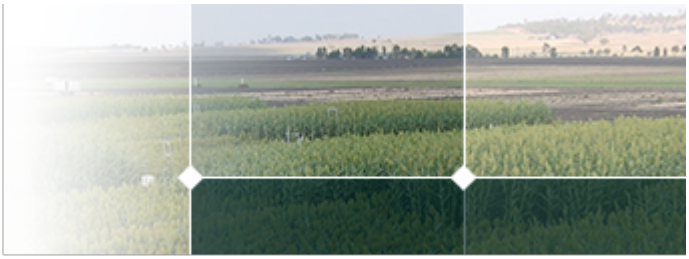

1 The APSIM RedClover Model

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1.1 Introduction

Red clover (*Trifolium pratense*) is a herbaceous perennial herb in the Fabaceae family (former Leguminosae) native of Europe, west Asia, and north Africa (Hay, 1985; Frame et al., 1998; Black et al., 2009). It can now be be found in swards around the world in places with temperate and subtropical climates. Although considered a perennial, red clover plants are typically short-lived in grazed conditions (2-4years). The plant has deep taproots and long segmented semi-erect stems. From each stem segment tri-foliate leaves grow alternately and from their axils a flower stalk (peduncle) may grow, petioles are 1-4 cm long. Roots are quite thick and can reach depths greater than 2.0 m. The inflorescence is typically pink/red and grows from peduncles that are less than 1cm long. As a legume, red clover can host N-fixing bacteria (*Rhizobium*) in a symbiotic relationship; from this, large quantities of N from the atmosphere can be incorporated to the soil (Heichel et al., 1985; Chmelikova et al., 2015). This is a major reason why red clover is sown alongside grasses in pastures, although red clover is also a valuable forage grown in monoculture, producing very high quality feed and is highly palatable to ruminants.

Objective: The model presented here was built using the Plant Modelling Framework (PMF) of Brown et al., 2014 to simulate the growth of red clover as forage crop. The model current focus is on describing biomass accumulation and regrowth after harvest on monocultural swards. As a derivate of APSIM's PMF, it is readily possible to use the red clover model for mixed swards, but this has not been properly tested yet and should be done with caution. The number of datasets available for the inital development of the model was quite limited, including data from only two environments and from experiments varying irrigation or fertiliser rates. It is expected that more datasets will be added in the future to broaden the tests and support model improvements.
The simulation of variations in N concentration over the growing season can also be considered as incipient and only reasonably good. The model should be updated and its performance revised in the future when more data becomes available.

Note: The model structure and paramaters were developed based on findings and data collated from a literature review and supported by analyses of the datasets presented in the validation section. Thus, the data from these datasets were not explicitly separated for calibration and validation. This was done firstly because calibration of any parameter against these data was minimal, and secondly because there was a limited amount of data and thus dividing them would be counter-productive. This would limit even more the amount of data and increase uncertainties, the method used to separate the data could become more important to define the success of the model calibration or validation than the model itself(e.g. Sinclair et al., 2000; Mourad et al., 2005).

1.2 Presentation

This model has been built using the Plant Modelling Framework (PMF) of Brown et al., 2014 to simulate the growth of red clover (*Trifolium pratense*) as a forage crop. The model focus primarily on describing the vegetative growth, with a simplified account of the reproductive phase, without explicit considering flowers and seeds. The red clover model simulates the above ground plant structure, including the photosynthesis process, using the SimpleLeaf procedure of PMF, which does not consider explicitly leaf age or placement in the canopy. The model describes a perennial crop, with phenology rewinding to the vegetative stage at the end of the reproductive phase.

1.3 Inclusion in APSIM simulations

To include red clover in a simulation the procedure is the same as any other APSIM crop:

- The red clover object can be dragged or copied from the Crop folder in the toolbox into a Field in your simulation;
- To become active and grow, the red clover crop needs to be sown using a manager script with a sowing rule. e.g.:

If a specified cultivar is not available, a fatal error will be thrown.

1.4 Harvest and biomass removal

Red clover biomass can be removed by raising one of the valid methods: Harvest, Cut, Graze, or Prune; this is done using a manager script, similarly to other crops. The proportion of the biomass of each organ that is removed from the system and/or added to the residue pools may be specified; otherwise defaults will be used. Note that the sum of fractions removed and added to residue should be <= 1.0. To specify the proportions for removal in a manager script, use a RemovalFractions class as shown below:

The RemovalFractions class can be sent with Harvest, Cut, Graze, or Prune events. All parameters are optional, defaults are used whenever any value is not specified.

1.5 Crop termination

To fully terminate a crop the EndCrop event should be raised:

Once a crop has been ended the field is open to be used by another APSIM plant model, or another red clover crop. Note that ending red clover is not necessary before sowing another crop, competition for resources will take place between crops when there is more than one in the field.

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
Phenology	Models.PMF.Phen.Phenology
Arbitrator	Models.PMF.OrganArbitrator
Leaf	Models.PMF.Organs.SimpleLeaf
Petiole	Models.PMF.Organs.GenericOrgan
Stem	Models.PMF.Organs.GenericOrgan
Inflorescence	Models.PMF.Organs.GenericOrgan
Nodule	Models.PMF.Organs.Nodule
Taproot	Models.PMF.Organs.GenericOrgan
Root	Models.PMF.Organs.Root
ShootRootRatio	Models.Functions.PhaseLookup
TargetShootRootRatio	Models.Functions.PhaseLookup
TargetAboveGroundFraction	Models.Functions.PhaseLookup
LowerAllocationFractionAboveG	Models.Functions.MaximumFunction
UpperAllocationFractionAboveG	Models.Functions.MinimumFunction
DeltaAnnualDayLength	Models.Functions.LinearInterpolationFunction
MortalityRate	Models.Functions.Constant

1.6 Phenology

The phenological development is simulated as the progression through a series of developmental phases, each bound by distinct growth stage.

The duration of each phenological phase in red clover is controlled either by the accumulation of thermal time or photoperiod.

1.6.1 ThermalTime

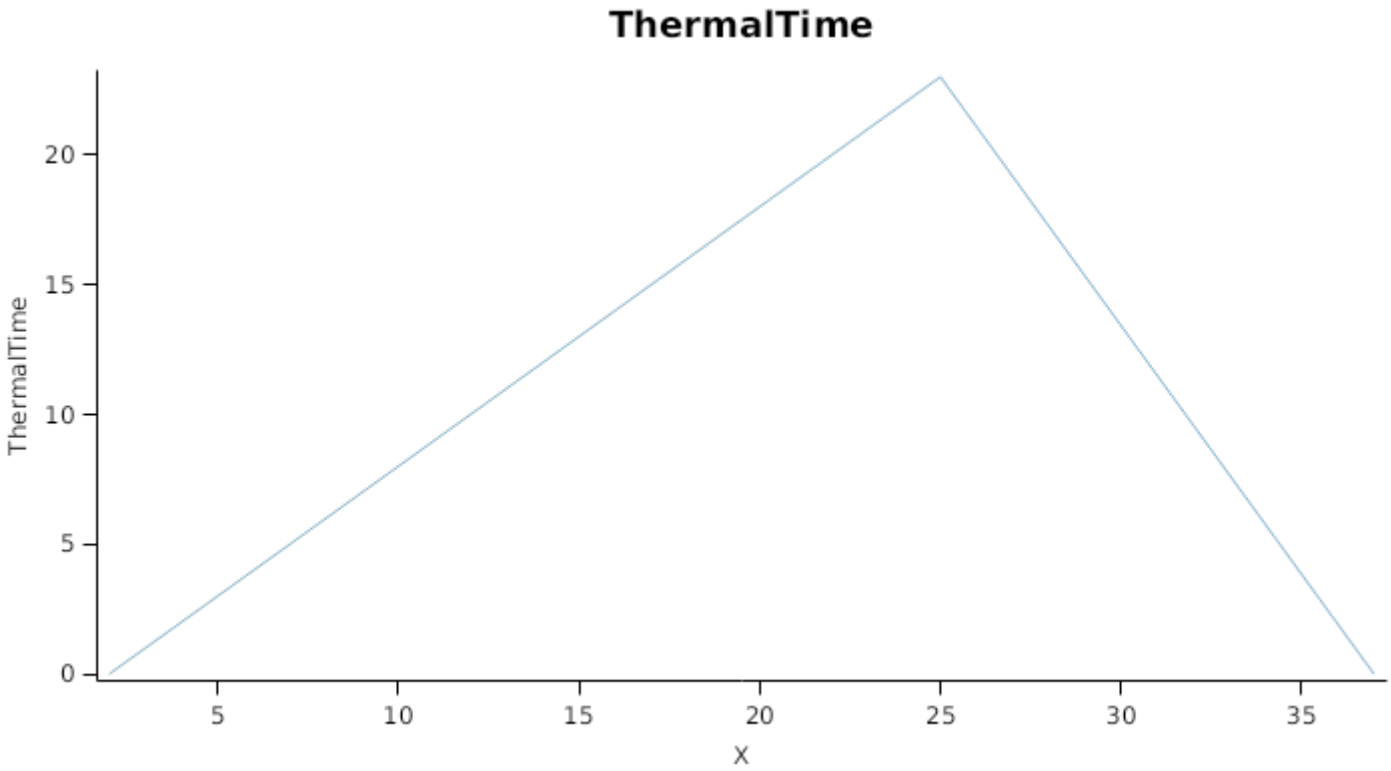
ThermalTime is the average of sub-daily values from a XYPairs.

The thermal time is used to control many of the phenological changes in red clover. It is calculated using the daily average temperature and three parameters, or cardinal temperatures: minimum, maximum, and optimum. Plant development accelerates as temperature increases from minimum to optimum and slows down after that, ceasing completely at maximum temperature. There is little information about these thresholds for red clover, especially about their variation between cultivars. The minimum, or base, temperature seems to vary from -1.0 to 5oC (Hampton et al., 1987; Monks et al., 2009; Moot et al., 2000). Even less data is found for the other parameters, and they are quite variable too; optimum temperature is around 25oC and 35oC for maximum temperature (Black et al., 2009; Monks et al., 2009).

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 ThermalTime

X	ThermalTime
2.0	0.0
25.0	23.0
37.0	0.0



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

Phase Number	Phase Name	Initial Stage	Final Stage
1	Germinating	Sowing	Germination
2	Emerging	Germination	Emergence
3	Vegetative	Emergence	Induction
4	Inductive	Induction	Flowering
5	Reproductive	Flowering	Ripening
6	GotoPhase	Ripening	Emergence

1.6.2 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.

Germination in most clover species is very variable (e.g. Hampton et al., 1987; Murray, 2012), with about 60-85% of seeds germinating for red clover. Temperatures between 5 and 20oC do not affect germination rate, but do slow it down (Hampton et al., 1987). The model does not consider variable germination rate, thus the population should be adjusted by the user to account for less than 100% germination when sowing. Also, following default PMF behaviour, red clover germination will occur one day after sowing, provided that the amount of soil extractable water is greater than zero.

1.6.3 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 = 15 (deg day/mm),

ShootLag = 50 (deg day),

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

Red clover has small seeds and these need to be placed near the soil surface to emergence successfully. Best emergence rate occur when seeds are sown at depth of 5mm (Hyde, 1950; Murray et al., 1993), and few plants will emerge from seeds deeper than 40mm. Variations in germination rate due to depth are not currently simulated by the model, however the sowing depth does affect timing of emergence, in combination with temperature. This is controlled by the parameter ShootRate, which is the shoot elongation rate as function of thermal time (mm/oCd).
Emergence of red clover occur a few days after germination (Hyde, 1950; Moot et al., 2000), but this is quite variable (taking 5-20 days). Both temperature and depth of seed are important factors. Thermal time for the emergence of red clover (cv. Huia and Nomad) has been reported as being approximately 150oCd (Moot et al., 2000; Murray, 2012), and there seem to be no significant variations between NZ cultivars (Hampton et al., 1987).

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

ThermalTime = [Phenology].ThermalTime

1.6.4 Vegetative

This phase goes from emergence to induction.

During this phase, red clover plants allocates new biomass to only leaf+petiole, stems, and root+taproot organs. Initially, this phase starts when plants emerge, but it is also triggered as phenology resets after the end of the reproductive phase. The vegetative phase ends when the inductive phase starts.
Red clover is a long day species, with flowering starting in spring when day light is increasing (Aitken, 1964; Bowley et al., 1987; Fagerberg, 1988), and although temperature has a small effect on flowering date and intensity, red clover does not need vernalisation to start flower initiation. Red clover plants can flower on the same year of planting, if that is done early enough in spring, but swards sown in later summer and autumn will not be developed enough to start flowering before the winter. The model uses accumulation of days under favourable conditions (mild temperature) to trigger the change of phase from vegetative to inductive to ensure that flower is not triggered in autumn.

The *Target* for completion is calculated as:

Target = 500 (oCd)

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

Progression = [Phenology].ThermalTime

1.6.5 Inductive

This phase goes from induction to flowering.

During this phase the red clover plants await for the environmental cue to start the reproductive growth. Physiologic and metabolic processes remain the same as for the vegetative phase with plants allocating biomass to leaf+petiole, stems, and root+taproot organs. As red clover requires long days for flowering, the trigger to end this phase is defined by the length of day, or more spcifically by the increase in daily photoperiod. The plants need a few days under favourable

conditions, photoperiod increasing and greater than a threshold, to start the reproductive phase.
Cultivars of red clover are often grouped by flowering date, as in early, intermediate, or late flowering; thus different cultivars require different photoperiods to trigger flower initiation (Aitken, 1964; Fagerberg, 1988; Claydon et al., 1993). The variability in response of induction to environmental condition is considerably in red clover and not well understood (e.g. Jones et al., 1993; Fan et al., 2004). In most stands at least some plants will show reproductive growth, but often not all the plants in the stand. This, and genetic variability, results in considerable variation in flower initiation is any given sward. As the model attempts to simulated an average plant, such variations are not accounted for.

The *Target* for completion is calculated as:

Target = 10 (days)

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

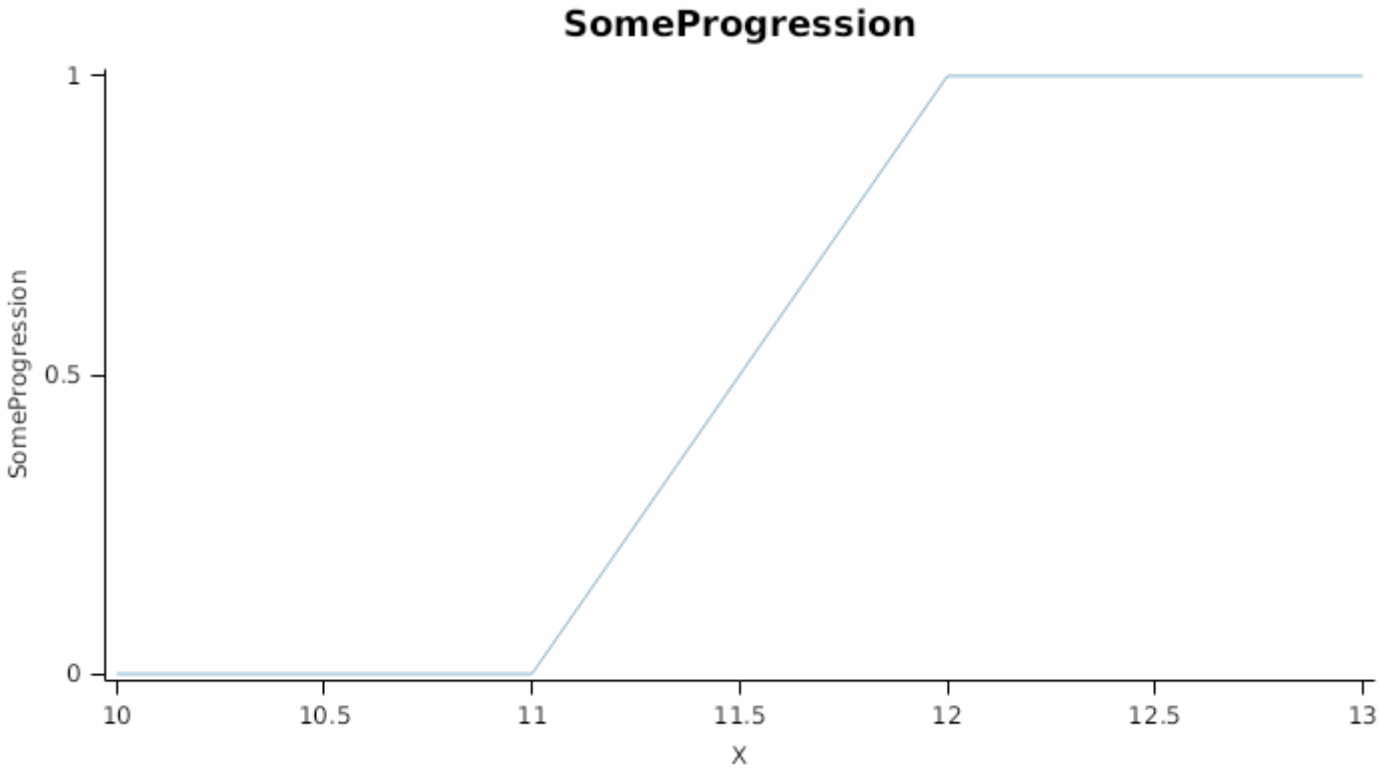
IF [Phenology].PhotoperiodVariation < Zero THEN

NoProgression = 0

ELSE

SomeProgression is calculated using linear interpolation

X	SomeProgression
10.0	0.0
11.0	0.0
12.0	1.0
13.0	1.0



1.6.6 Reproductive

This phase goes from flowering to ripening.

During this phase the plant is partitioning biomass to all organs, including reproductive organs (peduncles, inflorescence, and seeds). The current model does not describe the development of flower and seeds explicitly, only a generic organ referred to as *inflorescence* is defined. The reason for this is because there isn't enough data to devise and parameterise these processes while there is considerable variability in the phenology of reproduction of red clover. Often there are seeds maturing while new flowers are still being initiated over summer (e.g. Aitken, 1964; Clifford et al., 1980). Also due to their similarities and the fact that a population is describe in the model (instead of single plants), peduncles and

petioles are simulated as a single organ.
Flower emergence starts in spring when day light is increasing, heading peaks in summer, and ceases in early autumn (Aitken, 1964; Clifford et al., 1980; Claydon et al., 1993). The actual periods vary for different cultivars, with early flowering ones having typically longer reproductive phases. The model uses the accumulation of degrees-day to simulate the progression and to trigger the end of this phase.
Management practices, such as applying N fertiliser, irrigation, and defoliations, may have an impact on flower and seed production (Brougham, 1959; Clifford et al., 1980; Fan et al., 2004), but there is large variation in the responses, depending on the cultivars as well as the extent and timing of the intervention. Currently, the model does not account for the effect of this practices explicitly, although it is expected that some effects are captured by changes in biomass allocation caused by actions such as irrigation or defoliation.

The *Target* for completion is calculated as:

Target = 2500 (oCd)

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

Progression = [Phenology].ThermalTime

1.6.7 GotoPhase

When the Ripening phase is reached, phenology is rewound to the Vegetative phase.

1.6.8 Photoperiod

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

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

Twilight = -6 (degrees)

1.6.9 PhotoperiodVariation

1.6.9.1 PhotoperiodVariation

Returns the difference between today's and yesterday's photoperiods in hours.

1.7 Arbitrator

1.7.1 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.

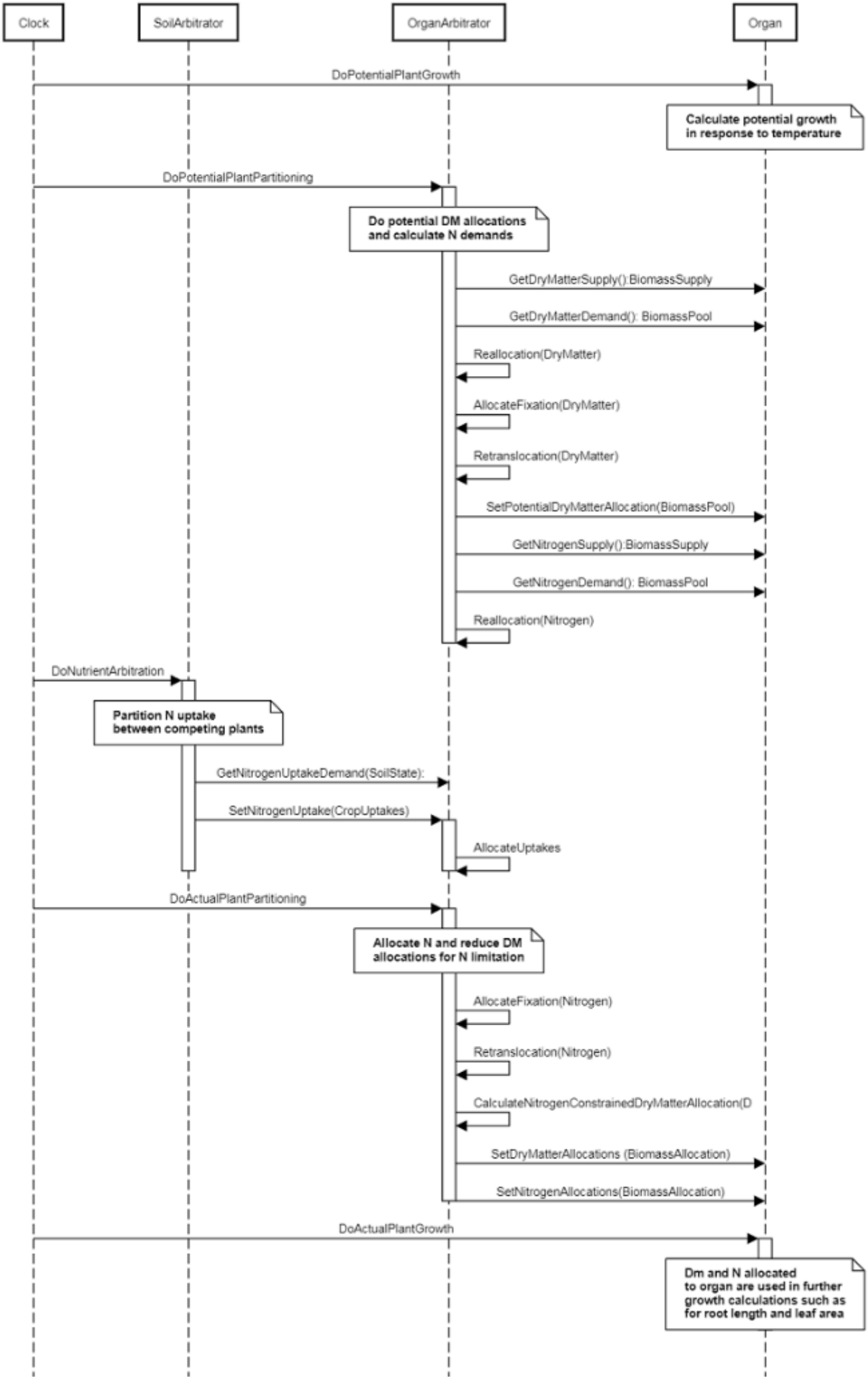

Clock
SoilArbitrator
OrganArbitrator
Organ
DoPotentialPlantGrowth
Calculate potential growth in response to temperature
DoPotentialPlantPartitioning
Do potential DM allocations and calculate N demands
GetDryMatterSupply():BiomassSupply
GetDryMatterDemand(): BiomassPool
Reallocation(DryMatter)
AllocateFixation(DryMatter)
Retranslocation(DryMatter)
SetPotentialDryMatterAllocation(BiomassPool)
GetNitrogenSupply():BiomassSupply
GetNitrogenDemand(): BiomassPool
Reallocation(Nitrogen)
DoNutrientArbitration
Partition N uptake between competing plants
GetNitrogenUptakeDemand(SoilState):
SetNitrogenUptake(CropUptakes)
AllocateUptakes
DoActualPlantPartitioning
Allocate N and reduce DM allocations for N limitation
AllocateFixation(Nitrogen)
Retranslocation(Nitrogen)
CalculateNitrogenConstrainedDryMatterAllocation(D
SetDryMatterAllocations (BiomassAllocation)
SetNitrogenAllocations(BiomassAllocation)
DoActualPlantGrowth
Dm and N allocated to organ are used in further growth calculations such as for root length and leaf area

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.

1.8 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.

Note: this organ represents all the leaves in the plant, it has only a basic representation of canopy structure and does not distinguish leaves for ages or placement in the canopy.

1.8.1 Initial Dry Matter

It is assumed that approximately 1/3 of the seed biomass is allocated to shoot upon emergence. The weight of red clover seeds varies between 2.0 and 4.5 g/1000 seeds (Claydon et al., 1993; Murray, 2012).

InitialWt = *InitialOrganWt* x [Plant].Population

InitialOrganWt = 0.0002 (g/plant)

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 = *StructuralFraction* x *DMDemandFunction*

This is the default value for PMF.

StructuralFraction = 0.95 (g/g)

The DM demand as defined here is a weighting factor, actual values are computed by the OrganArbitrator. The value is computed as the sum of a base demand, simply based on the potential partition according to the target proportions, and a deficit demand, which diverts more biomass to organs that deviate from their targeted proportions. This ensures faster regrowth of above ground organs after defoliation. The target proportion may vary with growth stage and environmental conditions.

DMDemandFunction = Max(*Zero*, *OrganDMDemand*)

Where:

Zero = 0

The DM demand as defined here is a weighting factor, actual values are computed by the OrganArbitrator. The value is computed as the sum of a base demand, simply based on the potential partition according to the target proportions, and a deficit demand, which diverts more biomass to organs that deviate from their targeted proportions. This ensures faster regrowth of above ground organs after defoliation. The target proportion may vary with growth stage and environmental conditions.

OrganDMDemand = BaseBiomassDemand + DeficitBiomassDemand

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

BaseBiomassDemand = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction = [TargetAboveGroundFraction] x [Leaf].TargetBiomassProportion

DeficitBiomassDemand = *TargetBiomass* - [Leaf].Live.Wt

TargetBiomass = [TargetAboveGroundFraction] x [Leaf].TargetBiomassProportion x [TotalLive].Wt

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.8.3 Nitrogen Demand

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

1.8.3.1 NDemands

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

Structural = [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 = [Leaf].NitrogenDemandSwitch

MaxNconc = [Leaf].MaximumNConc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.8.4 Nitrogen Concentration Thresholds

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

1.8.4.1 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 = [Leaf].NitrogenDemandSwitch

MaxNconc = [Leaf].MaximumNConc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.8.5 Dry Matter Supply

This is the default value for PMF.

DMReallocationFactor = 1

DMRetranslocationFactor = 0 (/day)

1.8.6 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.

There has been a number of studies on the photosynthetesis rate of red clover (e.g. Joggi et al., 1983; den Hollander et al., 2007; Riesinger et al., 2009), including its variation due to water defficiency, nutrition, and shading. The values and trends for CO2 assimilation rates are generally consistent across the various studies and these have been used to help defining the limiting factor for photoynthesis in the model. Reported values RUE for red clover are in general around 2.5-3.0 g DM/MJ for aboveground biomass (Riesinger et al., 2009; Torssell et al., 2007).
The parameters used for the stress factors are mostly generic ones based on typical response form plants to the various environmental factors.

RUE = 1.5 (g/MJ)

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

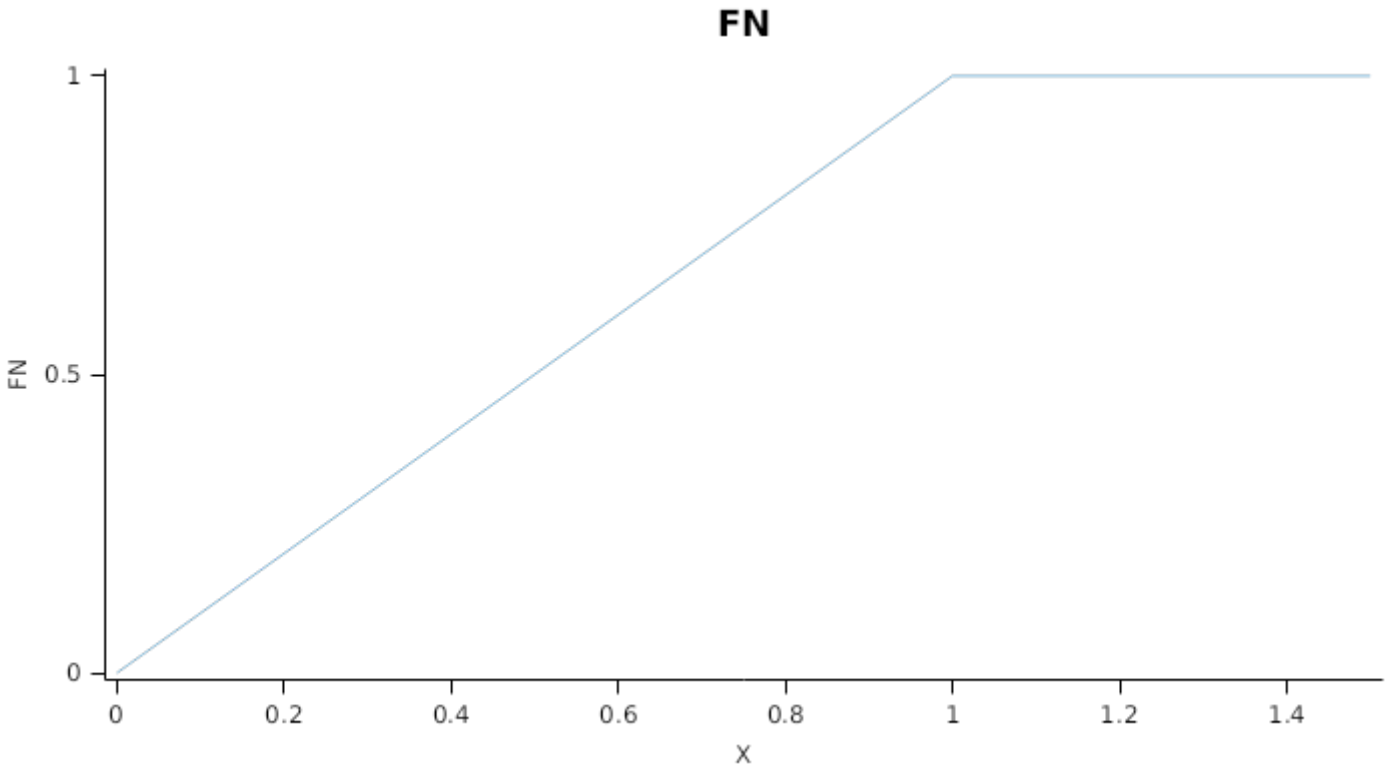
$CP = (163.0 - T) / (5.0 - 0.1 * T)$

For C4 plants,

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

FN is calculated using linear interpolation

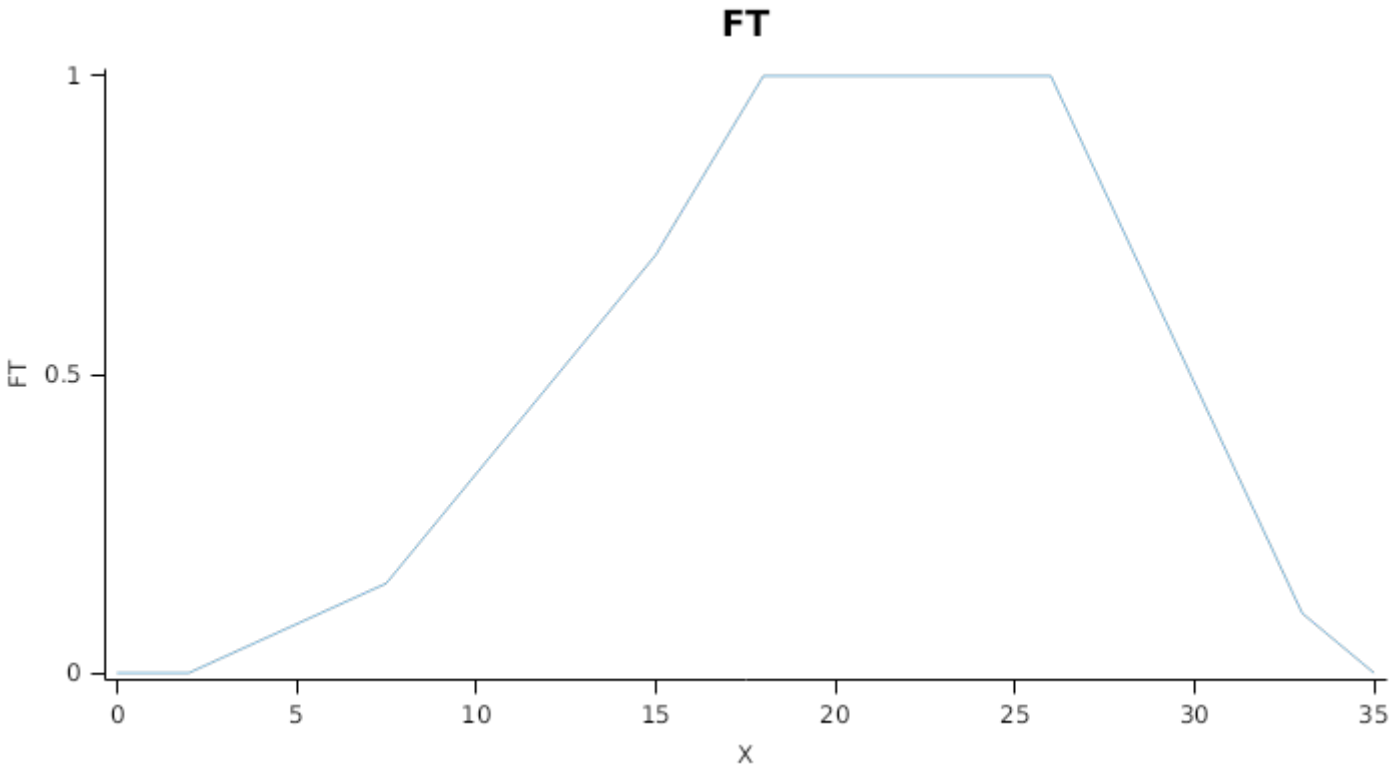
X	FN
0.0	0.0
0.5	0.5
1.0	1.0
1.5	1.0

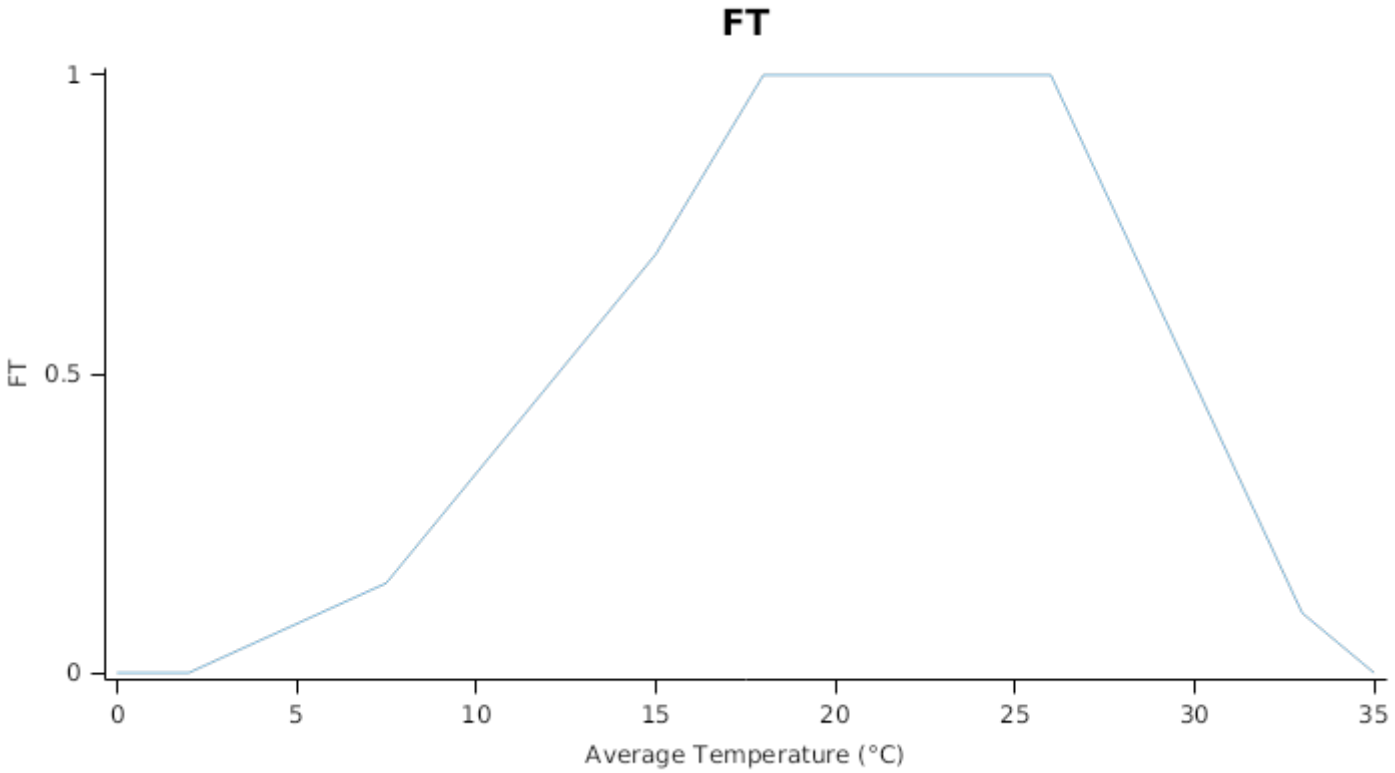


FT is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.75

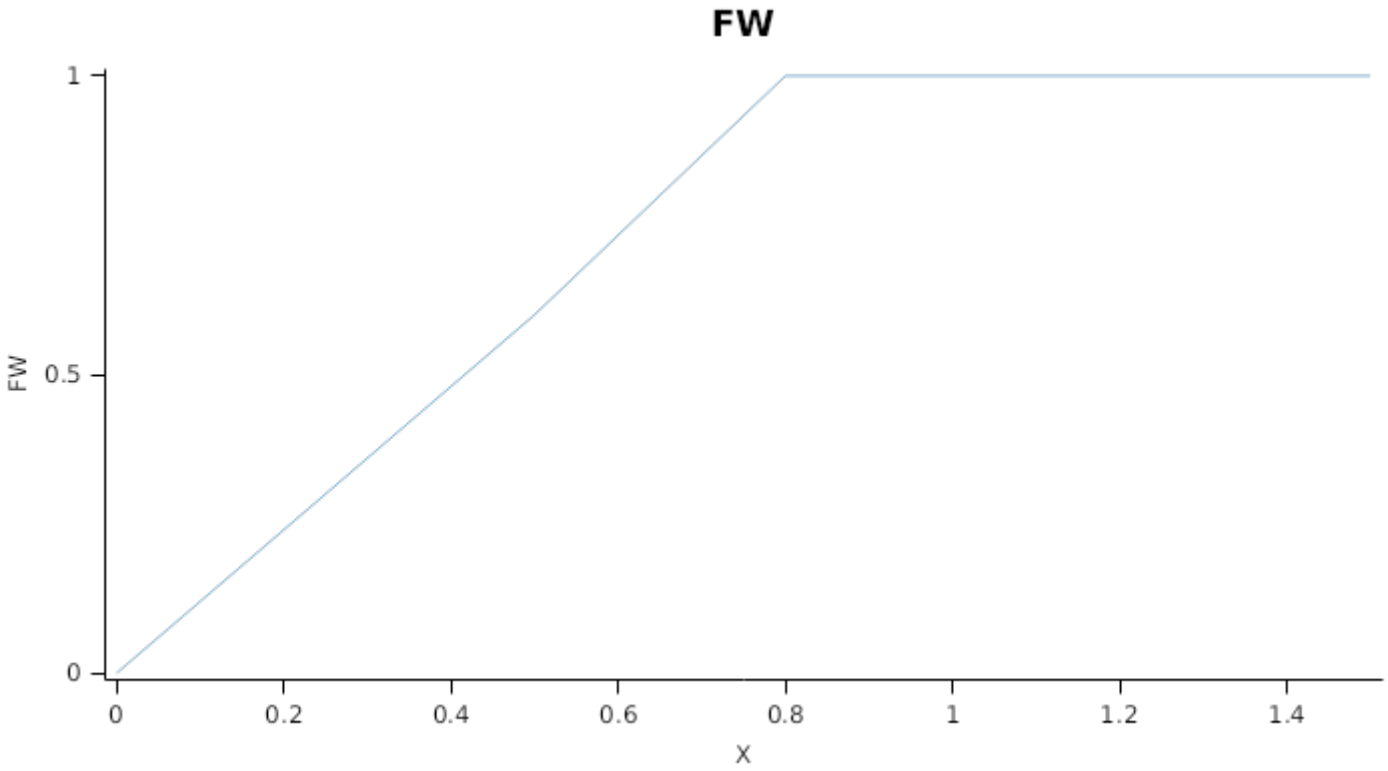
X	FT
0.0	0.0
2.0	0.0
7.5	0.1
15.0	0.7
18.0	1.0
26.0	1.0
33.0	0.1
35.0	0.0





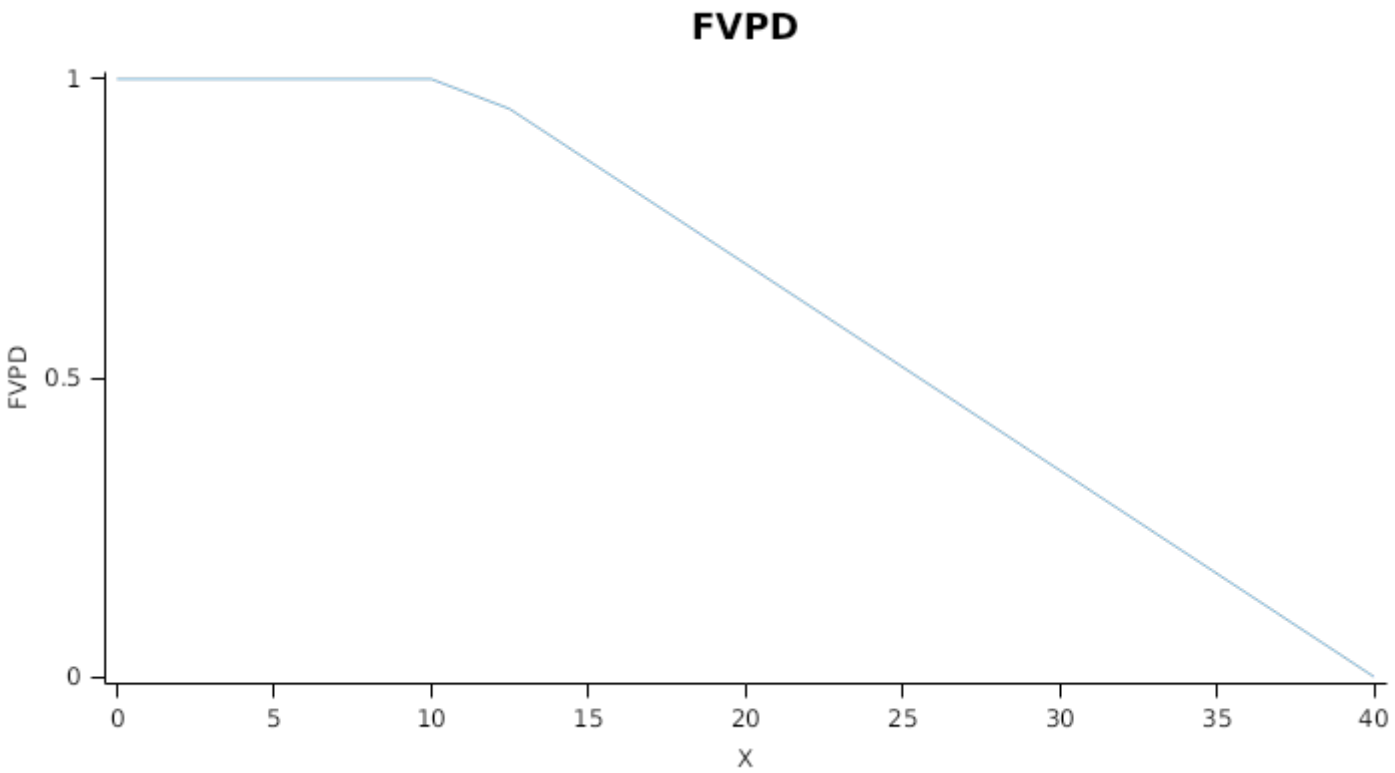
FW is calculated using linear interpolation

X	FW
0.0	0.0
0.5	0.6
0.8	1.0
1.5	1.0



FVPD is calculated using linear interpolation

X	FVPD
0.0	1.0
10.0	1.0
12.5	0.9
40.0	0.0



RadnInt = [Leaf].RadiationIntercepted

1.8.7 Nitrogen Supply

This is the default value for PMF.

NReallocationFactor = 1 (/day)

A generic relationship between retranslocation and environmental factors is assumed, this is done so that retranslocation is enhanced when conditions are good for growth. Retranslocation from leaves is enable any time.

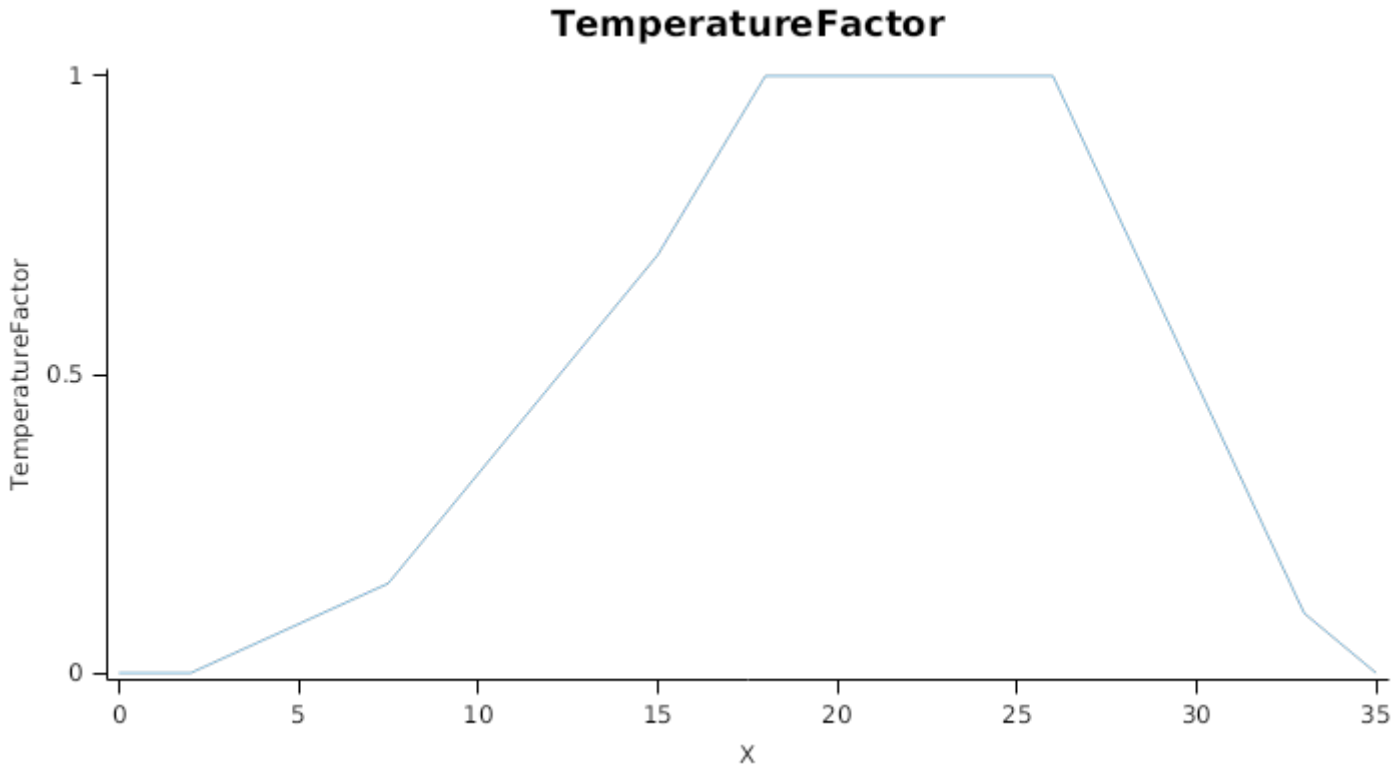
NRetranslocationFactor = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor*

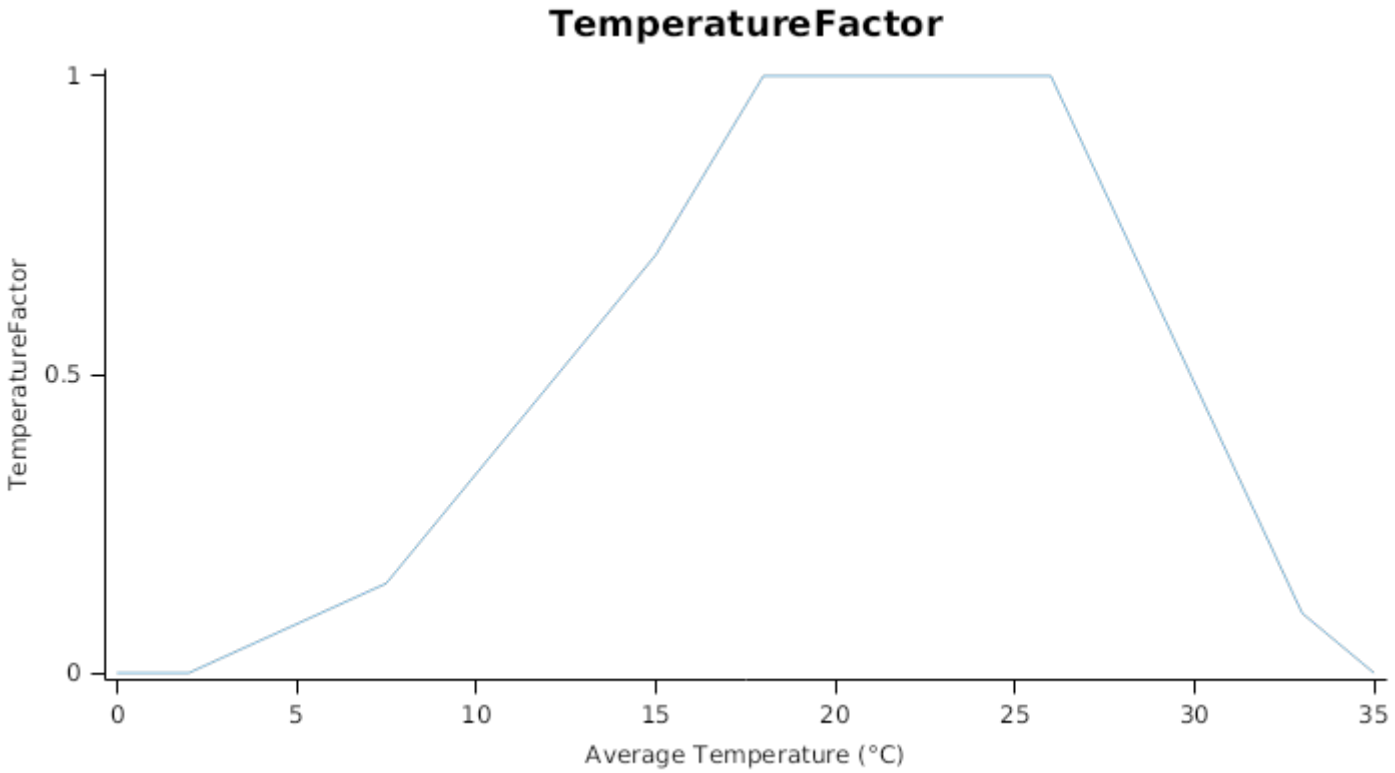
ReferenceRate = 0.1 (/day)

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

MaximumTemperatureWeighting = 0.5

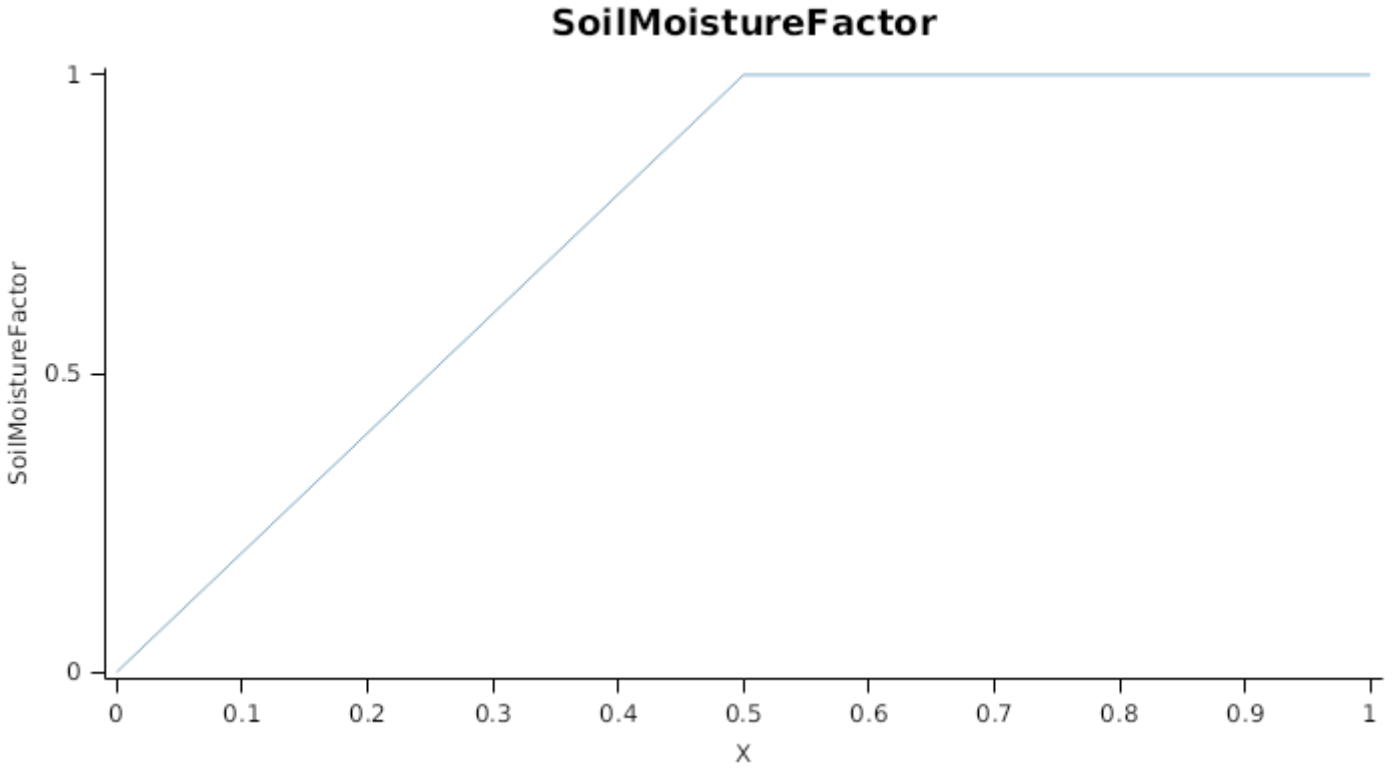
X	TemperatureFactor
0.0	0.0
2.0	0.0
7.5	0.1
15.0	0.7
18.0	1.0
26.0	1.0
33.0	0.1
35.0	0.0





SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.0
0.5	1.0
1.0	1.0



1.8.8 Canopy Properties

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

The leaf area index (LAI) for green leaves of red clover is defined based on their biomass and specific leaf area (SLA). The value for SLA is currently assumed to be constant, although factors such as age and environmental conditions (shading and nutrient status) should have an effect on this value. Variations due to age can ignored because the model simulates a generic population, and thus it represents leaves of varing ages at the same time. According to available studies, the effects of shading and nutrition, as well as water deficiency, are typically only manifested when these conditions are mantained for some time (e.g. Heraut-Bron et al., 2000; Joggi et al., 1983) and may not be important for average swards. The model may have to be revised in the future to account for some of these factors, preferably with some experimental data. Available data suggest that SLA of red clover varies approximately between 0.020 and 0.035 m2/g, with some variation due to cultivar; mean values for adult plants are around 0.030 m2/g (den Hollander et al., 2007; Murray, 2012; Mason et al., 2016).

Area = *SpecificLeafArea* x [Leaf].Live.Wt

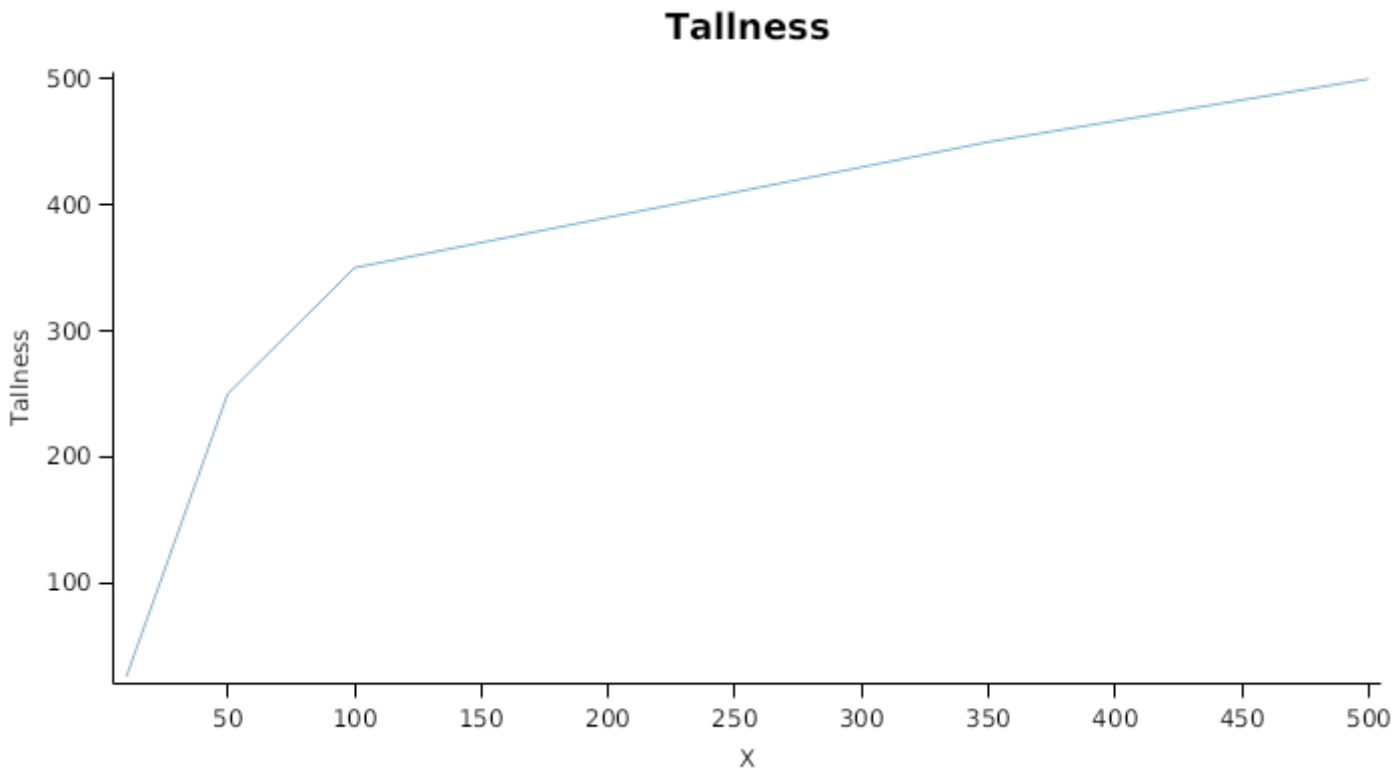
SpecificLeafArea = 0.03 (m^2/g)

Red clover has a high capacity for light interception due to the near horizontal placement of its leaves. Values for the light extinction coefficient reported in the literature are sparse and quite variable, depending on what light fraction they are related to and whether plants are considered in mixed swards or as separated plants; these vary from 0.80 up to 1.10 (Joggi et al., 1983; den Hollander et al., 2007).

ExtinctionCoefficient = 0.9 (0-1)

Tallness is calculated using linear interpolation

X	Tallness
10.0	25.0
50.0	250.0
100.0	350.0
350.0	450.0
500.0	500.0



1.8.9 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

StomatalConductanceCO2Modifier = 1

1.8.10 Senescence and Detachment

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

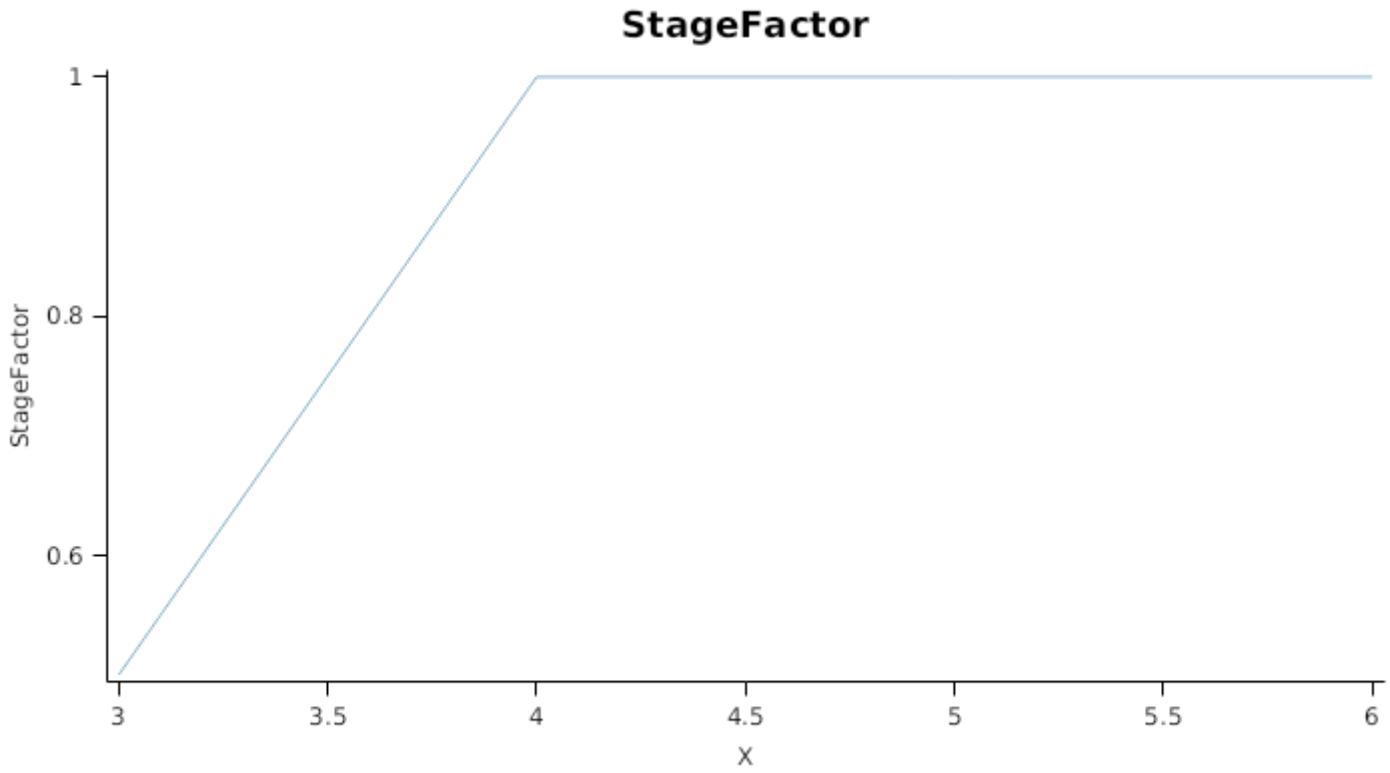
Red clover has, similar to otehr clovers, a relatively high rate of leaf senescence, with leaf area estabilising when LAI reaches about 5.0 m2/m2 (Brougham, 1958; Joggi et al., 1983; Murray, 2012). Generic relationships to enviromental factors, such as temperature and soil moisture, are assumed based on other plant models.

SenescenceRate = *ReferenceRate* x *StageFactor* x *CoverFactor* x *TemperatureFactor* x *SoilMoistureFactor*

ReferenceRate = 0.05 (/day)

StageFactor is calculated using linear interpolation

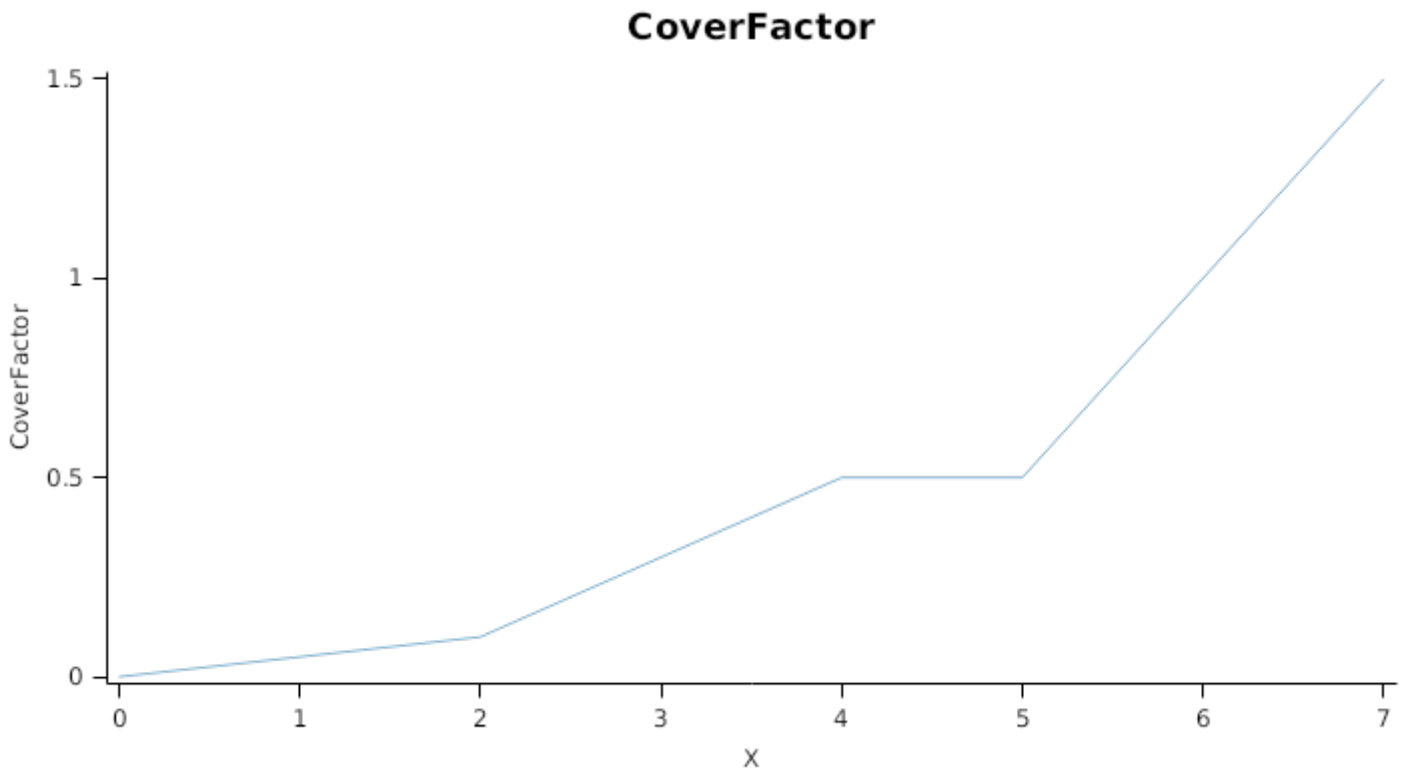
X	StageFactor
3.0	0.5
4.0	1.0
5.0	1.0
6.0	1.0



CoverFactor is calculated using linear interpolation

X	CoverFactor
0.0	0.0
2.0	0.1
4.0	0.5
5.0	0.5

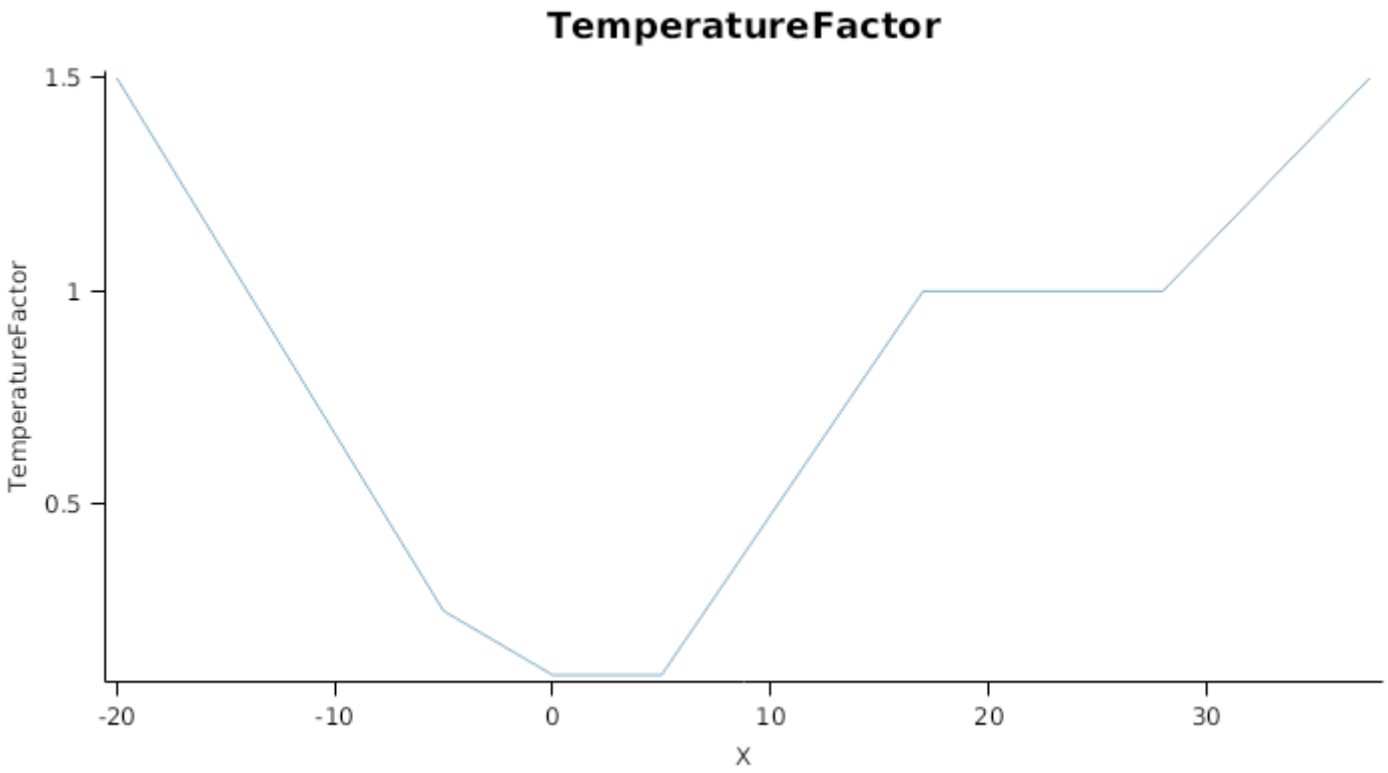
X	CoverFactor
7.0	1.5

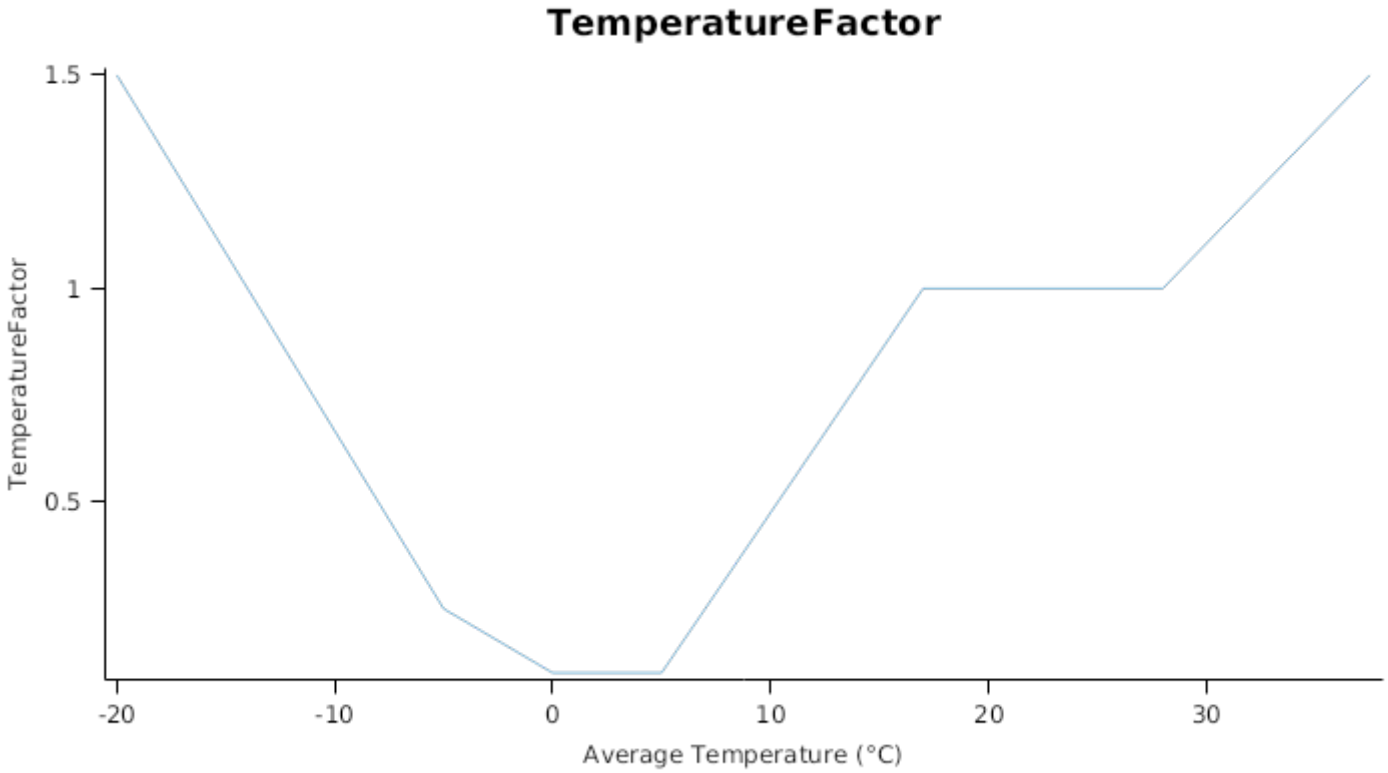


TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

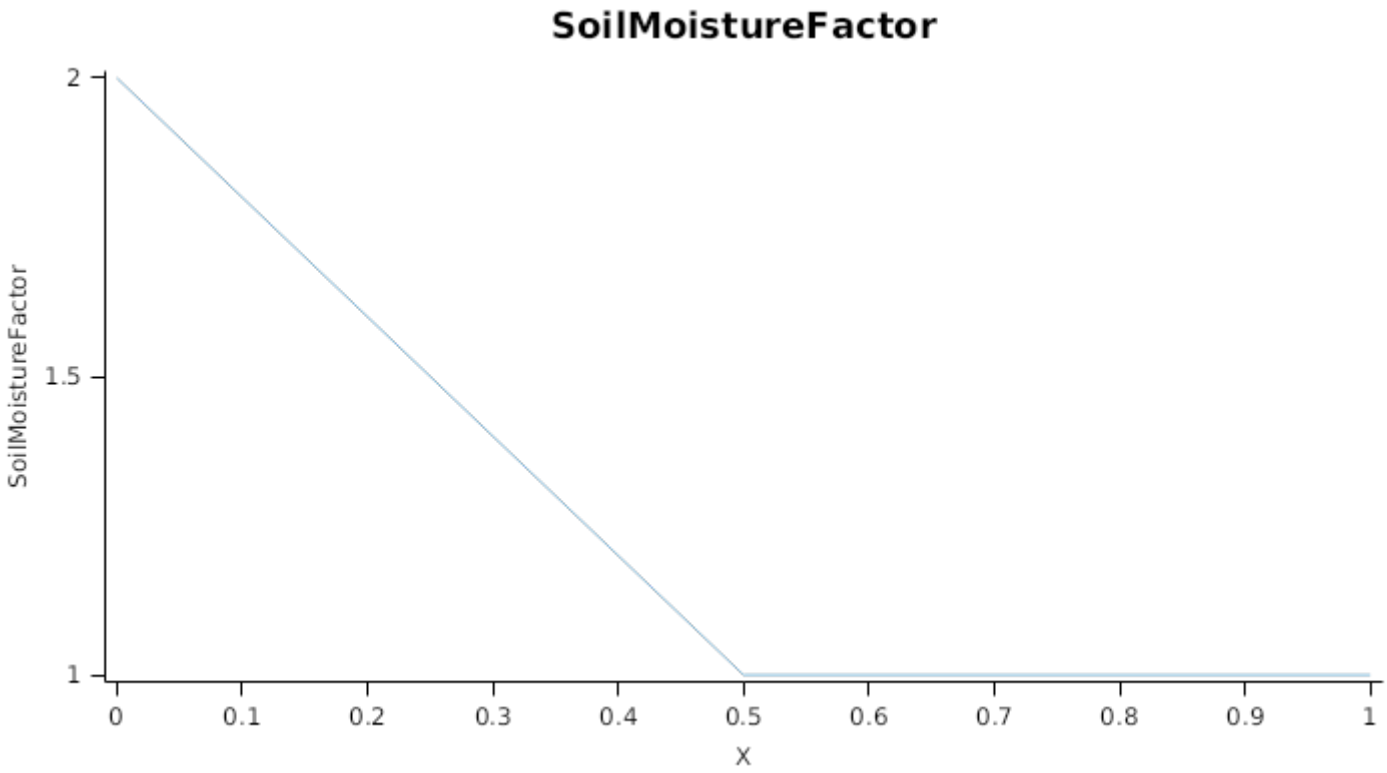
X	TemperatureFactor
-20.0	1.5
-5.0	0.2
0.0	0.1
5.0	0.1
17.0	1.0
28.0	1.0
37.5	1.5





SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	2.0
0.5	1.0
1.0	1.0



The proportion of Biomass that detaches and is passed to the surface organic matter model for decomposition is quantified by the DetachmentRateFunction.

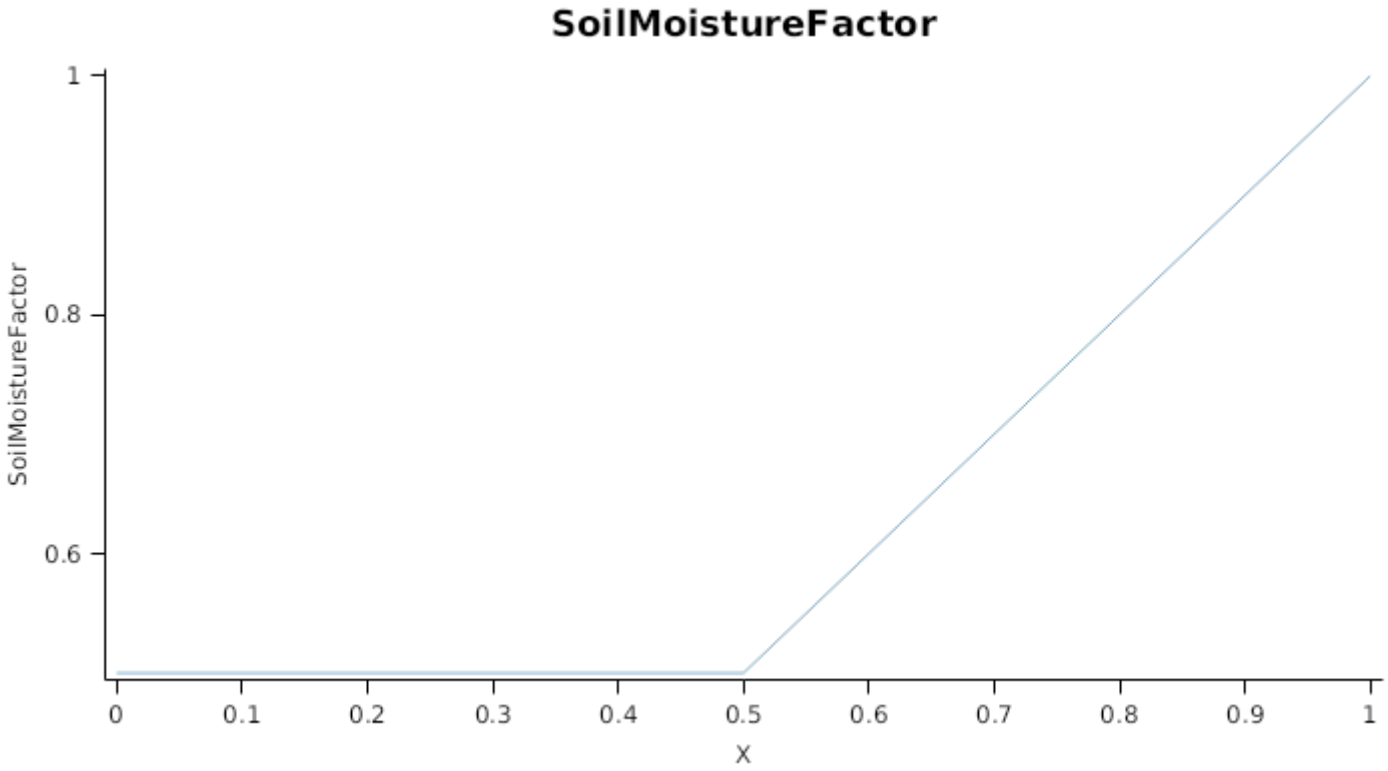
A generic relationship between detachment and soil moisture is assumed. It implies that under dry conditions the detachment rate decreases due to the lower level of activity of decomposing microorganisms.

DetachmentRate = *ReferenceRate* x *SoilMoistureFactor*

ReferenceRate = 0.1 (/day)

SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.5
0.5	0.5
1.0	1.0



1.8.11 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
Cut	65	52	15	13
Graze	60	60	25	25
Harvest	6	7	24	28
Prune	0	0	0	0

1.9 Petiole

1.9.1 Petiole

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.

1.9.2 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.

1.9.2.1 DMDemands

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

Structural = *StructuralFraction* x *DMDemandFunction*

StructuralFraction = 1 (g/g)

The DM demand as defined here is a weighting factor, actual values are computed by the OrganArbitrator. The value is computed as the sum of a base demand, simply based on the potential partition according to the target proportions, and a deficit demand, which diverts more biomass to organs that deviate from their targeted proportions. This ensures faster

regrowth of above ground organs after defoliation. The target proportion may vary with growth stage and environmental conditions.

DMDemandFunction = Max(*Zero*, *OrganDMDemand*)

Where:

Zero = 0

OrganDMDemand = *BaseBiomassDemand* + *DeficitBiomassDemand*

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

BaseBiomassDemand = *PartitionFraction x [Arbitrator].DM.TotalFixationSupply*

PartitionFraction = [TargetAboveGroundFraction] x [Petiole].TargetBiomassProportion

DeficitBiomassDemand = *TargetBiomass* - [Petiole].Live.Wt

TargetBiomass = [TargetAboveGroundFraction] x [Petiole].TargetBiomassProportion x [TotalLive].Wt

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.9.3 Nitrogen Demand

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

1.9.3.1 NDemands

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

Structural = [Petiole].MinimumNConc x [Petiole].potentialDMAllocation.Structural

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

MetabolicNconc = [Petiole].CriticalNConc - [Petiole].MinimumNConc

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

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

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

NitrogenDemandSwitch = [Petiole].NitrogenDemandSwitch

MaxNconc = [Petiole].MaximumNConc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.9.4 N Concentration Thresholds

MinimumNConc = 0.025 (gN/gDM)

CriticalNConc = 0.0275 (gN/gDM)

MaximumNConc = 0.03 (gN/gDM)

1.9.5 Dry Matter Supply

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

Petiole does not retranslocate non-structural DM.

1.9.6 Nitrogen Supply

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

Petiole can retranslocate up to 5% of non-structural N each day if required by the plant arbitrator to meet N demands.

1.9.7 Senescence and Detachment

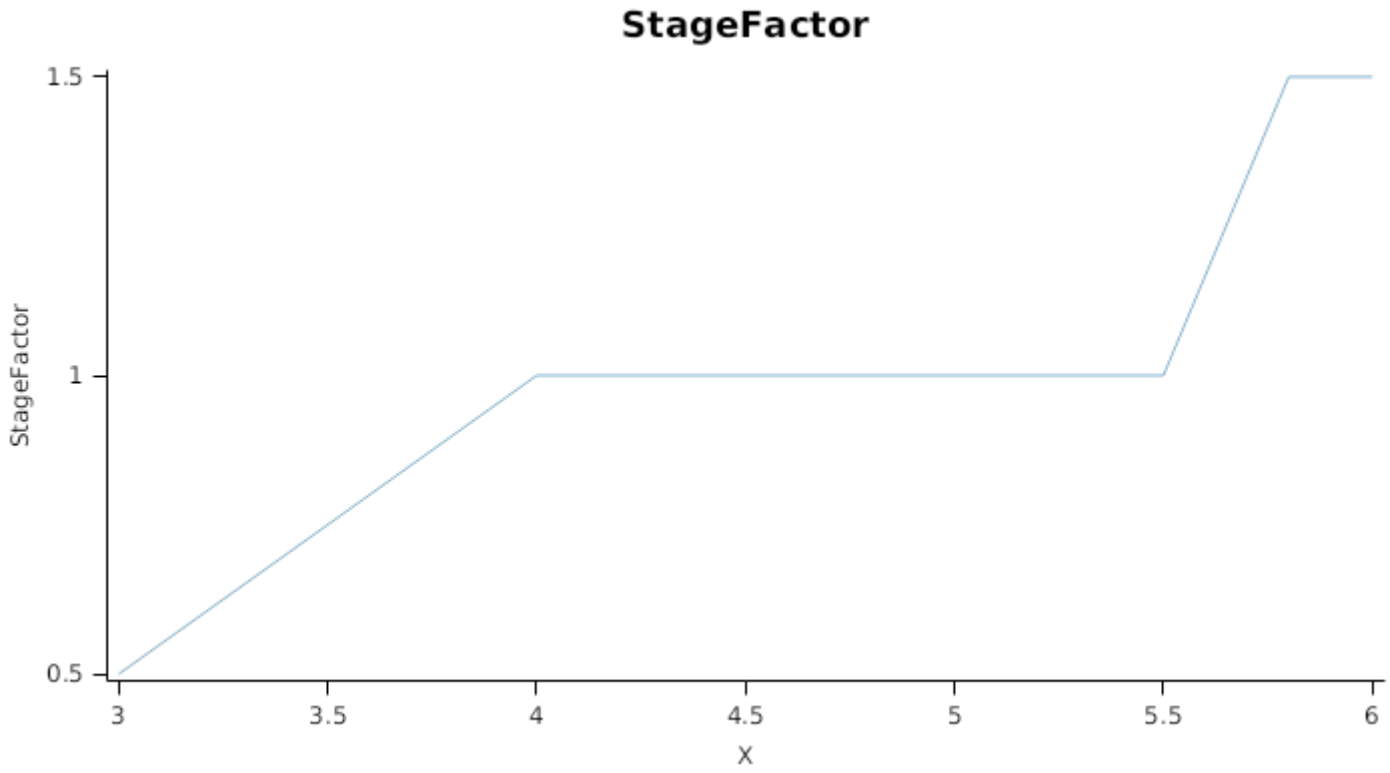
The proportion of live biomass that senesces and moves into the dead pool each day is quantified by the SenescenceRate.

The reference senescence rate is adjusted using generic relationships to environmental factors, such as temperature and soil moisture. These are based on general knowledge from other plant models.

SenescenceRate = [Leaf].SenescenceRate.ReferenceRate x *StageFactor* x *CoverFactor* x *TemperatureFactor* x *SoilMoistureFactor*

StageFactor is calculated using linear interpolation

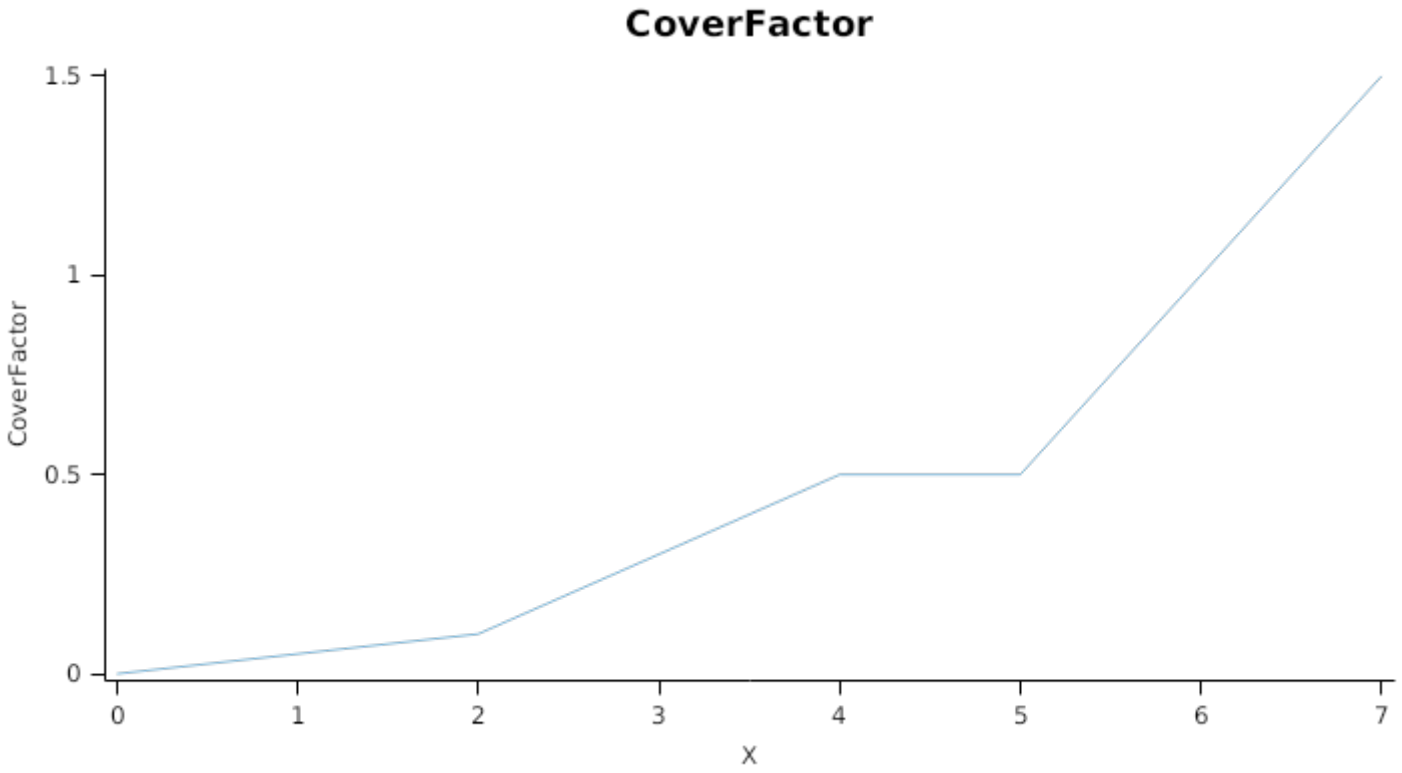
X	StageFactor
3.0	0.5
4.0	1.0
5.5	1.0
5.8	1.5
6.0	1.5



CoverFactor is calculated using linear interpolation

X	CoverFactor
0.0	0.0

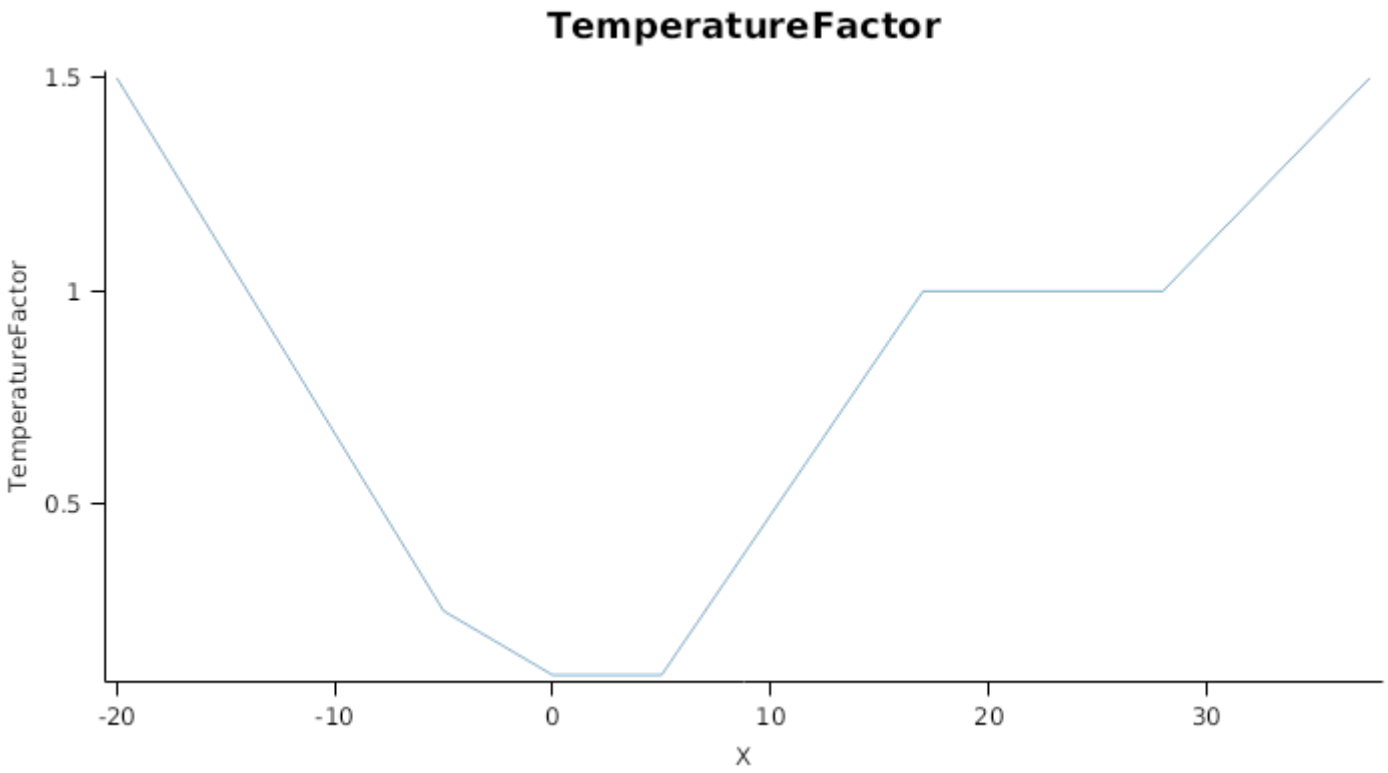
X	CoverFactor
2.0	0.1
4.0	0.5
5.0	0.5
7.0	1.5

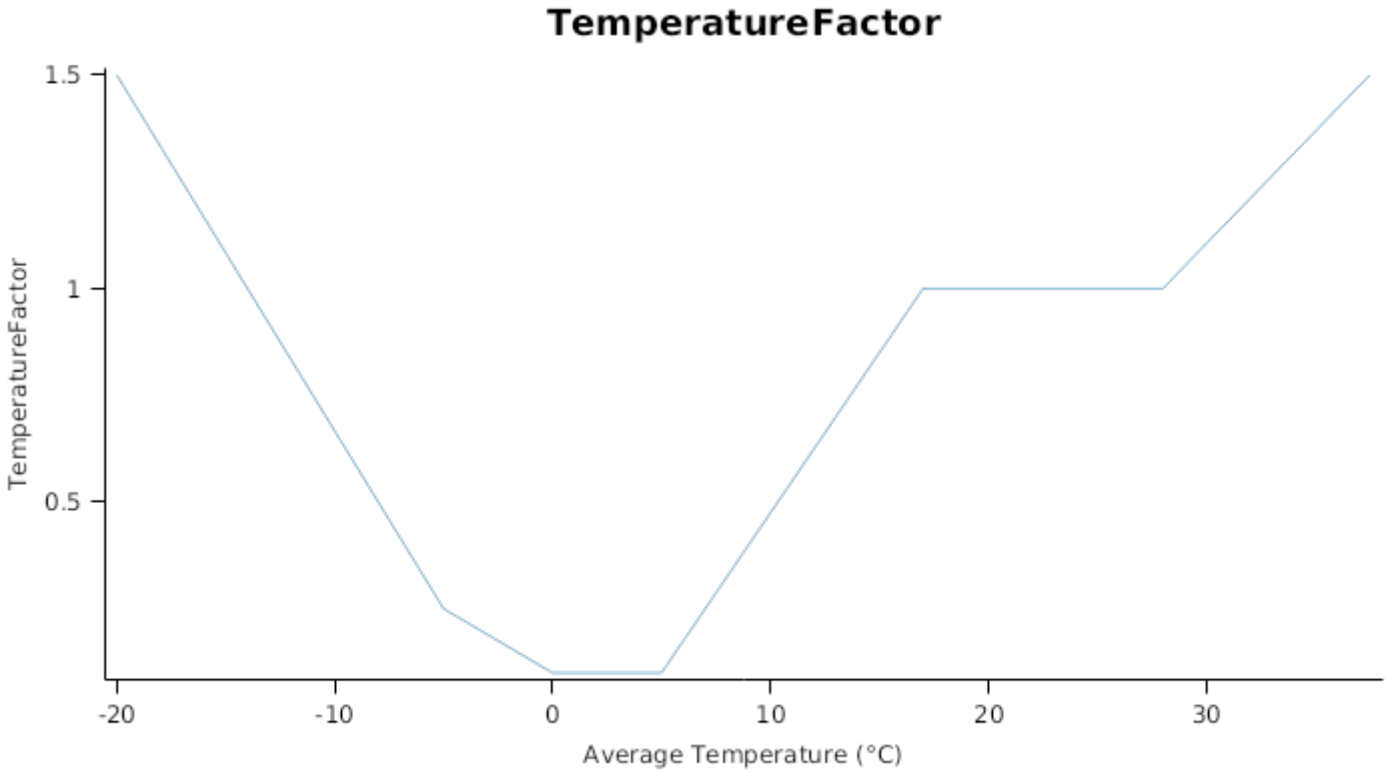


TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

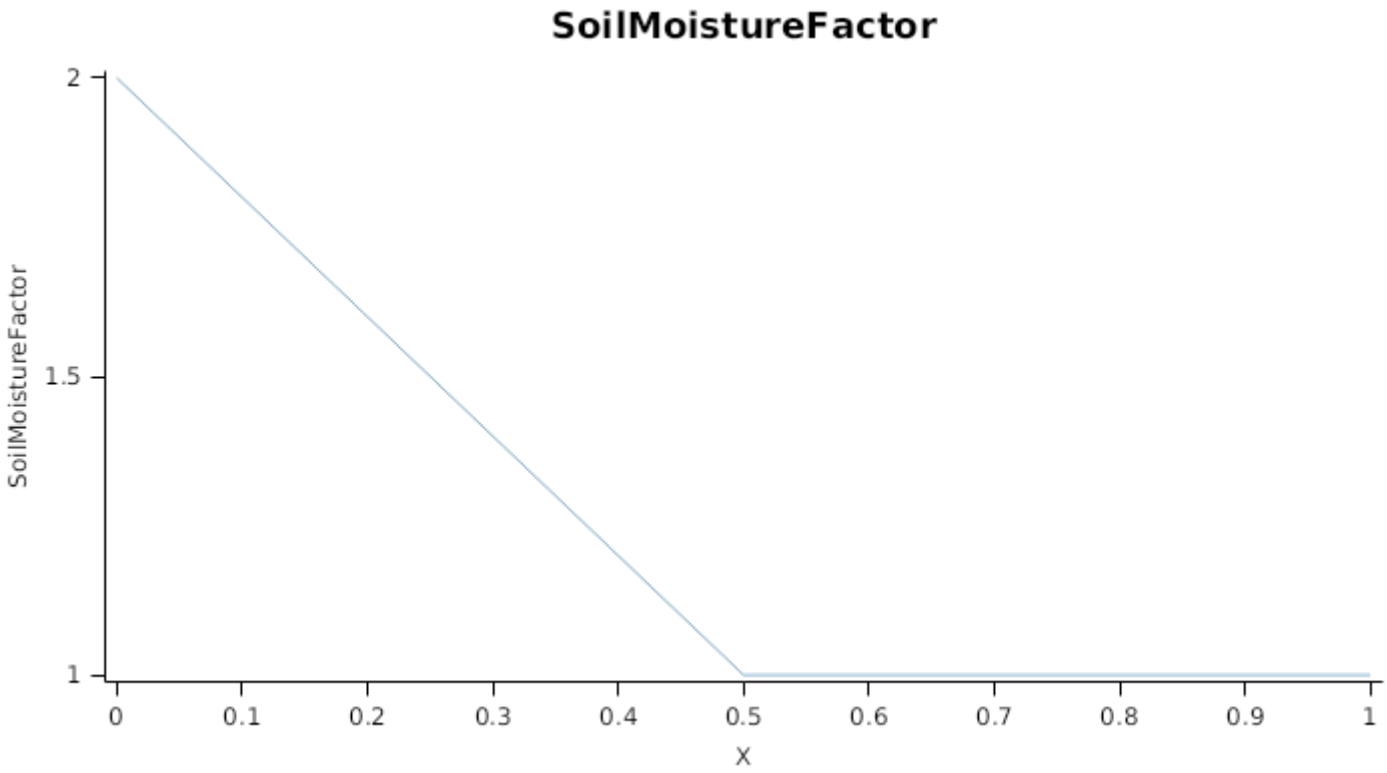
X	TemperatureFactor
-20.0	1.5
-5.0	0.2
0.0	0.1
5.0	0.1
17.0	1.0
28.0	1.0
37.5	1.5





SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	2.0
0.5	1.0
1.0	1.0



The proportion of Biomass that detaches and is passed to the surface organic matter model for decomposition is quantified by the DetachmentRateFunction.

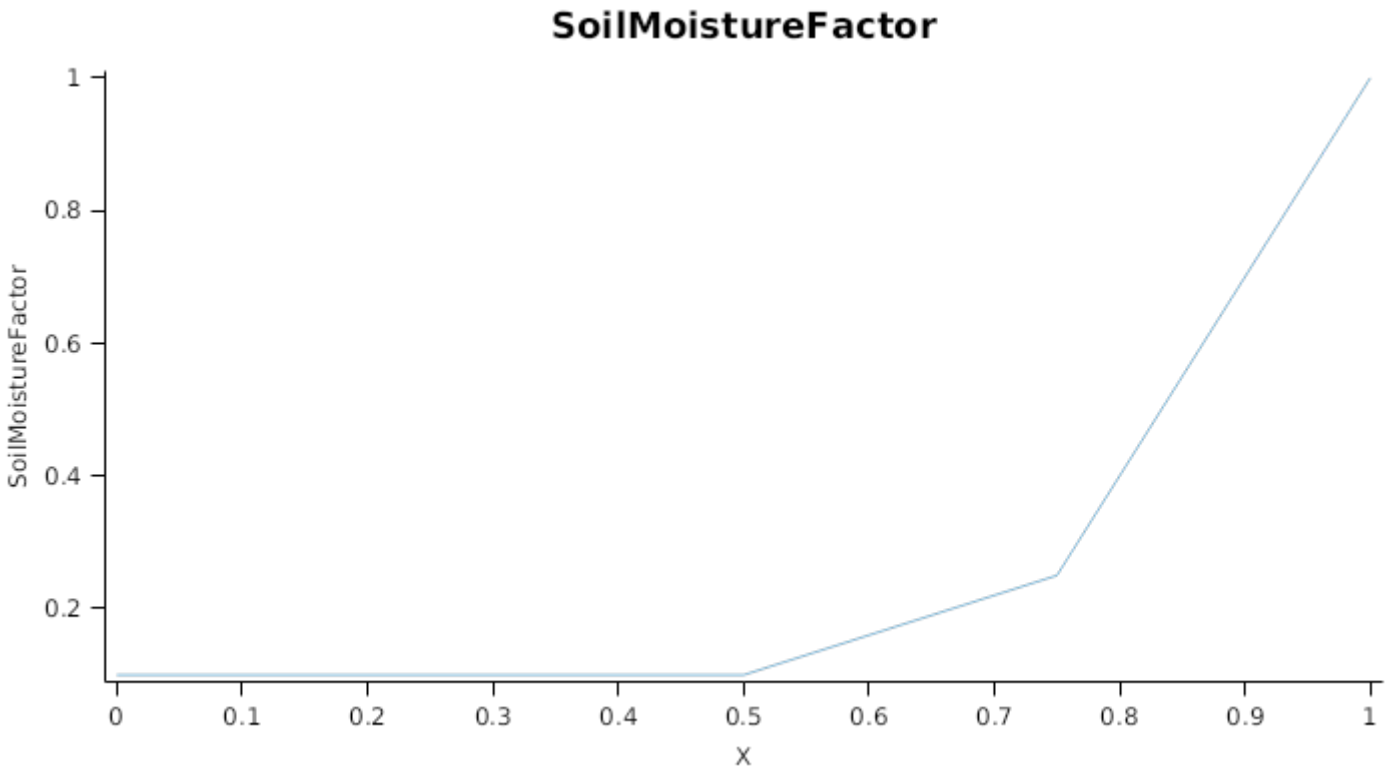
A generic relationship between detachment and soil moisture is assumed. It implies that under dry conditions the detachment rate decreases due to the lower level of activity of decomposing microorganisms.

DetachmentRateFunction = *ReferenceRate* x *SoilMoistureFactor*

ReferenceRate = 0.1 (/day)

SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.1
0.5	0.1
0.8	0.2
1.0	1.0



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
Cut	65	52	15	13
Graze	60	60	25	25
Harvest	8	9	32	36
Prune	0	0	0	0

1.10 Stem

1.10.1 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.

1.10.2 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.

1.10.2.1 DMDemands

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

Structural = *StructuralFraction* x *DMDemandFunction*

StructuralFraction = 0.85 (g/g)

The DM demand as defined here is a weighting factor, actual values are computed by the OrganArbitrator. The value is computed as the sum of a base demand, simply based on the potential partition according to the target proportions, and a deficit demand, which diverts more biomass to organs that deviate from their targeted proportions. This ensures faster regrowth of above ground organs after defoliation. The target proportion may vary with growth stage and environmental conditions.

DMDemandFunction = Max(*Zero*, *OrganDMDemand*)

Where:

Zero = 0

OrganDMDemand = *BaseBiomassDemand* + *DeficitBiomassDemand*

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

BaseBiomassDemand = *PartitionFraction x [Arbitrator].DM.TotalFixationSupply*

PartitionFraction = [TargetAboveGroundFraction] x [Stem].TargetBiomassProportion

DeficitBiomassDemand = *TargetBiomass* - [Stem].Live.Wt

TargetBiomass = [TargetAboveGroundFraction] x [Stem].TargetBiomassProportion x [TotalLive].Wt

Metabolic = *MetabolicFraction* x [Stem].DMDemands.Structural.DMDemandFunction

MetabolicFraction = 0 (g/g)

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

StorageFraction = 1 - [Stem].DMDemands.Structural.StructuralFraction - [Stem]
.DMDemands.Metabolic.MetabolicFraction

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.10.3 Nitrogen Demand

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

1.10.3.1 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

1.10.4 N Concentration Thresholds

MinimumNConc = 0.025 (gN/gDM)

CriticalNConc = 0.03 (gN/gDM)

MaximumNConc = 0.045 (gN/gDM)

1.10.5 Dry Matter Supply

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

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

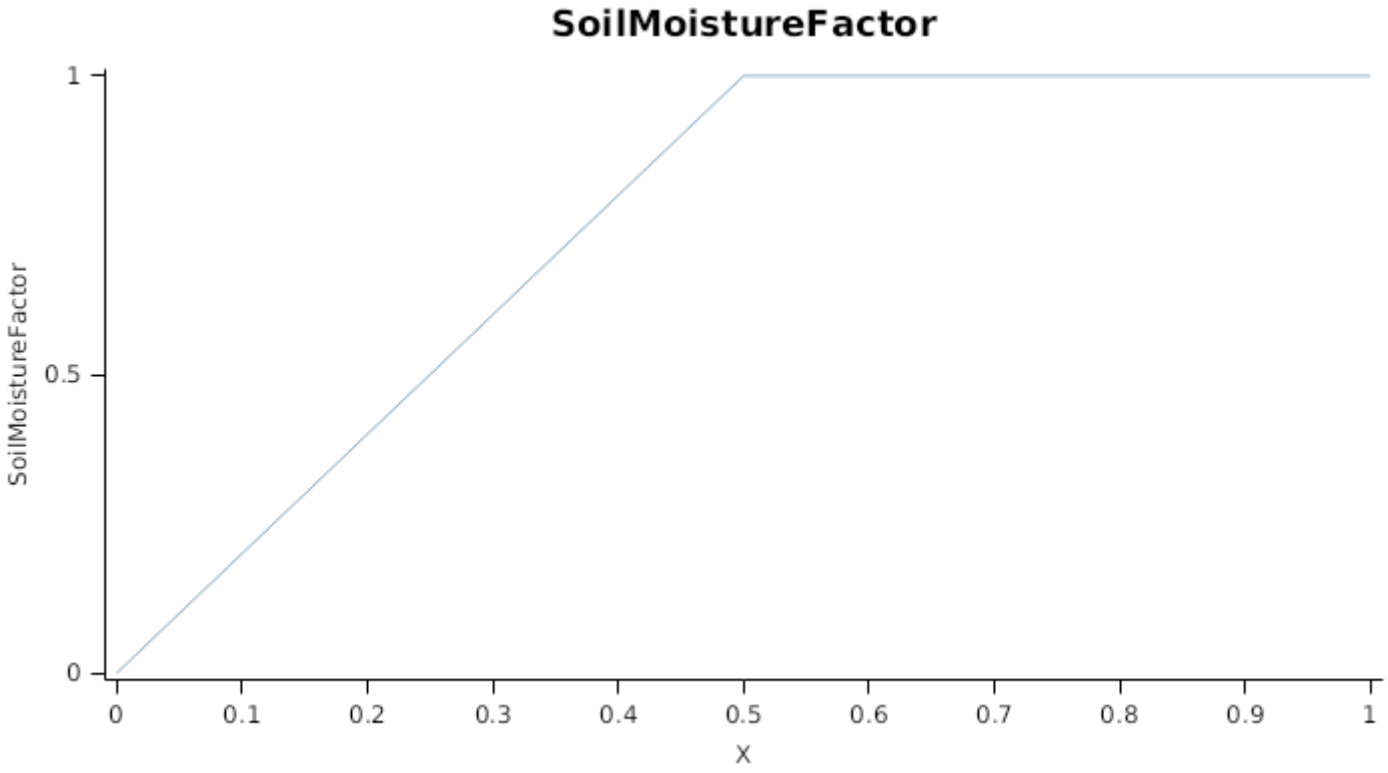
A generic relationship between retranslocation and environmental factors is assumed, this is done so that retranslocation is enhanced when conditions are good for growth. Plus retranslocation is only allowed when days are increasing, thus helping growth in spring and allowing for some replenishing in late summer and autumn.

DMRetranslocationFactor = *ReferenceRate* x [Leaf].NRetranslocationFactor.TemperatureFactor x *SoilMoistureFactor* x *PhotoPeriodFactor*

ReferenceRate = 0.05 (/day)

SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.0
0.5	1.0
1.0	1.0



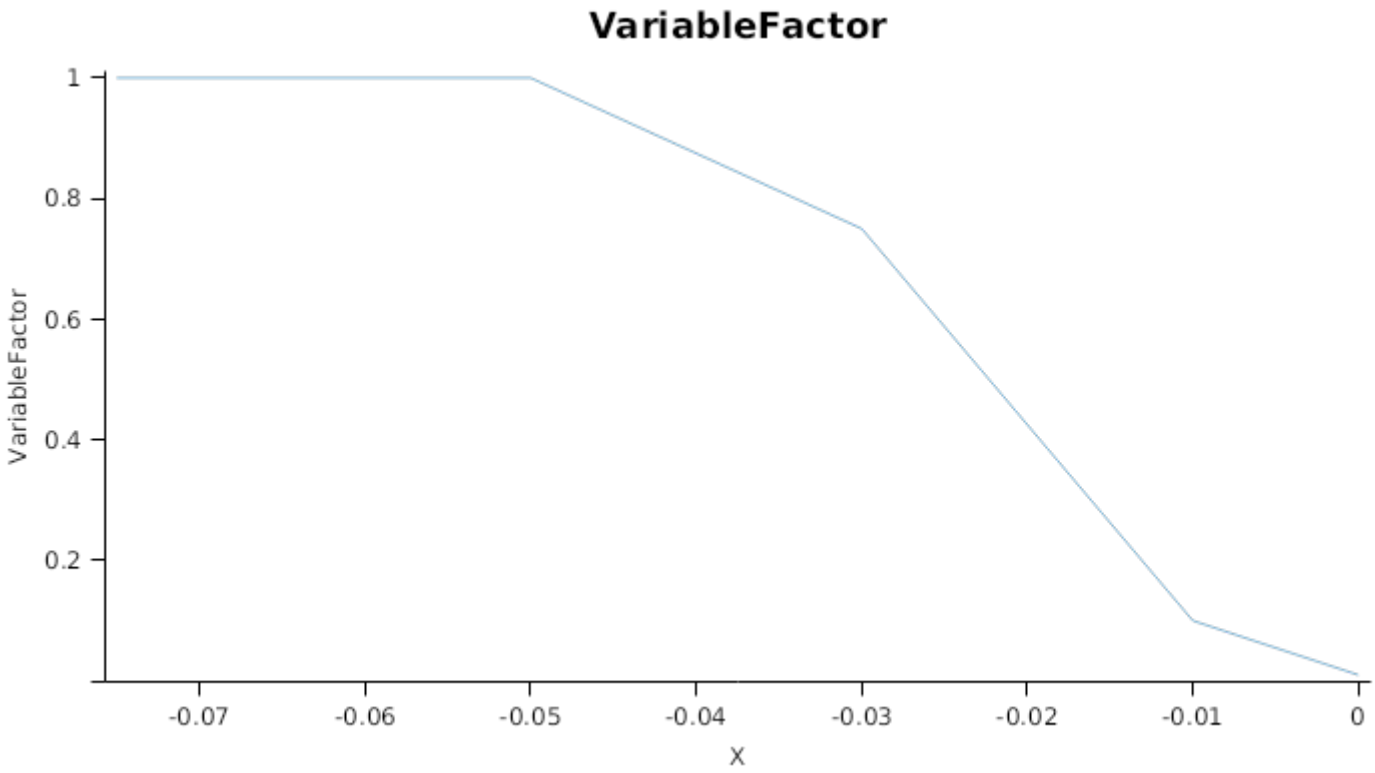
IF [Phenology].PhotoperiodVariation < Zero THEN

BaseFactor = 0.01

ELSE

VariableFactor is calculated using linear interpolation

X	VariableFactor
-0.1	1.0
-0.1	1.0
-0.0	0.8
-0.0	0.1
0.0	0.0



1.10.6 Nitrogen Supply

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

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

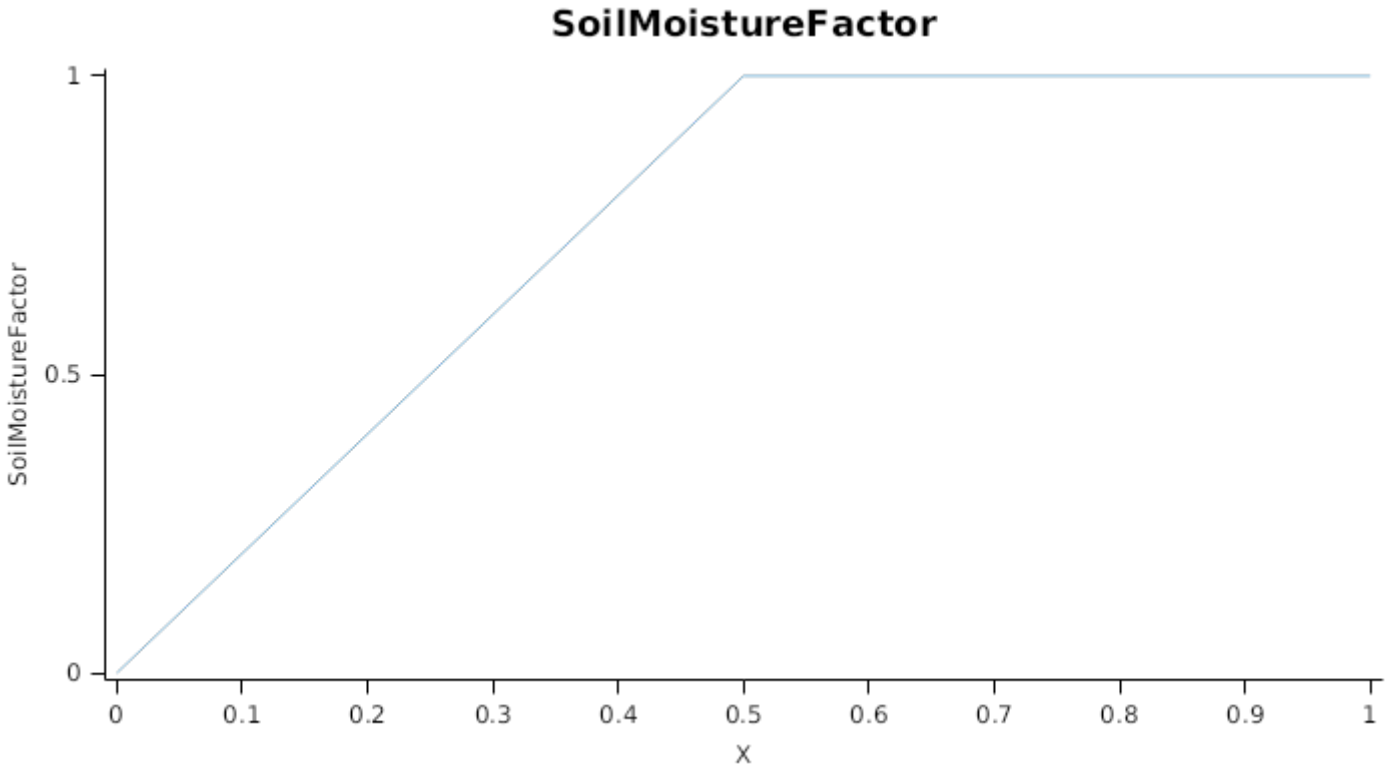
A generic relationship between retranslocation and environmental factors is assumed, this is done so that retranslocation is enhanced when conditions are good for growth. Plus retranslocation is only allowed when days are increasing, thus helping growth in spring and allowing for some replenishing in late summer and autumn.

NRetranslocationFactor = *ReferenceRate* x [Leaf].NRetranslocationFactor.TemperatureFactor x *SoilMoistureFactor* x [Stem].DMRetranslocationFactor.PhotoPeriodFactor

ReferenceRate = 0.1 (/day)

SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.0
0.5	1.0
1.0	1.0



1.10.7 Senescence and Detachment

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

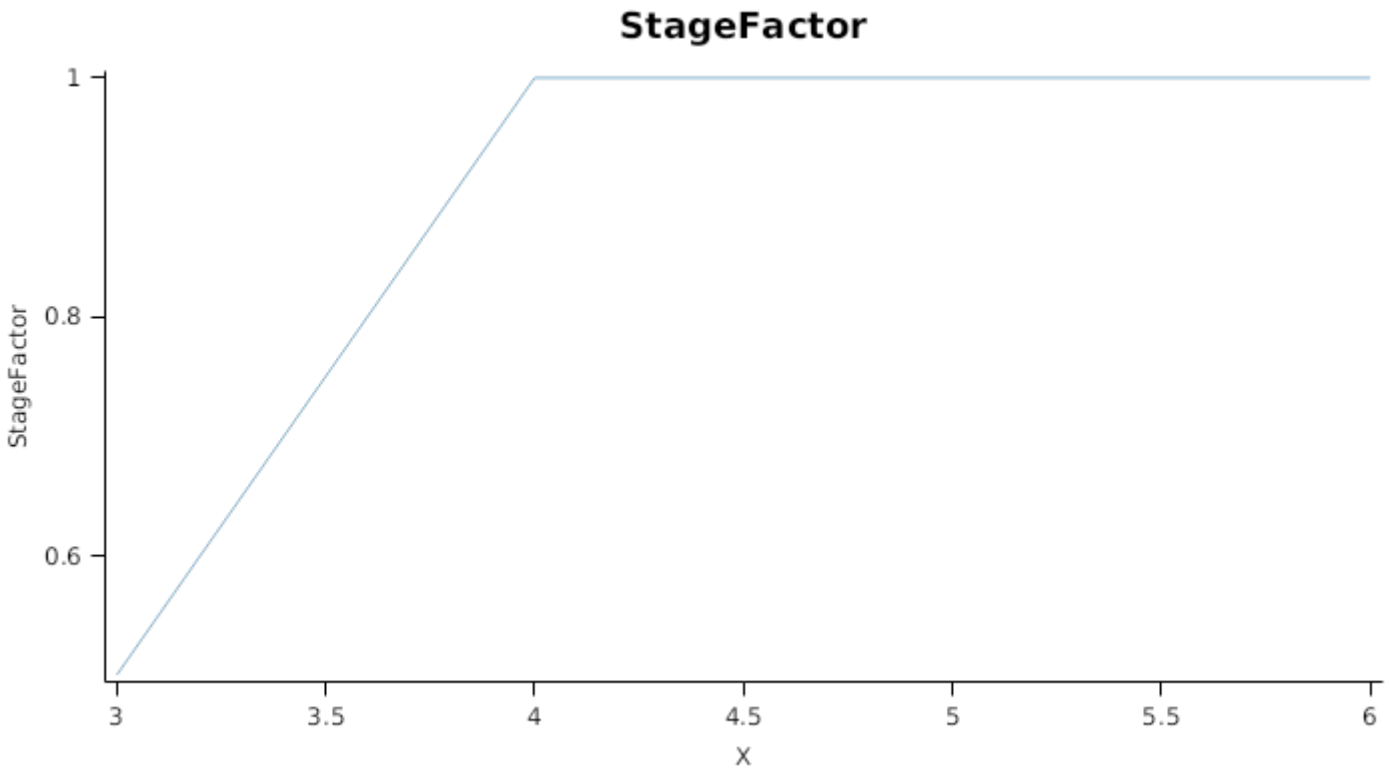
The reference senescence rate is adjusted using generic relationships to environmental factors, such as temperature and soil moisture. These are based on general knowledge from other plant models.

SenescenceRate = *ReferenceRate* x *StageFactor* x *TemperatureFactor* x *SoilMoistureFactor*

ReferenceRate = 0.01 (/day)

StageFactor is calculated using linear interpolation

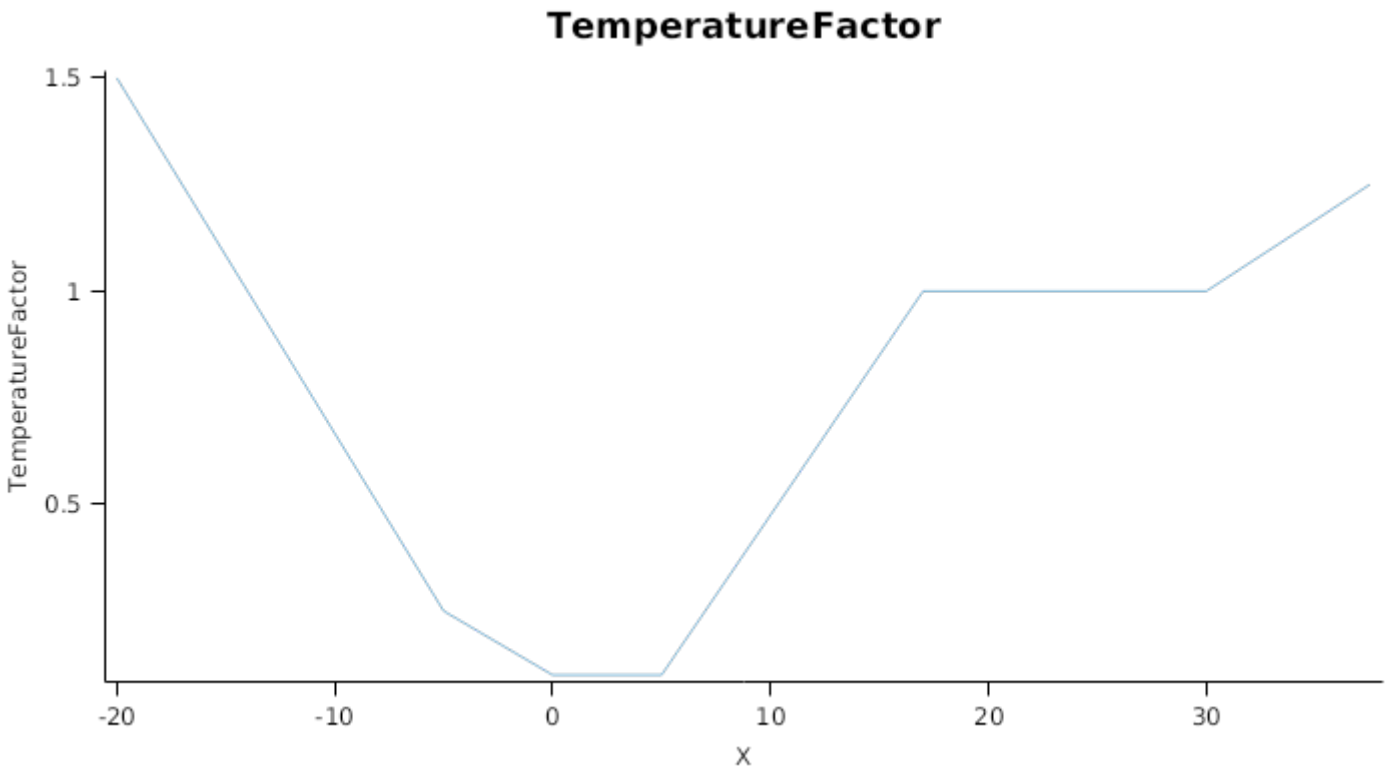
X	StageFactor
3.0	0.5
4.0	1.0
6.0	1.0

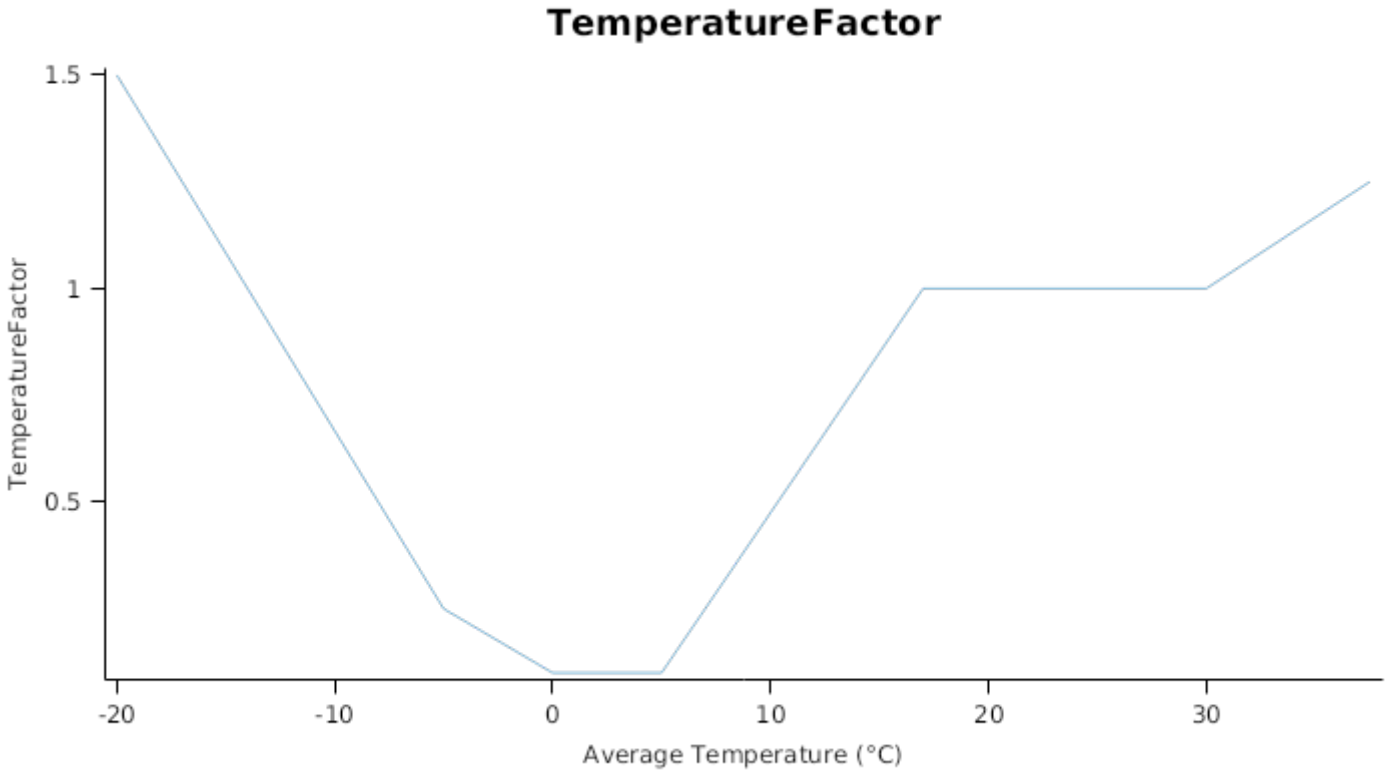


TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

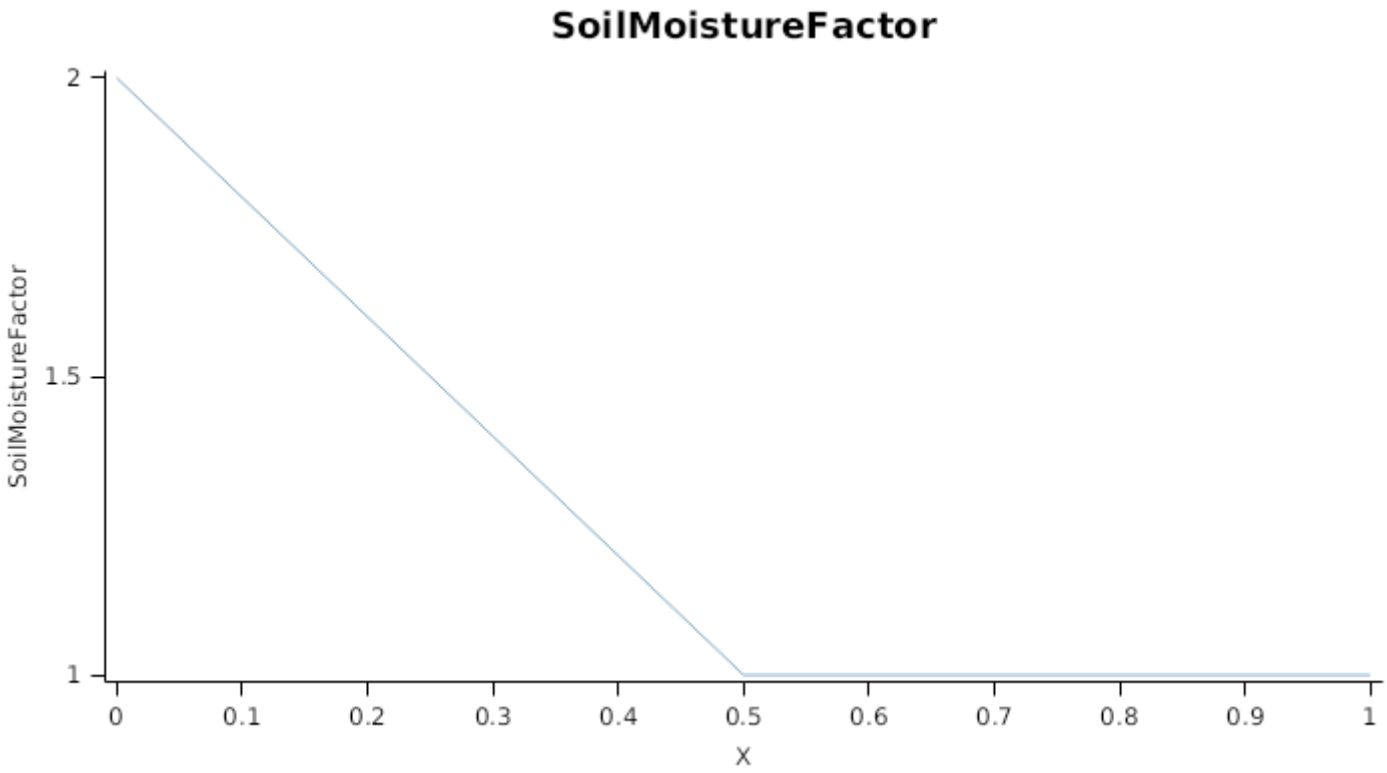
X	TemperatureFactor
-20.0	1.5
-5.0	0.2
0.0	0.1
5.0	0.1
17.0	1.0
30.0	1.0
37.5	1.2





SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	2.0
0.5	1.0
1.0	1.0



The proportion of Biomass that detaches and is passed to the surface organic matter model for decomposition is quantified by the DetachmentRateFunction.

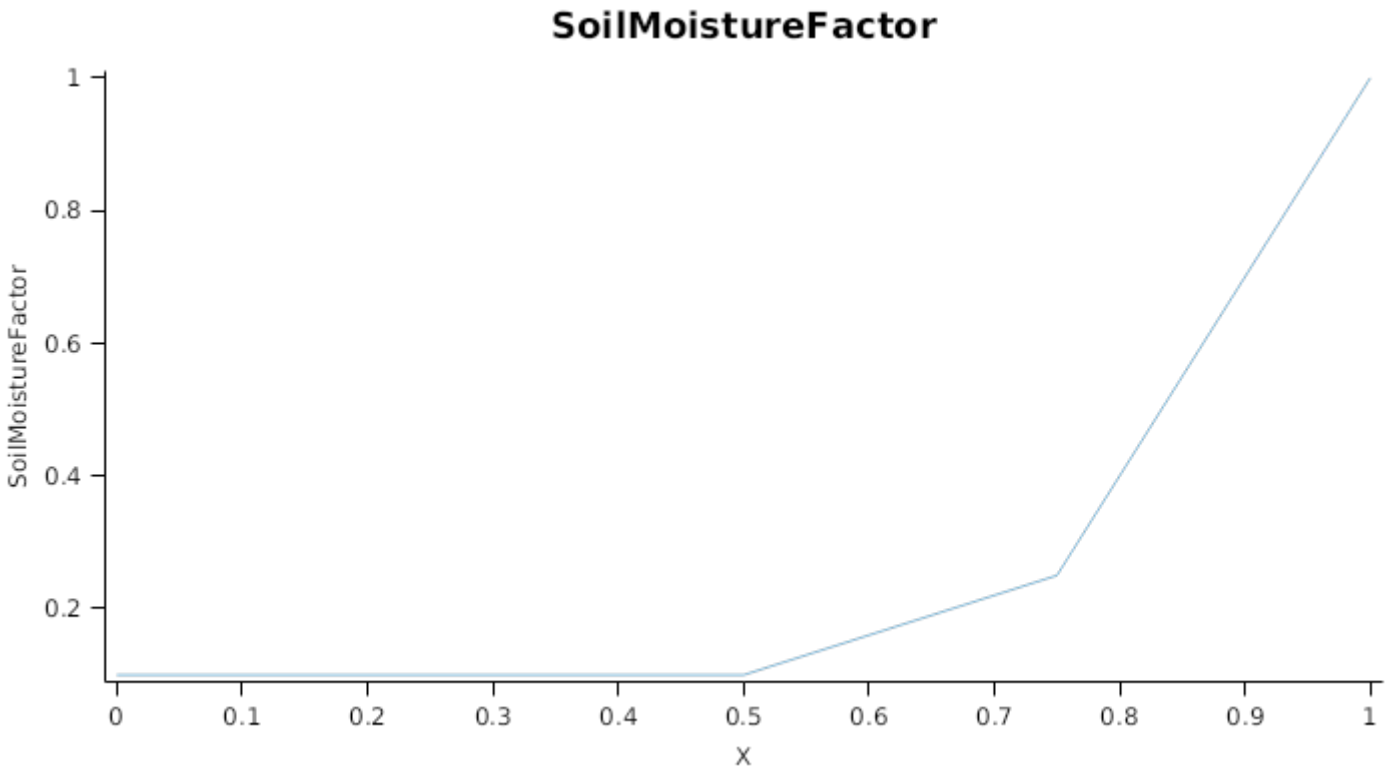
A generic relationship between detachment and soil moisture is assumed. It implies that under dry conditions the detachment rate decreases due to the lower level of activity of decomposing microorganisms.

DetachmentRateFunction = *ReferenceRate* x *SoilMoistureFactor*

ReferenceRate = 0.05 (/day)

SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.1
0.5	0.1
0.8	0.2
1.0	1.0



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
Cut	68	55	7	5
Graze	45	45	15	15
Harvest	3	4	12	14
Prune	0	0	0	0

1.11 Inflorescence

1.11.1 Inflorescence

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.

1.11.2 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.

1.11.2.1 DMDemands

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

Structural = *StructuralFraction* x *DMDemandFunction*

StructuralFraction = 1 (g/g)

The DM demand as defined here is a weighting factor, actual values are computed by the OrganArbitrator. The value is computed as the sum of a base demand, simply based on the potential partition according to the target proportions, and a deficit demand, which diverts more biomass to organs that deviate from their targeted proportions. This ensures faster regrowth of above ground organs after defoliation. The target proportion may vary with growth stage and environmental conditions.

DMDemandFunction = Max(*Zero*, *OrganDMDemand*)

Where:

Zero = 0

OrganDMDemand = *BaseBiomassDemand* + *DeficitBiomassDemand*

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

BaseBiomassDemand = *PartitionFraction x [Arbitrator].DM.TotalFixationSupply*

PartitionFraction = [TargetAboveGroundFraction] x [Inflorescence].TargetBiomassProportion

DeficitBiomassDemand = *TargetBiomass* - [Inflorescence].Live.Wt

TargetBiomass = [TargetAboveGroundFraction] x [Inflorescence].TargetBiomassProportion x [TotalLive].Wt

Metabolic = 0

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

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

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.11.3 Nitrogen Demand

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

1.11.3.1 NDemands

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

Structural = [Inflorescence].MinimumNConc x [Inflorescence].potentialDMAllocation.Structural

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

MetabolicNconc = [Inflorescence].CriticalNConc - [Inflorescence].MinimumNConc

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

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

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

NitrogenDemandSwitch = [Inflorescence].NitrogenDemandSwitch

MaxNconc = [Inflorescence].MaximumNConc

QStructuralPriority = 1

QMetabolicPriority = 1

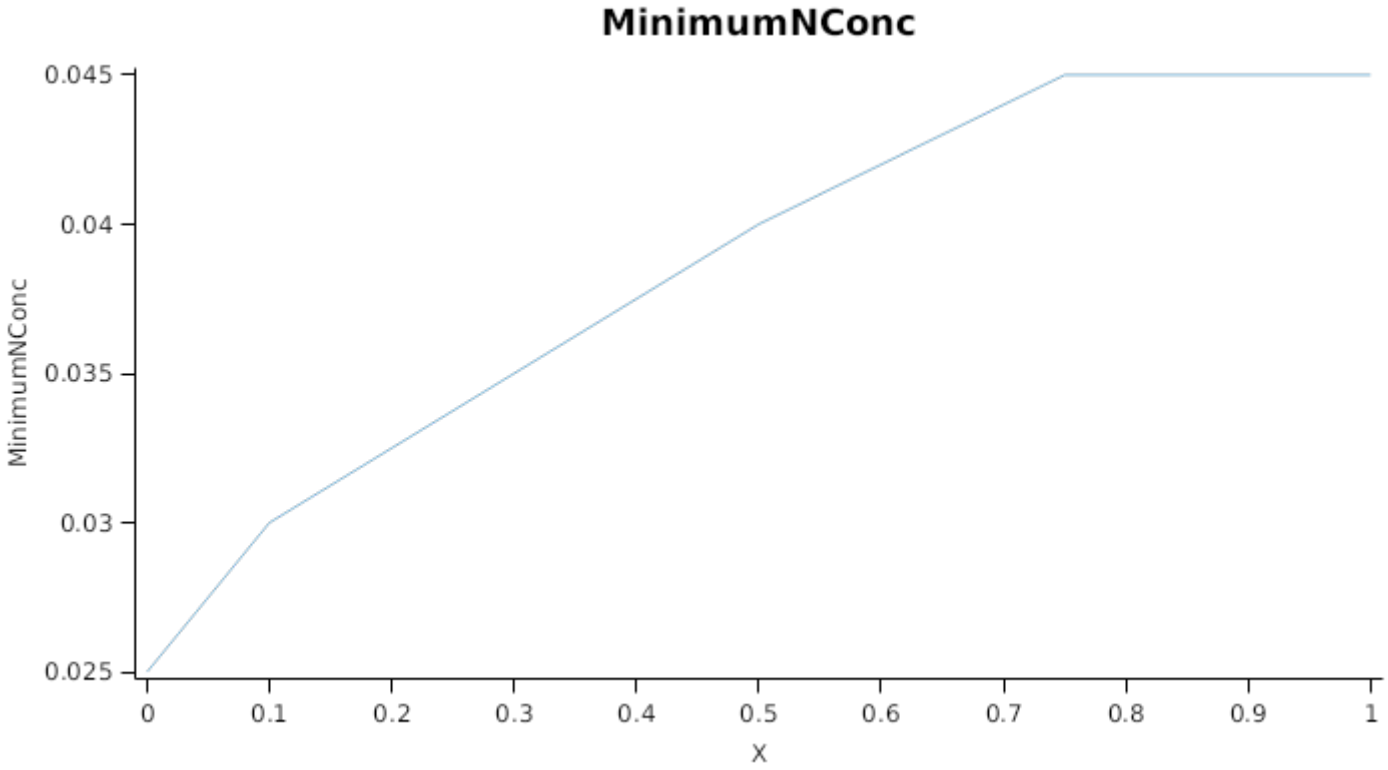
QStoragePriority = 1

1.11.4 N Concentration Thresholds

MinimumNConc is calculated using linear interpolation

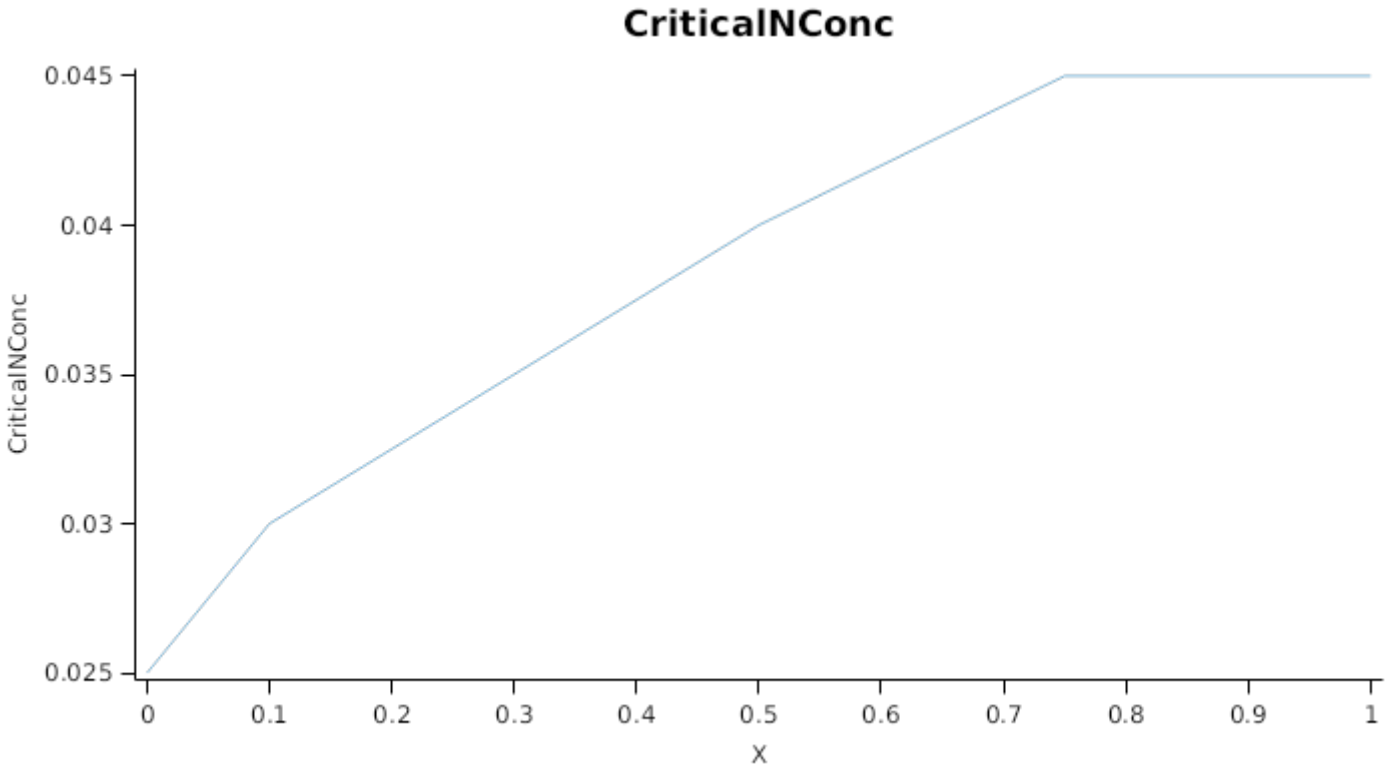
X	MinimumNConc
0.0	0.0
0.1	0.0
0.5	0.0

X	MinimumNConc
0.8	0.0
1.0	0.0



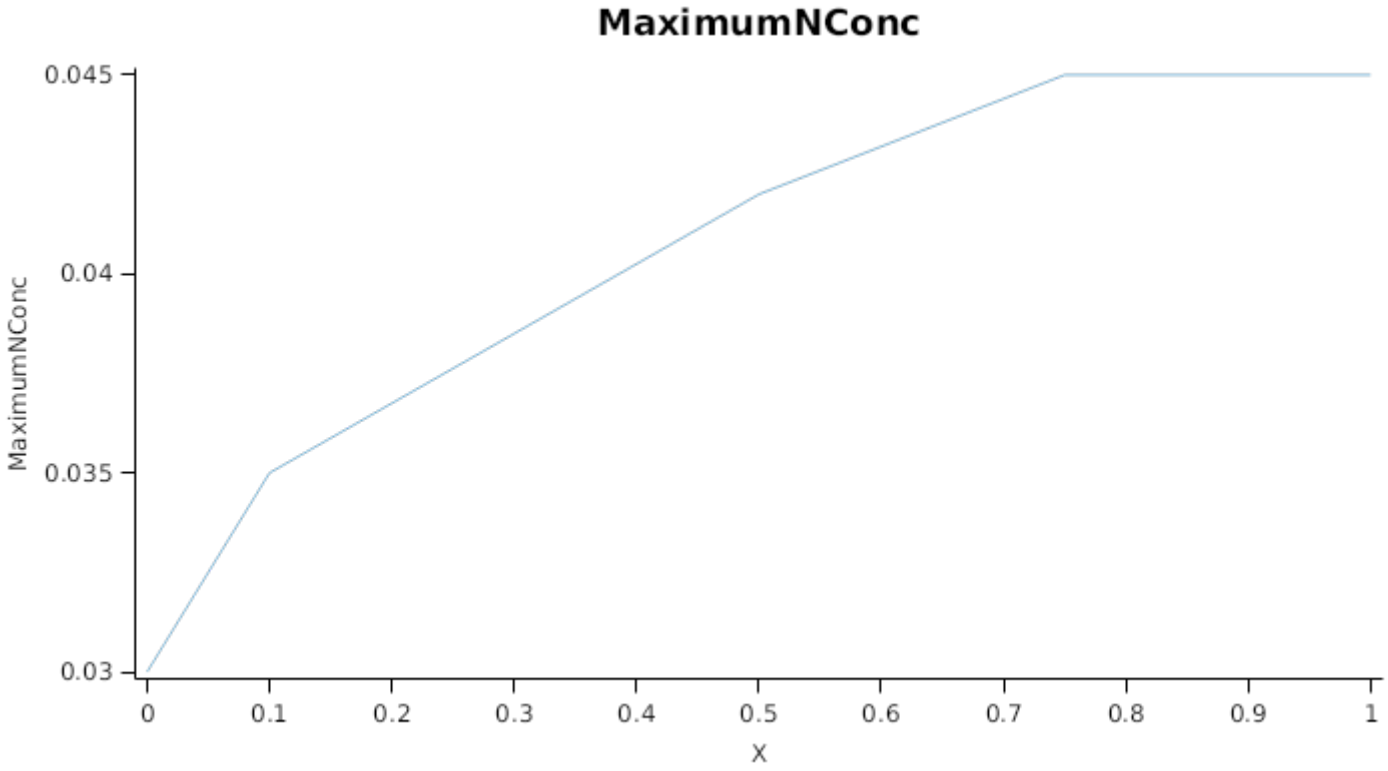
CriticalNConc is calculated using linear interpolation

X	CriticalNConc
0.0	0.0
0.1	0.0
0.5	0.0
0.8	0.0
1.0	0.0



MaximumNConc is calculated using linear interpolation

X	MaximumNConc
0.0	0.0
0.1	0.0
0.5	0.0
0.8	0.0
1.0	0.0



1.11.5 Dry Matter Supply

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

Inflorescence does not retranslocate non-structural DM.

1.11.6 Nitrogen Supply

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

Inflorescence does not retranslocate non-structural N.

1.11.7 Senescence and Detachment

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

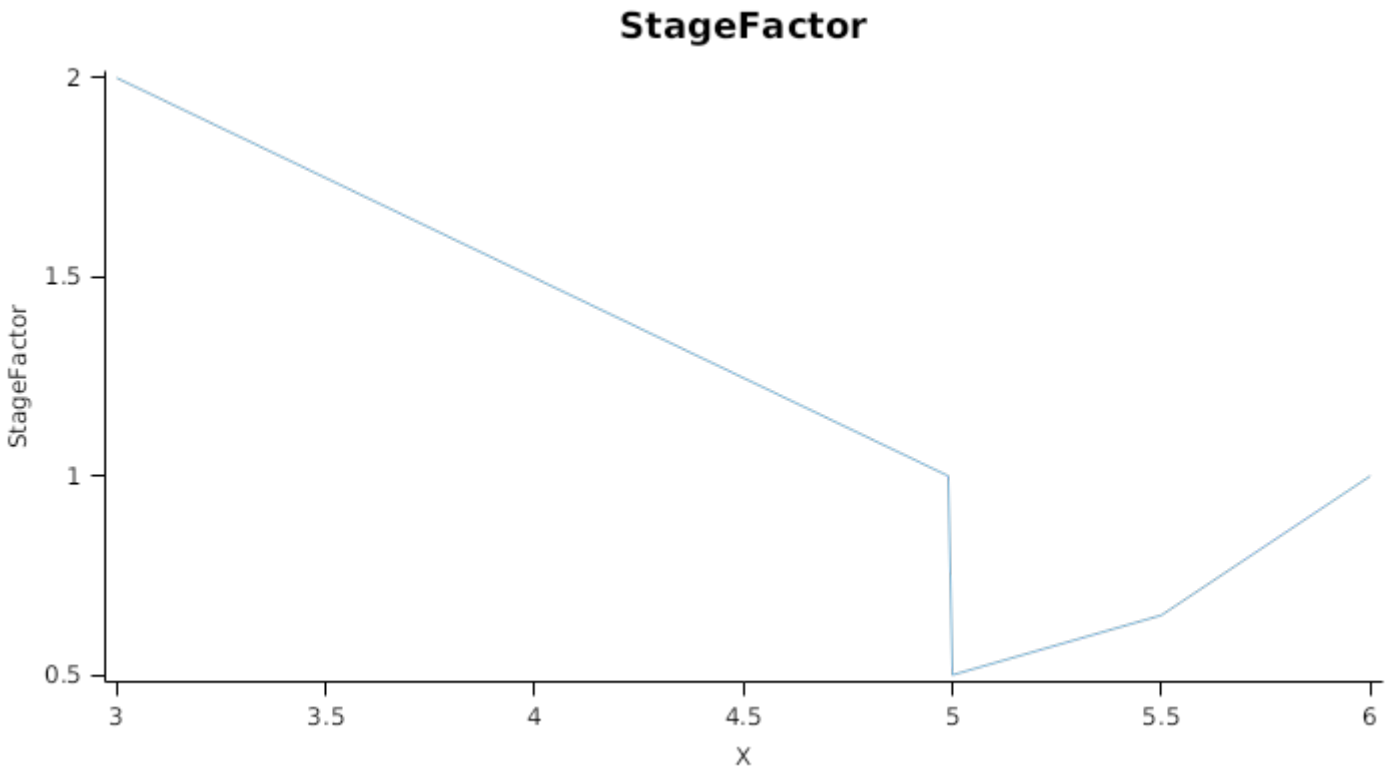
The reference senescence rate is adjusted using generic relationships to environmental factors, such as temperature and soil moisture. These are based on general knowledge from other plant models.

SenescenceRate = *ReferenceRate* x *StageFactor* x *TemperatureFactor* x *SoilMoistureFactor*

ReferenceRate = 0.1 (/day)

StageFactor is calculated using linear interpolation

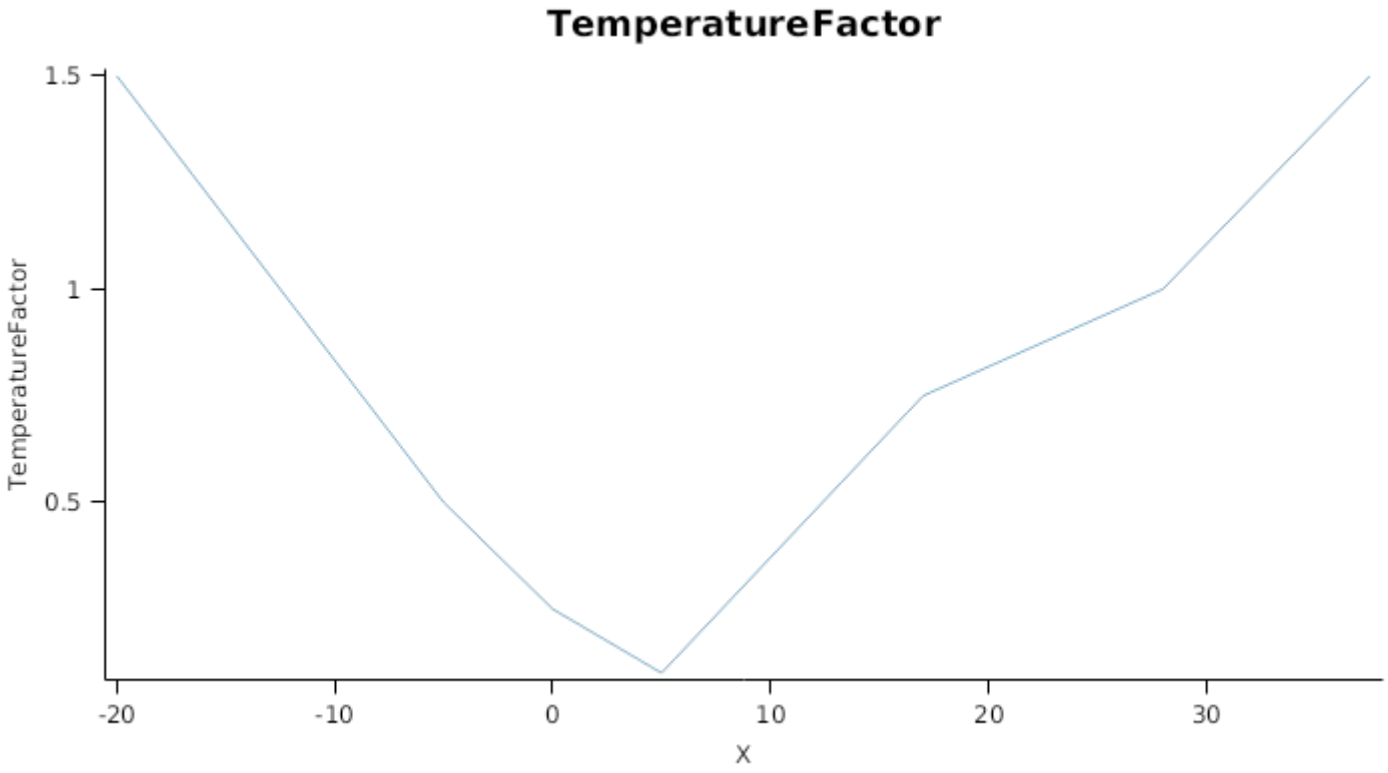
X	StageFactor
3.0	2.0
5.0	1.0
5.0	0.5
5.5	0.7
6.0	1.0

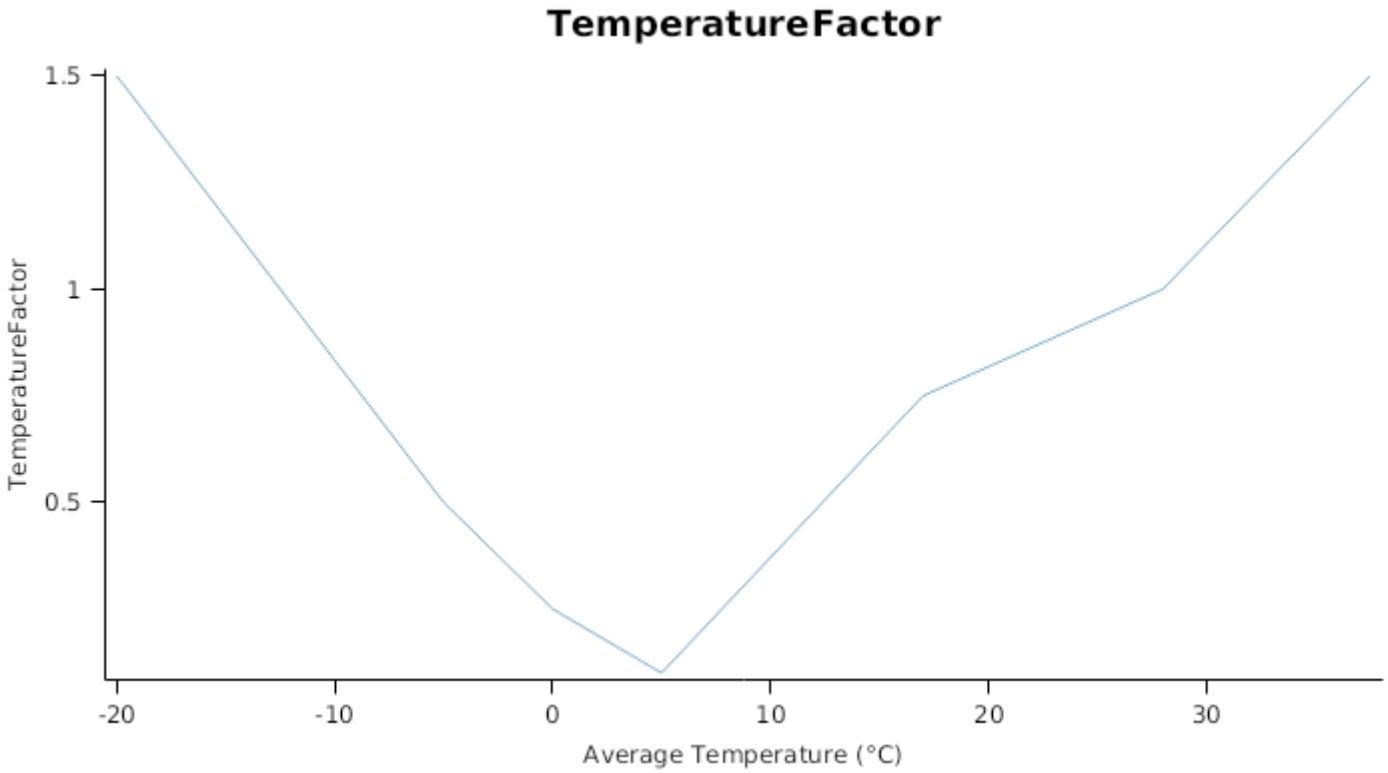


TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

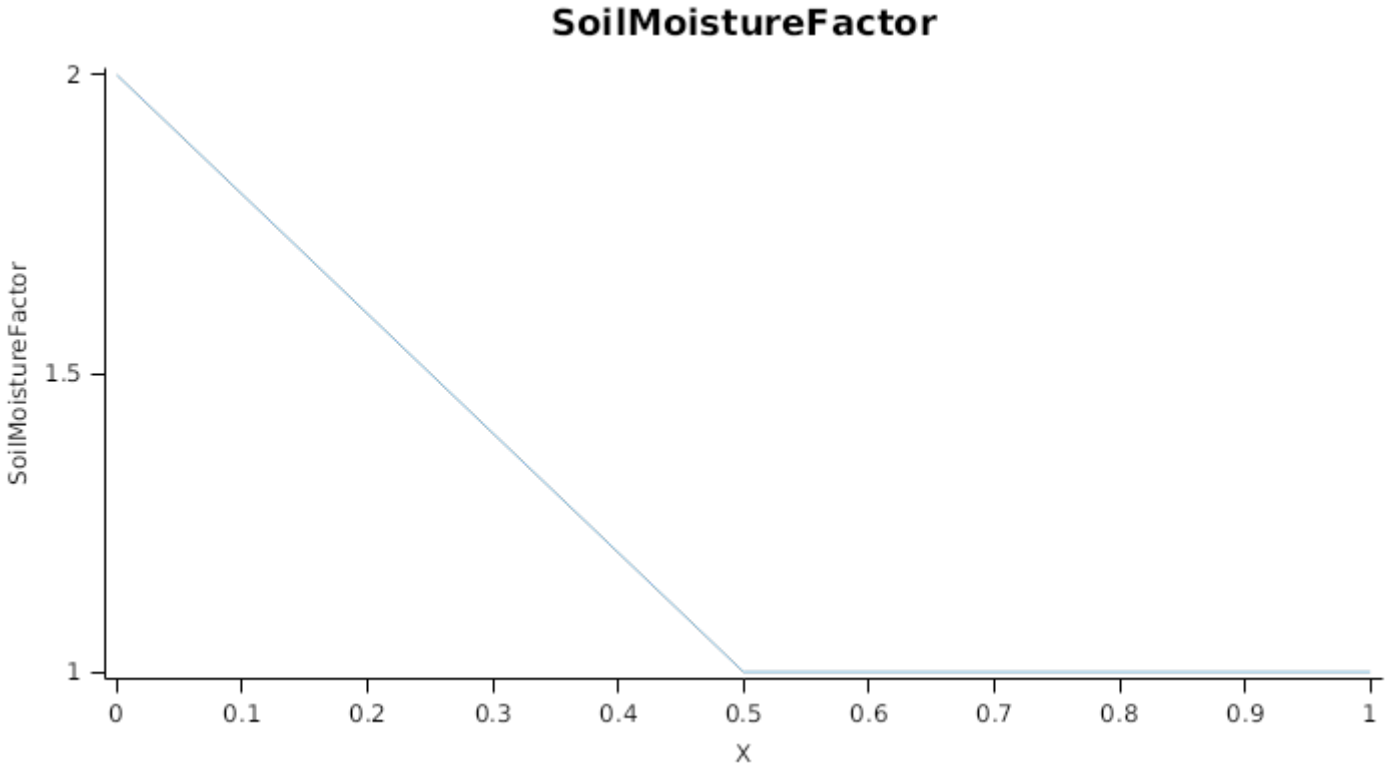
X	TemperatureFactor
-20.0	1.5
-5.0	0.5
0.0	0.2
5.0	0.1
17.0	0.8
28.0	1.0
37.5	1.5





SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	2.0
0.5	1.0
1.0	1.0



The proportion of Biomass that detaches and is passed to the surface organic matter model for decomposition is quantified by the DetachmentRateFunction.

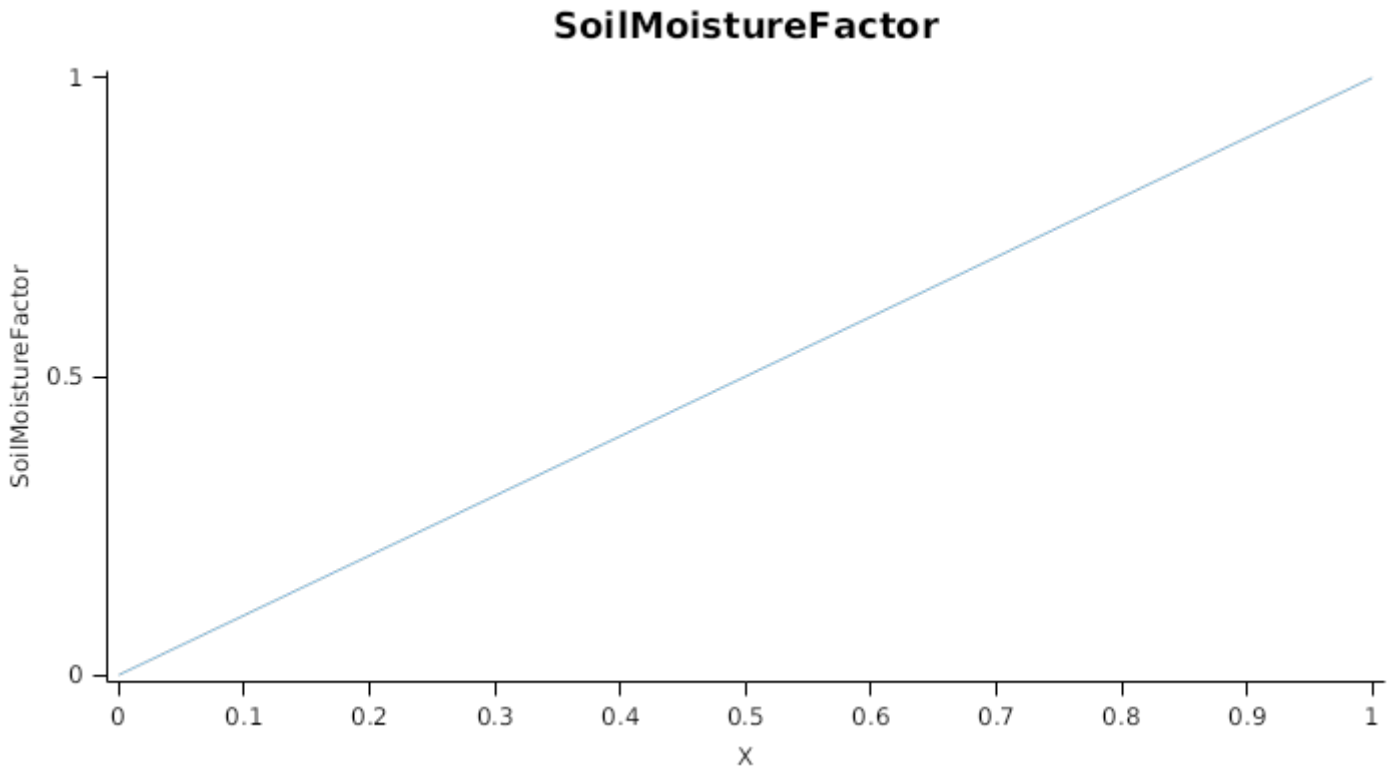
A generic relationship between detachment and soil moisture is assumed. It implies that under dry conditions the detachment rate decreases due to the lower level of activity of decomposing microorganisms.

DetachmentRateFunction = *ReferenceRate* x *SoilMoistureFactor*

ReferenceRate = 0.1 (/day)

SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.0
0.5	0.5
1.0	1.0



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
Cut	68	55	17	15
Graze	63	63	27	27
Harvest	60	70	15	20
Prune	0	0	0	0

1.12 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.

1.12.1 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 = *StructuralFraction* x *DMDemandFunction*

StructuralFraction = 1 (g/g)

The DM demand as defined here is a weighting factor, actual values are computed by the OrganArbitrator. The value is computed as the sum of a base demand, simply based on the potential partition according to the target proportions, and a deficit demand, which diverts more biomass to organs that deviate from their targeted proportions. This ensures faster regrowth of above ground organs after defoliation. The target proportion may vary with growth stage and environmental conditions.

DMDemandFunction = Max(*Zero*, *OrganDMDemand*)

Where:

Zero = 0

OrganDMDemand = *BaseBiomassDemand* + *DeficitBiomassDemand*

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

BaseBiomassDemand = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction = *TargetBelowGroundProp* x [Nodule].TargetBiomassProportion

TargetBelowGroundProp = 1 - [TargetAboveGroundFraction]

DeficitBiomassDemand = *TargetBiomass* - [Nodule].Live.Wt

TargetBiomass = *TargetBelowGroundProp* x [Nodule].TargetBiomassProportion x [TotalLive].Wt

TargetBelowGroundProp = 1 - [TargetAboveGroundFraction]

Metabolic = 0

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

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

1.12.2 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 = 0.05 (gN/gDM)

CriticalNConc = 0.055 (gN/gDM)

MaximumNConc = 0.055 (gN/gDM)

1.12.3 Dry Matter Supply

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

Nodule does not retranslocate non-structural DM.

1.12.4 Nitrogen Supply

Nodule will reallocate 100% of N that senesces each day.

Nodule does not retranslocate non-structural N.

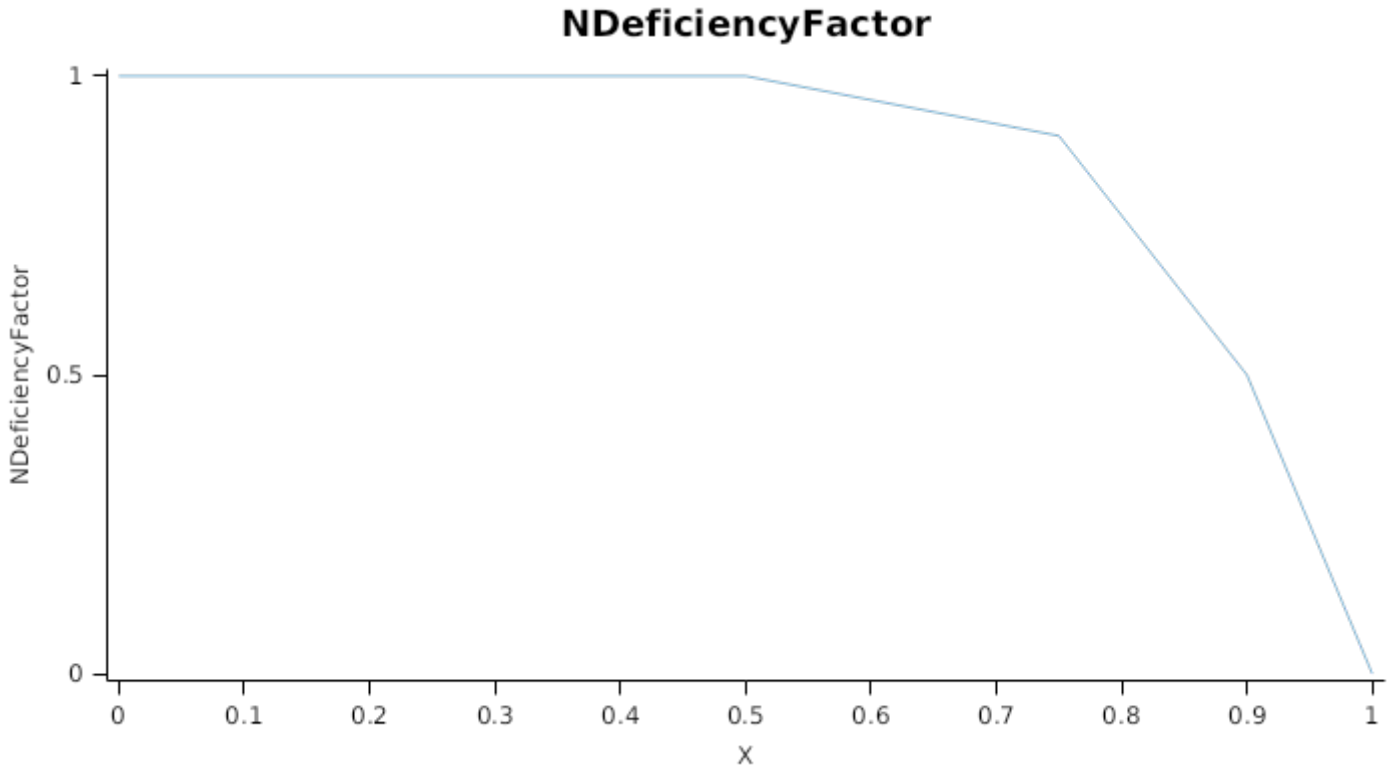
The rate of N fixation in legumes is highly regulated by the host plant, but in its basis it is defined by the presence and quantity of symbiont bacteria. The RedClover model uses an approach whereby the basic fixation rate is directly proportional to the biomass of nodules (Rys et al., 1985; Ledgard et al., 1990; Warembourg et al., 1997; Hogh-Jensen et al., 2002; Russelle et al., 2008). This is then regulated by environmental factors and the plant (Crush, 1987; Russelle et al., 2008). The plants control N fixation by limiting the supply of sugars and oxygen to the nodules (Puppo et al., 2005; Russelle et al., 2008; Haag et al., 2013). In the model, this is simulated as a function of N deficiency, with fixation rate being inversely proportional to the plant's N deficiency factor. The mechanism regulating N fixation is quite fast, with fixation nearly ceasing soon after fertilisation or defoliation (e.g. Carroll et al., 1983; Russelle et al., 2008). By linking potential fixation to nodule biomass, the model is capable of describing both a upper limit for fixation and the temporal lag between the inception of N stress and an elevated N fixation rate.

FixationRate = *MaxFixationRate* x [Nodule].Live.Wt x *NDeficiencyFactor* x *EnvironmentalFactor*

MaxFixationRate = 0.05 (gN/gDM nodule/day)

NDeficiencyFactor is calculated using linear interpolation

X	NDeficiencyFactor
0.0	1.0
0.5	1.0
0.8	0.9
0.9	0.5
1.0	0.0

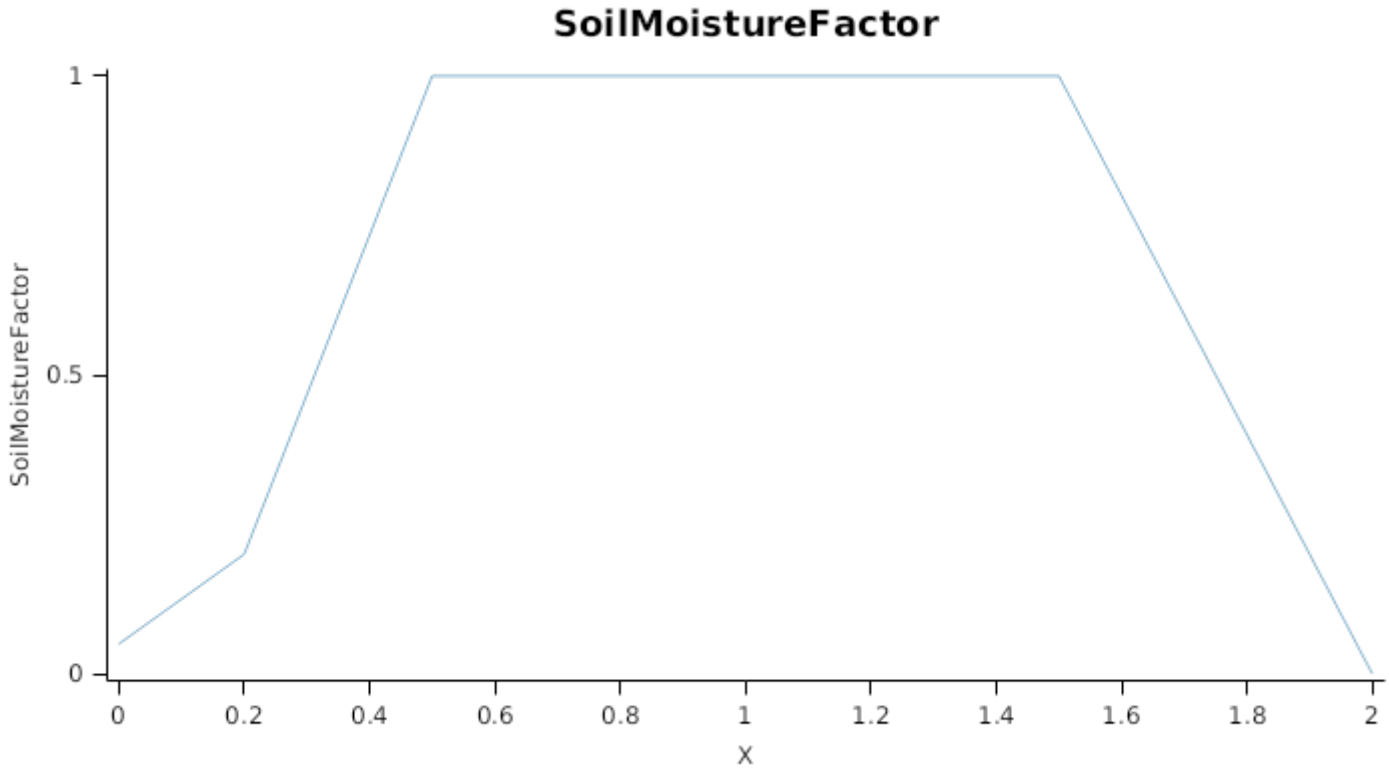


EnvironmentalFactor = Min(*SoilMoistureFactor*, *TemperatureFactor*)

Where:

SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.1
0.2	0.2
0.5	1.0
1.0	1.0
1.5	1.0
2.0	0.0



TemperatureFactor = [Leaf].NRetranslocationFactor.TemperatureFactor

1.12.5 Senescence and Detachment

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

The reference senescence rate is adjusted according to enviromental factors, temperature and soil water status.

SenescenceRate = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor* x *SoilAerationFactor*

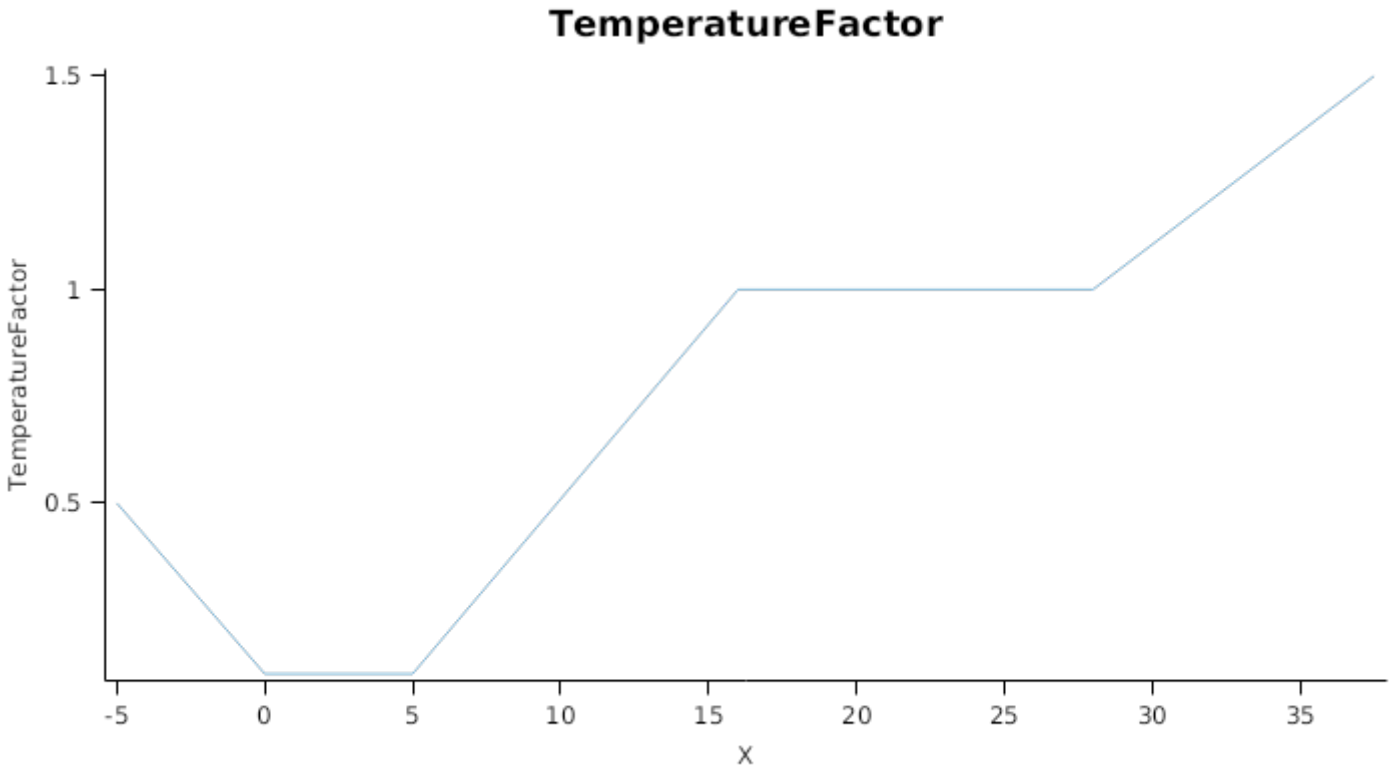
ReferenceRate = 0.005 (/day)

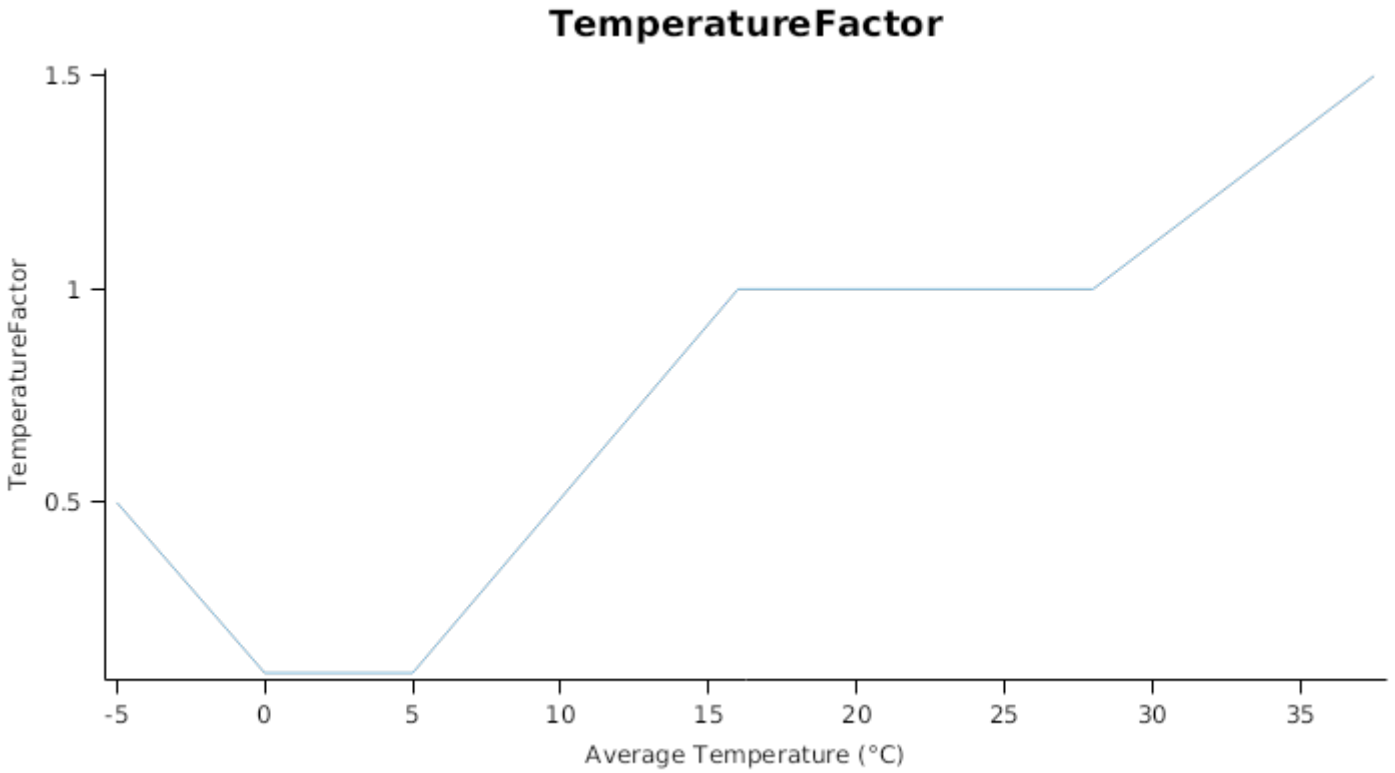
TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

X	TemperatureFactor
-5.0	0.5
0.0	0.1

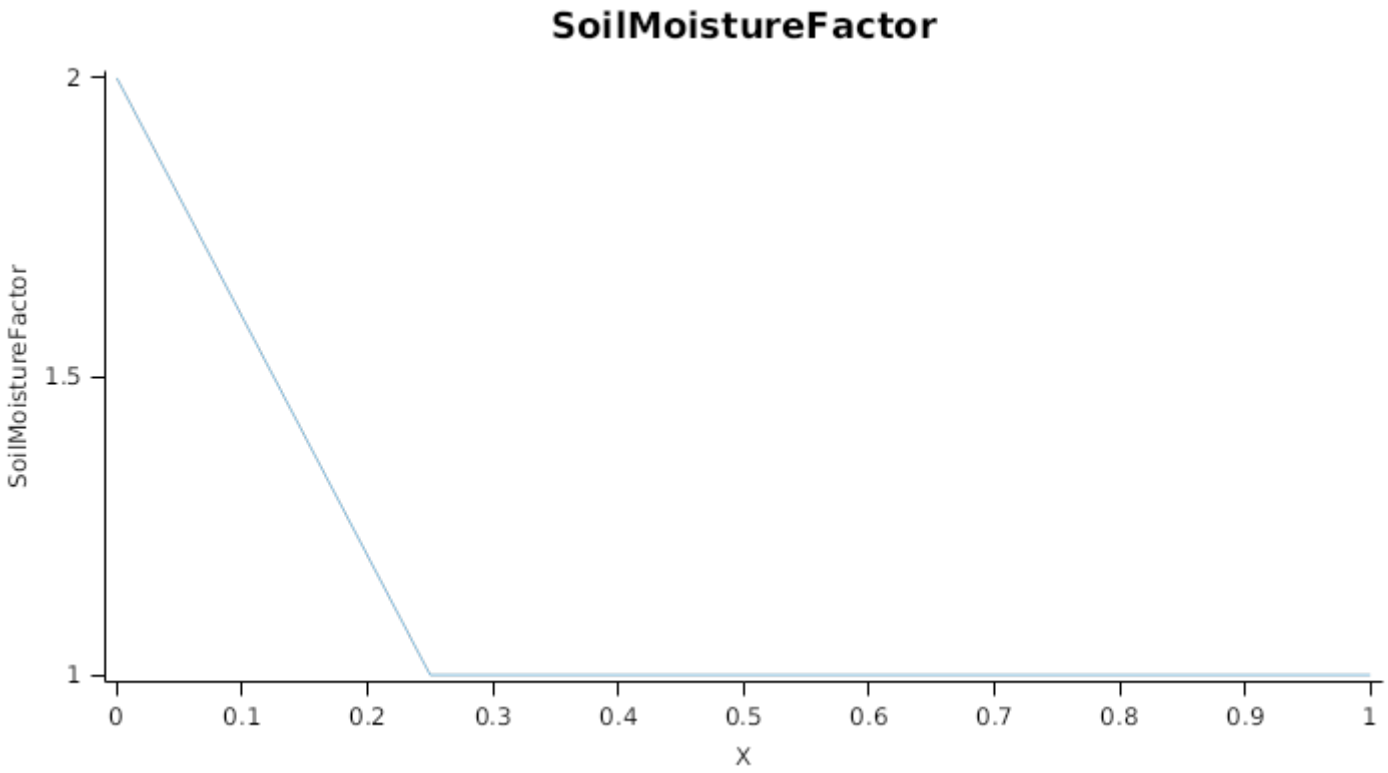
X	TemperatureFactor
5.0	0.1
16.0	1.0
28.0	1.0
37.5	1.5





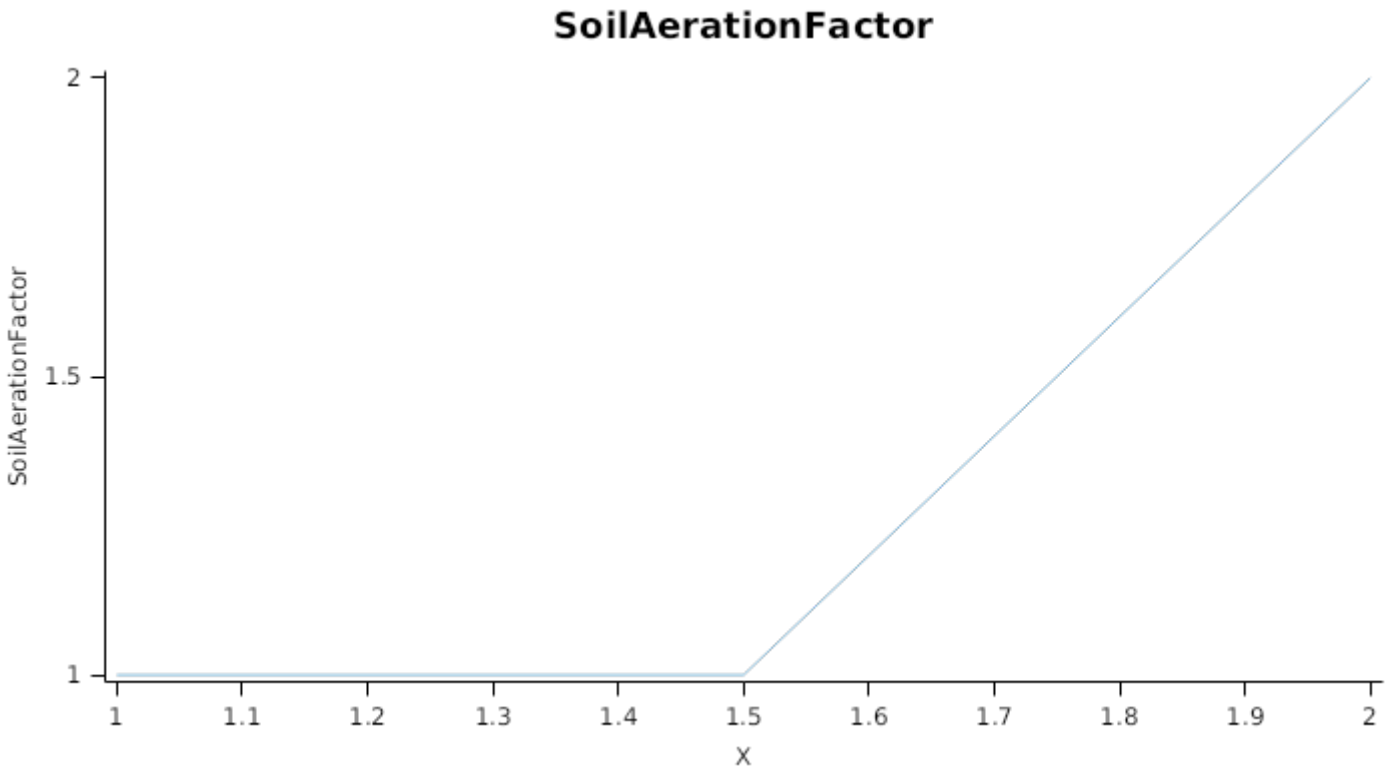
SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	2.0
0.2	1.0
1.0	1.0



SoilAerationFactor is calculated using linear interpolation

X	SoilAerationFactor
1.0	1.0
1.5	1.0
2.0	2.0



Nodule detaches 100% of its live biomass each day, passing it to the surface organic matter model for decomposition.

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	10	0
Cut	0	0	10	0
Prune	0	0	5	0
Graze	0	0	0	0

1.13 Taproot

1.13.1 Taproot

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.

1.13.2 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.

1.13.2.1 DMDemands

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

Structural = *StructuralFraction* x *DMDemandFunction*

StructuralFraction = 0.85 (g/g)

The DM demand as defined here is a weighting factor, actual values are computed by the OrganArbitrator. The value is computed as the sum of a base demand, simply based on the potential partition according to the target proportions, and a deficit demand, which diverts more biomass to organs that deviate from their targeted proportions. This ensures faster

regrowth of above ground organs after defoliation. The target proportion may vary with growth stage and environmental conditions.

DMDemandFunction = Max(*Zero*, *OrganDMDemand*)

Where:

Zero = 0

OrganDMDemand = *BaseBiomassDemand* + *DeficitBiomassDemand*

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

BaseBiomassDemand = *PartitionFraction x [Arbitrator].DM.TotalFixationSupply*

PartitionFraction = *TargetBelowGroundProp* x [Taproot].TargetBiomassProportion

TargetBelowGroundProp = 1 - [TargetAboveGroundFraction]

DeficitBiomassDemand = *TargetBiomass* - [Taproot].Live.Wt

TargetBiomass = *TargetBelowGroundProp* x [Taproot].TargetBiomassProportion x [TotalLive].Wt

TargetBelowGroundProp = 1 - [TargetAboveGroundFraction]

Metabolic = *MetabolicFraction* x [Taproot].DMDemands.Structural.DMDemandFunction

MetabolicFraction = 0 (g/g)

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

StorageFraction = 1 - [Taproot].DMDemands.Structural.StructuralFraction - [Taproot] .DMDemands.Metabolic.MetabolicFraction

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.13.3 Nitrogen Demand

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

1.13.3.1 NDemands

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

Structural = [Taproot].MinimumNConc x [Taproot].potentialDMAllocation.Structural

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

MetabolicNconc = [Taproot].CriticalNConc - [Taproot].MinimumNConc

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

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

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

NitrogenDemandSwitch = [Taproot].NitrogenDemandSwitch

MaxNconc = [Taproot].MaximumNConc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.13.4 N Concentration Thresholds

MinimumNConc = 0.025 (gN/gDM)

CriticalNConc = 0.025 (gN/gDM)

MaximumNConc = 0.0325 (gN/gDM)

1.13.5 Dry Matter Supply

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

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

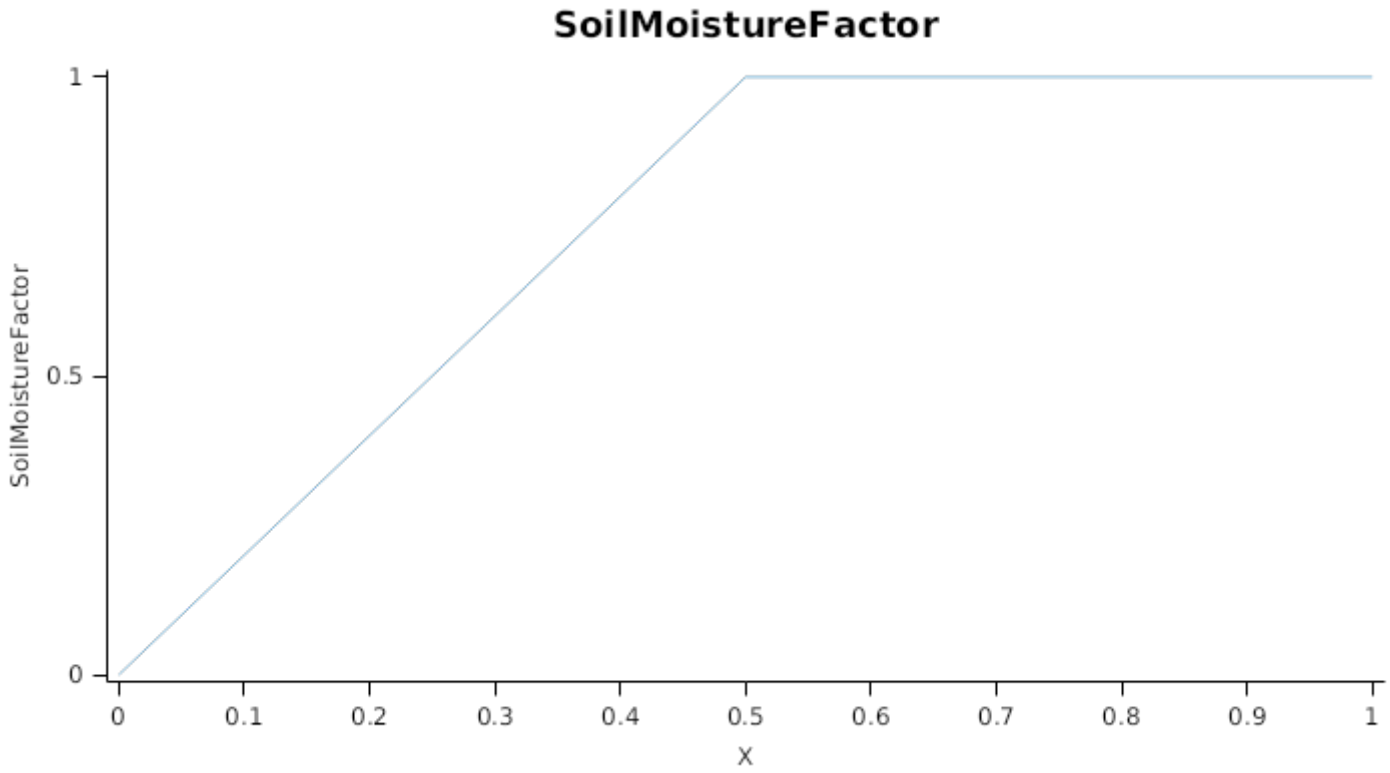
A generic relationship between retranslocation and environmental factors is assumed, this is done so that retranslocation is enhanced when conditions are good for growth. Plus retranslocation is only allowed when days are increasing, thus helping growth in spring and allowing for some replenishing in late summer and autumn.

DMRetranslocationFactor = *ReferenceRate* x [Leaf].NRetranslocationFactor.TemperatureFactor x *SoilMoistureFactor* x [Stem].DMRetranslocationFactor.PhotoPeriodFactor

ReferenceRate = 0.05 (/day)

SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.0
0.5	1.0
1.0	1.0



1.13.6 Nitrogen Supply

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

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

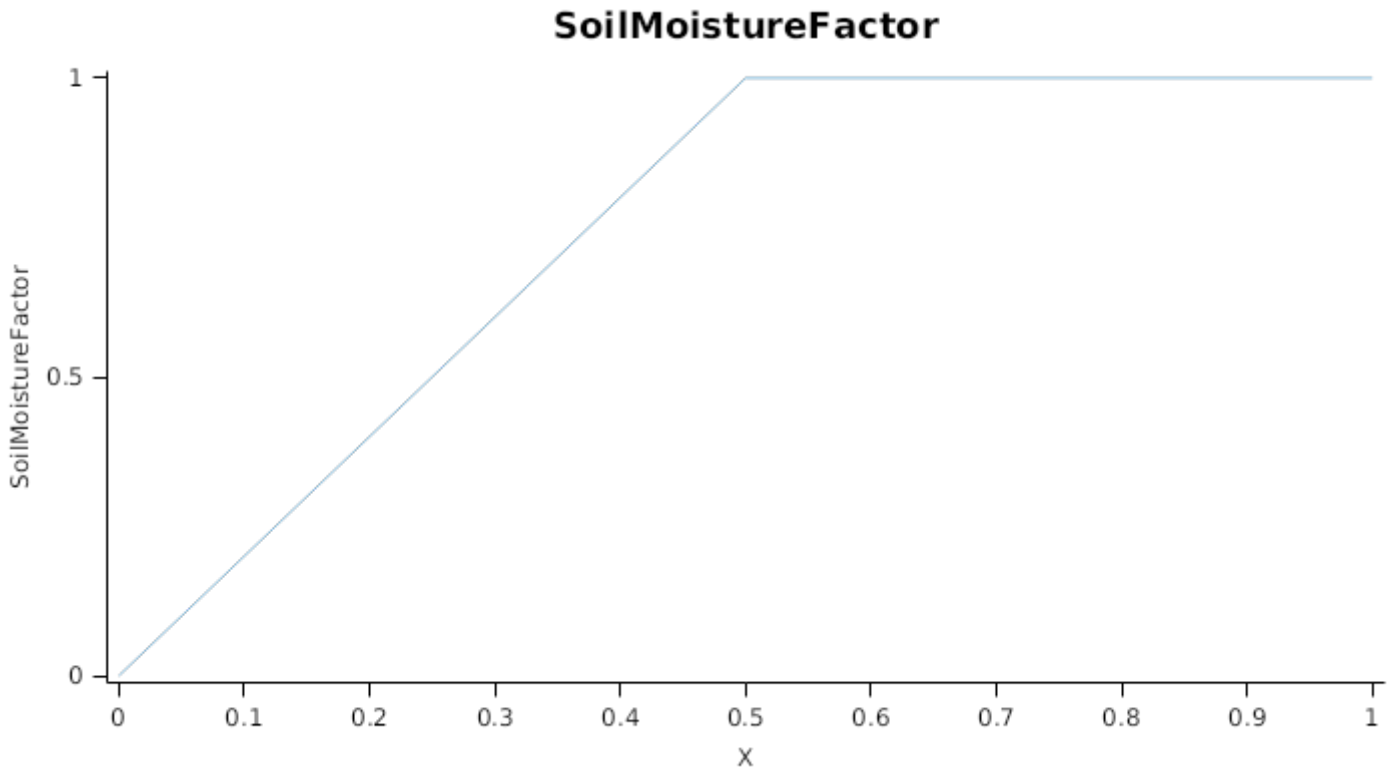
A generic relationship between retranslocation and environmental factors is assumed, this is done so that retranslocation is enhanced when conditions are good for growth. Plus retranslocation is only allowed when days are increasing, thus helping growth in spring and allowing for some replenishing in late summer and autumn.

NRetranslocationFactor = *ReferenceRate* x [Leaf].NRetranslocationFactor.TemperatureFactor x *SoilMoistureFactor* x [Stem].DMRetranslocationFactor.PhotoPeriodFactor

ReferenceRate = 0.1 (/day)

SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.0
0.5	1.0
1.0	1.0



1.13.7 Senescence and Detachment

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

The reference senescence rate is adjusted according to environmental factors, temperature and soil water status.

SenescenceRate = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor* x *SoilAerationFactor*

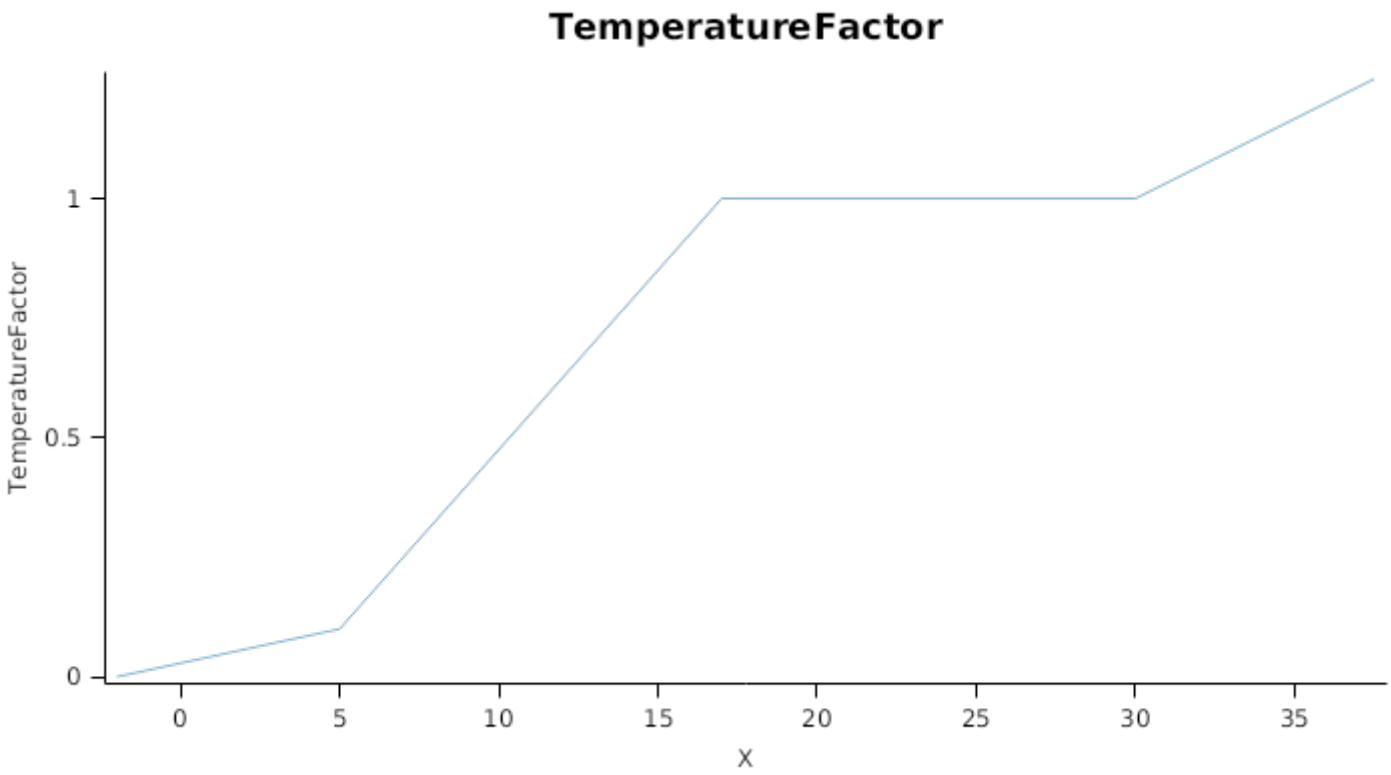
ReferenceRate = 0.01 (/day)

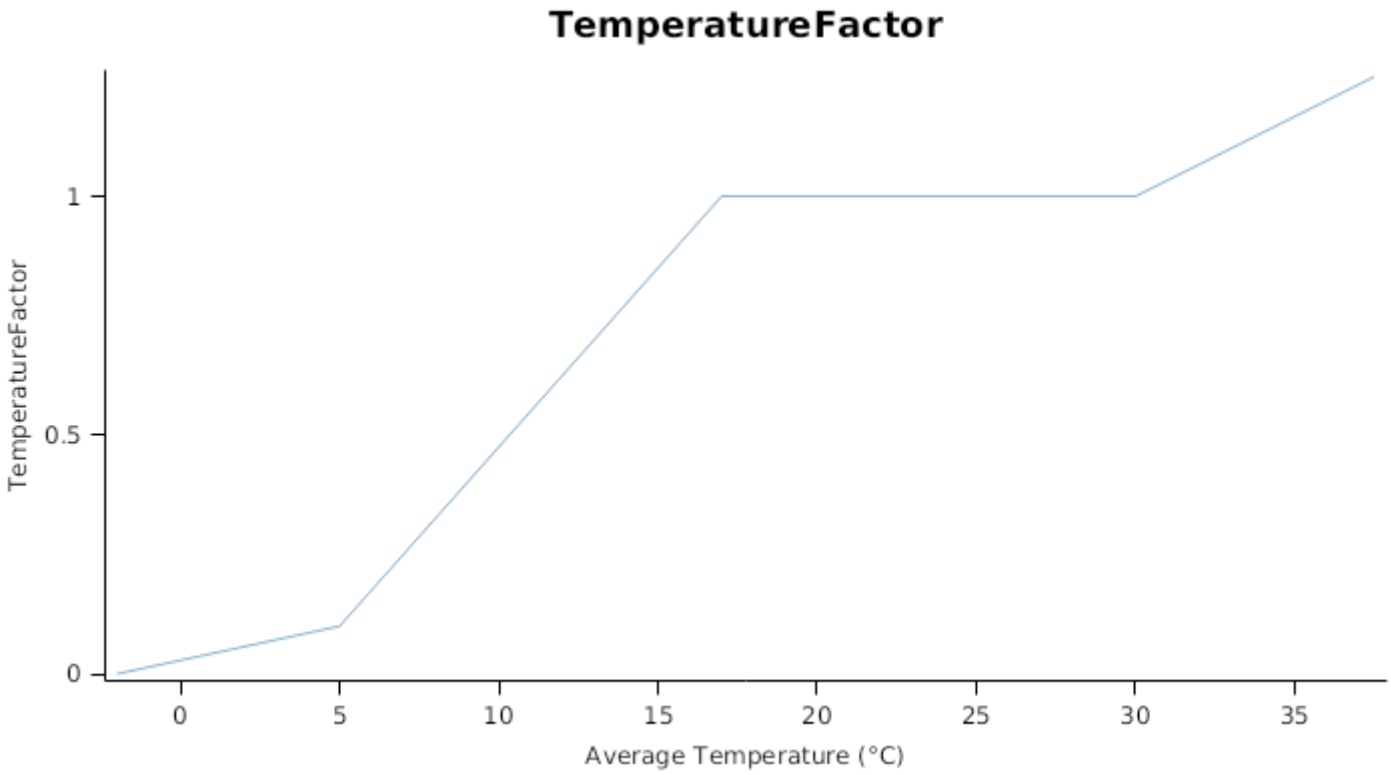
TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

X	TemperatureFactor
-2.0	0.0
5.0	0.1
17.0	1.0
30.0	1.0

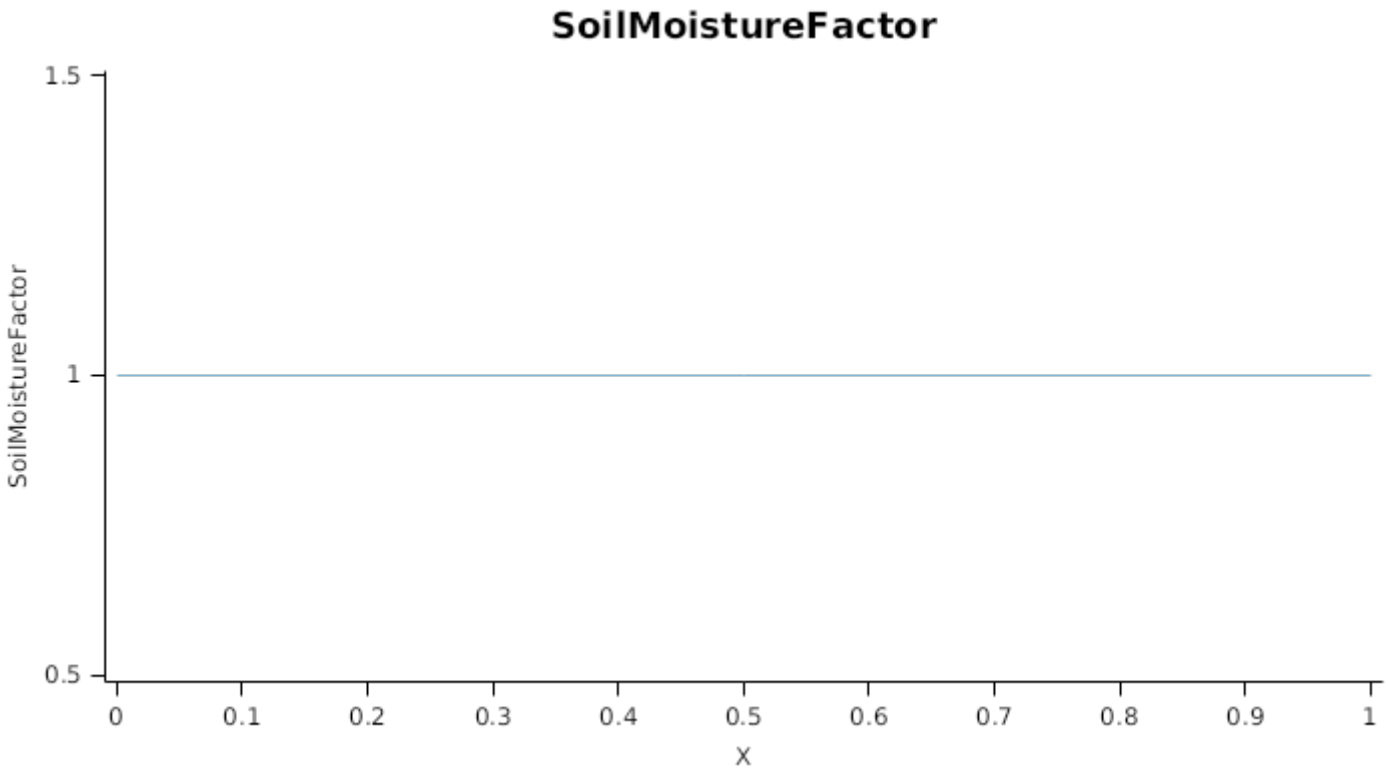
X	TemperatureFactor
37.5	1.2





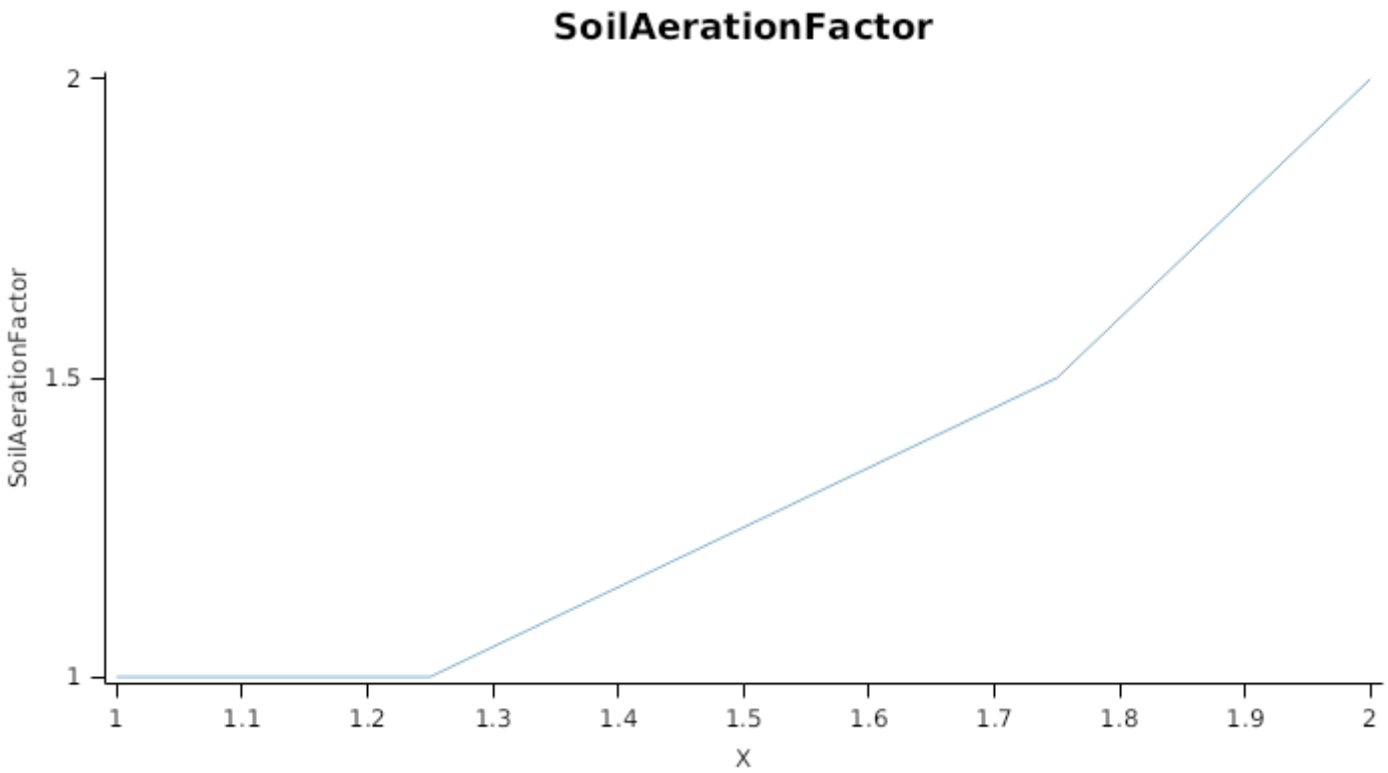
SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	1.0
0.5	1.0
1.0	1.0



SoilAerationFactor is calculated using linear interpolation

X	SoilAerationFactor
1.0	1.0
1.2	1.0
1.8	1.5
2.0	2.0



Taproot detaches 100% of its live biomass each day, passing it to the surface organic matter model for decomposition.

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
Cut	0	0	3	0
Graze	0	0	3	0
Harvest	0	0	1	0
Prune	0	0	0	0

1.14 Root

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

1.14.1 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 x XF_i *x 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

$DMAllocated_i = TotalDMAllocated \times RAw_i / TotalRAw$

1.14.2 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.

1.14.3 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.

1.14.4 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. $NO3\ uptake = NO3_i \times kNO3 \times NO3_{ppm,\ i} \times NUptakeSWFactor$ _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.

1.14.5 Water Uptake

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

1.14.6 Constants

CarbonConcentration = 0.4

MinimumNConc = 0.025 (gN/gDM)

CriticalNConc = 0.025 (gN/gDM)

MaximumNConc = 0.03 (gN/gDM)

DMConversionEfficiency = 1

MaintenanceRespirationFunction = 1

MaximumRootDepth = 750 (mm)

SpecificRootLength = 100 (m/g)

DMReallocationFactor = 1 (/day)

NReallocationFactor = 1 (/day)

RemobilisationCost = 0

MaxDailyNUptake = 10 (kgN/ha)

RootDepthStressFactor = 1

1.14.7 RootShape

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

1.14.8 Description

Note: this represents all the fine roots of the plant. The root organ demands and can supply both N and DM, although the later is typically samll and due to remobilisation of non-structural biomass upon senescence. The root depth increases through time, but currently it does not retreat. Roots provide N and water uptake supply.

1.14.9 NitrogenDemandSwitch

NitrogenDemandSwitch has a value between Germination and Ripening calculated as:

Constant = 1

1.14.10 TargetBiomassProportion

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

The targeted biomass proportion in below ground organs is linked to the variations in nodule growth. This means that if the plant experiences N deficiency it will favour the growth of the N fixing nodules instead of root and taproot. Note that this reffers only to the relative propotions of below ground organs, plant can still alter the shoot-to-root ratio so that more roots as well as noduels are growth in conditions of N deficiency.

This is the 'ideal' proportion of biomass for this organ within the above ground biomass (not total).

AllPhases has a value between Emergence and Ripening calculated as:

TargetProportion = *BaseProportion* x *VariationInOrgan*

BaseProportion = 0.5 (g/g)

VariationInOrgan = 1 - *VariationInNodule*

VariationInNodule = *DeltaNoduleProp* / *RootsBaseProp*

DeltaNoduleProp = [Nodule].TargetBiomassProportion - [Nodule]
.TargetBiomassProportion.AllPhases.TargetProportion.BaseProportion

RootsBaseProp = [Taproot].TargetBiomassProportion.AllPhases.TargetProportion.BaseProportion + [Root]
.TargetBiomassProportion.AllPhases.TargetProportion.BaseProportion

1.14.11 DMDemands

1.14.11.1 DMDemands

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

Structural = *StructuralFraction* x *DMDemandFunction*

StructuralFraction = 1 (g/g)

The DM demand as defined here is a weighting factor, actual values are computed by the OrganArbitrator. The value is computed as the sum of a base demand, simply based on the potential partition according to the target proportions, and a deficit demand, which diverts more biomass to organs that deviate from their targeted proportions. This ensures faster regrowth of above ground organs after defoliation. The target proportion may vary with growth stage and environmental conditions.

DMDemandFunction = Max(*Zero*, *OrganDMDemand*)

Where:

Zero = 0

OrganDMDemand = *BaseBiomassDemand* + *DeficitBiomassDemand*

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

BaseBiomassDemand = *PartitionFraction x [Arbitrator].DM.TotalFixationSupply*

PartitionFraction = *TargetBelowGroundProp* x [Root].TargetBiomassProportion

TargetBelowGroundProp = 1 - [TargetAboveGroundFraction]

DeficitBiomassDemand = *TargetBiomass* - [Root].Live.Wt

TargetBiomass = *TargetBelowGroundProp* x [Root].TargetBiomassProportion x [TotalLive].Wt

TargetBelowGroundProp = 1 - [TargetAboveGroundFraction]

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

1.14.12 NDemands

1.14.12.1 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

1.14.13 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:

ReferenceVelocity = 4.5 (mm/day)

VegetativeInductive has a value between Emergence and Flowering calculated as:

GrowthVelocity = *ReferenceVelocity* x *EnvironmentalFactor*

ReferenceVelocity = 9 (mm/day)

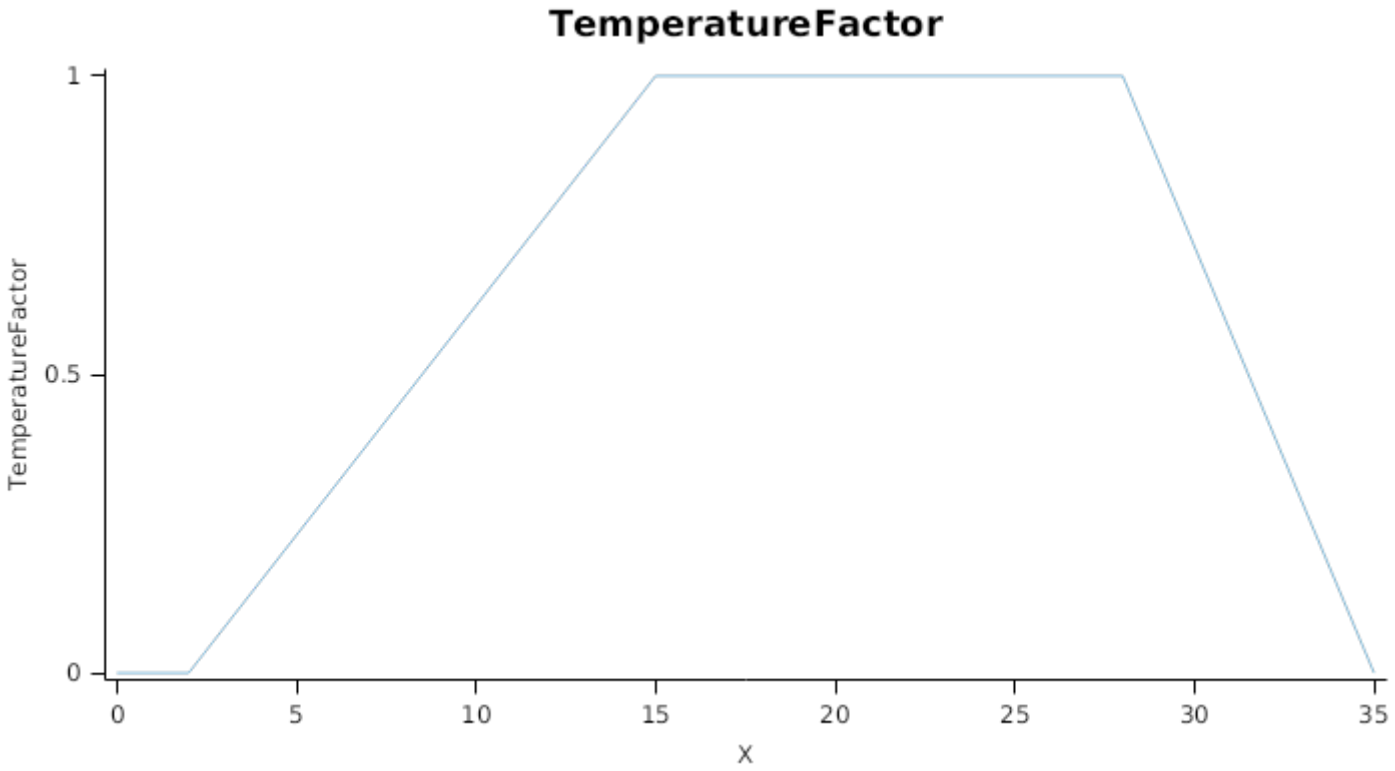
EnvironmentalFactor = Min(*TemperatureFactor*, *SoilMoistureFactor*, *SoilAerationFactor*)

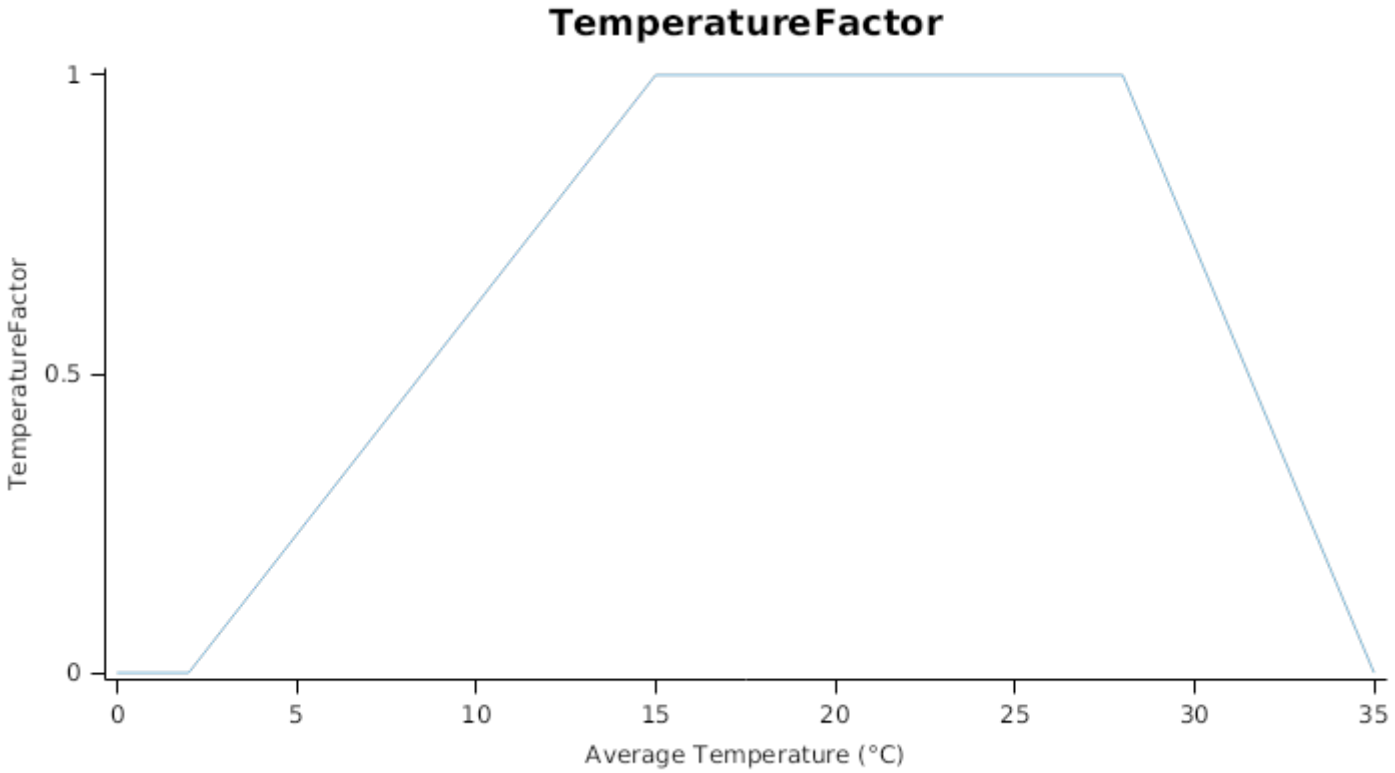
Where:

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

MaximumTemperatureWeighting = 0.5

X	TemperatureFactor
0.0	0.0
2.0	0.0
15.0	1.0
28.0	1.0
35.0	0.0





SoilMoistureFactor = 1

SoilAerationFactor = 1

Reproductive has a value between Flowering and Ripening calculated as:

GrowthVelocity = *ReferenceVelocity* x *EnvironmentalFactor*

ReferenceVelocity = 5 (mm/day)

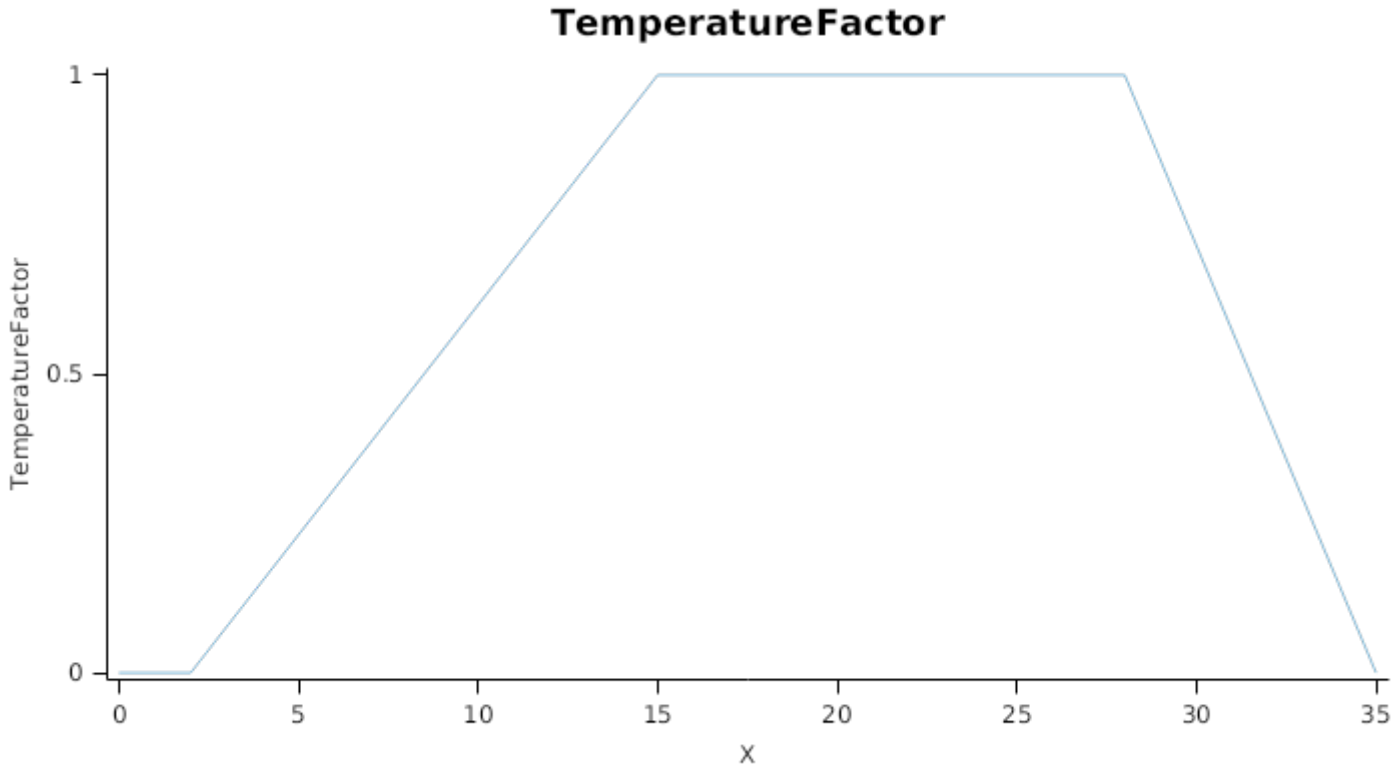
EnvironmentalFactor = Min(*TemperatureFactor*, *SoilMoistureFactor*, *SoilAerationFactor*)

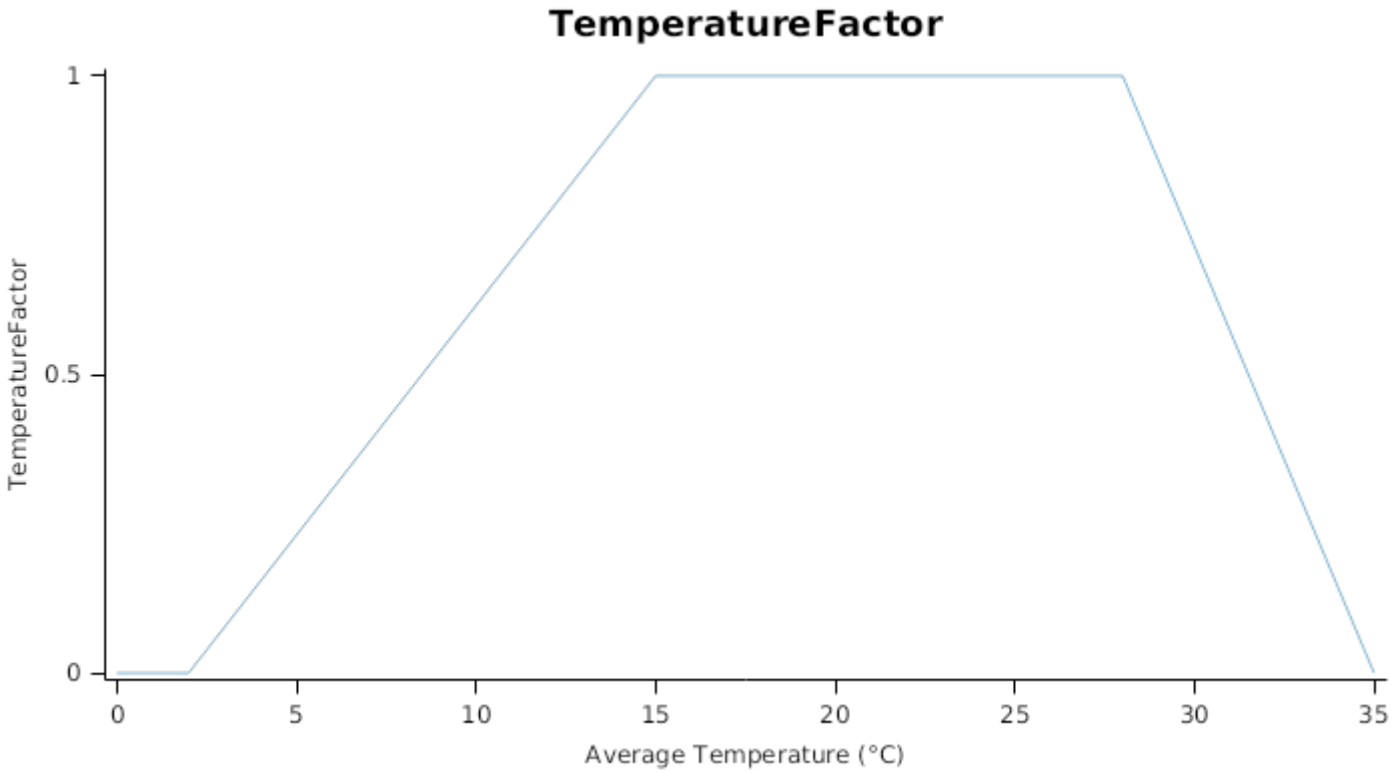
Where:

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

MaximumTemperatureWeighting = 0.5

X	TemperatureFactor
0.0	0.0
2.0	0.0
15.0	1.0
28.0	1.0
35.0	0.0





SoilMoistureFactor = 1

SoilAerationFactor = 1

1.14.14 SenescenceRate

The reference senescence rate is adjusted according to environmental factors, temperature and soil water status.

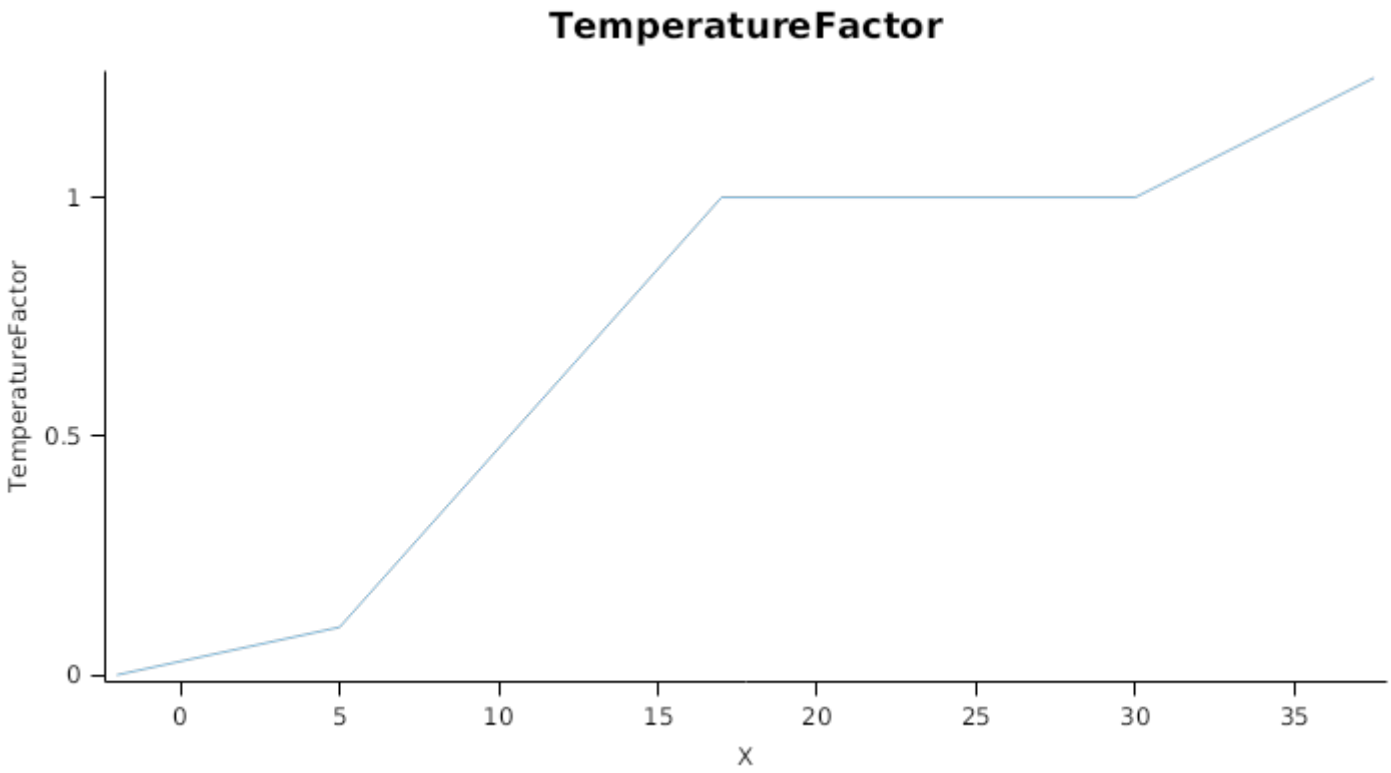
SenescenceRate = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor* x *SoilAerationFactor*

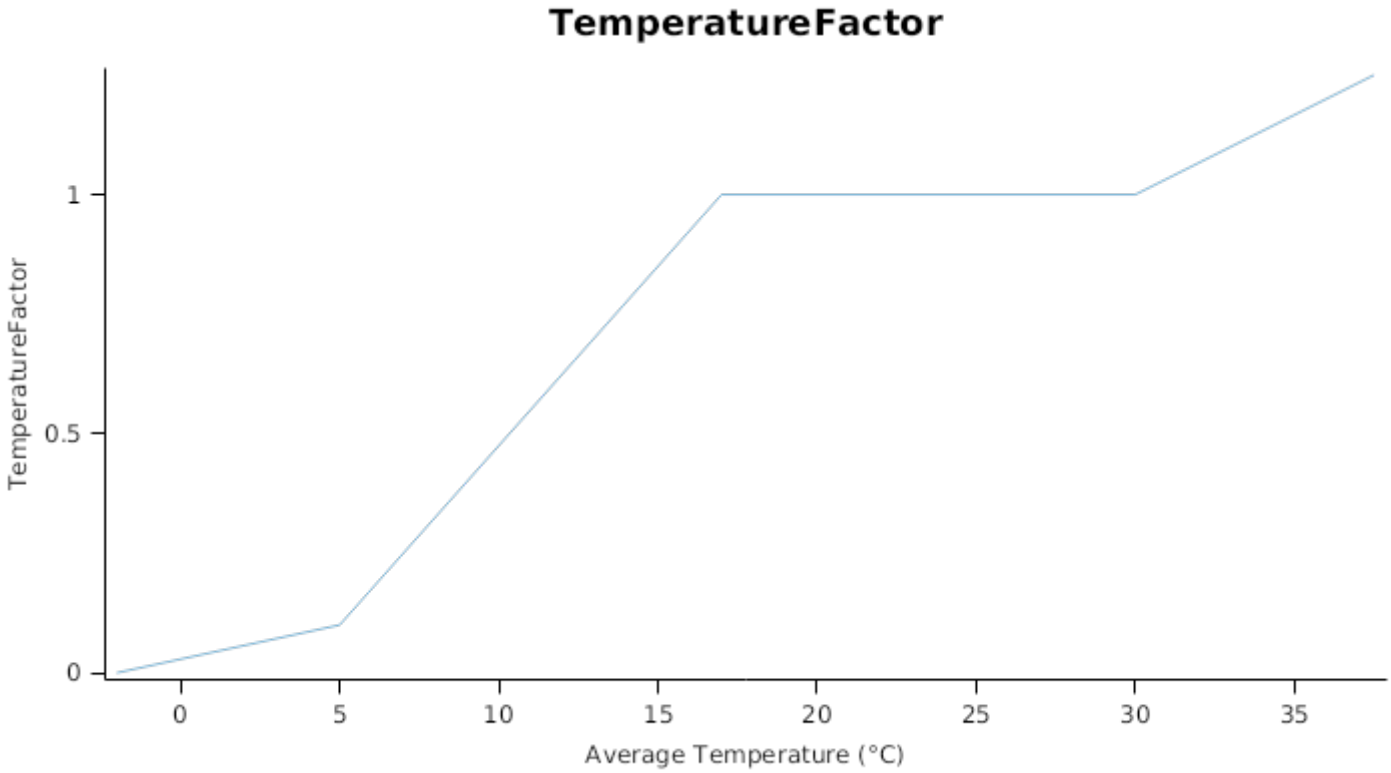
ReferenceRate = 0.02 (/day)

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

MaximumTemperatureWeighting = 0.5

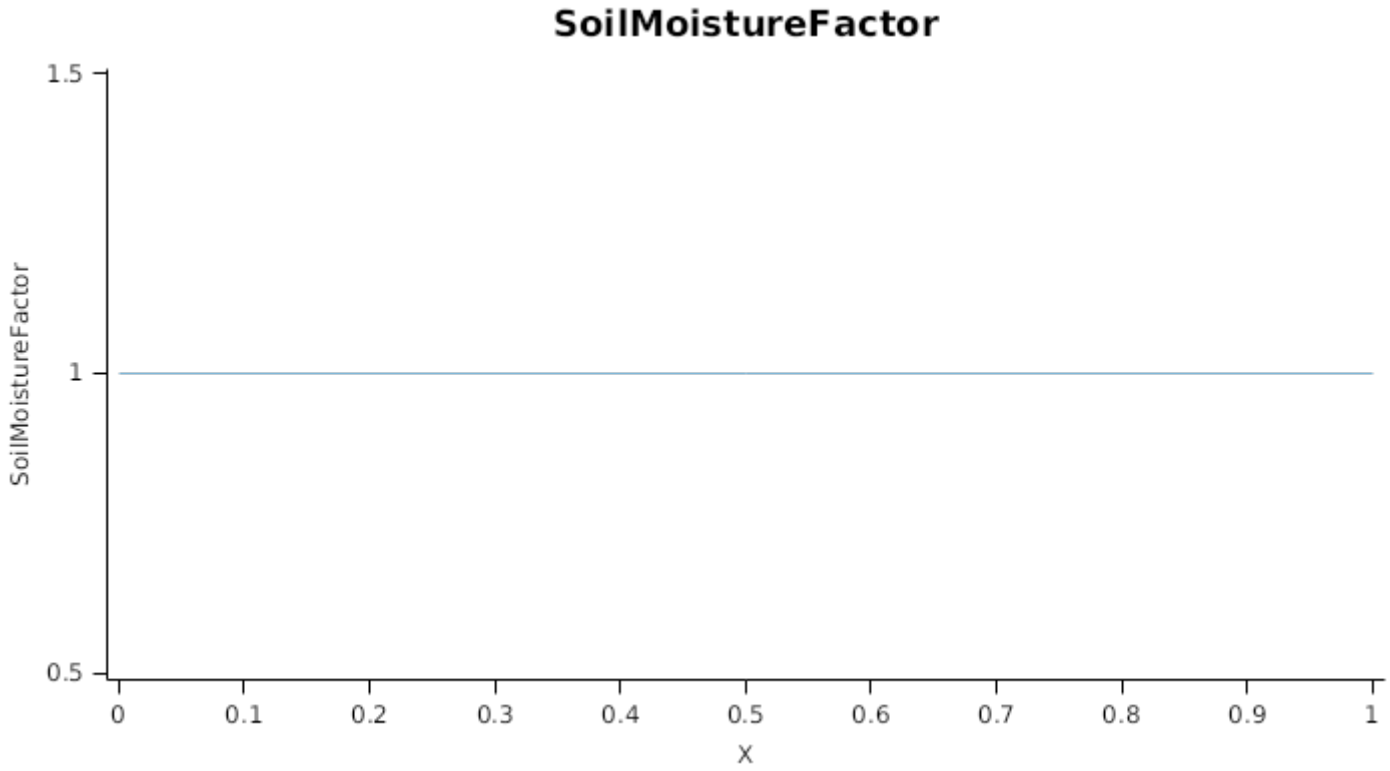
X	TemperatureFactor
-2.0	0.0
5.0	0.1
17.0	1.0
30.0	1.0
37.5	1.2





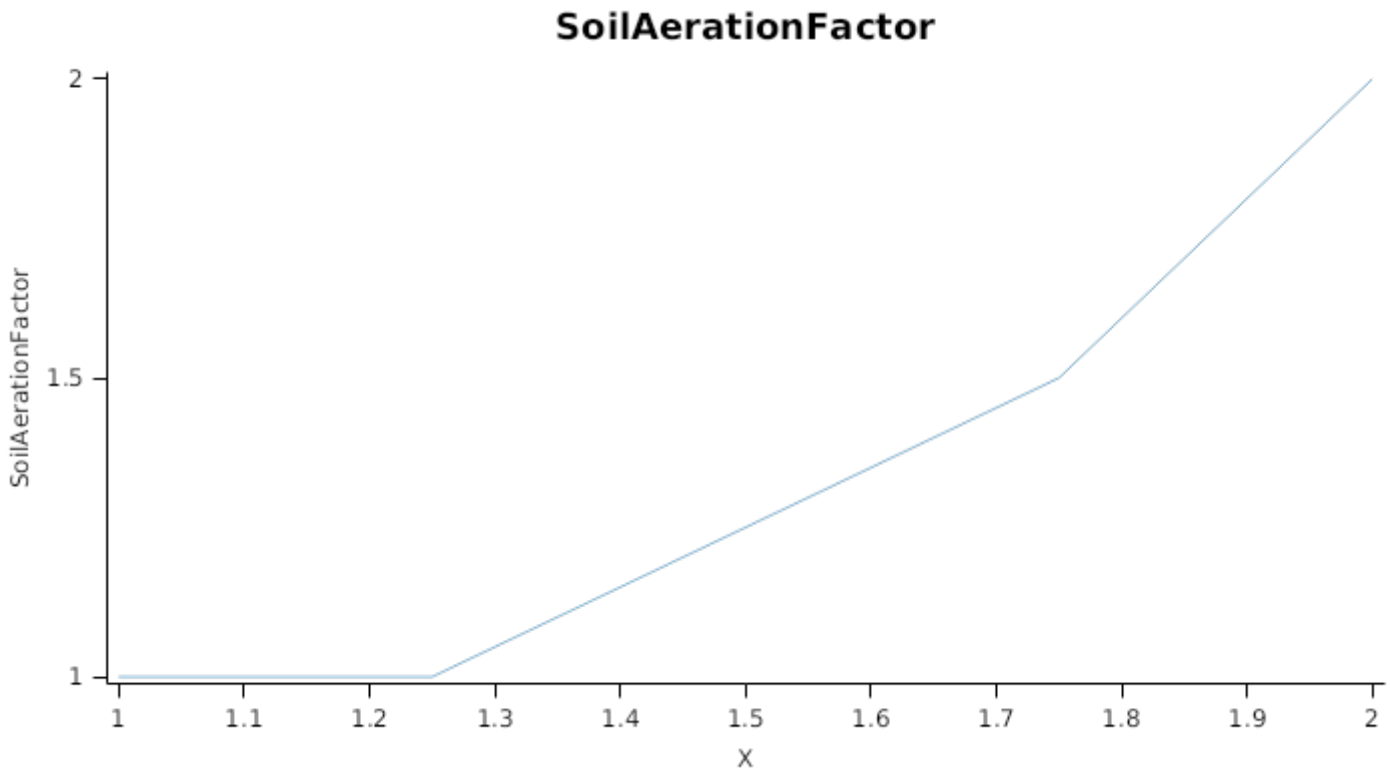
SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	1.0
0.5	1.0
1.0	1.0



SoilAerationFactor is calculated using linear interpolation

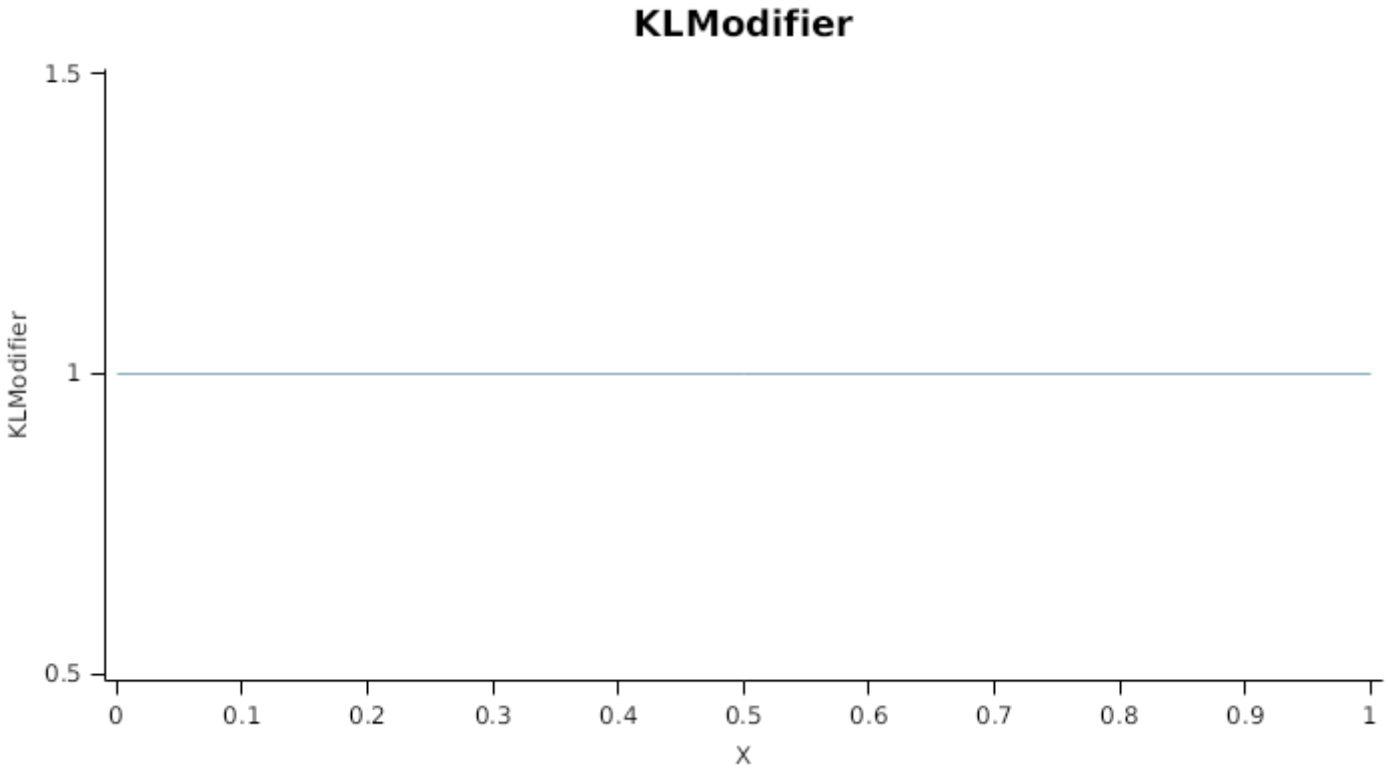
X	SoilAerationFactor
1.0	1.0
1.2	1.0
1.8	1.5
2.0	2.0



1.14.15 KLModifier

KLModifier is calculated using linear interpolation

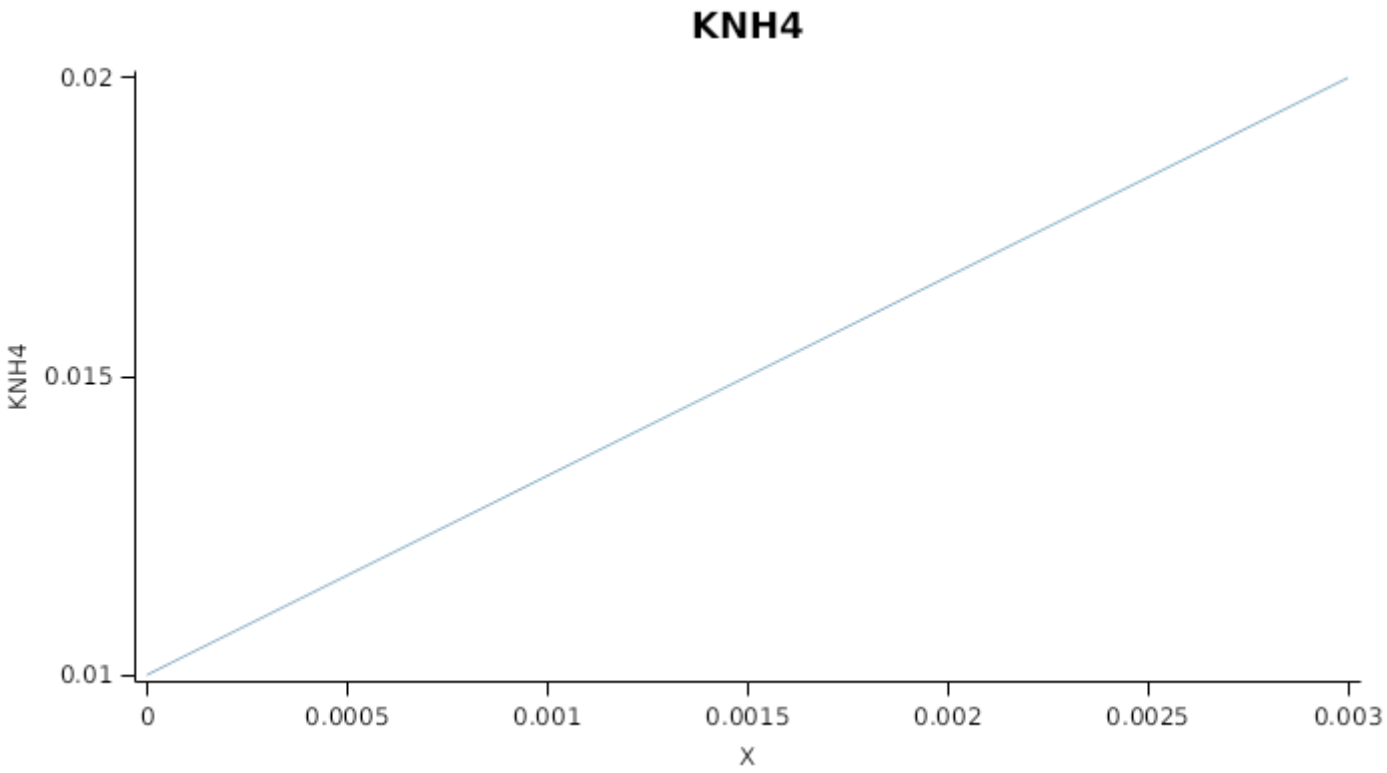
X	KLModifier
0.0	1.0
1.0	1.0



1.14.16 KNH4

KNH4 is calculated using linear interpolation

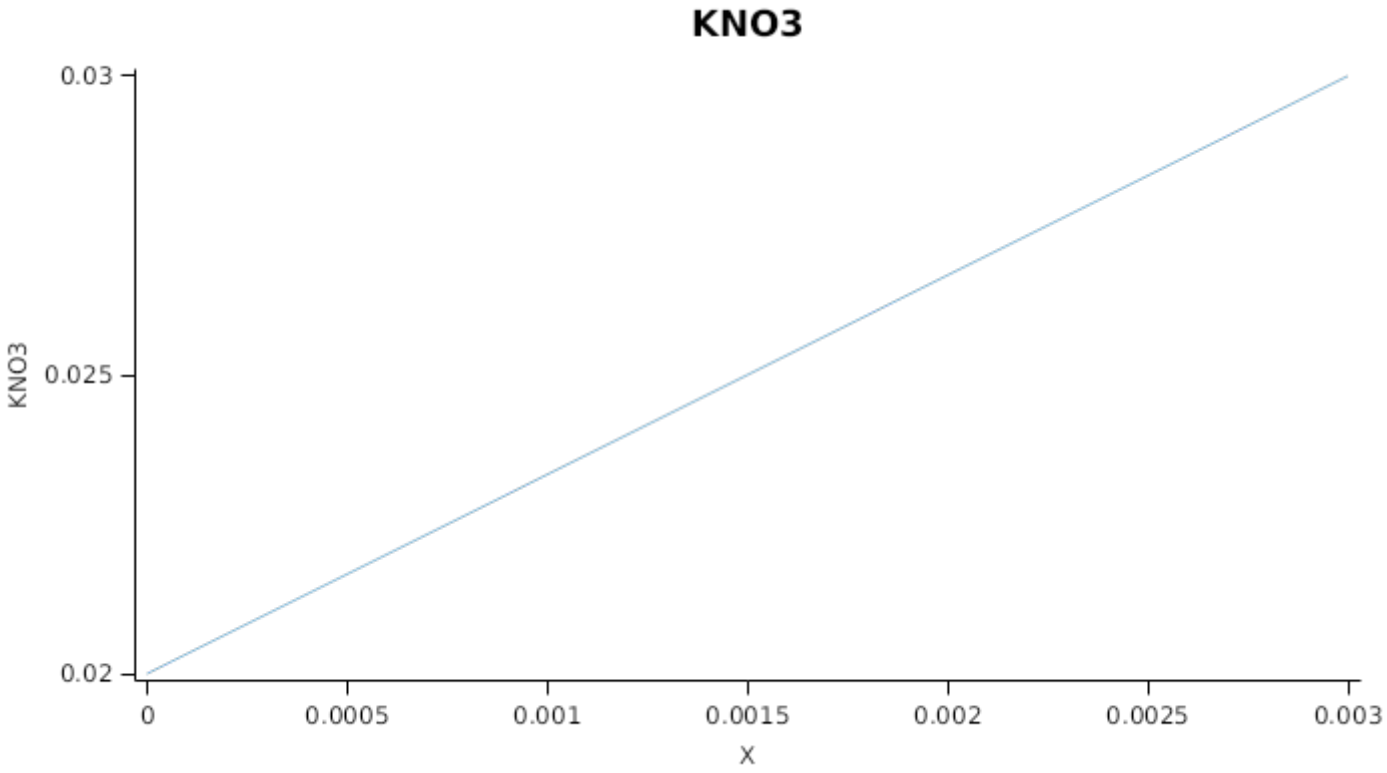
X	KNH4
0.0	0.0
0.0	0.0



1.14.17 KNO3

KNO3 is calculated using linear interpolation

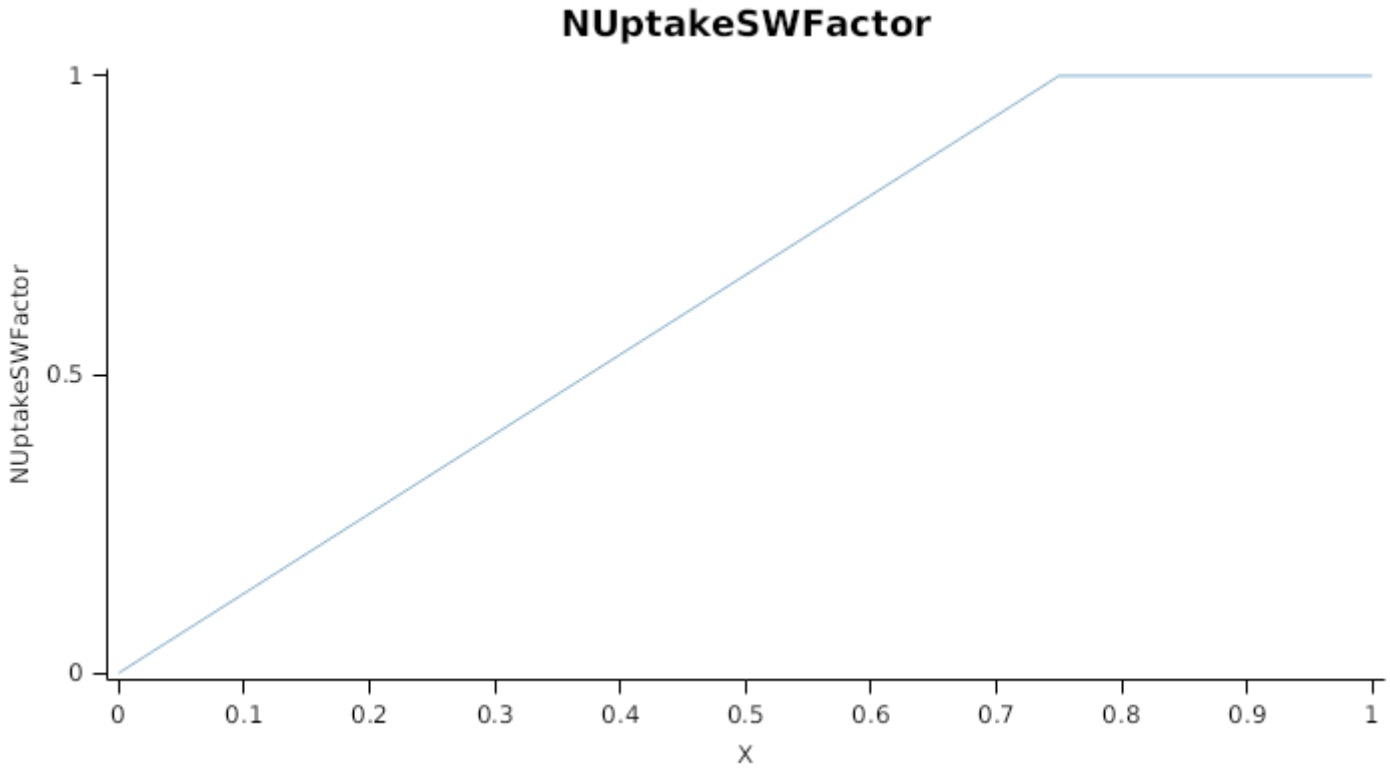
X	KNO3
0.0	0.0
0.0	0.0



1.14.18 NUptakeSWFactor

NUptakeSWFactor is calculated using linear interpolation

X	NUptakeSWFactor
0.0	0.0
0.8	1.0
1.0	1.0



1.14.19 SoilWaterScale

1.14.19.1 SoilWaterScale

A simple scale to convert soil water content into a value between 0 and 2 where 0 = LL15, 1 = DUL and 2 = SAT

1.14.20 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
Cut	0	0	5	0
Graze	0	0	5	0
Harvest	0	0	5	0
Prune	0	0	0	0

1.14.21 InitialWt

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

It is assumed that approximately 2/3 of the seed biomass is allocated to roots upon emergence. The weight of red clover seeds varies between 2.0 and 4.5 g/1000 seeds (Claydon et al., 1993; Murray, 2012).

Structural = 0.00035 (g/plant)

Metabolic = 0

Storage = 0

1.15 AboveGround

1.15.1 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
* Petiole
* Inflorescence

1.16 AboveGroundLive

1.16.1 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
* Petiole
* Inflorescence

1.17 AboveGroundDead

1.17.1 AboveGroundDead

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

AboveGroundDead summarises the following biomass objects:

* Leaf
* Stem
* Petiole
* Inflorescence

1.18 BelowGround

1.18.1 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
* Taproot
* Nodule

1.19 BelowGroundLive

1.19.1 BelowGroundLive

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

BelowGroundLive summarises the following biomass objects:

* Root
* Taproot
* Nodule

1.20 BelowGroundDead

1.20.1 BelowGroundDead

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

BelowGroundDead summarises the following biomass objects:

* Root
* Taproot
* Nodule

1.21 Total

1.21.1 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
* Petiole
* Inflorescence
* Root
* Taproot
* Nodule

1.22 TotalLive

1.22.1 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
* Petiole
* Inflorescence
* Root
* Taproot
* Nodule

1.23 TotalDead

1.23.1 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
* Petiole
* Inflorescence
* Root
* Taproot
* Nodule

1.24 ShootRootRatio

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

AllPhases has a value between Emergence and Ripening calculated as:

CurrentSR = [AboveGroundLive].Wt / [BelowGroundLive].Wt

1.25 TargetShootRootRatio

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

The target shoot-to-root is used to alter the allocation of biomass when the balance between the various organs is disturbed, such as after a defoliation.
Published data for the shoot-to-root ratio in red clover show considerable variability, with values between 1.5 to 8.0 for a wide range of conditions (Evans, 1973; Evans, 1977; Heichel et al., 1985; Chmelikova et al., 2015). For typical enviromental conditions (low stress levels) the data suggest a strong seasonality in biomass allocation. Similar to other forages that are strongly taprooted, basically all growth in spring is allocated to above ground organs, whereas in summer-autumn the allocation is more even, replenishing the below ground reserves (e.g. Evans, 1973; Heichel et al., 1985; Teixeira et al., 2008). The partition can be further affected by environmental conditions, with water or nutrient deficiency inducing greater root growth, while low light conditions lead to a higher allocation above ground (Gist et al., 1957; Kendall et al., 1994). The current model does not explicitly consider these variations, this should be upgraded when data becomes available.

AllPhases has a value between Emergence and Ripening calculated as:

TargetSR = [TargetAboveGroundFraction] / *BaseTargetBelowGroundAllocation*

BaseTargetBelowGroundAllocation = 1 - [TargetAboveGroundFraction]

1.26 TargetAboveGroundFraction

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

The model attempts to keep the proportion of the plant biomass above and below ground at a given value. The 'target' value is the 'ideal' relative proportion of biomass above and below ground for the plant at a given growth phase. The approach used here mimics the allocation pattern in strongly taprooted forages (e.g. Teixeira et al., 2008). In spring, nearly all biomass is allocated to above ground organs, with the proportion reducing as the length of day increases. In summer-autumn the allocation evenly distributed amoung all organs, favouring the replenishment of below ground reserves (Evans, 1973; Heichel et al., 1985).
The approach used in the RedClover model is based on that used for describing biomass partitioning in lucerne (Teixeira et al., 2008), which was parameterised for Lincoln, NZ, only. This was generalised by assuming that miminum and maximum allocations are a function of the annual variation in day length (which is a function of latitude). Thus, the variation in allocation to above ground organs is small in the tropics and reaches a maximum near the polar circle. This function allows for smooth transition between seasons and describe the general pattern sensibly, but it should be revised when more data becomes available.

AllPhases has a value between Emergence and Ripening calculated as:

IF [Phenology].PhotoperiodVariation < Zero THEN

BaseAllocationFraction = *[LowerAllocationFractionAboveG]*

ELSE

VariableAllocationFraction = [LowerAllocationFractionAboveG] + *AdditionalAllocation*

AdditionalAllocation = *DeltaAllocation* x *DayLengthFactor*

DeltaAllocation = [UpperAllocationFractionAboveG] - [LowerAllocationFractionAboveG]

DayLengthFactor = 1 - *PowerFactor*

1.26.1 PowerFactor

Raises the value of the child to the power of the exponent specified

1.27 LowerAllocationFractionAboveG

This is the lower limit for biomass allocation in above ground organs, assumed to be a function of latitude.

LowerAllocationFractionAboveG = Max(*MinimumAllocation*, *EstimatedAllocation*)

Where:

MinimumAllocation = 0.4 (g/g)

EstimatedAllocation = *MedianAllocation* - *LatitudeFactor*

MedianAllocation = 0.75 (g/g)

LatitudeFactor = *AbsLatitude* x *Variation*

IF [Weather].Latitude < Zero THEN

SouthLatitude = *MinusOne* x [Weather].Latitude

MinusOne = -1

ELSE

NorthLatitude = *[Weather].Latitude*

Variation = *DeltaAllocation* / *ReferenceLatitude*

DeltaAllocation = [LowerAllocationFractionAboveG].EstimatedAllocation.MedianAllocation - [LowerAllocationFractionAboveG].MinimumAllocation

ReferenceLatitude = 65 (degrees)

1.28 UpperAllocationFractionAboveG

This is the upper limit for biomass allocation in above ground organs, assumed to be a function of latitude. It is the values used for partitioning growth in early spring.

UpperAllocationFractionAboveG = Min(*MaximumAllocation*, *EstimatedAllocation*)

Where:

MaximumAllocation = 0.99 (g/g)

EstimatedAllocation = [LowerAllocationFractionAboveG].EstimatedAllocation.MedianAllocation + *LatitudeFactor*

LatitudeFactor = *AbsLatitude* x *Variation*

IF [Weather].Latitude < Zero THEN

SouthLatitude = *MinusOne* x [Weather].Latitude

MinusOne = -1

ELSE

NorthLatitude = *[Weather].Latitude*

Variation = *DeltaAllocation* / *ReferenceLatitude*

DeltaAllocation = [UpperAllocationFractionAboveG].MaximumAllocation - [LowerAllocationFractionAboveG] .EstimatedAllocation.MedianAllocation

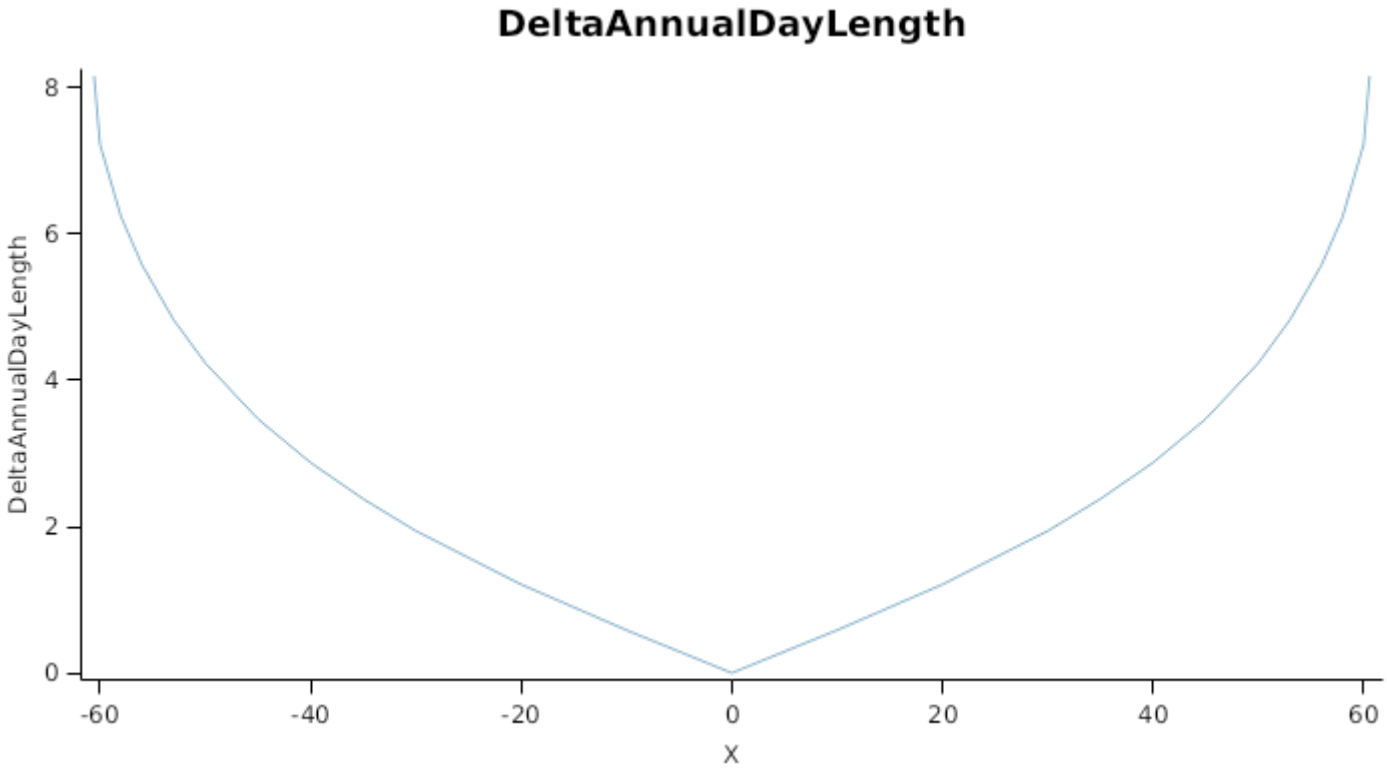
ReferenceLatitude = 50 (degrees)

1.29 DeltaAnnualDayLength

DeltaAnnualDayLength is calculated using linear interpolation

X	DeltaAnnualDayLength
-60.6	8.2
-60.0	7.2
-58.0	6.2
-56.0	5.6
-53.0	4.8
-50.0	4.2
-45.0	3.5

X	DeltaAnnualDayLength
-40.0	2.9
-35.0	2.4
-30.0	1.9
-20.0	1.2
-10.0	0.6
0.0	0.0
10.0	0.6
20.0	1.2
30.0	1.9
35.0	2.4
40.0	2.9
45.0	3.5
50.0	4.2
53.0	4.8
56.0	5.6
58.0	6.2
60.0	7.2
60.6	8.2



1.30 Cultivars

1.30.1 Colenso

Colenso overrides the following properties:

1.30.2 Pawera

Pawera overrides the following properties:

[Leaf].Photosynthesis.FT.XYPairs.X = 0,4,9,15,18.5,27,35,37.5

[Leaf].Photosynthesis.FT.XYPairs.Y = 0,0,0.15,0.6,1,1,0.1,0

[Leaf].NRetranslocationFactor.TemperatureFactor.XYPairs.X = 0,4,9,15,18.5,27,35,37.5

[Leaf].NRetranslocationFactor.TemperatureFactor.XYPairs.Y = 0,0,0.15,0.6,1,1,0.1,0

[Phenology].Inductive.Target.FixedValue = 20

[Phenology].Inductive.Progression.SomeProgression.XYPairs.X = 12,13,14,15

[Phenology].Reproductive.Target.FixedValue = 2000

1.30.3 Rajah

Rajah overrides the following properties:

[Leaf].Photosynthesis.FT.XYPairs.X = 0,2.5,8,15,18,26,34,37.5

[Leaf].Photosynthesis.FT.XYPairs.Y = 0,0,0.15,0.68,1,1,0.1,0

[Leaf].NRetranslocationFactor.TemperatureFactor.XYPairs.X = 0,2.5,8,15,18,26,34,37.5

[Leaf].NRetranslocationFactor.TemperatureFactor.XYPairs.Y = 0,0,0.15,0.68,1,1,0.1,0

[Phenology].Inductive.Target.FixedValue = 15

[Phenology].Inductive.Progression.SomeProgression.XYPairs.X = 12,12.5,13.5,14

[Phenology].Reproductive.Target.FixedValue = 2200

1.31 MortalityRate

MortalityRate = 0

2 Validation

The performance of the red clover model is evaluated in simulations based on experiments conducted in New Zealand and Denmark. These represent significant differences in environment and cover variations in irrigation and fertiliser rates, but the number of interactions are limited and thus more tests should be done for areas and management not considered here. It is expected that more datasets will be added in the future with colaboration with end-users.

Note: The definition of the main values compared (predicted versus measured) are given below to improve clarity.

- AboveGroundWt: total biomass weight of plant material aboveground at the end of a given day;
- HarvestedWt: biomass removed from the field at a given day;
- RotationHarvestedWt: biomass removed from the field at the end of a defoliation event (used when defoliation occured over a few days);
- CumulativeHarvestedWt: amount of harvested biomass accumulated over a growing season (between winters);
- HerbageNc: average nitrogen concentration in the harvested material;
- NTakenOff: amount of nitrogen taken off filed with the harvested material;
- CumNTakenOff: amount of N harvested accumulated over a growing season;

2.1 New Zealand

List of experiments.

Experiment Name	Design (Number of Treatments)
FRNLLincoln	NRate (6)
Iversen	Irrigation (2)

2.1.1 FRNLLincoln

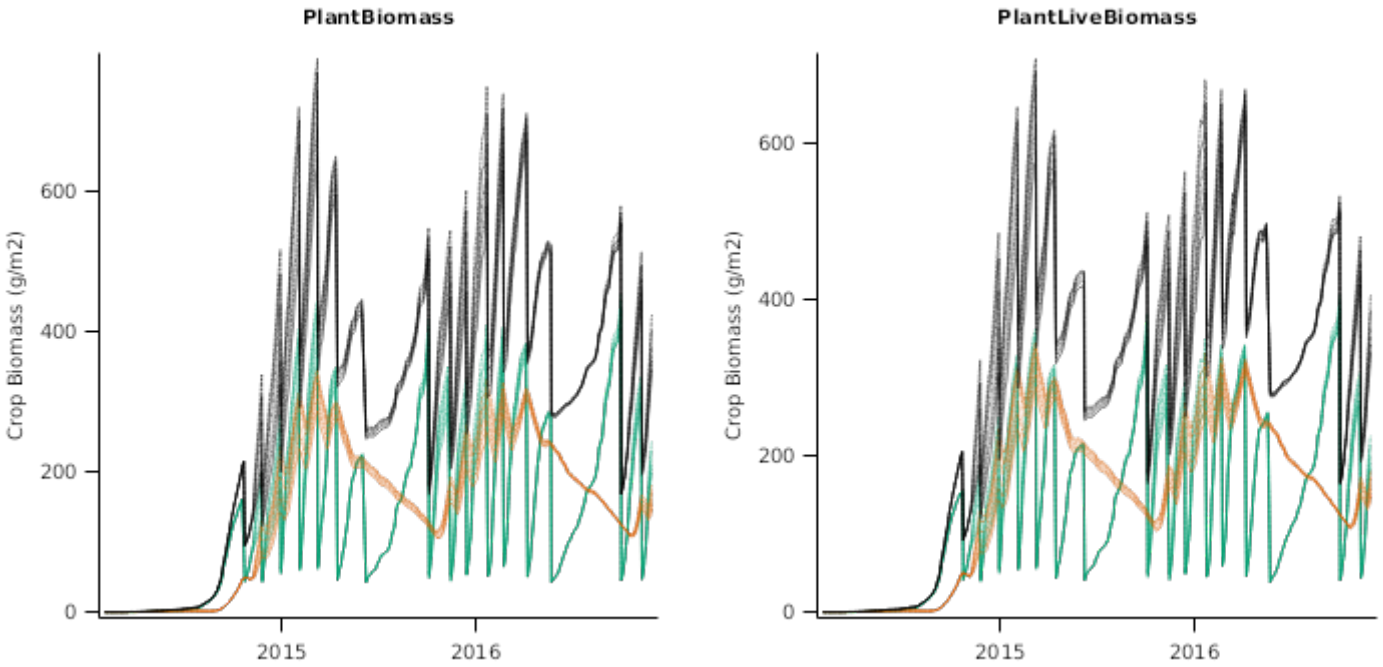
###FRNL Lincoln###

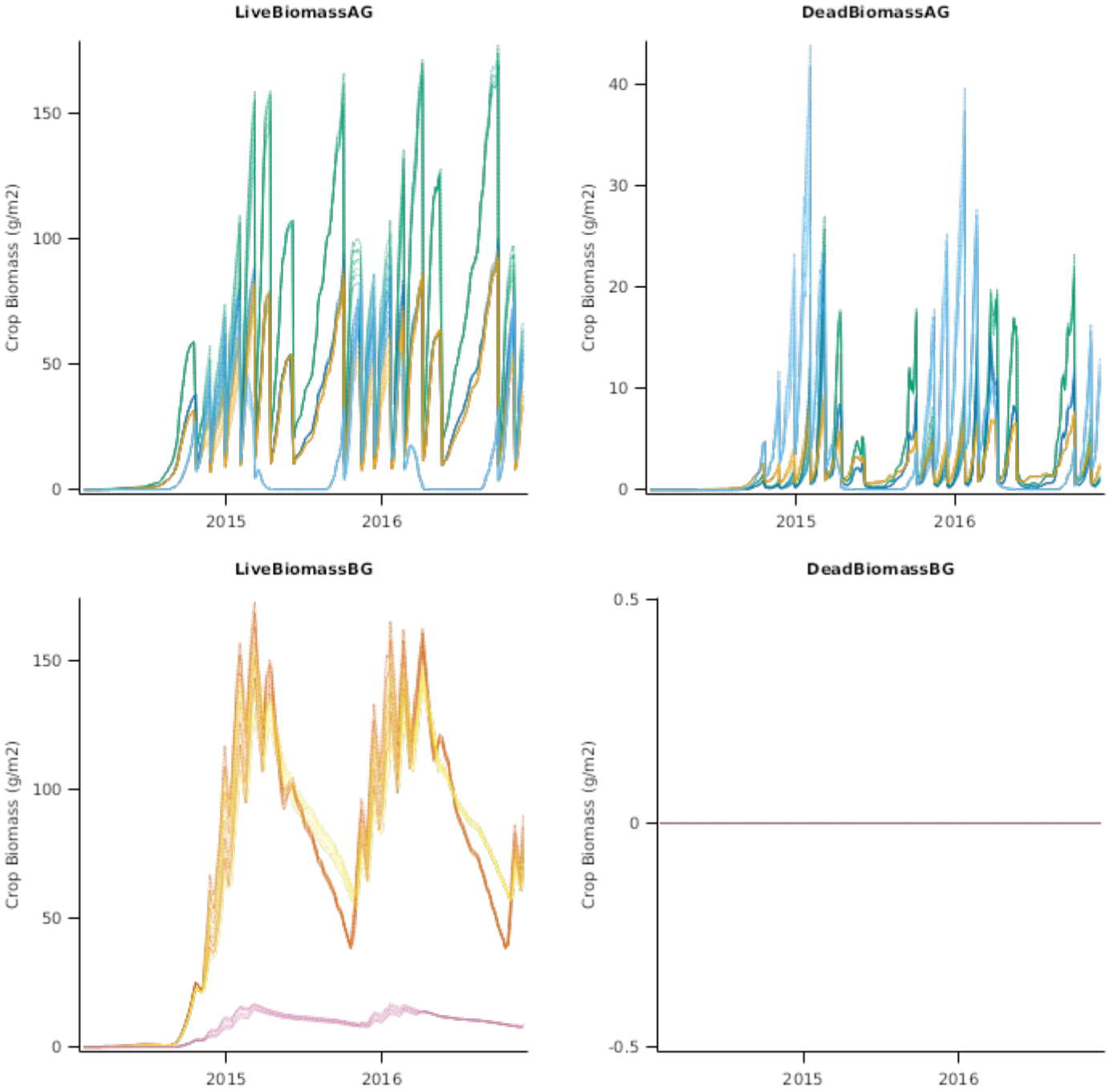
Simulation setup based on field trial performed at Lincoln University Research Dairy Farm, New Zealand, between 2014 and 2016. The experiment was part of the FRNL (Forages for Reduced Nitrogen Leaching) program (for more details see Martin et al., 2017). Here only plots with pure red clover are used.
The experiment consisted of six fertiliser treatments (N rates of 0, 50, 100, 200, 350 and 500 kg/ha/yr) in four replicates, and measurements comprised yield and quality indicators (here N content is used).
Data supplied by Grant Edwards, Lincoln University.

The soil at the experimental site was a Templeton fine sandy loam (an Immature Pallic soil, USDA: Udic Haplustept), the required parameters were inferred based on data from the New Zealand National Soils Database (Landcare Research). Weather data was obtained from nearby Broadfields weather station (NIWA).

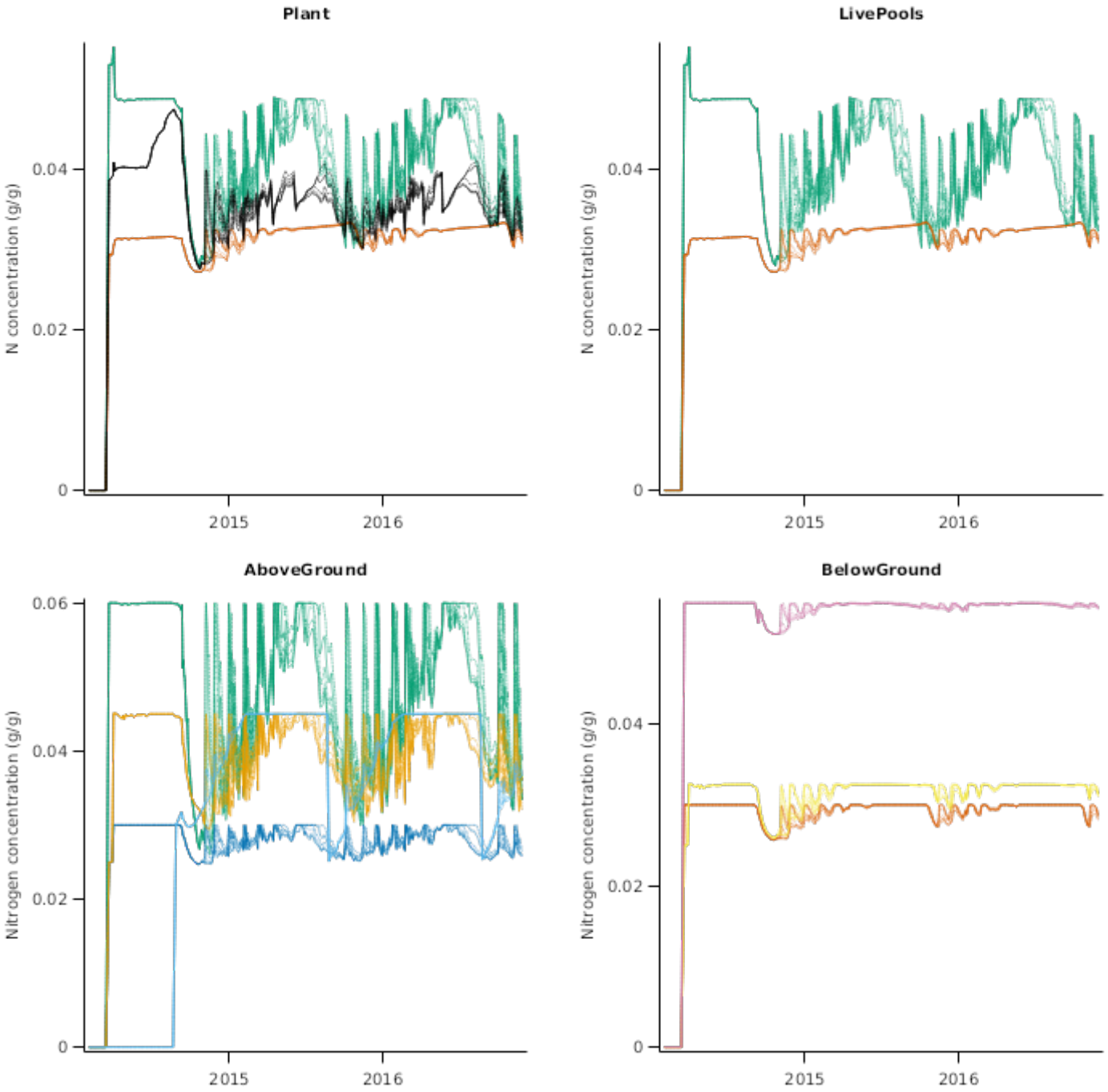
2.1.1.1 Results

2.1.1.1.1 PlantDM



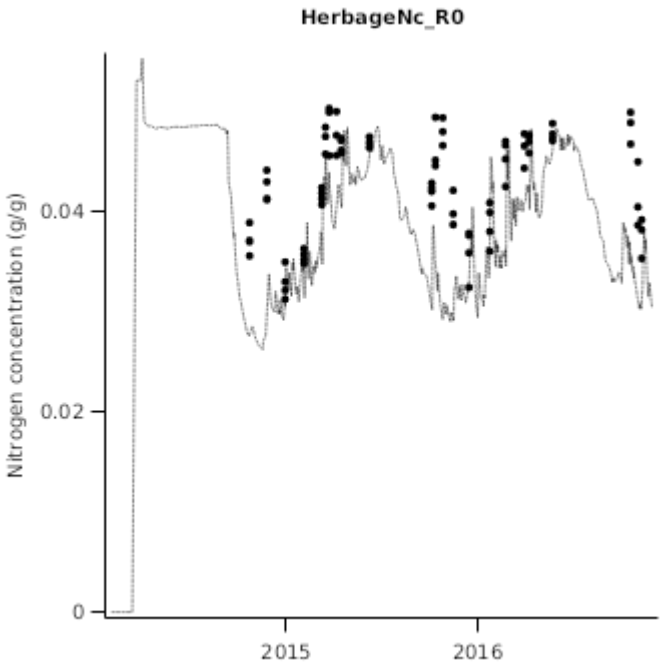


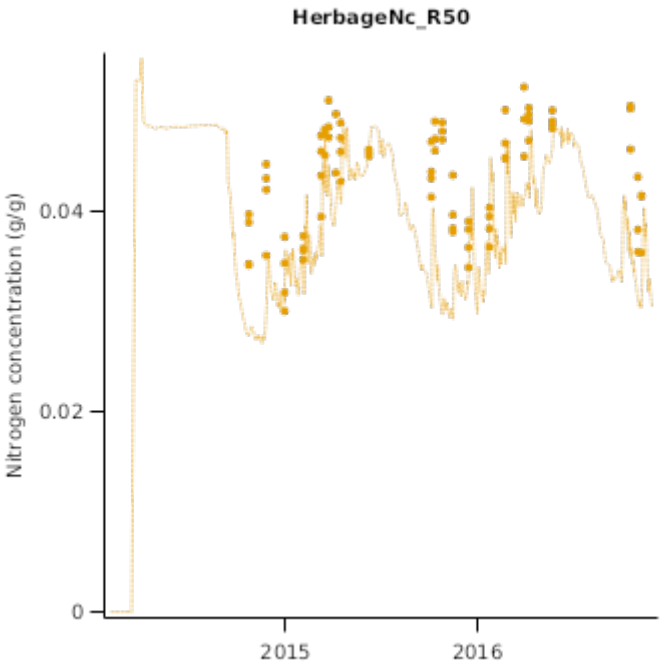
2.1.1.1.2 PlantNc

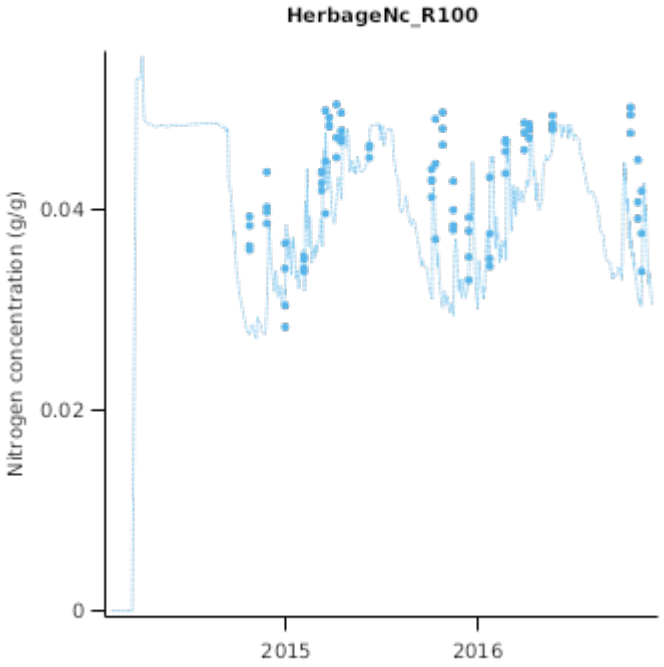


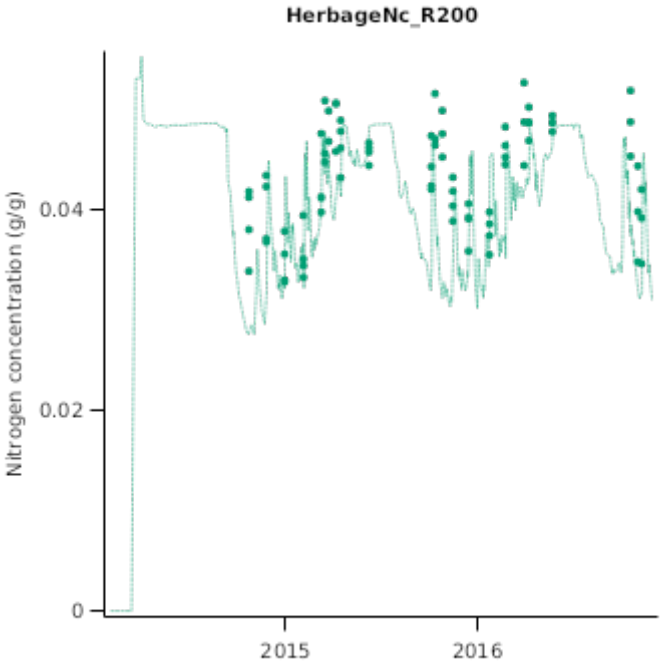
2.1.1.2 ObservedResults

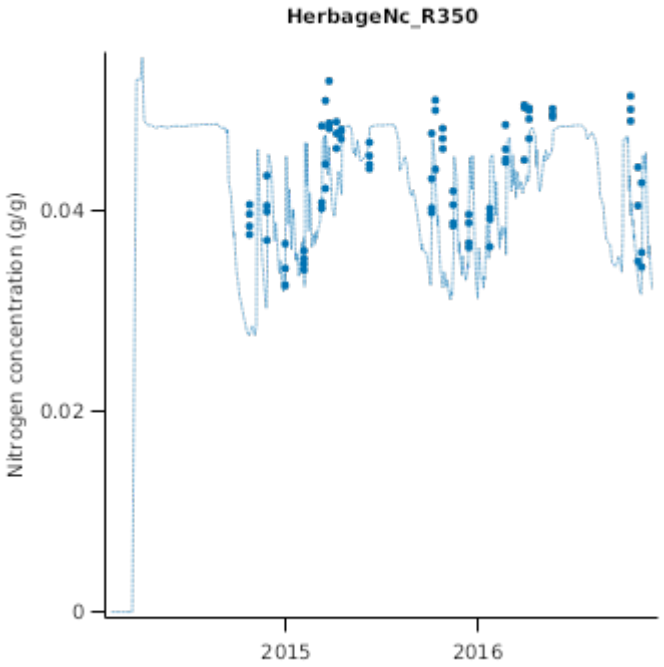
2.1.1.2.1 Nconcentration

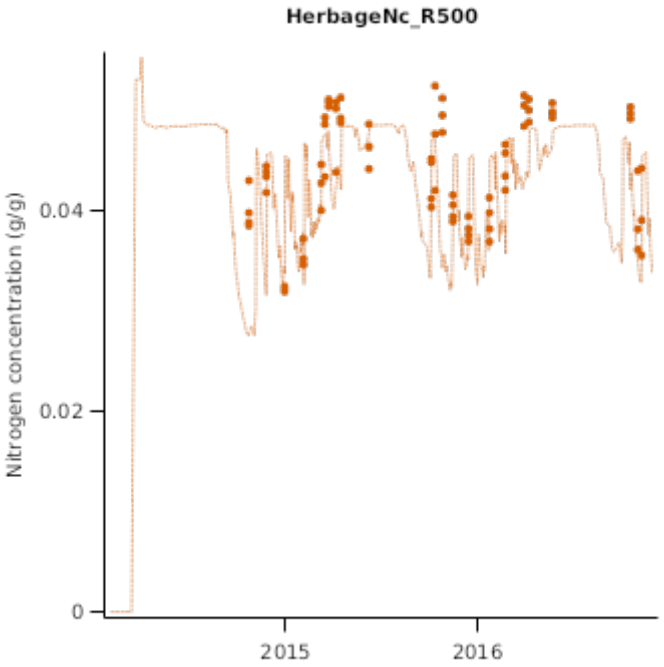

HerbageNc_R0
Nitrogen concentration (g/g)
0
0.02
0.04
2015
2016


HerbageNc_R50
Nitrogen concentration (g/g)
0
0.02
0.04
2015
2016

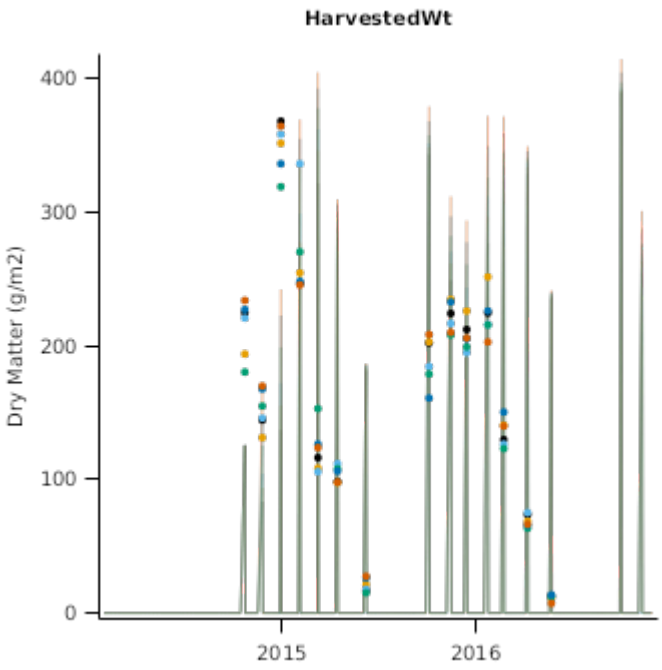

HerbageNc_R100
Nitrogen concentration (g/g)
0
0.02
0.04
2015
2016

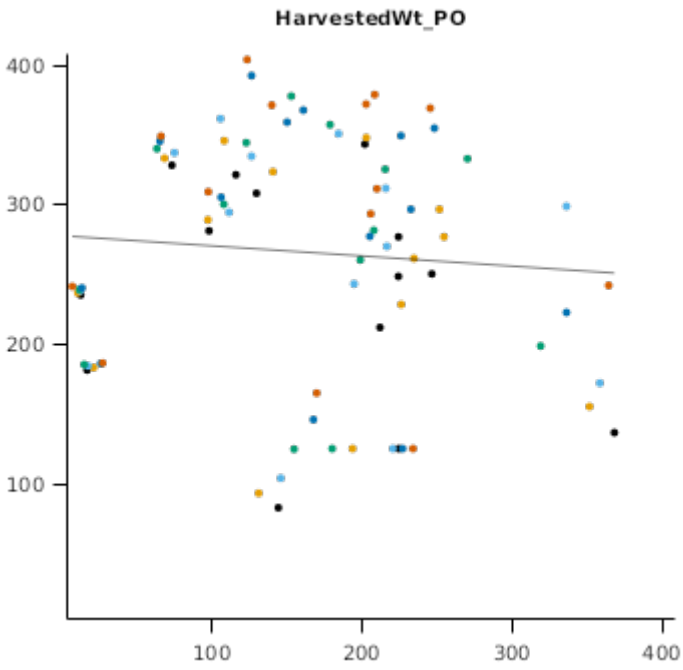

HerbageNc_R200
Nitrogen concentration (g/g)
0
0.02
0.04
2015
2016

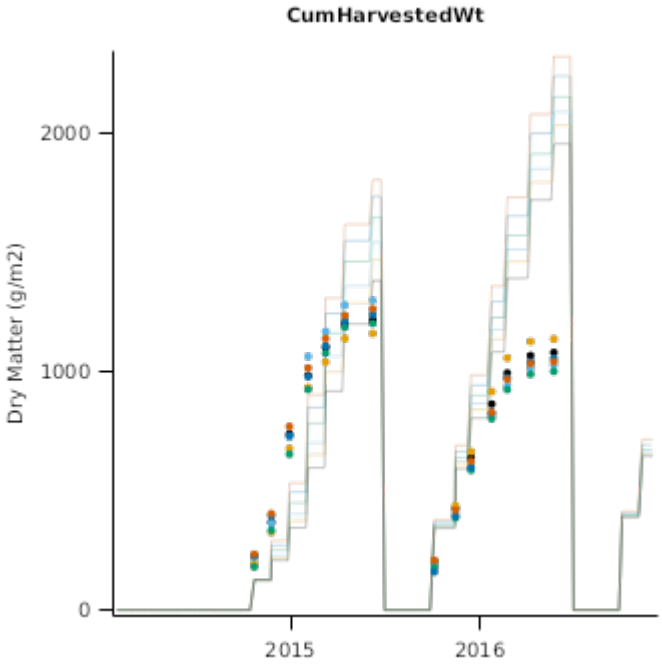

HerbageNc_R350
Nitrogen concentration (g/g)
0
0.02
0.04
2015
2016

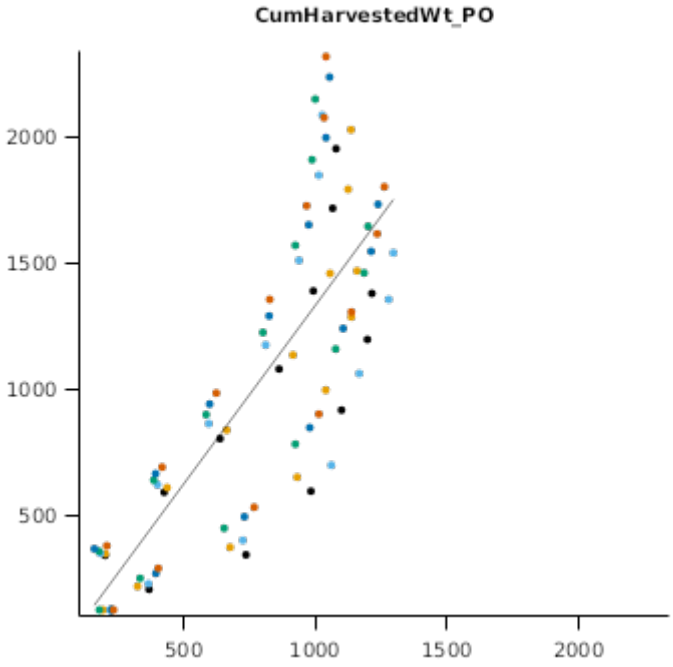

HerbageNc_R500
Nitrogen concentration (g/g)
0
0.02
0.04
2015
2016

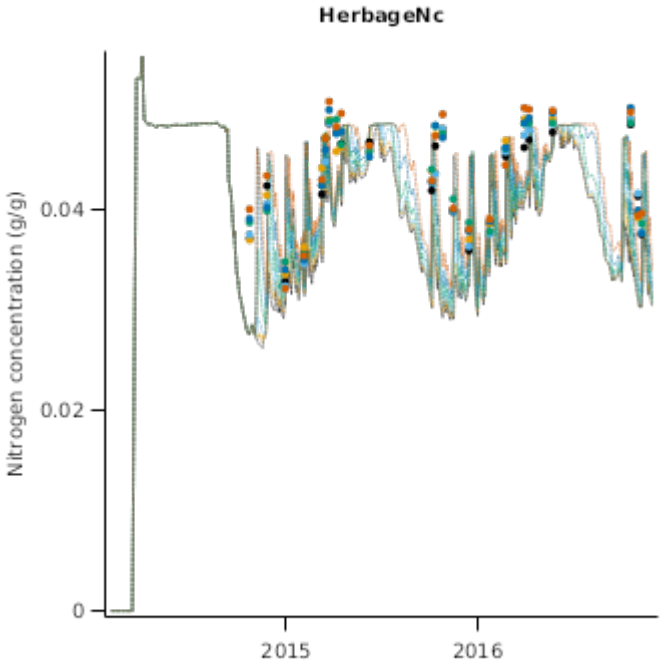
2.1.1.3 ObservedMeans

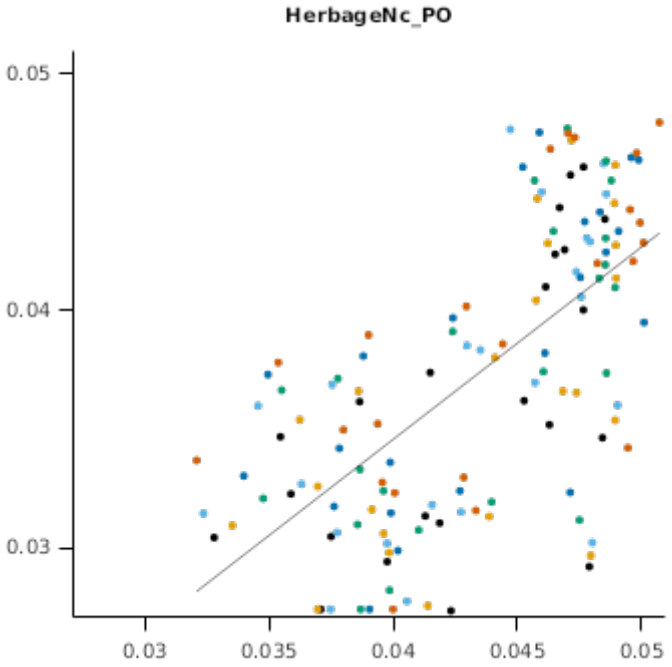


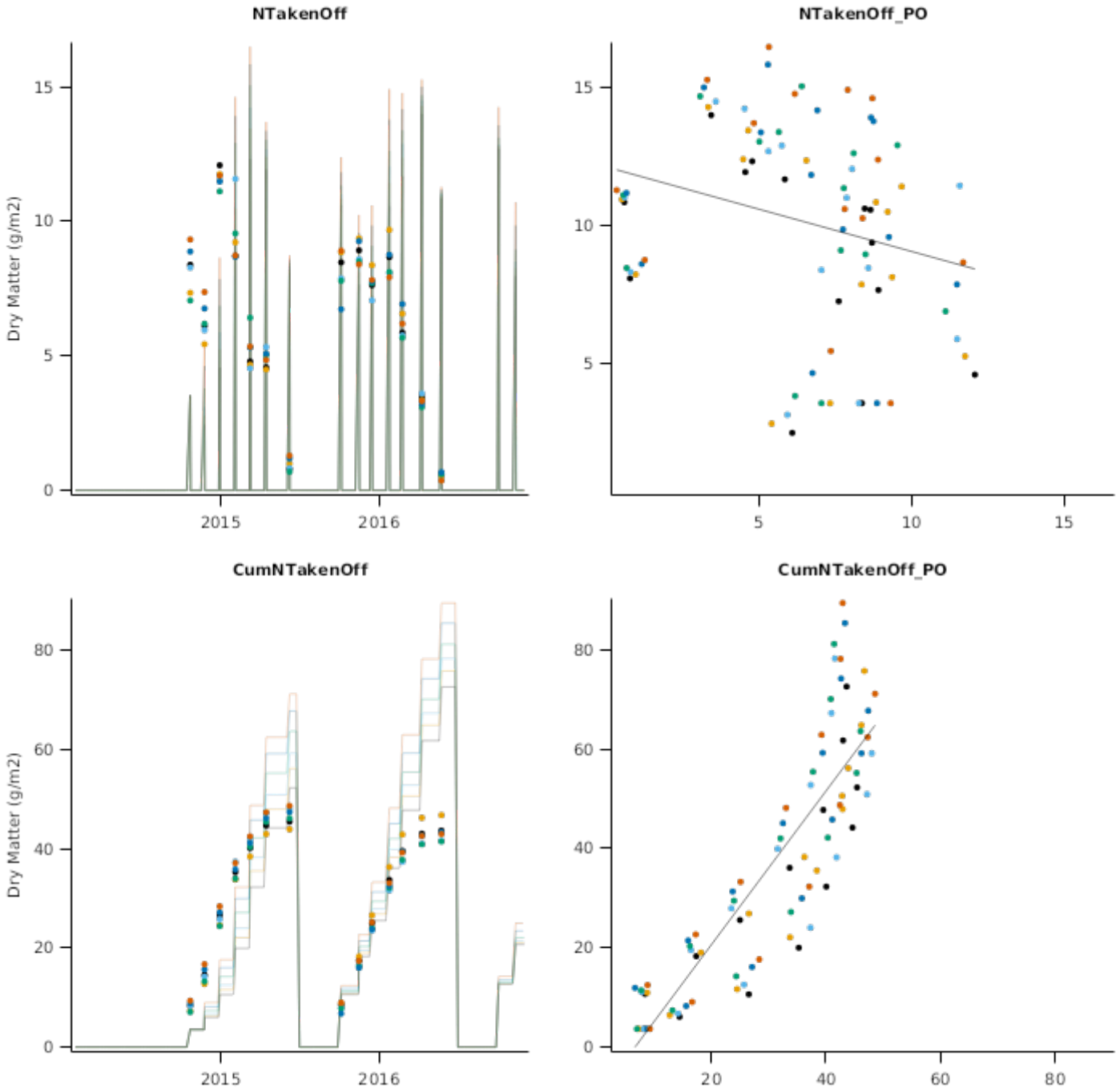



CumHarvestedWt
Dry Matter (g/m2)
2000
1000
0
2015
2016


CumHarvestedWt_PO
2000
1500
1000
500
500
1000
1500
2000


HerbageNc
Nitrogen concentration (g/g)
0.04
0.02
0
2015
2016


HerbageNc_PO
0.05
0.04
0.03
0.03
0.035
0.04
0.045
0.05

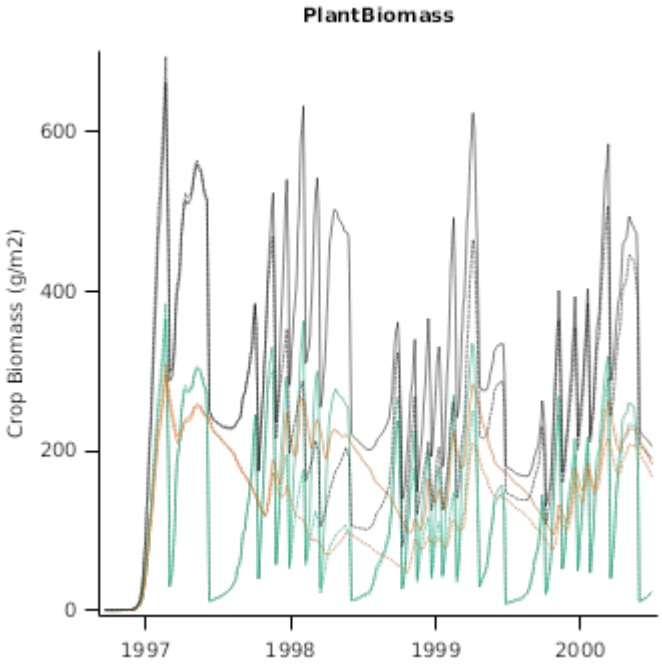


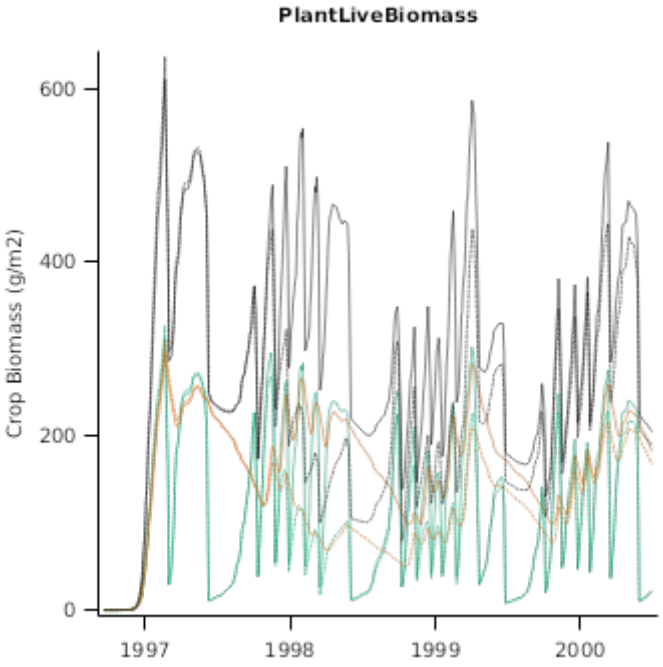
2.1.2 Iversen

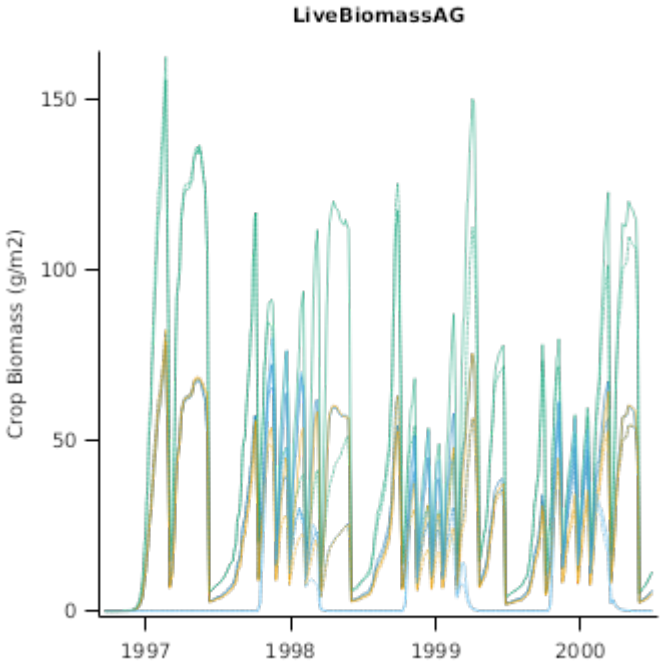
This simulation setup was based on a dataset supplied by Hamish Brown, which was collected for his PhD thesis. The trial was conducted at the Iversen field of Lincoln University, in Lincoln, New Zealand between 1996 and 2002 (Brown, 2004; Brown et al., 2005). The work was focused on understanding water use and its interaction with yield of dryland and irrigated forage crops (lucerne, chicory and red clover were used).
The trial was implemented in spring of 1996, after conventional cultivation, including sub soiling and liming. Red clover (cultivar '*Pawera*') was sown at a rate of 10.0 kg/ha and was grazed regularly by sheep. There were annual applications of superphosphate but no N fertilisation (except excreta from grazing sheep). The treatments consisted of irrigation versus dryland conditions. The major parameters analysed were herbage growth and yield, population, nutritive characteristics, and water utilisation. N concentration was inferred from the few measurements of crude protein and interpolated over time using a sinusoidal function; these values are for reference only and cannot be used to actually validate the model.
Soil data was obtained from measurements presented by H. Brown Thesis (Brown, 2004) and complemented by S-MAP database from Landcare Research Limited. Weather data was obtained from the nearby Broadfield met station in Lincoln.

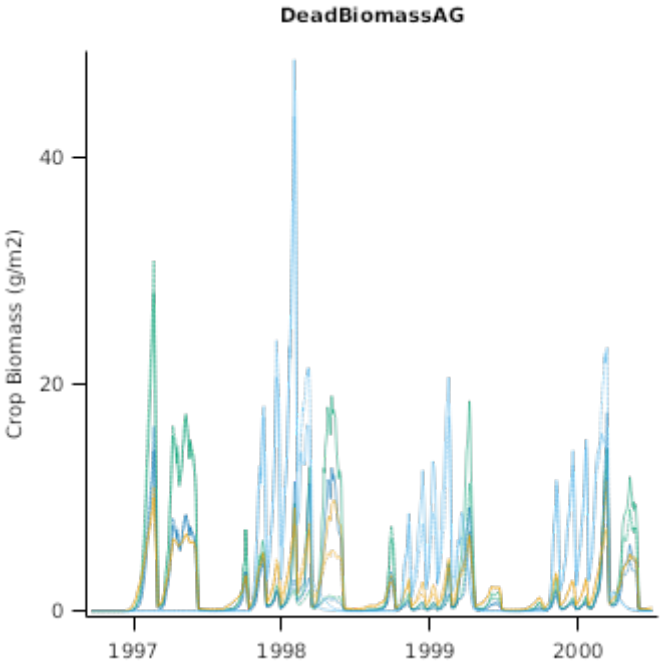
2.1.2.1 Results

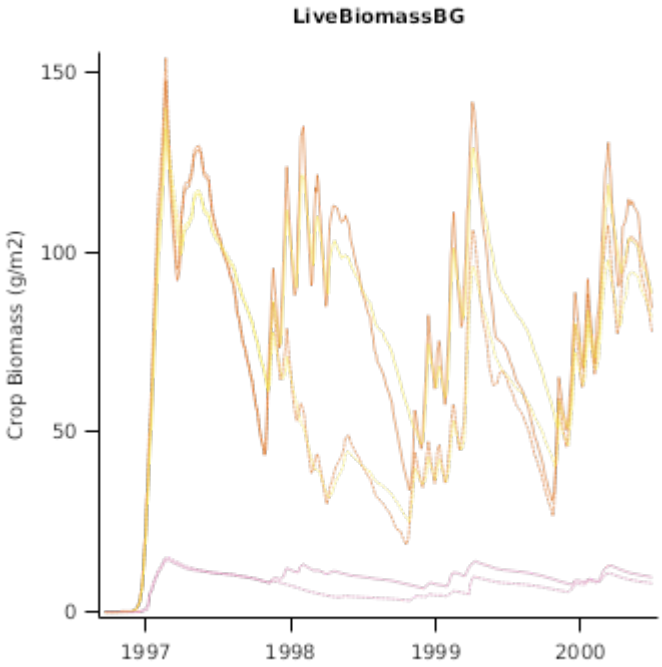
2.1.2.1.1 PlantDM

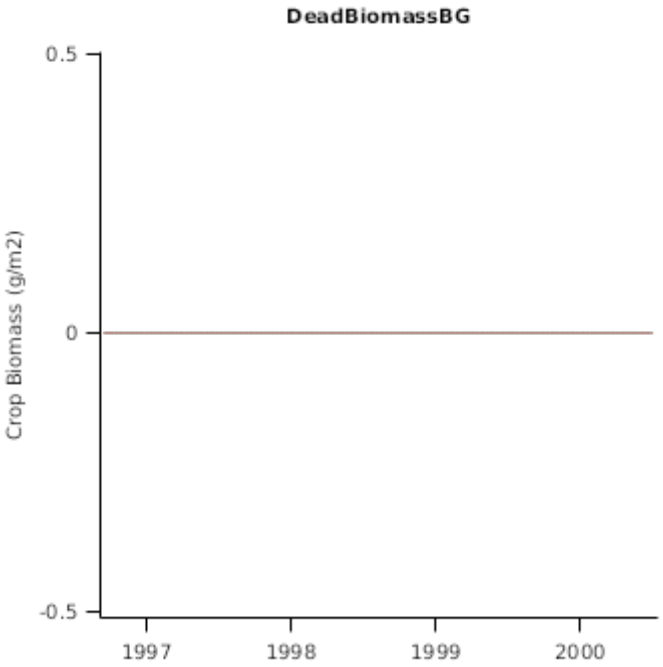

PlantBiomass
Crop Biomass (g/m2)
0
200
400
600
1997
1998
1999
2000


PlantLiveBiomass
Crop Biomass (g/m2)
0
200
400
600
1997
1998
1999
2000

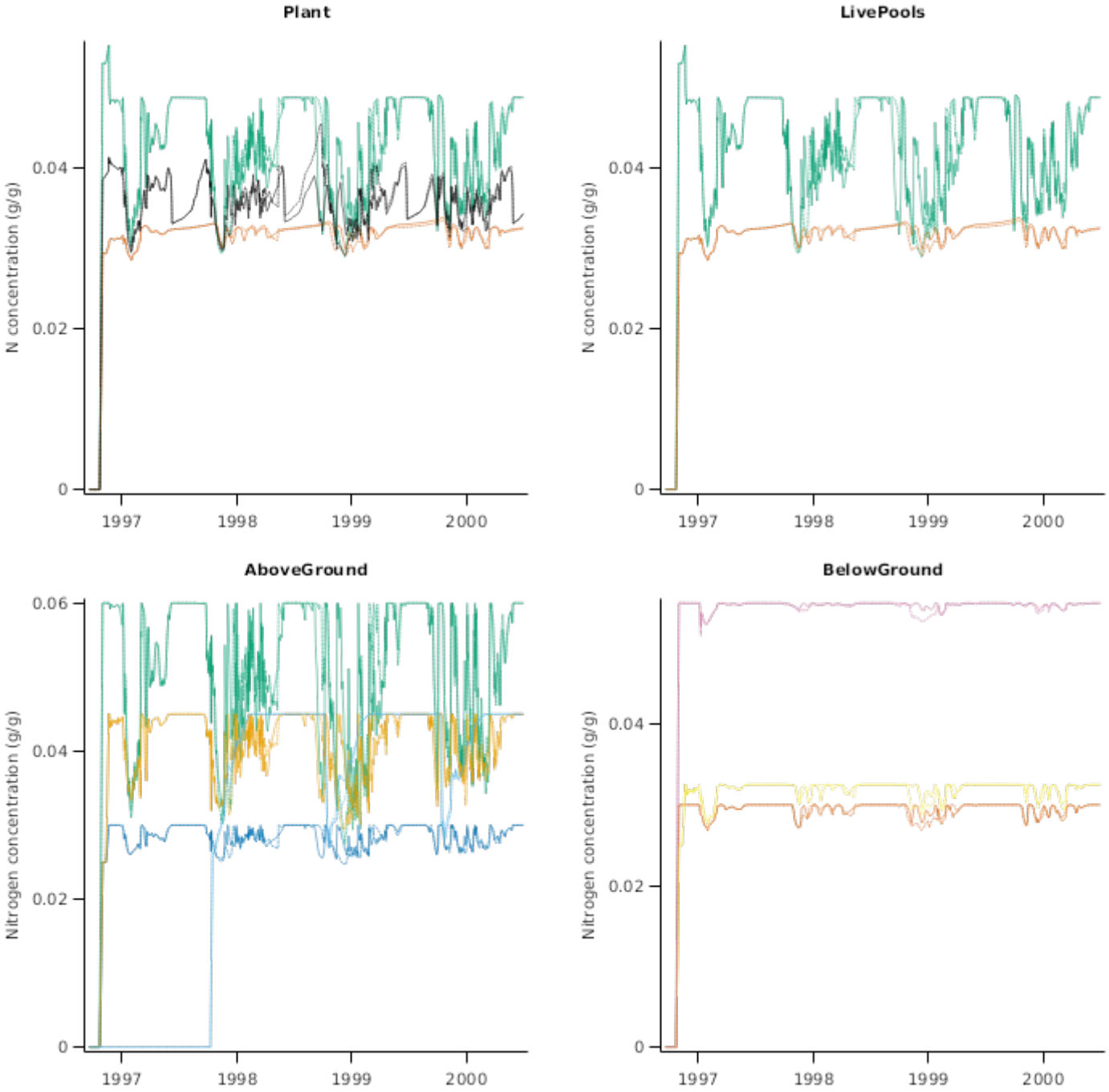

LiveBiomassAG
Crop Biomass (g/m2)
0
50
100
150
1997
1998
1999
2000


DeadBiomassAG
Crop Biomass (g/m2)
0
20
40
1997
1998
1999
2000


LiveBiomassBG
Crop Biomass (g/m2)
0
50
100
150
1997
1998
1999
2000

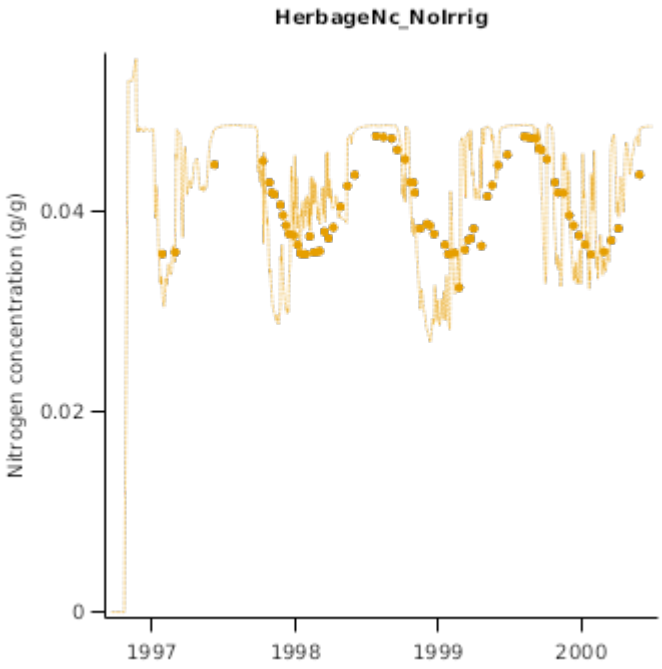

DeadBiomassBG
Crop Biomass (g/m2)
-0.5
0
0.5
1997
1998
1999
2000

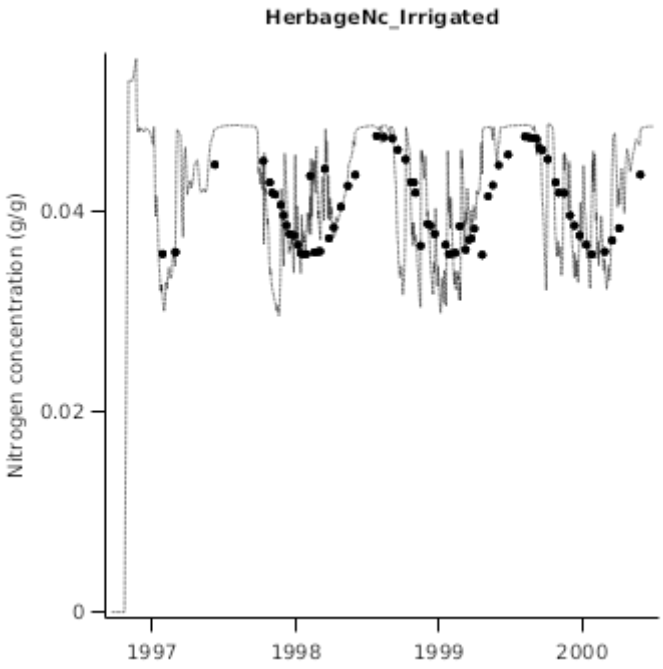
2.1.2.1.2 PlantNc



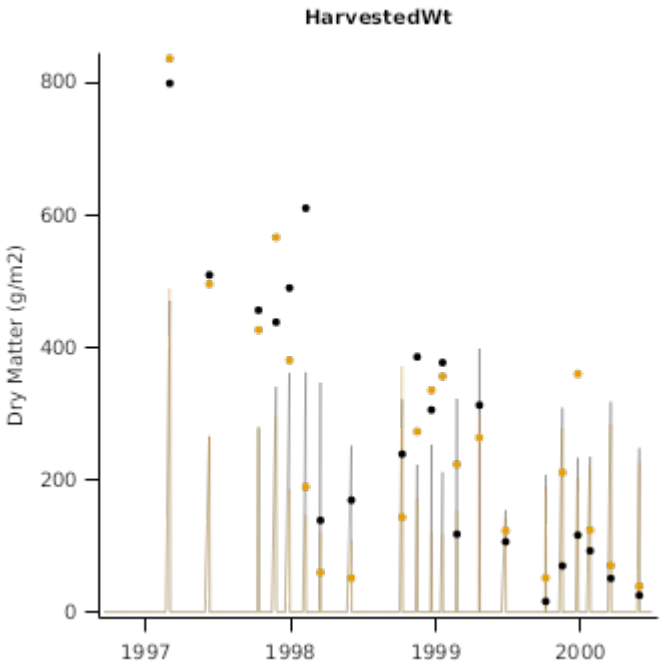
2.1.2.2 ObservedResults

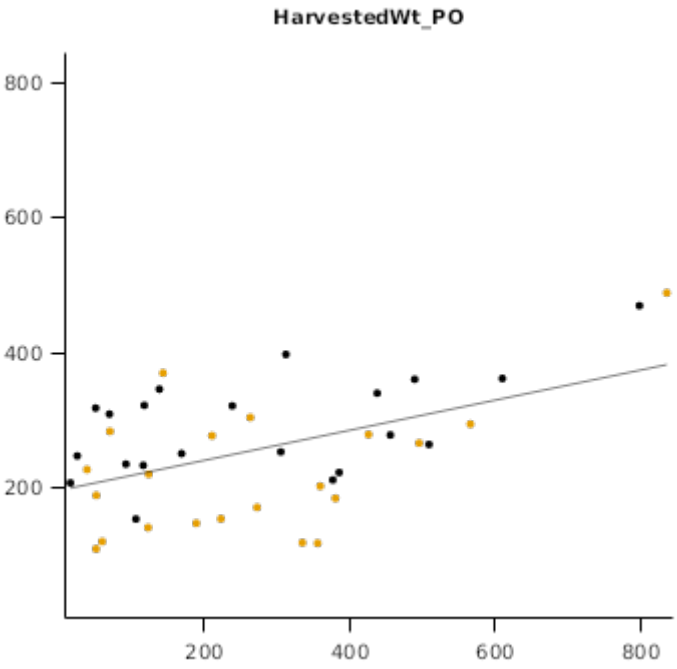
2.1.2.2.1 Nconcentration

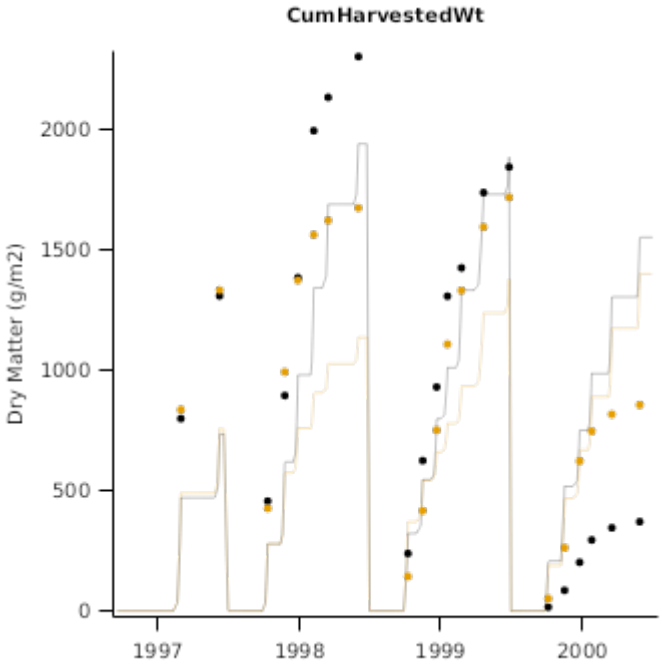


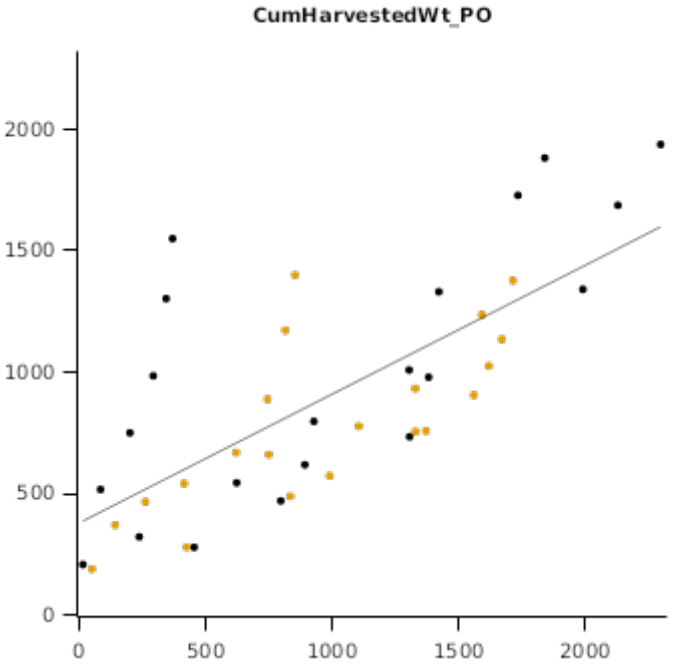


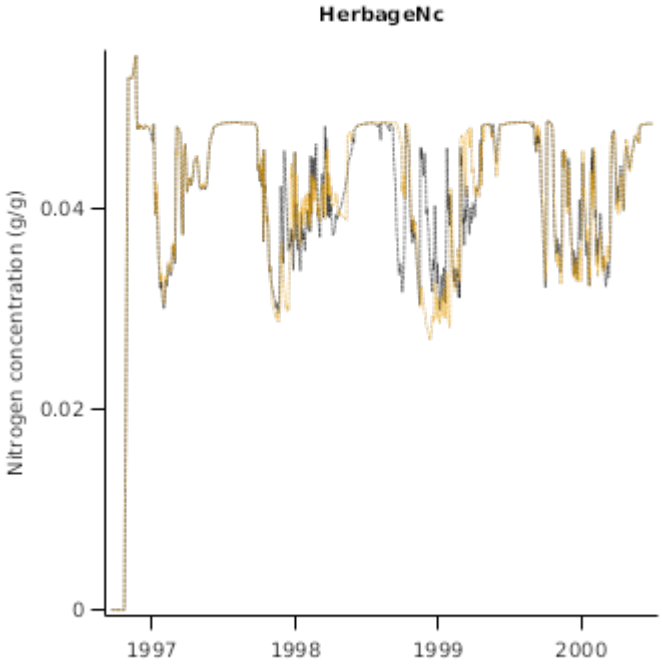
2.1.2.3 ObservedMeans

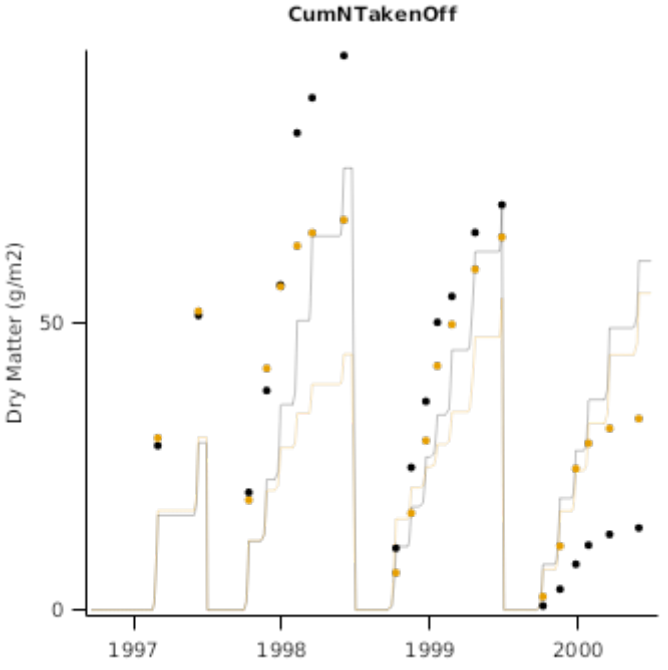

HarvestedWt
Dry Matter (g/m2)
800
600
400
200
0
1997
1998
1999
2000

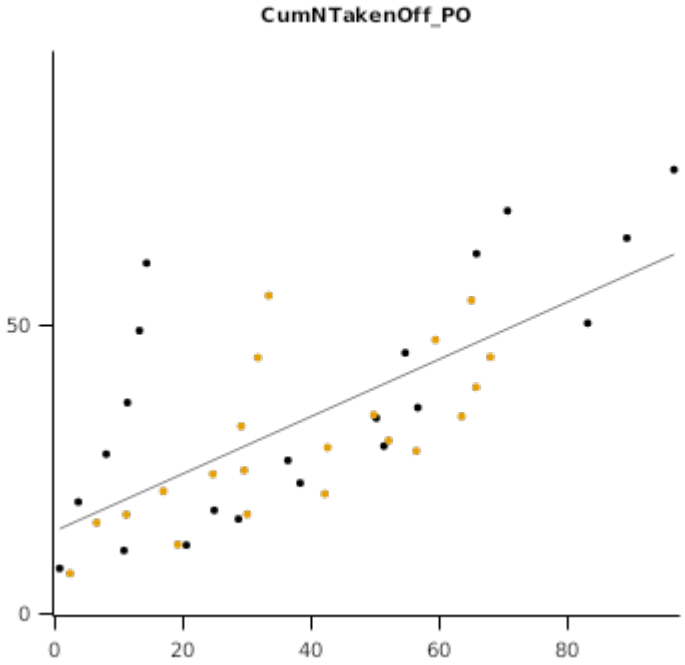

HarvestedWt_PO
800
600
400
200
200
400
600
800


CumHarvestedWt
Dry Matter (g/m2)
2000
1500
1000
500
0
1997
1998
1999
2000


CumHarvestedWt_PO
2000
1500
1000
500
0
0
500
1000
1500
2000


HerbageNc
Nitrogen concentration (g/g)
0.04
0.02
0
1997
1998
1999
2000


CumNTakenOff
Dry Matter (g/m2)
50
0
1997
1998
1999
2000



2.2 Denmark

List of experiments.

Experiment Name	Design (Number of Treatments)
Foulum	NInputs (2)

2.2.1 Foulum

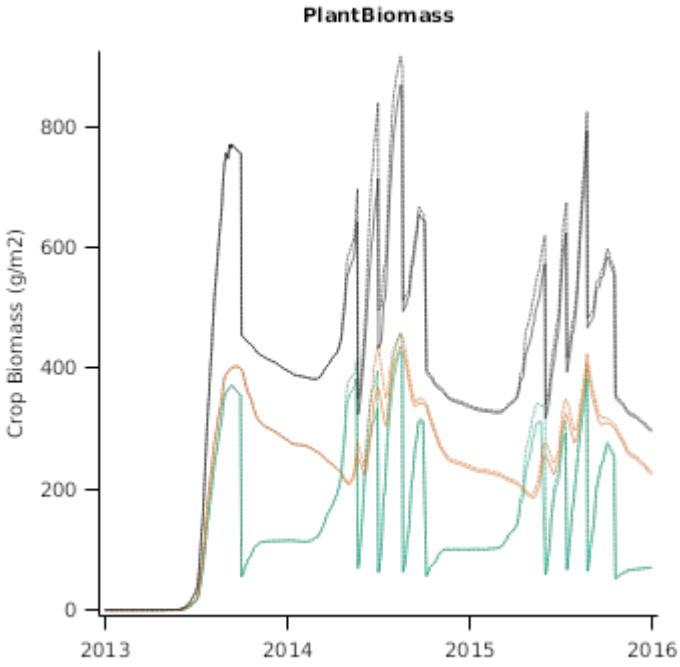
###Foulum species competition###

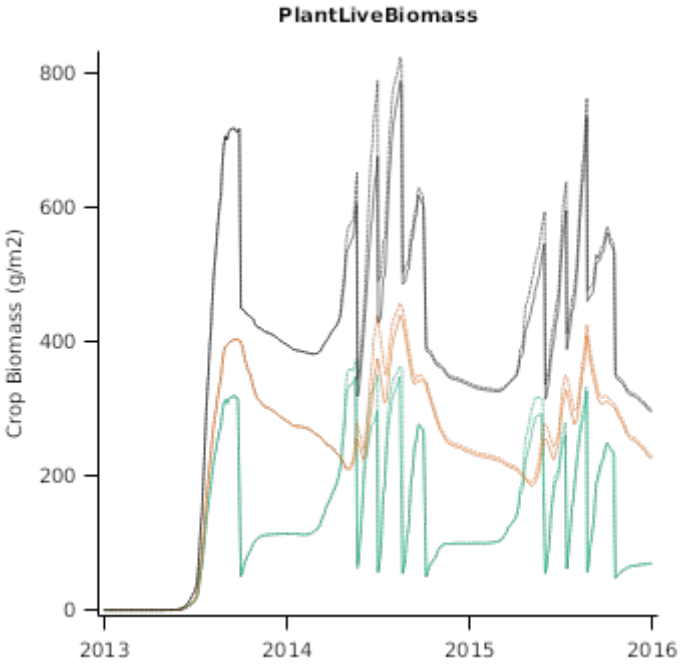
This simulation setup was based on field trials performed at the the Foulumgaard Experimental Station, Aarhus University, Denmark, between 2013 and 2015. The trial was part of an experiment studying species competition in multi-species sward in a dairy organic farming context. This comprises the establishement of plots sown with various species in monoculture and in a few combinations, either varying the number and type of species or the relative sowing rate. The plots received either no N fertiliser or a nominal annual rate of 250 kgN/ha applied as cattle slurry. Details of the site and trial can be found in publications (Cong et al., 2017; Cong et al., 2018; and Cong et al., 2018). Here only a selection of plots with red clover are used, with each treatment having three replicates.
Observed data supplied by Wen Feng Cong and Jorgen Eriksen, Aarhus University.

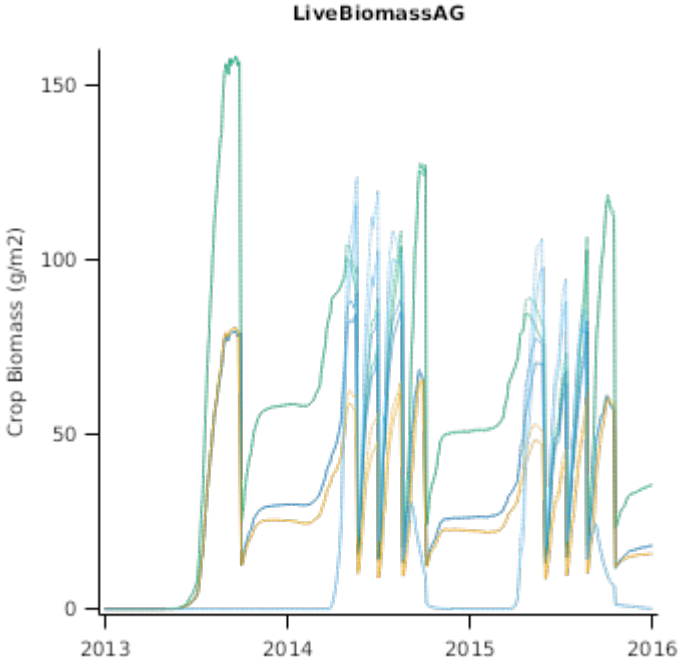
The soil at the experimental site was a loamy sand (a Typic Hapludult on the USDA classification), the parameters required were derived from data published and slightly adjusted with measurements done at the experimental site ([JacobsenFoulum1989]; [HeidmannFoulum1989]).
Weather data was obtained from nearby weather station (Aarhus University).

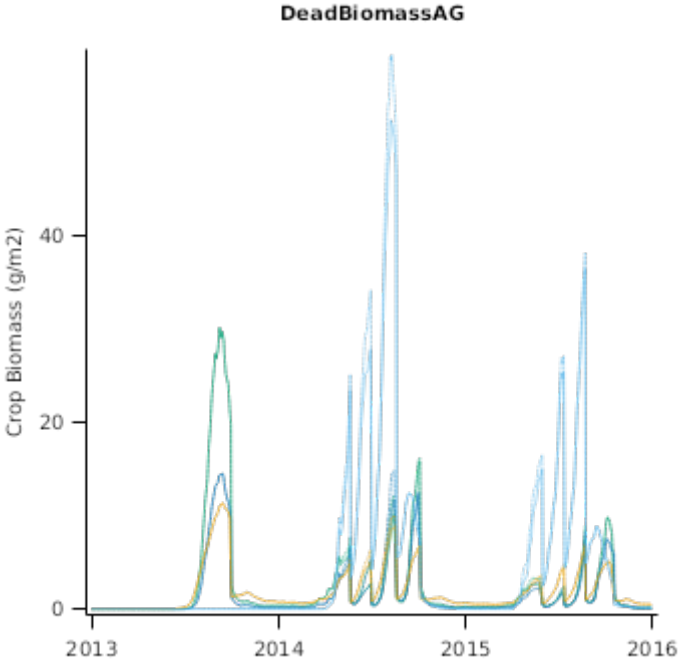
2.2.1.1 Results

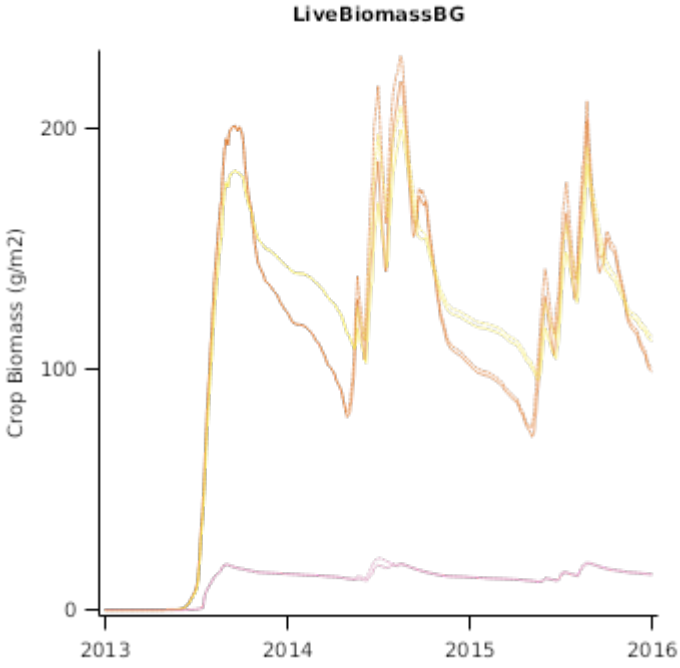
2.2.1.1.1 PlantDM

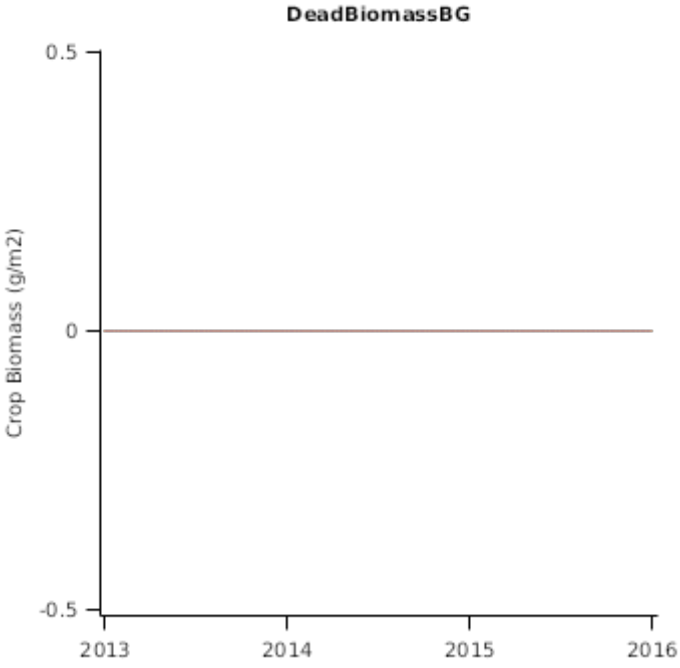

PlantBiomass
Crop Biomass (g/m2)
0
200
400
600
800
2013
2014
2015
2016


PlantLiveBiomass
Crop Biomass (g/m2)
0
200
400
600
800
2013
2014
2015
2016

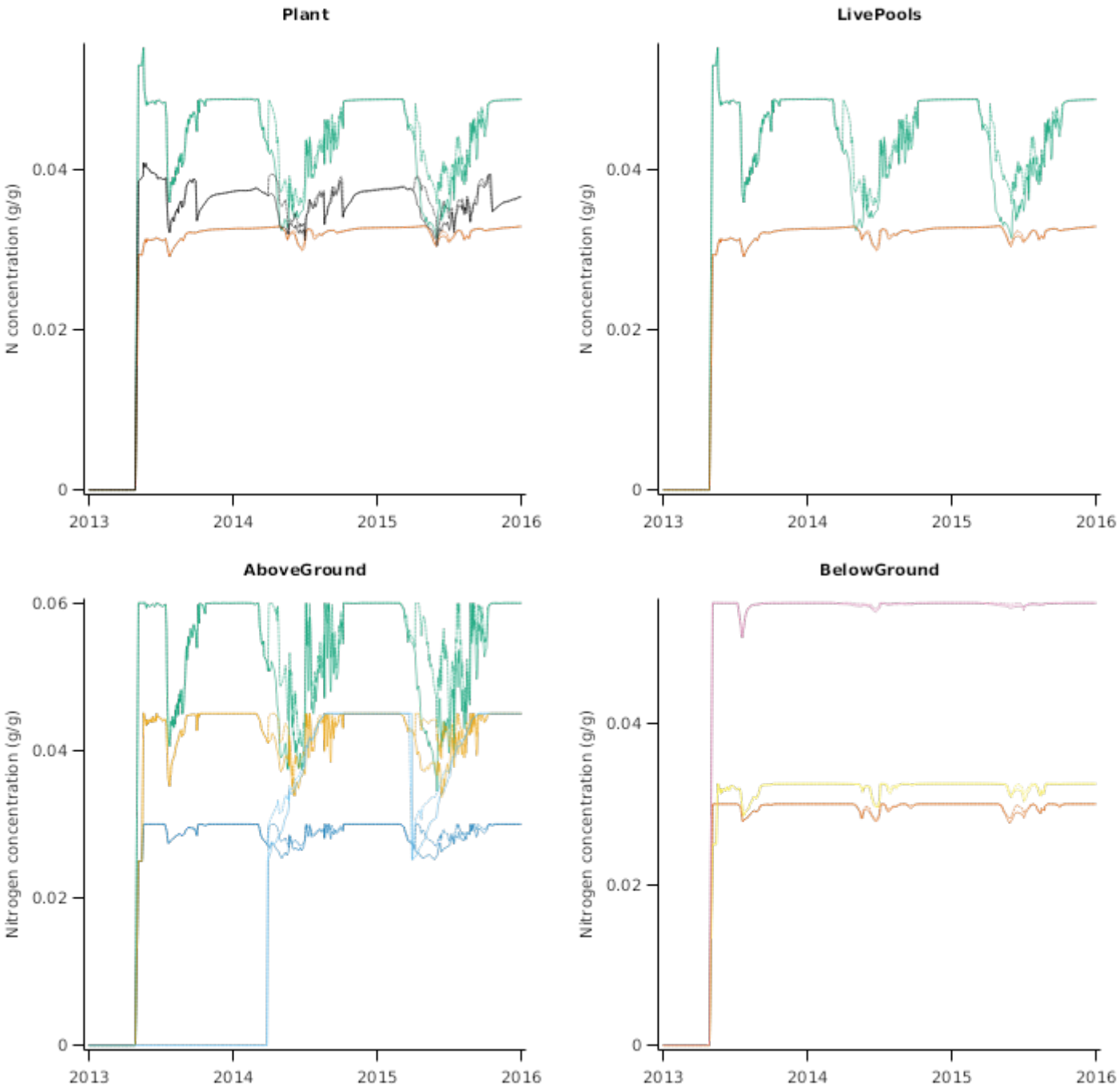

LiveBiomassAG
Crop Biomass (g/m2)
0
50
100
150
2013
2014
2015
2016


DeadBiomassAG
Crop Biomass (g/m2)
0
20
40
2013
2014
2015
2016

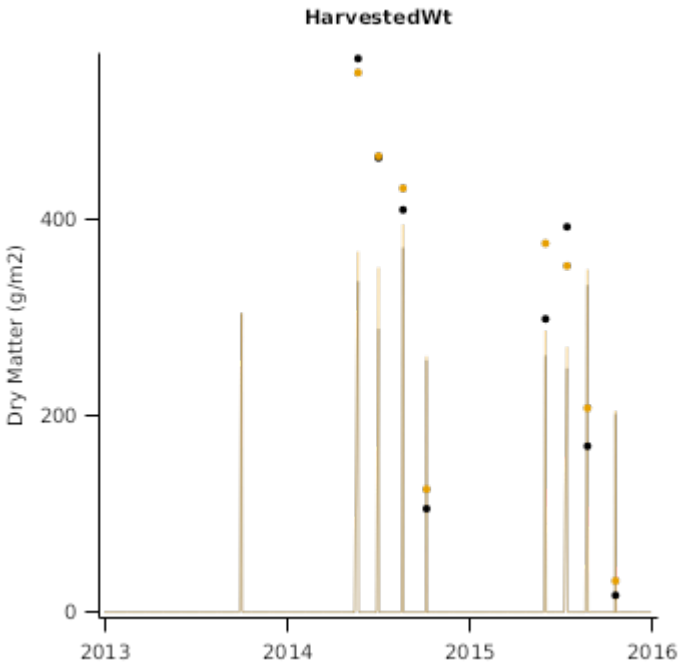

LiveBiomassBG
Crop Biomass (g/m2)
0
100
200
2013
2014
2015
2016

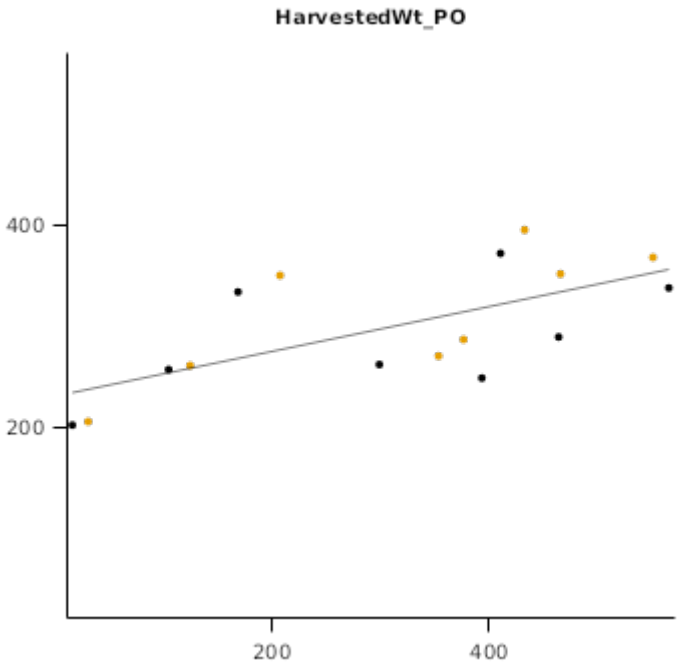

DeadBiomassBG
Crop Biomass (g/m2)
-0.5
0
0.5
2013
2014
2015
2016

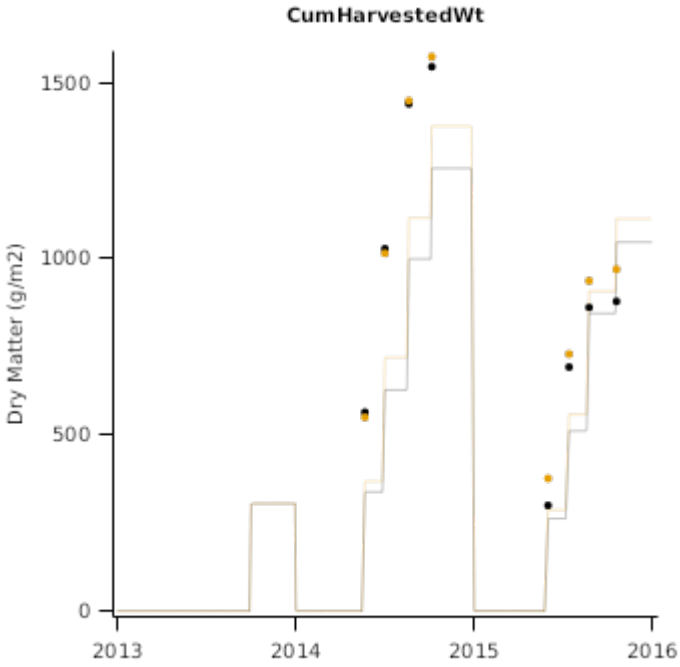
2.2.1.1.2 PlantNc

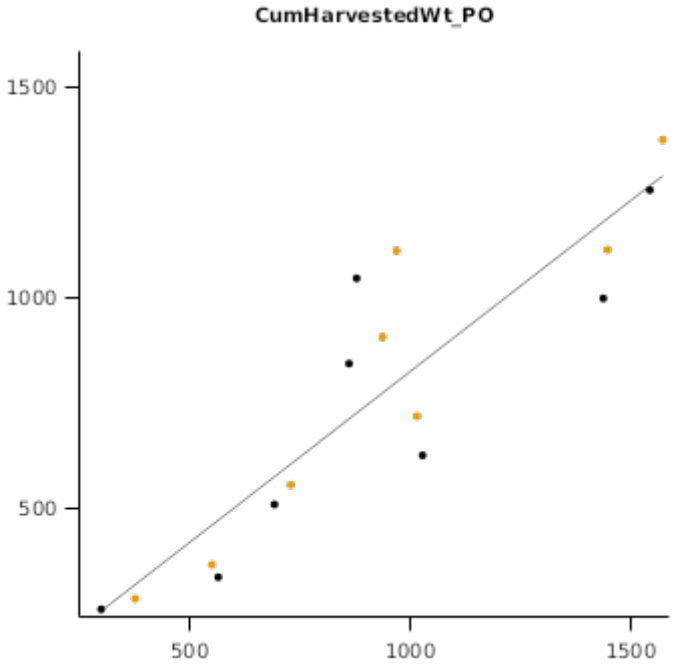


2.2.1.2 ObservedMeans









3 Acknowledgements

This model was developed with support and datasets provided by the Forages for Reduced Nitrogen Leaching (FRNL) programme, funded by the New Zealand Ministry of Business, Innovation and Employment. The programme is a partnership between DairyNZ, AgResearch, Plant & Food Research, Lincoln University, the Foundation for Arable Research, and Landcare Research.
The author is also thankful to Drs. Hamish Brown, Wen Feng Cong, and Grant Edwards for supplying the experimental data, acknowledging that many other people also contributed to their collection.

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