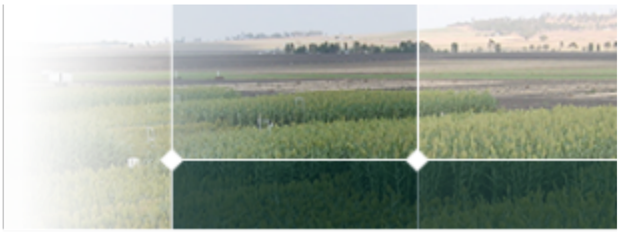


1 The APSIM Soybean Model

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

1.1 Arbitrator

1.1.1 Arbitrator

The Arbitrator class determines the allocation of dry matter (DM) and Nitrogen between each of the organs in the crop model. Each organ can have up to three different pools of biomass:

* **Structural biomass** which is essential for growth and remains within the organ once it is allocated there.
* **Metabolic biomass** which generally remains within an organ but is able to be re-allocated when the organ senesces and may be retranslocated when demand is high relative to supply.
* **Storage biomass** which is partitioned to organs when supply is high relative to demand and is available for retranslocation to other organs whenever supply from uptake, fixation, or re-allocation is lower than demand.

The process followed for biomass arbitration is shown in the figure below. Arbitration calculations are triggered by a series of events (shown below) that are raised every day. For these calculations, at each step the Arbitrator exchange information with each organ, so the basic computations of demand and supply are done at the organ level, using their specific parameters.

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

* **Fixation supply**. From photosynthesis (DM) or symbiotic fixation (N)
* **Uptake supply**. Typically uptake of N from the soil by the roots but could also be uptake by other organs (eg foliage application of N).

* **Retranslocation supply**. Storage biomass that may be moved from organs to meet demands of other organs.
* **Reallocation supply**. Biomass that can be moved from senescing organs to meet the demands of other organs.

1. **doPotentialPlantPartitioning.** On this event the Arbitrator first executes the DoDMSetup() method to gather the DM supplies and demands from each organ, these values are computed at the organ level. It then executes the DoPotentialDMAllocation() 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, DoActualDMAllocation 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.

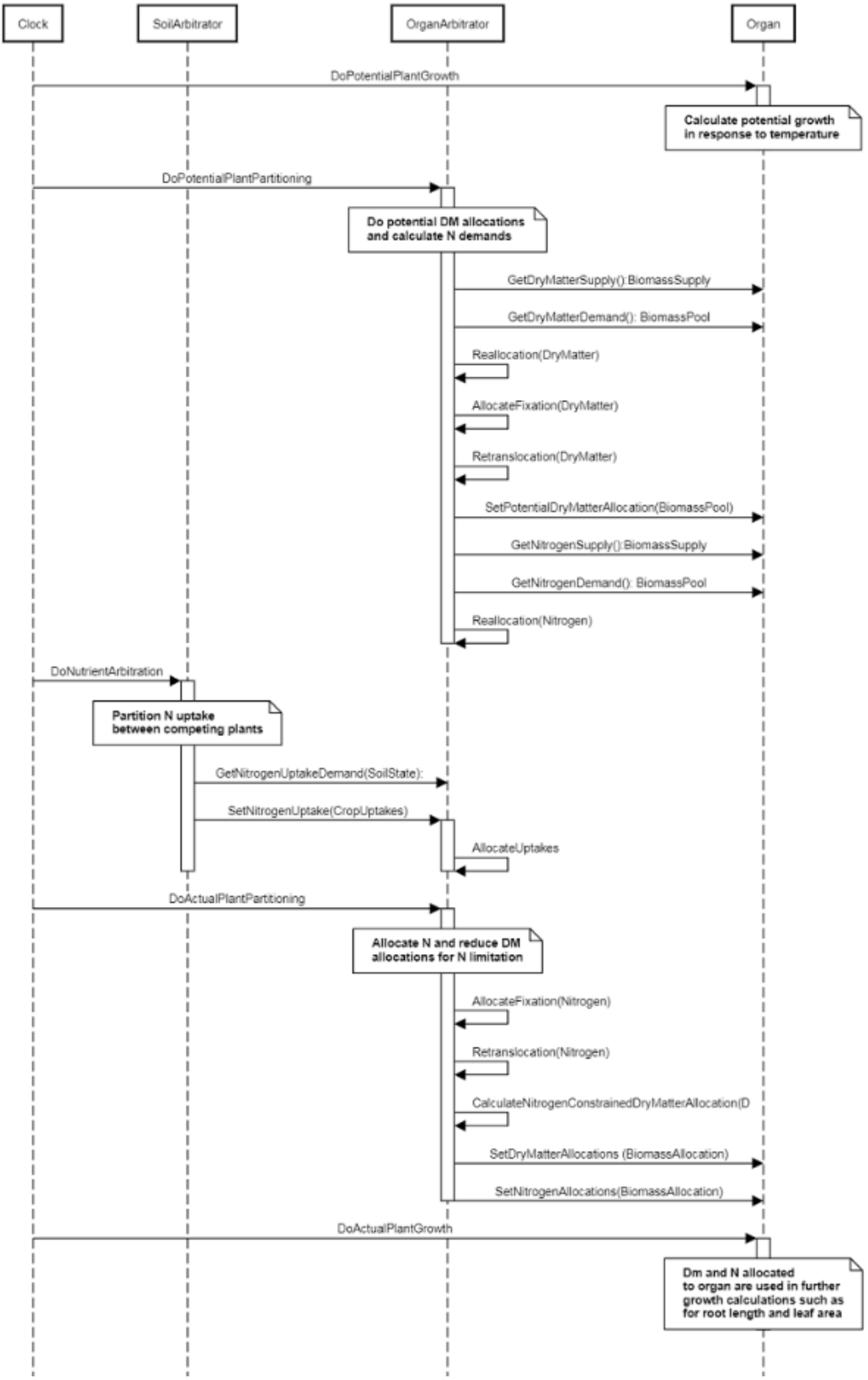


Figure 1: Schematic showing the procedure for arbitration of biomass partitioning. Pink boxes represent events that occur every day and their numbering shows the order of calculations. Blue boxes represent the methods that are called when these events occur. Orange boxes contain properties that make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

In the new model we simplified phenology by taking out stages that are not measurable (e.g. end of juvenile stage) and by adding new stages that are measurable (e.g. start pod). The new phenology follows the V/R staging system.

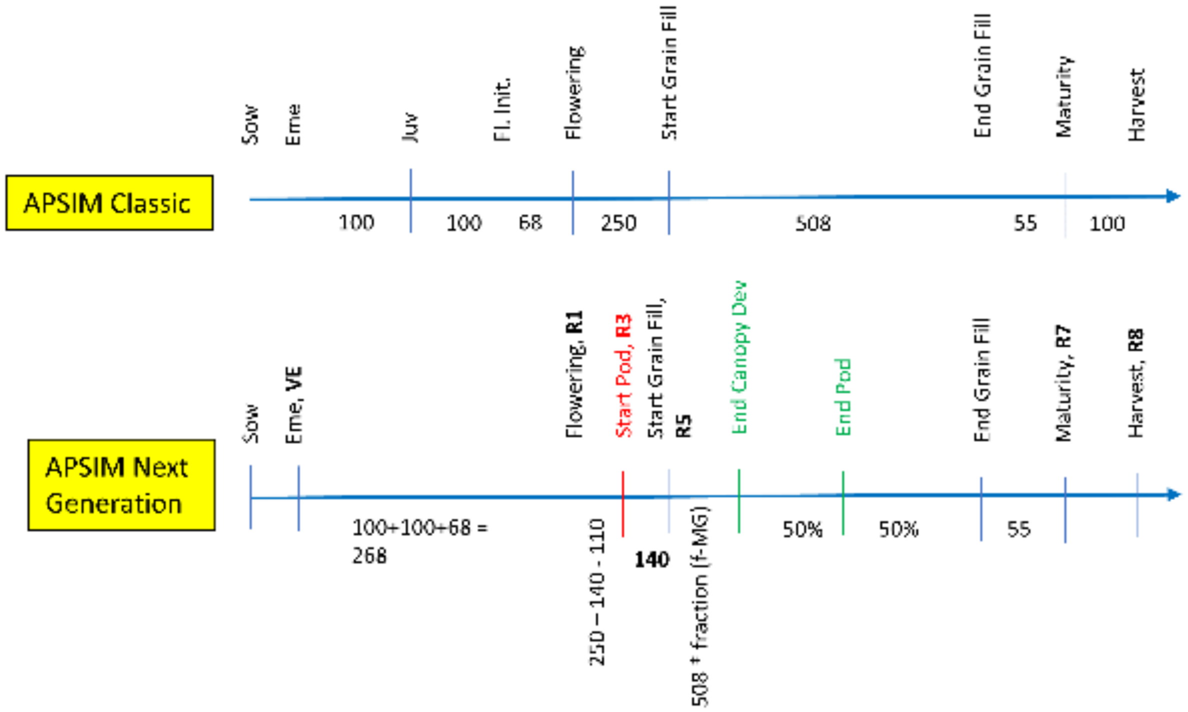


Figure 2: Alt Text

Figure [FigureNumber]: Comparison of soybean phenological stages for APSIM Classic and APSIM Next Generation.

The key differences for cultivars are mostly phenological parameters (e.g., Vegetative.Target, ReproductivePhotoperiodModifier). In some cases, some additional parameters have been changed, see parameter values in the cultivar section.

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 Sowing and Emergence calculated as:

Base = [Phenology].VegetativeThermalTime

VegetativeGrowth has a value between Emergence and EndCanopyDevelopment calculated as:

TT = [Phenology].VegetativeThermalTime x [Phenology].VegetativePhotoperiodModifier

ReproductiveGrowth has a value between EndCanopyDevelopment and HarvestRipe calculated as:

TT = [Phenology].ReproductiveThermalTime x [Phenology].ReproductivePhotoperiodModifier

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	StartFlowering

Phase Number	Phase Name	Initial Stage	Final Stage
4	EarlyFlowering	StartFlowering	StartPodDevelopment
5	EarlyPodDevelopment	StartPodDevelopment	StartGrainFilling
6	EarlyGrainFilling	StartGrainFilling	EndCanopyDevelopment
7	MidGrainFilling	EndCanopyDevelopment	EndPodDevelopment
8	LateGrainFilling	EndPodDevelopment	EndGrainFill
9	Maturing	EndGrainFill	Maturity
10	Ripening	Maturity	HarvestRipe
11	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* x *ShootRate* + *ShootLag*

Where:

ShootRate = 1 (deg day/mm),

ShootLag = 10 (deg day),

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

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

ThermalTime = [Phenology].VegetativeThermalTime

1.2.4 Vegetative

This phase goes from emergence to startflowering.

The *Target* for completion is calculated as:

Target = 200 (oD)

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

Progression = [Phenology].ThermalTime

1.2.5 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 = 200 (oD)

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

Progression = [Phenology].ThermalTime

1.2.6 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:

Target = 140 (oD)

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

Progression = [Phenology].ThermalTime

1.2.7 EarlyGrainFilling

This phase goes from startgrainfilling to endcanopydevelopment.

The *Target* for completion is calculated as:

Target = *FractionofGrainfilling* x [Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue

FractionofGrainfilling = 0.05

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

Progression = [Phenology].ThermalTime

1.2.8 MidGrainFilling

This phase goes from endcanopydevelopment to endpoddevelopment.

The *Target* for completion is calculated as:

Target = *FractionofMidToLateGrainfilling* x *MidToLateGrainfilling*

FractionofMidToLateGrainfilling = 0.5

MidToLateGrainfilling = [Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue - [Phenology].EarlyGrainFilling.Target

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

Progression = [Phenology].ThermalTime

1.2.9 LateGrainFilling

This phase goes from endpoddevelopment to endgrainfill.

The *Target* for completion is calculated as:

Target = *EntireGrainfillPeriod* - [Phenology].EarlyGrainFilling.Target - [Phenology].MidGrainFilling.Target

EntireGrainfillPeriod = 500

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

Progression = [Phenology].ThermalTime

1.2.10 Maturing

This phase goes from endgrainfill to maturity.

The *Target* for completion is calculated as:

Target = 45 (oD)

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

Progression = [Phenology].ThermalTime

1.2.11 Ripening

This phase goes from maturity to harvestripe.

The *Target* for completion is calculated as:

Target = 45 (oD)

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

Progression = [Phenology].ThermalTime

1.2.12 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

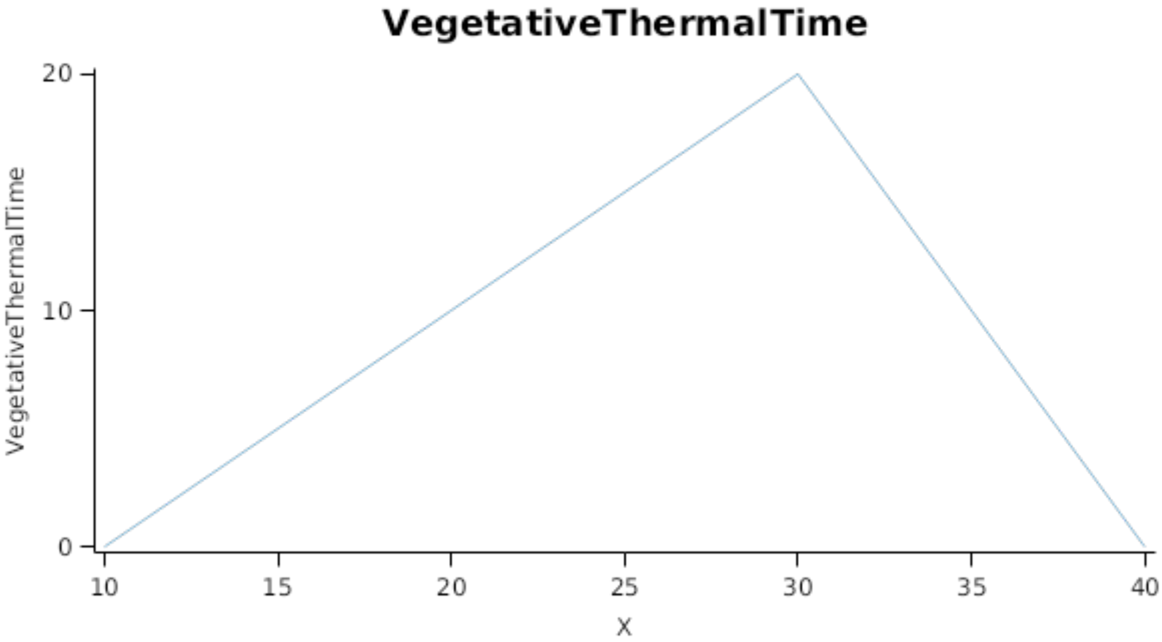
1.2.13 VegetativeThermalTime

VegetativeThermalTime 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 VegetativeThermalTime

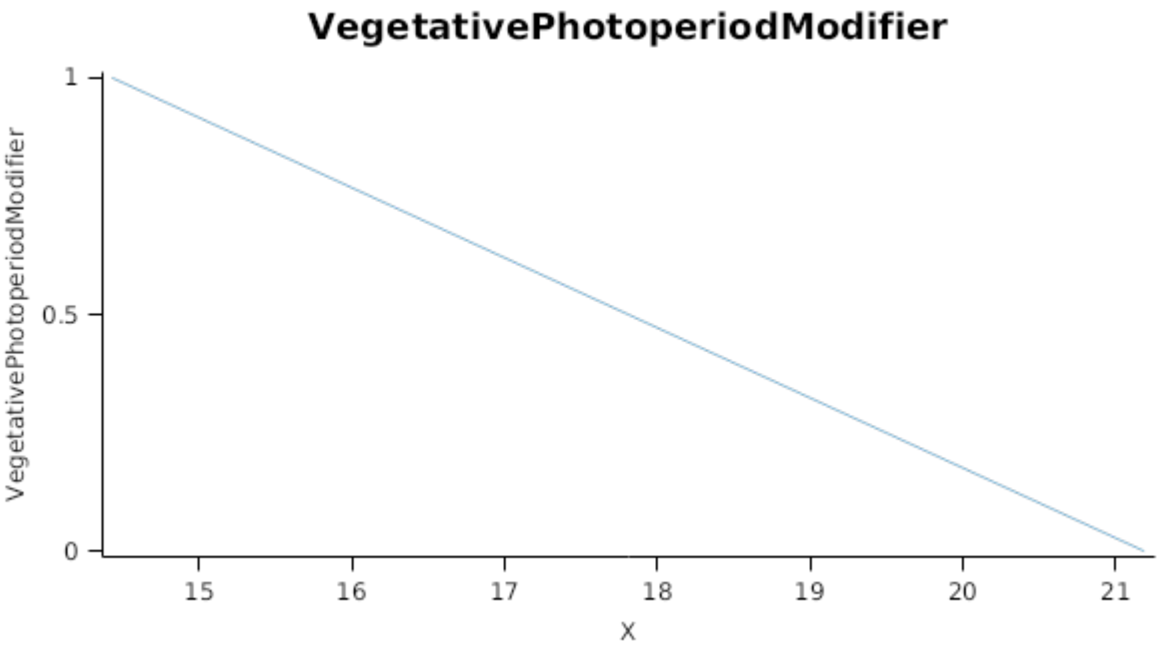
X	VegetativeThermalTime
10.0	0.0
20.0	10.0
30.0	20.0
40.0	0.0



1.2.14 VegetativePhotoperiodModifier

VegetativePhotoperiodModifier is calculated using linear interpolation

X	VegetativePhotoperiodModifier
14.4	1.0
21.2	0.0



1.2.15 ReproductiveThermalTime

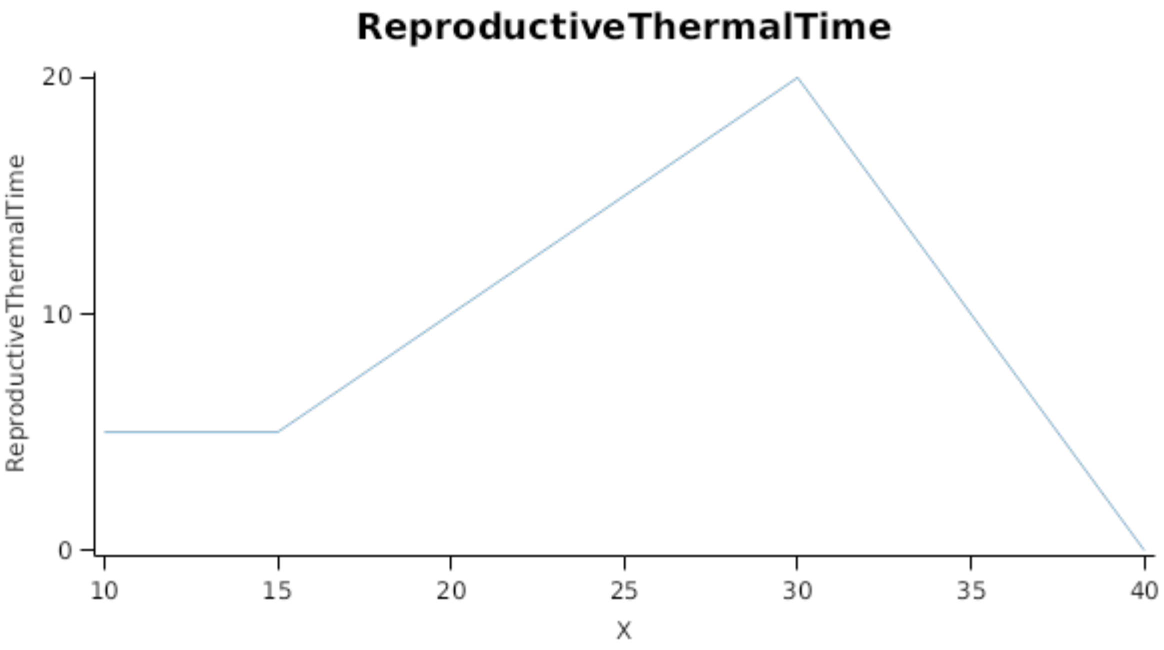
ReproductiveThermalTime is the average of sub-daily values from a XYPairs.

Cardinal temperatures for vegetative and reproductive thermal time are the same except the range of 0-15 C. A base temperature of 10 C is used for vegetative phase, which temperature has been used to calibrate 56 soybean cultivars in the USA (Archontoulis et al., 2014) and 72 soybean cultivars in China (Wu et al., 2019). The small changes in cardinal temperatures for reproductive thermal time was important for solving issues related to photoperiod response for some Australian cultivars. Such a differentiation in base temperature between V and R stages is supported by Boote et al., 1998, DSSAT-CROPGRO soybean model, who showed that cardinal temperatures may differ for vegetative and reproductive development for soybean. This is something to further explore as new data from other environments are added to the APSIM NG database.

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 ReproductiveThermalTime

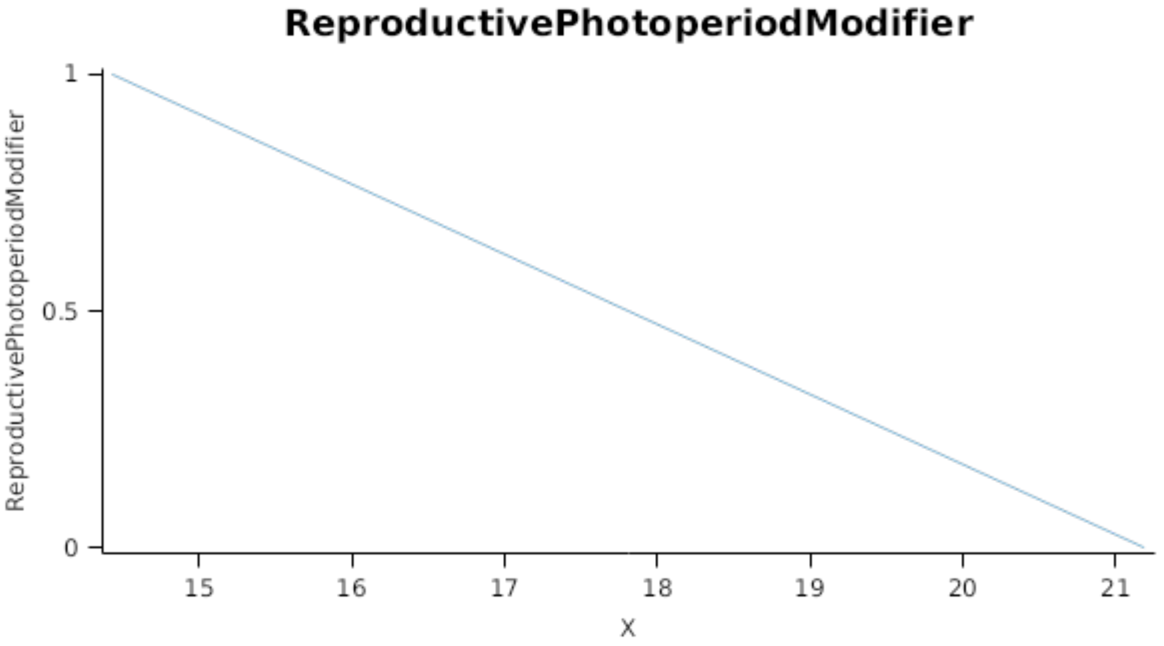
X	**ReproductiveThermalTime**
10.0	5.0
15.0	5.0
30.0	20.0
40.0	0.0



1.2.16 ReproductivePhotoperiodModifier

ReproductivePhotoperiodModifier is calculated using linear interpolation

X	ReproductivePhotoperiodModifier
14.4	1.0
21.2	0.0



1.2.17 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 = 0 (degrees)

1.2.18 EmergenceDAS

Before Emergence

PreEventValue = 0

On Emergence the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.19 FloweringDAS

Before StartFlowering

PreEventValue = 0

On StartFlowering the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.2.20 MaturityDAS

Before Maturity

PreEventValue = 0

On Maturity the value is set to:

PostEventValue = [Plant].DaysAfterSowing

1.3 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.

1.3.1 Initial Dry Matter

InitialWt = 1

1.3.2 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.

1.3.2.1 DMDemands

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

Growth in leaf area is used to calculate the leaf dry matter demand. The same was assumed in the original crop models in APSIM. Further model development can be taken once new experimental data for metabolic, structural and storage forms are provided.

DeltaLAI describes the LAI variation over the cycle and is calculated using the Area of Largest Leaf, relative leaf area, plant number, branch number and leaf appearance rate (thermal time/phyllochron).

Structural = [Leaf].DeltaLAI / [Leaf].SpecificArea

Storage = 0

Metabolic = 0

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.3.3 Nitrogen Demand

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

1.3.3.1 NDemands

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

Structural = [Leaf].minimumNconc x [Leaf].potentialDMAllocation.Structural

Metabolic = *MetabolicNconc* x [Leaf].potentialDMAllocation.Structural

MetabolicNconc = [Leaf].criticalNConc - [Leaf].minimumNconc

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

Storage = [Leaf].maximumNconc × ([Leaf].Live.Wt + potentialAllocationWt) - [Leaf].Live.N

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

NitrogenDemandSwitch = 1

MaxNconc = [Leaf].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.3.4 Nitrogen Concentration Thresholds

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

1.3.4.1 NDemands

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

Structural = [Leaf].minimumNconc x [Leaf].potentialDMAllocation.Structural

Metabolic = *MetabolicNconc* x [Leaf].potentialDMAllocation.Structural

MetabolicNconc = [Leaf].criticalNConc - [Leaf].minimumNconc

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

Storage = [Leaf].maximumNconc × ([Leaf].Live.Wt + potentialAllocationWt) - [Leaf].Live.N

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

NitrogenDemandSwitch = 1

MaxNconc = [Leaf].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.3.5 Dry Matter Supply

DMReallocationFactor = 0

DMRetranslocationFactor = 0

1.3.6 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 CO_2 concentration (FCO2).
NOTE: RUE in this model is expressed as g/MJ for a whole plant basis, including both above and below ground growth.

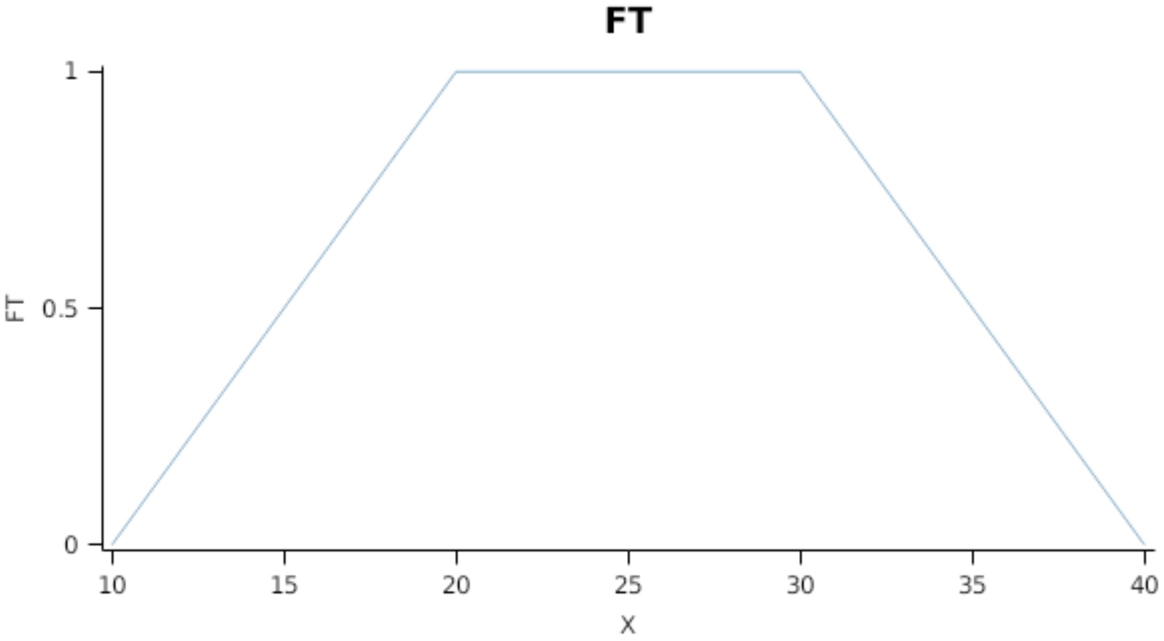
This value has been fitted to available data. In contrast to Classic, the RUE value in NG refers to the whole plant (above and below ground) and the calibrated value is 1.2 g/MJ. There are no literature references for whole plant RUE in soybean. To come up with this value we considered: RUE for above ground biomass (Sinclair et al., 1989; Van Roekel et al., 2014), biomass and root data from Iowa FACTS experiments and model fitting to available data.

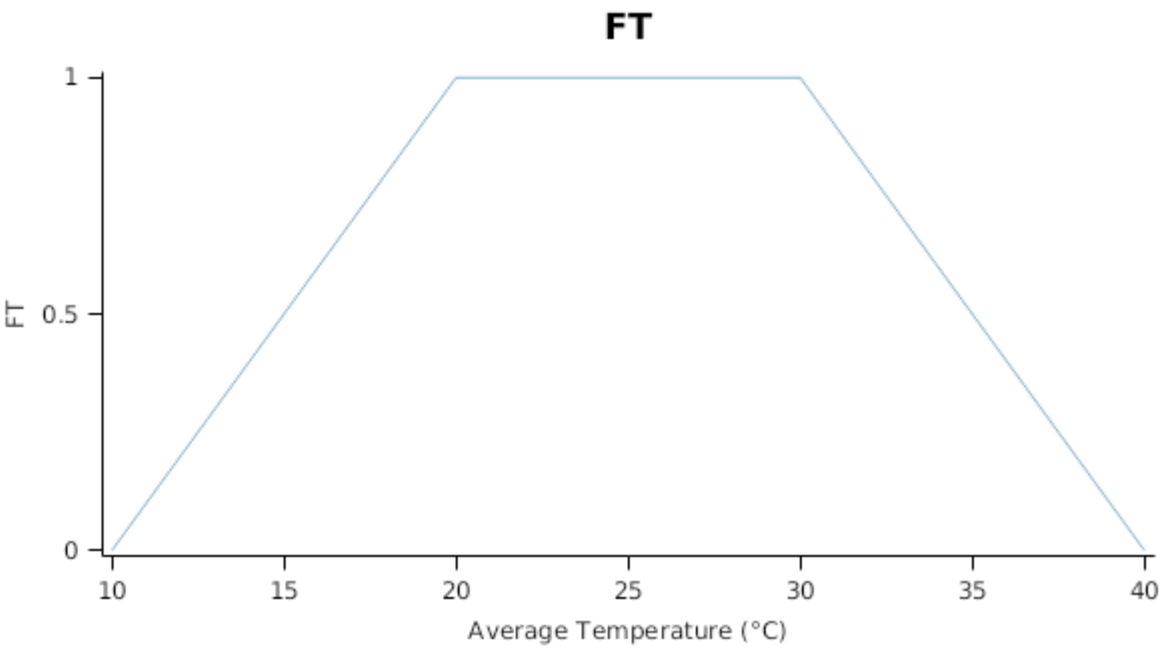
RUE = 1.2

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 = 0.5

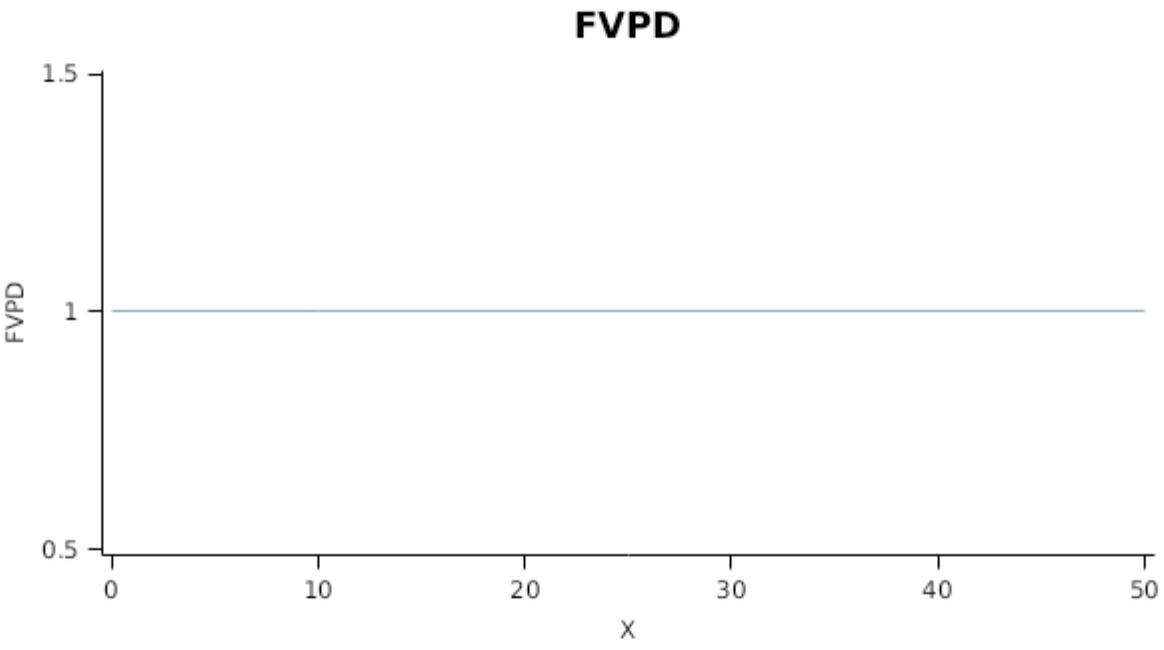
X	FT
10.0	0.0
20.0	1.0
30.0	1.0
40.0	0.0





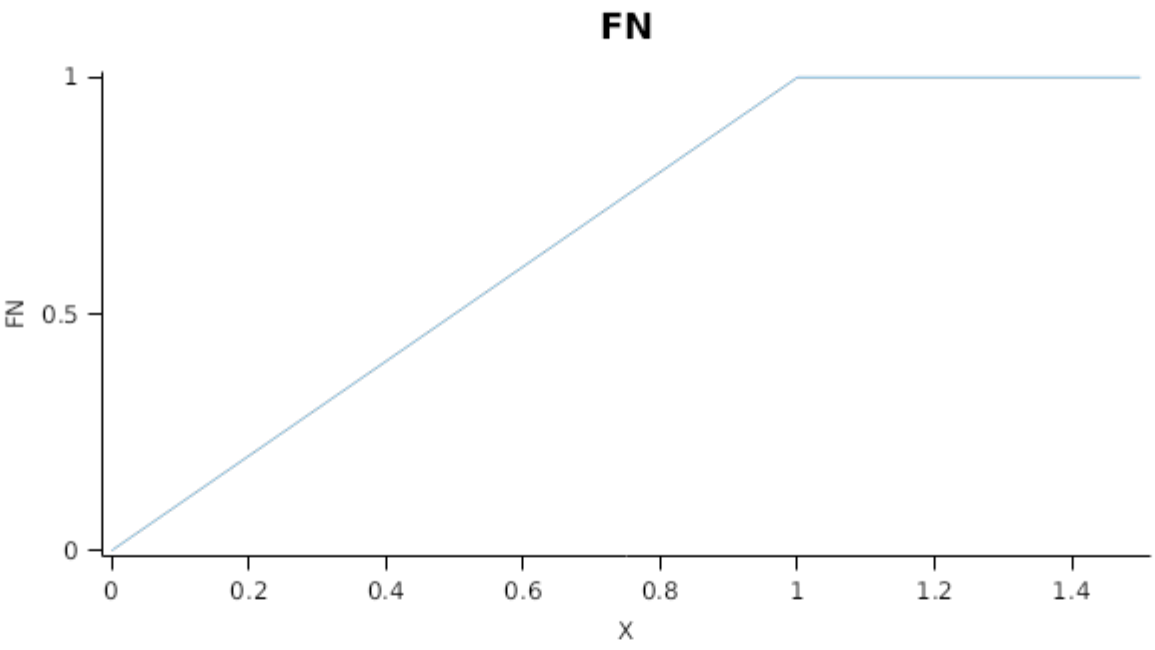
FVPD is calculated using linear interpolation

X	FVPD
0.0	1.0
10.0	1.0
50.0	1.0



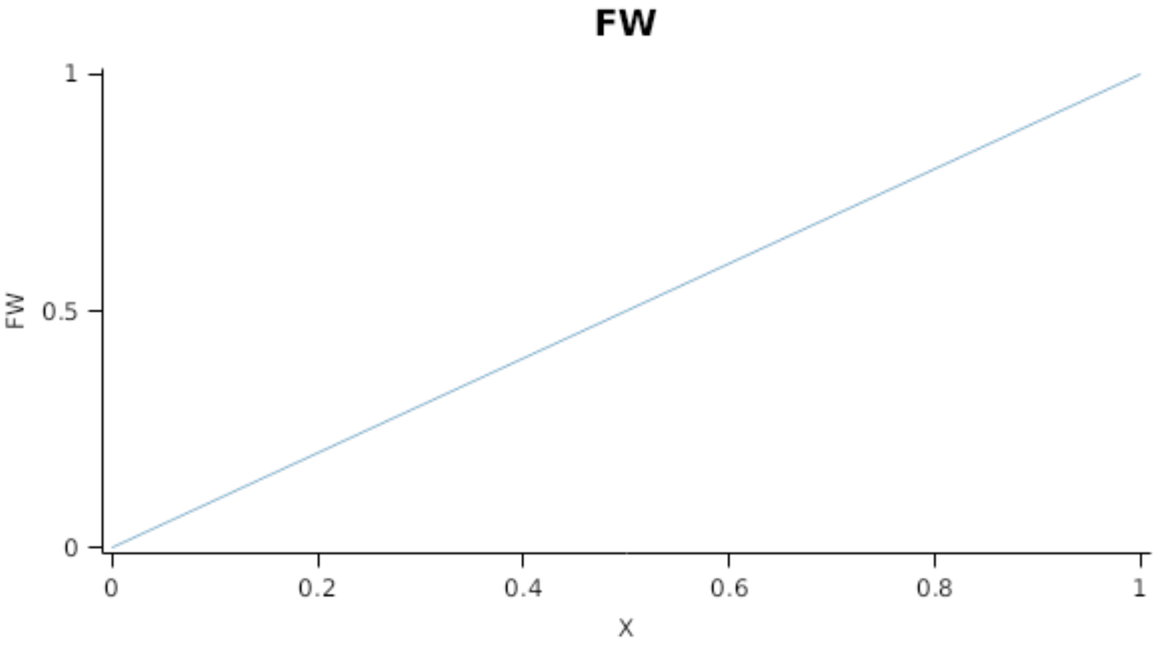
FN is calculated using linear interpolation

X	FN
0.0	0.0
1.0	1.0
1.5	1.0



FW is calculated using linear interpolation

X	FW
0.0	0.0
1.0	1.0



This model calculates the CO_2 impact on RUE using the approach of Reyenga et al., 1999.

For C3 plants,

$F_{CO2} = (CO_2 - CP) \times (350 + 2 \times CP)/(CO_2 + 2 \times CP) \times (350 - CP)$

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

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

For C4 plants,

$F_{CO2} = 0.000143 * CO_2 + 0.95$

RadnInt = [Leaf].RadiationIntercepted

1.3.7 Nitrogen Supply

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

NReallocationFactor = 1

NRetranslocationFactor = 0.5

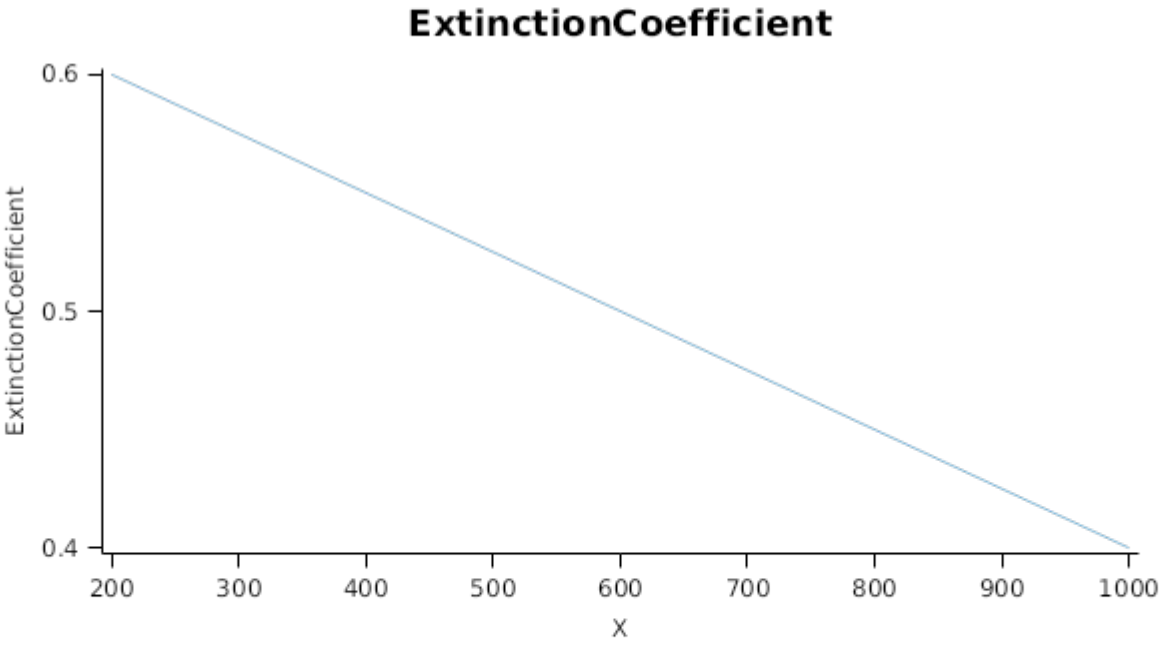
1.3.8 Canopy Properties

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

Area = [Leaf].SpecificArea x [Leaf].Live.Wt

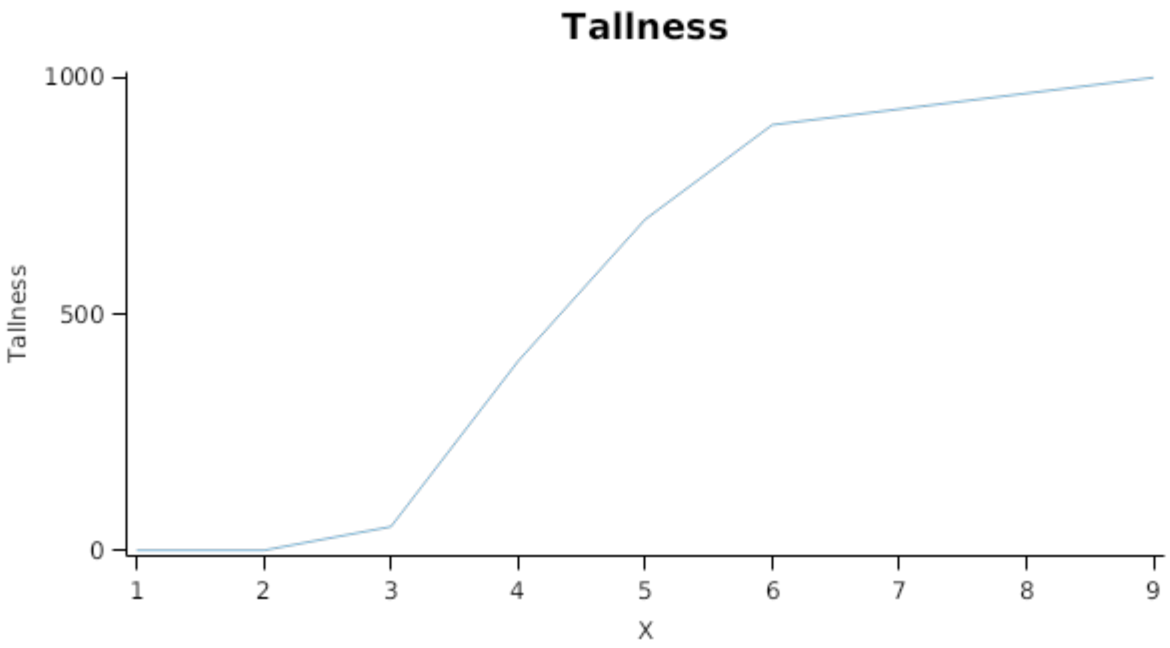
ExtinctionCoefficient is calculated using linear interpolation

X	ExtinctionCoefficient
200.0	0.6
1000.0	0.4



Tallness is calculated using linear interpolation

X	Tallness
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



1.3.9 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 = Gsmax350 x FRGR x stomatalConductanceCO2Modifier

This model calculates the CO_2 impact on stomatal conductance using the approach of Elli et al., 2020.

StomatalConductanceCO2Modifier = PhotosynthesisCO2Modifier x (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

1.3.10 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 EndCanopyDevelopment calculated as:

Rate = 0

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

There is no data on detachment rates and so a simple value was chosen to ensure that leaves were not retained in the canopy. In the future, with more data available a thermal time basis leaf detachment rate will be explored.

Reproductive has a value between EndCanopyDevelopment and Maturity calculated as:

Rate = [Phenology].ThermalTime / *TTRemaining*

TTRemaining = TTRequired - TTComplete

TTRequired = [Phenology].MidGrainFilling.Target + [Phenology].LateGrainFilling.Target + [Phenology].Maturing.Target

TTComplete = [Phenology].MidGrainFilling.ProgressThroughPhase + [Phenology].LateGrainFilling.ProgressThroughPhase + [Phenology].Maturing.ProgressThroughPhase

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

There is no data on detachment rates and so a simple value was chosen to ensure that leaves were not retained in the canopy. In the future, with more data available a thermal time basis leaf detachment rate will be explored.

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

1.3.11 Biomass removal

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

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	100	100
Cut	0	0	100	100

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

MinimumNConc = 0.05

MaximumNConc = 0.058

WaterContent = 0.12

DMConversionEfficiency = 0.89

RemobilisationCost = 0

CarbonConcentration = 0.4

This parameter is not used. Grain growth is calculated from harvest index increase.

MaximumPotentialGrainSize = 0

Grain number is not estimated by this model.

NumberFunction = 0

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 StartGrainFilling and EndGrainFill calculated as:

HIGrainDemand = [AboveGround].Wt x *HarvestIndexIncrease* x [Phenology].ThermalTime

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

1.4.4 NFillingRate

NFillingRate = [Grain].MaximumNConc x [Grain].DMDemandFunction x [Grain].DMConversionEfficiency

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	100	0	0
Cut	0	0	100	100

1.4.6 HarvestIndex

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

1.4.7 DMDemandPriorityFactors

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

Structural = 1

Metabolic = 1

Storage = 1

1.4.8 NDemandPriorityFactors

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

Structural = 1

Metabolic = 1

Storage = 1

1.5 Root

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

1.5.1 Growth

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

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

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

$DMAllocated_i = TotalDMAllocated \times RAw_i / TotalRAw$

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 then 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. *NO3 uptake = $NO3_i$ x kNO3 x $NO3_{ppm, i}$ x NUptakeSWFactor* _NH4 uptake = $NH4_i$ x kNH4 x $NH4_{ppm, i}$ x 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 demandeach 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 uptake = $(SW_i - LL_i)$ x KL_i x KLModifier*

1.5.6 Constants

No effect of soil water or temperature is considered for daily increases in rooting depth.

RootDepthStressFactor = 1

There is no intrinsic limit to maximum rooting depth. Roots will be limited by the depth of the soil profile, or via values of XF in each layer.

MaximumRootDepth = 1000000

No modification to water extraction rate is assumed in this model.

KLModifier = 1 (0-1)

Roots are assumed to simply senesce at a small and constant rate during the entire growth period.

SenescenceRate = 0.005 (/d)

MaximumNConc = 0.01

MinimumNConc = 0.005

KNO3 = 0.02

The current model version considers only NO3 uptake but NH4 option can be activated by the user . We do not expect activation of NH4 to change total plant N uptake because the nitrification rate (conversion of NH4 to NO3) is very fast in the model. In the future we will re-valuate this.

KNH4 = 0

SpecificRootLength = 40 (m/g)

DMConversionEfficiency = 1

MaintenanceRespirationFunction = 1

RemobilisationCost = 0

CarbonConcentration = 0.4

1.5.7 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 = 30

late has a value between StartGrainFilling and Maturity calculated as:

Function = 5

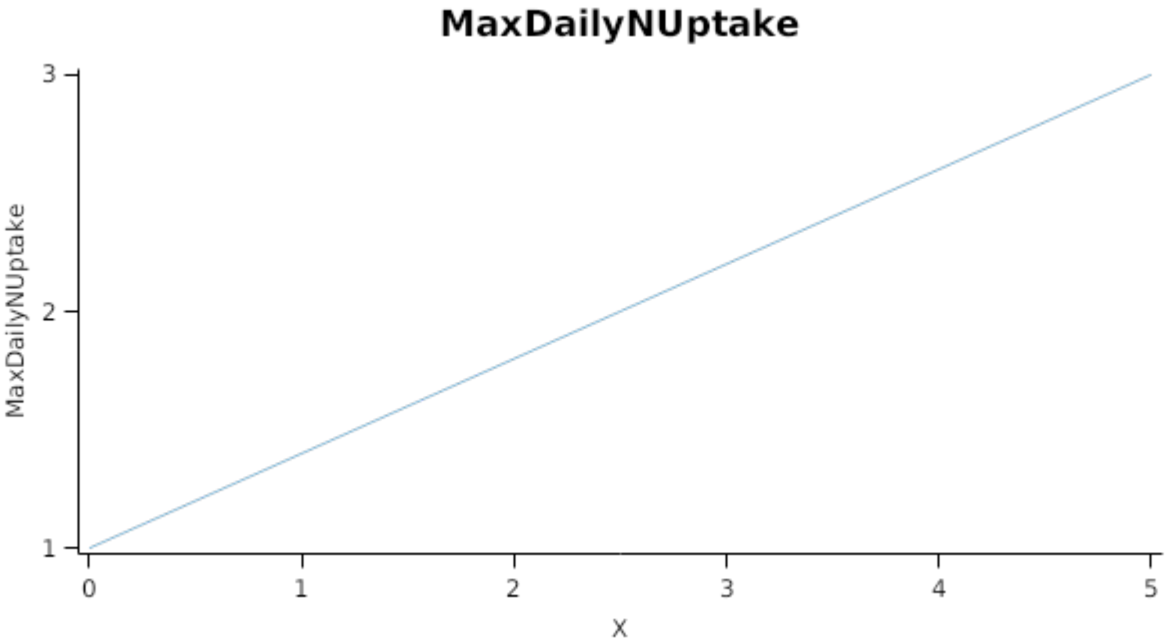
1.5.8 RootShape

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

1.5.9 MaxDailyNUptake

MaxDailyNUptake is calculated using linear interpolation

X	MaxDailyNUptake
0.0	1.0
5.0	3.0



1.5.10 NitrogenDemandSwitch

NitrogenDemandSwitch has a value between Emergence and EndGrainFill calculated as:

Constant = 1

1.5.11 BiomassRemovalDefaults

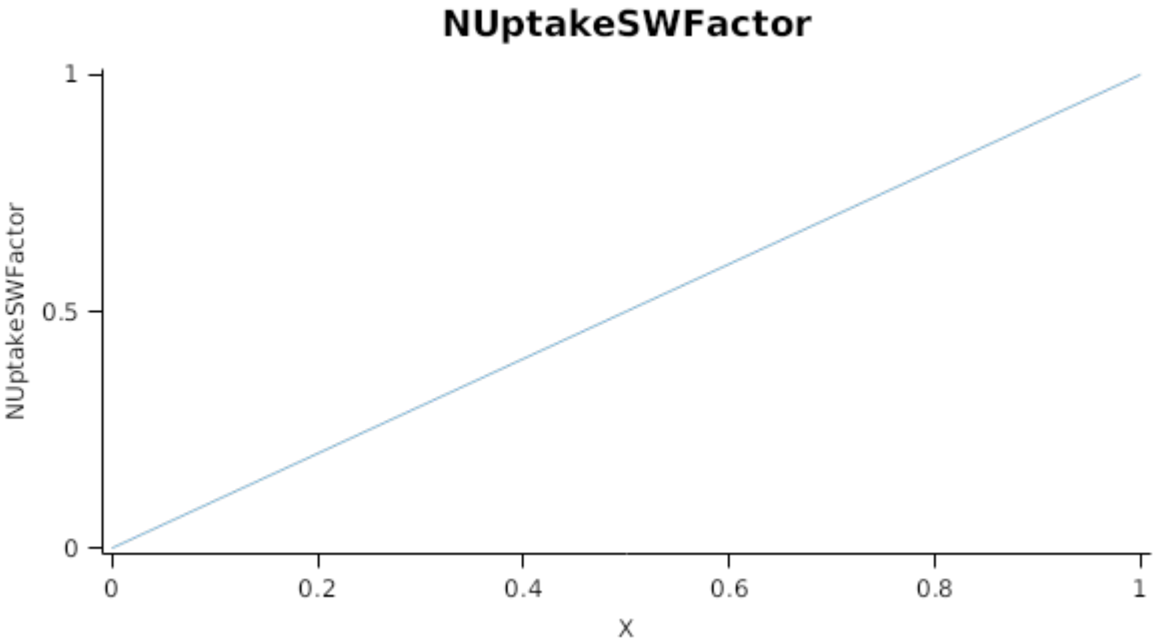
This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "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	20	0
Cut	0	0	20	0

1.5.12 NUptakeSWFactor

NUptakeSWFactor is calculated using linear interpolation

X	NUptakeSWFactor
0.0	0.0
1.0	1.0



1.5.13 DMDemands

1.5.13.1 DMDemands

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

Structural = *DMDemandFunction* x *StructuralFraction*

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

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

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

Early has a value between Emergence and StartFlowering calculated as:

Function = 0.2

Middle has a value between StartFlowering and StartGrainFilling calculated as:

Function = 0.2

Late has a value between StartGrainFilling and Maturity calculated as:

Function = 0.05

StructuralFraction = 1

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.5.14 NDemands

1.5.14.1 NDemands

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

Structural = [Root].minimumNconc x [Root].potentialDMAllocation.Structural

Metabolic = *MetabolicNconc* x [Root].potentialDMAllocation.Structural

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

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

Storage = [Root].maximumNconc × ([Root].Live.Wt + potentialAllocationWt) - [Root].Live.N

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

NitrogenDemandSwitch = [Root].nitrogenDemandSwitch

MaxNconc = [Root].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.5.15 CriticalNConc

CriticalNConc = [Root].MinimumNConc

1.5.16 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 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.

1.6.1 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 x *StructuralFraction*

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

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

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

Early has a value between Emergence and StartFlowering calculated as:

Function = 0.03

Middle has a value between StartFlowering and StartGrainFilling calculated as:

Function = 0.02

Late has a value between StartGrainFilling 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

1.6.2 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 x [Nodule].potentialDMAllocation.Structural

Metabolic = *MetabolicNconc* x [Nodule].potentialDMAllocation.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 × ([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

1.6.3 Dry Matter Supply

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

Nodule does not retranslocate non-structural DM.

1.6.4 Nitrogen Supply

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

Nodule does not retranslocate non-structural N.

FixationRate = *DailyPotentialFixationRate* until StartGrainFilling after which the value is fixed.

DailyPotentialFixationRate = Min(*PotentialFixationRate*, *MaximumFixationRate*)

Where:

PotentialFixationRate = [AboveGroundLive].Wt x *SpecificFixationRate*

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

VegetativeGrowth has a value between Emergence and StartFlowering calculated as:

Rate = 0.006

ReproductiveGrowth has a value between StartFlowering and EndGrainFill calculated as:

Rate = 0.002

MaximumFixationRate = 0.6 (g/g)

1.6.5 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	20	0
Cut	0	0	20	0

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.

Shell harvest index is used to calculate shell biomass demand, which follows the same approach than grain harvest index. It represents the fraction of shell biomass in relation to total aboveground biomass.

Structural = *DMDemandFunction* x *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 StartPodDevelopment and EndPodDevelopment calculated as:

HIPodDemand = [AboveGround].Wt x *HarvestIndexIncrease* x [Phenology].ThermalTime

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

StructuralFraction = 1

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

1.7.3 Nitrogen Demand

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

1.7.3.1 NDemands

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

Structural = [Shell].minimumNconc x [Shell].potentialDMAllocation.Structural

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

Storage = [Shell].maximumNconc × ([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

Metabolic = 0

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

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 StartPodDevelopment and Maturity calculated as:

Rate = Min(*Fraction*, *One*)

Where:

Fraction = [Phenology].ThermalTime / *TTRemaining*

TTRemaining = ReproductiveTT - ReproductiveTT1Complete

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

ReproductiveTT1Complete = [Phenology].EarlyPodDevelopment.ProgressThroughPhase+[Phenology].EarlyGrainFilling.ProgressThroughPhase+[Phenology].MidGrainFilling.ProgressThroughPhase+[Phenology].LateGrainFilling.ProgressThroughPhase

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	0	0	100	100
Cut	0	0	100	100

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* x [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.

StemGrowthPhase has a value between Emergence and StartPodDevelopment calculated as:

Fraction = 0.75

PodAndGrainGrowth has a value between StartPodDevelopment and EndGrainFill calculated as:

Fraction = 0

Metabolic = 0

Storage = [Stem].PotentialGrowth x *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 x [Stem].potentialDMAllocation.Structural

Metabolic = *MetabolicNconc* x [Stem].potentialDMAllocation.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 × ([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

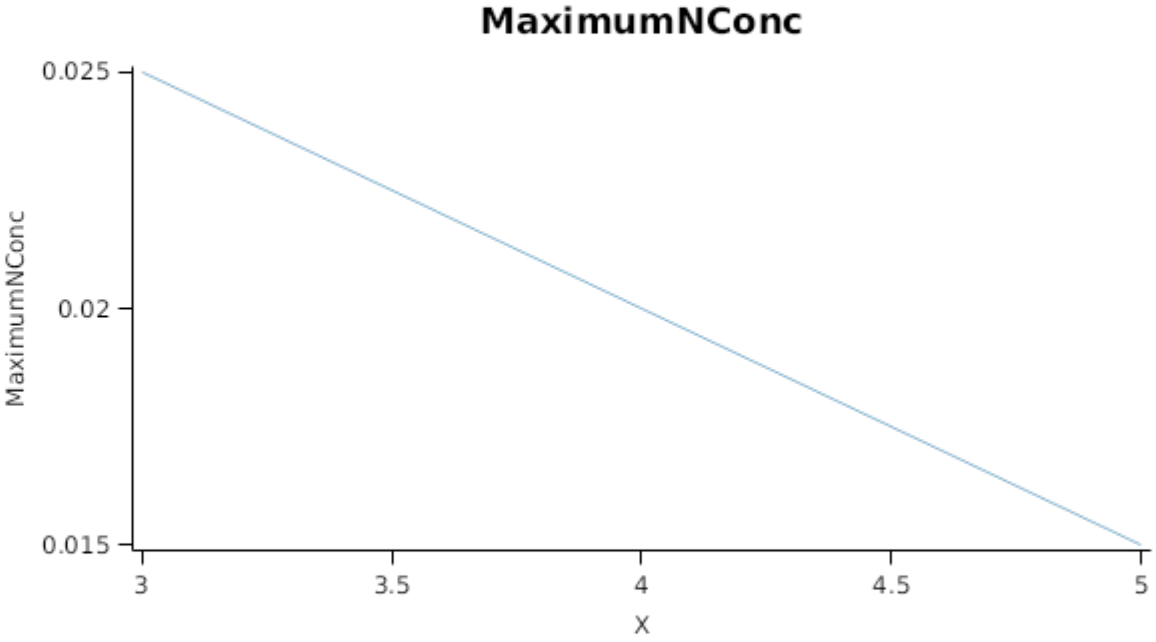
1.8.4 N Concentration Thresholds

MinimumNConc = 0.006

CriticalNConc = [Stem].MinimumNConc

MaximumNConc is calculated using linear interpolation

X	MaximumNConc
3.0	0.0
4.0	0.0
5.0	0.0



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

There is no evidence of stem N storage during grain filling. Also, there is no stem structural growth during this time.

NitrogenDemandSwitch has a value between Emergence and StartGrainFilling calculated as:

There is no evidence of stem N storage during grain filling. Also, there is no stem structural growth during this time.

Constant = 1

1.8.5 Dry Matter Supply

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

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

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

GrainFilling has a value between EndCanopyDevelopment and EndGrainFill calculated as:

RetranslocationFactor = 0.2

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 EndCanopyDevelopment and Maturity calculated as:

Rate = Min(*Fraction*, *One*)

Where:

Fraction = [Phenology].ThermalTime / *TTRemaining*

TTRemaining = *PostCanopyTT* - *PostCanopyTTComplete*

PostCanopyTT = [Phenology].EarlyPodDevelopment.Target+[Phenology].EarlyGrainFilling.Target+[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	0	0	100	100
Cut	0	0	100	100

1.9 AboveGround

1.9.1 AboveGround

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

AboveGround summarises the following biomass objects:

* Leaf
* Stem
* Grain
* Shell

1.10 BelowGround

1.10.1 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

1.11 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 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 Australia

1.17.1.1 Buchanan

Buchanan overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 480

[Phenology].EarlyFlowering.Target.FixedValue = 100

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.015

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 467

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.39, 15.61

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.39, 15.61

[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.33

[Grain].MaximumNConc.FixedValue = 0.067

[Stem].PotentialGrowth.PartitionFraction.StemGrowthPhase.StemFraction.FixedValue = 0.5

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.2 Djakal

Djakal overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 380

[Phenology].EarlyFlowering.Target.FixedValue = 100

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 405

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 17

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 11.9, 15.5

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.3 Davis

Davis overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 480

[Phenology].EarlyFlowering.Target.FixedValue = 100

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.015

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 467

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.39, 15.61

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.39, 15.61

[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.33

[Grain].MaximumNConc.FixedValue = 0.067

[Stem].PotentialGrowth.PartitionFraction.StemGrowthPhase.StemFraction.FixedValue = 0.5

[Leaf].AreaLargestLeaf.FixedValue=0.012

1.17.1.4 Hooper_MG40

Hooper_MG40 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 380

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 440

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.26, 16.67

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.26, 16.67

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.5 Stephens_MG40

Stephens_MG40 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 360

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 440

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.26, 16.67

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.26, 16.67

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.6 FiskebyV

FiskebyV overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 285

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 405

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 18

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.75, 18

1.17.1.7 F148_7

F148_7 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 314

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 485

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 17

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12, 18

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.8 Bowyer

Bowyer overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 377

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 405

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 15.5

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 11.9, 15.5

1.17.1.9 Bunya

Bunya overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 550

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 405

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 18

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 10.9, 15.5

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.10 Cowrie

Cowrie overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 390

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 16

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 16

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.11 Soya791

Soya791 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 430

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 15.3

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 15.3

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.12 Manark

Manark overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 440

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 15

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 15

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.13 Warrigal

Warrigal overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 490

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 15

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 15

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.14 Leichhardt

Leichhardt overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 806

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 14.7

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 14.7

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.1.15 Djakal1

Djakal1 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 332

[Phenology].EarlyFlowering.Target.FixedValue = 80

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 440

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.26, 16.67

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.26, 16.67

[Leaf].AreaLargestLeaf.FixedValue=0.009

1.17.2 USA

1.17.2.1 Trial_MG00

Trial_MG00 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 268

[Phenology].EarlyFlowering.Target.FixedValue = 76

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 432

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.43, 21.19

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.43, 21.19

1.17.2.2 Lambert_MG0

Lambert_MG0 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 294

[Phenology].EarlyFlowering.Target.FixedValue = 81

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 442

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.29, 20.14

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.29, 20.14

1.17.2.3 IA1006_MG10

IA1006_MG10 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 336

[Phenology].EarlyFlowering.Target.FixedValue = 118

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 518

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.37, 19.30

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.37, 19.30

1.17.2.4 IA2008_MG20

IA2008_MG20 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 329

[Phenology].EarlyFlowering.Target.FixedValue = 150

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 580

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.92, 17.93

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.92, 17.93

1.17.2.5 PioneerP22T61_MG22

PioneerP22T61_MG22 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 328

[Phenology].EarlyFlowering.Target.FixedValue = 106

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.3

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 499

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.6

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.6

1.17.2.6 PioneerP22T69R_MG22

PioneerP22T69R_MG22 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 328

[Phenology].EarlyFlowering.Target.FixedValue = 106

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.35

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 580

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.6

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.6

1.17.2.7 Pioneer92MGI_MG26

Pioneer92MGI_MG26 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 271

[Phenology].EarlyFlowering.Target.FixedValue = 120

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.125

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 529

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.77, 17.57

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.77, 17.57

1.17.2.8 PioneerP92Y75_MG27

PioneerP92Y75_MG27 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 328

[Phenology].EarlyFlowering.Target.FixedValue = 106

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.14

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 499

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.6

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.6

1.17.2.9 Macon_MG30

Macon_MG30 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 367

[Phenology].EarlyFlowering.Target.FixedValue = 163

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.175

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 607

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.05, 17.56

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.05, 17.56

1.17.2.10 PioneerP93M11_MG31

PioneerP93M11_MG31 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 250

[Phenology].EarlyFlowering.Target.FixedValue = 110

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 457

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.4, 16.0

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.4, 16.0

[Grain].MaximumNConc.FixedValue = 0.065

[Shell].PotentialHarvestIndex.FixedValue = 0.5

[Leaf].AreaLargestLeaf.FixedValue=0.013

1.17.2.11 Becks321NRR_MG32

Becks321NRR_MG32 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 272

[Phenology].EarlyFlowering.Target.FixedValue = 117

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.20

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 522

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.45, 18.0

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.45, 18.0

1.17.2.12 PioneerP932T16R_MG32

PioneerP932T16R_MG32 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 328

[Phenology].EarlyFlowering.Target.FixedValue = 106

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.40

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 499

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.6

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.6

1.17.2.13 Becks367NRR_MG37

Becks367NRR_MG37 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 267

[Phenology].EarlyFlowering.Target.FixedValue = 112

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.26

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 506

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.27, 17.2

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.27, 17.2

1.17.2.14 AsgrowAG4403_MG40

AsgrowAG4403_MG40 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 292

[Phenology].EarlyFlowering.Target.FixedValue = 123

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 535

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.09, 16.49

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.09, 16.49

1.17.2.15 HornbeckHBK4891_MG40

HornbeckHBK4891_MG40 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 292

[Phenology].EarlyFlowering.Target.FixedValue = 123

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 535

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.09, 16.49

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.09, 16.49

1.17.2.16 Pioneer94B01_MG40

Pioneer94B01_MG40 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 322

[Phenology].EarlyFlowering.Target.FixedValue = 143

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 567

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.05, 16.46

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.05, 16.46

1.17.2.17 PioneerP9504_MG50

PioneerP9504_MG50 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 404

[Phenology].EarlyFlowering.Target.FixedValue = 112

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 505

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.83, 16.13

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.83, 16.13

1.17.2.18 AsgrowAG5701_MG50

AsgrowAG5701_MG50 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 404

[Phenology].EarlyFlowering.Target.FixedValue = 131

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 549

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.83, 16.13

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.83, 16.13

1.17.2.19 Hutcheson_MG50

Hutcheson_MG50 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 438

[Phenology].EarlyFlowering.Target.FixedValue = 112

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 505

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.58, 15.88

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.58, 15.88

1.17.2.20 NK622_MG60

NK622_MG60 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 436

[Phenology].EarlyFlowering.Target.FixedValue = 93

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 467

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.39, 15.61

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.39, 15.61

1.17.3 China

1.17.3.1 Nandou12

Nandou12 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 500

[Phenology].EarlyFlowering.Target.FixedValue = 120

[Phenology].EarlyPodDevelopment.Target.FixedValue = 180

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.2

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 440

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.63, 15.13

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.63, 15.13

[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.45

[Leaf].AreaLargestLeaf.FixedValue=0.013

[Grain].PotentialHarvestIndex.FixedValue=0.35

1.17.3.2 Texuan13

Texuan13 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 500

[Phenology].EarlyFlowering.Target.FixedValue = 200

[Phenology].EarlyPodDevelopment.Target.FixedValue = 170

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.2

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 460

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.63, 15.13

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.63, 15.13

[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.45

[Leaf].AreaLargestLeaf.FixedValue=0.013

[Grain].PotentialHarvestIndex.FixedValue=0.35

1.17.3.3 Jiuyuehuang

Jiuyuehuang overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 540

[Phenology].EarlyFlowering.Target.FixedValue = 140

[Phenology].EarlyPodDevelopment.Target.FixedValue = 140

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.2

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 420

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.94, 15.44

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.94, 15.44

[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.45

[Leaf].AreaLargestLeaf.FixedValue=0.013

[Grain].PotentialHarvestIndex.FixedValue=0.25

1.17.3.4 Hedou19

Hedou19 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 370

[Phenology].EarlyFlowering.Target.FixedValue = 120

[Phenology].EarlyPodDevelopment.Target.FixedValue = 180

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.361

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 600

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.57, 16.07

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.57, 16.07

[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.45

[Leaf].AreaLargestLeaf.FixedValue=0.02

[Leaf].Phyllochron.FixedValue=45

1.17.4 Generic

1.17.4.1 Generic_MG000

Generic_MG000 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 310

[Phenology].EarlyFlowering.Target.FixedValue = 100

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.475

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 590

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.6, 22.35

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.6, 22.35

1.17.4.2 Generic_MG00

Generic_MG00 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 320

[Phenology].EarlyFlowering.Target.FixedValue = 100

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.467

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 600

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.35, 21.11

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.35, 21.11

1.17.4.3 Generic_MG0

Generic_MG0 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 336

[Phenology].EarlyFlowering.Target.FixedValue = 120

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.422

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 616

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.1, 19.95

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.1, 19.95

1.17.4.4 Generic_MG1

Generic_MG1 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 340

[Phenology].EarlyFlowering.Target.FixedValue = 120

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.411

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 632

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.84, 18.77

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.84, 18.77

1.17.4.5 Generic_MG2

Generic_MG2 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 348

[Phenology].EarlyFlowering.Target.FixedValue = 120

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.386

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 648

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.61

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.61

1.17.4.6 Generic_MG3

Generic_MG3 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 380

[Phenology].EarlyFlowering.Target.FixedValue = 120

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.361

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 664

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.4, 16.91

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.4, 16.91

1.17.4.7 Generic_MG4

Generic_MG4 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 388

[Phenology].EarlyFlowering.Target.FixedValue = 140

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.324

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 664

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.1, 16.49

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.1, 16.49

1.17.4.8 Generic_MG5

Generic_MG5 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 396

[Phenology].EarlyFlowering.Target.FixedValue = 160

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.072

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 696

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.83, 16.13

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.83, 16.13

1.17.4.9 Generic_MG6

Generic_MG6 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 404

[Phenology].EarlyFlowering.Target.FixedValue = 180

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.056

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 712

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.58, 15.8

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.58, 15.8

1.17.4.10 Generic_MG7

Generic_MG7 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 416

[Phenology].EarlyFlowering.Target.FixedValue = 200

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.055

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 728

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.33, 15.46

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.33, 15.46

1.17.4.11 Generic_MG8

Generic_MG8 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 430

[Phenology].EarlyFlowering.Target.FixedValue = 200

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.054

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 744

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.07, 15.1

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.07, 15.1

1.17.4.12 Generic_MG9

Generic_MG9 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 460

[Phenology].EarlyFlowering.Target.FixedValue = 200

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.053

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 748

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 11.88, 14.82

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 11.88, 14.82

1.17.4.13 Generic_MG10

Generic_MG10 overrides the following properties:

[Phenology].Vegetative.Target.FixedValue = 470

[Phenology].EarlyFlowering.Target.FixedValue = 200

[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.053

[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 748

[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 11.78, 14.65

[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 11.78, 14.65

2 The APSIM Soybean Model

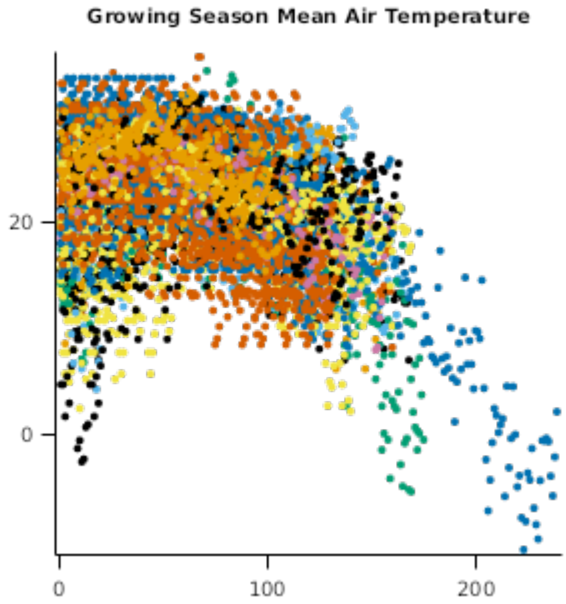
The APSIM Soybean model has been developed using the Plant Modelling Framework (PMF) of (Brown et al., 2014). This new framework provides a library of plant organ and process submodels that can be coupled, at runtime, to construct a model in much the same way that models can be coupled to construct a 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.

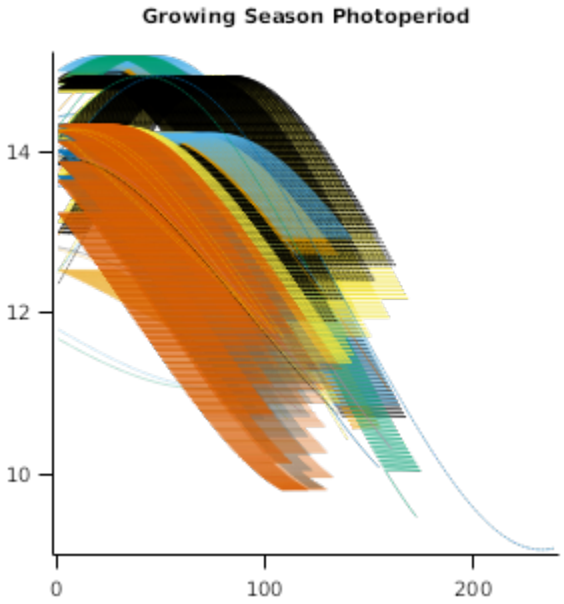
The model consists of:

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

3 Validation

The soybean model has been tested across a range of planting and agronomic conditions. These include datasets from Australia, USA and China covering a wide range of weather conditions (See graphs that follow) and agronomic factors (irrigation, fertiliser, sowing dates).





3.1 USA

3.1.1 FACTS

This trial was conducted on deep fertile soils, in central Iowa (Ames) and in northwest Iowa (Sutherland), USA, in years 2015, 2016 and 2017. In each year two planting date were studied, early versus late. Row spacing was 76 cm, and plant population was around 35 plants/m2 (see details in APSIM managers). No nitrogen or irrigation applied. This region has shallow water tables (about 1.2 m below surface, range 0.3 to 3m) and the soil has no subsurface drainage. Data from years 2015 and 2017 have been incorporated while data from year 2016 will be added later. Local weather data (the station was positioned 10 m from the trial) and actual soil profile data (measured in Nov 2014 up to 1.2 meter, soil organic matter, texture, and pH by layer) were used. Additional soil data were taken from ssurgo. The following measurements were taken per plot (each treatment was replicated 3 times): Phenology (visual observations in the field using the V/R coding system); biomass samplings 6-9 times per season and per treatment (destructive sampling of 1 m2 per plot); biomass partitioning and dry weight of each plant tissue including green and yellow leaves, stem plus petioles, and pod-walls plus seeds (note that seeds were separated at the final harvest only); carbon and nitrogen concentration of each plant tissue (LECO CN analyzer); green leaf area index (LI Area Meter); node number and pod number per plant; leaf area per node in year 2015 only; root front depth over time (manual soil core technique) and maximum root depth, mass and length (mechanical gidding prode technique, depth of 240 cm) at approximately middle grain fill stage; daily soil water and temperature at two depths, 15 and 45 cm (5TM sensors placed horizontally, METEO group), daily water table depth (CTD-10 sensors, METEO group), and soil nitrate and ammonium approximately 10 times over each season and treatment at two depths 0-30 and 30-60 cm (sample was extracted in 2 M potassium chloride), and N-fixation over time (Isotope dilution method); soybean leaf senescence (gages to measure drop leaves dry matter and CN concentration, 1m2 size, 3-4 measurements per season per treatment); crop residue dry matter, soil cover and soil nitrogen and water measurements (manual samplings 10 times from crop harvest to planting of the next crop). This dataset is licensed by the Iowa State University Research Foundation.

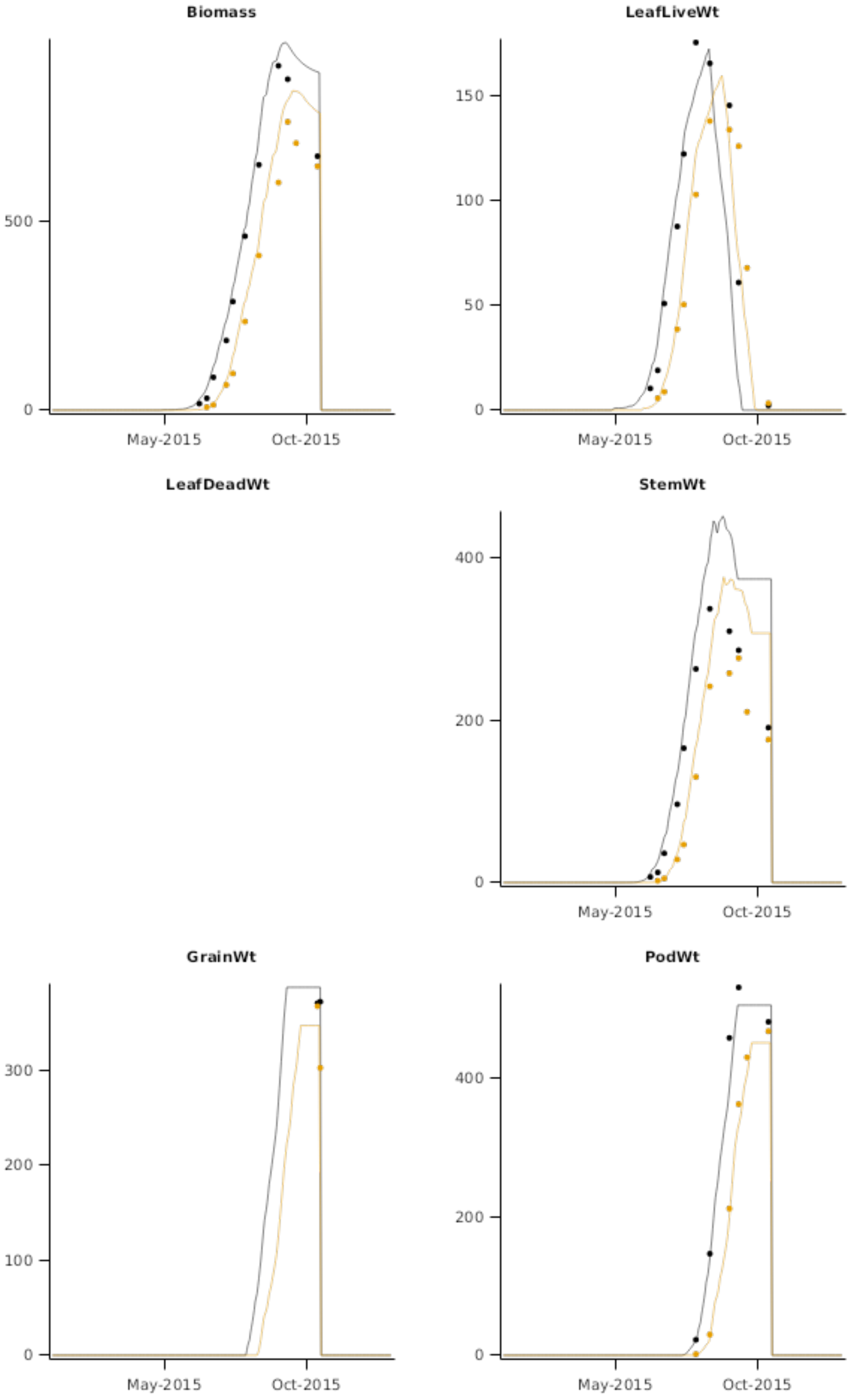
List of experiments.

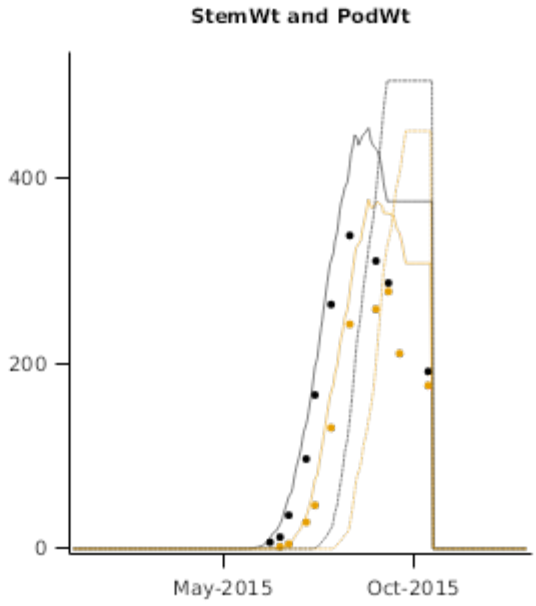
Experiment Name	Design (Number of Treatments)
Ames2015	Sow (2)
Ames2017	Sow (2)
Sutherland2015	Sow (2)
Sutherland2017	Sow (2)

3.1.1.1 Ames2015

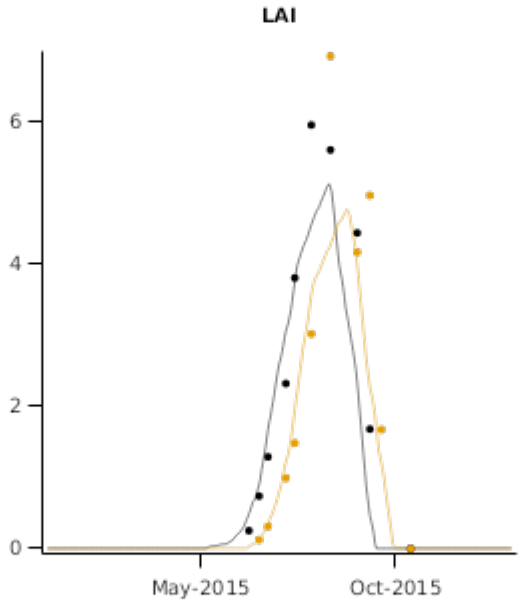
3.1.1.1.1 Graphs

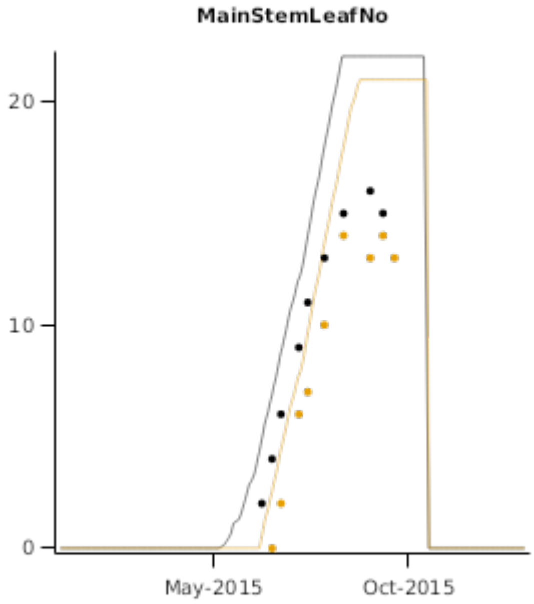
3.1.1.1.1.1 Biomass

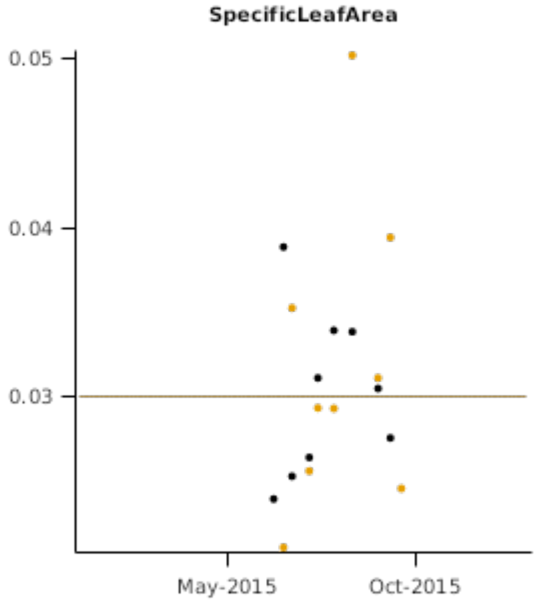

Biomass
500
0
May-2015
Oct-2015
LeafLiveWt
150
100
50
0
May-2015
Oct-2015
LeafDeadWt
StemWt
400
200
0
May-2015
Oct-2015
GrainWt
300
200
100
0
May-2015
Oct-2015
PodWt
400
200
0
May-2015
Oct-2015



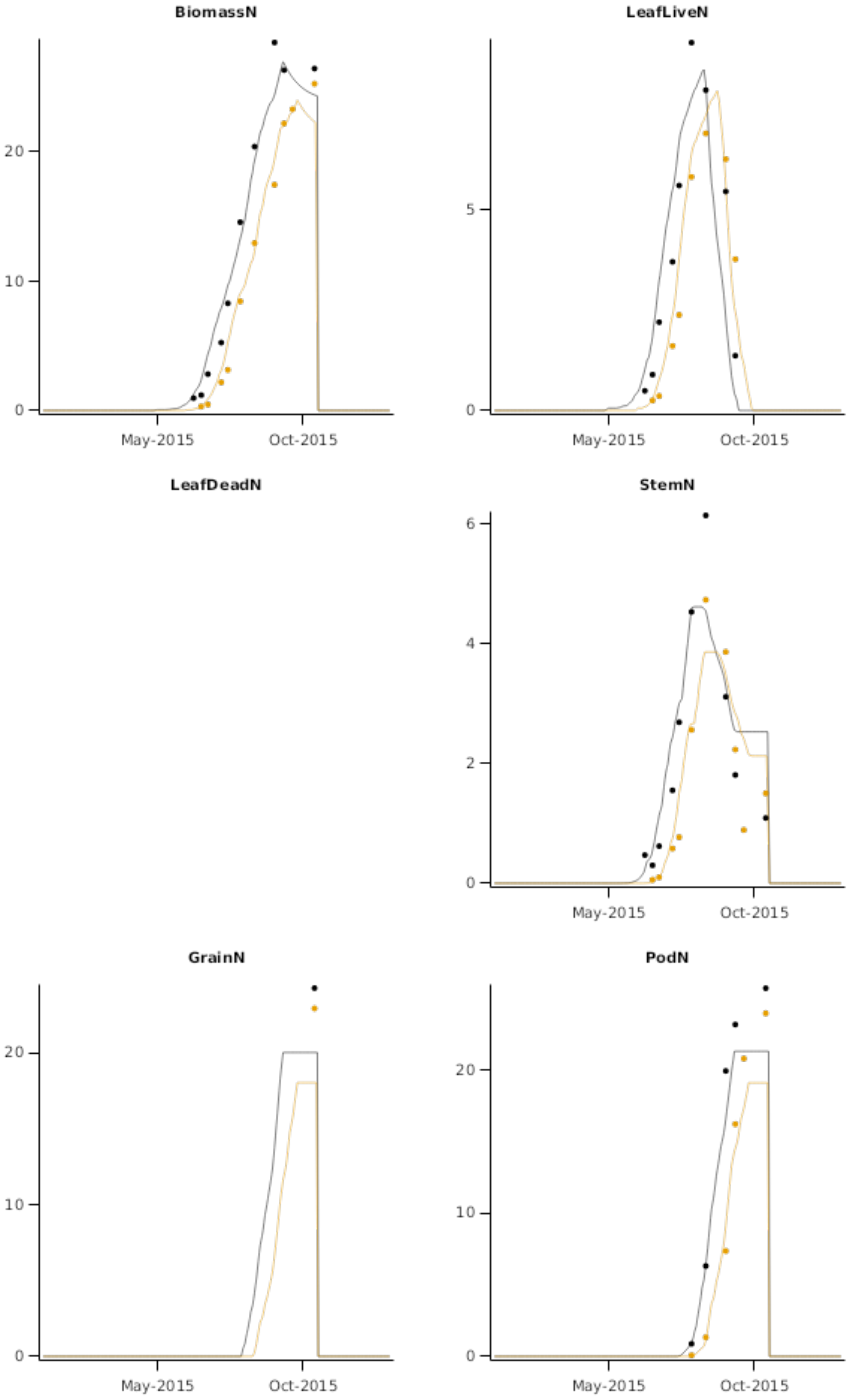
3.1.1.1.1.2 Canopy

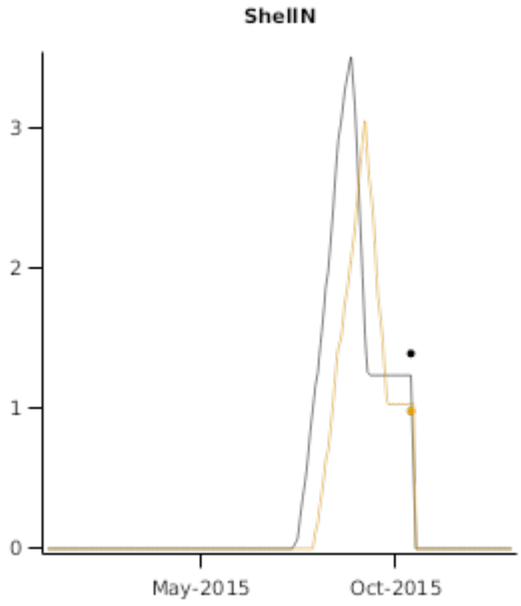




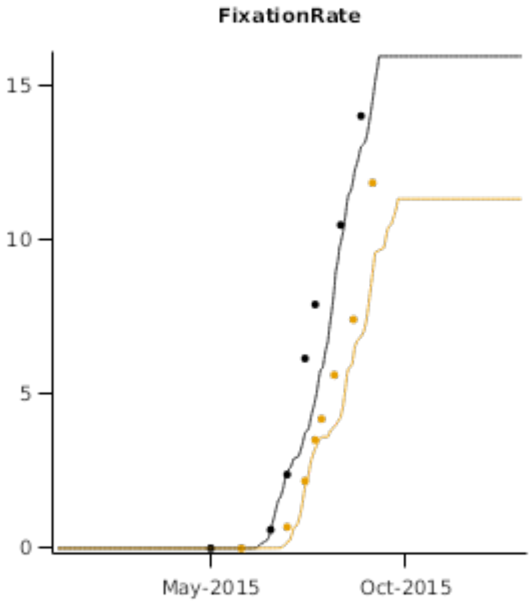


3.1.1.1.1.3 Nitrogen


BiomassN
0
10
20
May-2015
Oct-2015
LeafLiveN
0
5
May-2015
Oct-2015
LeafDeadN
StemN
0
2
4
6
May-2015
Oct-2015
GrainN
0
10
20
May-2015
Oct-2015
PodN
0
10
20
May-2015
Oct-2015



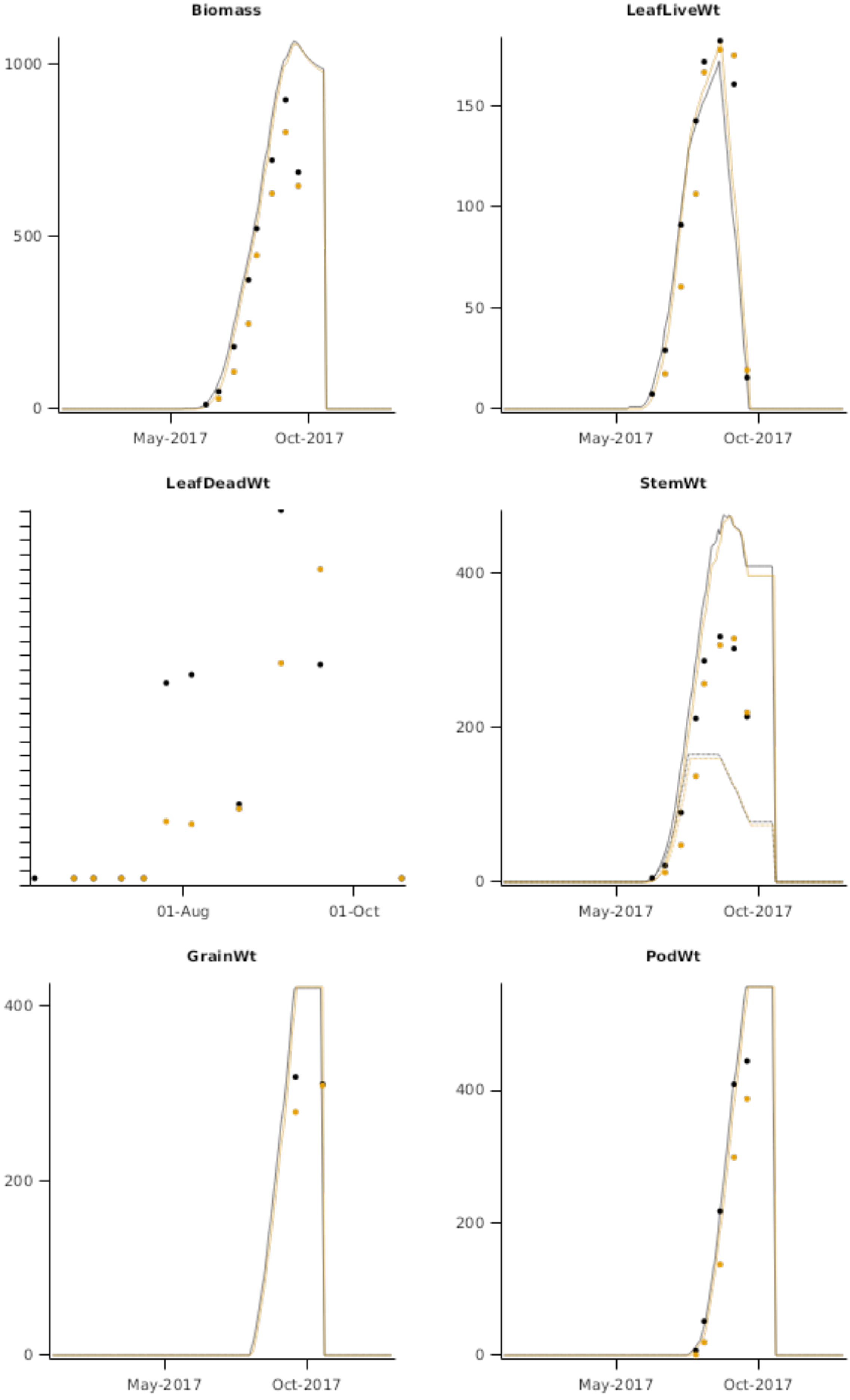
3.1.1.1.1.4 Fixation

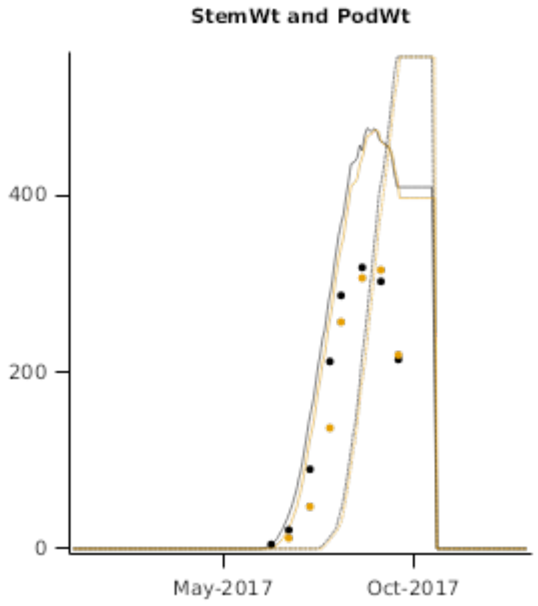


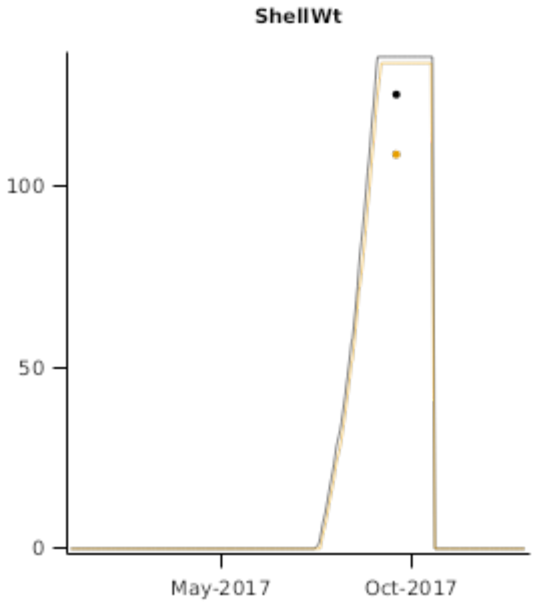
3.1.1.2 Ames2017

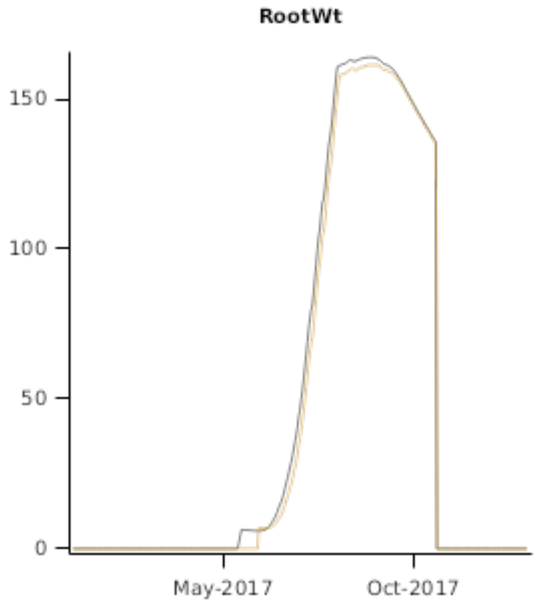
3.1.1.2.1 Graphs

3.1.1.2.1.1 Biomass

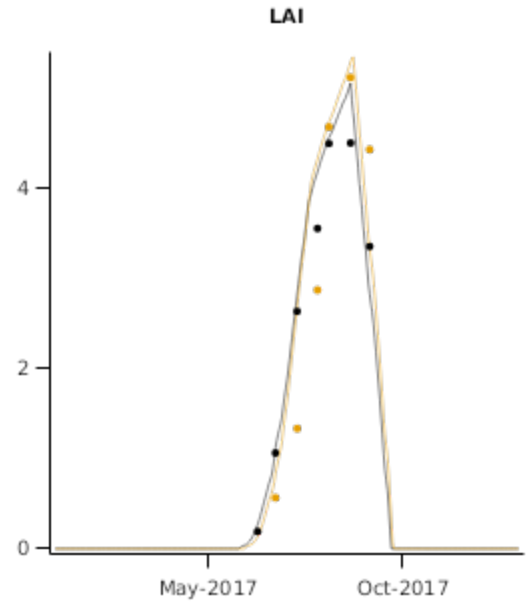

Biomass
1000
500
0
May-2017
Oct-2017
LeafLiveWt
150
100
50
0
May-2017
Oct-2017
LeafDeadWt
01-Aug
01-Oct
StemWt
400
200
0
May-2017
Oct-2017
GrainWt
400
200
0
May-2017
Oct-2017
PodWt
400
200
0
May-2017
Oct-2017

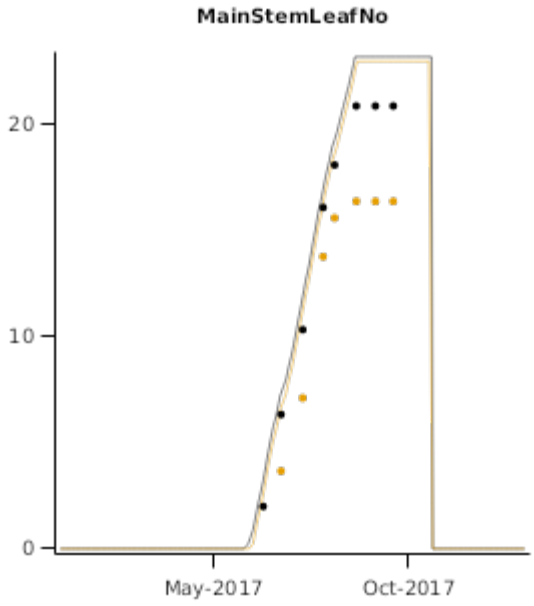


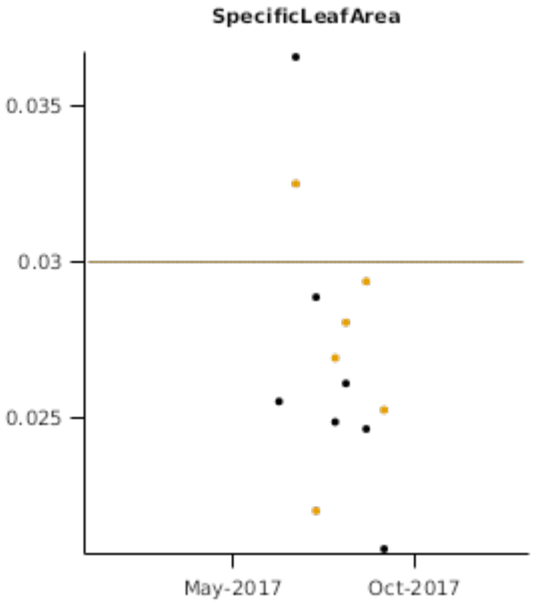




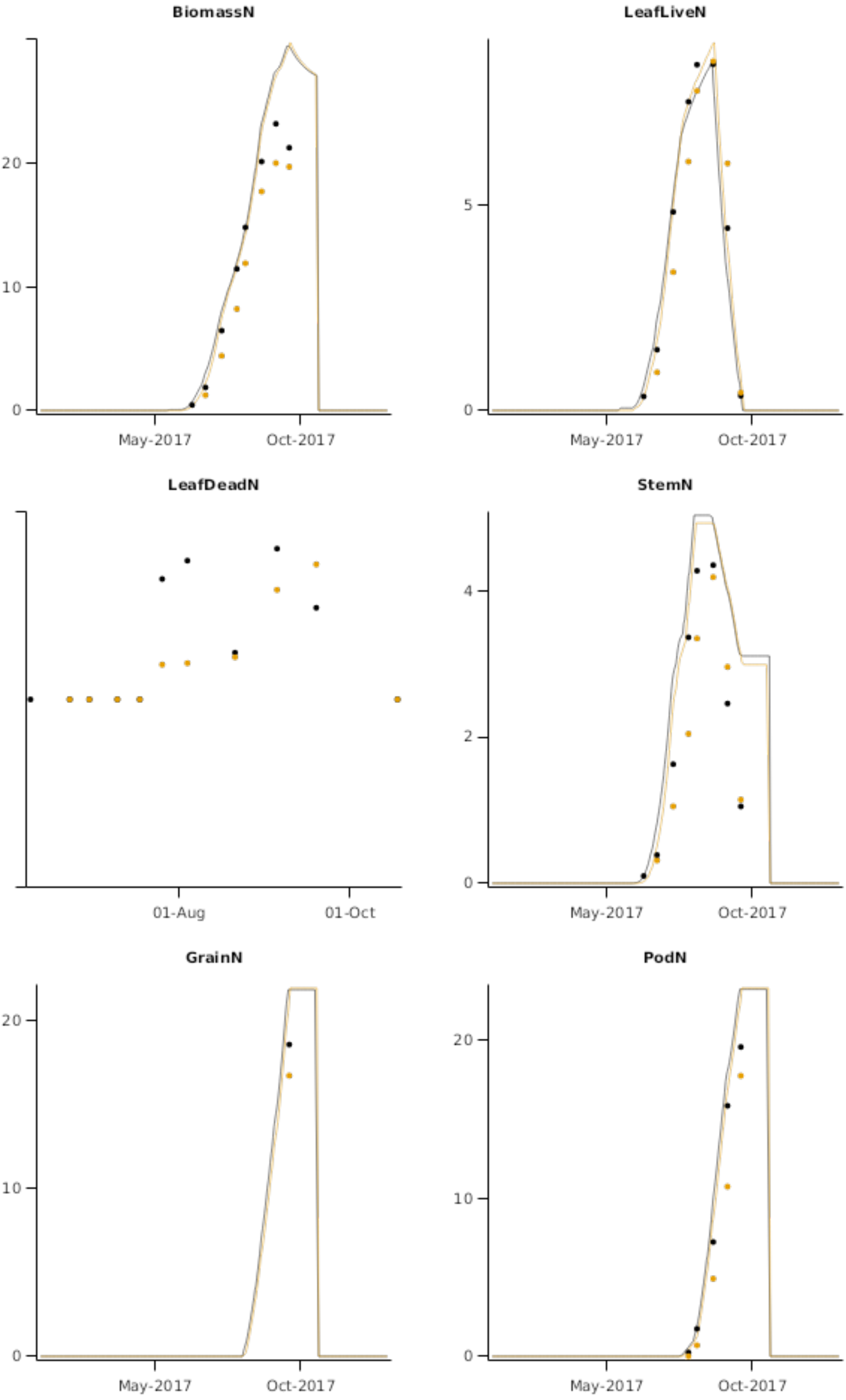
3.1.1.2.1.2 Canopy

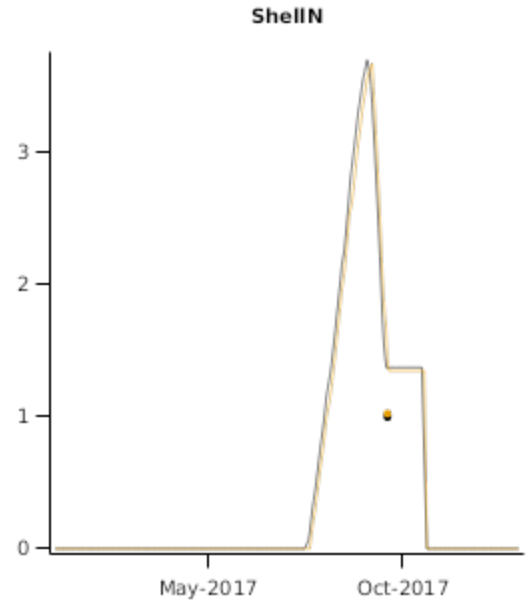






3.1.1.2.1.3 Nitrogen

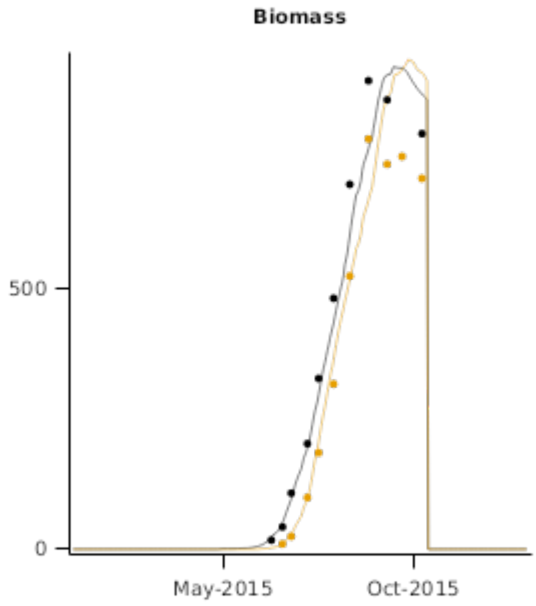

BiomassN
0
10
20
May-2017
Oct-2017
LeafLiveN
0
5
May-2017
Oct-2017
LeafDeadN
01-Aug
01-Oct
StemN
0
2
4
May-2017
Oct-2017
GrainN
0
10
20
May-2017
Oct-2017
PodN
0
10
20
May-2017
Oct-2017

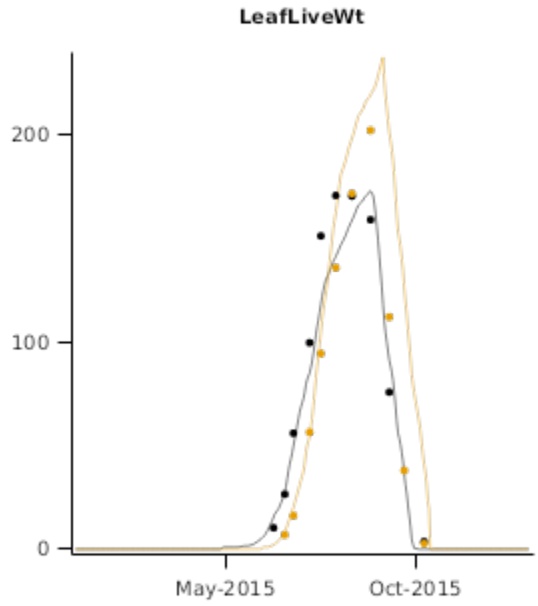


3.1.1.3 Sutherland2015

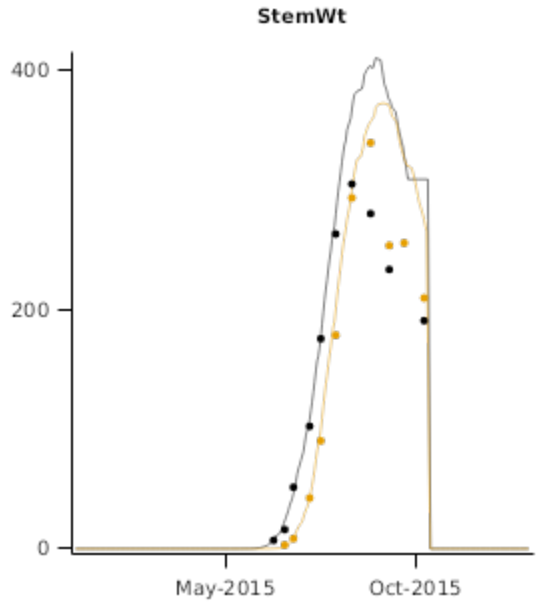
3.1.1.3.1 Graphs

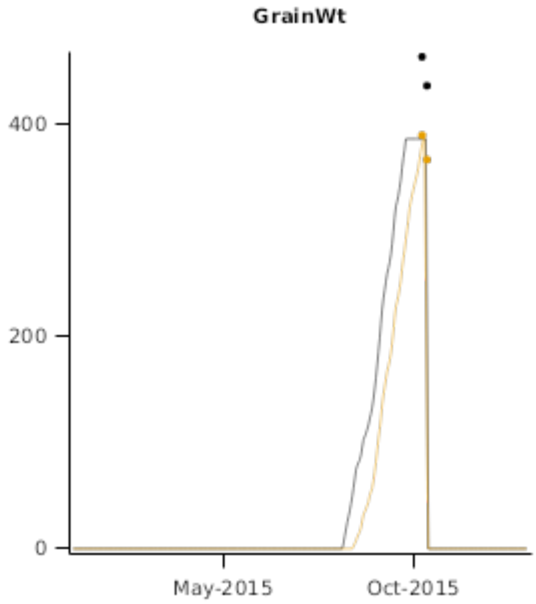
3.1.1.3.1.1 Biomass

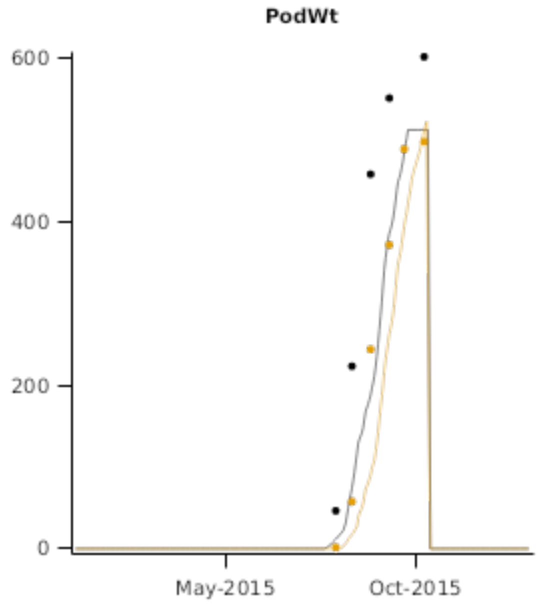




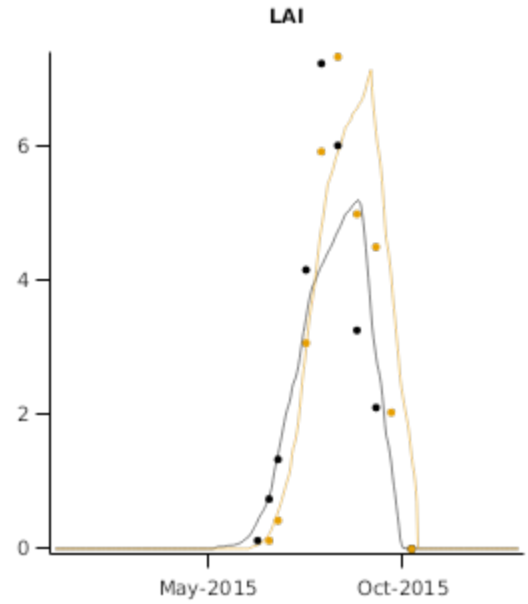
LeafDeadWt

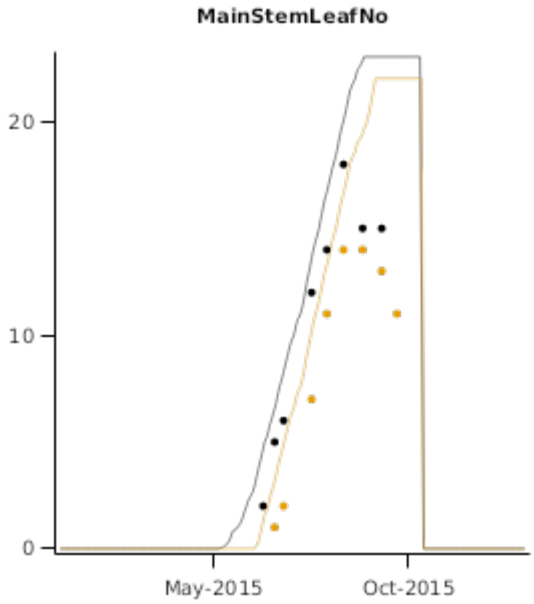


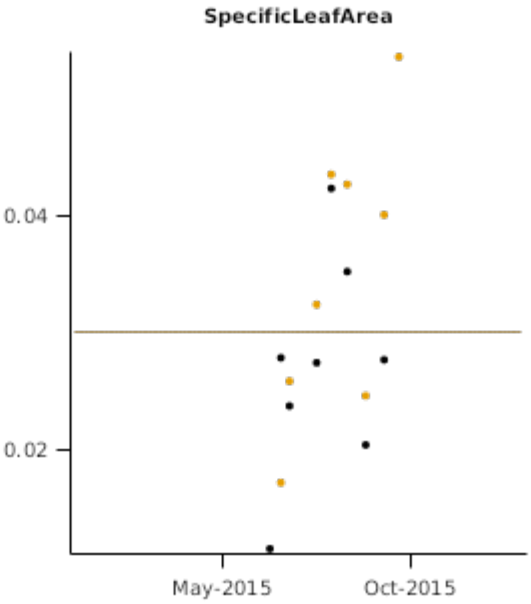




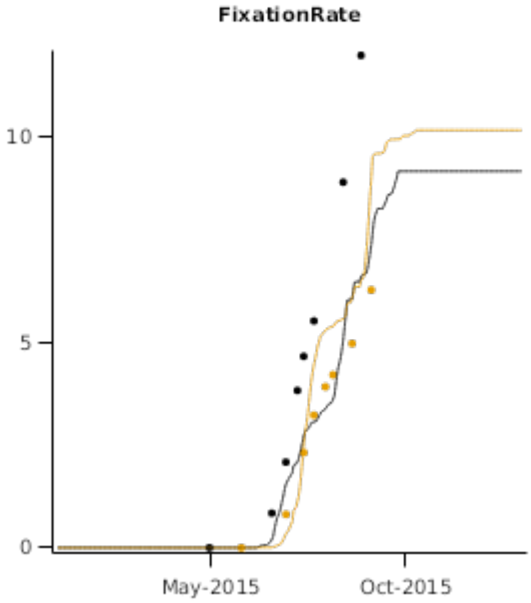
3.1.1.3.1.2 Canopy



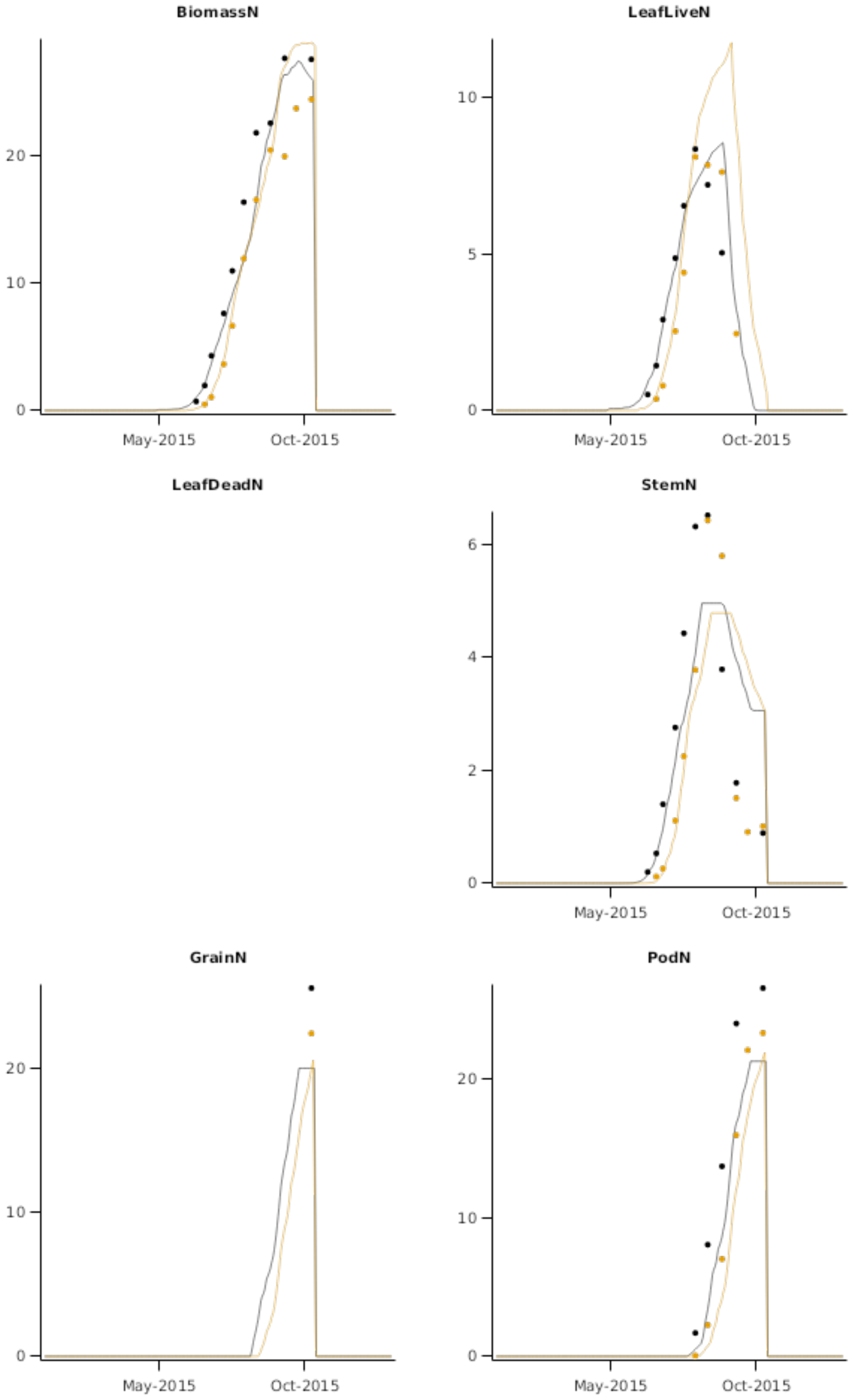


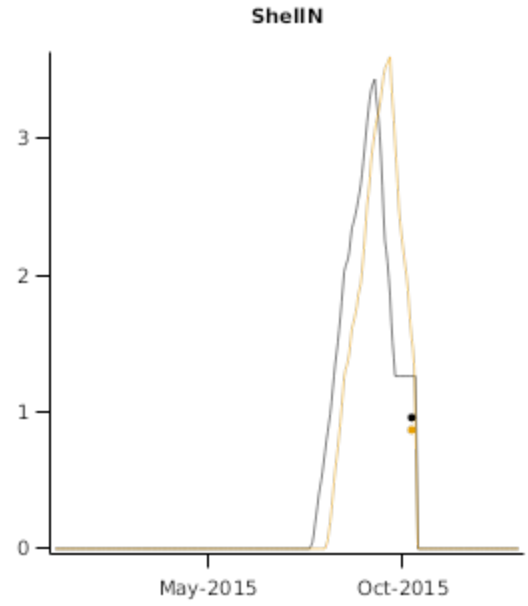


3.1.1.3.1.3 Fixation



3.1.1.3.1.4 Nitrogen

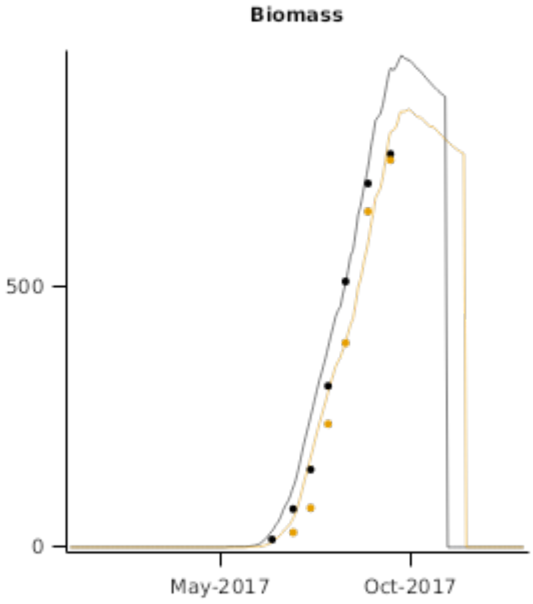

BiomassN
0
10
20
May-2015
Oct-2015
LeafLiveN
0
5
10
May-2015
Oct-2015
LeafDeadN
StemN
0
2
4
6
May-2015
Oct-2015
GrainN
0
10
20
May-2015
Oct-2015
PodN
0
10
20
May-2015
Oct-2015

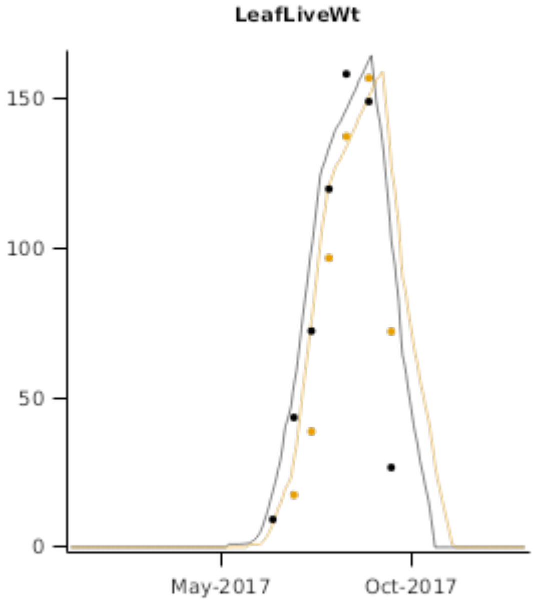


3.1.1.4 Sutherland2017

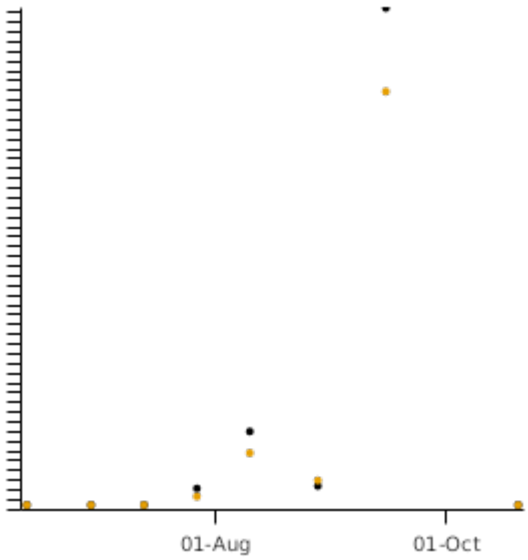
3.1.1.4.1 Graphs

3.1.1.4.1.1 Biomass

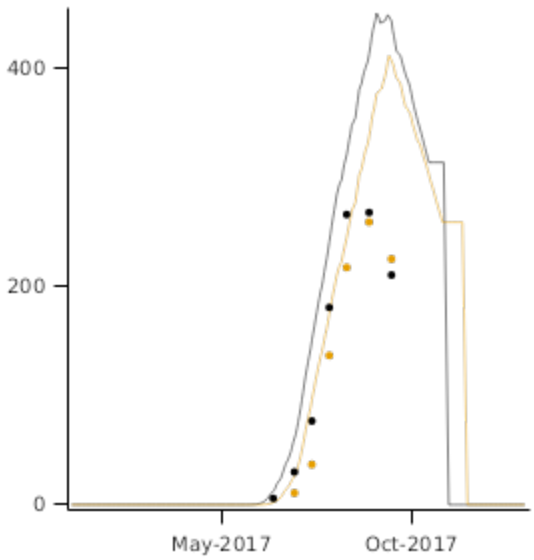




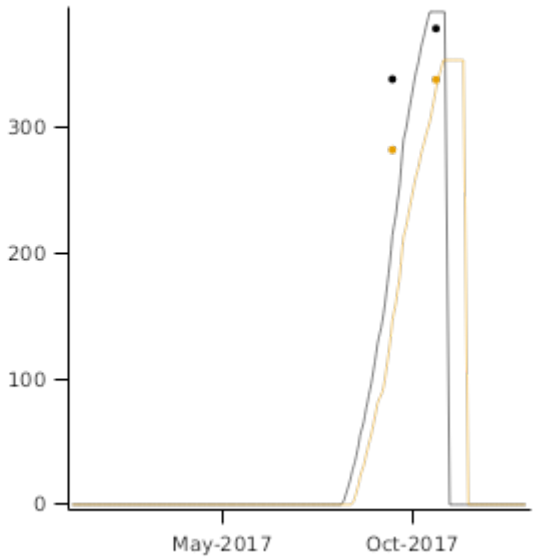
LeafDeadWt



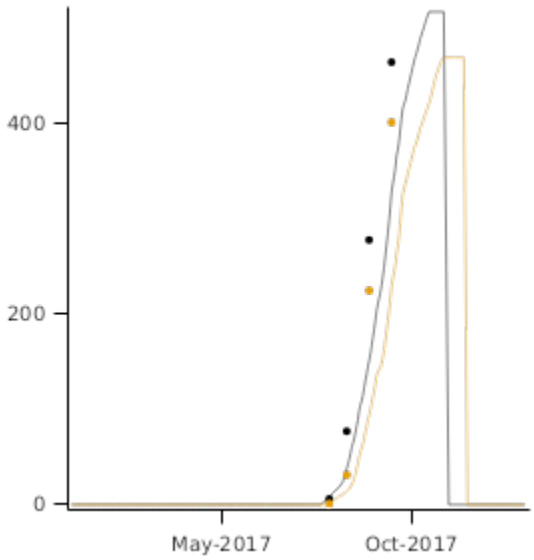
StemWt



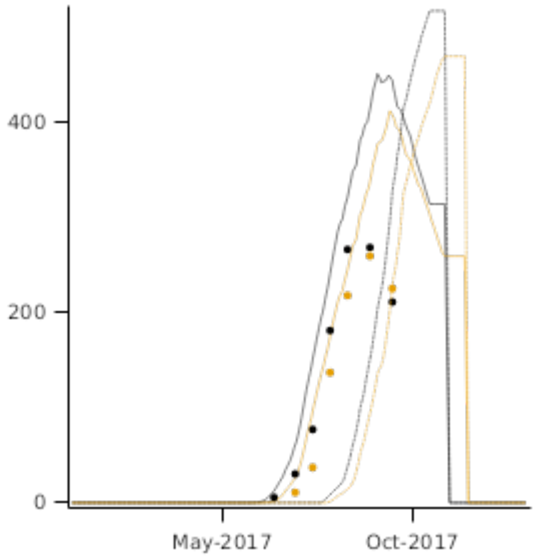
GrainWt



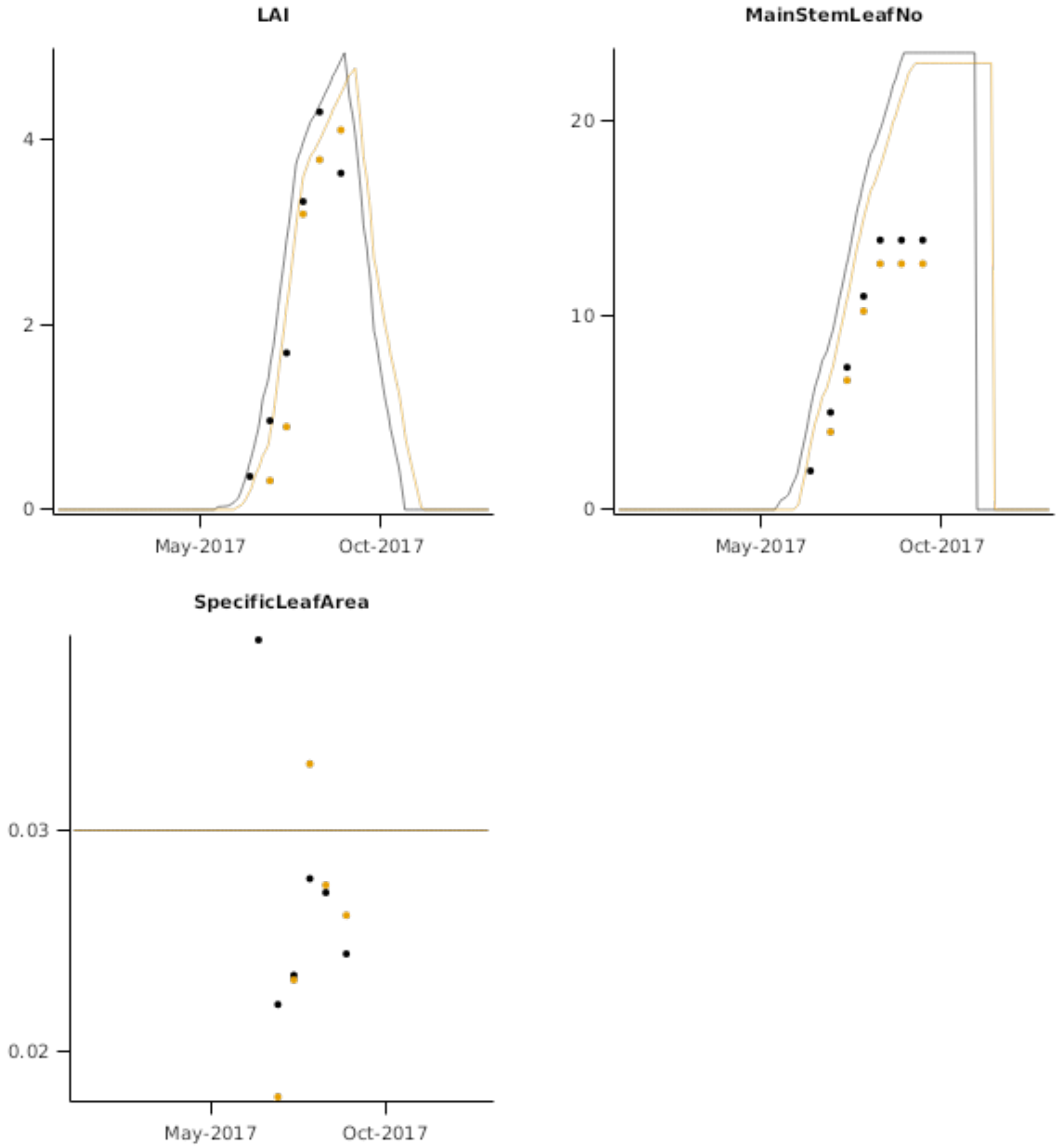
PodWt



StemWt and PodWt



3.1.1.4.1.2 Canopy

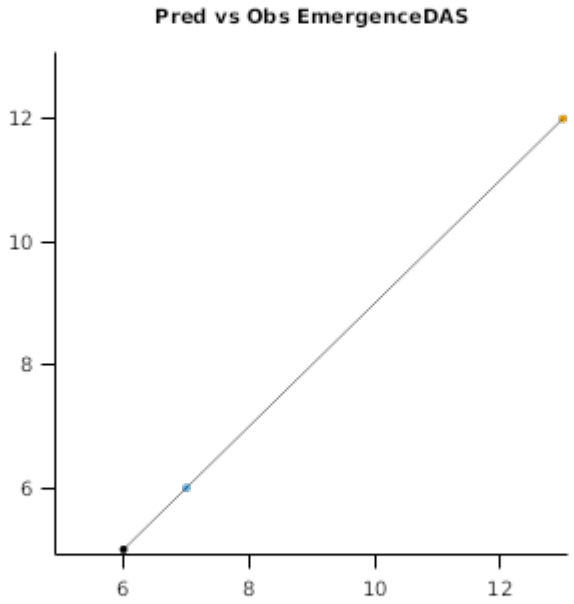


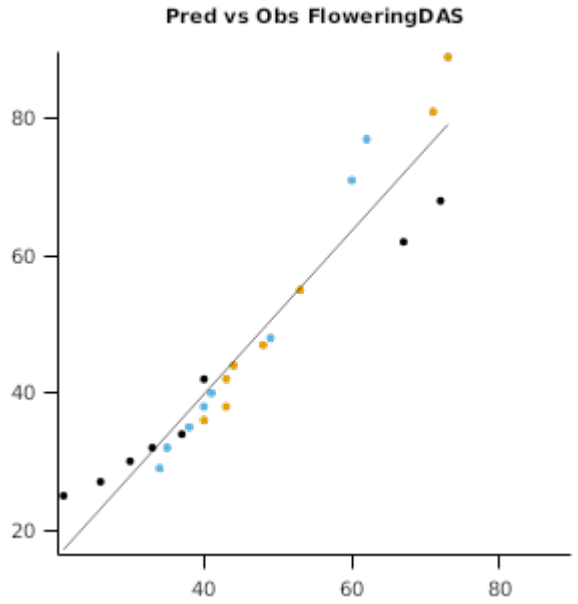
3.1.2 Arkansas

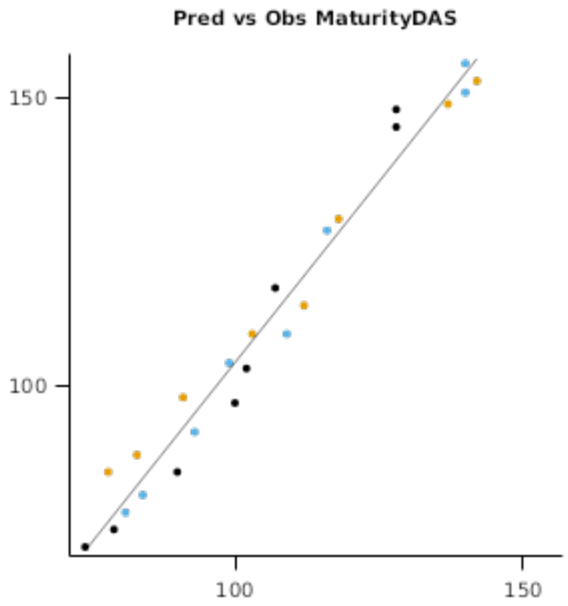
This trial (Edwards, 2005) was conducted on a silt loam soil in Fayetteville Arkansas, USA, in years 2001, 2002 and 2003. The factor studied were seven soybean maturity groups (from mg 00 to mg 6) and in some year multiple varieties within a maturity group. Crops were irrigated. No N fertilization was applied. This region has no shallow water tables. Phenology data were collected at different growth stages and were used in this work. Weather and soil data for the site were estimated from public sources. For additional information about this trial, see Archontoulis et al., 2014.

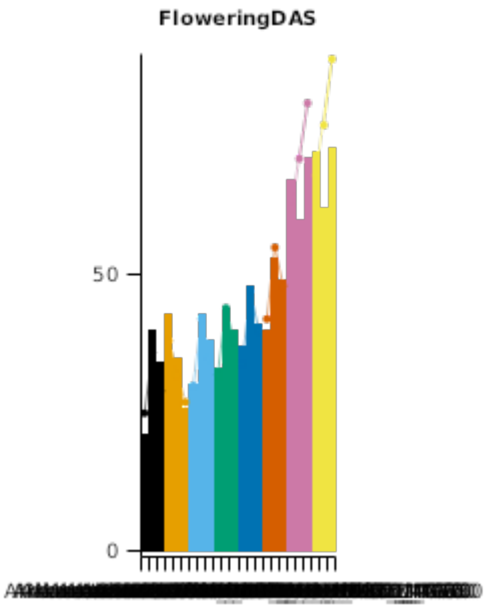
List of experiments.

Experiment Name	Design (Number of Treatments)
Arkansas2001	Cv (8)
Arkansas2002	Cv (8)
Arkansas2003	Cv (8)







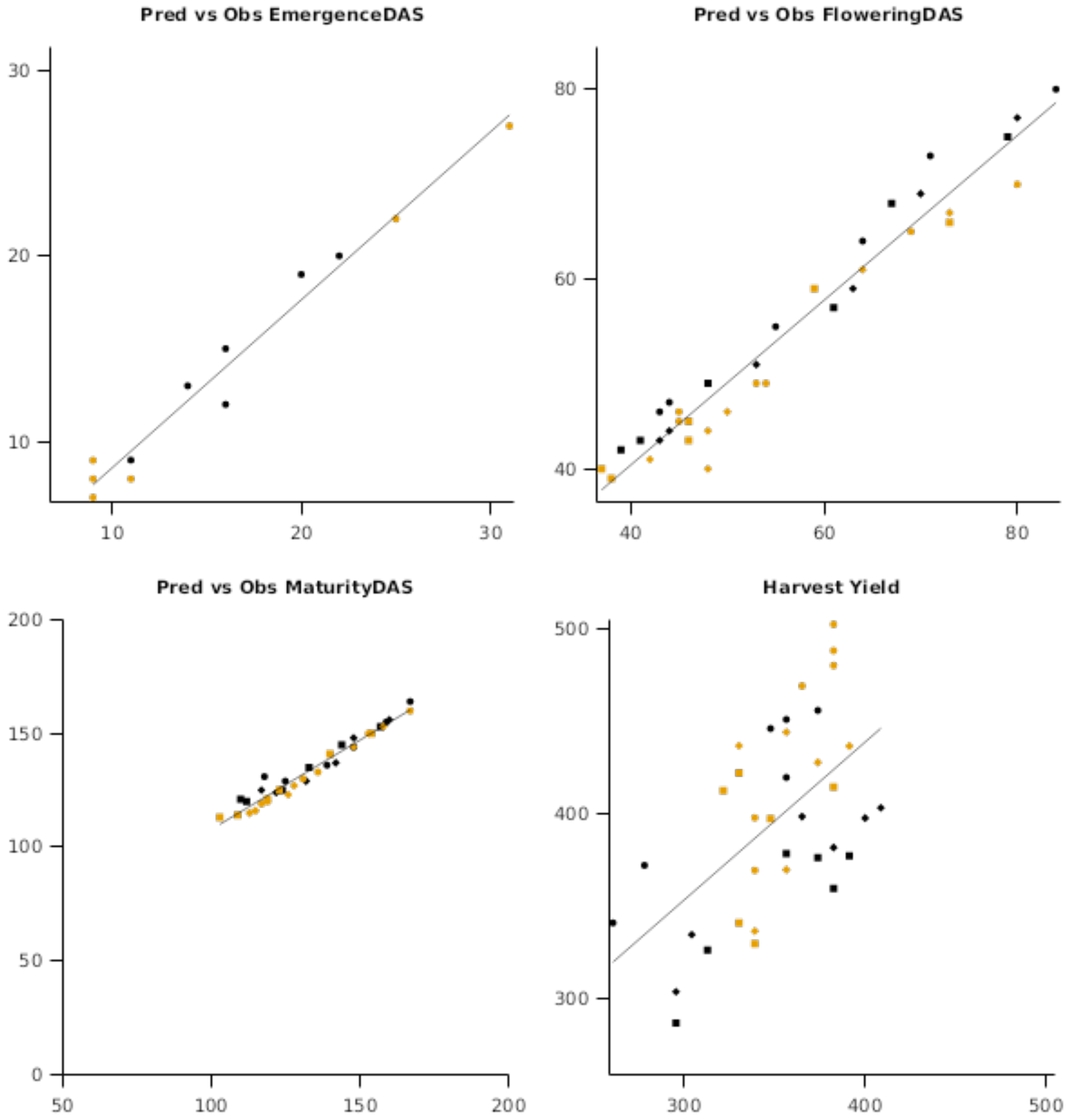


3.1.3 Indiana

This trial (Robinson, 2009) conducted in West Lafayette Indiana, USA, in years 2006 and 2007. The factors studied were six planting dates x three varieties (from mg 2.6 to mg 3.7). No irrigation or fertilization applied. Phenology, gravimetric soil moisture at three depth (manual soil cores), pod numbers, seed size, grain yield, protein and oil data were collected. Weather and soil data for the site were estimated from public sources. For additional information about this trial, see Archontoulis et al., 2014.

List of experiments.

Experiment Name	Design (Number of Treatments)
Indiana2006	Sow x Cv (18)
Indiana2007	Sow x Cv (18)

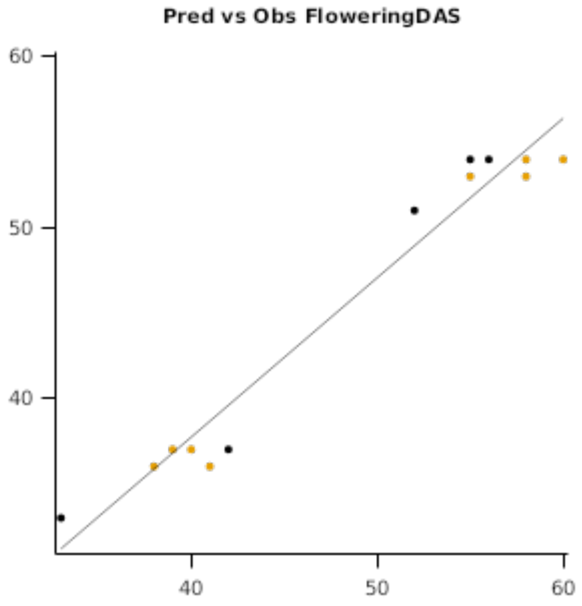


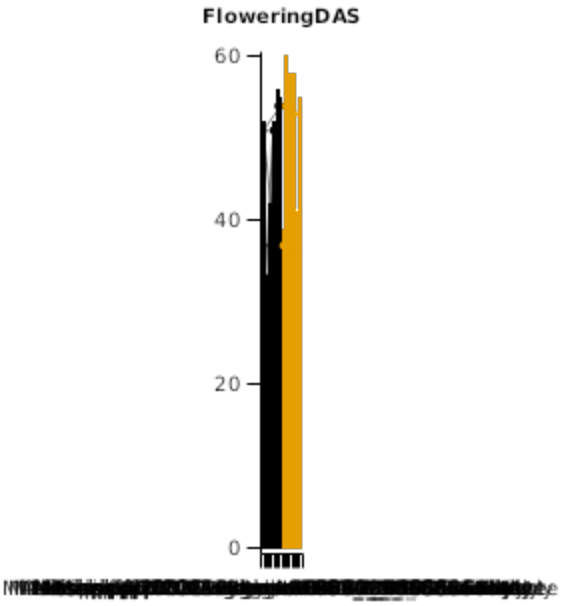
3.1.4 Mississippi

This trial (Zhang, 2004) was conducted in Stoneville Mississippi USA, in years 1998 to 2002. The factors studied were planting dates (ranged from early March to early July) and varieties (from mg 3.4 to mg 5.6). Crops were irrigated. Phenological measurements were obtained in the field following the V/R staging system. For additional information about this trial, see Archontoulis et al., 2014.

List of experiments.

Experiment Name	Design (Number of Treatments)
Mississippi2002	Cv x Sow (8)
Mississippi2003	Cv x Sow (8)





3.1.5 Nebraska

This trial ([Salvagiotti, 2009](#))was conducted on a deep silt loam soil in Lincoln Nebraska USA, in years 2006 and 2007. The factors studied were different crop histories (normal N applied to corn-soy rotation and high N applied to the rotation) and 4 N fertilization treatments to the soybean crop (zero N, 180 kg N/ha at planting, 180 kg N/ha as split between preplanting and V6 leaf stage, and 180 kg N/ha at R5 stage). Crops were irrigated. Row spacing was 76 cm, plant density about 31 pl/m2 and planting date around late april to early May. The following measurements were taken: initial soil nitrate, destructive biomass samples six times during the season (size 0.46 m2 per plot) per year and per treatment, biomass partitioning, dry weight and N concentrations of each tissue (Dumas method in Rapid N Cube; Elementer, Germany), fallen leaves, phenology, and N-fixation during the growing season using the ureide method. Local weather data and public soil data were used to drive the simulations.

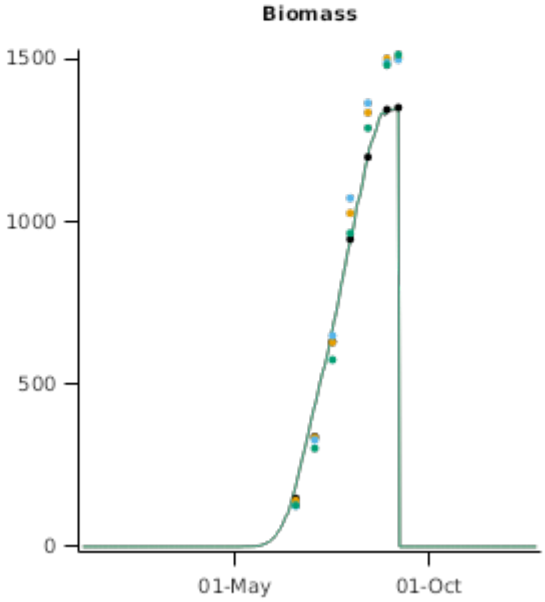
List of experiments.

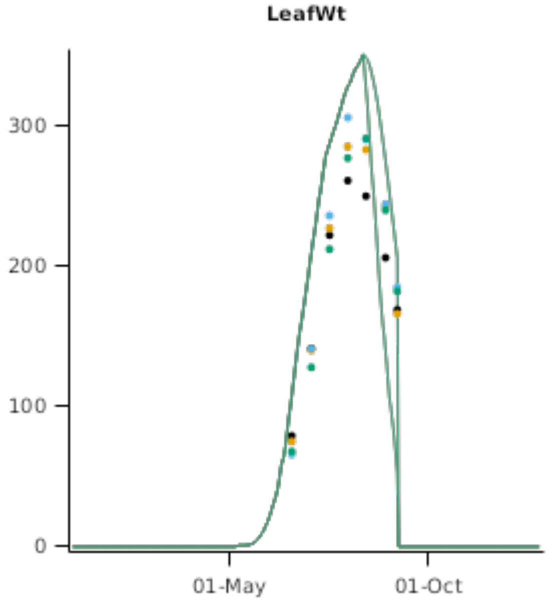
Experiment Name	Design (Number of Treatments)
Nebraska2006	N (4)
Nebraska2007	N (4)

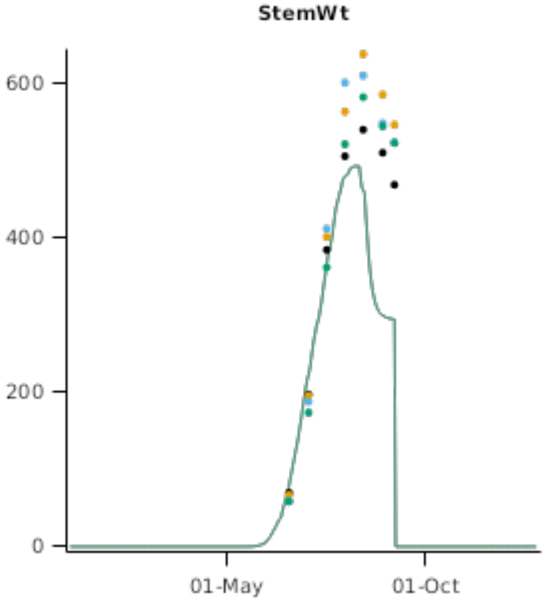
3.1.5.1 Nebraska2006

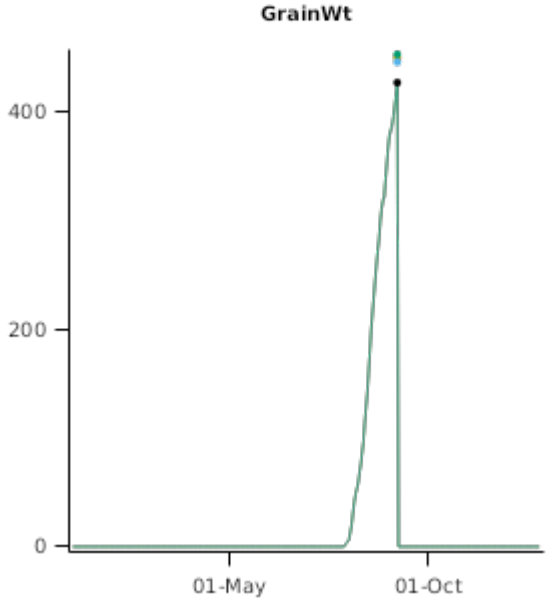
3.1.5.1.1 Graphs

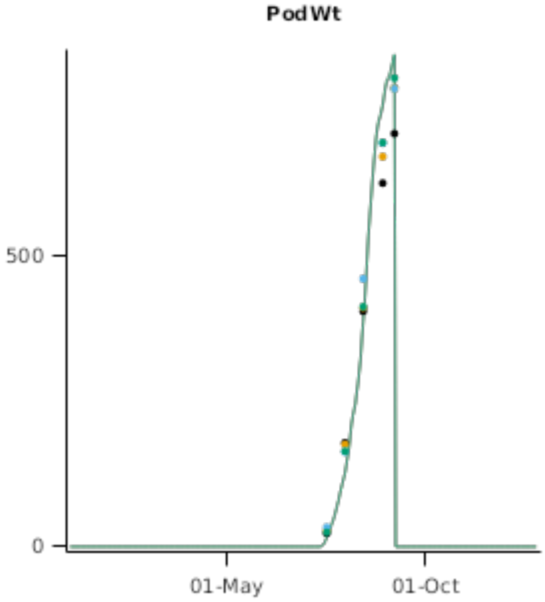
3.1.5.1.1.1 Biomass

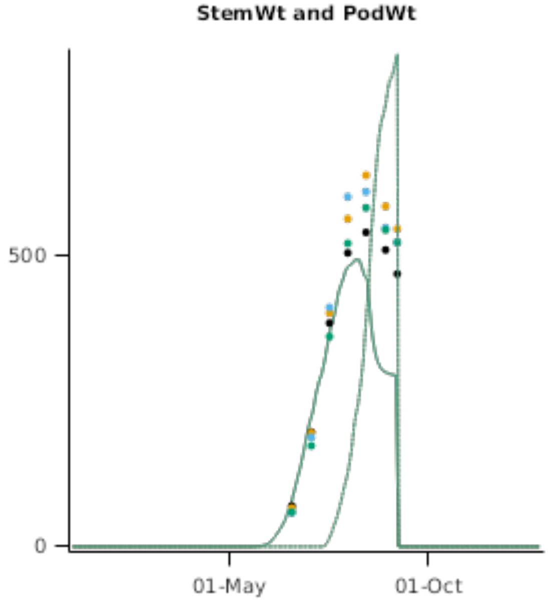

Biomass

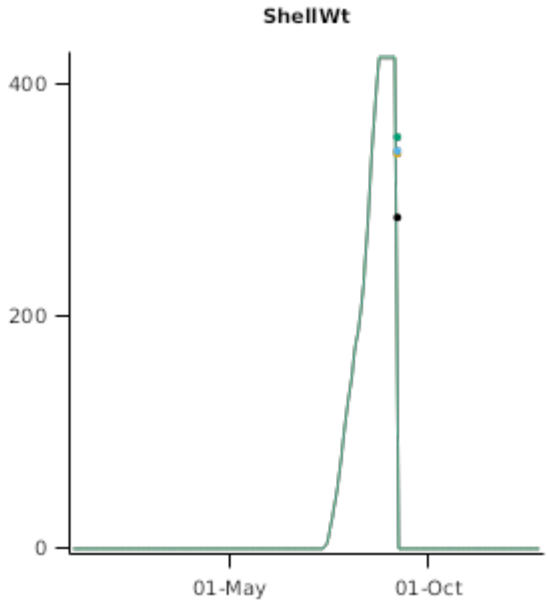

LeafWt


StemWt

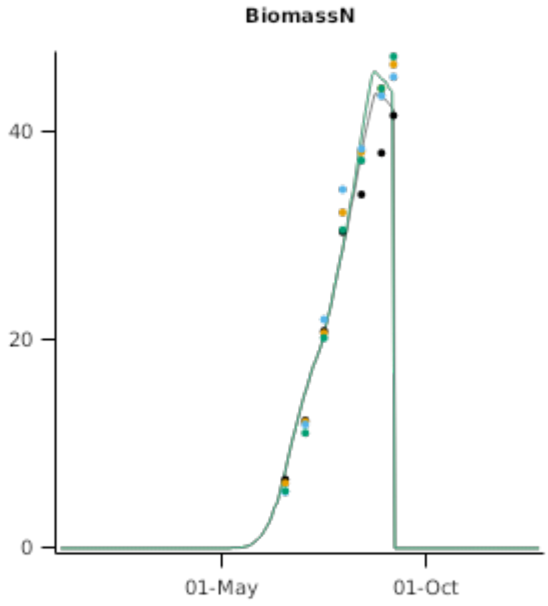

GrainWt

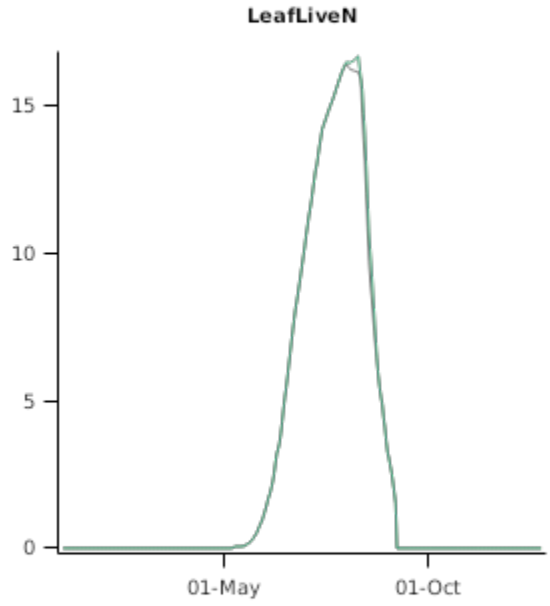

PodWt

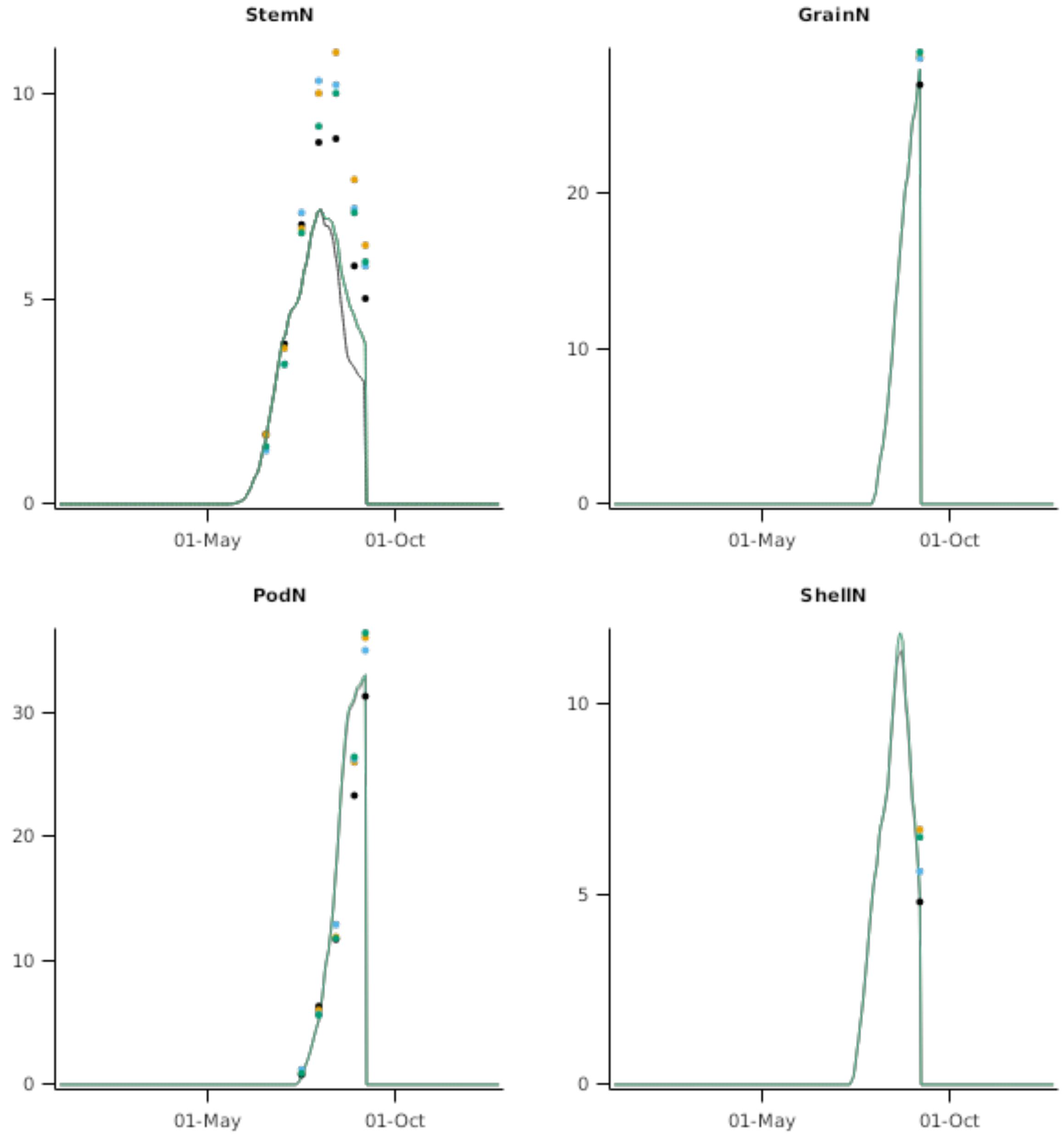

StemWt and PodWt



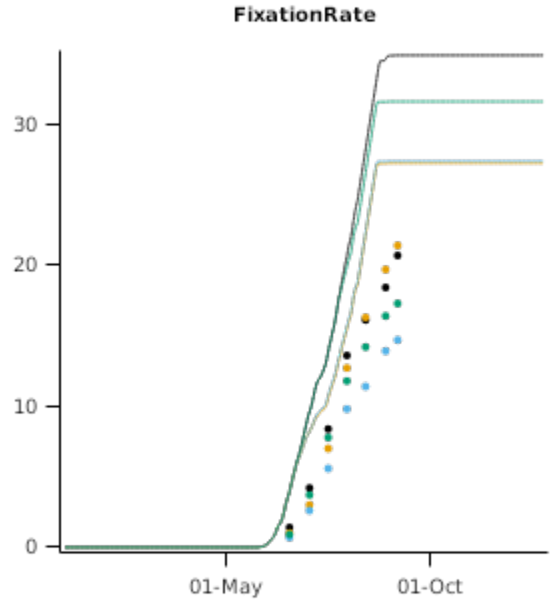
3.1.5.1.1.2 Nitrogen







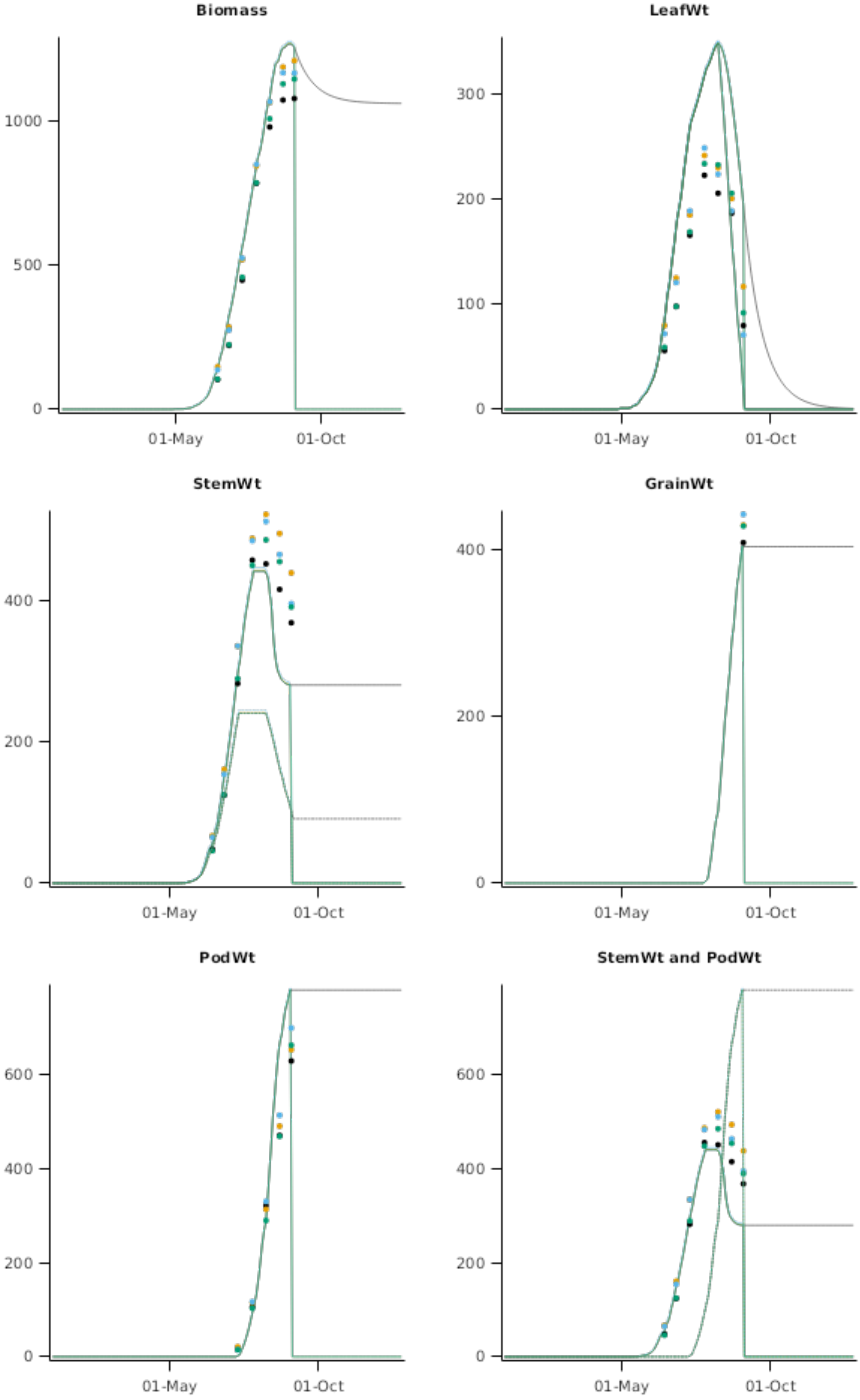
3.1.5.1.1.3 Fixation

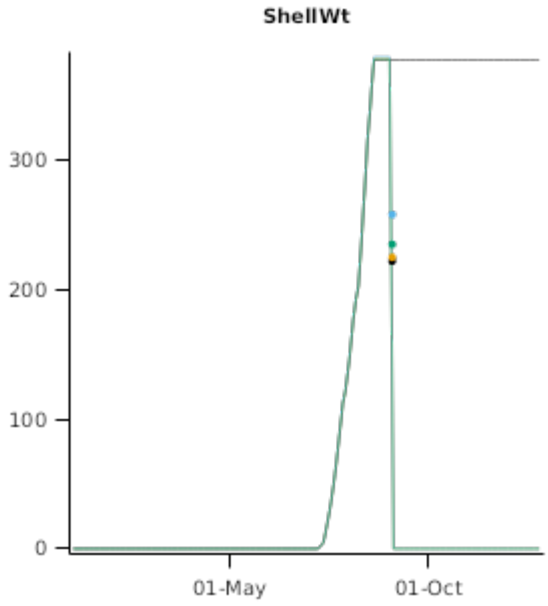


3.1.5.2 Nebraska2007

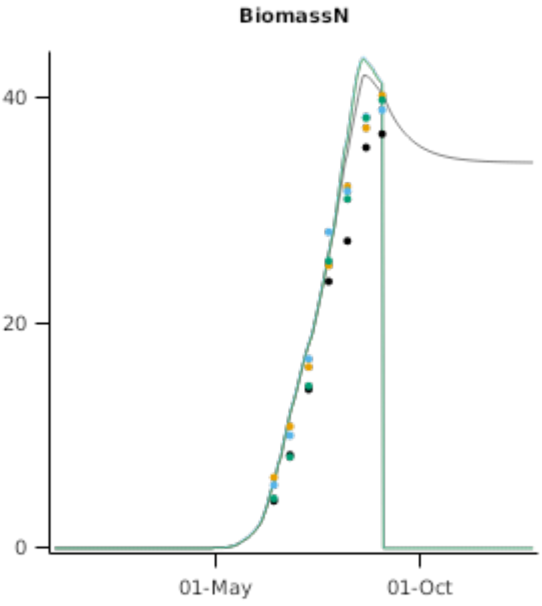
3.1.5.2.1 Graphs

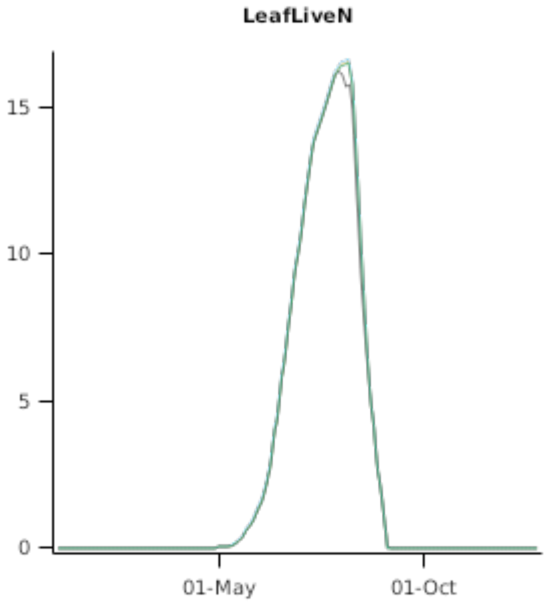
3.1.5.2.1.1 Biomass

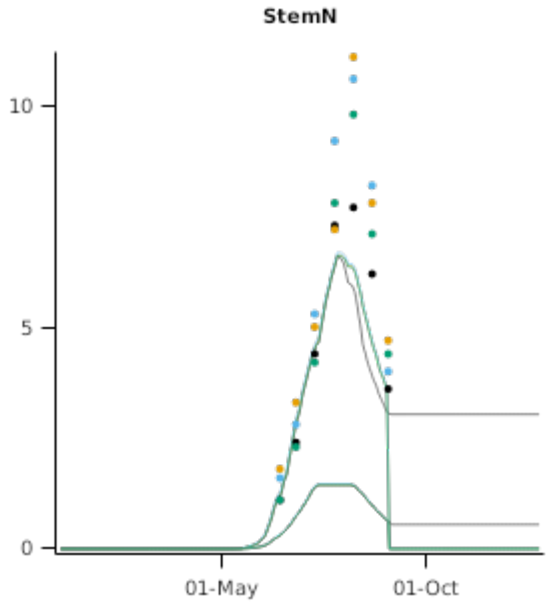


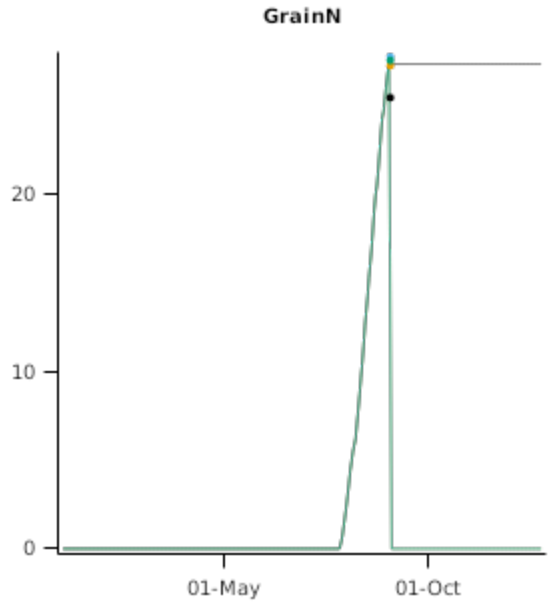


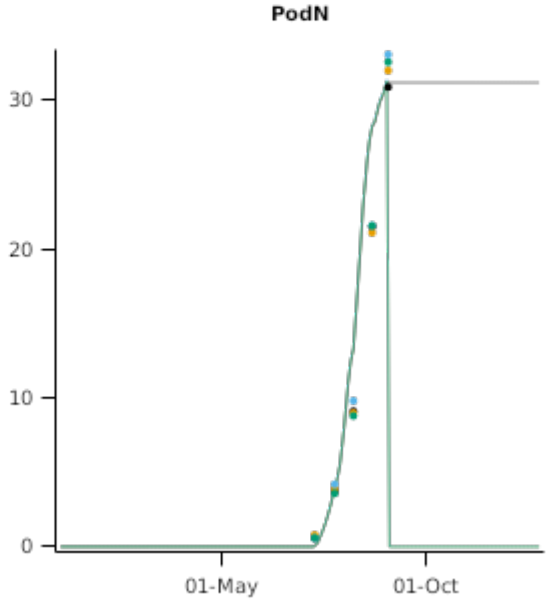
3.1.5.2.1.2 Nitrogen

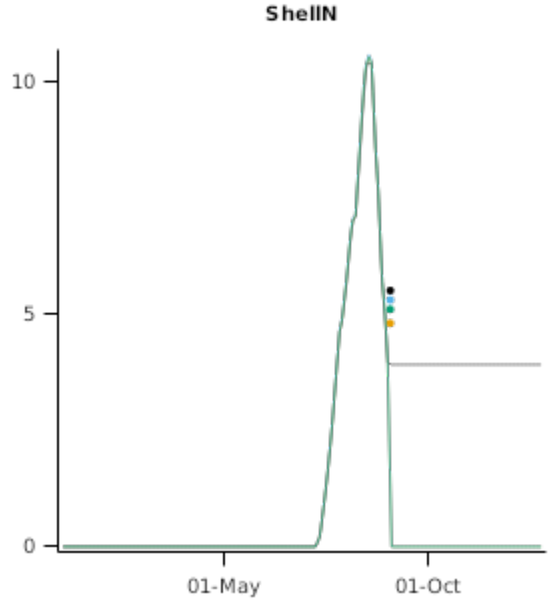




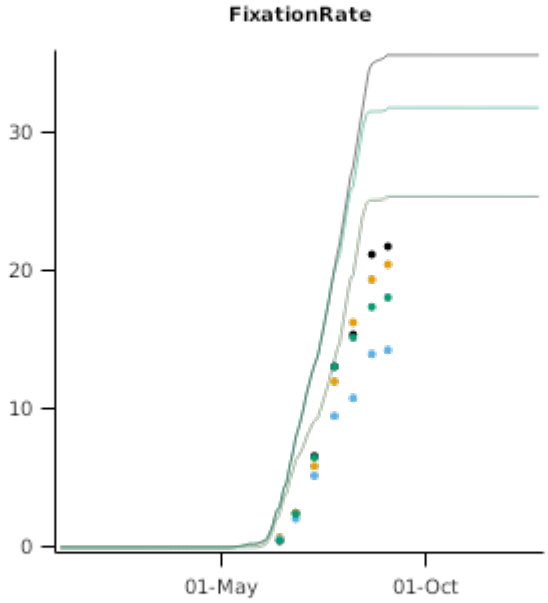








3.1.5.2.1.3 Fixation



3.2 Australia

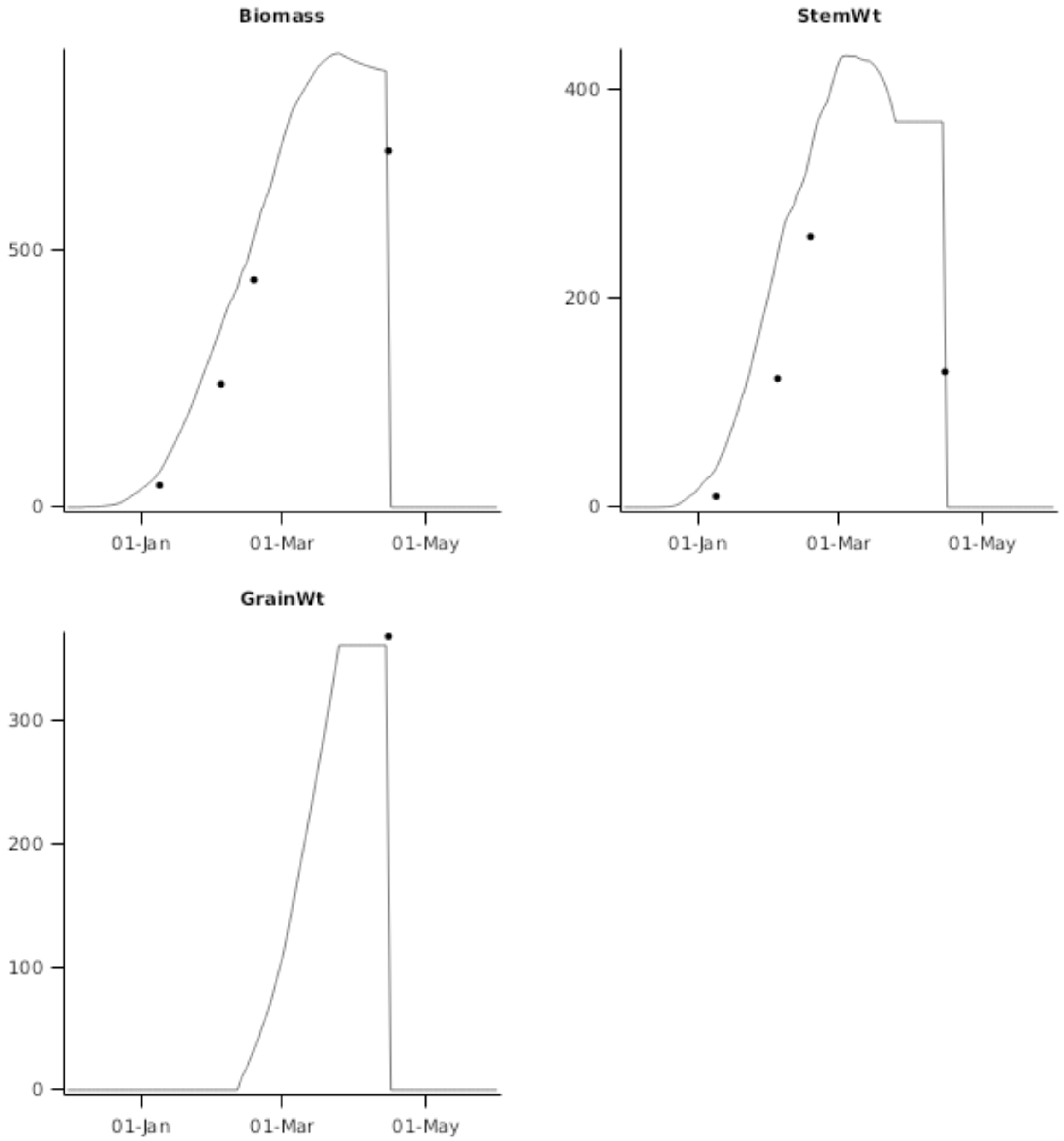
3.2.1 Coleambally

List of experiments.

Experiment Name	Design (Number of Treatments)
Coleambally	Sow (1)

3.2.1.1 Graphs

3.2.1.1.1 Biomass



3.2.2 Gatton

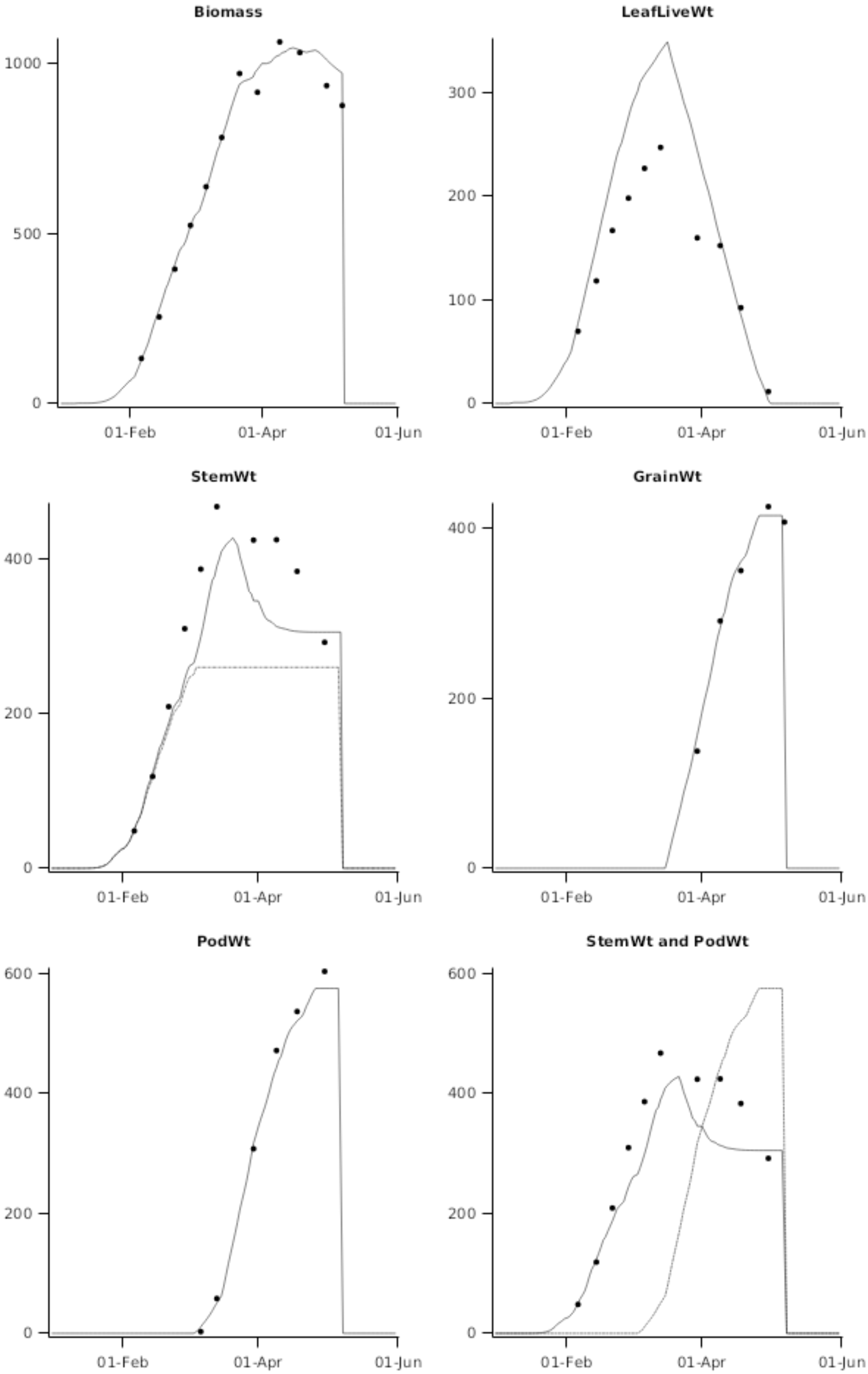
This dataset (Muchow et al., 1993) includes the cultvar "Davis" grown under irrigated conditions in a subtropical environment at the Gatton Research Station in southeastern Queensland, Australia. Plants were sampled almost weekly for biomass partitioning, nitrogen and plant development.

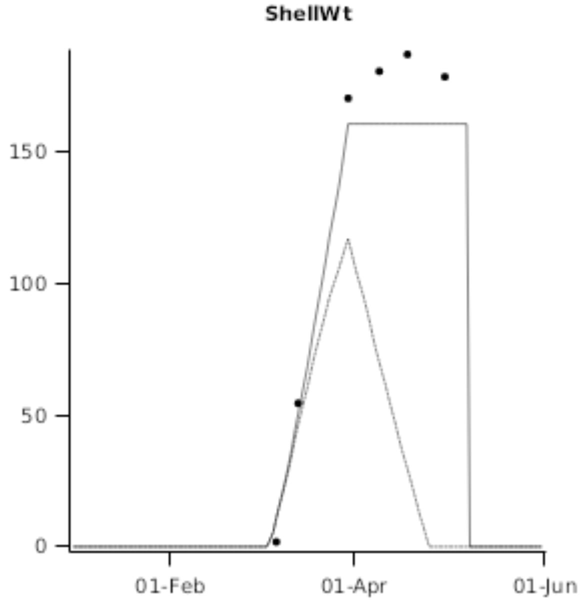
List of experiments.

Experiment Name	Design (Number of Treatments)
Gatton	Sow (1)

3.2.2.1 Graphs

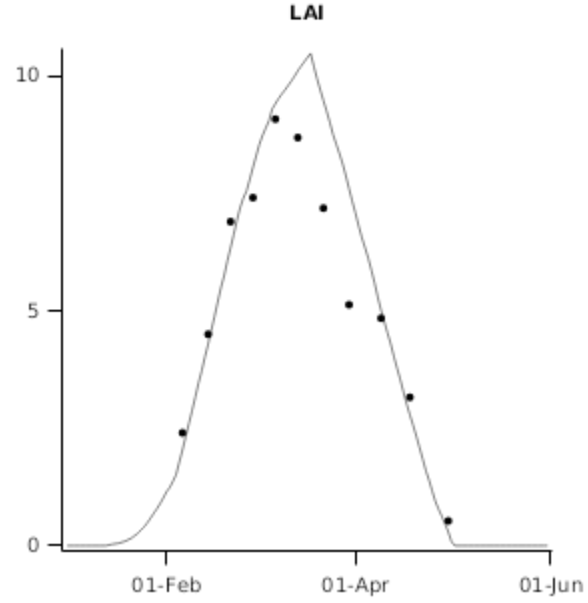
3.2.2.1.1 Biomass

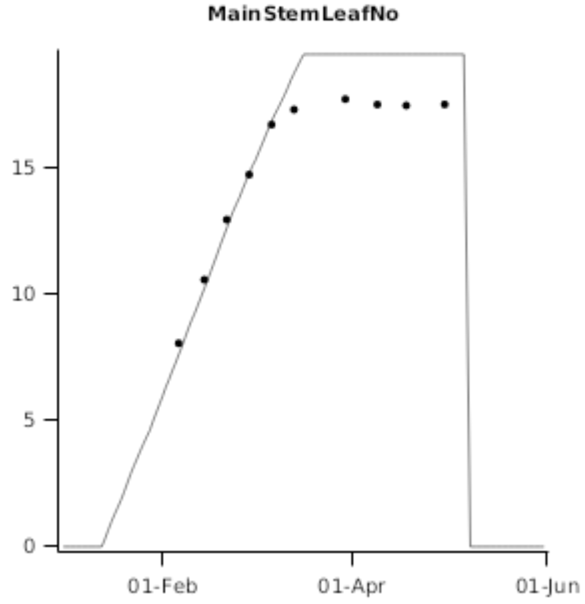

Biomass
1000
500
0
01-Feb
01-Apr
01-Jun
LeafLiveWt
300
200
100
0
01-Feb
01-Apr
01-Jun
StemWt
400
200
0
01-Feb
01-Apr
01-Jun
GrainWt
400
200
0
01-Feb
01-Apr
01-Jun
PodWt
600
400
200
0
01-Feb
01-Apr
01-Jun
StemWt and PodWt
600
400
200
0
01-Feb
01-Apr
01-Jun

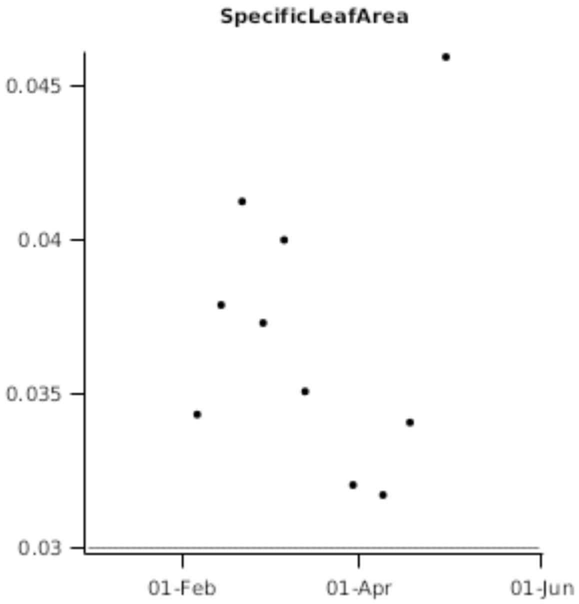


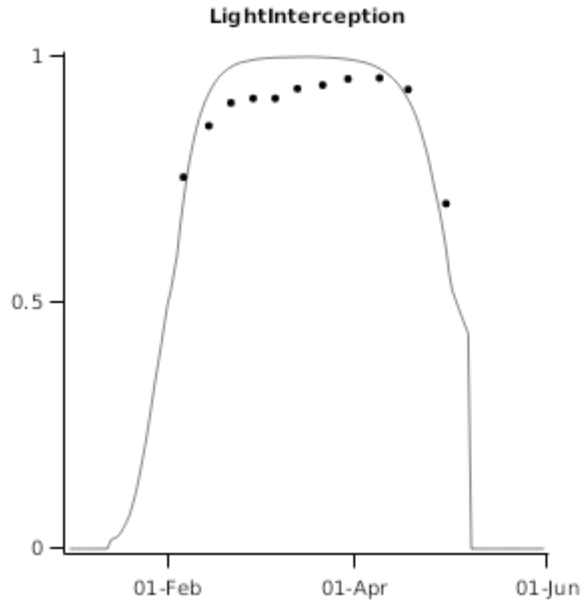
HarvestIndex

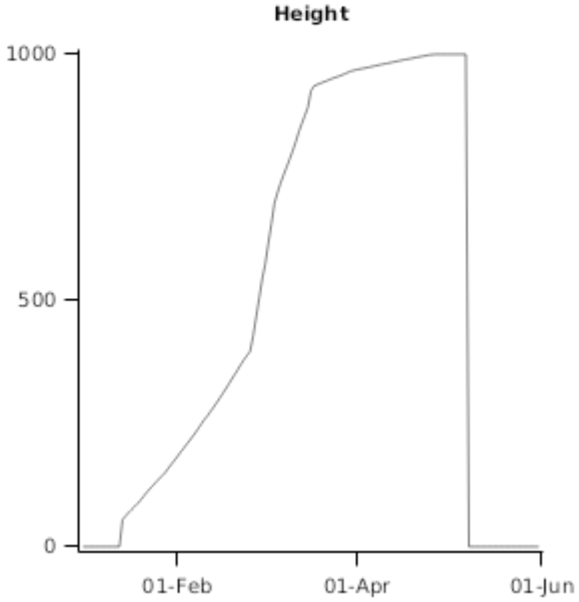
3.2.2.1.2 Canopy



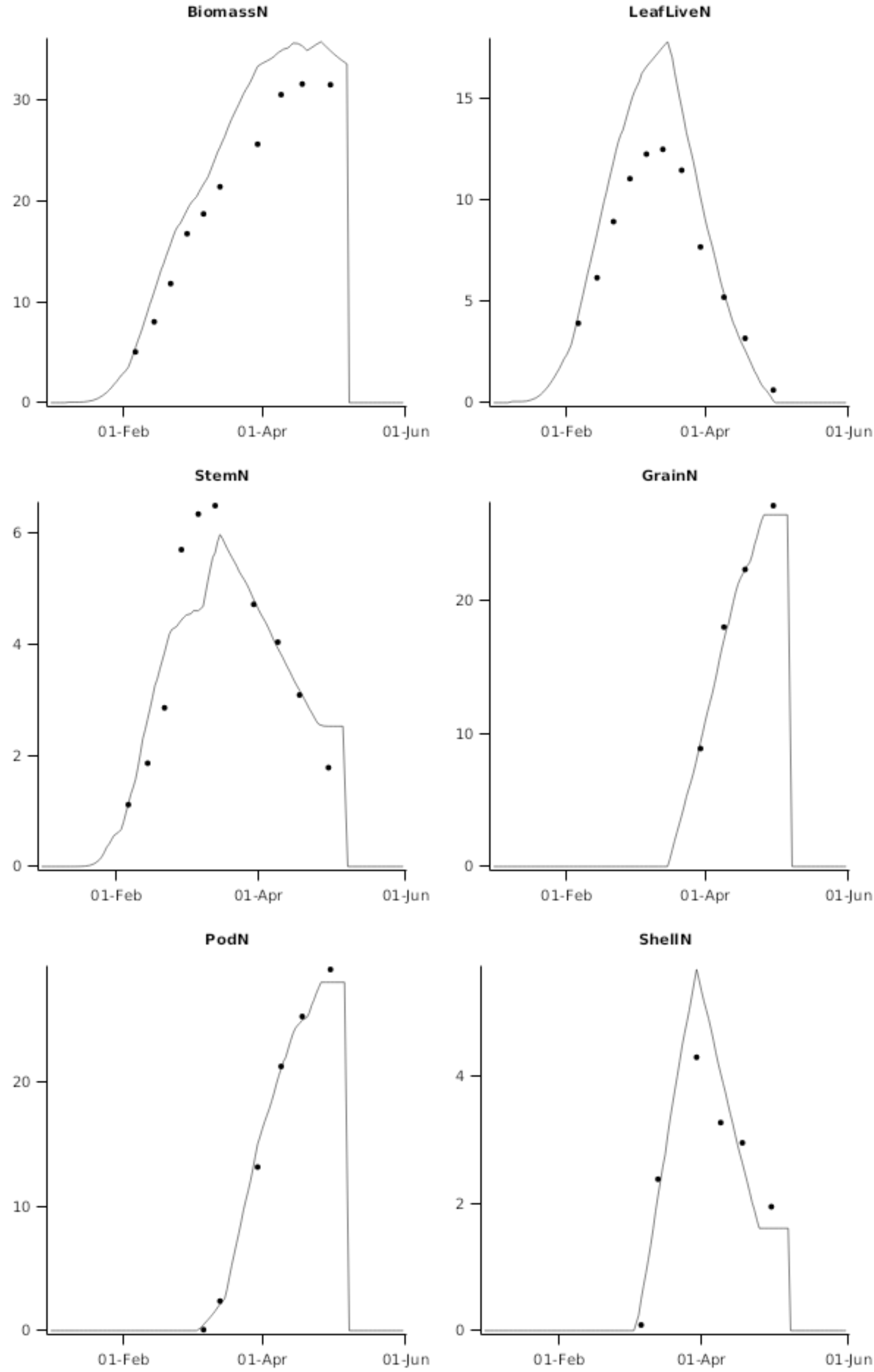




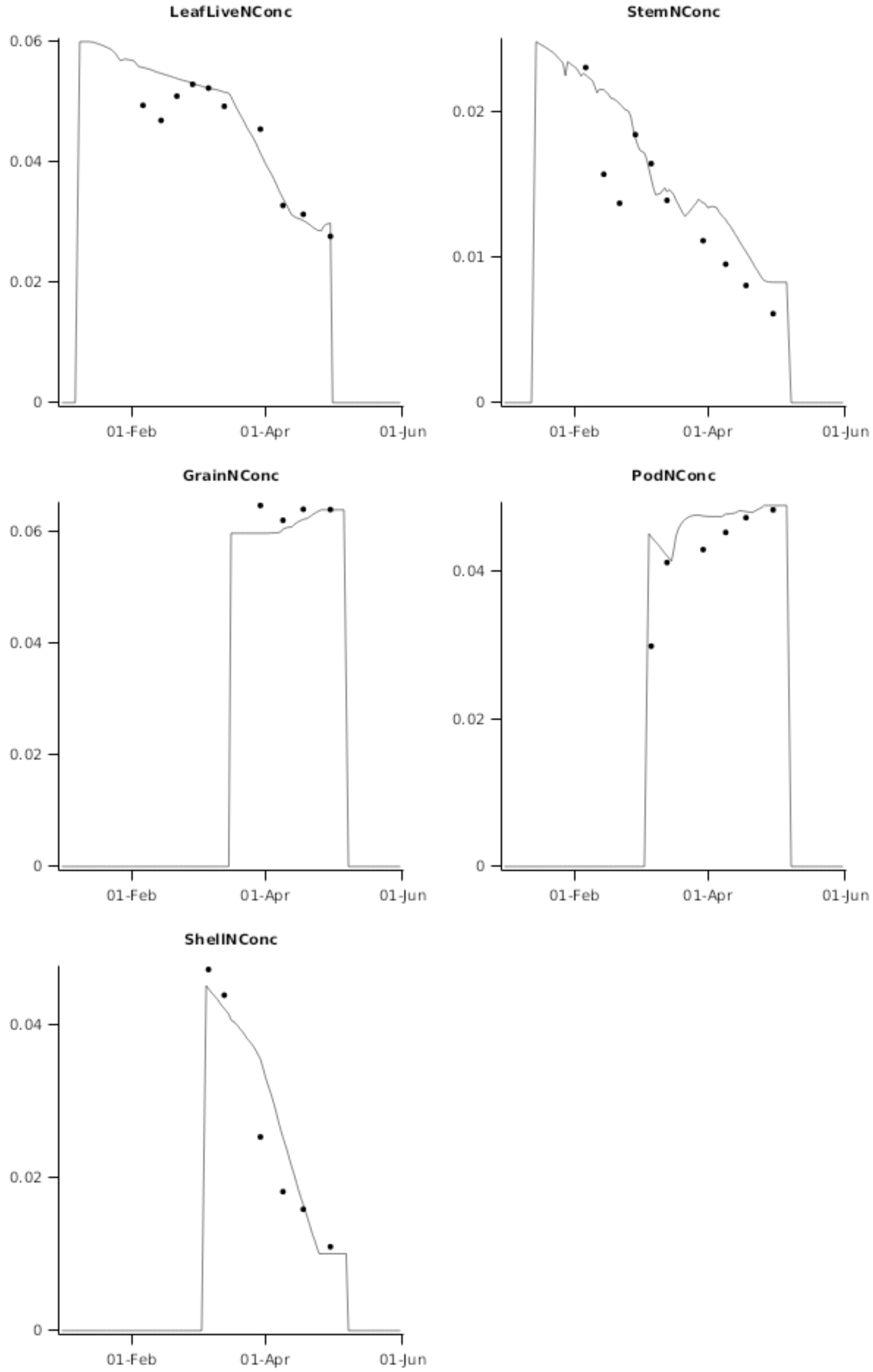




3.2.2.1.3 Nitrogen



3.2.2.1.4 NitrogenConcentration



3.2.3 Griffith

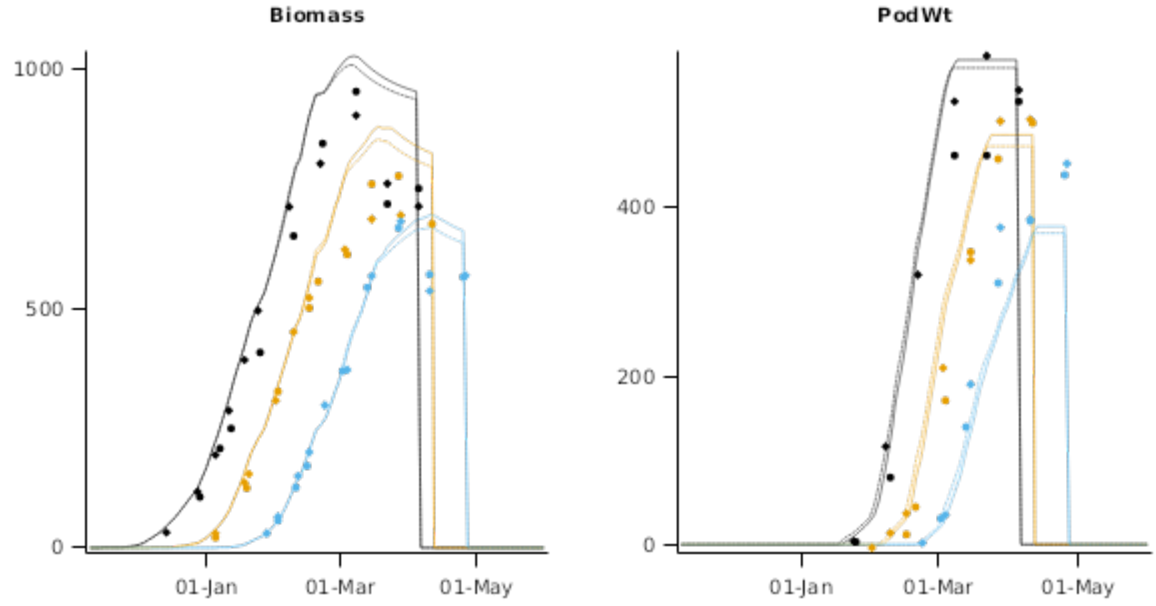
These data Timsina et al., 2007 were obtained from a field experiment conducted in 1999–2000 on a Hanwood loam soil at CSIRO Land and Water, Griffith, Australia. Two indeterminate soybean cultivars (Hooper and Stephens belonging to late maturity group [MG] 3 or early MG 4) were on 15 November, 8 December, and 6 January.

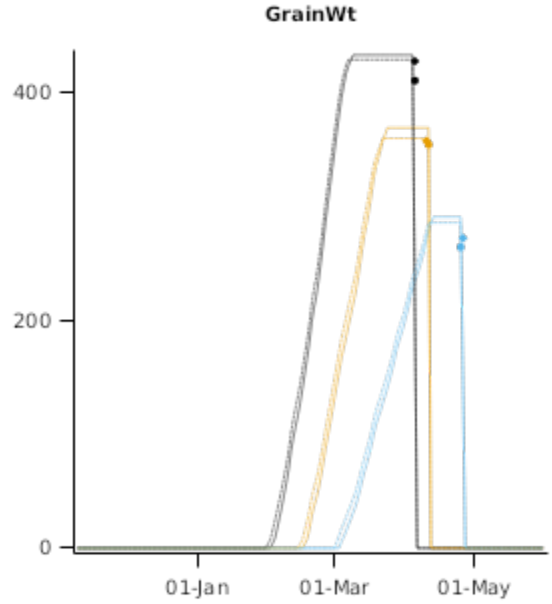
List of experiments.

Experiment Name	Design (Number of Treatments)
Griffith	Sow x Cv (6)

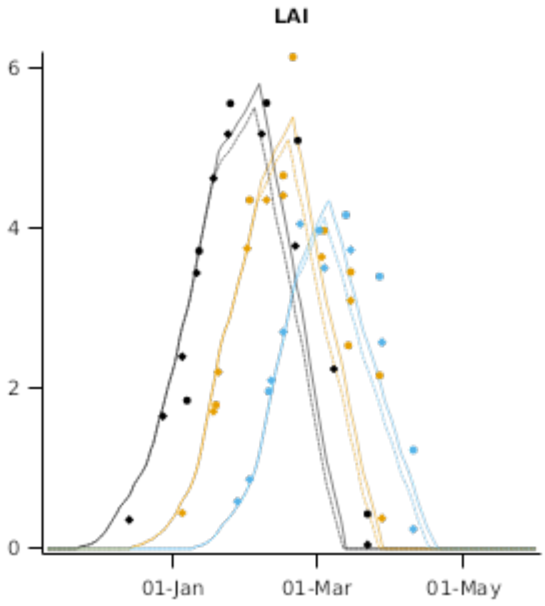
3.2.3.1 Griffith

3.2.3.1.1 Biomass





3.2.3.1.2 Canopy



3.2.4 Katherine

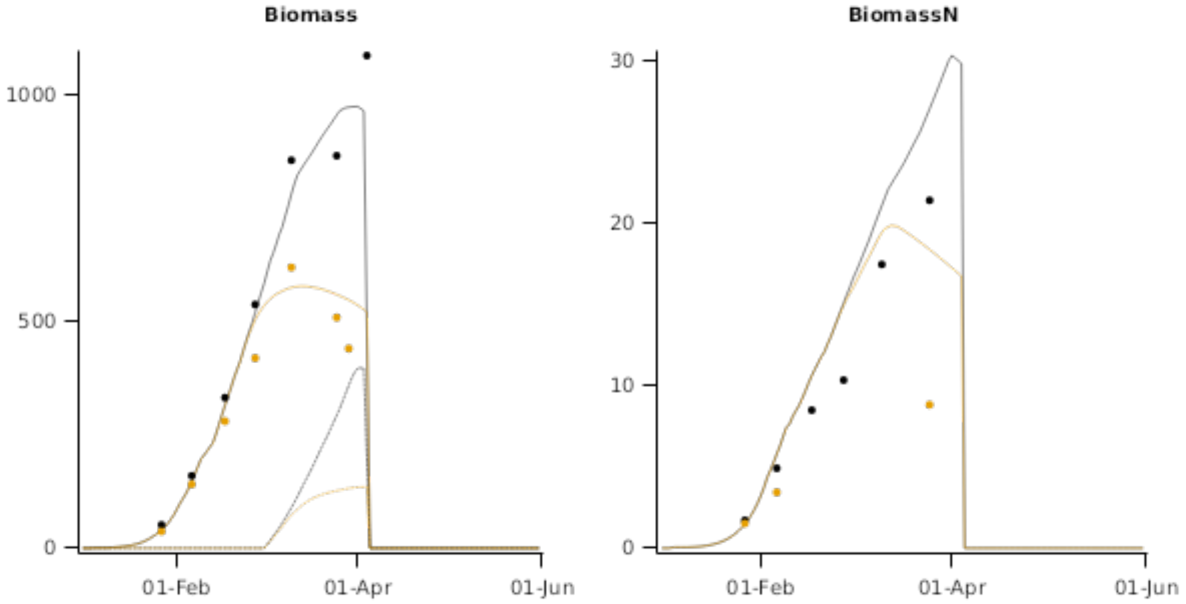
This dataset (Muchow et al., 1993) includes the cultvar "Buchanan" grown under a range of conditions in a tropical environment at the Katherin Research Station in the Northern Territory, Australia. This includes two irrigated conditions in 1988 and two planting dates in 1989.

List of experiments.

Experiment Name	Design (Number of Treatments)
Katherine1988	Water (2)
Katherine1989	Sow (2)

3.2.4.1 Katherine1988

3.2.4.1.1 Biomass



3.2.5 Kununurra

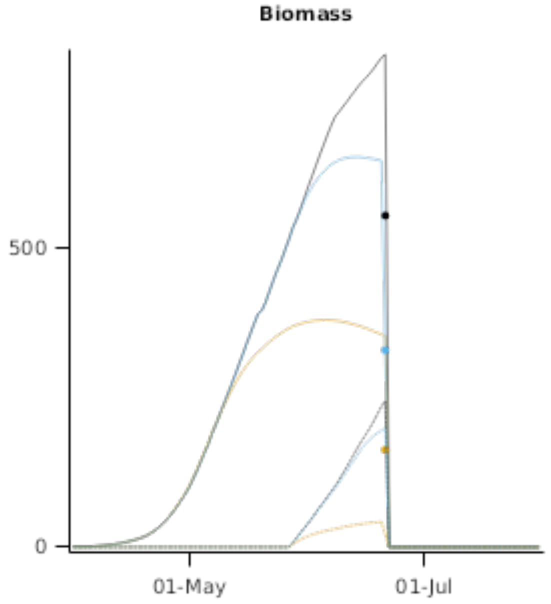
This dataset Muchow et al., 1986 includes a short-season and a long-season cultivar grown on two different soil types under both irrigated and water-limited conditions in a semi-arid tropical environment at the Kimberley Research Station (15 ° 38' S, 128°43 ' E) in northern Western Australia. Crops were grown over the winter months because of the tropical location.

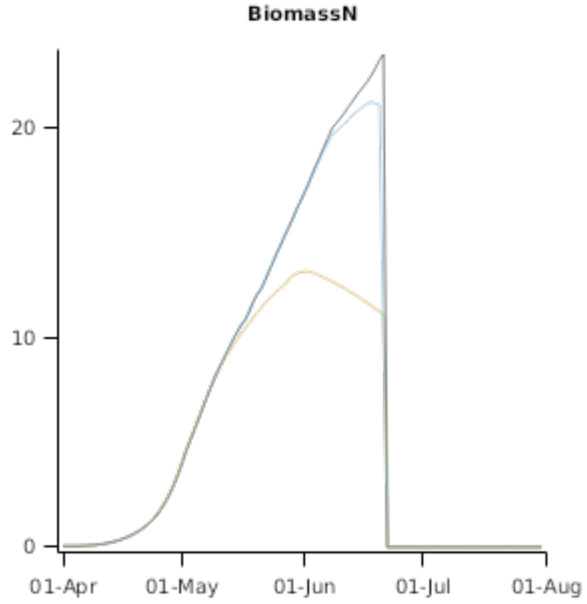
List of experiments.

Experiment Name	Design (Number of Treatments)
Kununurra1980	Water (3)
Kununurra1979	Water (3)

3.2.5.1 Kununurra1980

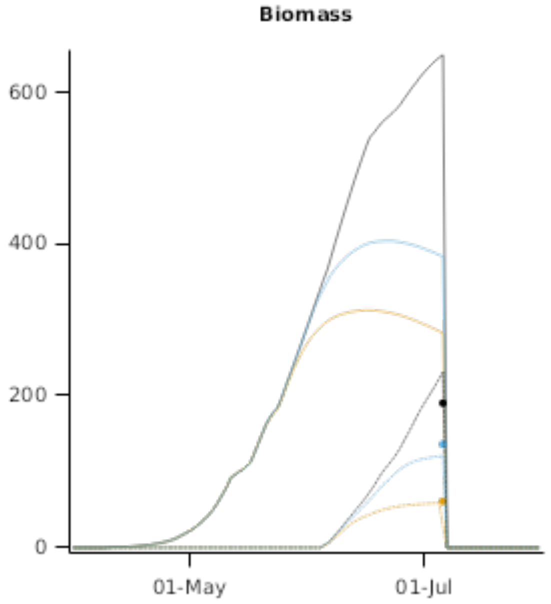
3.2.5.1.1 Biomass

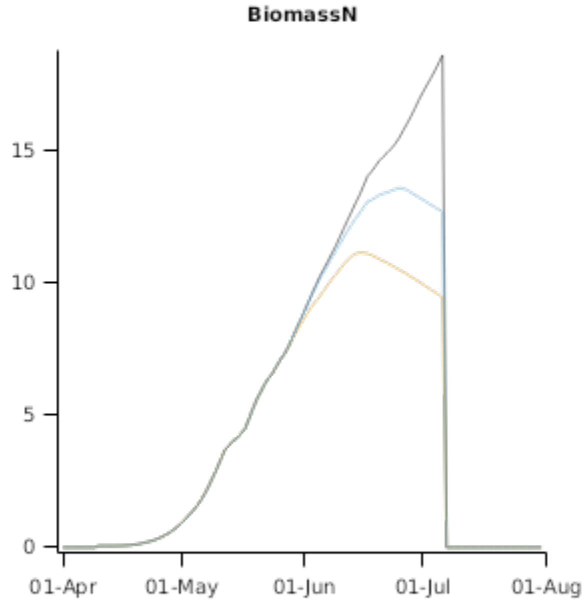




3.2.5.2 Kununurra1979

3.2.5.2.1 Biomass



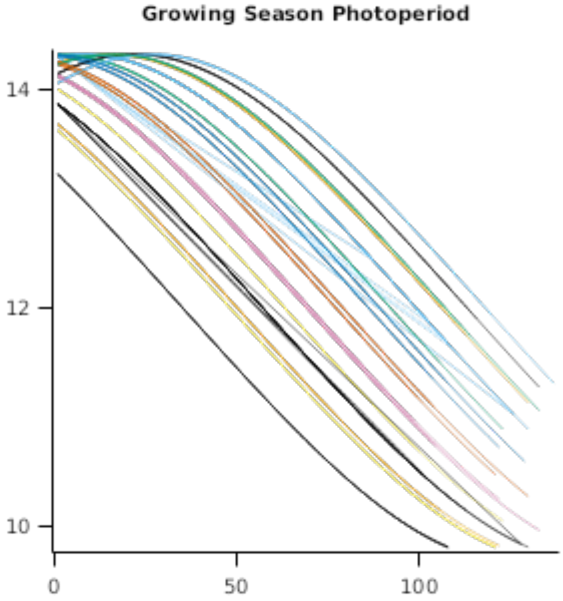


3.2.6 Leeton

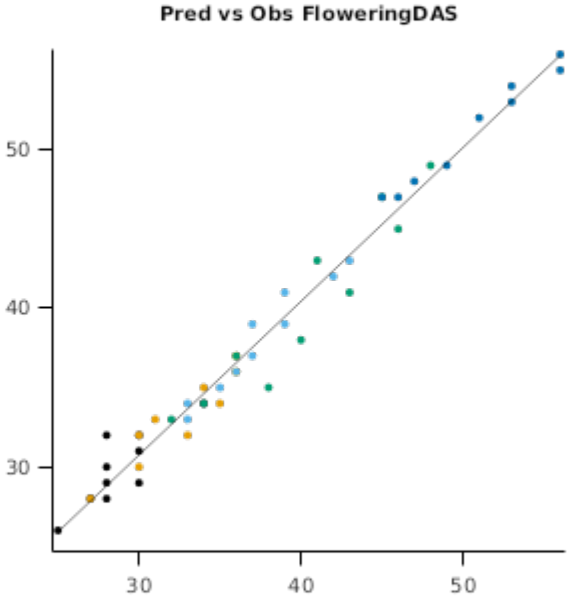
This dataset Gaynor et al., 2011 is derived from a small-plot serial sowing date study were conducted over the summers of 2006–07 and 2007–08, at the NSW Department of Primary Industries' Leeton Field Station, New South Wales, Australia (348280S, 1468250E). The soil was a grey self-mulching clay, described as a Vertosol under the Australian Soil Classification. Ten diverse soybean genotypes ranging from very early to very late maturity were grown with 10 sowing dates in the first season and 9 in the second.

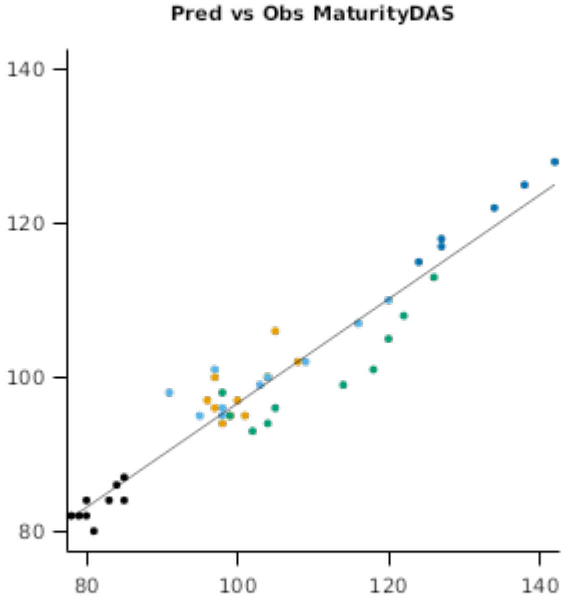
List of experiments.

Experiment Name	Design (Number of Treatments)
Leeton2006	Sow x Cv (50)
Leeton2007	Sow x Cv (45)



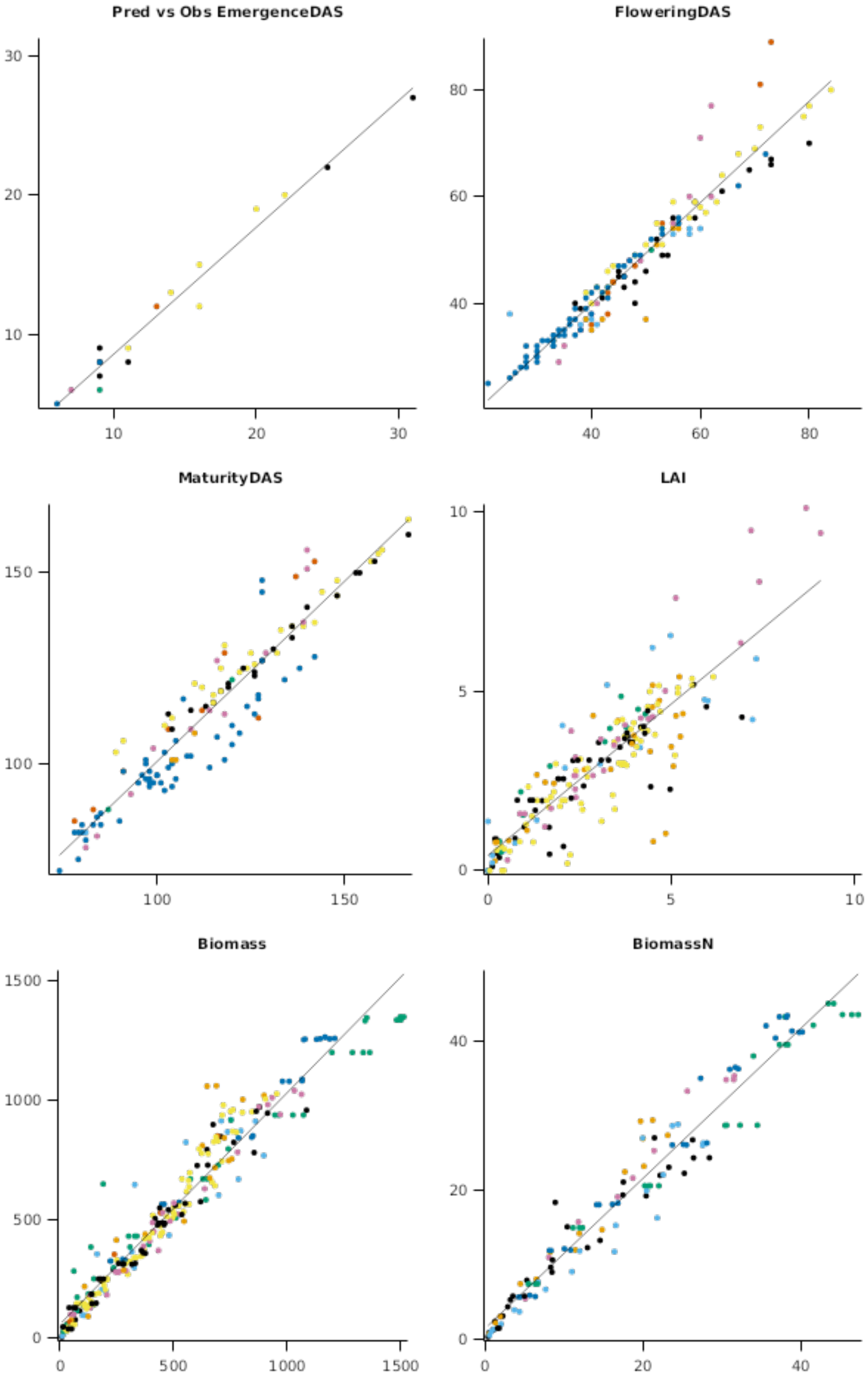
3.2.6.1 Phenology

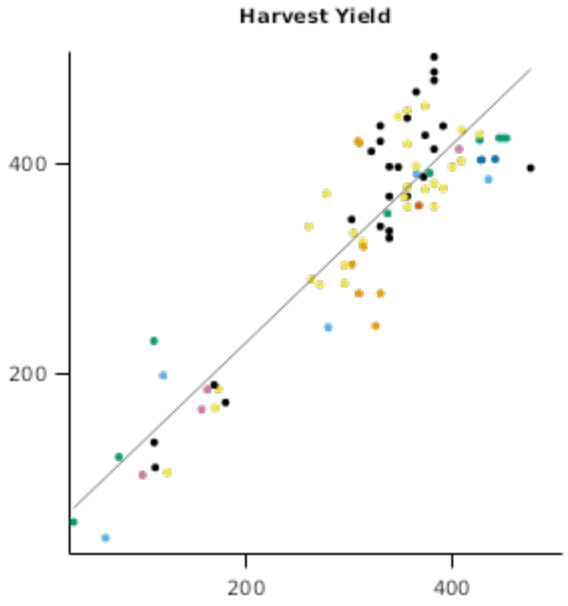


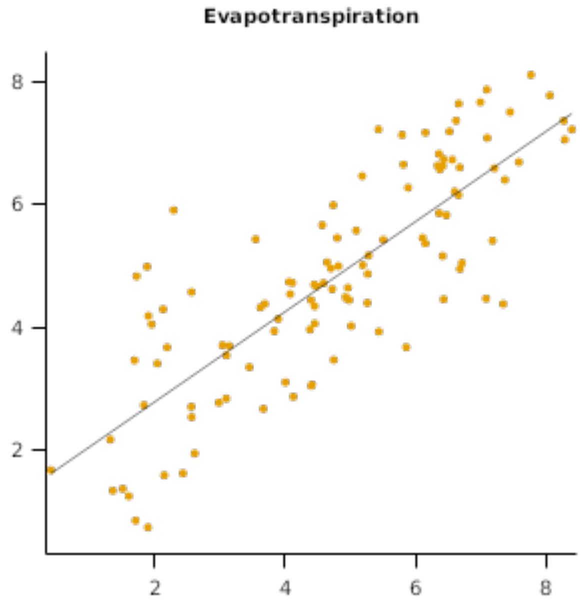


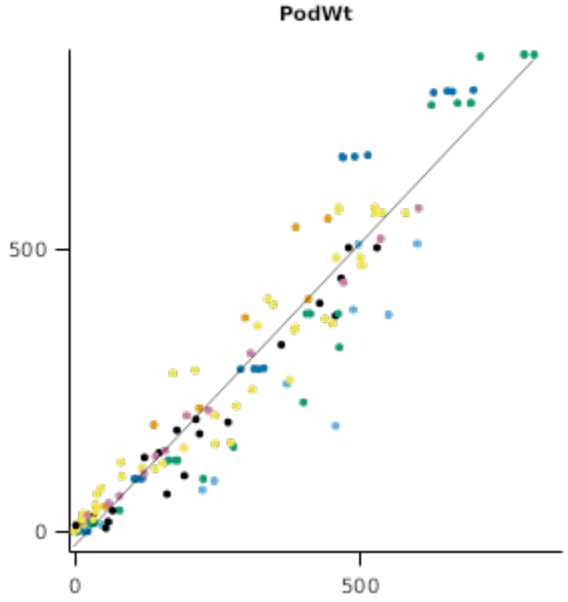
3.3 Combined Results

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


Pred vs Obs EmergenceDAS
30
20
10
10
20
30
FloweringDAS
80
60
40
40
60
80
MaturityDAS
150
100
100
150
LAI
10
5
0
0
5
10
Biomass
1500
1000
500
0
0
500
1000
1500
BiomassN
40
20
0
0
20
40







3.4 China

3.4.1 Yaan

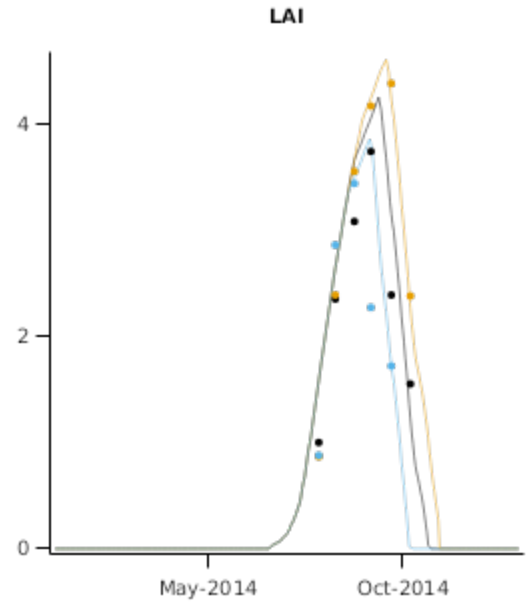
These data [Wu2019] were obtained from a field experiment conducted in 2014–2016 on a a Purple clay loam(XI-Luvic Xerosols, FAO classification) at Sichuan Agricultural University, Yaan, China. Three soybean cultivars (Jiuyuehuang,Nandou12, and Texuan13 belonging to maturity group [MG] 5-7) were sown on 15 Jun 2014, 18 Jun 2015, and 18 Jun 2016.

List of experiments.

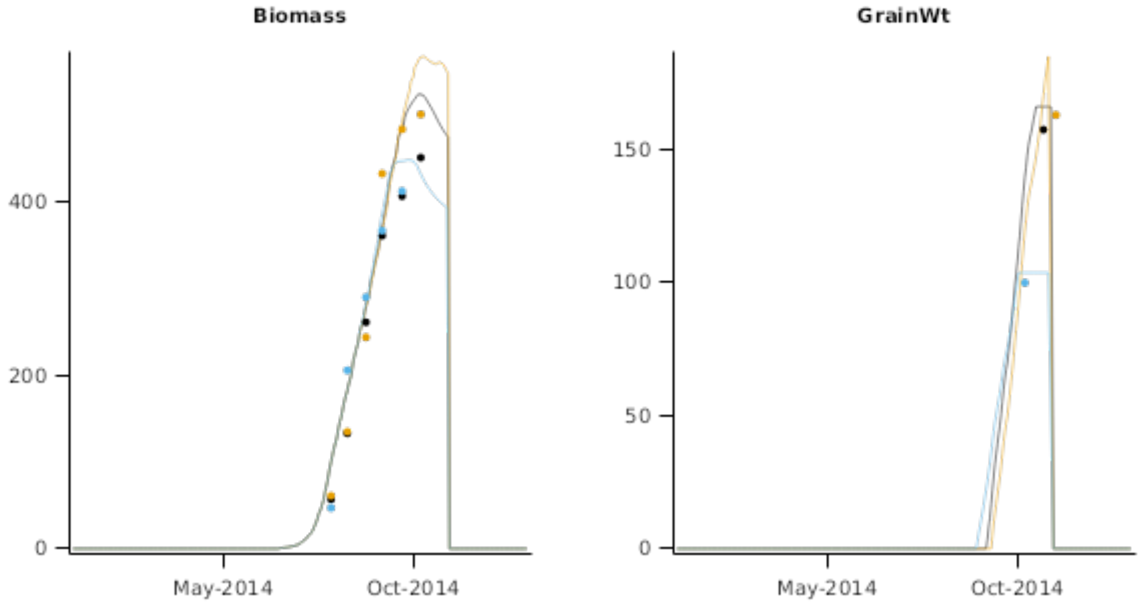
Experiment Name	Design (Number of Treatments)
Yaan2014	Cv (3)
Yaan2015	Cv (3)
Yaan2016	Cv (3)

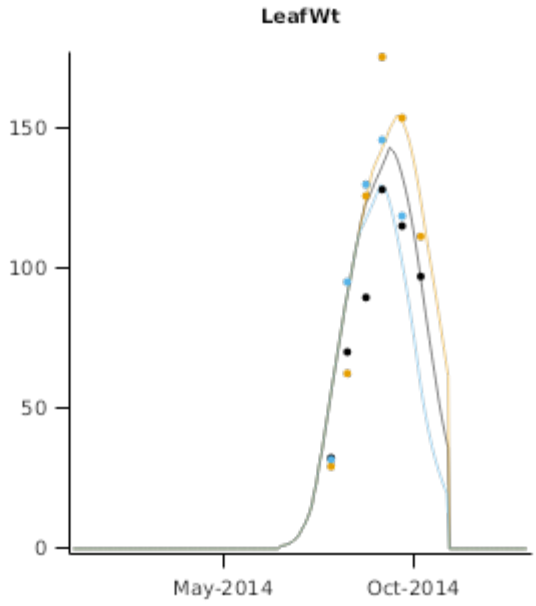
3.4.1.1 Yaan2014

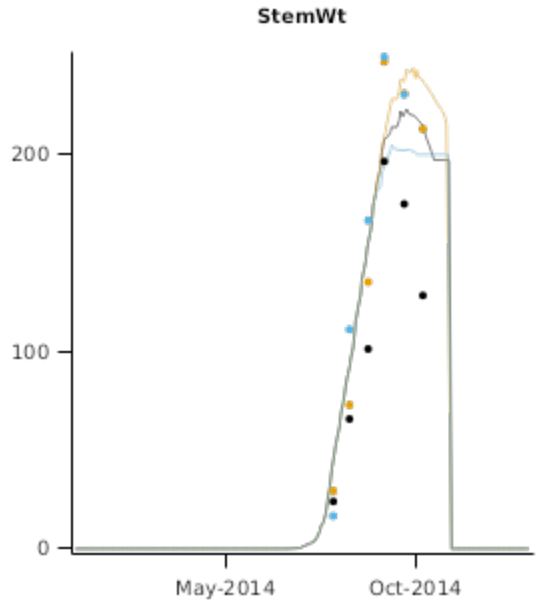
3.4.1.1.1 Canopy

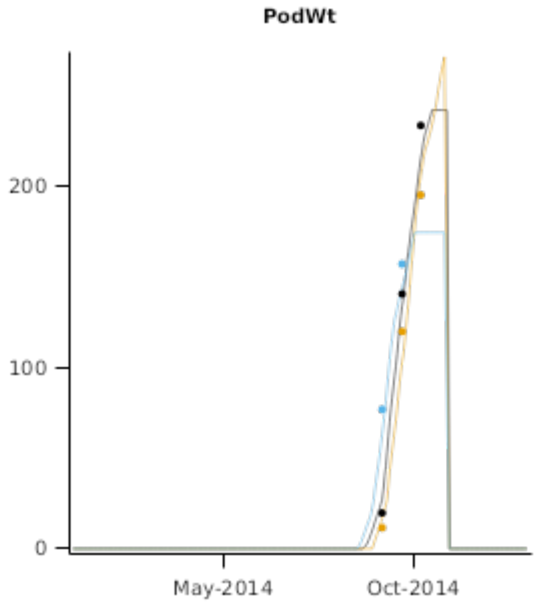


3.4.1.1.2 Biomass



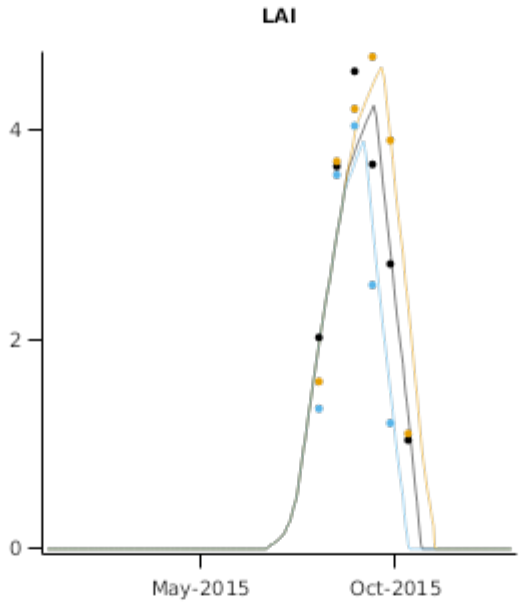




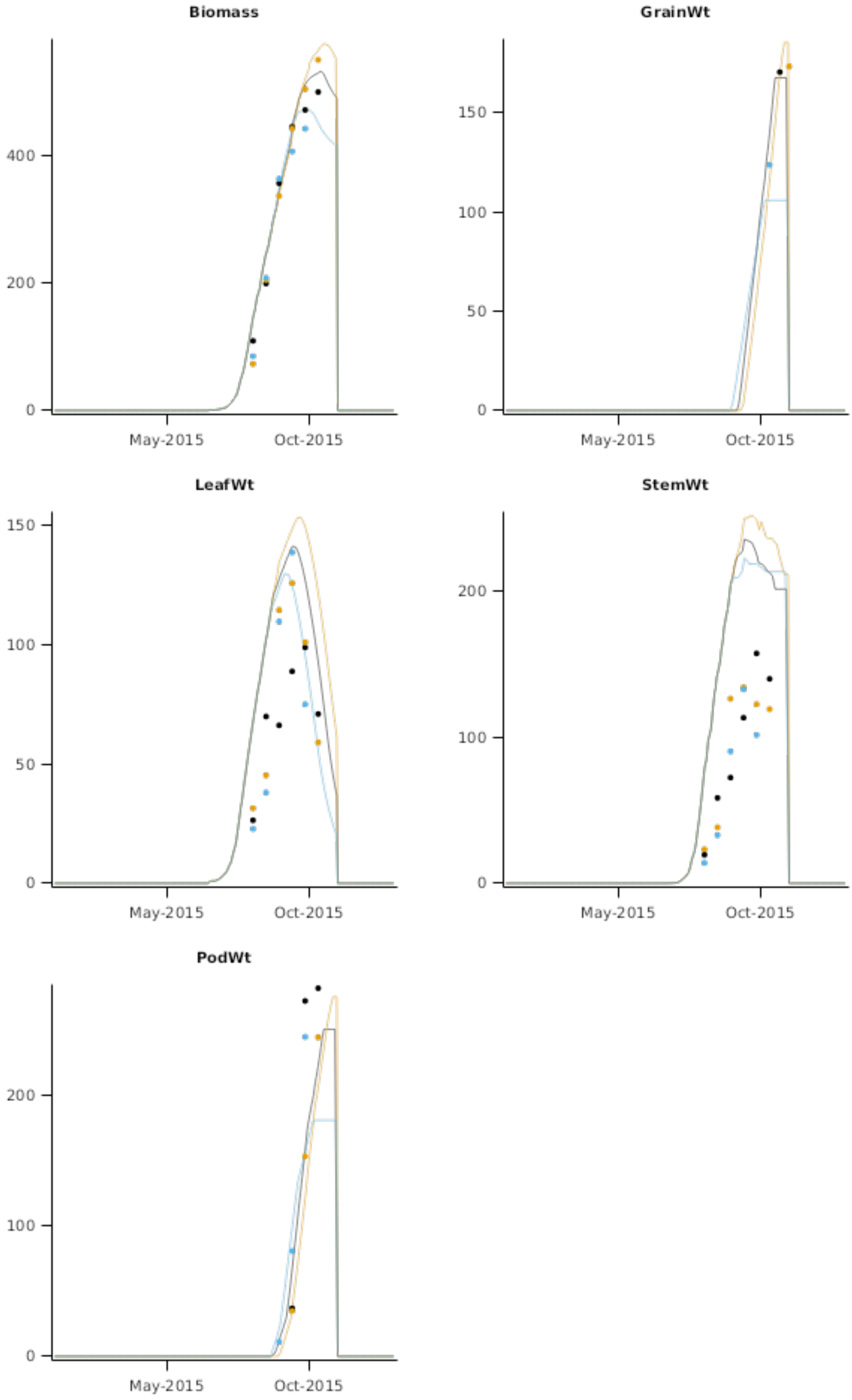


3.4.1.2 Yaan2015

3.4.1.2.1 Canopy

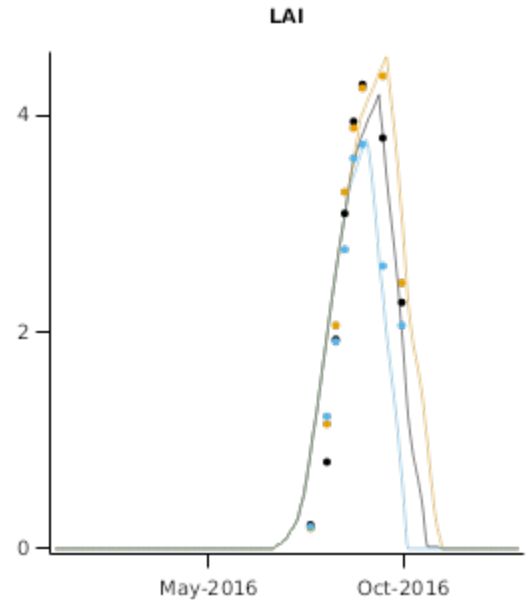


3.4.1.2.2 Biomass

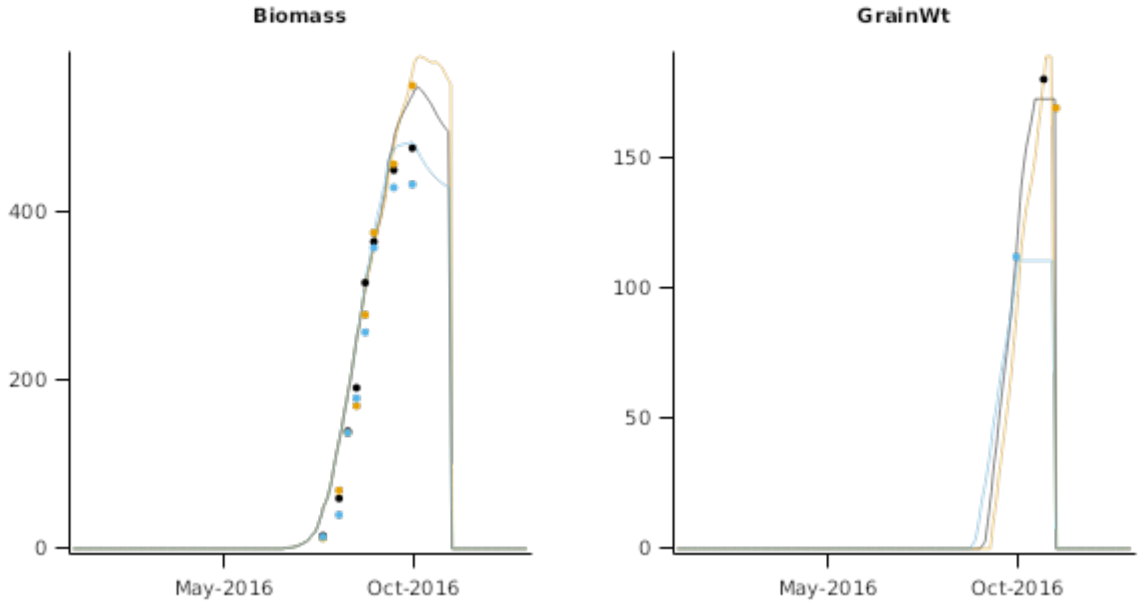


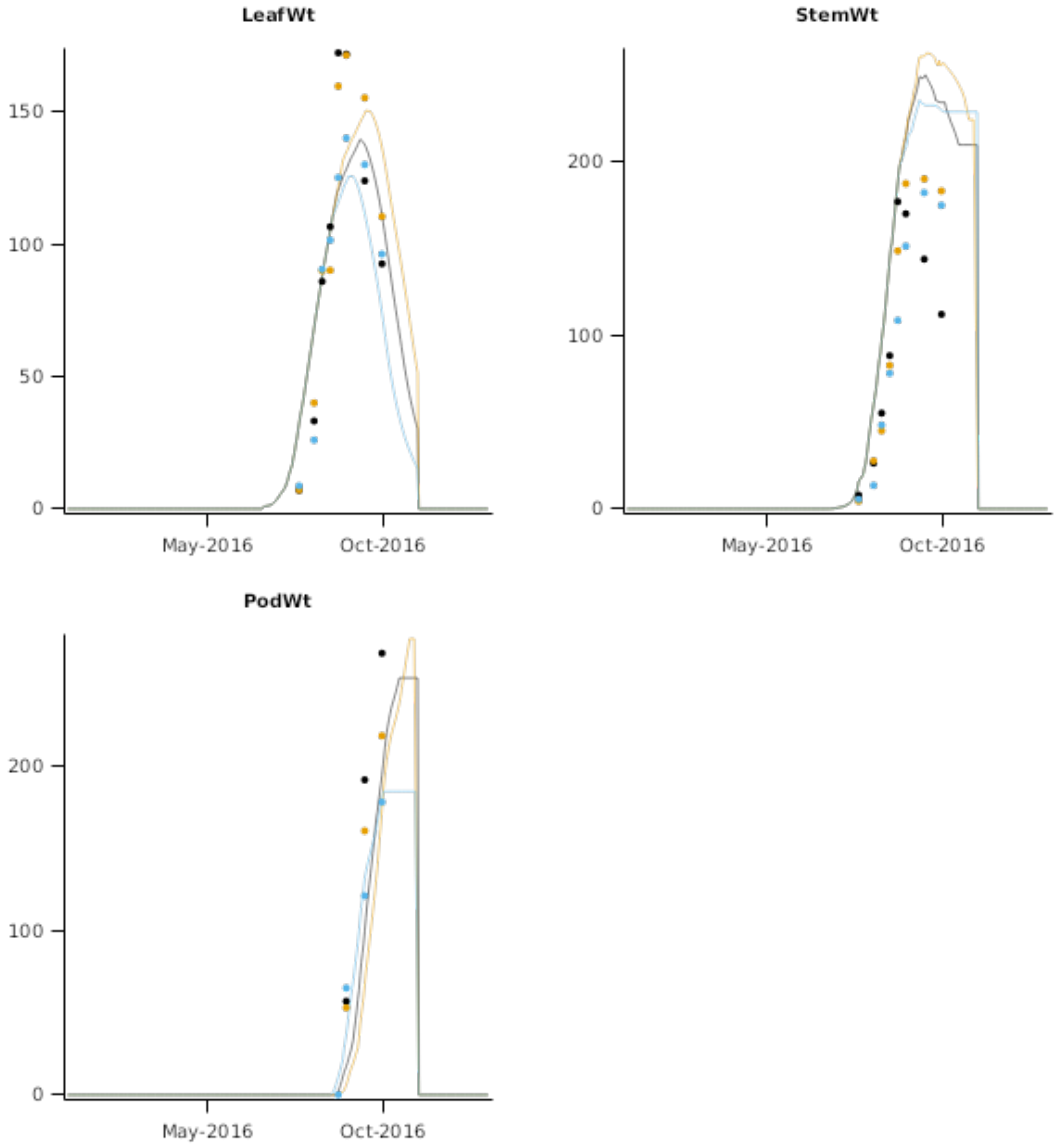
3.4.1.3 Yaan2016

3.4.1.3.1 Canopy



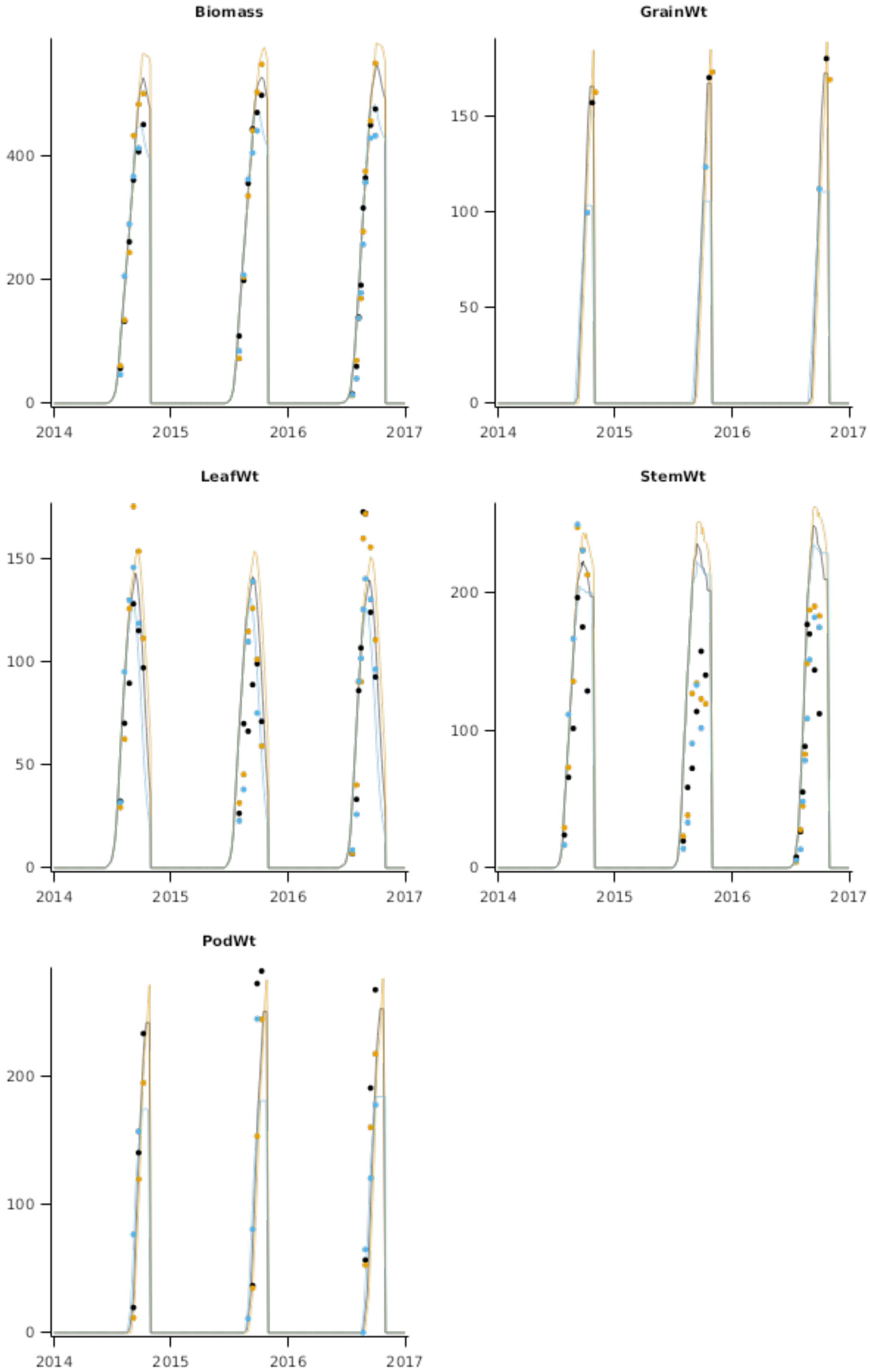
3.4.1.3.2 Biomass



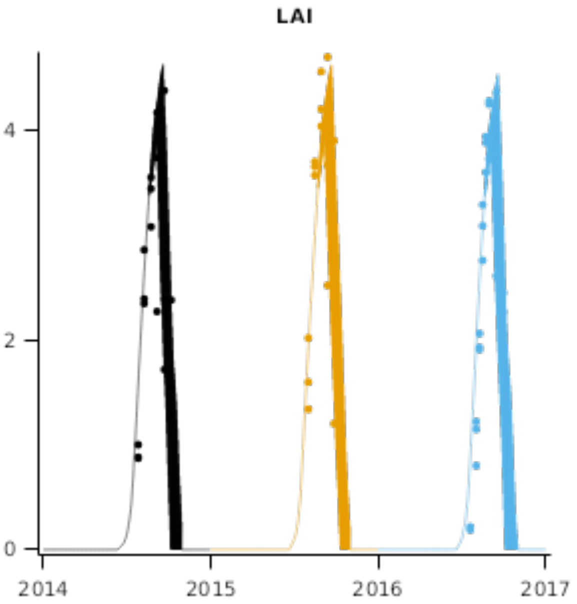


3.4.1.4 Graphs

3.4.1.4.1 Biomass



3.4.1.4.2 Canopy



3.4.2 Heze

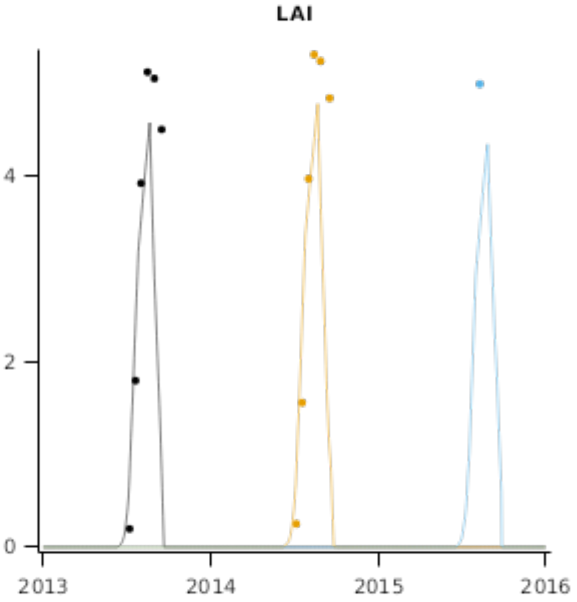
These data [Wu2019] were obtained from a field experiment conducted in 2013–2015 on sandy loam (J-Fluvisols, FAO classification) in the surface 0.5 m, changing to loam at depth with a deep soil profile (> 2 m) in Heze city, China. One soybean cultivar (Hedou19 belonging to maturity group [MG]3) were sown on 15 Jun 2014, 18 Jun 2015, and 18 Jun 2016.

List of experiments.

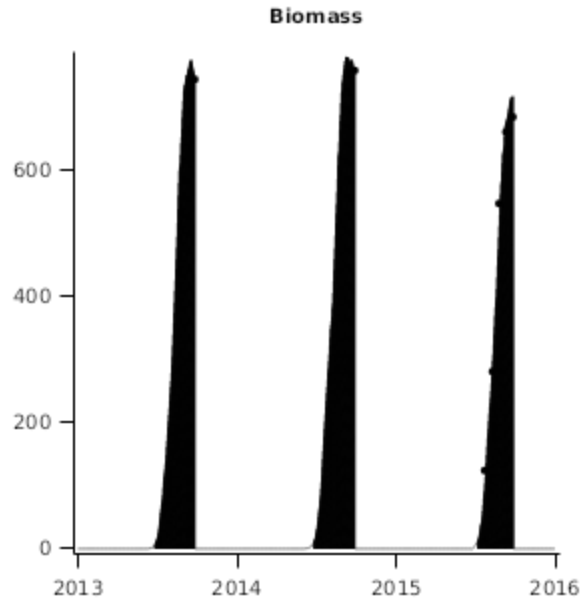
Experiment Name	Design (Number of Treatments)
Hedou19	Sow (3)

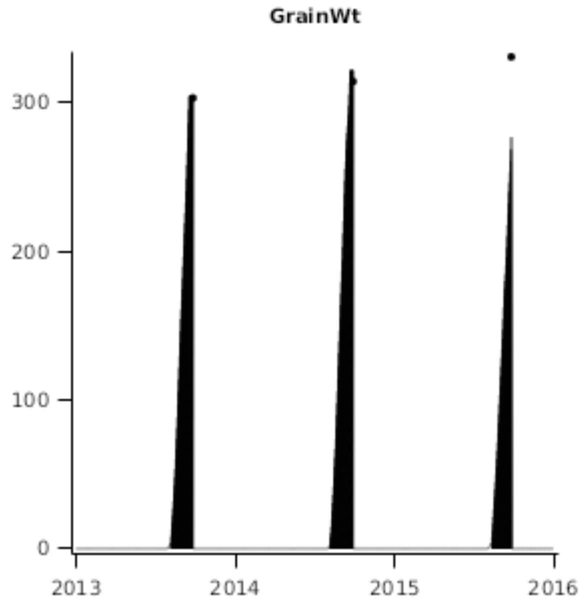
3.4.2.1 Hedou19

3.4.2.1.1 Canopy



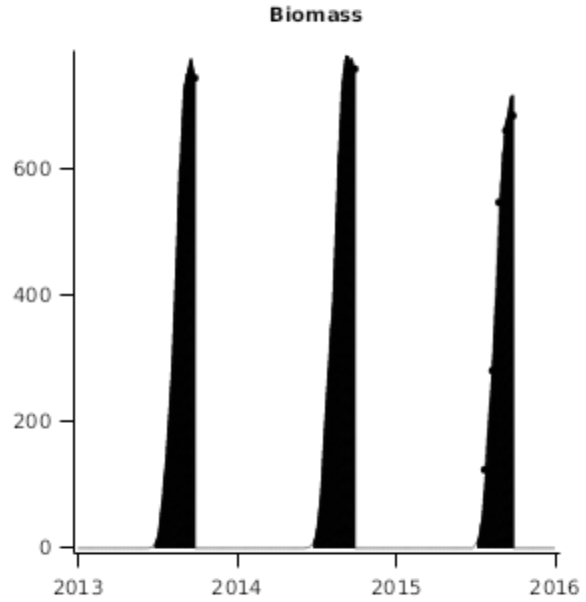
3.4.2.1.2 Biomass

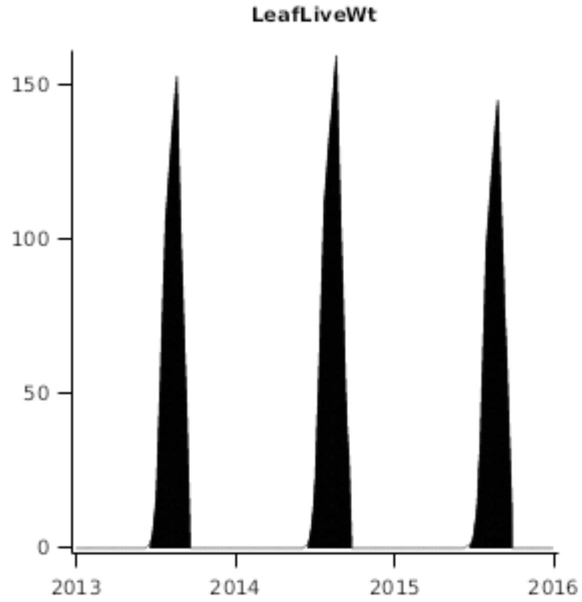


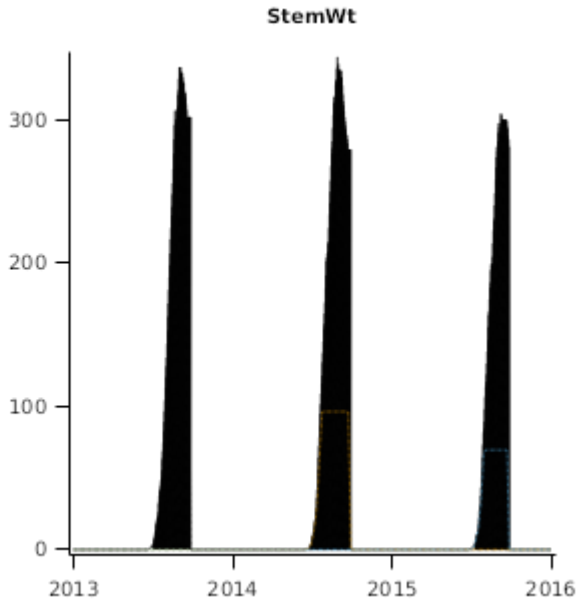


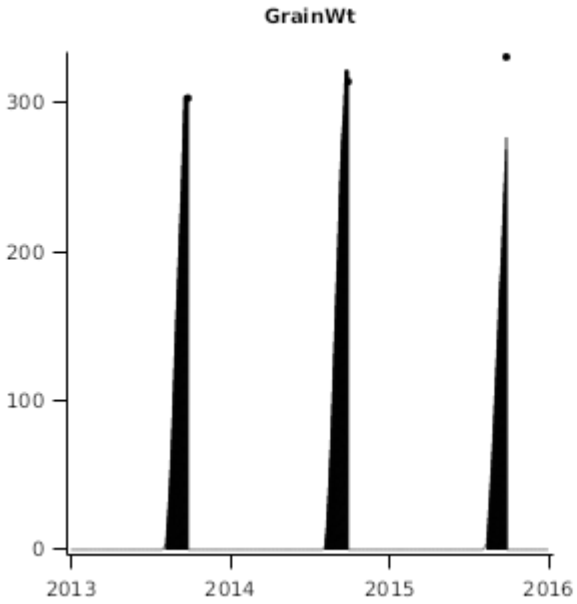
3.4.2.2 Graphs

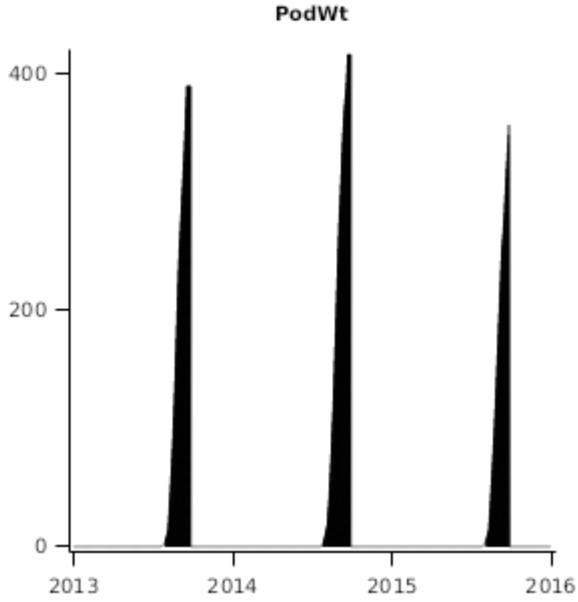
3.4.2.2.1 Biomass



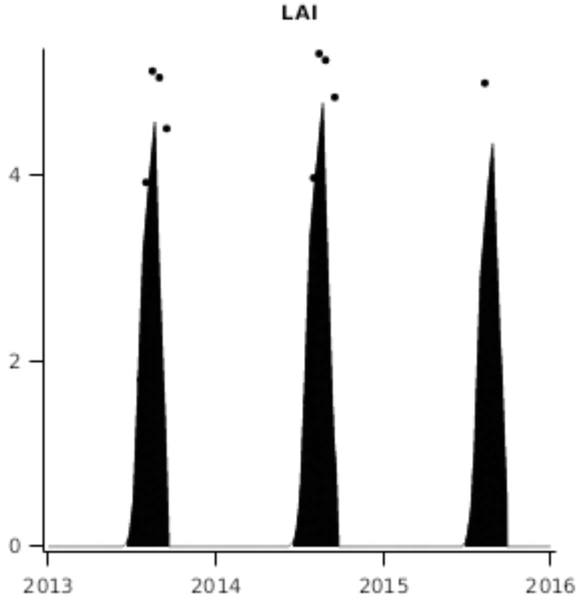








3.4.2.2.2 Canopy



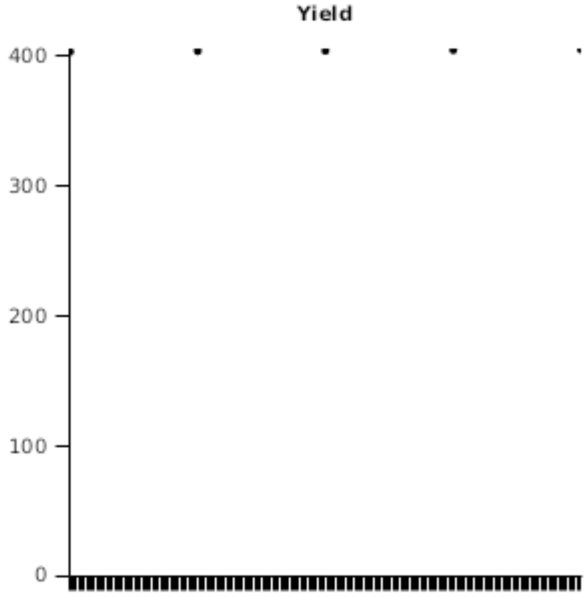
4 Sensibility

4.1 FertiliserResponse

This sensibility test checks that Soybean yield response to N fertiliser is modest under normal field conditions. A simulation experiment has been constructed to simulate yield in Nebraska for different rates of N applied at sowing. Yield variation in response to this should be low.

List of experiments.

Experiment Name	Design (Number of Treatments)
FertiliserResponse	N (5)

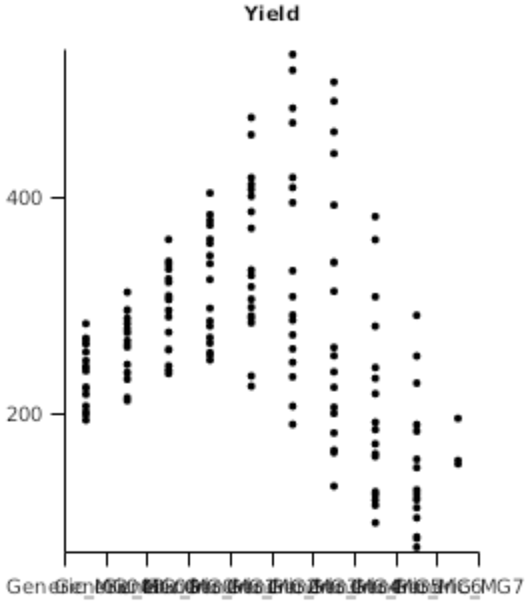


4.2 MaturityGroups

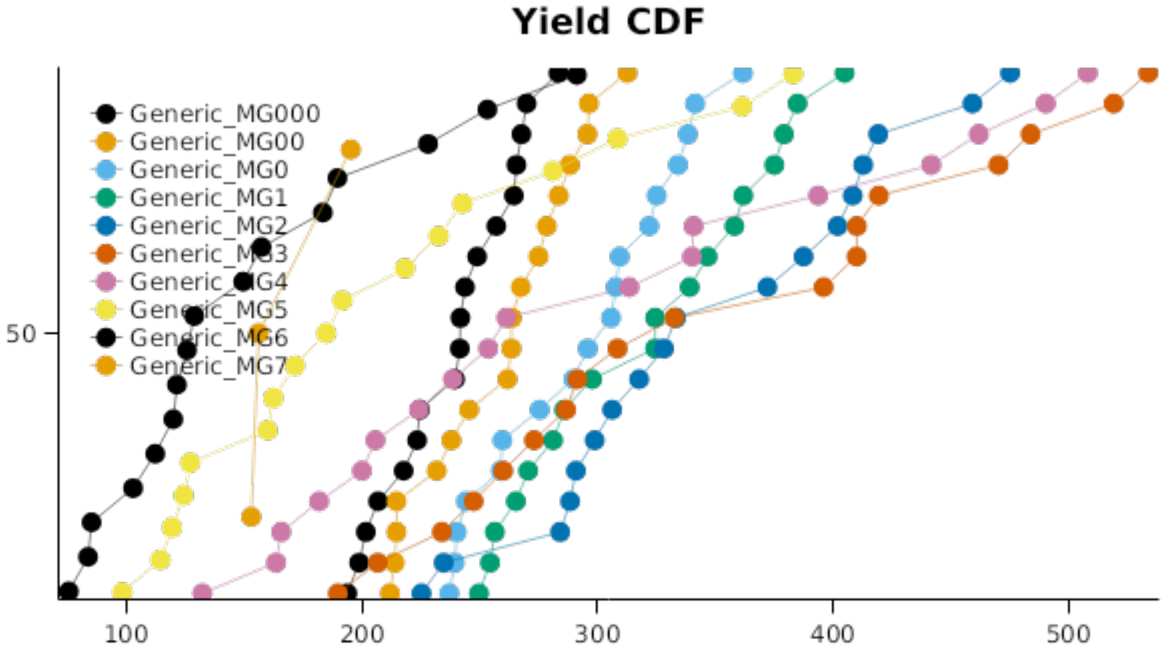
The optimum maturity class for soybean in Iowa should be approximately 2 to 3. Simulations are provided for the entire range of generic cultivars for several years at Ames, Iowa.

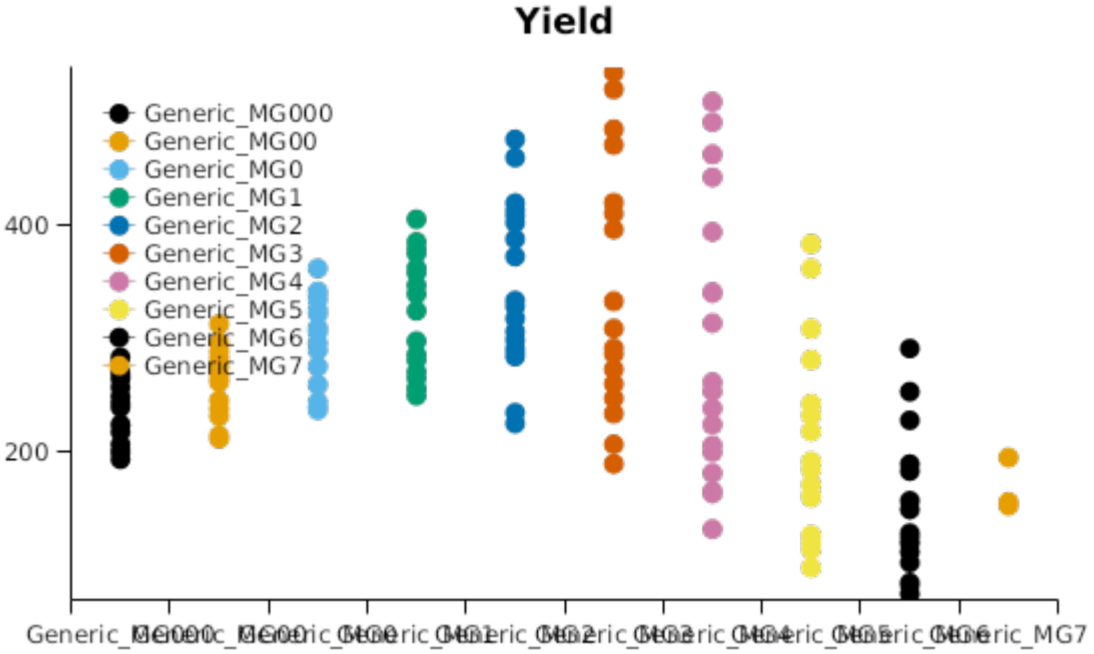
List of experiments.

Experiment Name	Design (Number of Treatments)
MaturityGroupsIowa	Cv (13)



4.2.1 MaturityGroupsIowa


Yield CDF
Generic_MG000
Generic_MG00
Generic_MG0
Generic_MG1
Generic_MG2
Generic_MG3
Generic_MG4
Generic_MG5
Generic_MG6
Generic_MG7
50
100
200
300
400
500


Yield
Generic_MG000
Generic_MG00
Generic_MG0
Generic_MG1
Generic_MG2
Generic_MG3
Generic_MG4
Generic_MG5
Generic_MG6
Generic_MG7
400
200
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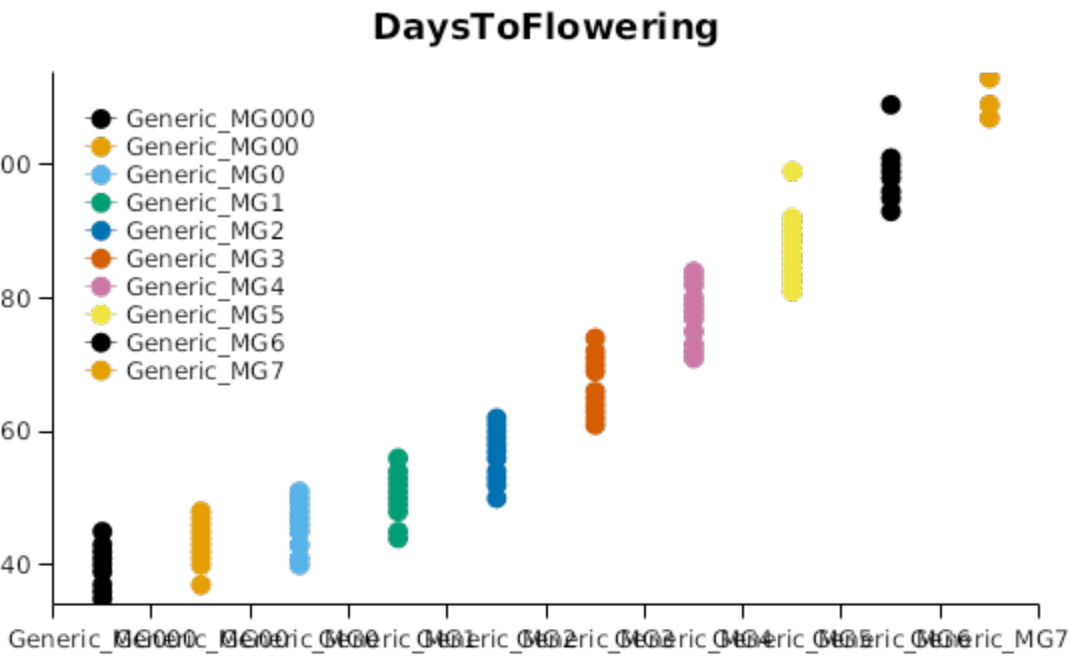
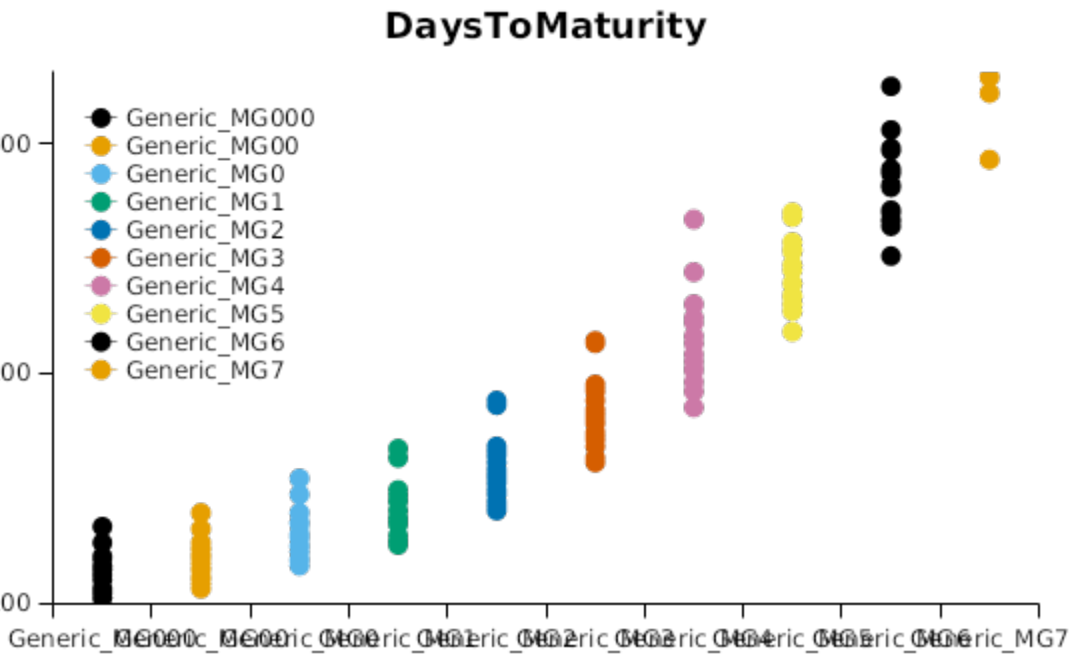
Generic_MG3
Generic_MG4
Generic_MG5
Generic_MG6
Generic_MG7



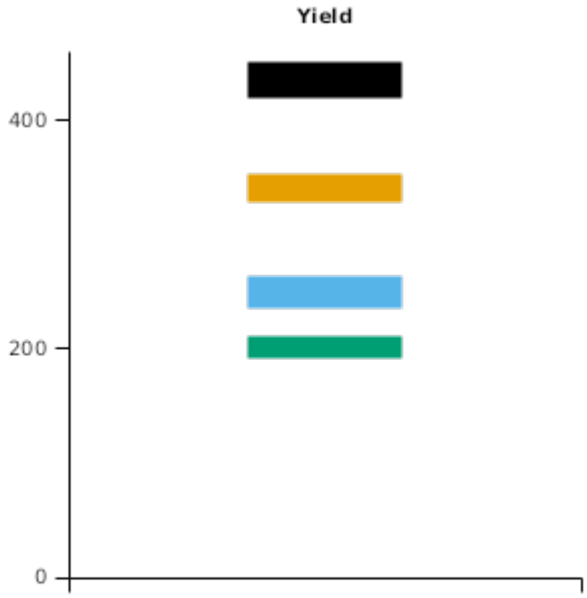


4.3 TimeOfSowing

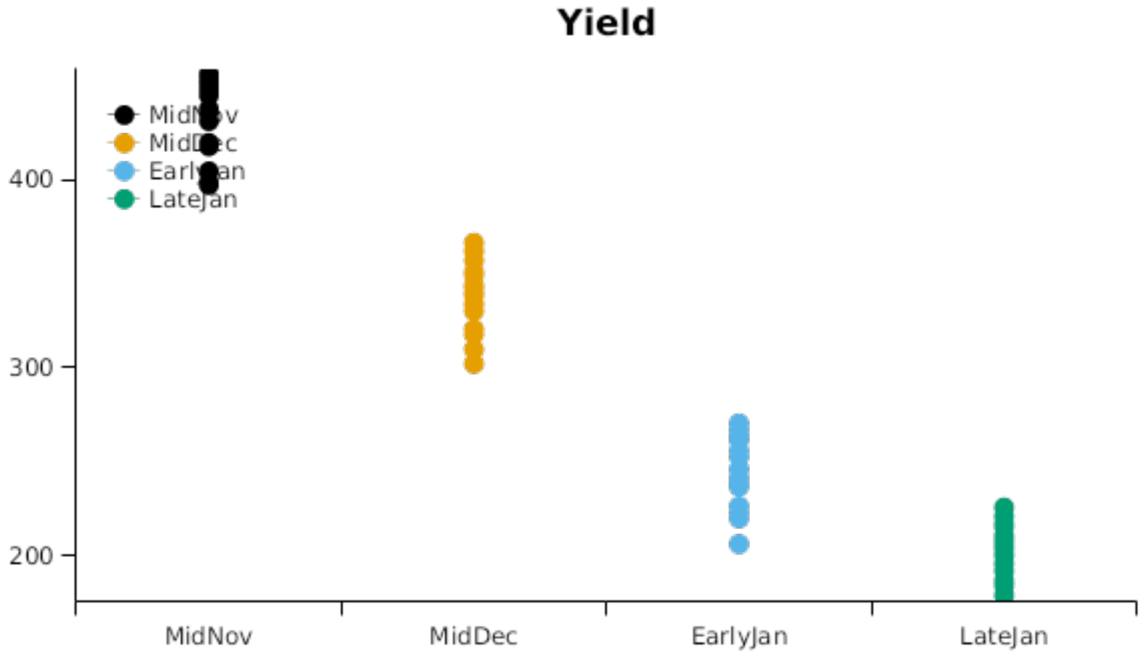
The data of Gaynor et al., 2011 show that Soybean yield should be approximately 4t/ha for early sown soybean (Mid November) in the Australian Riverina region and decrease across the growing season to lower values (1.5-2t/ha) by late January.

List of experiments.

Experiment Name	Design (Number of Treatments)
TimeOfSowingGriffith	TOS (4)



4.3.1 TimeOfSowingGriffith



DaysToFlowering

DaysToMaturity

4.4 DetailedDynamics

List of experiments.

Experiment Name	Design (Number of Treatments)
DetailedDynamics	Sow (1)

5 References

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