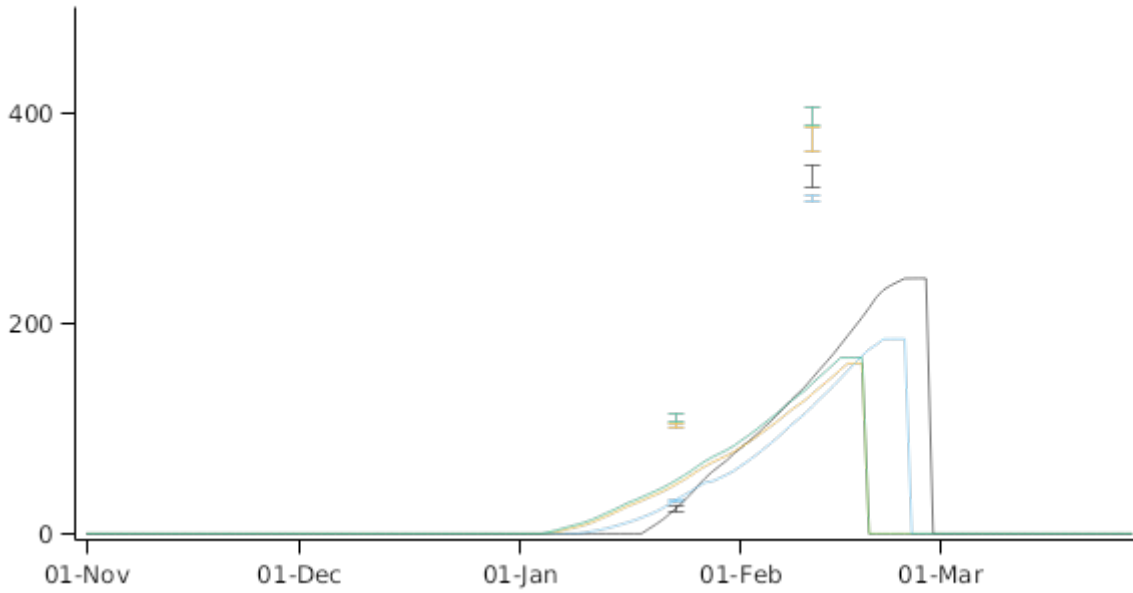
Shell Mass



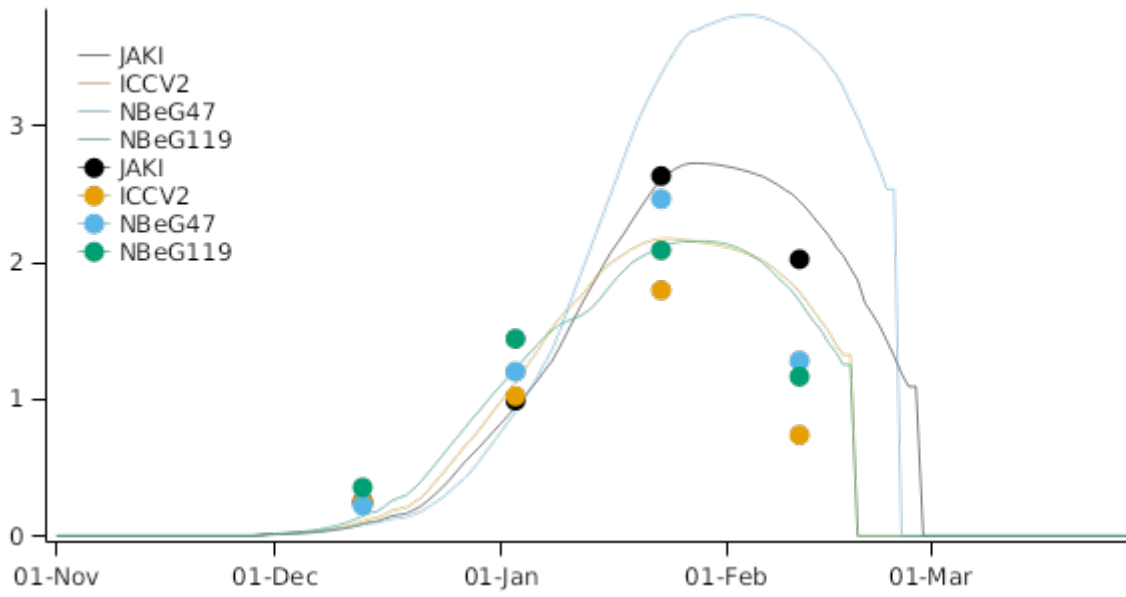
Dead Stem Mass



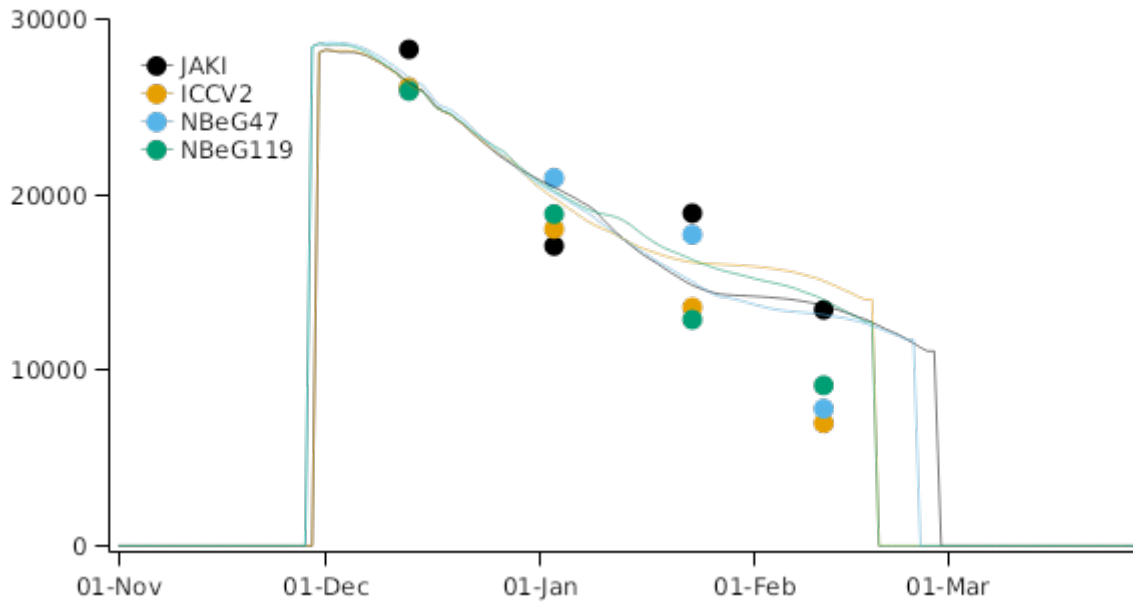
PodPlusGrainWt



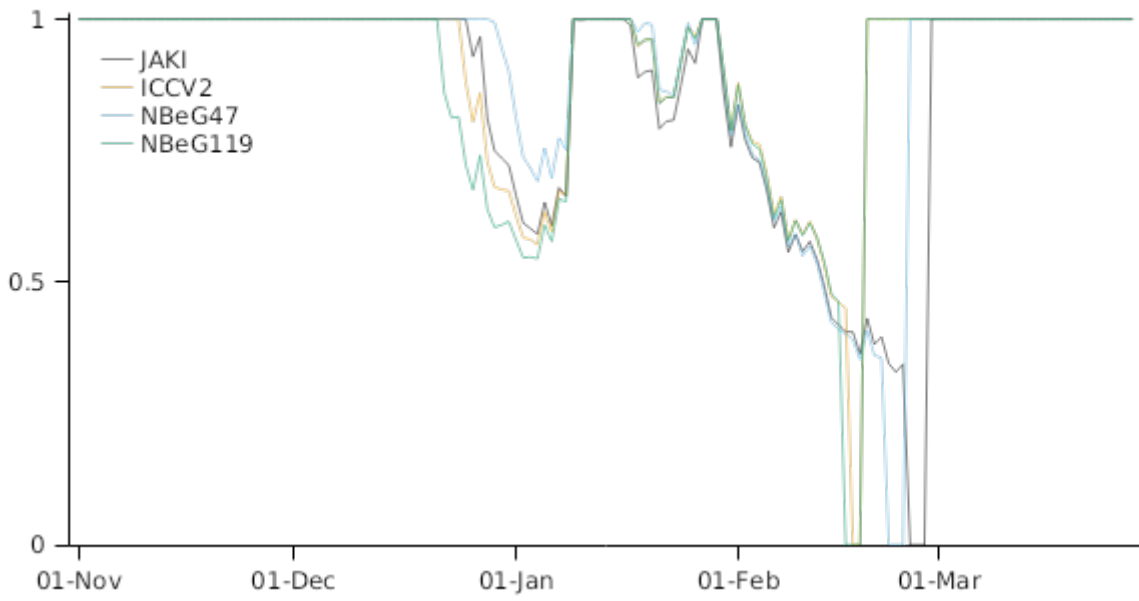
LAI



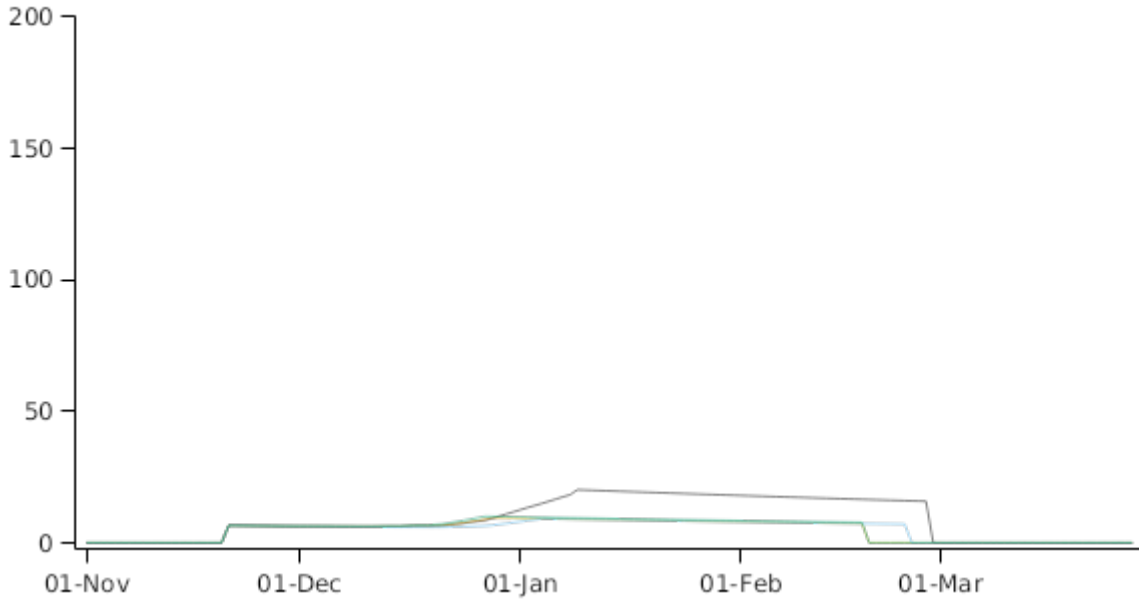
SpecificLeafArea



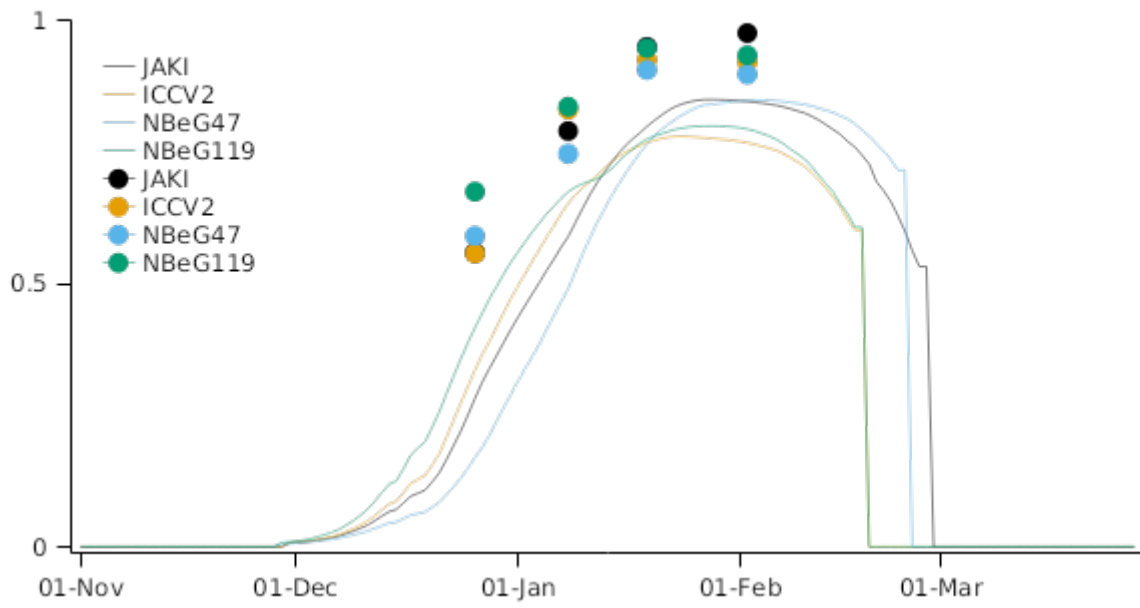
WaterStress



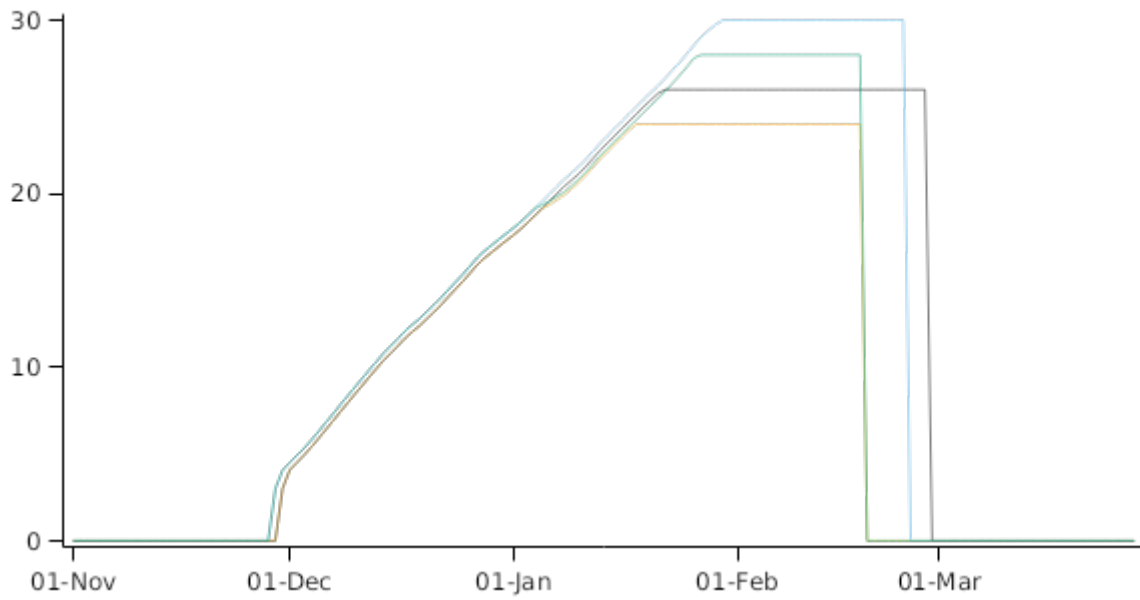
RootBiomass



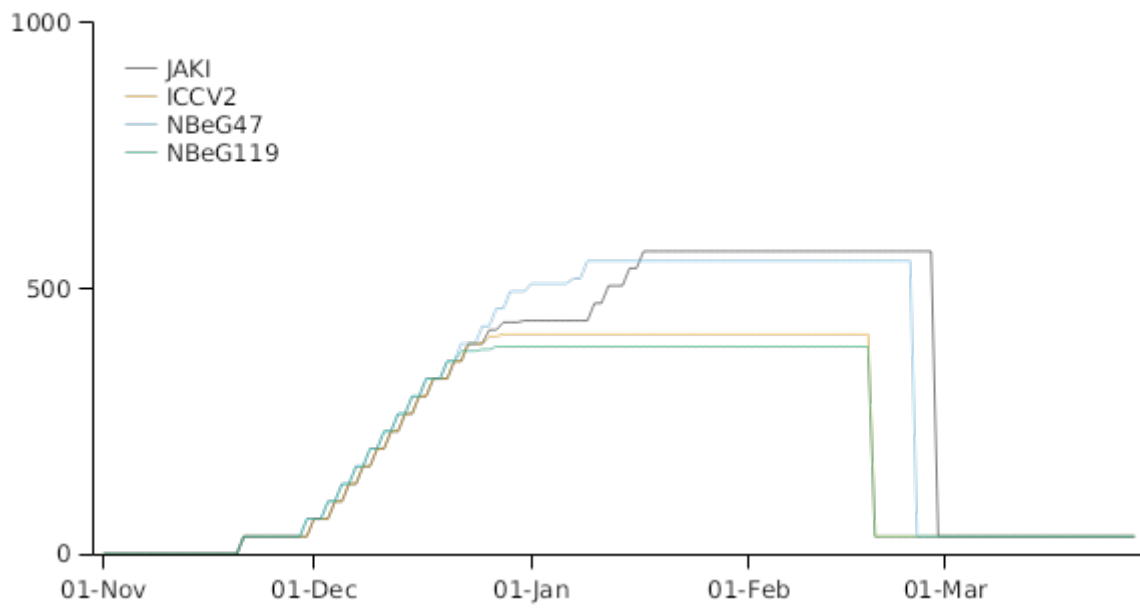
Cover



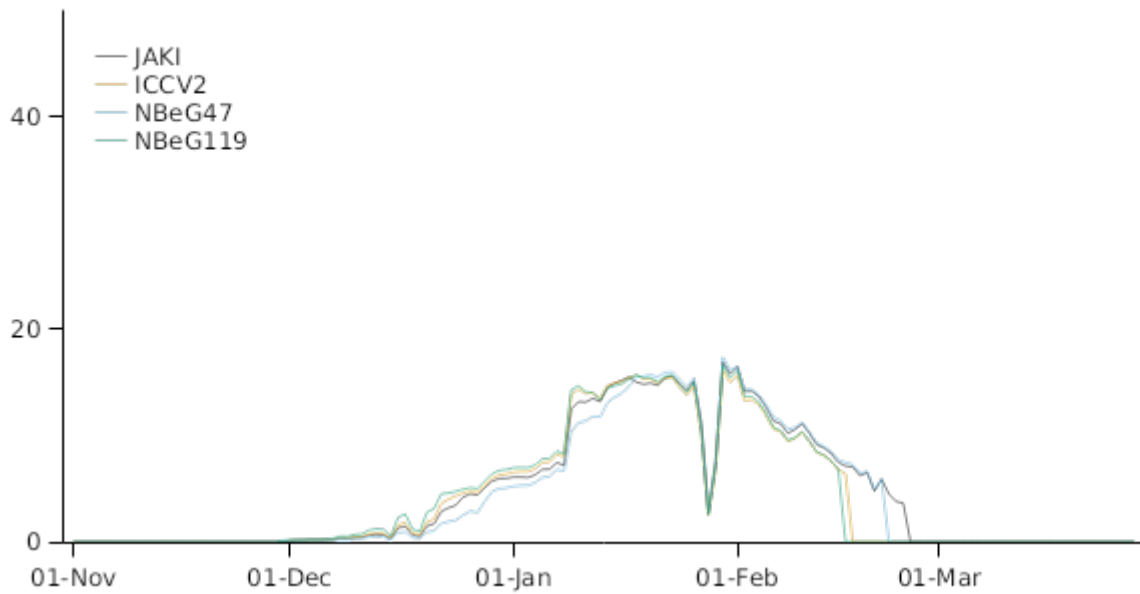
MSLeafNo



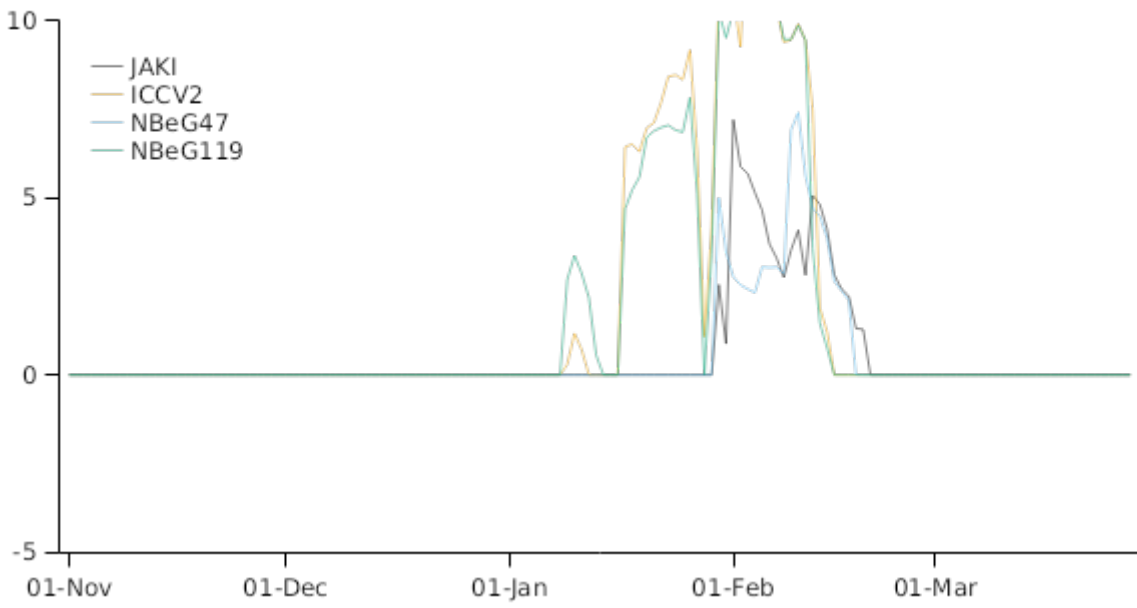
Branches_vs_time



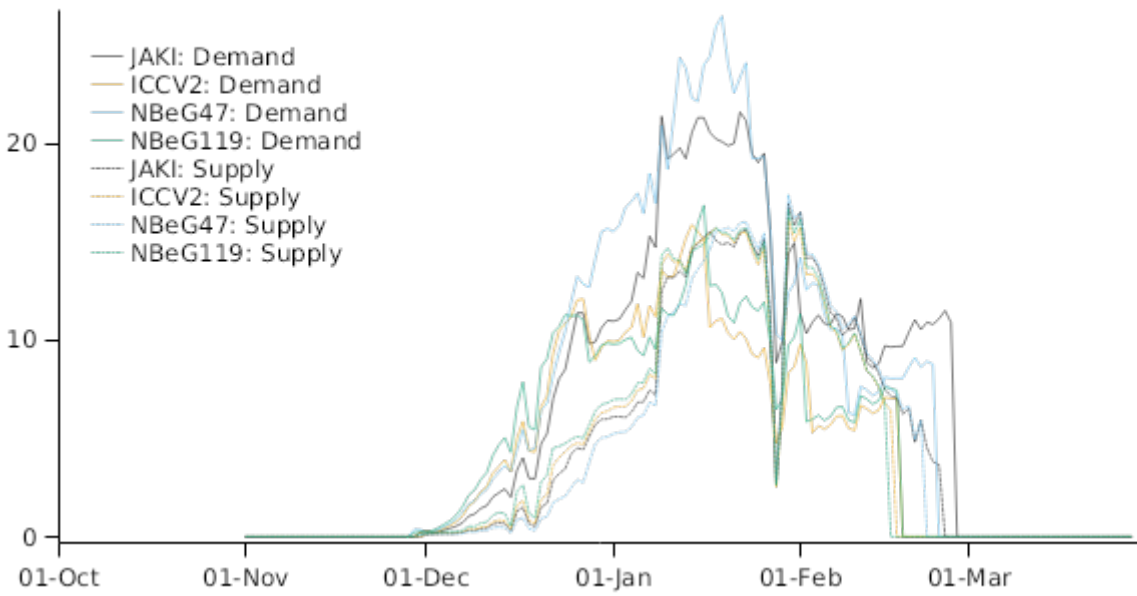
LeafPhotosynthesis



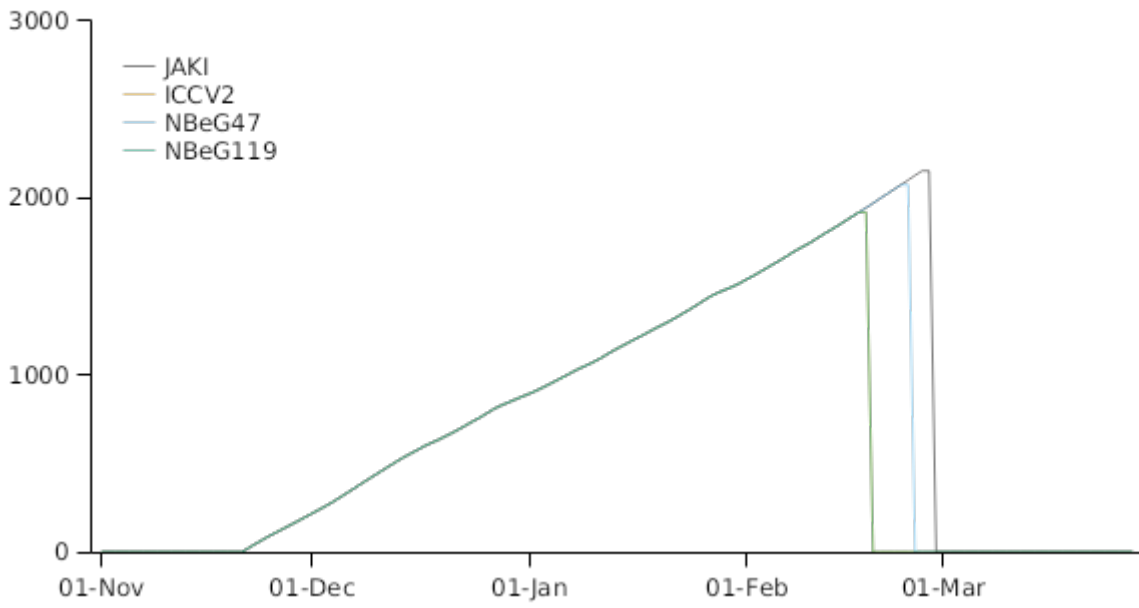
DMDemands



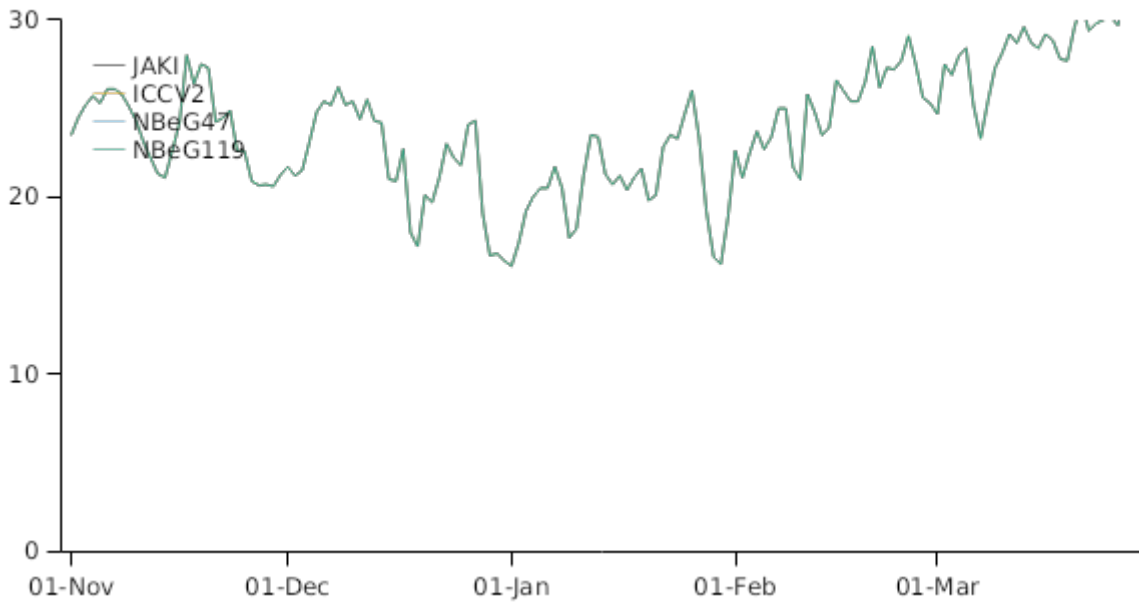
DMSupplyDemand



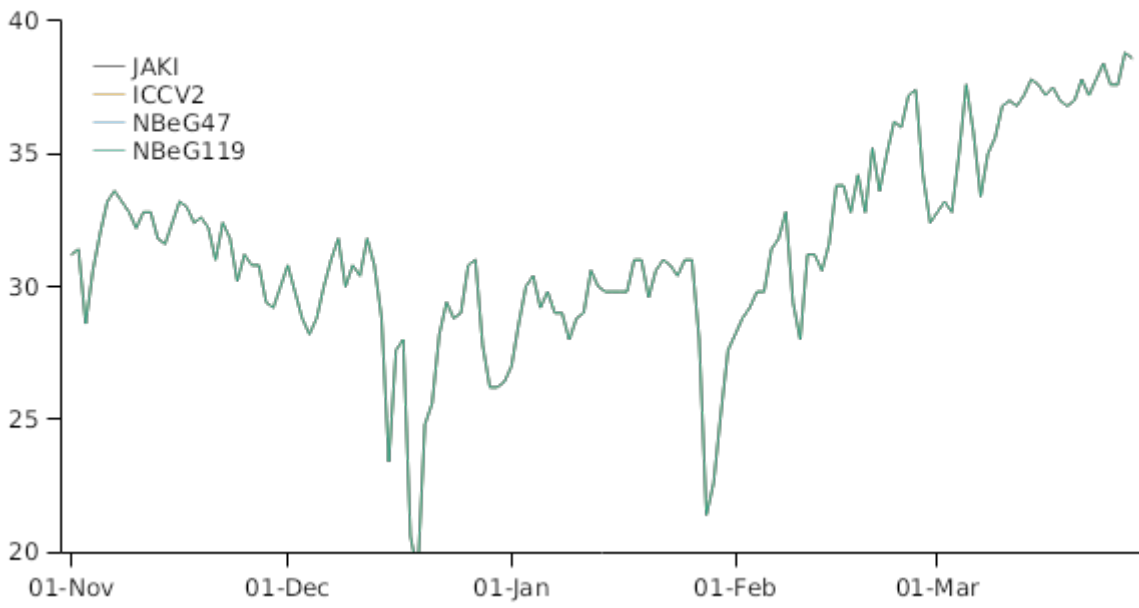
ThermalTime



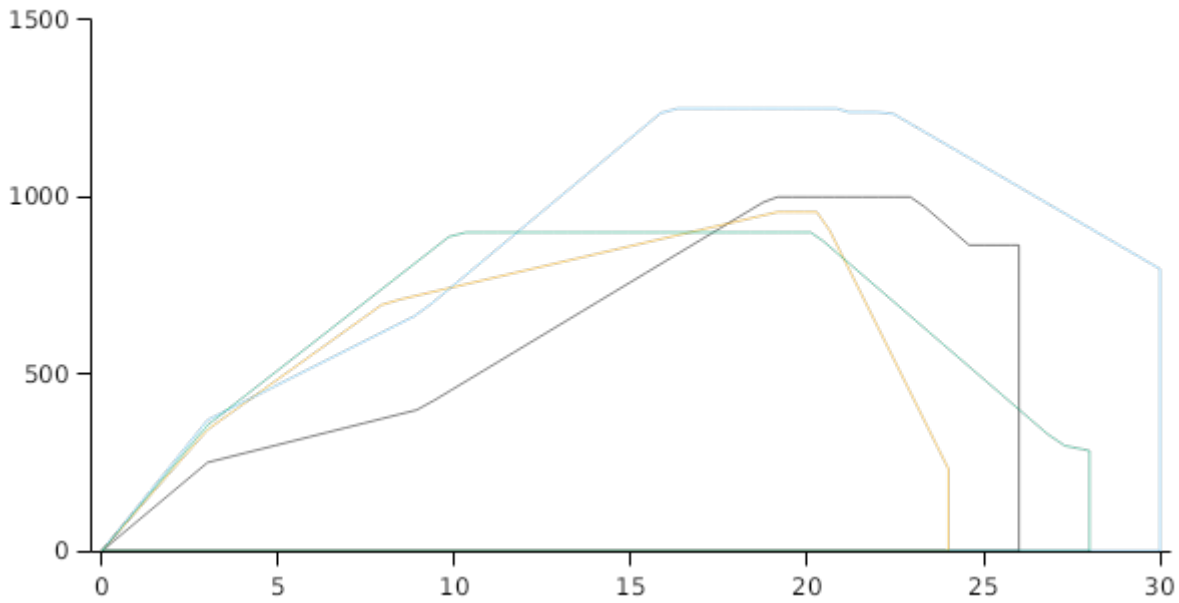
MeanT



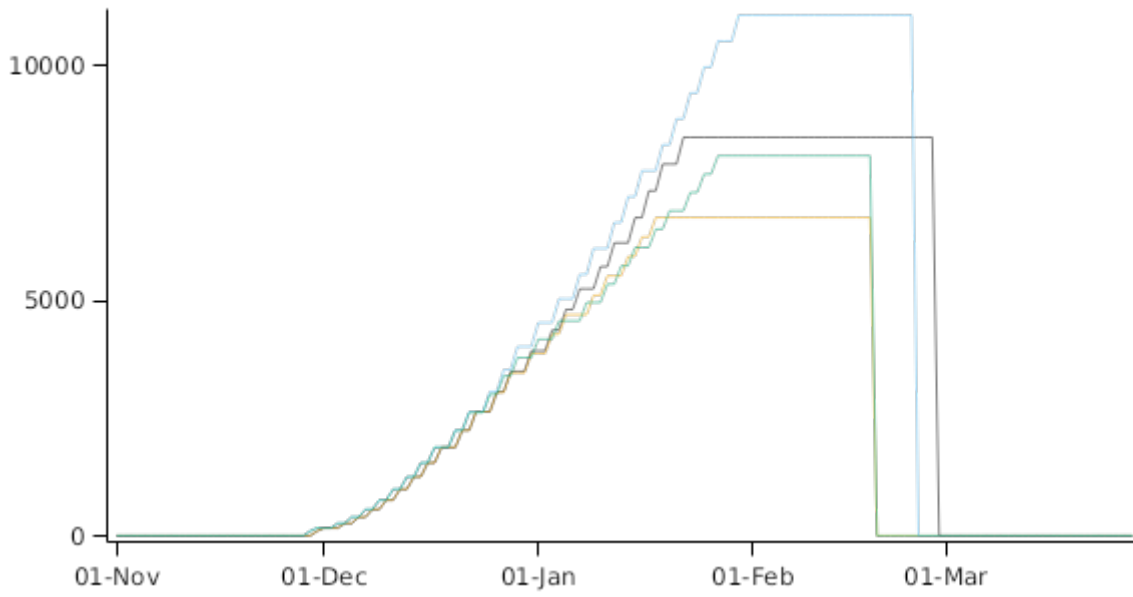
MaxT



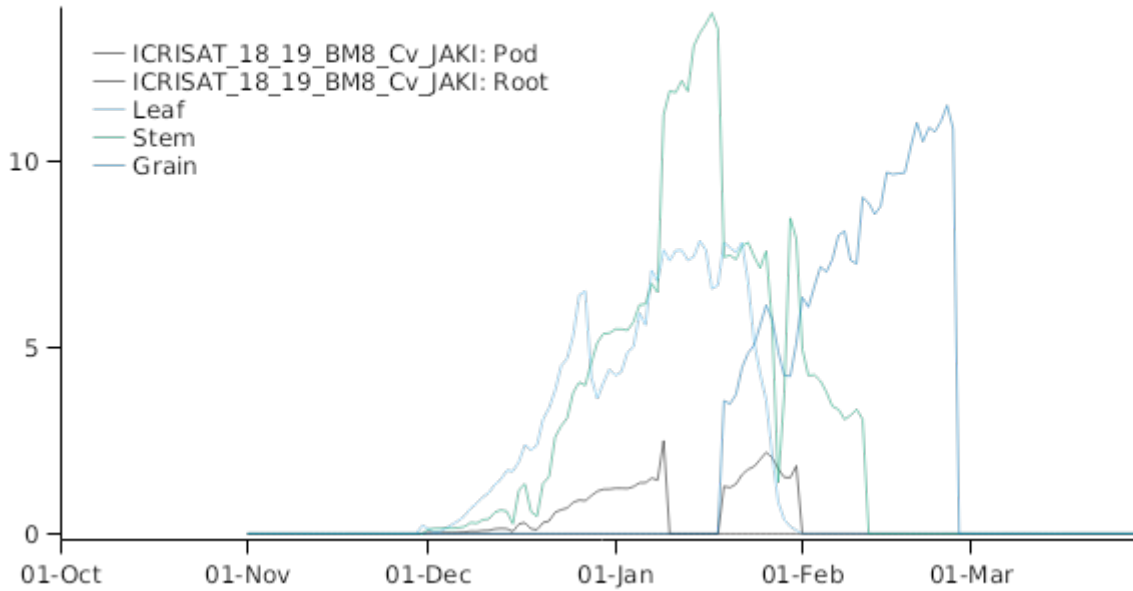
LeafSize



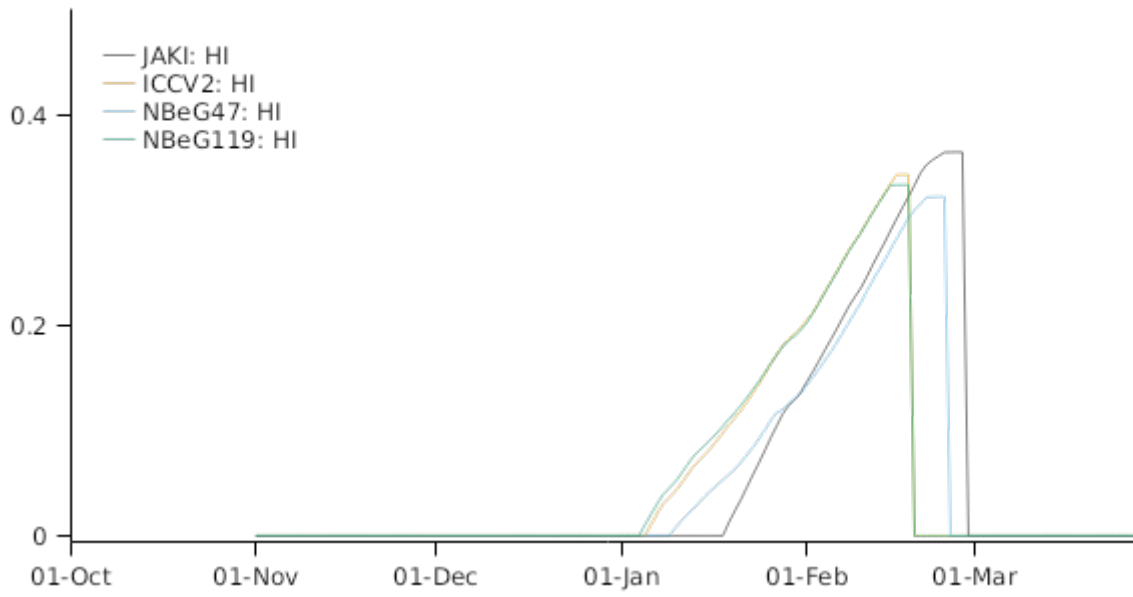
TotalLeaves



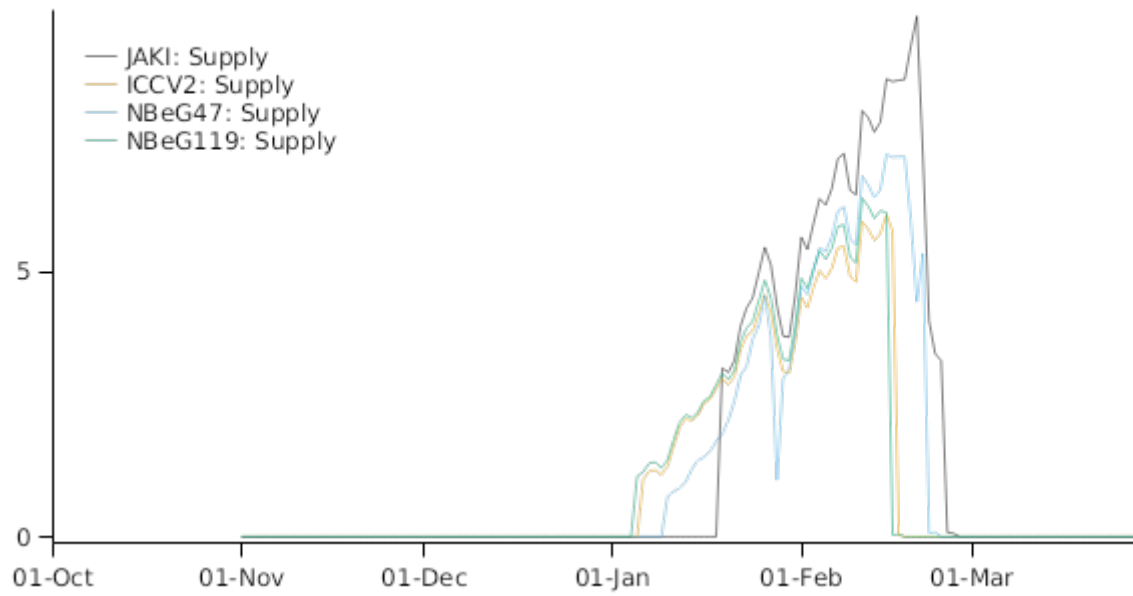
OrganDemand



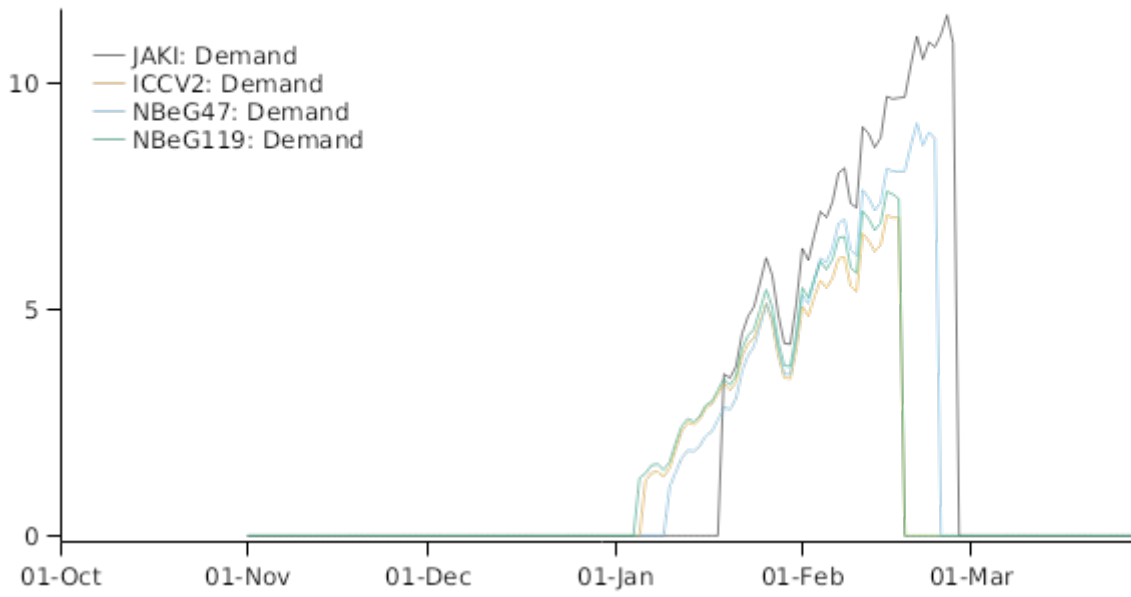
HI



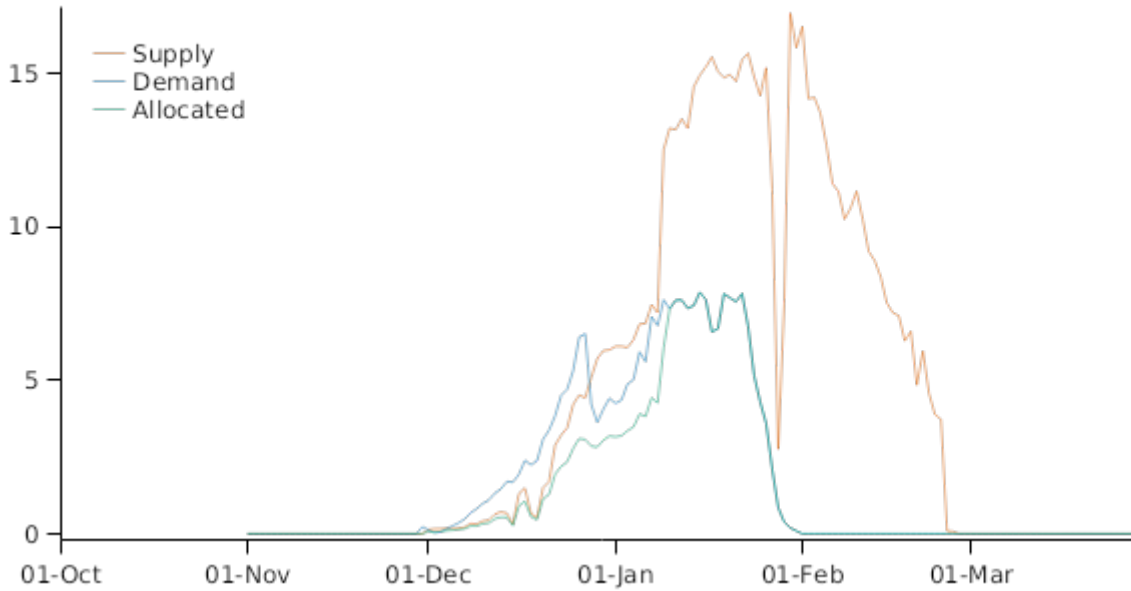
GrainSupply



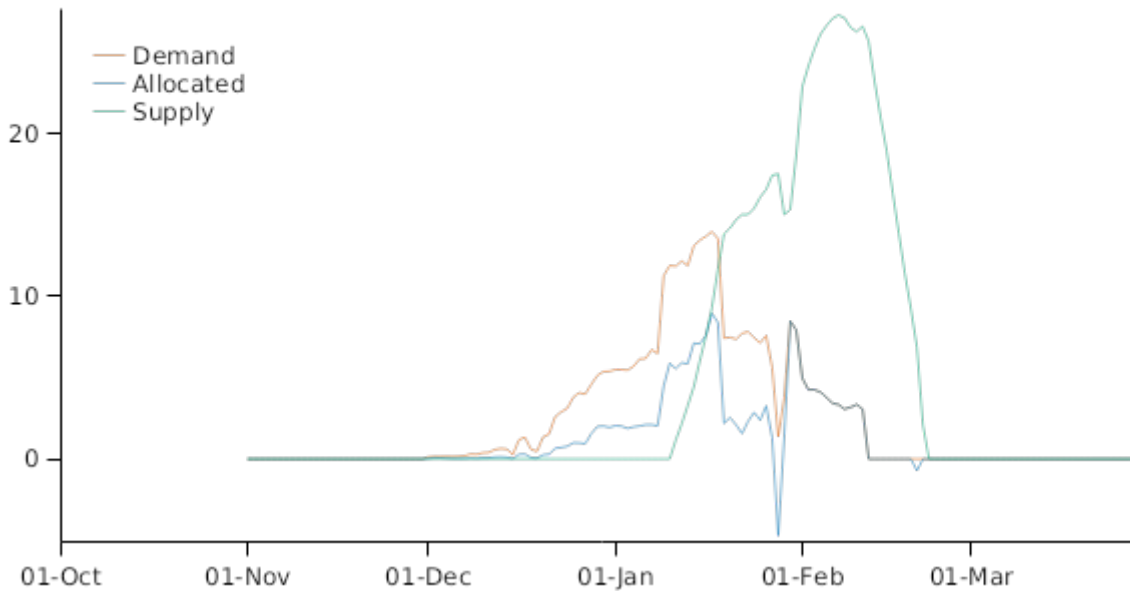
GrainDemand



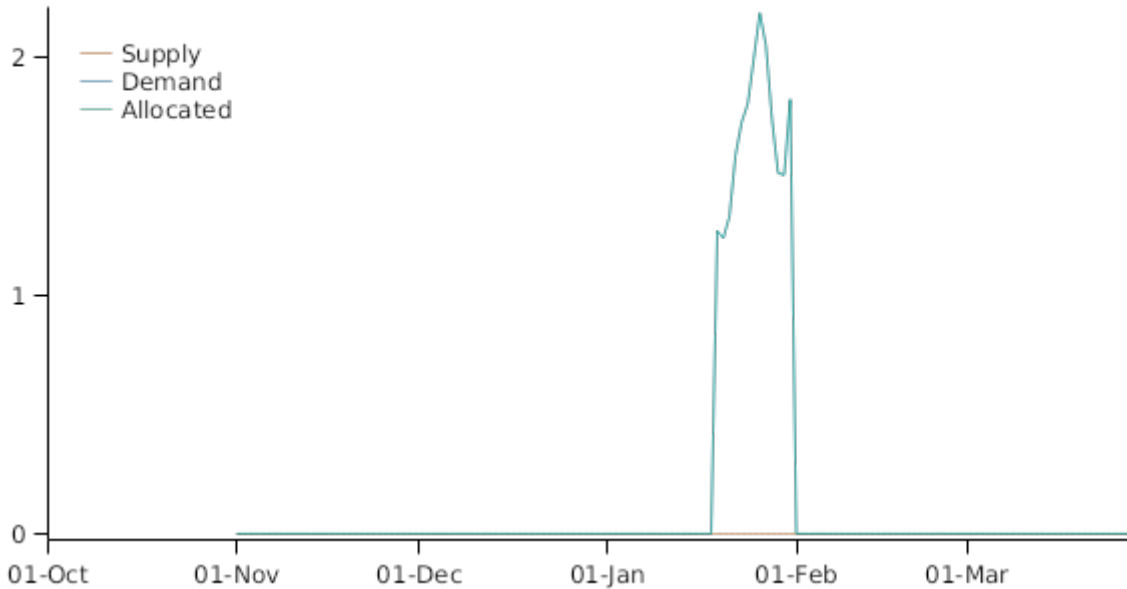
LeafDemandSupply1



StemDemandSupply2



PodDemandSupply3



3 Sensibility

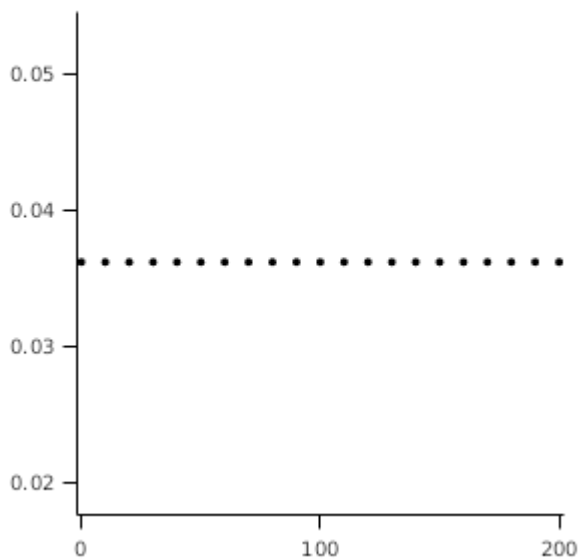
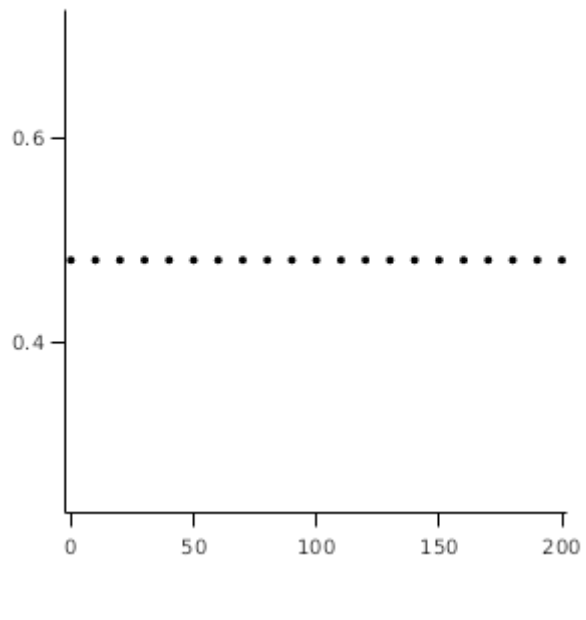
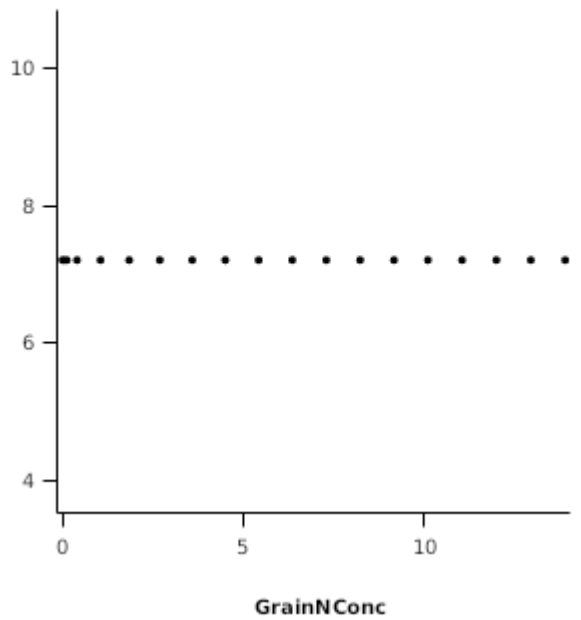
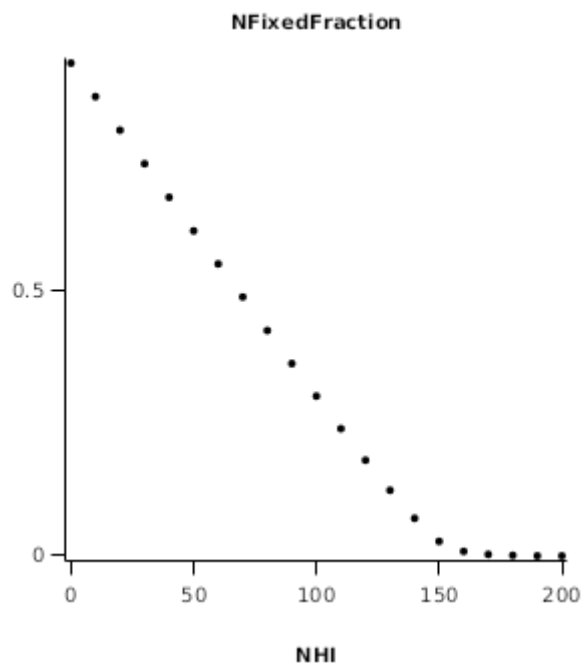
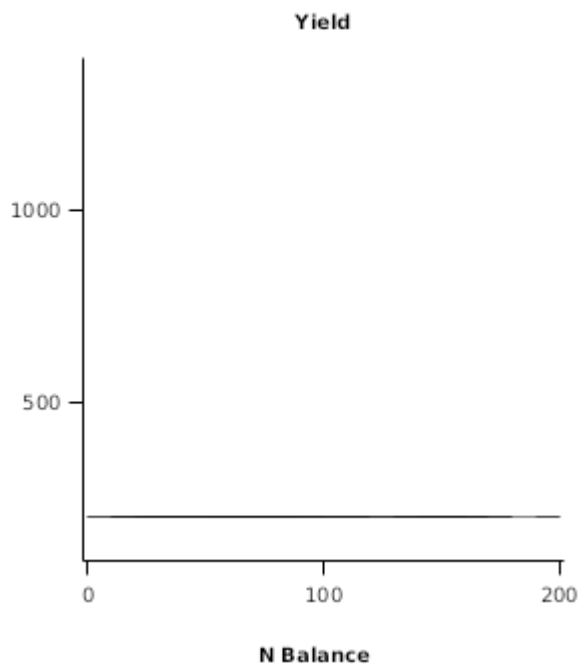
List of experiments.

Experiment Name	Design (Number of Treatments)
FixationResponse	N (21)
DetailedDynamics	Sowing (1)
CO2TE	CO2 (2)
ExtremeEnvironmentsKatherine	TOS (6)
ExtremeEnvironmentsLaunceston	TOS (6)

3.1 FixationResponse

Field studies by [Schwenke et al., 1998](#) showed that, for chickpea crops near Walgett/Moree in 1995, the proportion of total plan N derived from fixation decreased from about 90% when soil nitrate was very low at sowing, down to approximately 20% when soil nitrate was near 100kg/ha at sowing. Furthermore, N fixation was unable to account for N export in grain.

3.1.1 Graphs



3.2 DetailedDynamics

Peter Carberry unpublished data. Creek bank soil. Varies in short distances.

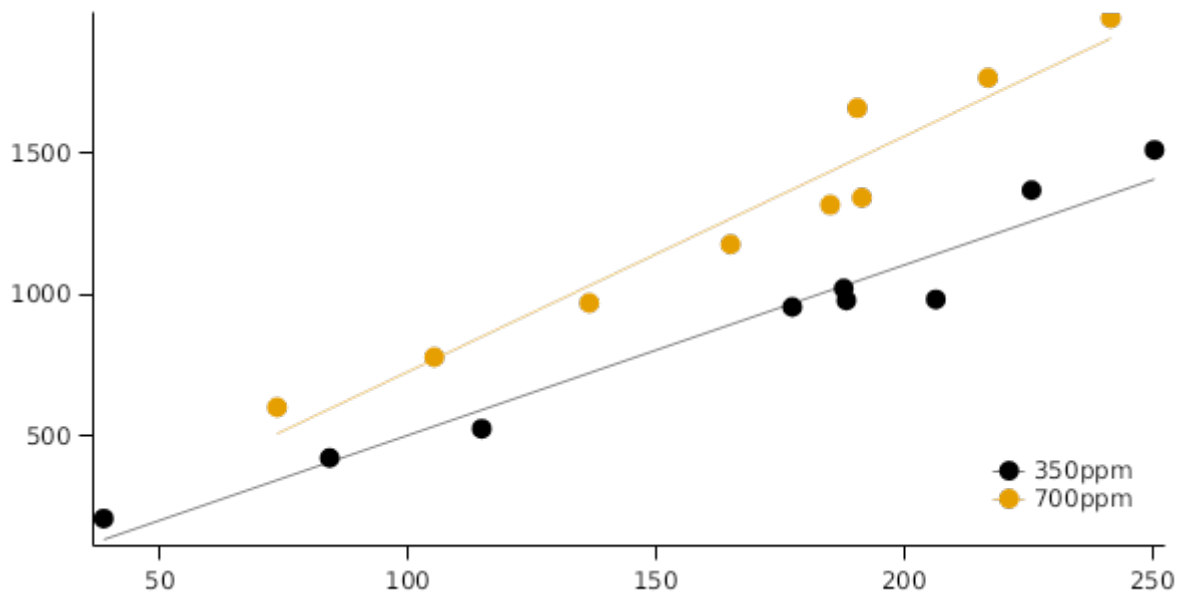
Note that Brinsmead paper says 1st sowing date was waterlogged, which would explain the delayed response on that experiment.

Note - auto-irrigate function has been used as no record of actual irrigation? Probably that they ran out of water at the end and actually wouldn't have achieved the yields we simulated

3.3 CO2TE

This test examines the impact of a doubling of CO₂ from historical (350ppm) on Transpiration Efficiency. [Reyenga et al., 1999](#) suggest an increase of approximately 37% in Transpiration Efficiency over this range in CO₂ concentration for c3 plants (wheat). In this test, a series of chickpea crops are simulated for Dalby, Queensland, Australia. The slope of plots of biomass production vs crop water use is used to quantify a gross seasonal TE. The change in slope should approximate the response suggested by [Reyenga et al., 1999](#).

Biomass production vs Crop water Use

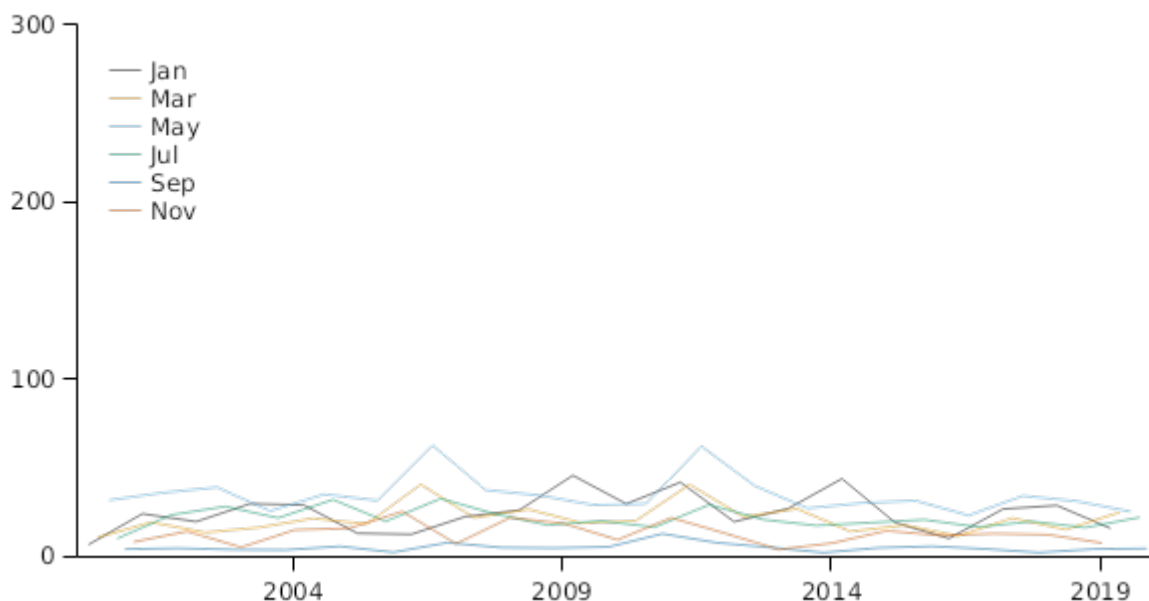


3.4 ExtremeEnvironmentsKatherine

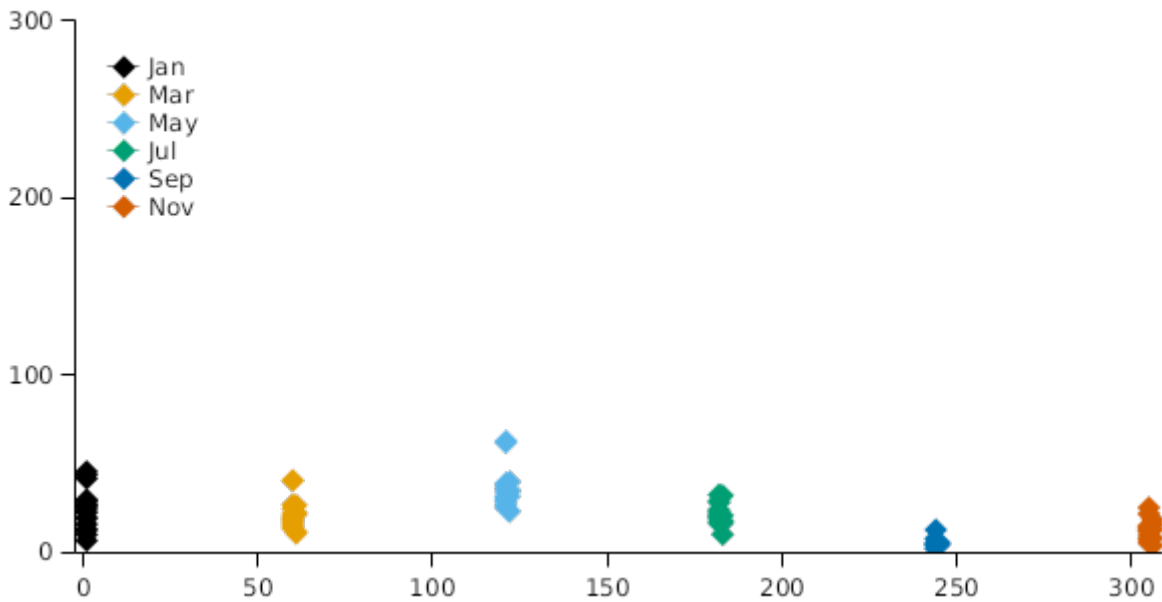
Testing ability of model to simulate rainfed chickpea production at Katherine RS, Northern Territory, Australia.

25mm irrigation applied on day of sowing to ensure germination on all sowing dates through the year

GrainYield



GrainYield1

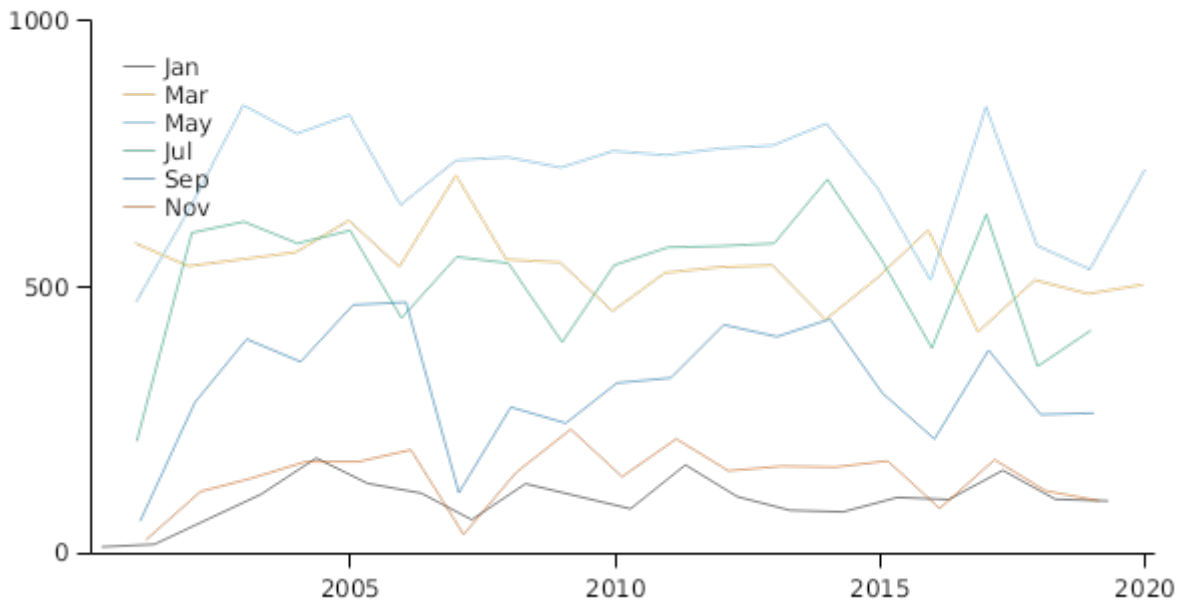


3.5 ExtremeEnvironmentsLaunceston

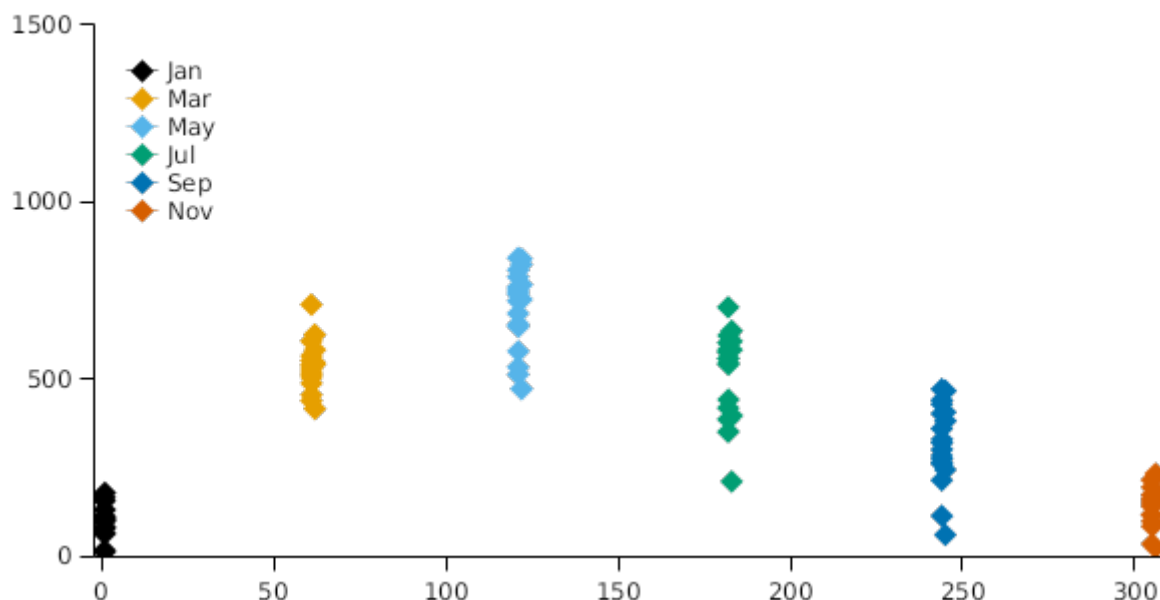
Testing ability of model to simulate rainfed chickpea production at Launceston, Tasmania, Australia.

25mm irrigation applied on day of sowing to ensure germination on all sowing dates through the year

GrainYield



GrainYield1



4 References

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