



1 The APSIM Canola Model

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
Root	Models.PMF.Organs.Root
Leaf	Models.PMF.Organs.SimpleLeaf
Grain	Models.PMF.Organs.ReproductiveOrgan
Stem	Models.PMF.Organs.GenericOrgan
Shell	Models.PMF.Organs.GenericOrgan
MortalityRate	Models.Functions.Constant
SeedMortalityRate	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.

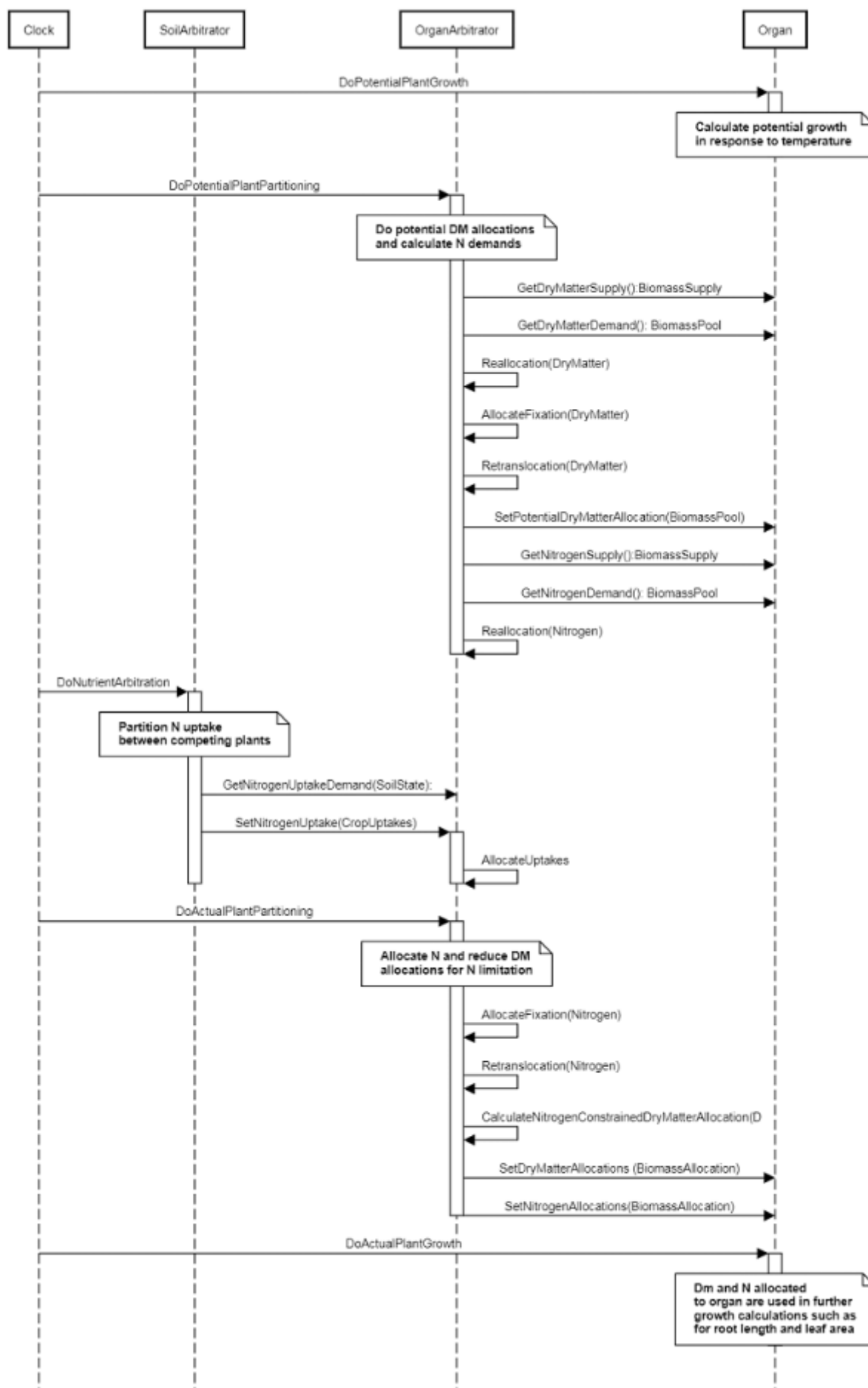


Figure 1: Schematic showing the procedure for arbitration of biomass partitioning. Pink boxes represent events that occur every day and their numbering shows the order of calculations. Blue boxes represent the methods that are called when these events occur. Orange boxes contain properties that make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

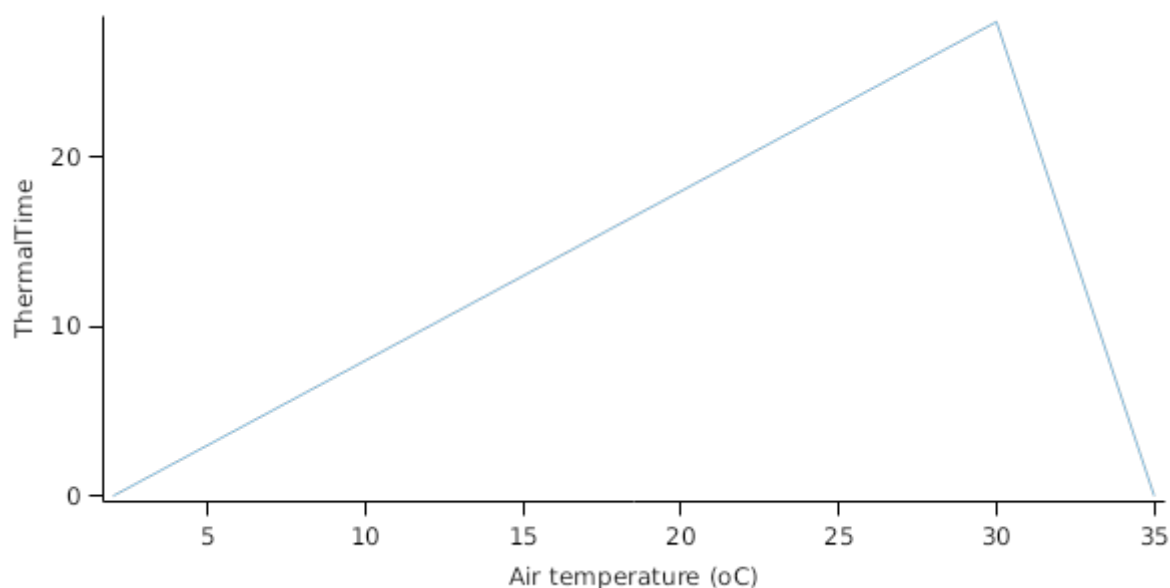
ThermalTime is the average of sub-daily values from a XYPairs.

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

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

Air temperature (oC)	ThermalTime
2.0	0.0
30.0	28.0
35.0	0.0

ThermalTime



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

Phase Number	Phase Name	Initial Stage	Final Stage
1	Germinating	Sowing	Germination
2	Emerging	Germination	Emergence
3	Vegetative	Emergence	FloralInitiation
4	BudDevelopment	FloralInitiation	GreenBud
5	StemElongation	GreenBud	StartFlowering
6	EarlyFlowering	StartFlowering	StartPodDevelopment
7	EarlyPodDevelopment	StartPodDevelopment	StartGrainFilling
8	EarlyGrainFilling	StartGrainFilling	EndFlowering
9	MidGrainFilling	EndFlowering	EndPodDevelopment

Phase Number	Phase Name	Initial Stage	Final Stage
10	LateGrainFilling	EndPodDevelopment	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:

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

Where:

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

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

$$ThermalTime = [Phenology].ThermalTime$$

1.2.4 Vegetative

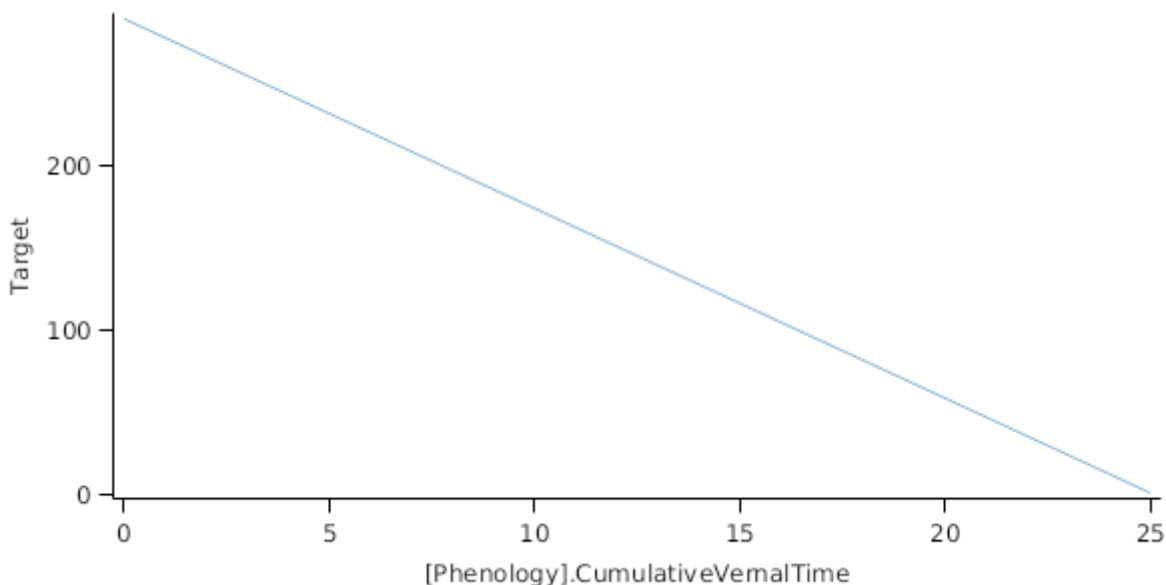
This phase goes from emergence to floralinitiation.

The *Target* for completion is calculated as:

Target is calculated using linear interpolation

[Phenology].CumulativeVernalTime	Target
0.0	290.0
25.0	1.0

Target



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

$$Progression = [Phenology].ThermalTime$$

1.2.5 BudDevelopment

1.2.5.1 BudDevelopment

This phase goes from the specified start stage to the specified end stage and its duration is determined by leaf appearance rate and the number of leaves to complete the phase.

1.2.6 StemElongation

This phase goes from greenbud to startflowering.

The *Target* for completion is calculated as:

$$Target = Base + PPResponse$$

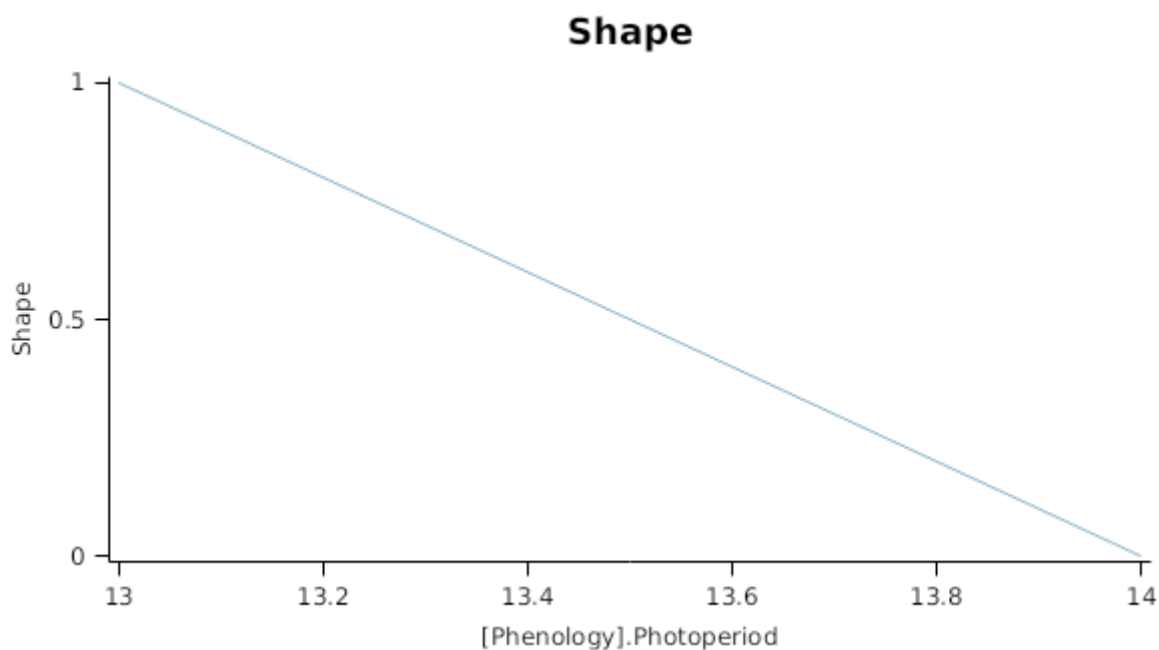
$$Base = 250$$

$$PPResponse = Amount \times Shape$$

$$Amount = 0$$

Shape is calculated using linear interpolation

[Phenology].Photoperiod	Shape
13.0	1.0
14.0	0.0



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

$$Progression = [Phenology].ThermalTime$$

1.2.7 EarlyFlowering

This phase goes from startflowering to startpoddevelopment.

The duration of the grain filling phase has been taken from the model of Robertson et al (2002).

The *Target* for completion is calculated as:

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

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

$$Progression = [Phenology].ThermalTime$$

1.2.8 EarlyPodDevelopment

This phase goes from startpoddevelopment to startgrainfilling.

The duration of the grain filling phase has been taken from the model of Robertson et al (2002).

The *Target* for completion is calculated as:

$$\text{Target} = 140 \text{ (oD)}$$

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

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

1.2.9 EarlyGrainFilling

This phase goes from startgrainfilling to endflowering.

The *Target* for completion is calculated as:

$$\text{Target} = \text{FractionofGrainfilling} \times [\text{Phenology}].\text{LateGrainFilling}.\text{Target}.\text{EntireGrainfillPeriod}.\text{FixedValue}$$

$$\text{FractionofGrainfilling} = 0.05$$

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

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

1.2.10 MidGrainFilling

This phase goes from endflowering to endpoddevelopment.

The *Target* for completion is calculated as:

$$\text{Target} = \text{FractionofMidToLateGrainfilling} \times \text{SubtractFunction}$$

$$\text{FractionofMidToLateGrainfilling} = 0.5$$

$$\text{SubtractFunction} = [\text{Phenology}].\text{LateGrainFilling}.\text{Target}.\text{EntireGrainfillPeriod}.\text{FixedValue} - [\text{Phenology}].\text{EarlyGrainFilling}.\text{Target}$$

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

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

1.2.11 LateGrainFilling

This phase goes from endpoddevelopment to endgrainfill.

The *Target* for completion is calculated as:

$$\text{Target} = \text{EntireGrainfillPeriod} - [\text{Phenology}].\text{EarlyGrainFilling}.\text{Target} - [\text{Phenology}].\text{MidGrainFilling}.\text{Target}$$

$$\text{EntireGrainfillPeriod} = 700$$

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

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

1.2.12 Maturing

This phase goes from endgrainfill to maturity.

The *Target* for completion is calculated as:

$$\text{Target} = 5 \text{ (oD)}$$

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

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

1.2.13 Ripening

This phase goes from maturity to harvestripe.

The *Target* for completion is calculated as:

Target = 1 (oD)

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

Progression = [Phenology].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 CumulativeThermalTime

CumulativeThermalTime = Accumulated *DailyValue* between germination and floralinitiation

DailyValue = [Phenology].ThermalTime

1.2.16 VernalTime

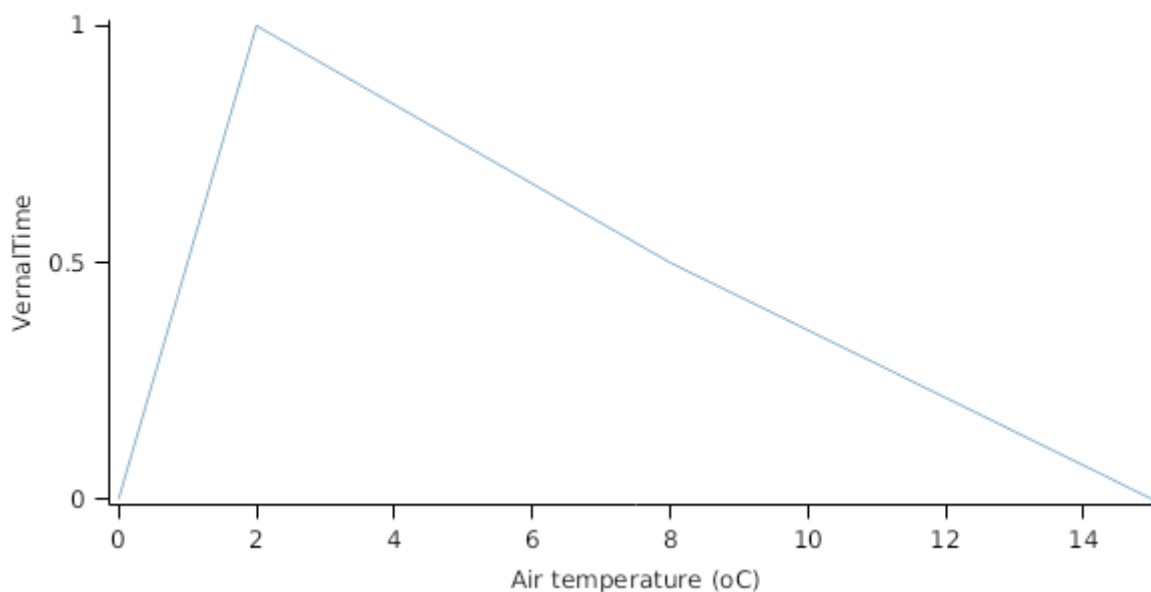
VernalTime is the average of sub-daily values from a XYPairs.

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

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

Air temperature (oC)	VernalTime
0.0	0.0
2.0	1.0
8.0	0.5
15.0	0.0

VernalTime



1.2.17 CumulativeVernalTime

CumulativeVernalTime = Accumulated *DailyValue* between germination and floralinitiation

DailyValue = [Phenology].VernalTime

1.2.18 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)

1.2.19 EmergenceDAS

Before Emergence

PreEventValue = 0

On Emergence the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.20 FlorallInitiationDAS

Before FlorallInitiation

PreEventValue = 0

On FlorallInitiation the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.21 GreenBudDAS

Before GreenBud

PreEventValue = 0

On GreenBud the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.22 StartFloweringDAS

Before StartFlowering

PreEventValue = 0

On StartFlowering the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.23 MaturityDAS

Before Maturity

PreEventValue = 0

On Maturity the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.3 Root

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

1.3.1 Growth

Roots grow downwards through the soil profile, with initial depth determined by sowing depth and the growth rate determined by RootFrontVelocity. The RootFrontVelocity is modified by multiplying it by the soil's XF value, which represents any resistance posed by the soil to root extension.

$$Root\ Depth\ Increase = RootFrontVelocity \times XF_i \times RootDepthStressFactor$$

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

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

1.3.2 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.

1.3.3 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.

1.3.4 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 (kNO_3 or kNH_4), the concentration of N form (ppm), and a soil moisture factor ($NUptakeSWFactor$) which typically decreases as the soil dries. $NO_3\ uptake = NO_{3i} \times kNO_3 \times NO_{3ppm,i} \times NUptakeSWFactor$ $NH_4\ uptake = NH_{4i} \times kNH_4 \times NH_{4ppm,i} \times NUptakeSWFactor$ As can be seen from the above equations, the values of kNO_3 and kNH_4 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.

1.3.5 Water Uptake

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

1.3.6 Constants

$$MaxDailyNUptake = 6$$

$$SenescenceRate = 0.005$$

$$MaximumRootDepth = 1000000$$

$$MaximumNConc = 0.01$$

$$MinimumNConc = 0.005$$

$$SpecificRootLength = 40\ (m/g)$$

$$DMConversionEfficiency = 1$$

$$MaintenanceRespirationFunction = 1$$

$$RemobilisationCost = 0$$

$$CarbonConcentration = 0.4$$

RootDepthStressFactor = 1

1.3.7 RootShape

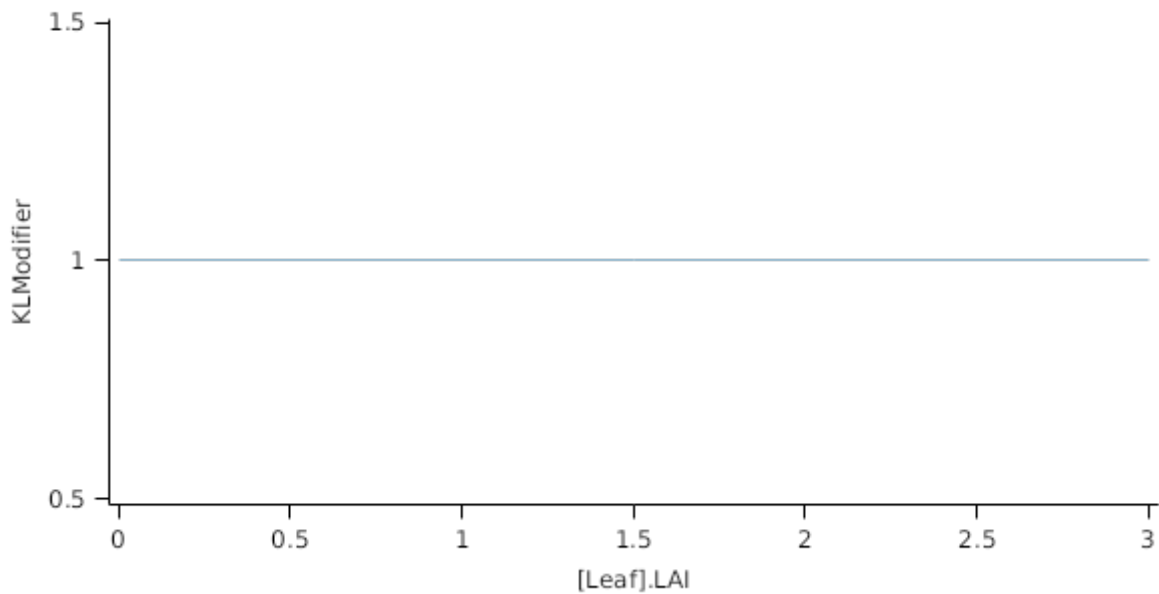
This model calculates the proportion of each soil layer occupied by roots.

1.3.8 KLModifier

KLModifier is calculated using linear interpolation

[Leaf].LAI	KLModifier
0.0	1.0
3.0	1.0

KLModifier



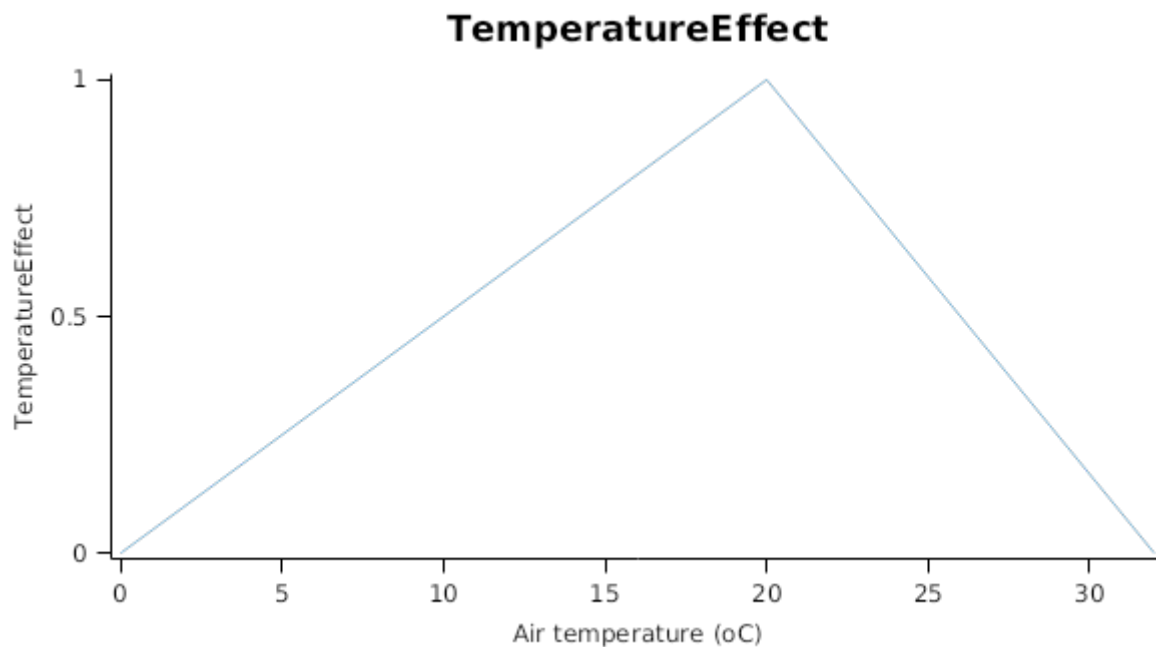
1.3.9 TemperatureEffect

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

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

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

Air temperature (oC)	TemperatureEffect
0.0	0.0
20.0	1.0
32.0	0.0



1.3.10 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 = 5

early has a value between Emergence and StartGrainFilling calculated as:

Function = 44

late has a value between StartGrainFilling and Maturity calculated as:

Function = 0

1.3.11 NitrogenDemandSwitch

NitrogenDemandSwitch has a value between Emergence and EndGrainFill calculated as:

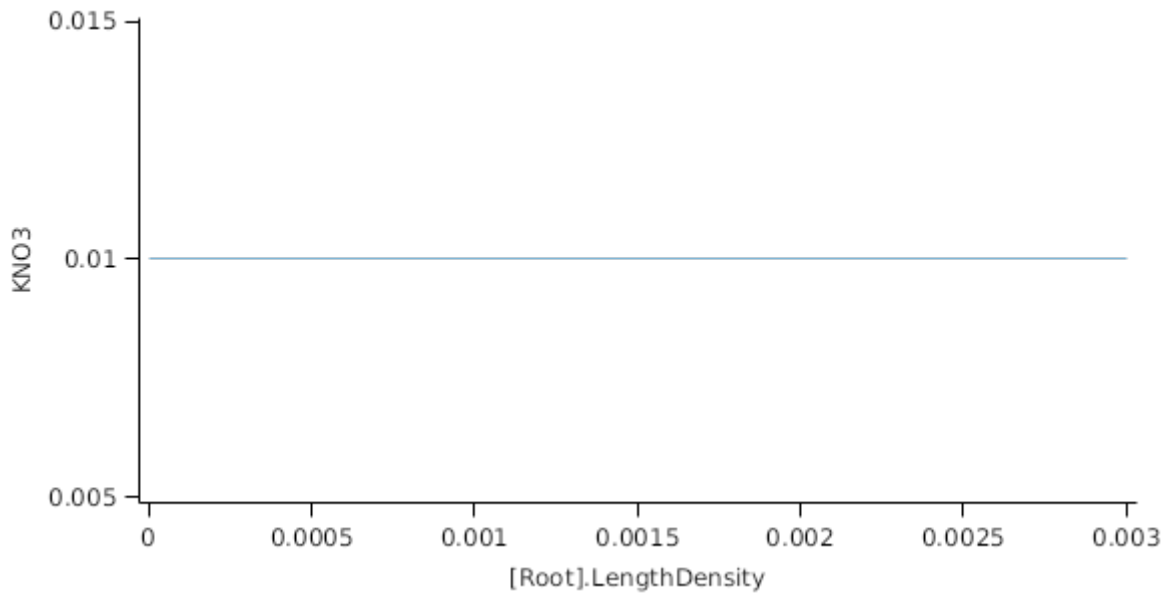
Constant = 1

1.3.12 KNO3

KNO3 is calculated using linear interpolation

[Root].LengthDensity	KNO3
0.0	0.01
0.003	0.01

KNO3

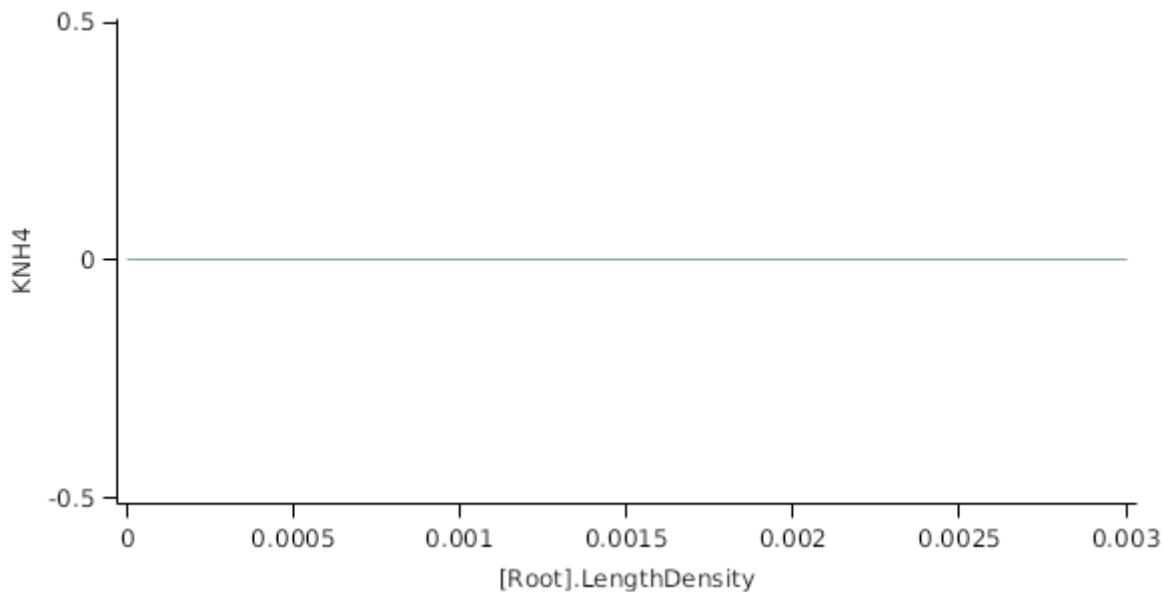


1.3.13 KNH4

KNH4 is calculated using linear interpolation

[Root].LengthDensity	KNH4
0.0	0.0
0.003	0.0

KNH4



1.3.14 BiomassRemovalDefaults

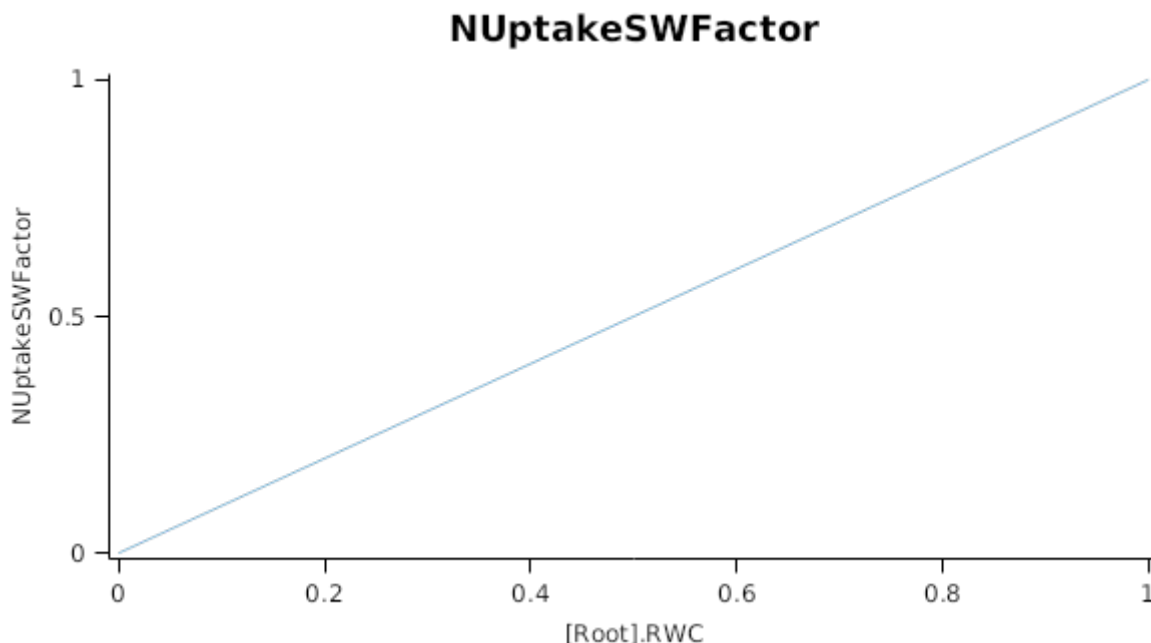
1.3.14.1 BiomassRemovalDefaults

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.

1.3.15 NUptakeSWFactor

NUptakeSWFactor is calculated using linear interpolation

[Root].RWC	NUptakeSWFactor
0.0	0.0
1.0	1.0



1.3.16 DMDemands

1.3.16.1 DMDemands

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

1.3.17 NDemands

1.3.17.1 NDemands

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

1.3.18 CriticalNConc

CriticalNConc = *[Root].MinimumNConc*

1.3.19 InitialWt

1.3.19.1 InitialWt

This class holds the functions for calculating values for each Nutrient component.

1.4 Leaf

This organ is simulated using a SimpleLeaf organ type. It provides the core functions of intercepting radiation, producing biomass through photosynthesis, and determining the plant's transpiration demand. The model also calculates the growth, senescence, and detachment of leaves. SimpleLeaf does not distinguish leaf cohorts by age or position in the canopy.

Radiation interception and transpiration demand are computed by the MicroClimate model. This model takes into account competition between different plants when more than one is present in the simulation. The values of canopy Cover, LAI, and plant Height (as defined below) are passed daily by SimpleLeaf to the MicroClimate model. MicroClimate uses an implementation of the Beer-Lambert equation to compute light interception and the Penman-Monteith equation to calculate potential evapotranspiration.

These values are then given back to SimpleLeaf which uses them to calculate photosynthesis and soil water demand.

NOTE: the summary above is used in the Apsim's autodoc.

SimpleLeaf has two options to define the canopy: the user can either supply a function describing LAI or a function describing canopy cover directly. From either of these functions SimpleLeaf can obtain the other property using the Beer-Lambert equation with the specified value of extinction coefficient. The effect of growth rate on transpiration is captured by the Fractional Growth Rate (FRGR) function, which is passed to the MicroClimate model.

1.4.1 Initial Dry Matter

$InitialWt = [Leaf].Area.Calculation.Initial / [Leaf].SpecificArea$

1.4.2 Dry Matter Demand

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

1.4.2.1 DMDemands

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

1.4.3 Nitrogen Demand

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

1.4.3.1 NDemands

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

1.4.4 Nitrogen Concentration Thresholds

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

1.4.4.1 NDemands

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

1.4.5 Dry Matter Supply

$DMReallocationFactor = 0$

$DMRetranslocationFactor = 0.5$

1.4.6 Photosynthesis

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

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

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

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

$RUE = Potential \times TriazineToleranceModifier$

This approach is based upon the value used in [Robertson et al., 2002](#) increased to account for partitioning to roots.

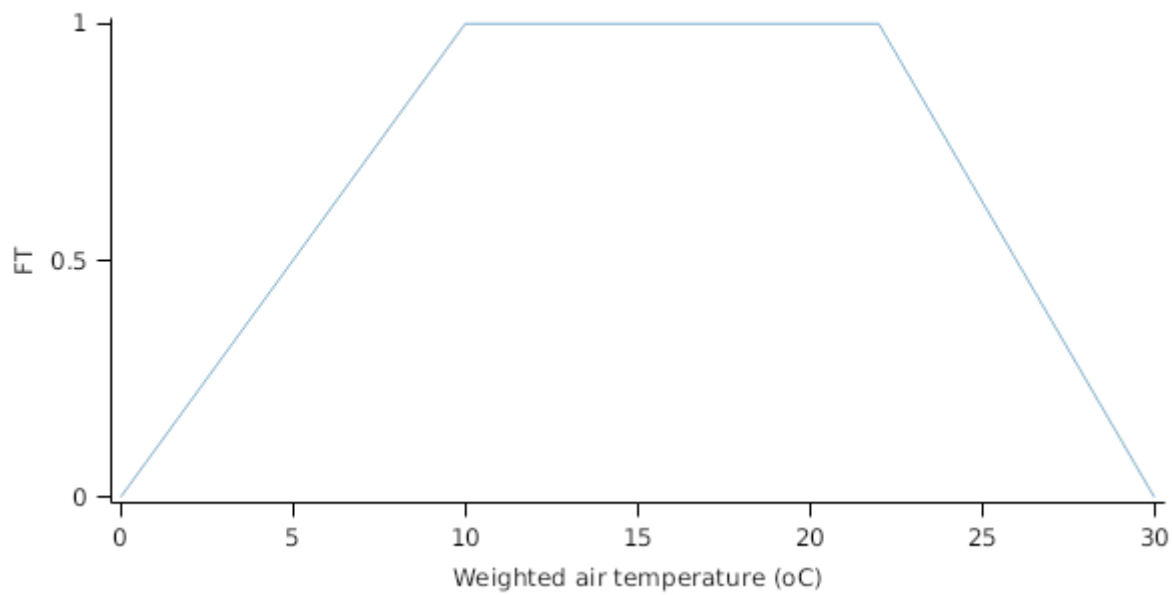
$Potential = 1.69$

$TriazineToleranceModifier = 1$

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

$MaximumTemperatureWeighting = 0.75$

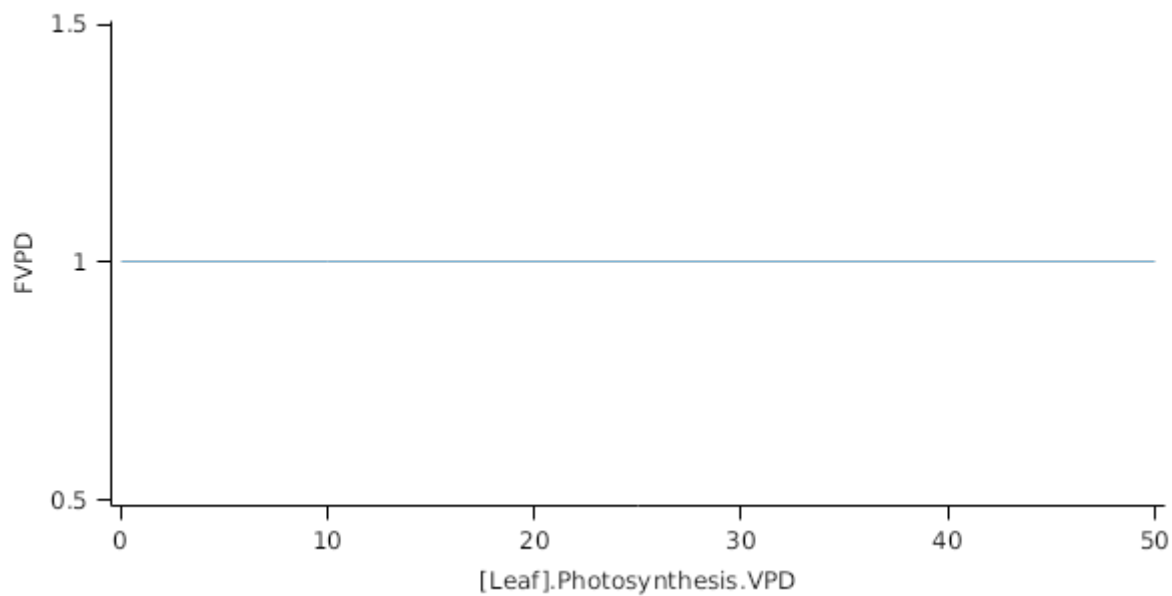
FT



FVPD is calculated using linear interpolation

[Leaf].Photosynthesis.VPD	FVPD
0.0	1.0
10.0	1.0
50.0	1.0

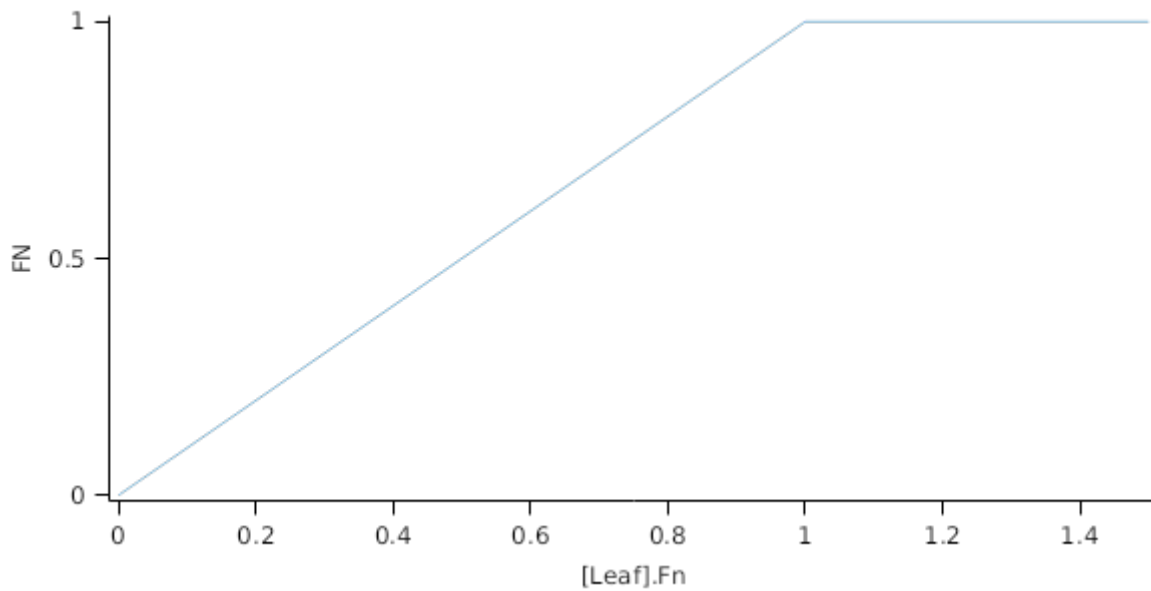
FVPD



FN is calculated using linear interpolation

[Leaf].Fn	FN
0.0	0.0
1.0	1.0
1.5	1.0

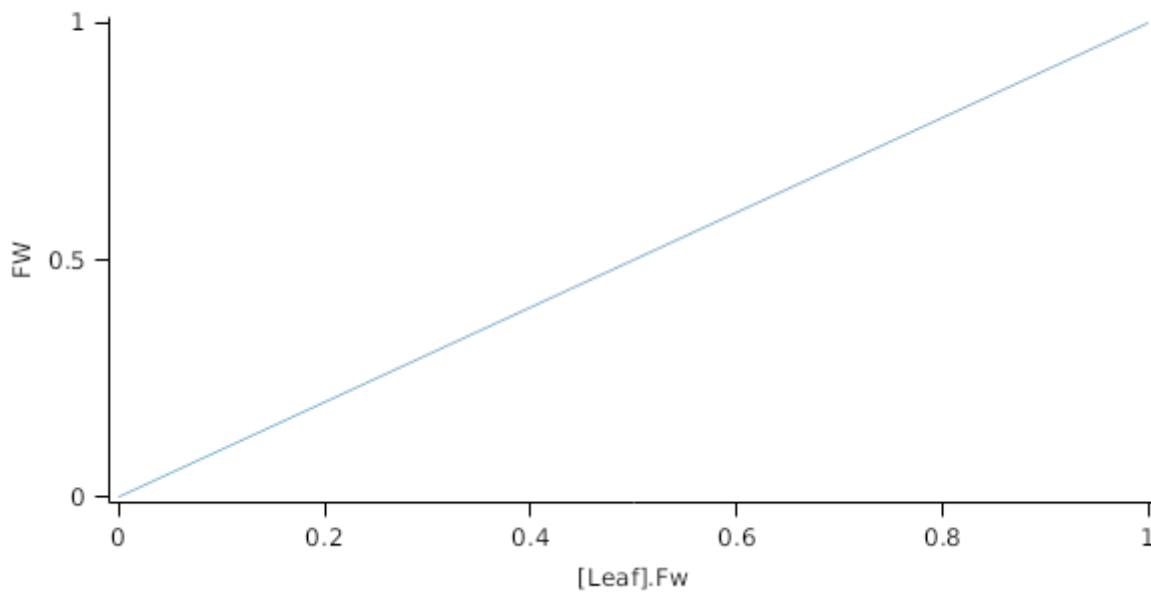
FN



FW is calculated using linear interpolation

$[Leaf].Fw$	FW
0.0	0.0
1.0	1.0

FW



This model calculates the CO_2 impact on RUE using the approach of [Reyenga et al., 1999](#).

For C3 plants,

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

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

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

For C4 plants,

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

$$RadnInt = [Leaf].RadiationIntercepted$$

1.4.7 Nitrogen Supply

This model assumes that all metabolic and storage N is available for reallocation from senescing leaves.

$N_{\text{ReallocationFactor}} = 0.5$

$N_{\text{RetranslocationFactor}} = 0.5$

1.4.8 Canopy Properties

Leaf has been defined with a LAIFunction, cover is calculated using the Beer-Lambert equation.

$Area = \text{Max}(\text{Calculation}, \text{Zero})$

Where:

$Calculation = Initial + Change$

$Initial = AreaPerPlant \times [Plant].SowingData.Population$

$AreaPerPlant = 0.0005$

$Change = AreaGrowth - AreaSenesced - AreaRemoved$

AreaGrowth is a daily accumulation of the values of functions listed below between the Emergence and StartFlowering stages. Function values added to the accumulate total each day are:

AreaSenesced is a daily accumulation of the values of functions listed below between the Emergence and HarvestRipe stages. Function values added to the accumulate total each day are:

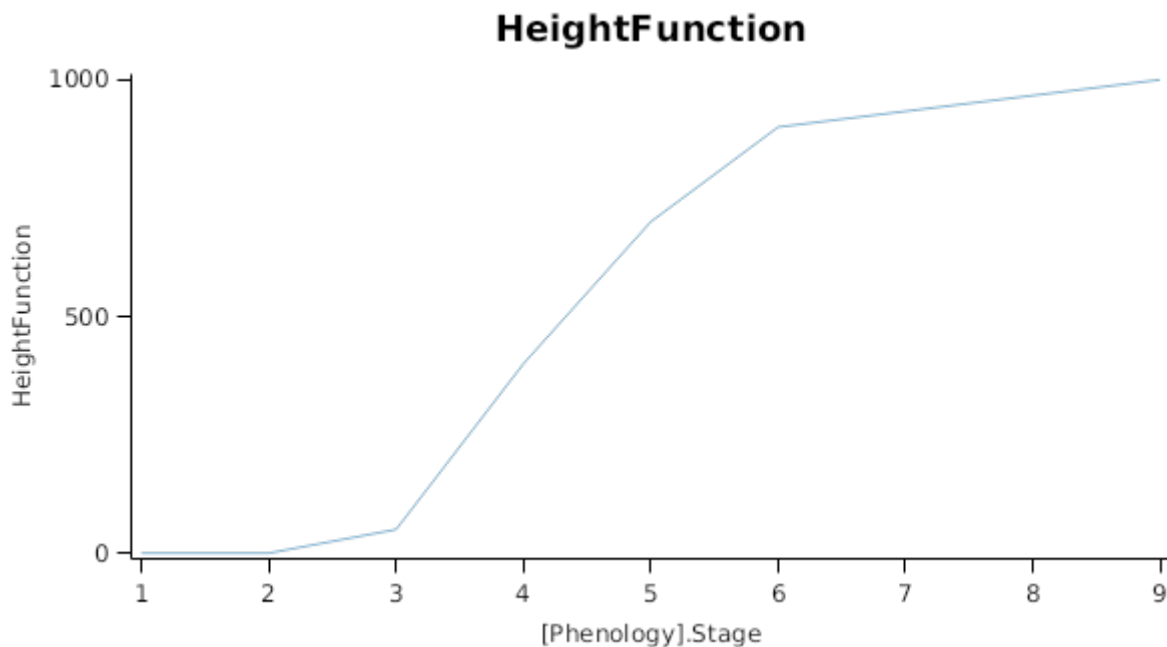
AreaRemoved is a daily accumulation of the values of functions listed below between the Emergence and HarvestRipe stages. Function values added to the accumulate total each day are:

$Zero = 0$

$ExtinctionCoefficient = 0.6$

HeightFunction is calculated using linear interpolation

[Phenology].Stage	HeightFunction
1.0	0.0
2.0	0.0
3.0	50.0
4.0	400.0
5.0	700.0
6.0	900.0
9.0	1000.0



1.4.9 StomatalConductance

Stomatal Conductance (gs) is calculated for use within the micromet model by adjusting a value provided for an atmospheric CO₂ concentration of 350 ppm. The impact of other stresses (e.g. Temperature, N) are captured through the modifier, Frgr.

$$gs = G_{max350} \times FRGR \times \text{stomatalConductanceCO2Modifier}$$

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

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

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

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

$$\text{PhotosynthesisCO2Modifier} = [\text{Leaf}].\text{Photosynthesis.FCO2}$$

1.4.10 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.

Vegetative has a value between Emergence and StartFlowering calculated as:

$$\text{Rate} = \text{Max}(\text{AgeSenescence}, \text{ShadeSenescence})$$

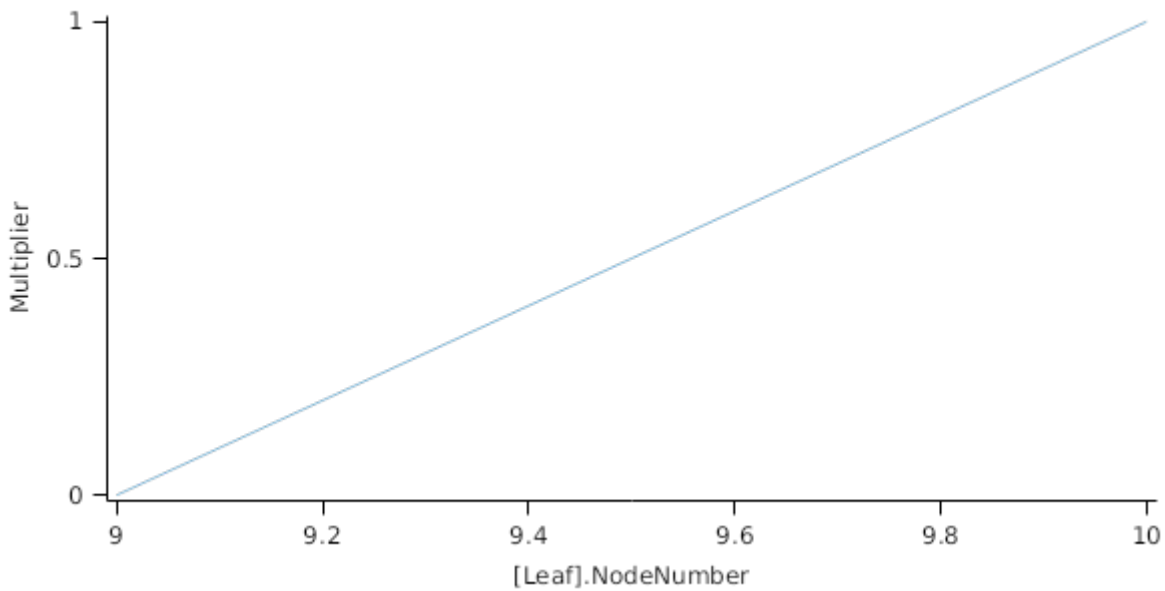
Where:

$$\text{AgeSenescence} = \text{Multiplier} \times \text{LeavesPerDay} \times 0$$

Multiplier is calculated using linear interpolation

[Leaf].NodeNumber	Multiplier
9.0	0.0
10.0	1.0

Multiplier

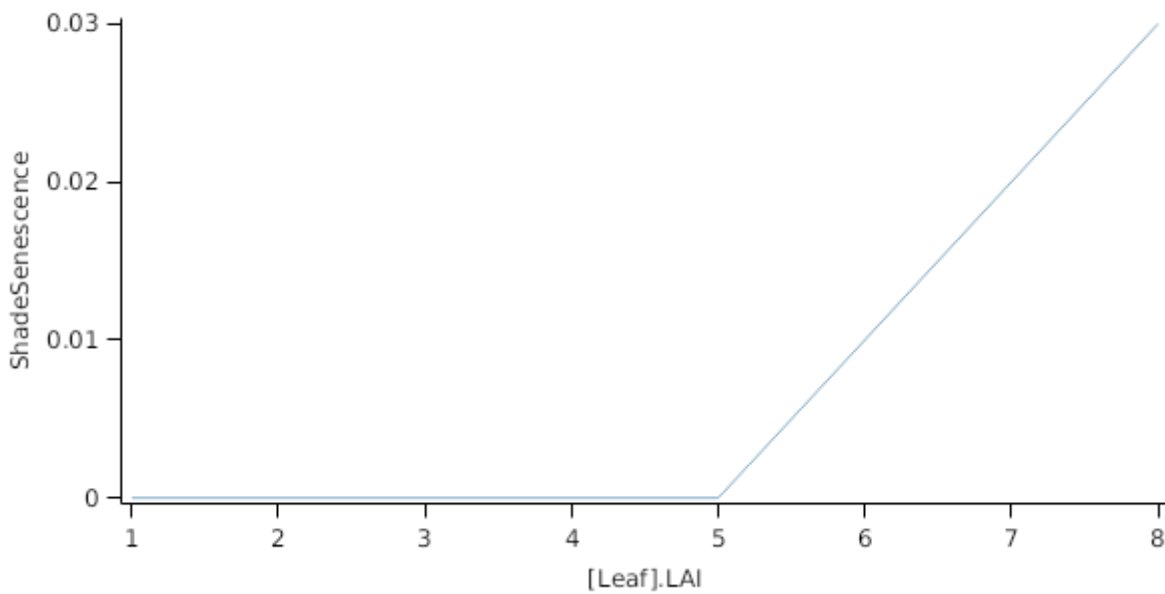


$LeavesPerDay = [Phenology].ThermalTime / [Leaf].Phyllochron / [Leaf].NodeNumber$

ShadeSenescence is calculated using linear interpolation

[Leaf].LAI	ShadeSenescence
1.0	0.0
5.0	0.0
8.0	0.03

ShadeSenescence



Leaf senescence rate is calculated to ensure that all leaves are senesced by crop maturity.

Reproductive has a value between StartFlowering and EndPodDevelopment calculated as:

Leaf senescence rate is calculated to ensure that all leaves are senesced by crop maturity.

Rate is the value of Fraction bound between a lower and upper bound where:

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

$$TTRemaining = TTRequired - TTComplete$$

$$TTRequired = [Phenology].EarlyFlowering.Target + [Phenology].EarlyPodDevelopment.Target + [Phenology].EarlyGrainFilling.Target + [Phenology].MidGrainFilling.Target$$

$$TTComplete = [Phenology].EarlyFlowering.ProgressThroughPhase + [Phenology].EarlyPodDevelopment.ProgressThroughPhase + [Phenology].EarlyGrainFilling.ProgressThroughPhase + [Phenology].MidGrainFilling.ProgressThroughPhase$$

$$Modifier = 1$$

$$Lower = 0$$

$$Upper = 1$$

Leaf senescence rate is calculated to ensure that all leaves are senesced by crop maturity.

Senescent has a value between EndPodDevelopment and HarvestRipe calculated as:

Leaf senescence rate is calculated to ensure that all leaves are senesced by crop maturity.

$$Rate = 0.1$$

Leaf detaches 5% of its dead biomass each day, passing it to the surface organic matter model for decomposition.

1.4.11 Biomass removal

1.4.11.1 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.

1.5 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).

1.5.1 Constants

$$MinimumNConc = 0.02$$

$$MaximumNConc = 0.058$$

$$WaterContent = 0.13$$

$$DMConversionEfficiency = 0.89$$

$$RemobilisationCost = 0$$

$$CarbonConcentration = 0.4$$

This parameter is only used to provide a very approximate estimate of final grain number. Grain growth is calculated from harvest index increase.

$$MaximumPotentialGrainSize = 0.0038$$

1.5.2 FillingDuration

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

1.5.3 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 StartGrainFilling and EndGrainFill calculated as:

$HI_{GrainDemand} = [AboveGround].Wt \times HarvestIndexIncrease \times [Phenology].ThermalTime$

$HarvestIndexIncrease = OutstandingHarvestIndexIncrease / TT_{Remaining}$

$OutstandingHarvestIndexIncrease = \text{Max}(Increase, Zero)$

Where:

$Increase = [Grain].PotentialHarvestIndex - [Grain].HarvestIndex$

$Zero = 0$

$TT_{Remaining} = ReproductiveTT - ReproductiveTT_{Complete}$

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

$ReproductiveTT_{Complete} = [Phenology].EarlyGrainFilling.ProgressThroughPhase + [Phenology].MidGrainFilling.ProgressThroughPhase + [Phenology].LateGrainFilling.ProgressThroughPhase$

1.5.4 NFillingRate

$N_{FillingRate} = [Grain].MaximumNConc \times [Grain].DMDemandFunction \times [Grain].DMConversionEfficiency$

1.5.5 BiomassRemovalDefaults

1.5.5.1 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.

1.5.6 HarvestIndex

$HarvestIndex = [Grain].Wt / [AboveGround].Wt$

1.5.7 PotentialHarvestIndex

$PotentialHarvestIndex = [Pod].PotentialHarvestIndex \times GrainFraction$

$GrainFraction = 0.72 \text{ (0-1)}$

1.5.8 DMDemandPriorityFactors

1.5.8.1 DMDemandPriorityFactors

This class holds the functions for calculating values for each Nutrient component.

1.5.9 NDemandPriorityFactors

1.5.9.1 NDemandPriorityFactors

This class holds the functions for calculating values for each Nutrient component.

1.5.10 NumberFunction

Grain number is simply estimated from grain mass and a constant potential grain size.

$NumberFunction = [Grain].Wt / [Grain].MaximumPotentialGrainSize$

1.6 Stem

1.6.1 Stem

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

1.6.2 Dry Matter Demand

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

1.6.2.1 DMDemands

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

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.

1.6.4 N Concentration Thresholds

MinimumNConc = 0.005

CriticalNConc = [Stem].MinimumNConc

MaximumNConc = [Leaf].MaximumNConc

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

NitrogenDemandSwitch has a value between Emergence and StartGrainFilling calculated as:

Constant = 1

1.6.5 Dry Matter Supply

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

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

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

Vegetative has a value between Emergence and StartGrainFilling calculated as:

RetranslocationFactor = 0

GrainFilling has a value between StartGrainFilling and EndGrainFill calculated as:

RetranslocationFactor = 0.2

1.6.6 Nitrogen Supply

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

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

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

Vegetative has a value between Emergence and StartGrainFilling calculated as:

RetranslocationFactor = 0

GrainFilling has a value between StartGrainFilling and EndGrainFill calculated as:

RetranslocationFactor = 0.1

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.

PostCanopyPhase has a value between EndPodDevelopment and Maturity calculated as:

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

Where:

$Fraction = [Phenology].ThermalTime / TTRemaining$

$TTRemaining = PostCanopyTT - PostCanopyTTComplete$

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

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

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.

1.6.8 BiomassRemovalDefaults

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

1.7 Shell

1.7.1 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.

1.7.2 Dry Matter Demand

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

1.7.2.1 DMDemands

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

1.7.3 Nitrogen Demand

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

1.7.3.1 NDemands

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

1.7.4 N Concentration Thresholds

MinimumNConc = 0.01

$CriticalNConc = [Shell].MinimumNConc$

MaximumNConc = 0.045

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

NitrogenDemandSwitch has a value between StartPodDevelopment and EndPodDevelopment calculated as:

Constant = 1

1.7.5 Dry Matter Supply

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

Shell will retranslocate 10% of non-structural DM each day.

1.7.6 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.

1.7.7 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 `EndPodDevelopment` and `Maturity` calculated as:

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

Where:

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

$$\text{TTRemaining} = \text{ReproductiveTT} - \text{ReproductiveTT1Complete}$$

$$\text{ReproductiveTT} = [\text{Phenology}].\text{LateGrainFilling.Target} + [\text{Phenology}].\text{Maturing.Target}$$

$$\text{ReproductiveTT1Complete} = [\text{Phenology}].\text{LateGrainFilling.ProgressThroughPhase} + [\text{Phenology}].\text{Maturing.ProgressThroughPhase}$$

$$\text{One} = 1$$

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

1.7.8 BiomassRemovalDefaults

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

1.8 Pod

1.8.1 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

1.9 MortalityRate

$$\text{MortalityRate} = 0$$

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 AboveGroundLive

1.11.1 AboveGroundLive

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

AboveGroundLive summarises the following biomass objects:

- * Leaf
- * Stem
- * Grain
- * Shell

1.12 BelowGround

1.12.1 BelowGround

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

BelowGround summarises the following biomass objects:

- * Root

1.13 Total

1.13.1 Total

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

Total summarises the following biomass objects:

- * Leaf
- * Stem
- * Grain
- * Shell
- * Root

1.14 TotalLive

1.14.1 TotalLive

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

TotalLive summarises the following biomass objects:

- * Leaf
- * Stem
- * Grain
- * Shell
- * Root

1.15 TotalDead

1.15.1 TotalDead

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

TotalDead summarises the following biomass objects:

- * Leaf
- * Stem
- * Grain
- * Shell
- * Root

1.16 CultivarFolder

1.16.1 CultivarFolder

Cultivar names include several codes for several traits.

- * RR = Roundup Ready - These cultivars are developed to provide tolerance for Glyphosate herbicide.
- * CL = Clearfield - These cultivars are developed for the Clearfield Canola weed control system.
- * TT = Triazine Tolerant - These cultivars are developed to provide tolerance for triazine herbicide
- * RT = Triazine and Roundup - These cultivars are developed to provide tolerance to both triazine and glyphosate herbicides.

1.17 SeedMortalityRate

SeedMortalityRate = 0

2 The APSIM Canola Model

3 Validation

A test dataset has been developed to test the APSIM Canola model for a range of environmental (soil and climate) conditions, management options (sowing dates, populations, nitrogen rates, irrigation) and genetic backgrounds (different regions, cultivar types). These tests have been grouped into experiments focusing on phenological development or growth and resource use. Graphs of model performance are provided for yield, biomass production, canopy development, phenological development, water and nitrogen uptake, and grain yield components.



3.1 Phenology Experiments

3.1.1 OCP Phenology

GRDC funded Optimised Canola Profitability project had experiments at Gatton in 2015, and Gatton and Canberra in 2016 and 2017 which consisted of 3 to 5 sowing dates [Whish et al., 2020](#). In 2016 and 2017 photoperiod treatments (daylength extension with lights) were also applied. Experiments were in the field in single rows of 1-3.5m in length and row spacing of 50cm. Plants were well watered and supplied with nutrients and were removed after flowering. The total number of cultivars included across the 5 experiments was 37, with each cultivar being included 4 to 28 combinations of location, year, TOS, and photoperiod (most cultivars between 13 and 18 combinations. Data collected: plant growth stage and leaf number was recorded 2 to 3 x weekly between emergence and flowering for 8 plants in each plot. Data was summarised as average sowing, emergence, floral initiation, green bud, flowering date for each cultivar/treatment.

Contact Jeremy Whish, Julianne Lilley (CSIRO)

List of experiments.

Experiment Name	Design (Number of Treatments)
Gatton2015	TOS x Cv x PP (90)
Gatton2016	TOS x Cv x PP (228)
Gatton2017	TOS x Cv x PP (132)
Canberra2016	TOS x Cv x PP (252)
Canberra2017	TOS x Cv x PP (198)

3.1.2 Omics Phenology

GRDC funded "CSP1901-002RTX: Optimising Canola Production in Diverse Australian Growing Environments" project had experiments at Gatton in 2019, 2020, Boorowa 2019, 2021, Cummins 2020, 2021, York 2020, 2021 which consisted of 2-4 sowing dates. Project aimed to use field observations and transcriptomic and genomic data to establish a genetic phenology model. This project assesses G x E effects on phenological traits (including flowering time) in a diverse set of modern Australian and globally important canola varieties (~350) across key growing environments and regions relevant to the Australian industry (14 combinations of site, year and TOS), as well as three controlled environments.

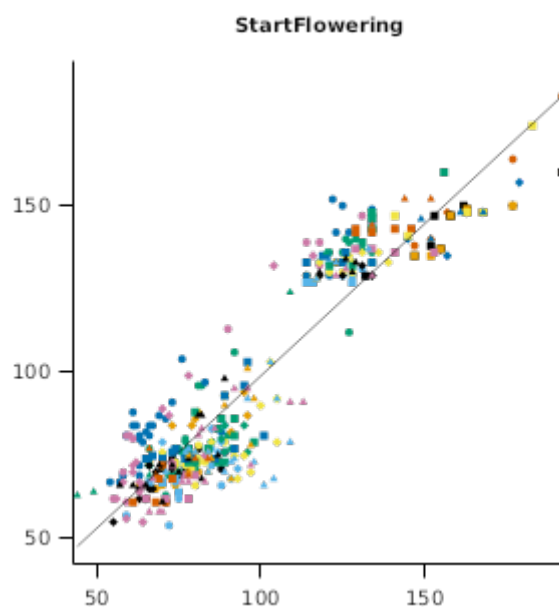
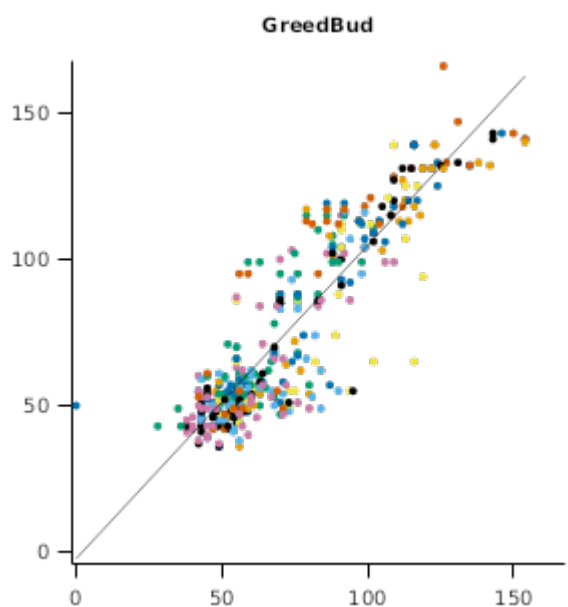
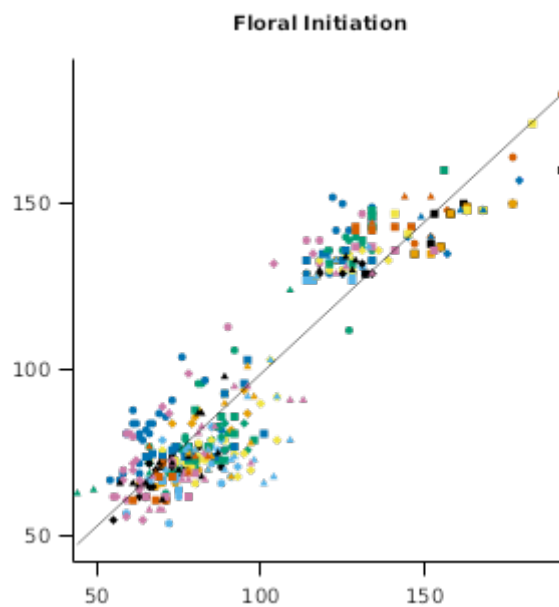
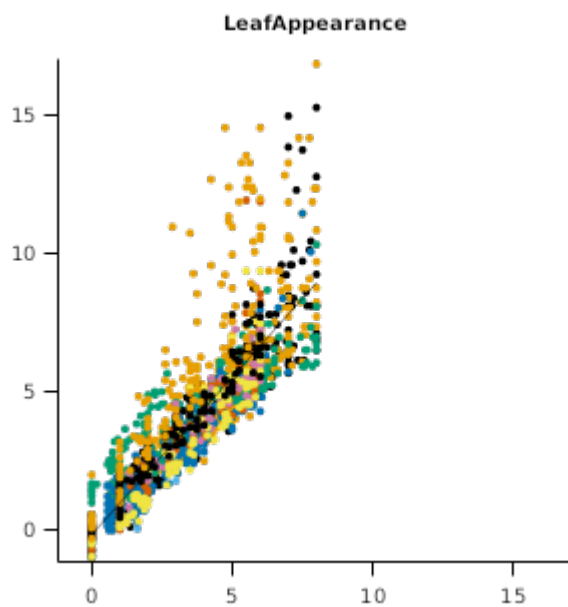
Data collected: plant growth stage and leaf number was recorded 2 to 3 x weekly between emergence and flowering for 4 plants in each plot. Data was summarised as average sowing, emergence, floral initiation, green bud, flowering date for each cultivar/treatment.

Contact Jeremy Whish, Julianne Lilley (CSIRO)

List of experiments.

Experiment Name	Design (Number of Treatments)
Gatton2019	TOS x Cv (28)
Gatton2020	TOS x Cv (18)
Boorowa2019	TOS x Cv (24)
Cummins2020	TOS x Cv (18)
York2020	TOS x Cv (18)

3.1.3 Combined Results



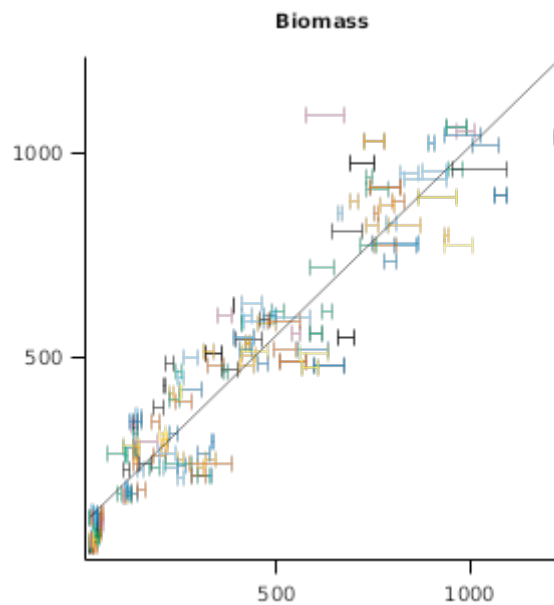
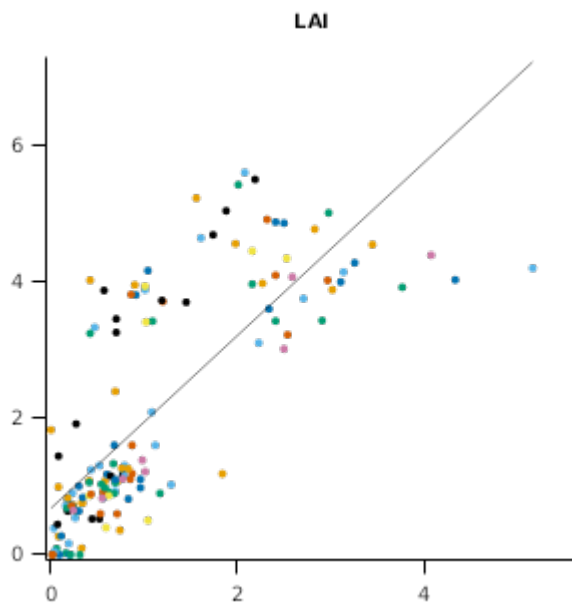
3.2 Growth Experiments

3.2.1 Kojonup

List of experiments.

Experiment Name	Design (Number of Treatments)
Kojonup2013	Cv x Fert (18)
Kojonup2014	Cv x Fert (20)

3.2.1.1 Combined Results

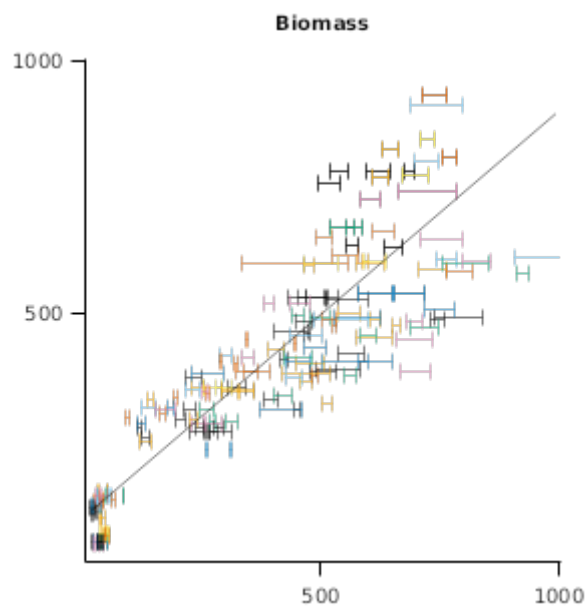
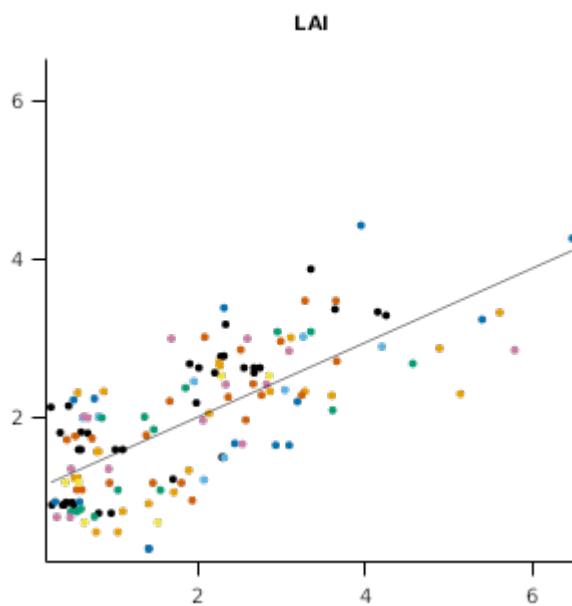


3.2.2 Cunderdin

List of experiments.

Experiment Name	Design (Number of Treatments)
Cunderdin2013	Cv x Fert (36)
Cunderdin2014	Cv x Fert (20)

3.2.2.1 Combined Results



3.2.3 Wagga

List of experiments.

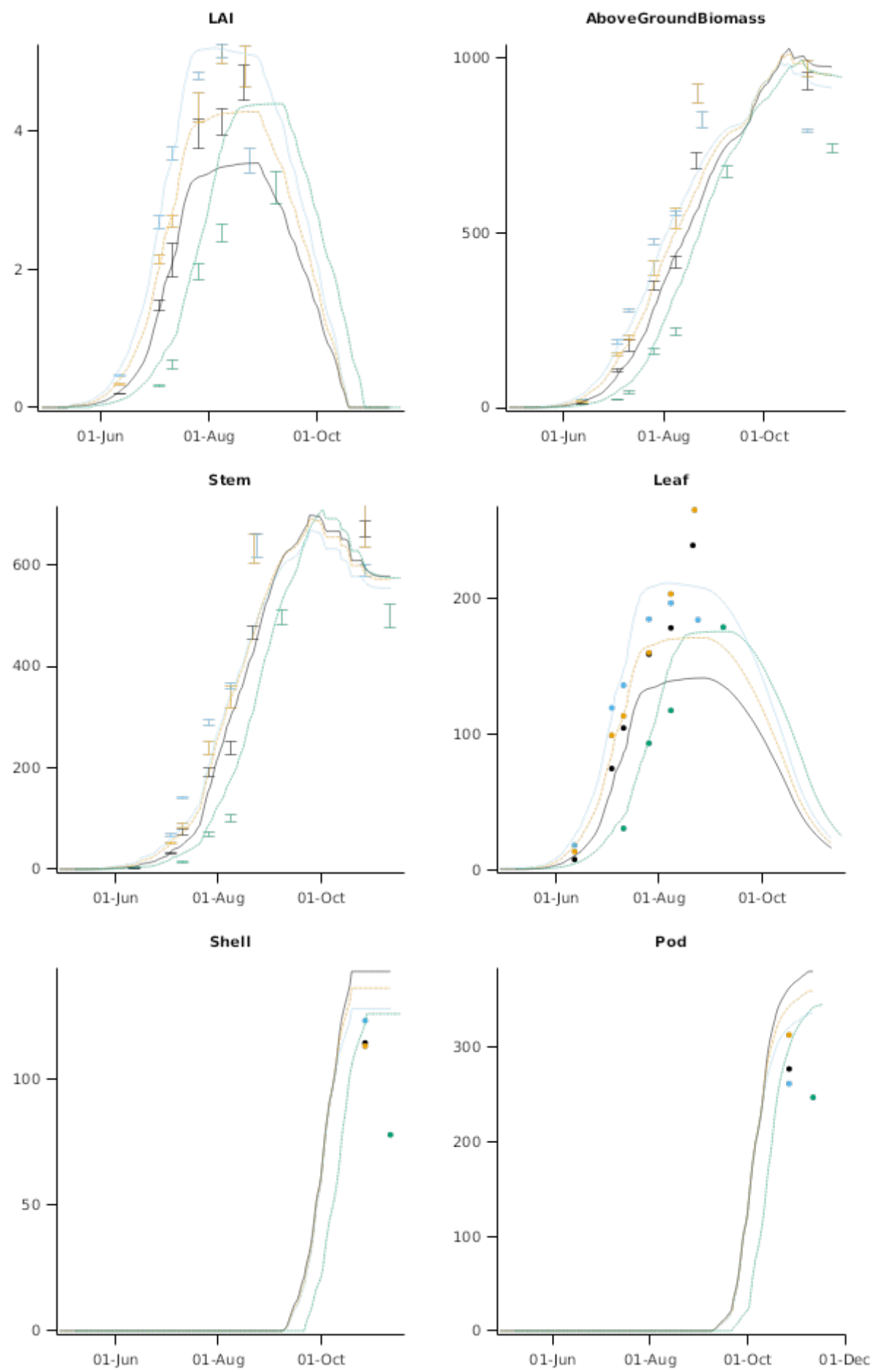
Experiment Name	Design (Number of Treatments)
Wagga2008	Cv x Treat (12)

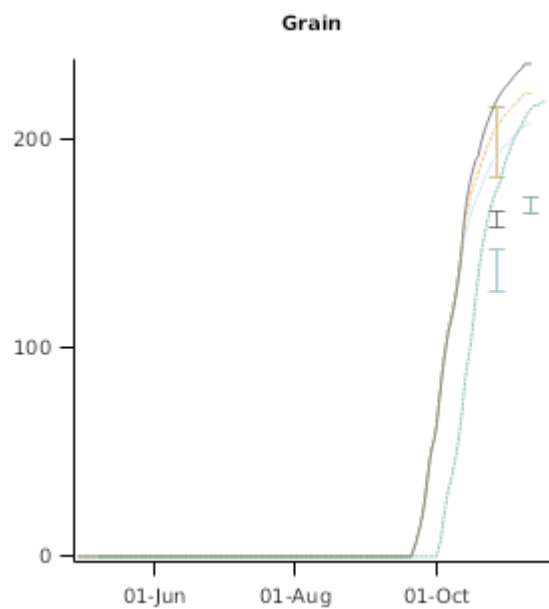
3.2.3.1 Wagga2008

McCormick et al 2012. irrigated experiment, 3 cultivars, 3 densities, grazed and ungrazed

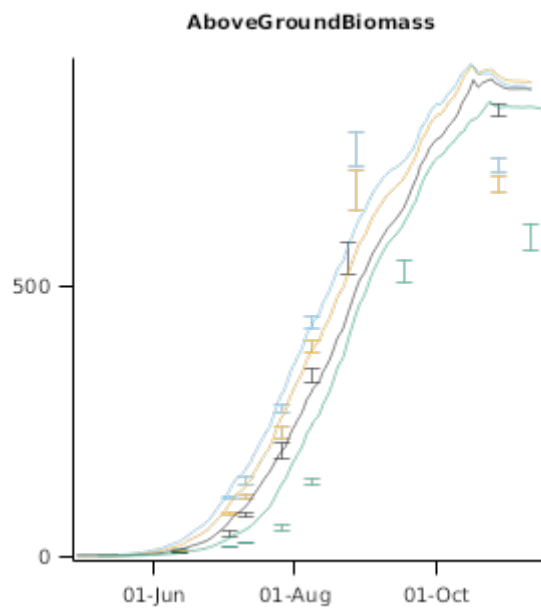
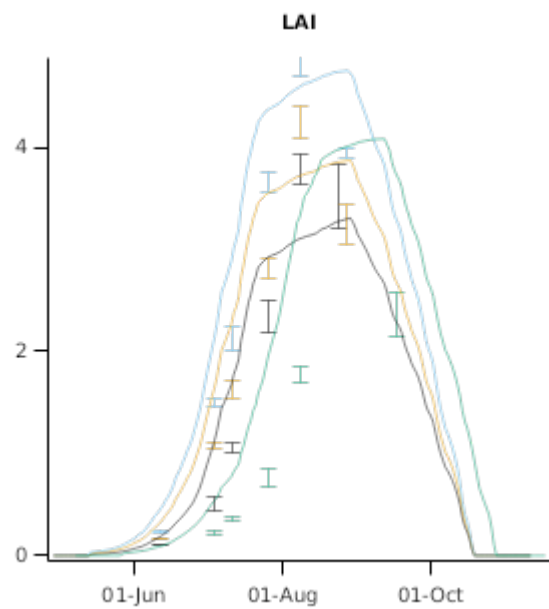
3.2.3.1.1 Graphs

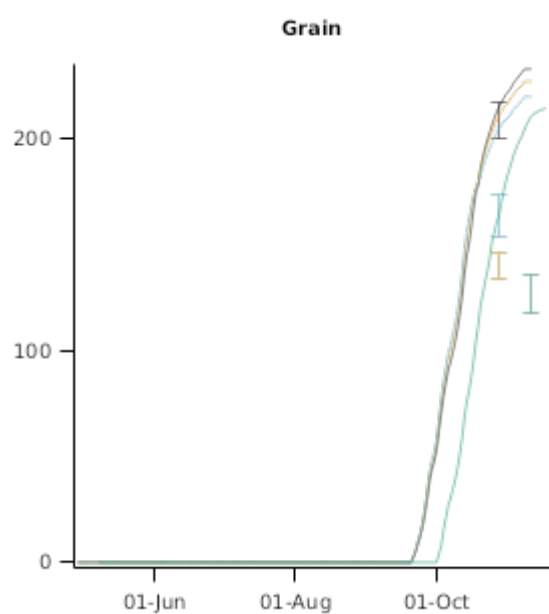
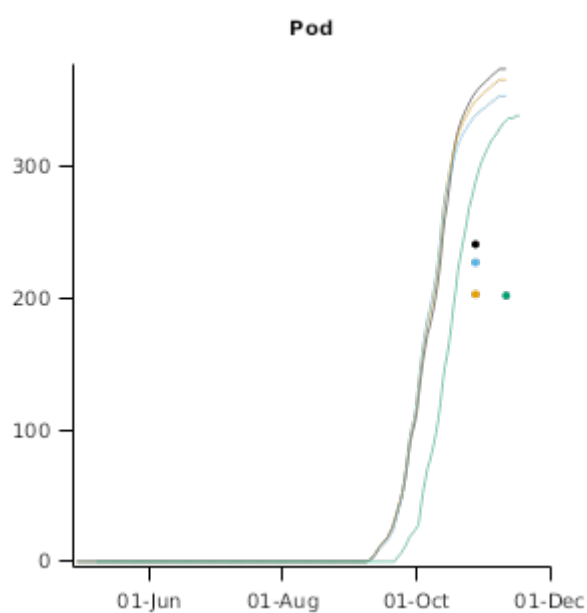
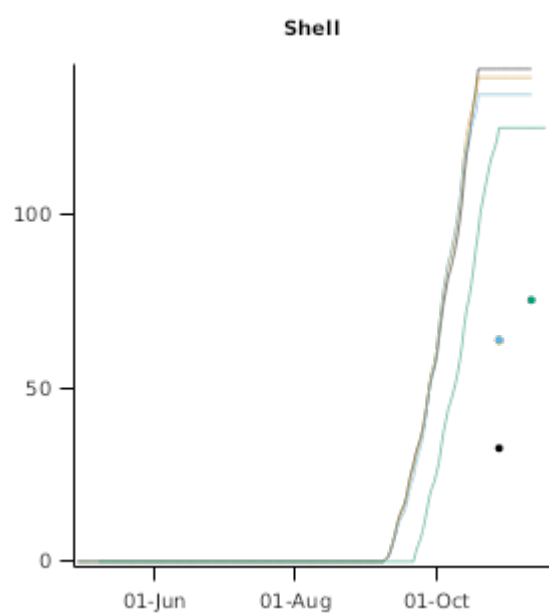
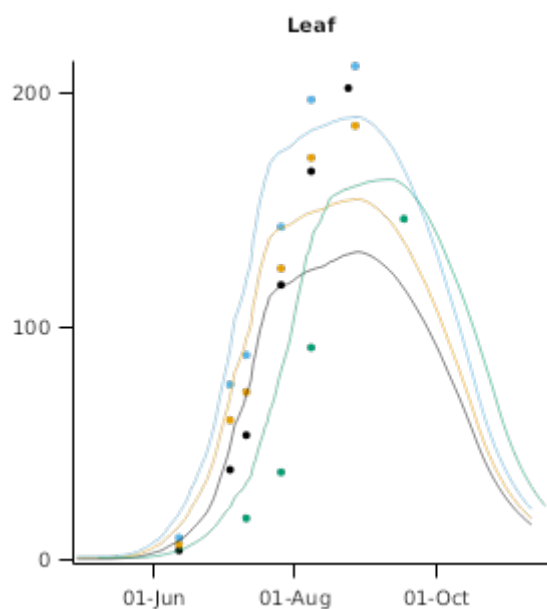
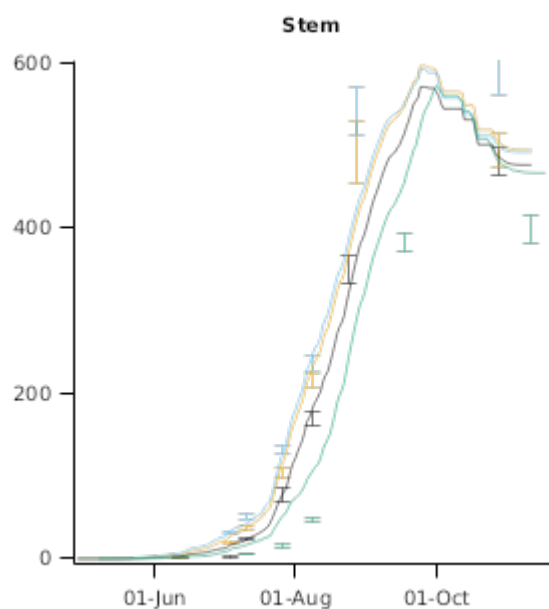
3.2.3.1.1.1 Garnet

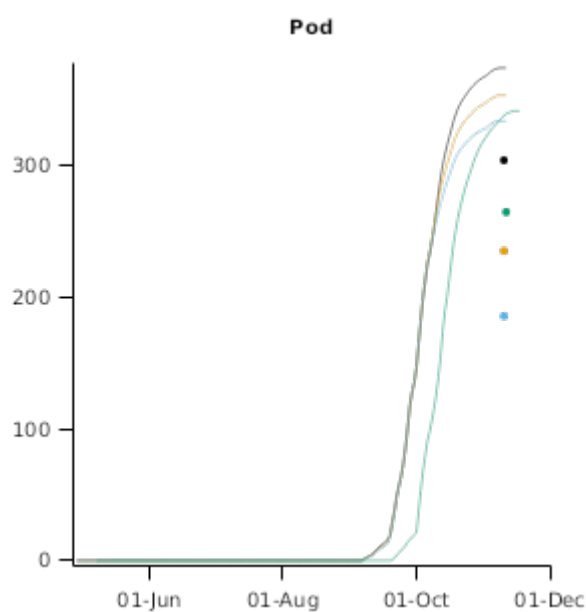
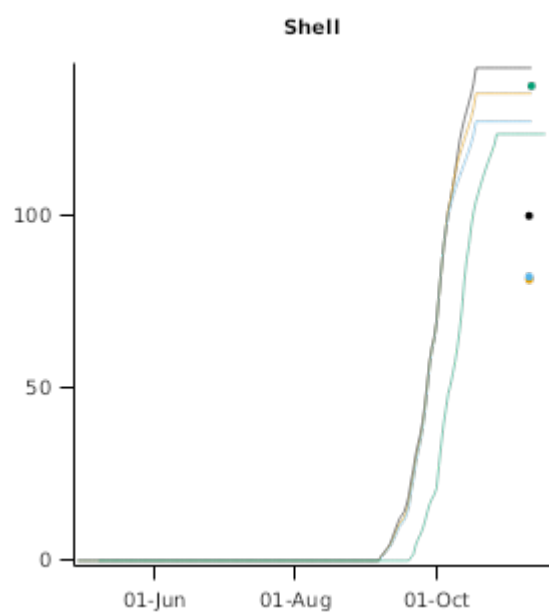
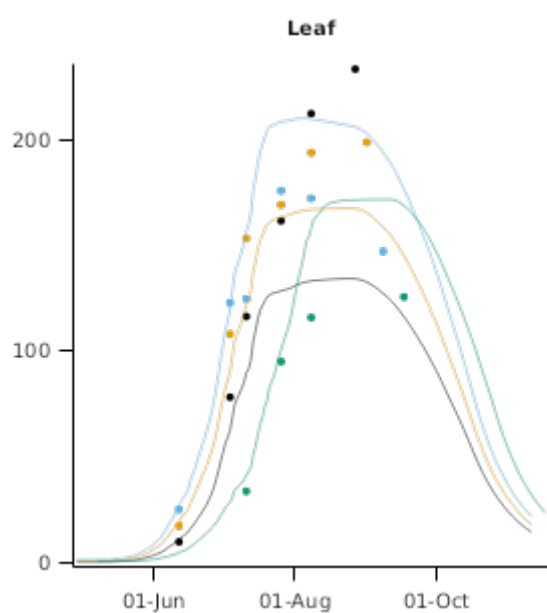
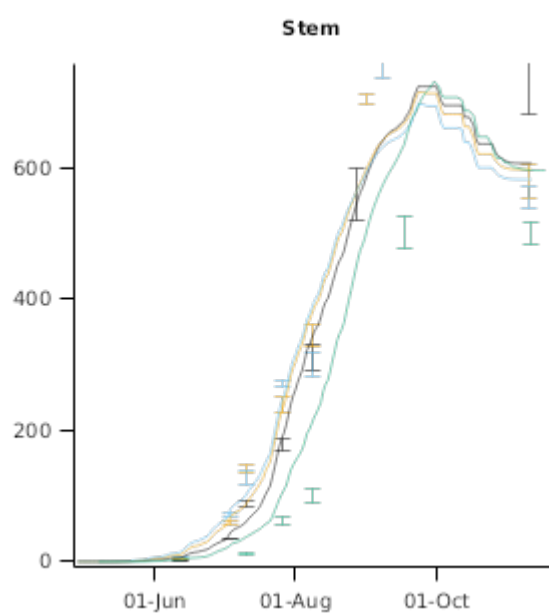
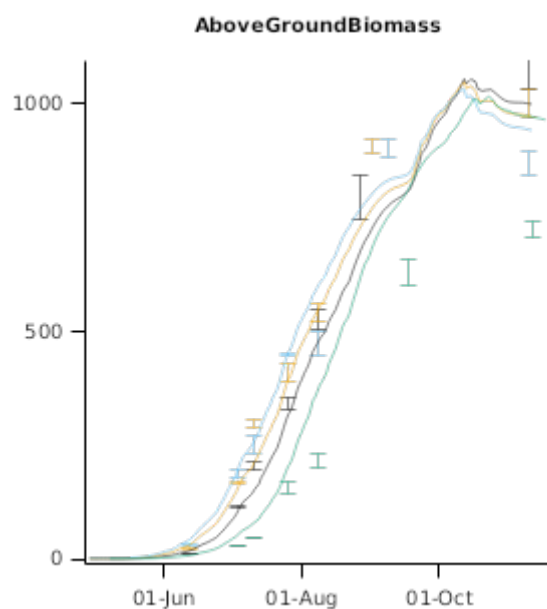
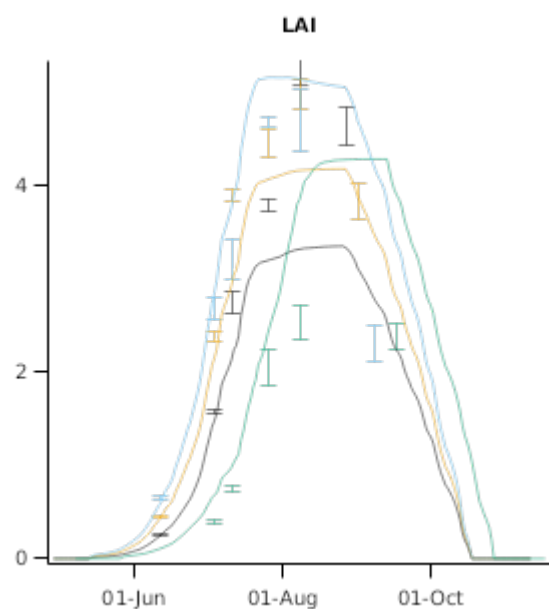


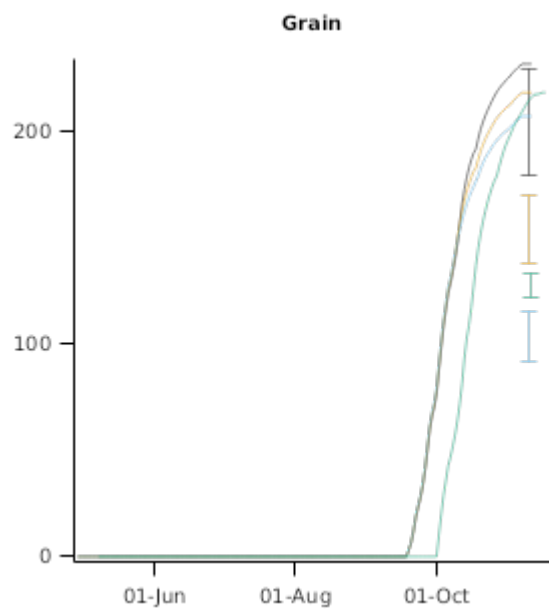


3.2.3.1.1.2 Marlin









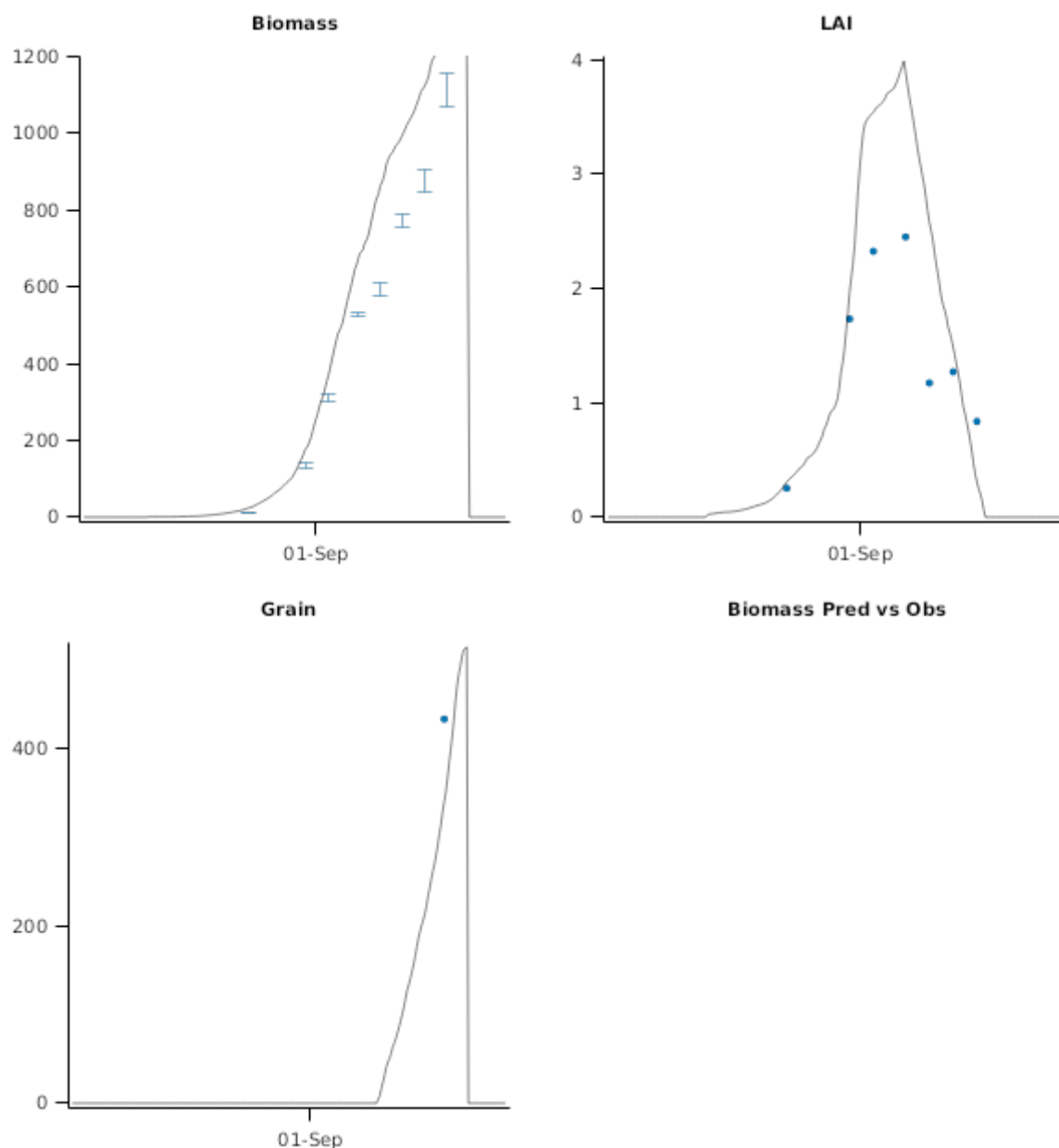
3.2.4 Harden

List of experiments.

Experiment Name	Design (Number of Treatments)
Harden1999	Cv (1)

3.2.4.1 Harden1999

3.2.4.1.1 Graphs

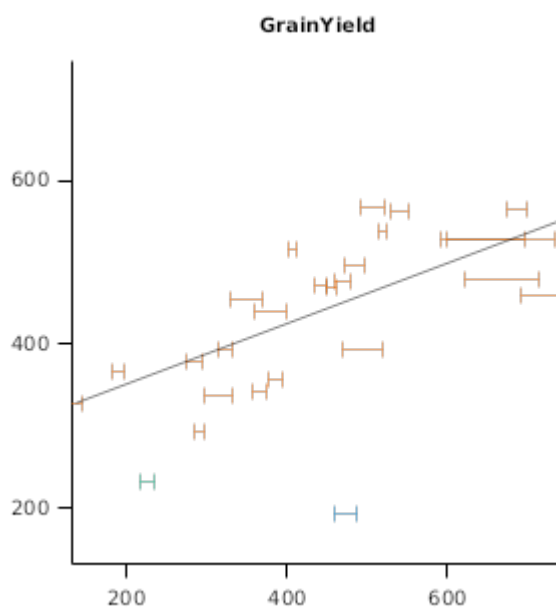
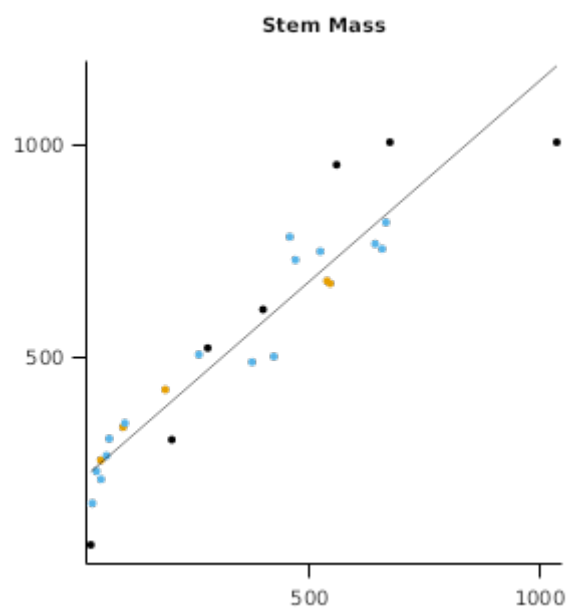
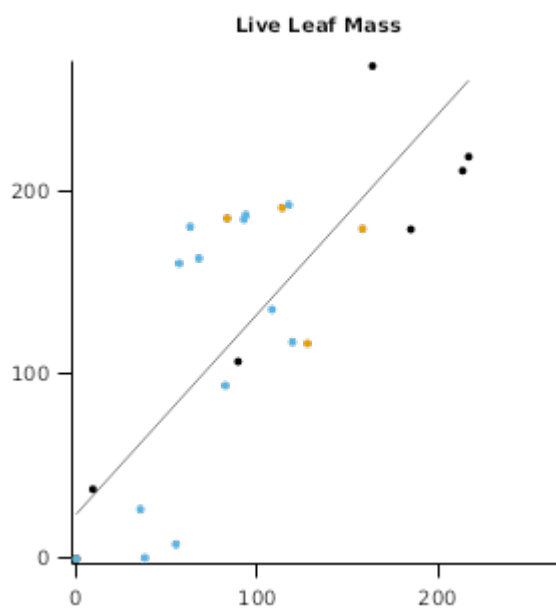
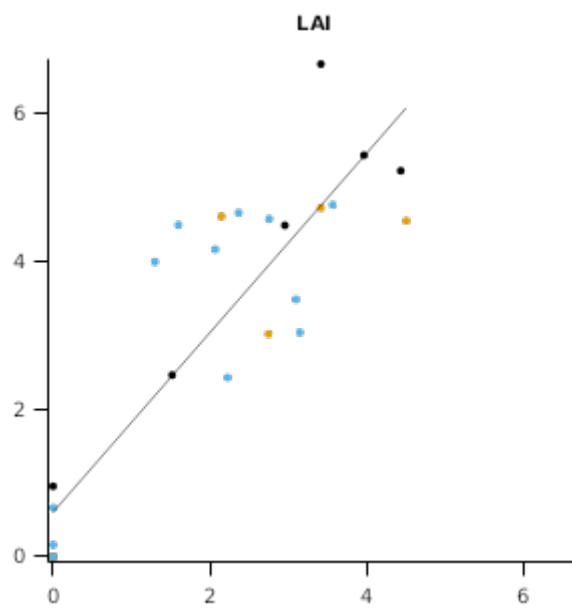
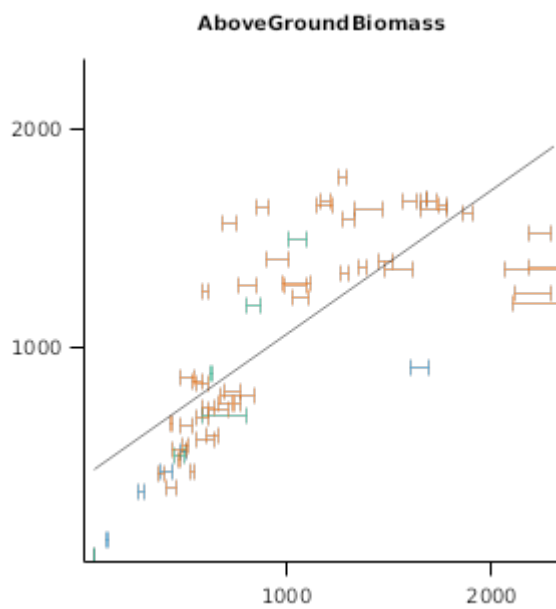


3.2.5 Greenthorpe

List of experiments.

Experiment Name	Design (Number of Treatments)
Greenethorpe2013_Ex1	Cv (1)
Greenethorpe2013_Ex2	Cv (1)
Greenethorpe2013_Ex3	Cv (3)
Greenethorpe2014_Ex1	Cv (1)
Greenethorpe2014_Ex2	Cv (1)
Greenethorpe2014_Ex3	Cv x TOS (24)

3.2.5.1 Combined Results



3.2.6 Merredin

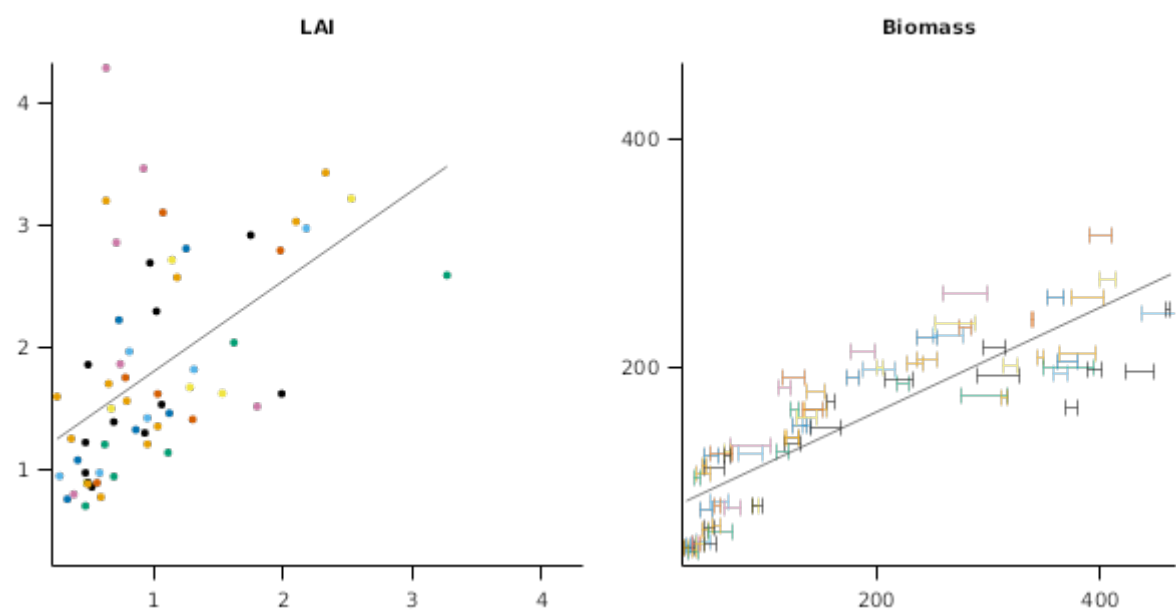
List of experiments.

Experiment Name	Design (Number of Treatments)
Merredin2014	Cv x Fert (20)

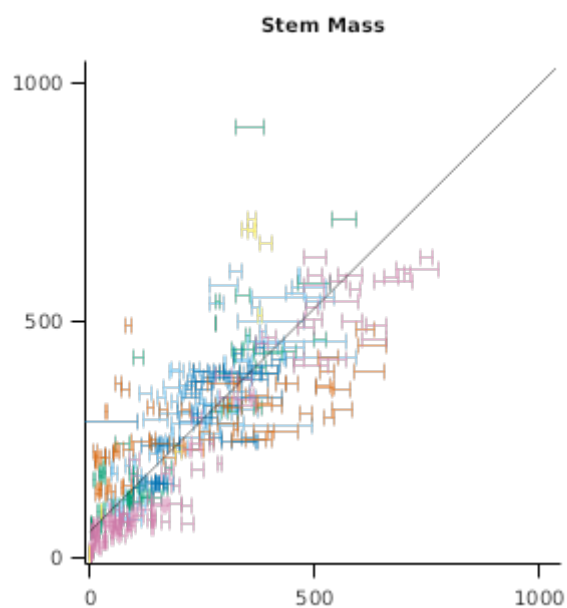
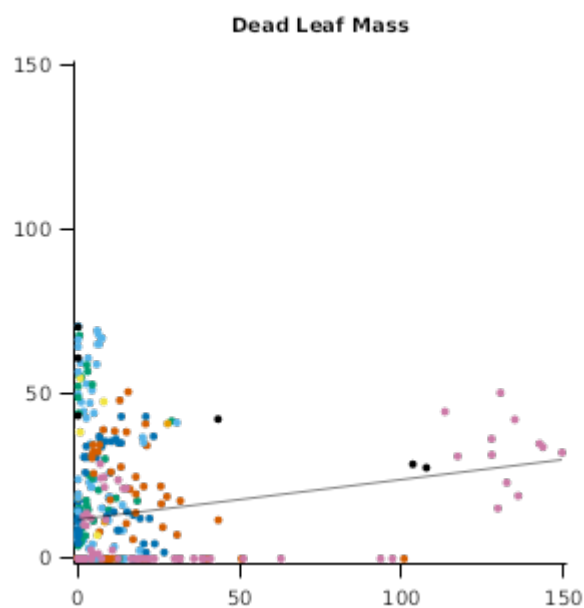
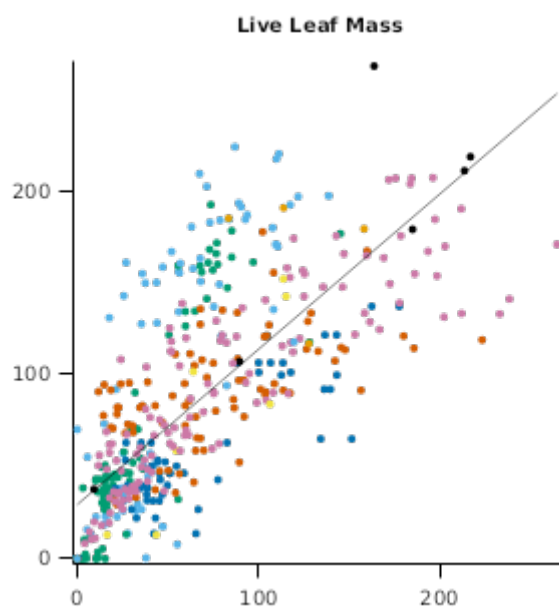
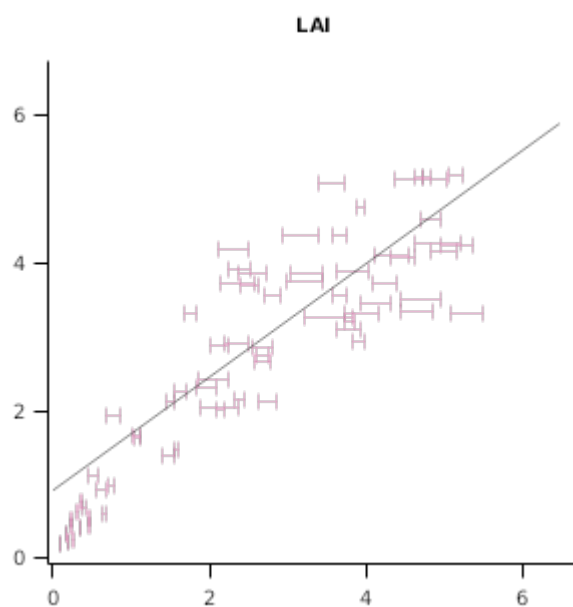
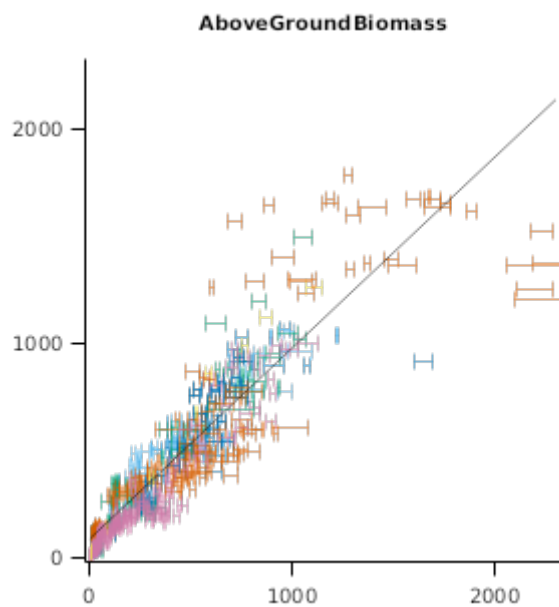
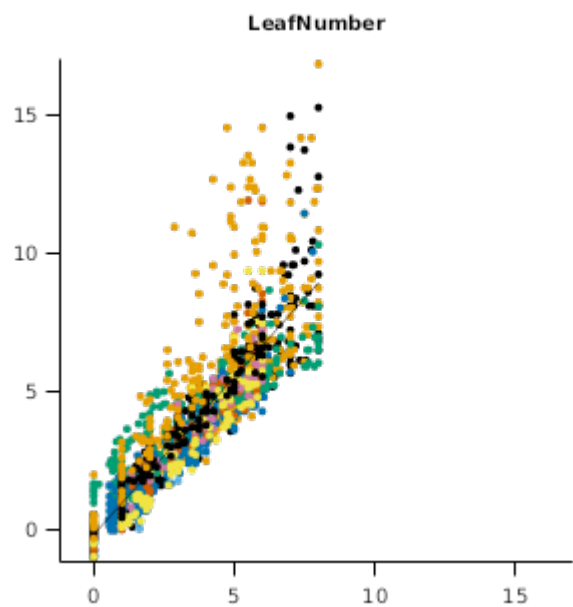
3.2.6.1 Merredin2014

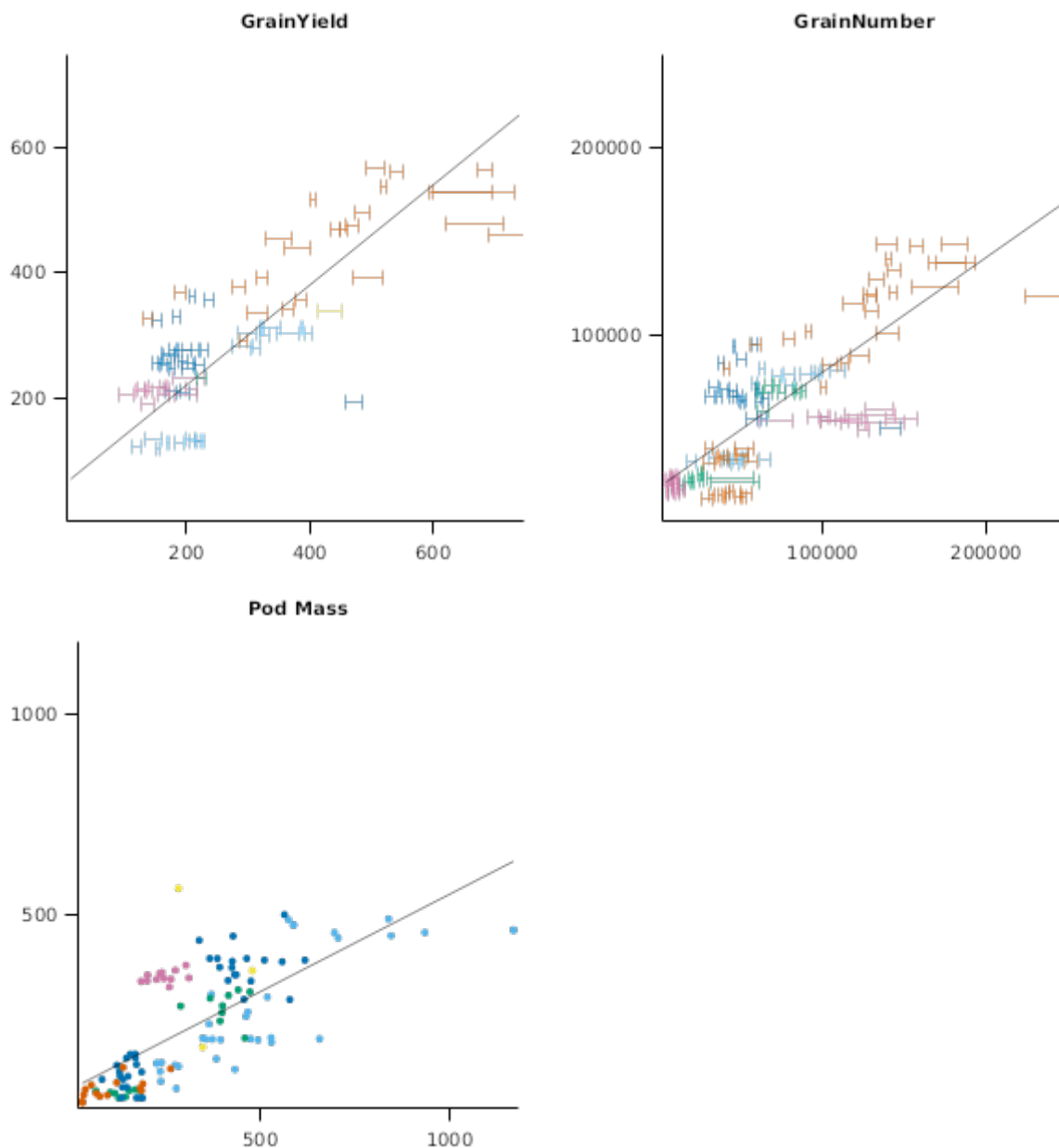
3.2.6.1.1 Graphs

3.2.6.1.1.1 Combined Results



3.3 Combined Results





4 Sensibility

List of experiments.

Experiment Name	Design (Number of Treatments)
DetailedDynamics	Cv (1)
CanolaGrazing	StockingRate (3)
Wagga	Cv x TOS (6)

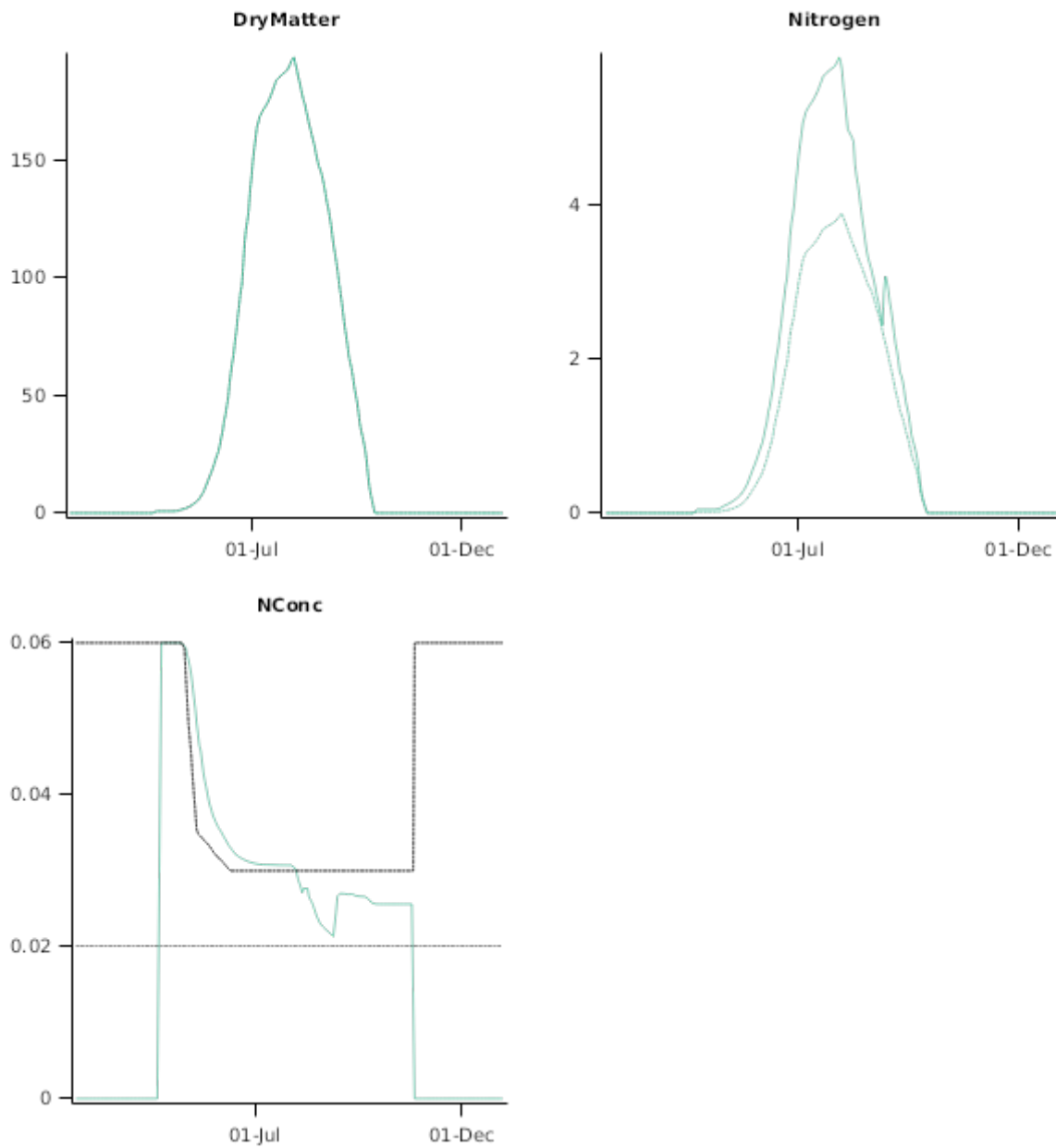
4.1 DetailedDynamics

This test demonstrates the detailed dynamics within a simple simulation of conola growth and resource use. This includes:

- * Dry matter and Nitrogen supply and demand for individual organs
- * Dry matter and Nitrogen content for live and dead components of each organ
- * Light interception for live and dead components for each organ

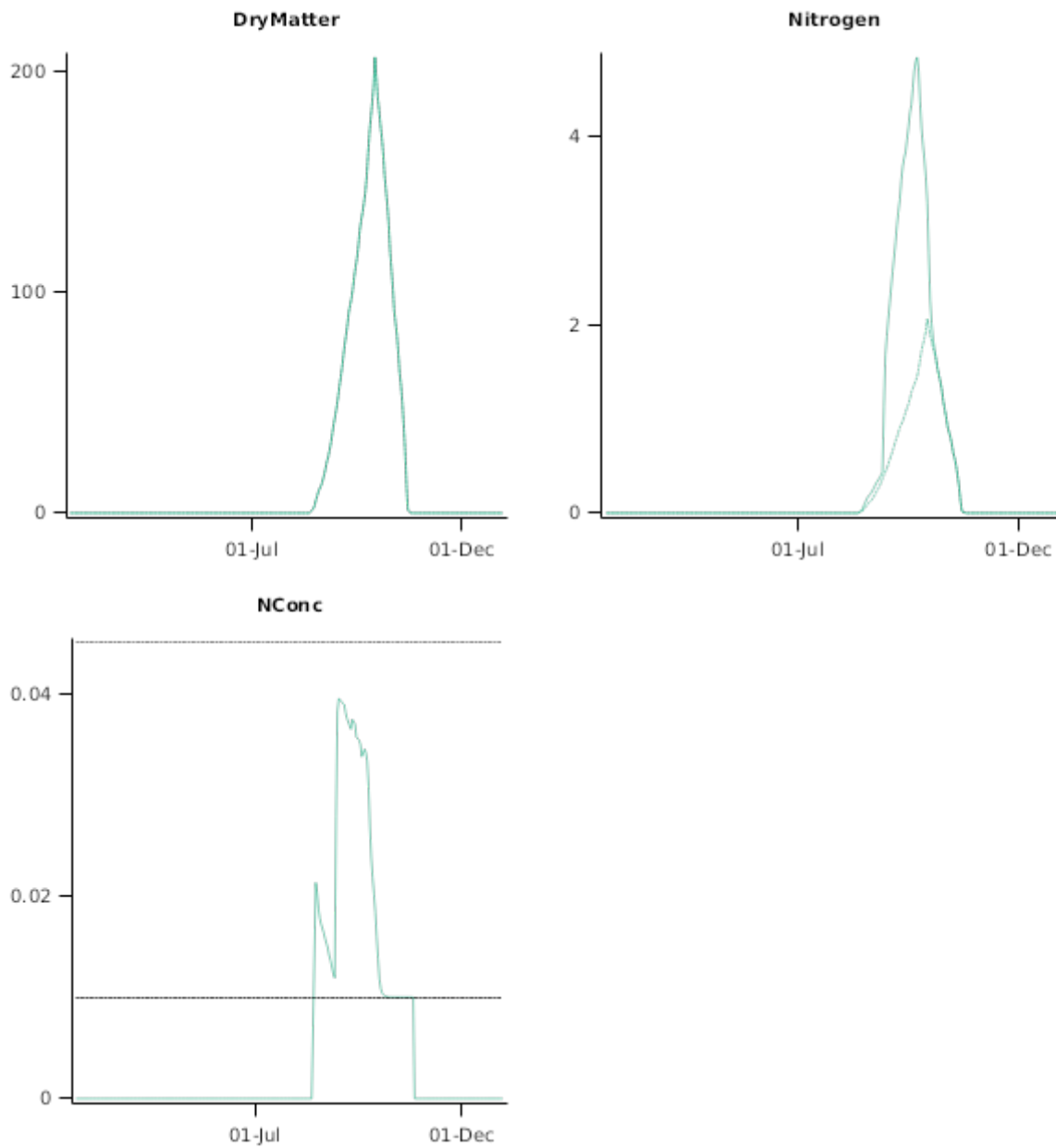
4.1.1 Leaf

These graphs demonstrate the development of live and dead leaf biomass over time, and the accumulation and retranslocation of N in the structural and non-structural pools as the plant develops.



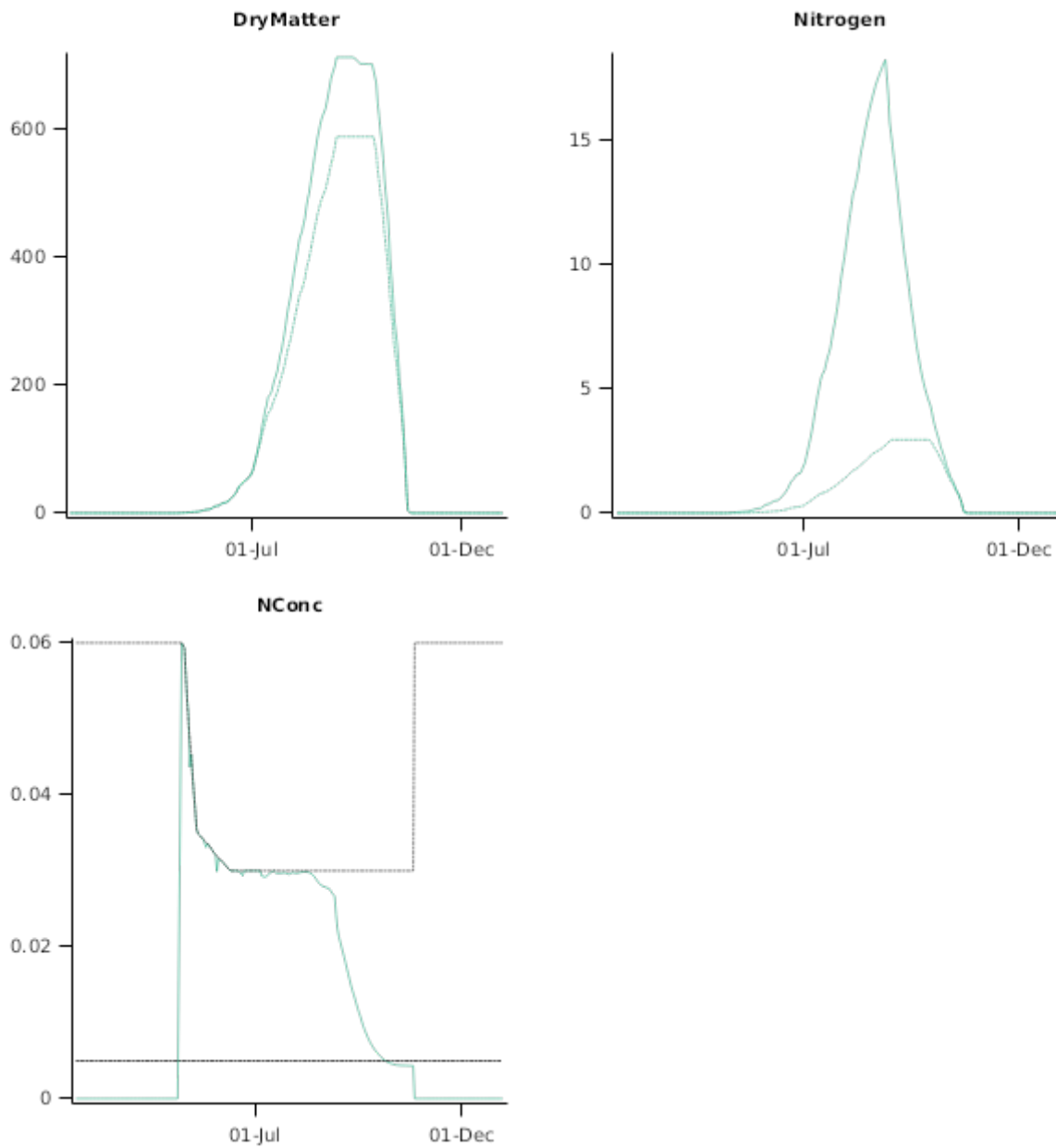
4.1.2 Shell

These graphs demonstrate the development of live and dead shell biomass over time, and the accumulation and retranslocation of N in the structural and non-structural pools as the plant develops.



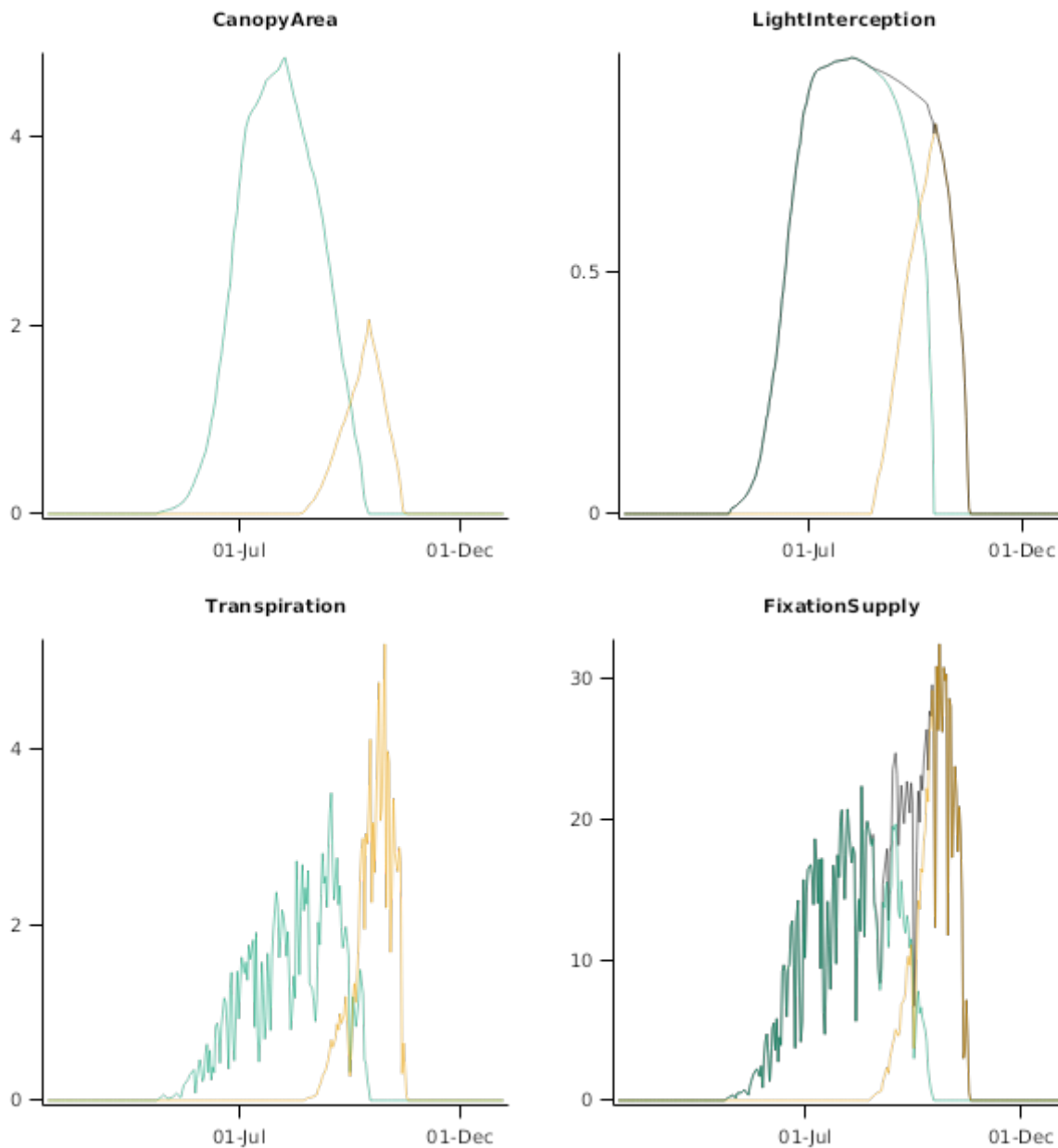
4.1.3 Stem

These graphs demonstrate the development of live and dead stem biomass over time, and the accumulation and retranslocation of N in the structural and non-structural pools as the plant develops.



4.1.4 Canopy

These graphs demonstrate the changing roles of leaf and pod in light interception, photosynthesis and transpiration over time



4.2 CanolaGrazing

This sensibility test performs a livestock grazing simulation for canola planted in March, and grazed in late May as a dual-purpose crop.

4.3 Wagga

This test demonstrates the effect of time of sowing and cultivar (generic early, late or winter cultivars) on yield, biomass and time to harvest for long term simulations at Wagga Wagga, NSW.

5 References

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