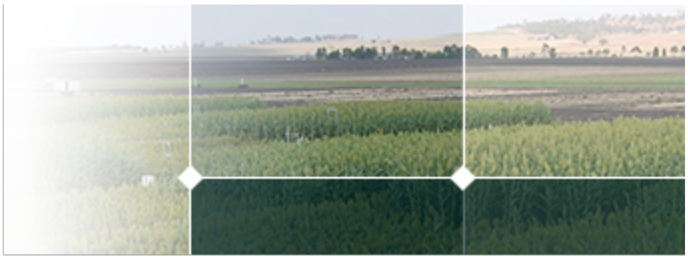

1 The APSIM WhiteClover Model

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1.1 Preamble

White clover (*Trifolium repens*) is a herbaceous perennial herb in the Fabaceae family (former Leguminosae) native of Europe and west Asia. It can now be be found in swards around the world in places with temperate and subtropical climates (Thomas, 1987; Brock et al., 1989). The plant aboveground consists of prostrate segmented stolons, from which tri-foliate leaves grow on top of a 5-15 cm petiole. From the axils of each leaf emerges either a flower stalk (peduncle) or a branching stolon. Roots are quite thick and relatively shallow; the initial taproot dies after a year or so, but roots can also grow from each branching stolon. These rooted stolon behave and can become independent plants. Cultivated varieties are commonly classified into small-, medium- and large-leaved cultivars, which besides leaf size also reflects variations in plant height and proportion of stolons (Caradus et al., 1989). The inflorescence is typically of white colour and grows about one third higher than the leaves. As a legume, white clover can host N-fixing bacteria (*Rhizobium*) in a symbiotic relationship. N fixation by rhyzobia can tranfer large quantities of N from the atmosphere into the soil. This is a major reason why white clover is typically sown alongside grasses in pastures. Nonetheless, white clover is also a valuable forage, producing very high quality feed and is highly palatable to ruminants.

Objective: The model presented here was built to simulate the growth of white clover as a forage crop. The current model focus on describing biomass accumulation and regrowth after defoliation in monocultural swards. The model was developed using the Plant Modelling Framework (PMF) and thus, it is readily possible to use the WhiteClover model in mixed swards, but this usage has not been properly tested yet and should be done with caution.
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.

1.2 Presentation

This model has been built using APSIM's Plant Modelling Framework (PMF), as introduced in Brown et al., 2014 and described in more detail in www.apsim.info. It aims to simulate the development and growth of white clover (*Trifolium repens*) as a forage crop. The model focus primarily on describing the vegetative growth with only a simplified account of the reproductive phase. Only an inflorescence organ is defined, so flowers and seeds and their development are not considered separately. This was done because the reproductive phase of white clover stands is quite long and undefined: different plants may start flowering at different times and single plants may have flower buds as well as ripen seed at the same time (e.g. Hyde et al., 1959; Thomas, 1987; Medeiros et al., 2000); more details in the phenology section below. With more comprehensive data, the implementation of this phase and the reproductive organs may be revisited in the future. The white clover model simulates the aboveground plant structure, including the photosynthesis process, using the SimpleLeaf procedure of PMF, which does not consider explicitly leaf age or their 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 white clover in a simulation the procedure is the same as any other APSIM crop:

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

```
WhiteClover.Sow(cultivar: Huia, population: 450, depth: 5, rowSpacing: 100);
```

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

1.4 Harvest and biomass removal

White 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 the residue should be <= 1.0. To specify the proportions for removal in a manager script, use a RemovalFractions class as shown below:

```
[EventSubscribe("Commencing")]
private void OnSimulationCommencing(object sender, EventArgs e)
{
RemoveFraction = new RemovalFractions(WhiteClover.Organs);
}
[EventSubscribe("DoManagement")]
private void OnDoManagement(object sender, EventArgs e)
{
if (Clock.Today.Date == HarvestDate)
{
RemoveFraction.SetFractionToRemove("Leaf", 0.80, "Live");
RemoveFraction.SetFractionToRemove("Petiole", 0.50, "Live");
RemoveFraction.SetFractionToResidue("Leaf", 0.05, "Live");
RemoveFraction.SetFractionToResidue("Petiole", 0.01, "Live");
WhiteClover.Harvest(RemoveFraction);
}
}
```

The default values for the fractions (%) to be removed or transferred to residue are shown below in the description of each organ.

1.5 Crop termination

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

```
WhiteClover.EndCrop();
```

Once a crop has been ended the field is open to be used by another APSIM plant model, or another white clover crop. Note that ending white 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
Stolon	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

Component Name	Component Type
TargetShootRootRatio	Models.Functions.PhaseLookup
TargetAboveGroundFraction	Models.Functions.DivideFunction
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 white clover is controlled either by the accumulation of thermal time or photoperiod.

1.6.1 ThermalTime

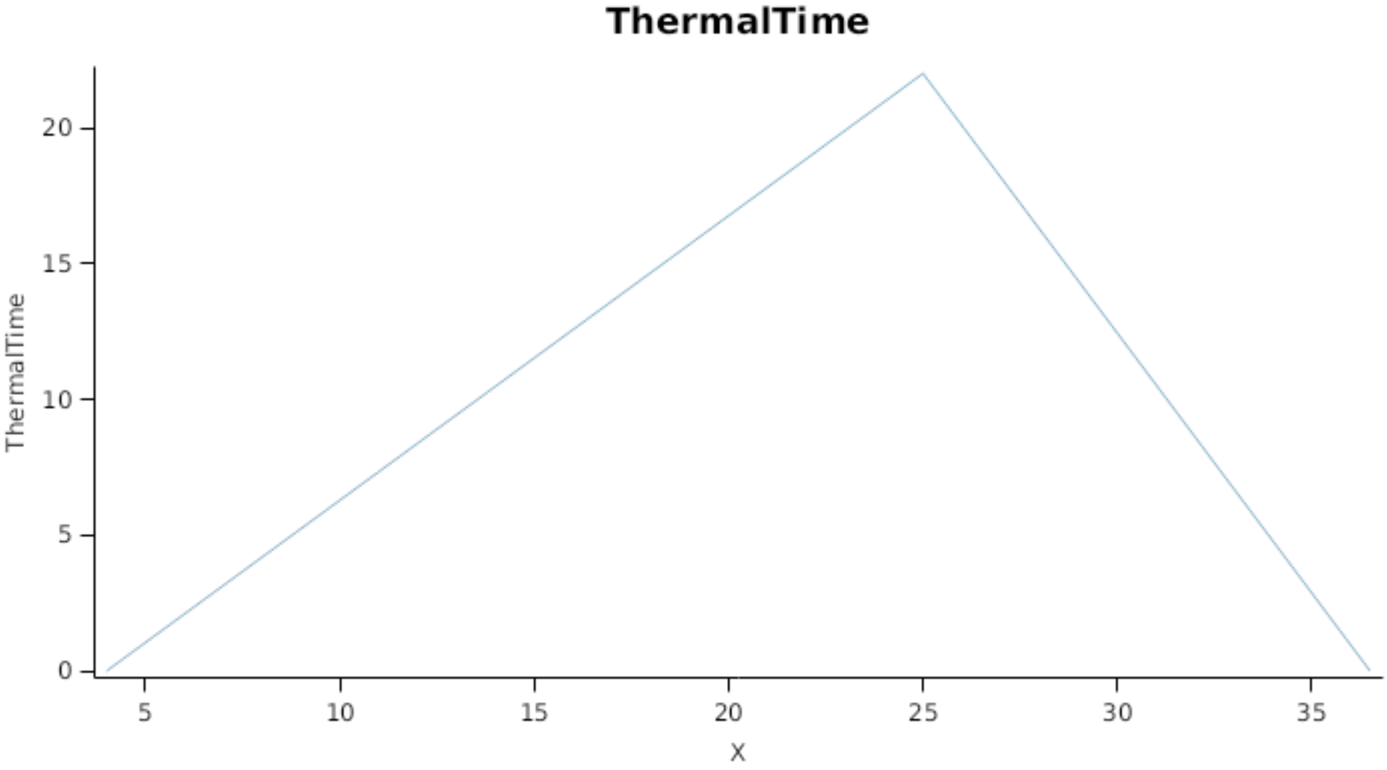
ThermalTime is the average of sub-daily values from a XYPairs.

The thermal time is used to control many of the phenological changes in white clover. It is calculated from the daily average temperature using three 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 white clover. The minimum, or base, temperature is quite variable among cultivars, varying from -1.0 to 5°C (Black et al., 2006; 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 28°C and 38°C for maximum temperature (Black et al., 2006; 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
4.0	0.0
25.0	22.0
36.5	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	PhenologyRewind	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 70-90% of seeds germinating for white clover. Temperatures between 5 and 20^{o}C affect the speed of germination but not the final percentage (Hampton et al., 1987). The model does not consider variable germination rate, thus the population should be adjusted by the user when sowing to account for less than 100% germination.

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.

White clover has small seeds and these need to be placed near the soil surface to emerge successfully. Best emergence rates 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 white clover occurs 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 white 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, white clover plants partition biomass to leaf+petiole, stolon, 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.
White clover is typically described as either short day or short-long day species (Thomas, 1961; Thomas, 1980), which means induction is caused by exposure to short daylight lengths but reproductive growth may also be triggered by a period with long photoperiod. Exposure to cold temperature can also lead to induction with subsequent initiation of inflorescence development when days become warmer and longer (Thomas, 1981; Beatty, 1959). The variability in response of induction to environmental conditions are considerably large in white clover. In most stands at least some plants will show reproductive growth regardless of environmental conditions. The variations show some trend when contrasting large- to short-leaved cultivars or for cultivars from different origins (especially latitude), but the effect of genotypes within each group was not found to be significant (e.g. Thomas, 1980; Thomas, 1982; Norris, 1984; Beatty,

1959).
Inducing daylight length seem to be 12 hours or less, while temperatures need to be below about 10°C (Thomas, 1979; Thomas, 1981; Thomas, 1982; Norris, 1984; Norris, 1985). The base white clover model uses the accumulation of days under either low temperature or short photoperiod to trigger the end of the vegetative phase.

The *Target* for completion is calculated as:

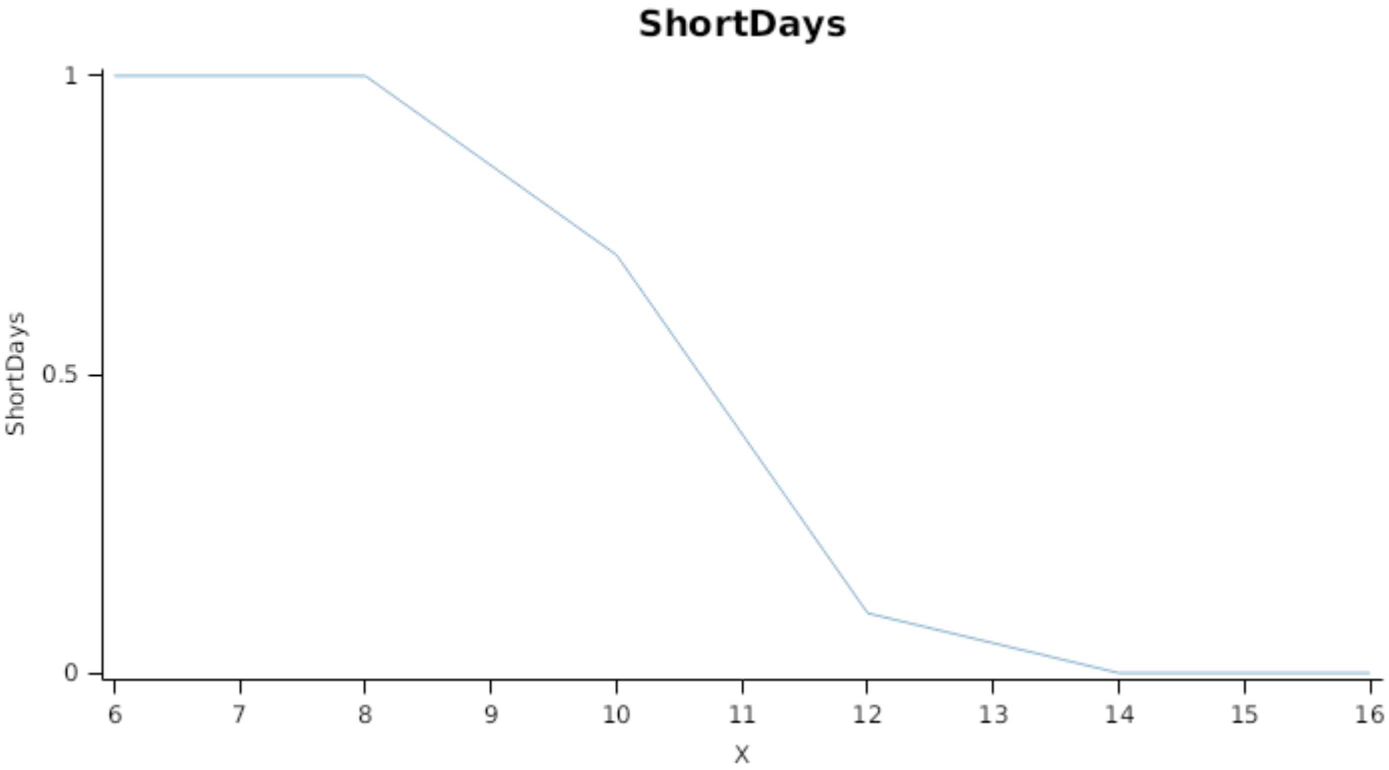
Target = 15 (days)

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

Progression = ShortDays + LowTemperatures

ShortDays is calculated using linear interpolation

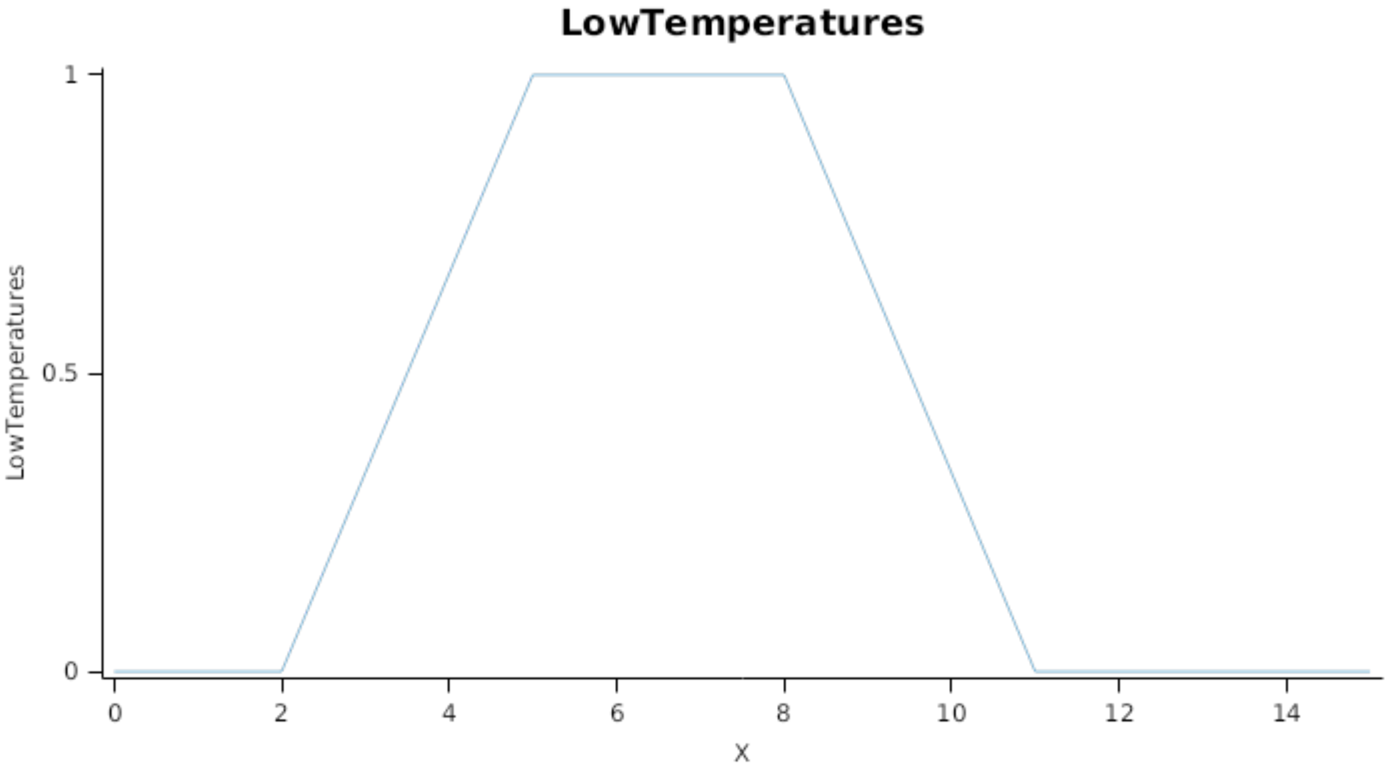
X	ShortDays
6.0	1.0
8.0	1.0
10.0	0.7
12.0	0.1
14.0	0.0
16.0	0.0



LowTemperatures is calculated using linear interpolation

X	LowTemperatures
0.0	0.0
2.0	0.0
5.0	1.0
8.0	1.0

X	LowTemperatures
11.0	0.0
15.0	0.0



1.6.5 Inductive

This phase goes from induction to flowering.

During this phase the white clover plants await for the environmental cue to start the reproductive growth. Physiological and metabolic processes remain the same as for the vegetative phase; plants partition biomass to leaf+petiole, stolon, and root+taproot organs. The inductive phase starts when plants accumulate a given number of days under inductive conditions, i.e. low temperatures and/or short daylight lengths (Thomas, 1979; Norris, 1984; Norris, 1985). The phase ends when the plants start reproduction growth, with the emergence of flower buds.
There is a large level of variation in white clover plants and their flowering response to environmental conditions, with some plants reaching reproductive growth in almost any stand (Thomas, 1979; Beatty, 1959). Nonetheless, in natural conditions reproductive growth is typically triggered by long daylight lengths, with reported values around 14 hours (Thomas, 1980; Thomas, 1981;Norris, 1984). The accumulation of days under long photoperiod is used by the model to trigger the end of the inductive phase.

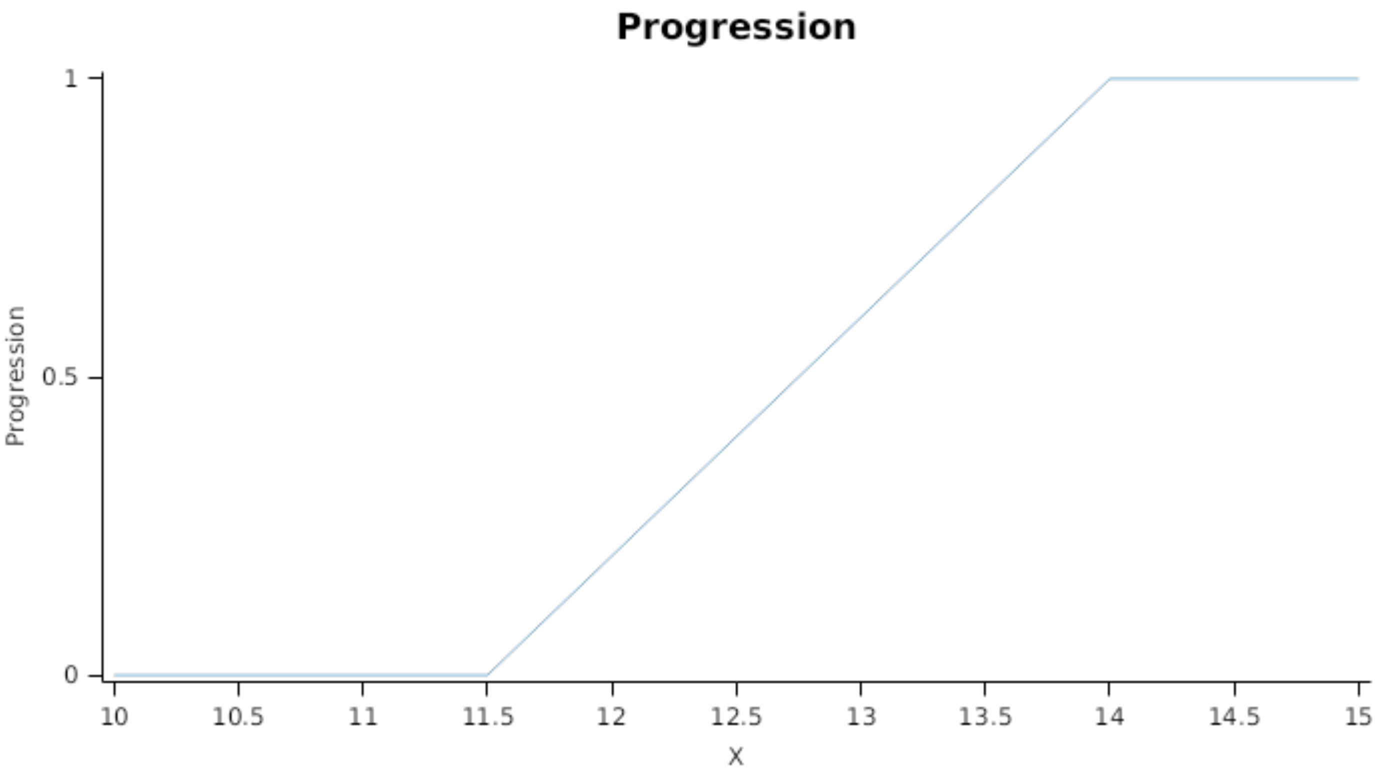
The *Target* for completion is calculated as:

Target = 10 (days)

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

Progression is calculated using linear interpolation

X	Progression
10.0	0.0
11.5	0.0
14.0	1.0
15.0	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 flower and seeds development explicitly, only a generic organ referred to as *inflorescence* is defined. The main reason for this is the variability and complex phenology of reproduction of white clover; with seeds maturing while new flowers are still being initiated over summer and early autumn (e.g. Hyde et al., 1959; Thomas, 1987; Medeiros et al., 2000). Also due to their similarities and the fact that a population is described in the model (instead of single plants), peduncles and petioles are simulated as a single organ.
Flower emergence typically starts in spring, peaks at the beginning of summer and continues until autumn (Thomas, 1980 ; Macfarlane et al., 1984; Marshall et al., 1993). The actual periods vary for different cultivars, and some have flowers nearly all year (albeit with low frequency over winter). A drop in flower numbers in mid-summer and subsequent increase in early autumn has been shown in some cultivars and has been linked to water deficit or inhibition due to long days (Thomas, 1980; Macfarlane et al., 1984). Management practices, such as applying N fertiliser, irrigation and defoliations, have, in general, a positive impact on flower and seed production (Thomas, 1980; Medeiros et al., 2000; Bissuel-Belaygue et al., 2002), 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 of application of fertilisers.

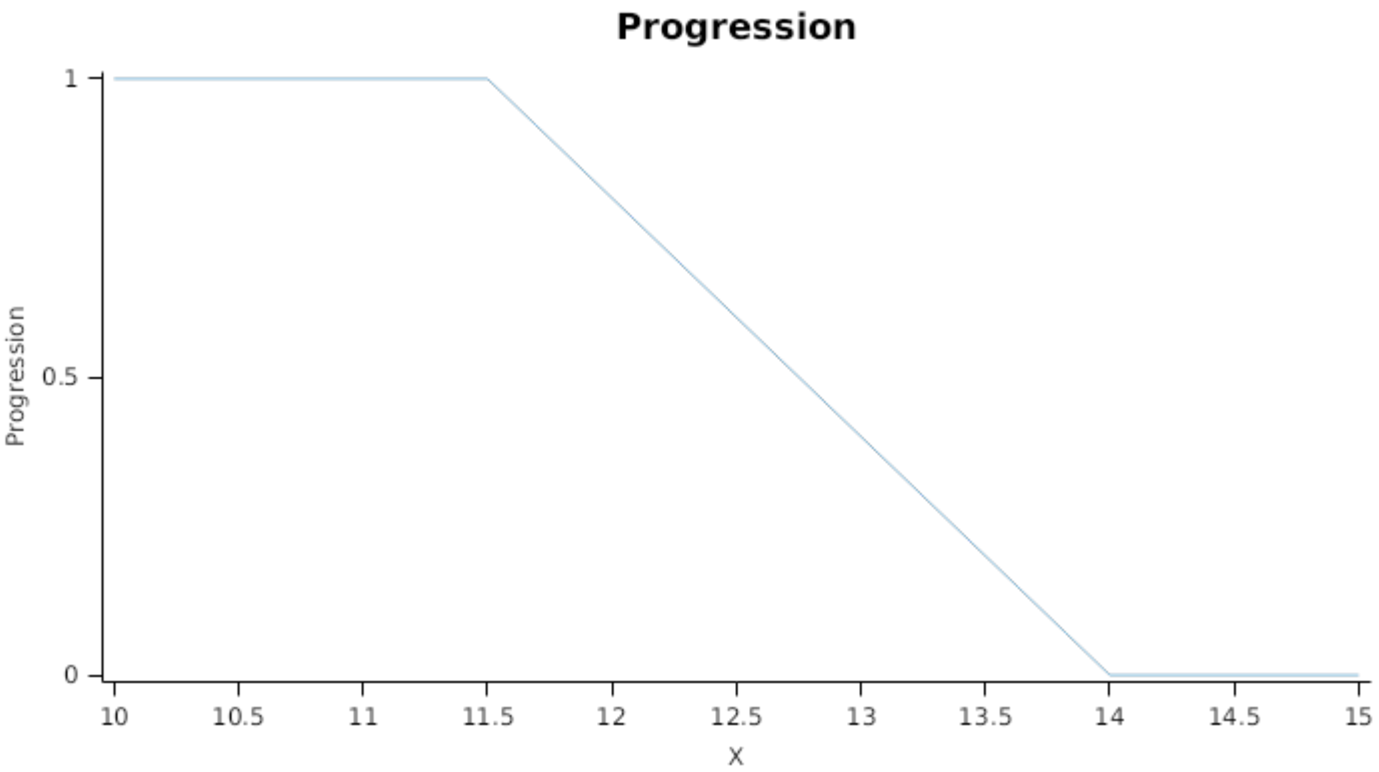
The *Target* for completion is calculated as:

Target = 30 (days)

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

Progression is calculated using linear interpolation

X	Progression
10.0	1.0
11.5	1.0
14.0	0.0
15.0	0.0



1.6.7 PhenologyRewind

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.

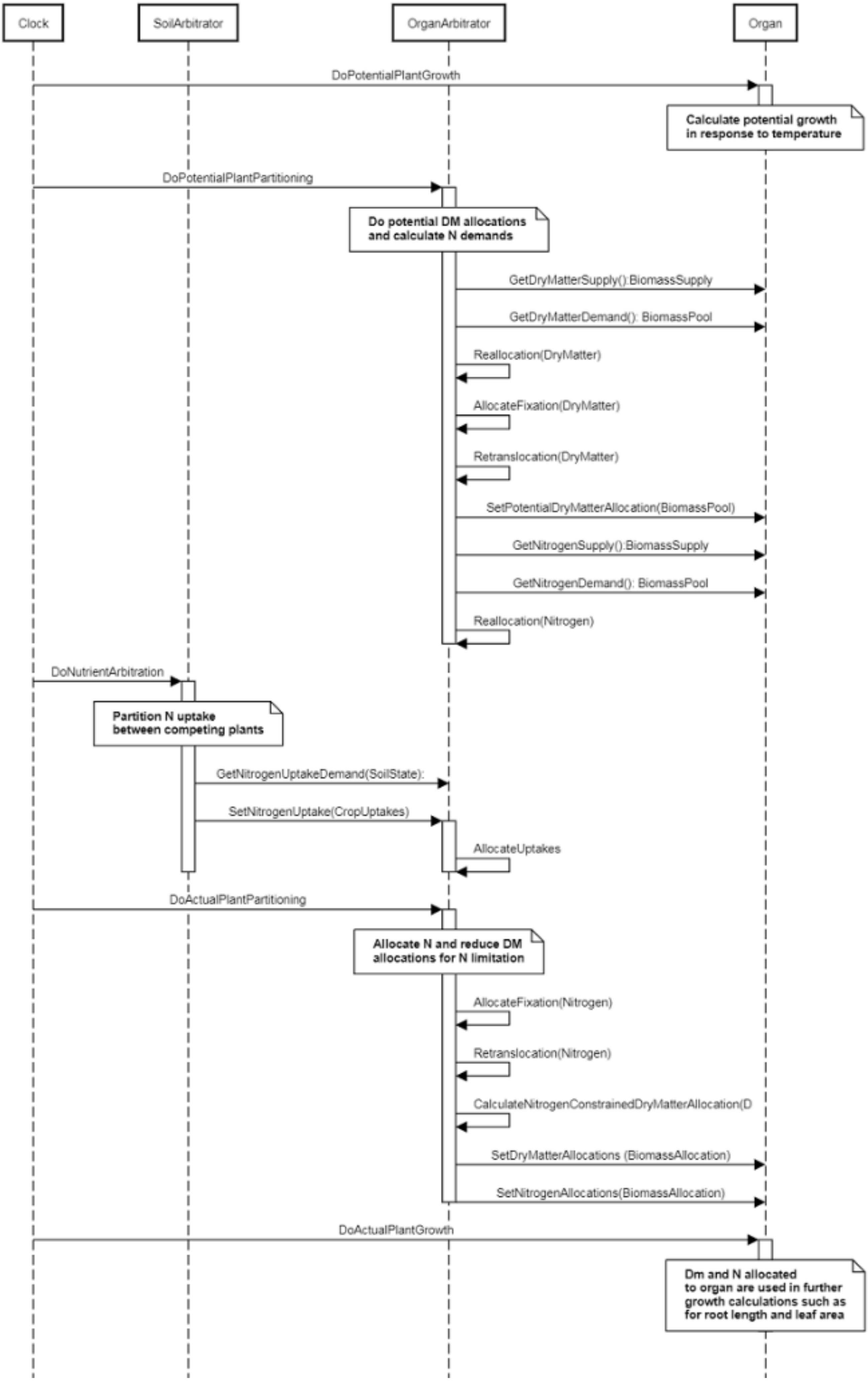

Clock
SoilArbitrator
OrganArbitrator
Organ
DoPotentialPlantGrowth
Calculate potential growth in response to temperature
DoPotentialPlantPartitioning
Do potential DM allocations and calculate N demands
GetDryMatterSupply():BiomassSupply
GetDryMatterDemand(): BiomassPool
Reallocation(DryMatter)
AllocateFixation(DryMatter)
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.

This organ represents all the leaves in the plant and has only a basic representation of the canopy structure, with all leaves considered to be distributed in one layer. The total leaf biomass is used to determine the height of the canopy, using a function that can vary for different cultivars but that currently it is not affected by competition with other plants.

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 white clover seeds varies between 0.5 and 0.8 g/1000 seeds (Thomas, 1987; Bissuel-Belaygue et al., 2002; 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.

The DM demands calculated here represent potential values, or a weighting factors, which are used by the OrganArbitrator to compute the allocated DM for all organs. The potential demand is computed as the sum of a *Base* and a *Deficit* demand. The *Base* demand is simply defined by the target proportion of leaf biomass, whereas the *Deficit* demand is defined by the difference between the actual and the targeted proportions. This approach is used to ensure promptly regrowth of aboveground organs after a defoliation; it relies in the assumption that a target biomass proportion for each organ exists. The *TargetBiomassProportion* is calculated based on a target shoot-to-root ratio and a biomass proportion for each organ above or below ground, these are defined elsewhere in this documentation and may vary with growth stage and environmental conditions.

The partitioning of daily demand towards structural biomass is based on the structural fraction:

Structural = *DMDemandFunction* x *StructuralFraction*

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

Where:

Zero = 0

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

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

StructuralFraction = 0.95 (g/g)

Currently there is no metabolic biomass in SimpleLeaf

Metabolic = 0 (g/g)

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.

These N demands also represent potential values that are used by the OrganArbitrator to get the total plant N demand. This and any source of N in the plant are used to determine soil N demand, and eventually the actual amounts allocated to each pool in each organ.

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.

These N demands also represent potential values that are used by the OrganArbitrator to get the total plant N demand. This and any source of N in the plant are used to determine soil N demand, and eventually the actual amounts allocated to each pool in each organ.

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 (/day)

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 white clover (e.g. McCree et al., 1966; Woledge et al., 1992; Malinowski et al., 1998; Heraut-Bron et al., 2000; Hofmann et al., 2007), including its variation due to water and N deficiency, shading and CO_2 changes. The values and trends for CO_2 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 white clover are in general around 2.5-3.0 g DM/MJ (Faurie et al., 1996; Manderscheid et al., 1997; Nassiri, 1998).

RUE = 1.25 (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

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

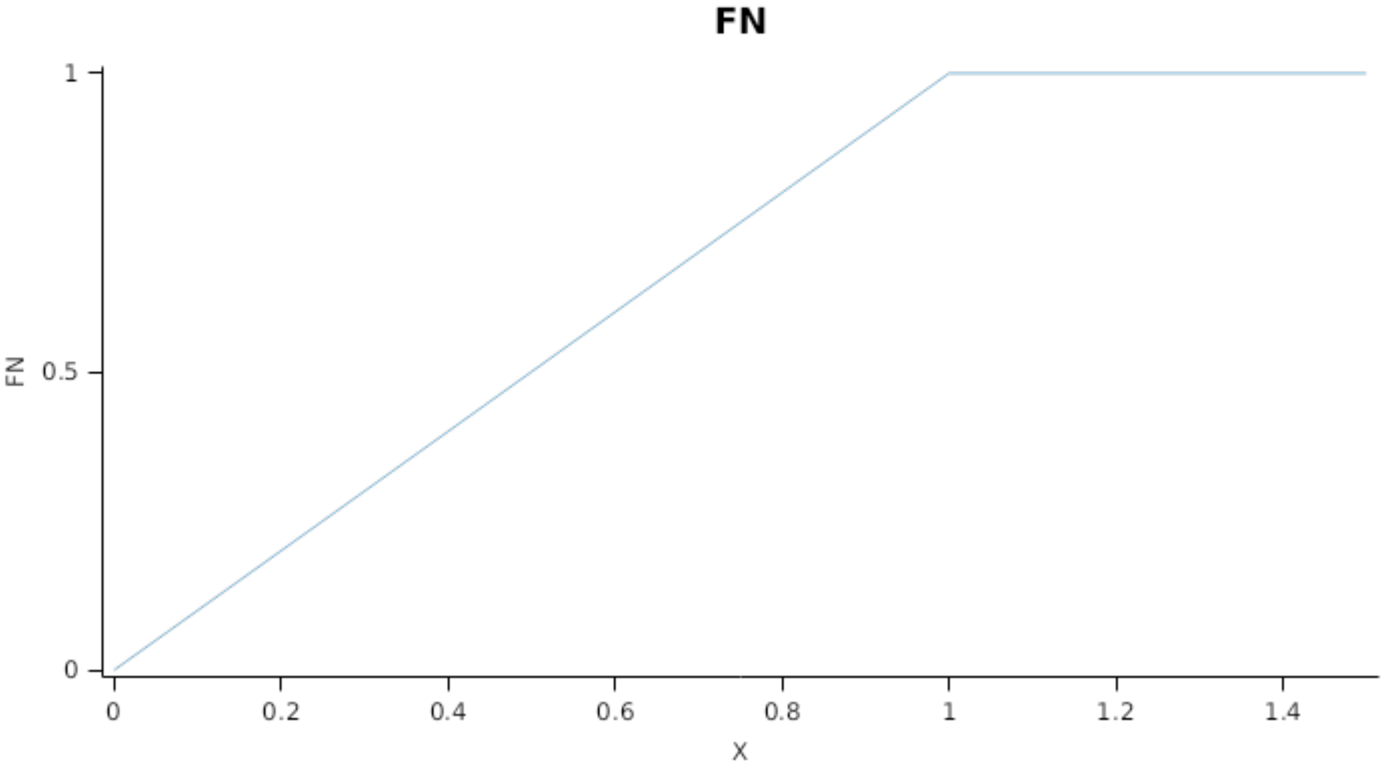
For C4 plants,

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

FN is calculated using linear interpolation

X	FN
0.0	0.0
0.5	0.5
1.0	1.0

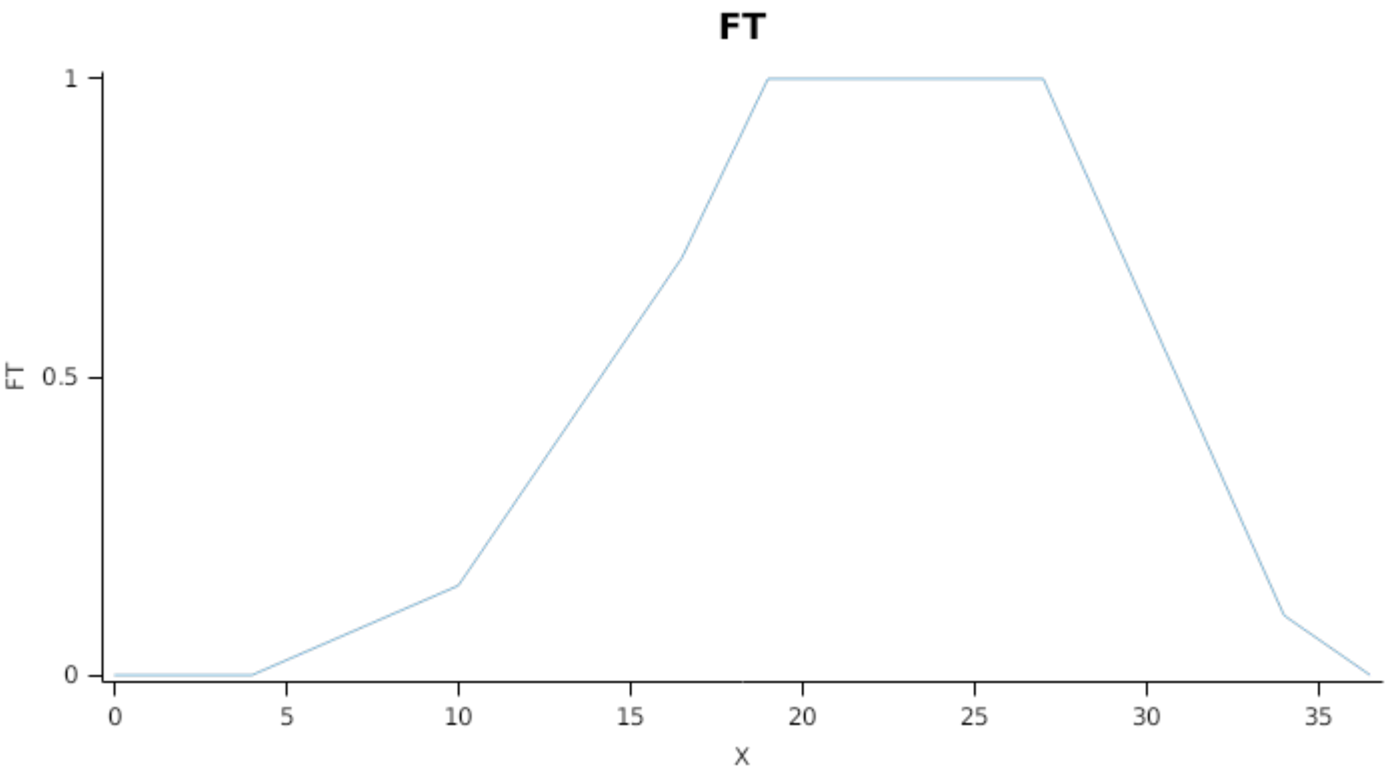
X	FN
1.5	1.0

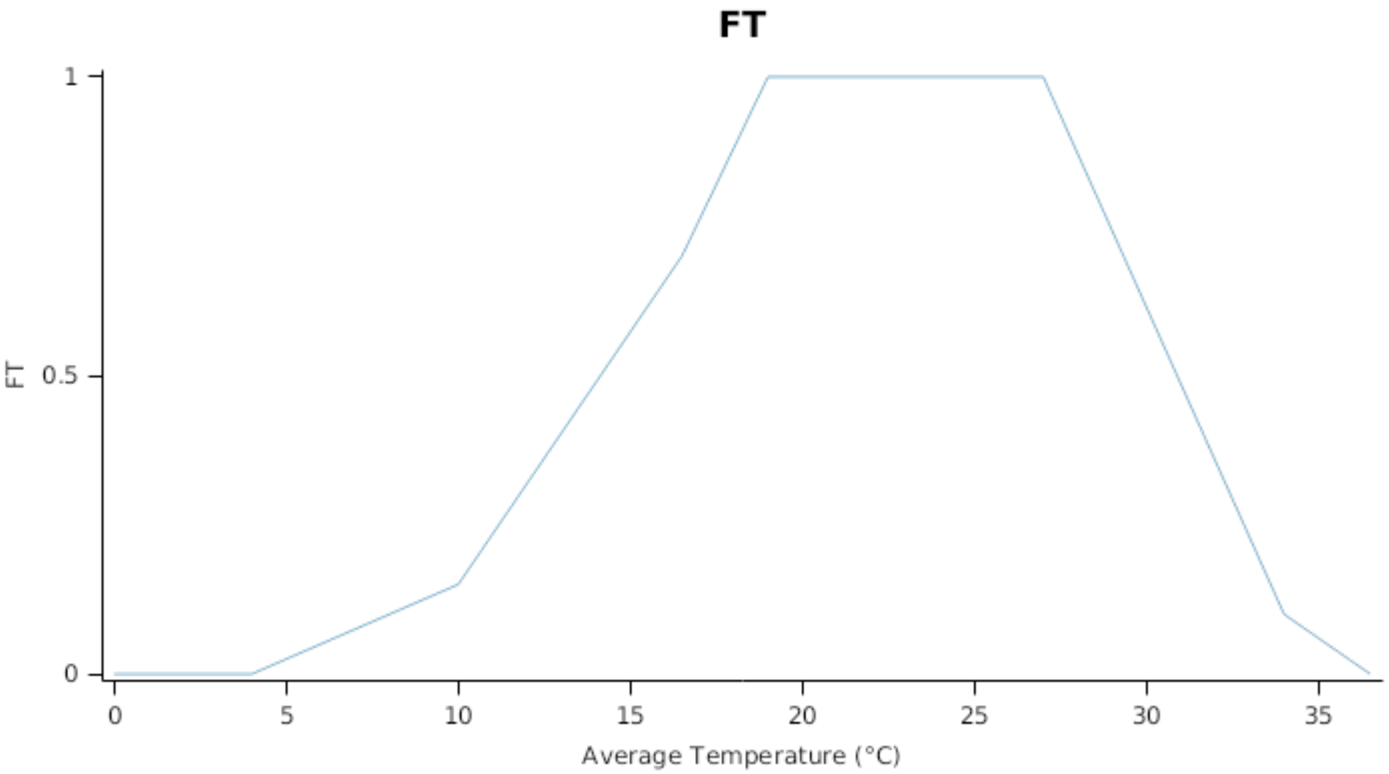


FT is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.75

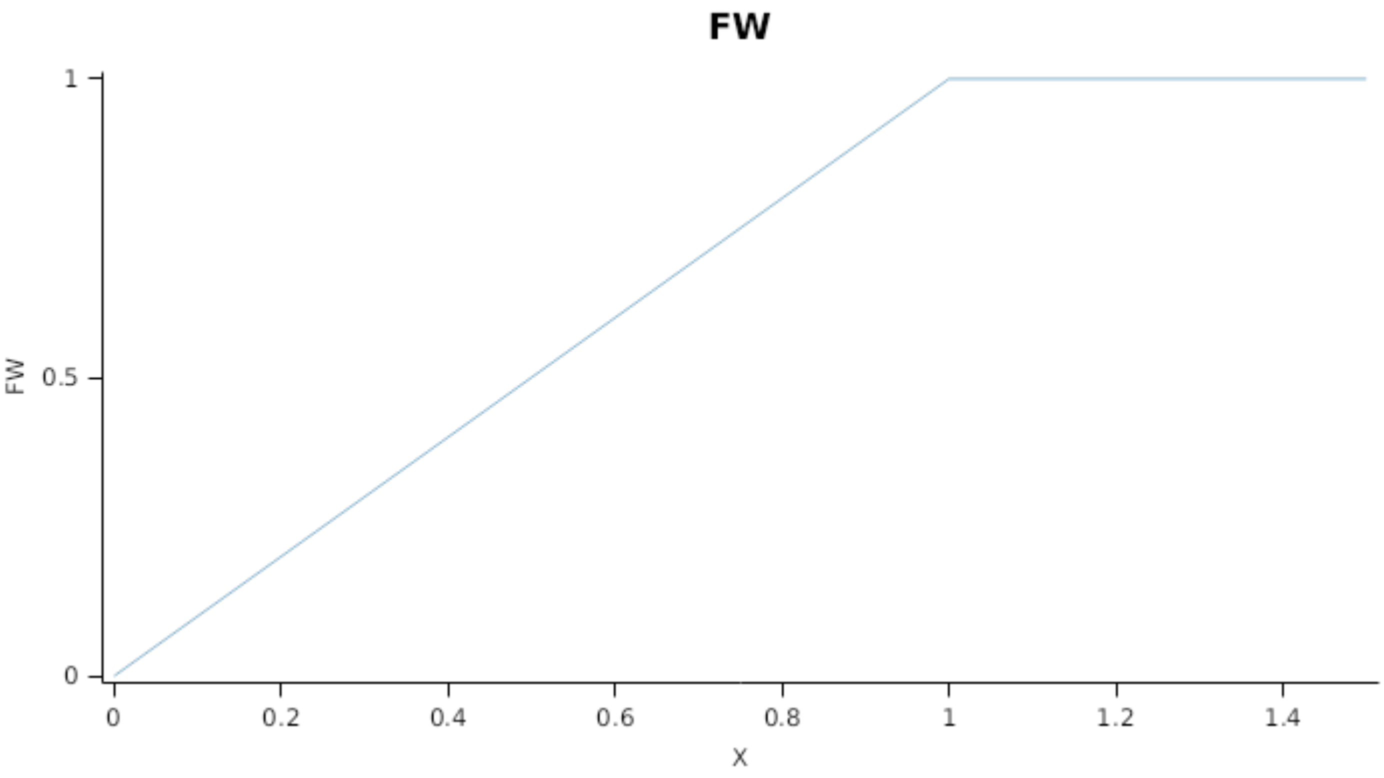
X	FT
0.0	0.0
4.0	0.0
10.0	0.1
16.5	0.7
19.0	1.0
27.0	1.0
34.0	0.1
36.5	0.0





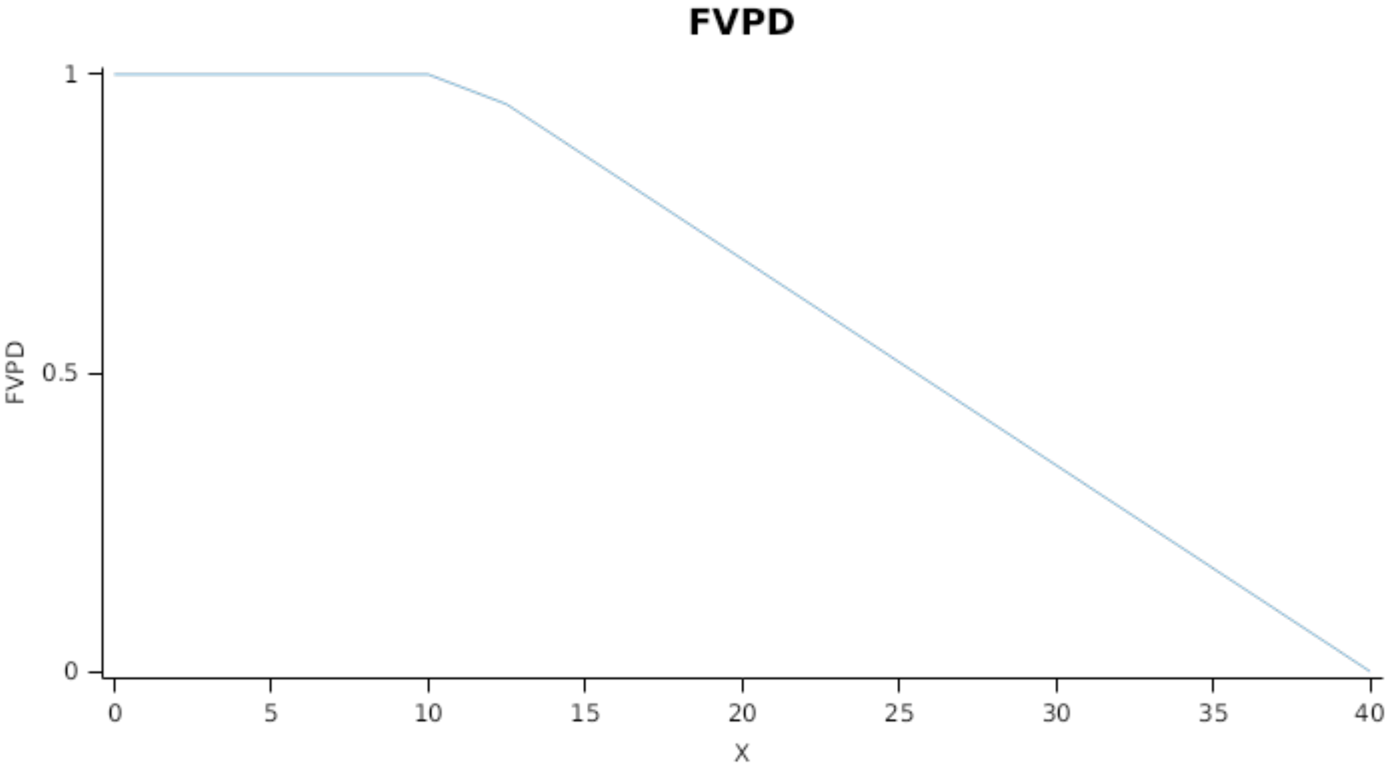
FW is calculated using linear interpolation

X	FW
0.0	0.0
0.8	0.8
1.0	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 favoured when conditions are good for growth. Retranslocation from leaves is enabled any time.

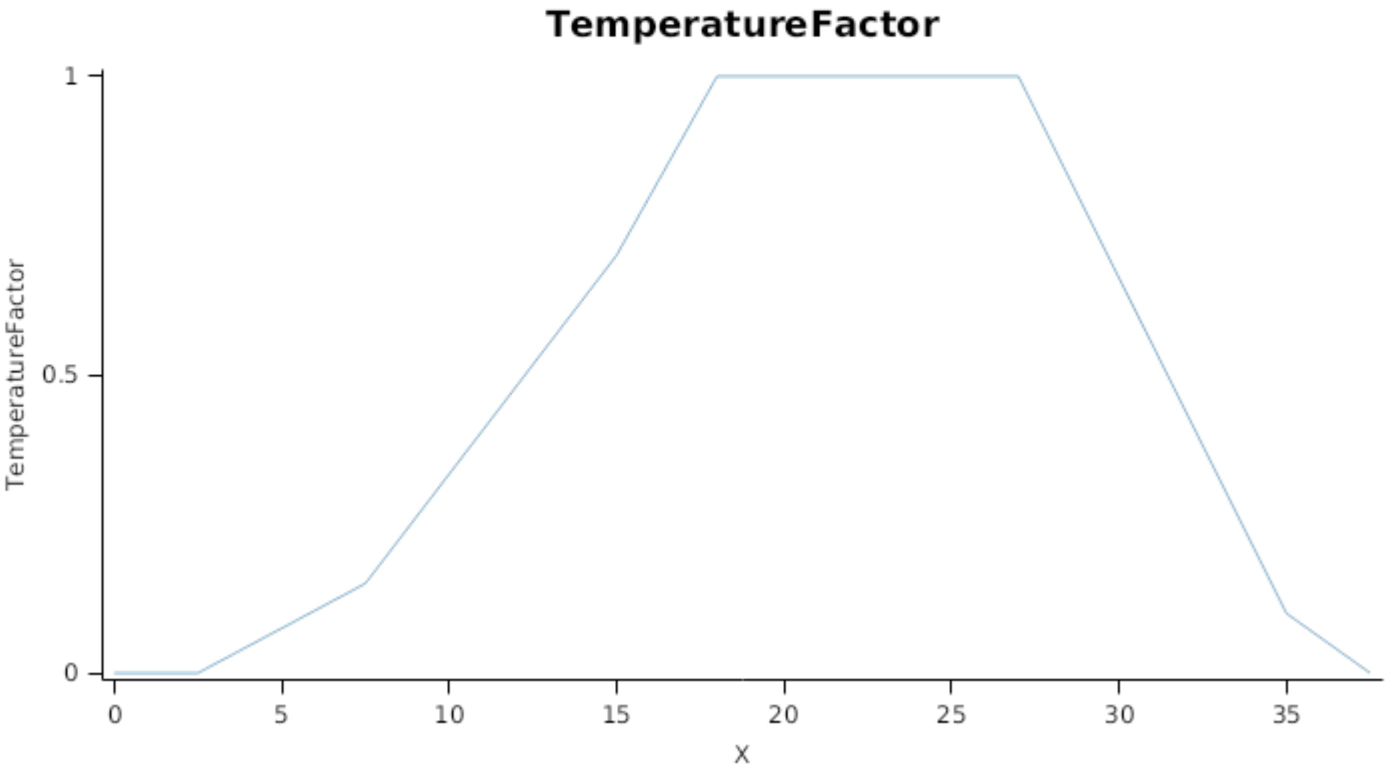
NRetranslocationFactor = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor*

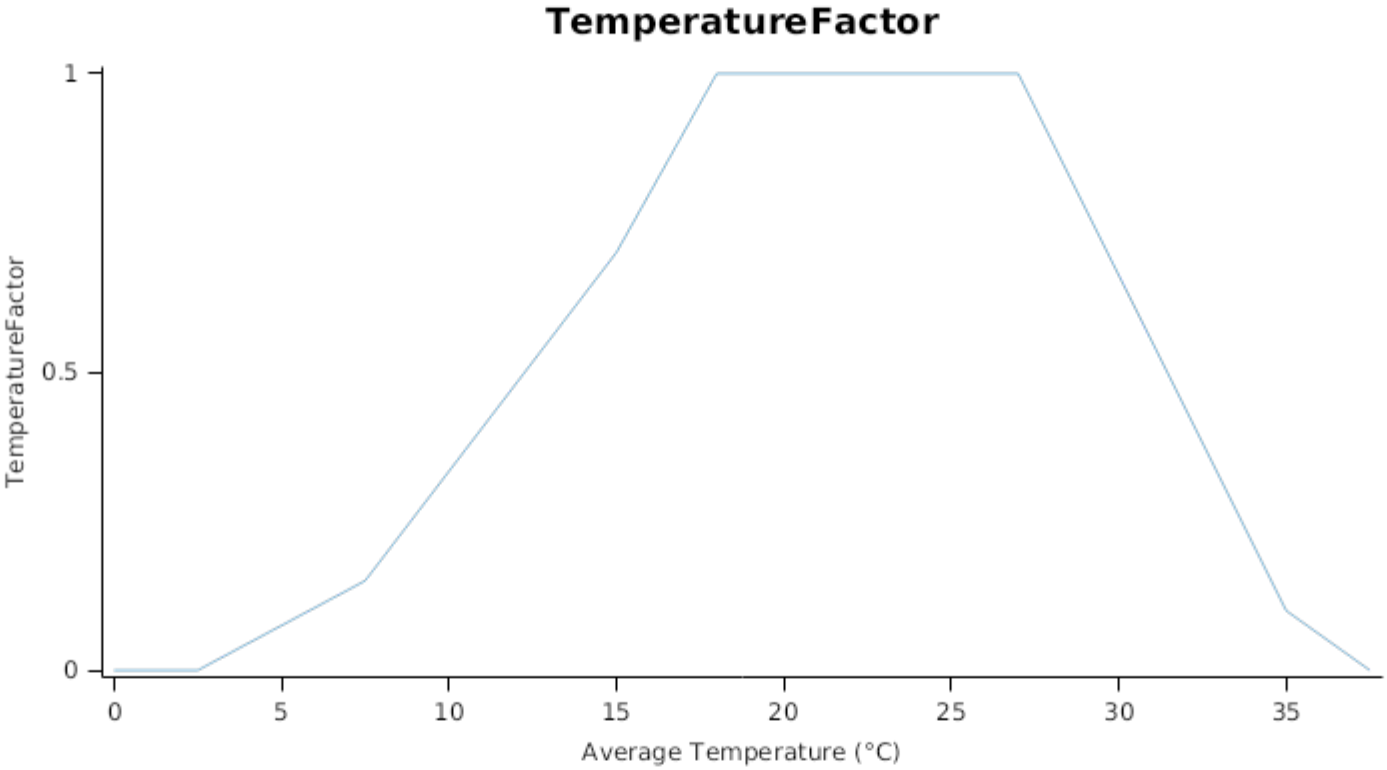
ReferenceRate = 0.1 (/day)

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

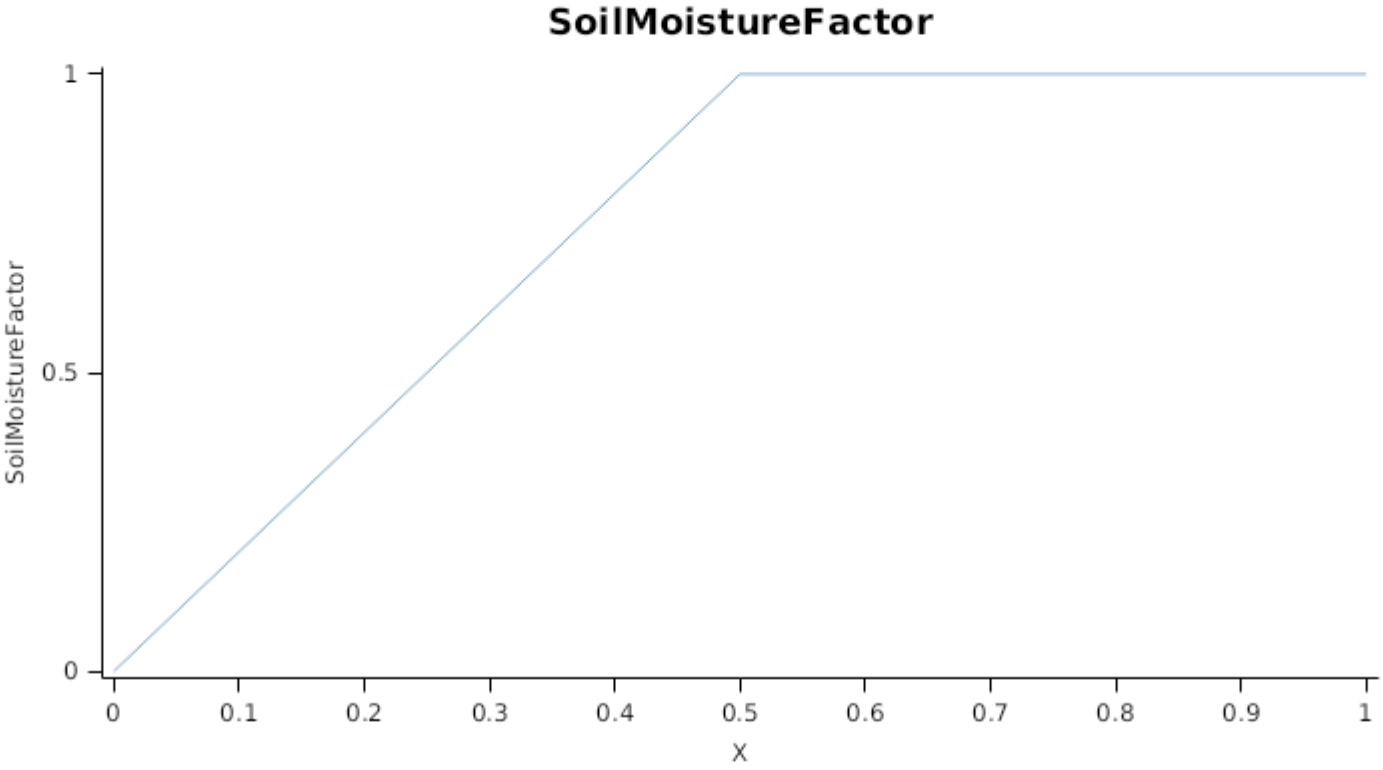
X	TemperatureFactor
0.0	0.0
2.5	0.0
7.5	0.1
15.0	0.7
18.0	1.0
27.0	1.0
35.0	0.1
37.5	0.0





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 is defined based on biomass and the specific leaf area (SLA). The value for SLA for white clover is assumed to be constant in the current model, although the data indicates that age and some environmental factors (shading and nutrient status) have some effect on this value. Variation due to age are ignored because the model simulates a population, as is intented to describe swards over long term, thus it should represent leaves of varing ages at the same time. The nutritional effects are generally not linked to N, which currently is the only nutrient simulated in APSIM, thus can be ignored. The effects of shading, as well as water deficiency, only occur when these conditions are mantained for some time, the model may have to be revised in the future to account for these factors, prefereably with some experimental data. Available data suggest that SLA of white clover varies between 0.020 and 0.045 m2/g, with mean values for the cultivar Huia being around 0.030 m2/g (Woledge, 1986; Chapman et al., 1992; Kang et al., 1995; Heraut-Bron et al., 2000; Castle et al., 2002; Nichols et al., 2014).

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

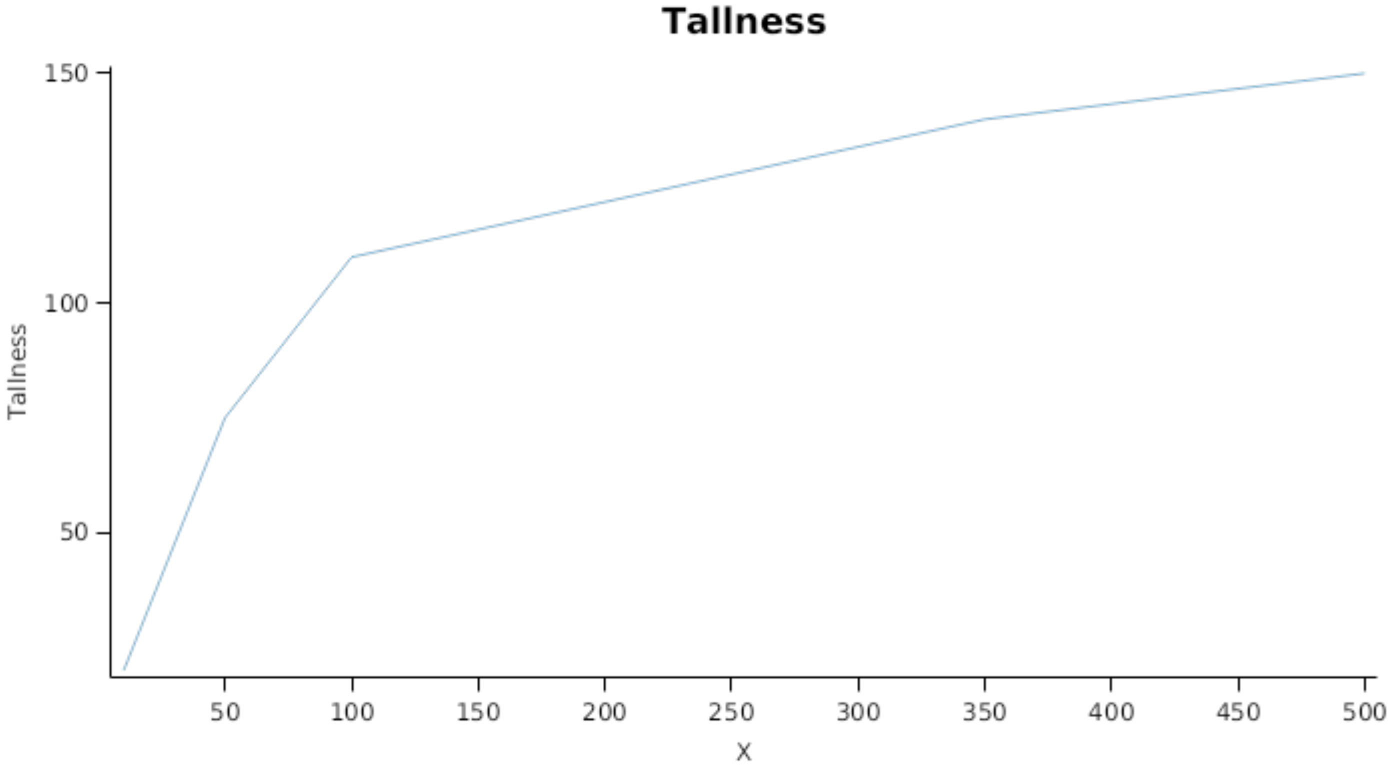
SpecificLeafArea = 0.03 (m^2/g)

Due to the near horizontal placement of its leaves, white clover has a high capacity for light interception. Values for the light extinction coefficient reported in the literature are quite variable, depending on which radiation was considered (total, direct, or PAR) to and whether plants were in mixed swards or in monoculture; these vary from 0.70 up to 1.0 (Lantinga et al., 1999; Sonohat et al., 2002; den Hollander et al., 2007).

ExtinctionCoefficient = 0.9 (0-1)

Tallness is calculated using linear interpolation

X	Tallness
10.0	20.0
50.0	75.0
100.0	110.0
350.0	140.0
500.0	150.0



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 (0-1)

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.

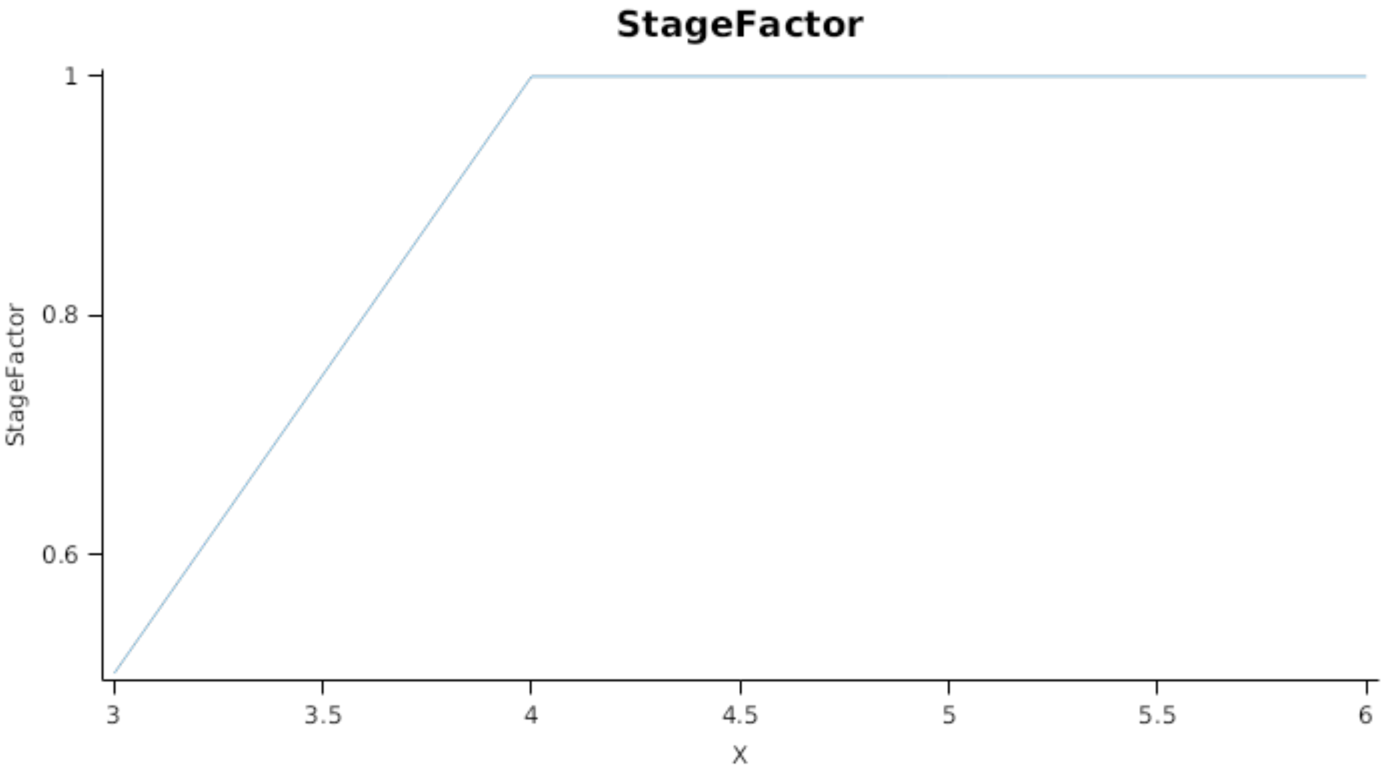
White clover has a relatively high rate of leaf senescence, with leaf area estabilising when LAI reaches about 5.0 (Brougham, 1958; Hart, 1987; Nichols et al., 2014). Generic relationships to enviromental factors, such as temperature and soil moisture, are assumed based on other plant models.

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

ReferenceRate = 0.05 (/day)

StageFactor is calculated using linear interpolation

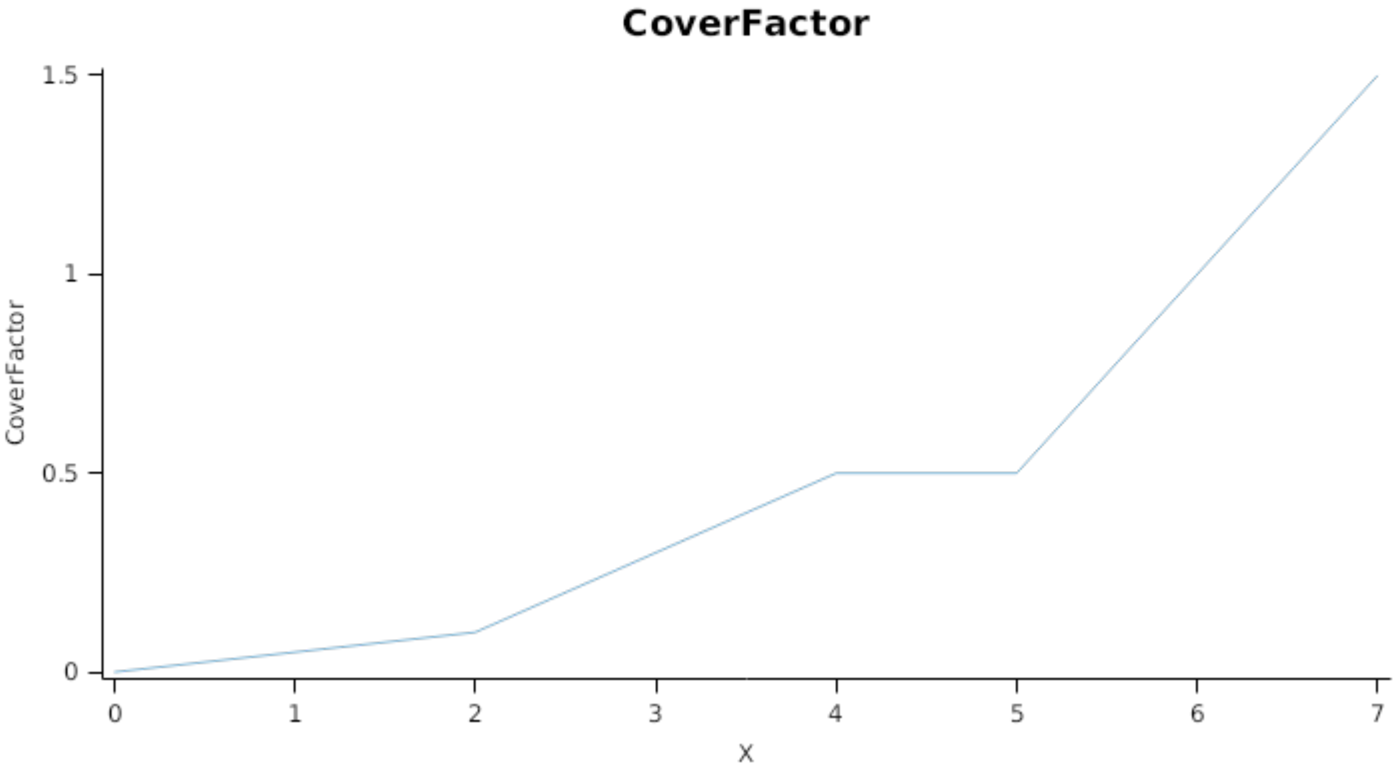
X	StageFactor
3.0	0.5
4.0	1.0
5.0	1.0
6.0	1.0



CoverFactor is calculated using linear interpolation

X	CoverFactor
0.0	0.0
2.0	0.1
4.0	0.5
5.0	0.5

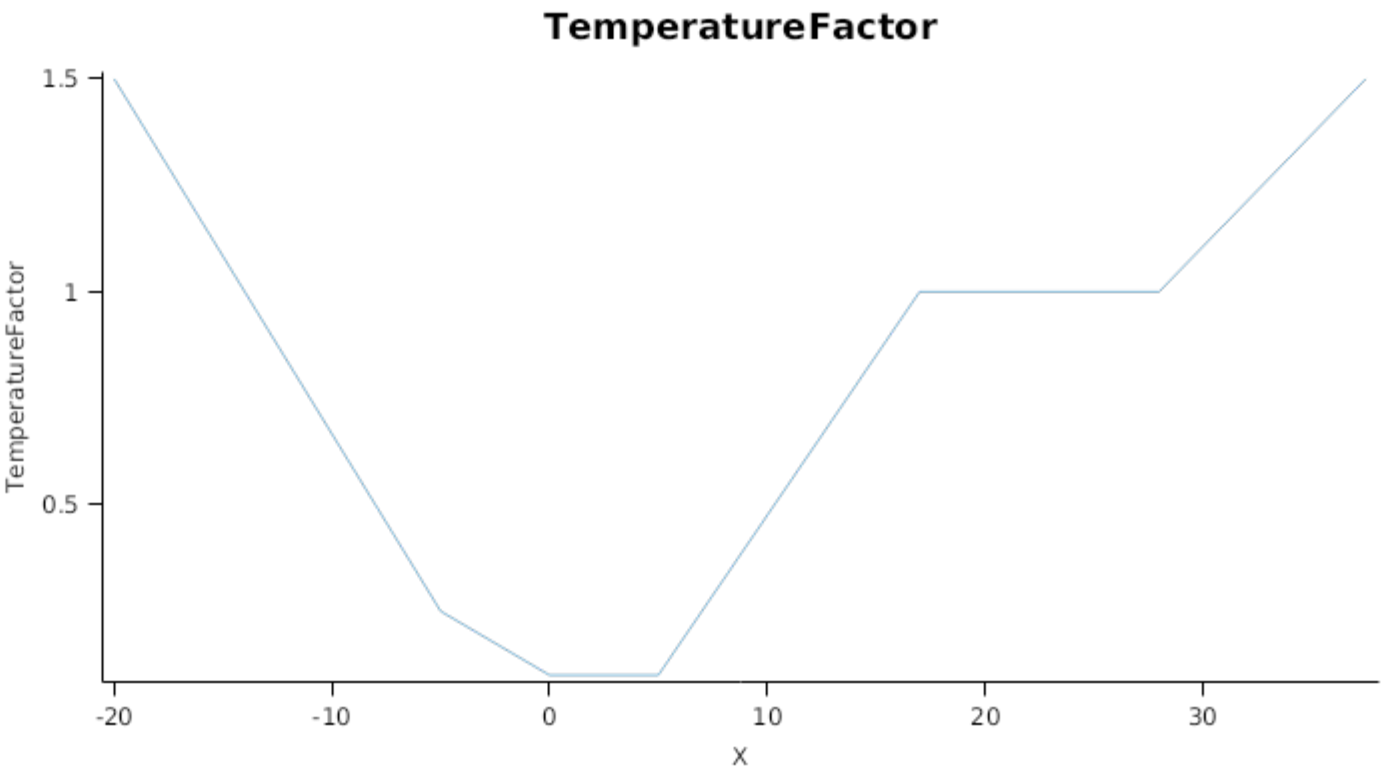
X	CoverFactor
7.0	1.5

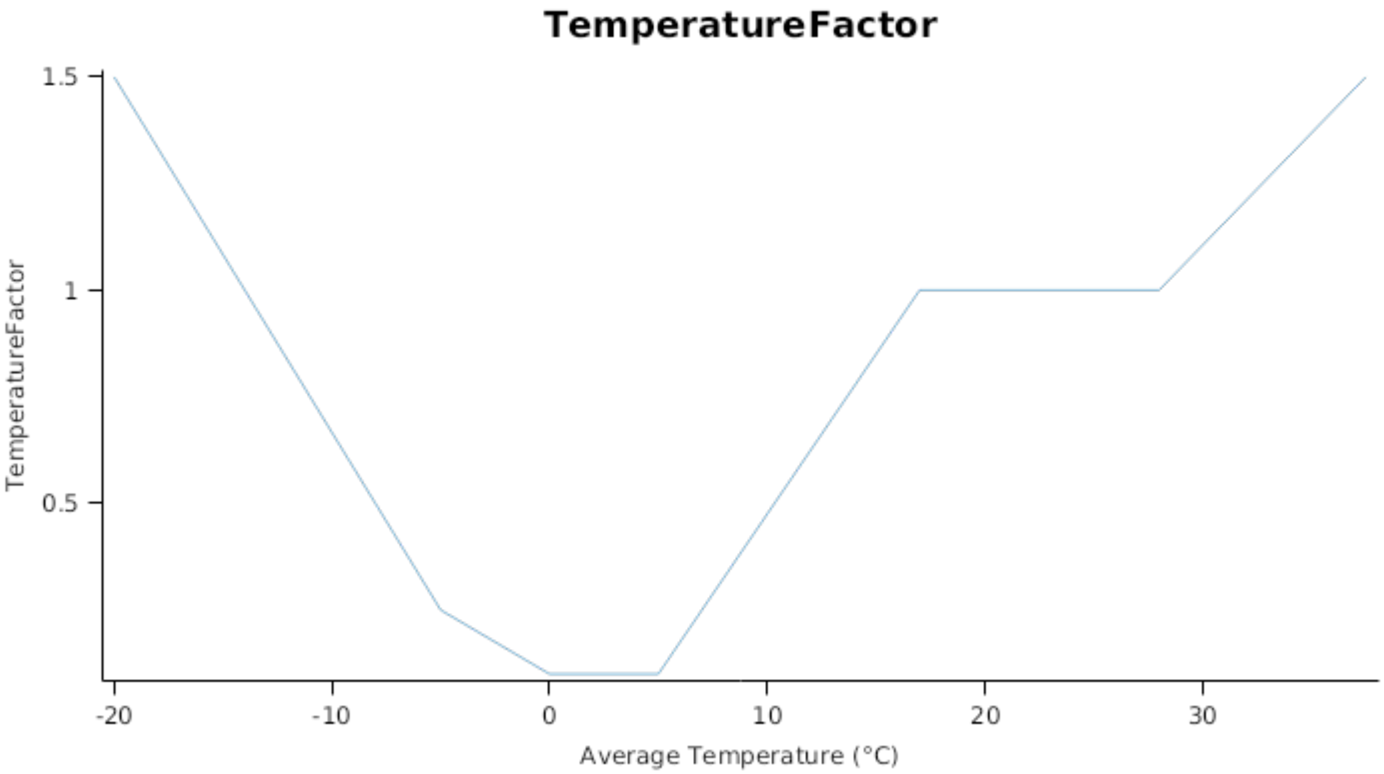


TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

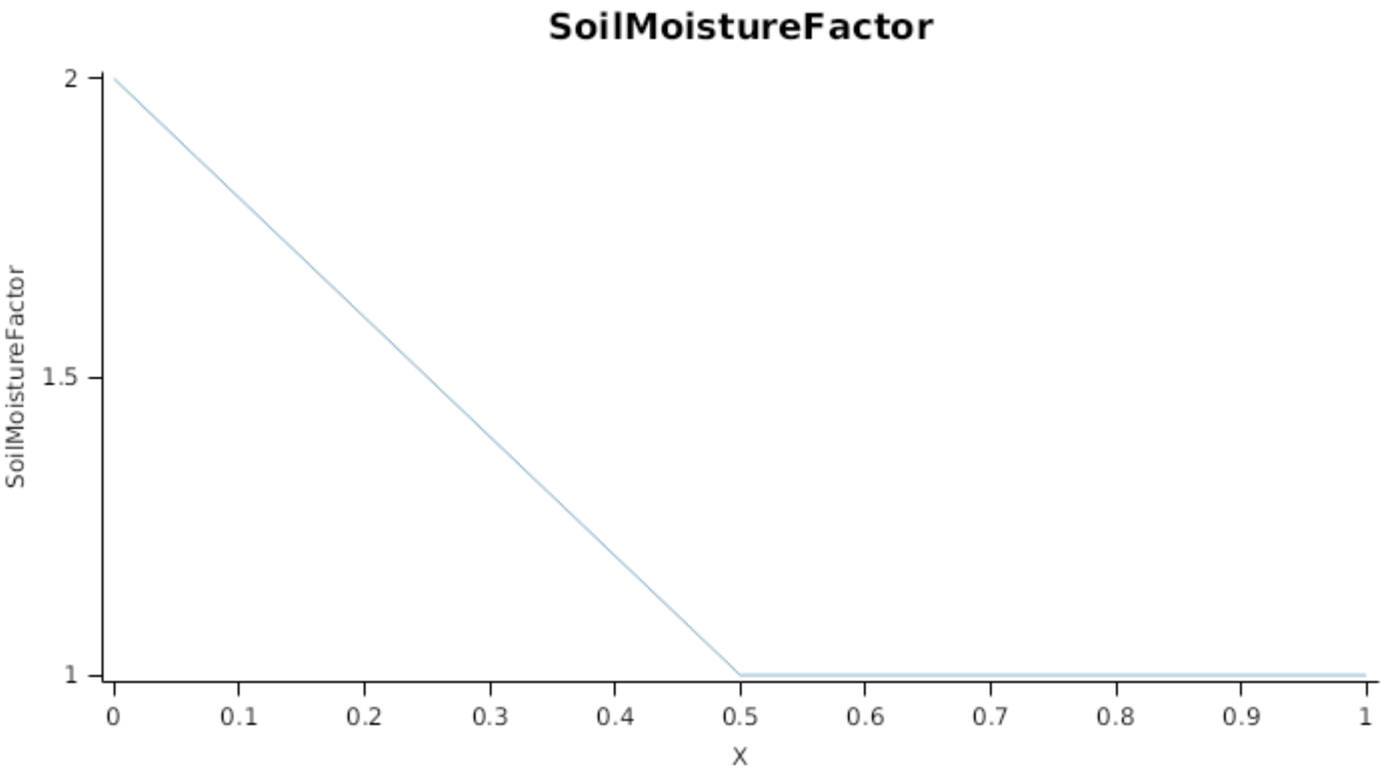
X	TemperatureFactor
-20.0	1.5
-5.0	0.2
0.0	0.1
5.0	0.1
17.0	1.0
28.0	1.0
37.5	1.5





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.

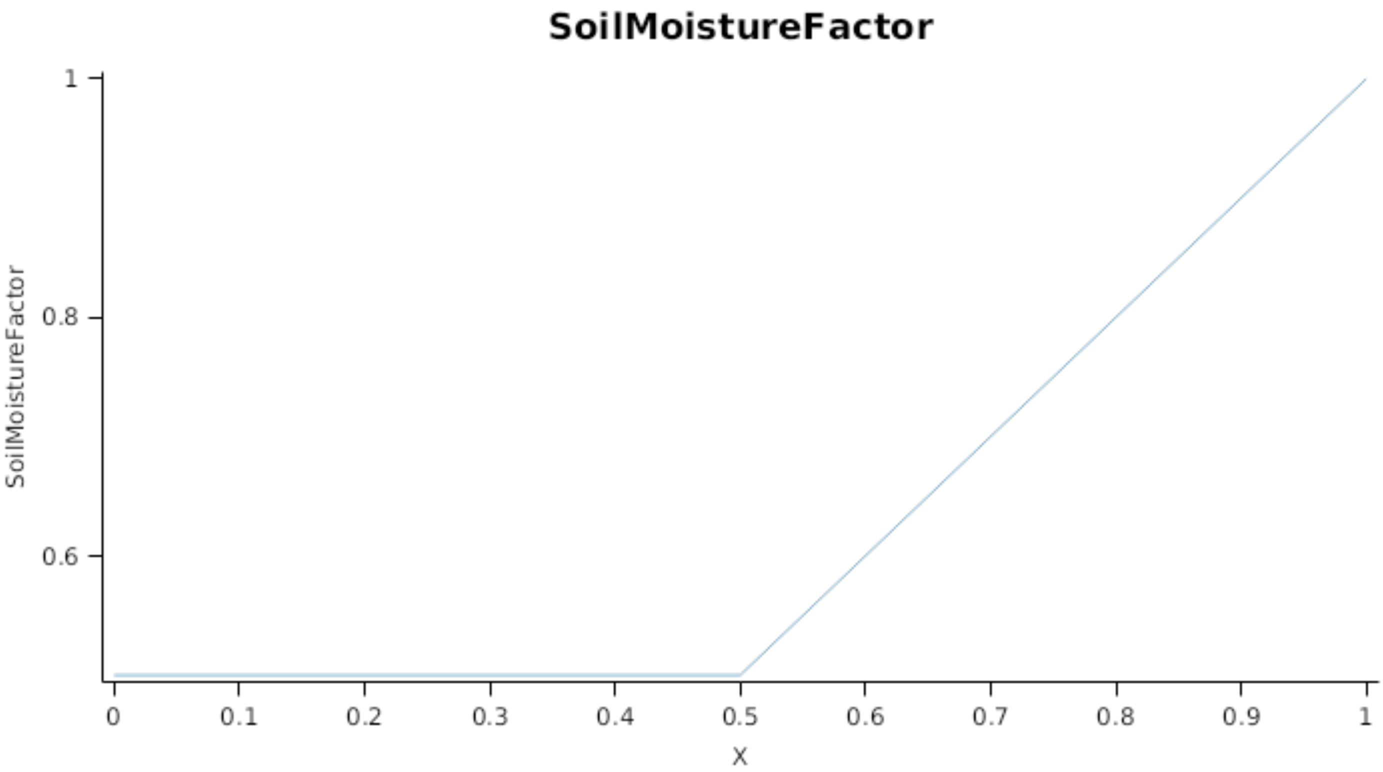
A generic relationship between detachment and soil moisture is assumed. It implies that under dry conditions the detachment rate decreases due to the lower level of activity of decomposing microorganisms.

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	80	20	0	0
Graze	70	10	10	20
Harvest	10	10	10	10
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.

The DM demands calculated here represent potential values, or a weighting factors, which are used by the OrganArbitrator to compute the allocated DM for all organs. The potential demand is computed as the sum of a *Base* and a *Deficit* demand. The *Base* demand is simply defined by the target proportion of leaf biomass, whereas the *Deficit* demand is defined by the difference between the actual and the targeted proportions. This approach is used to ensure promptly regrowth of aboveground organs after a defoliation; it relies in the assumption that a target biomass proportion for each organ exists. The *TargetBiomassProportion* is calculated based on a target shoot-to-root ratio and a biomass proportion for each organ above or below ground, these are defined elsewhere in this documentation and may vary with growth stage and environmental conditions.

Structural = *DMDemandFunction* x *StructuralFraction*

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

Where:

Zero = 0

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

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

StructuralFraction = 1 (g/g)

Metabolic = 0 (g/g)

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.

These N demands also represent potential values that are used by the OrganArbitrator to get the total plant N demand. This and any source of N in the plant are used to determine soil N demand, and eventually the actual amounts allocated to each pool in each organ.

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 = 0.035 (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

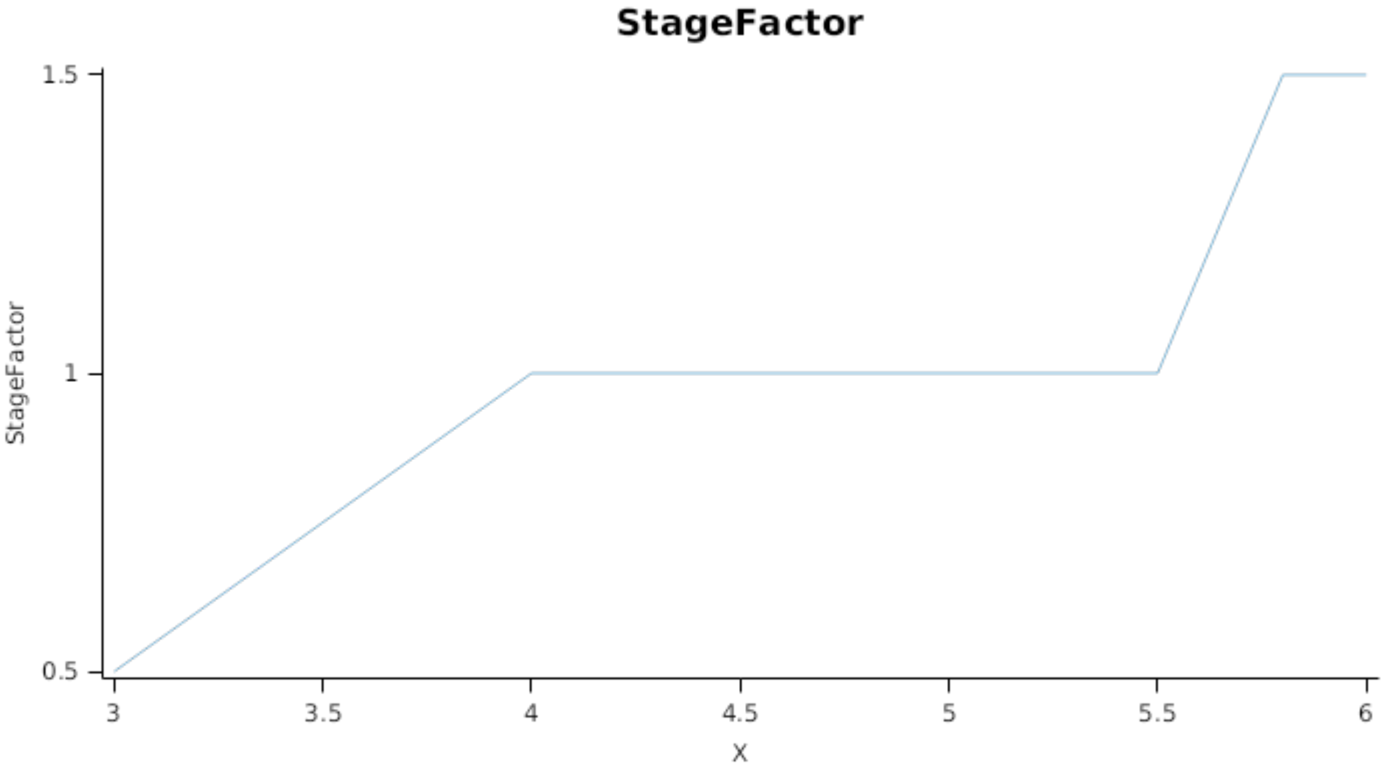
The proportion of live biomass that senesces and moves into the dead pool each day is quantified by the SenescenceRate.

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*

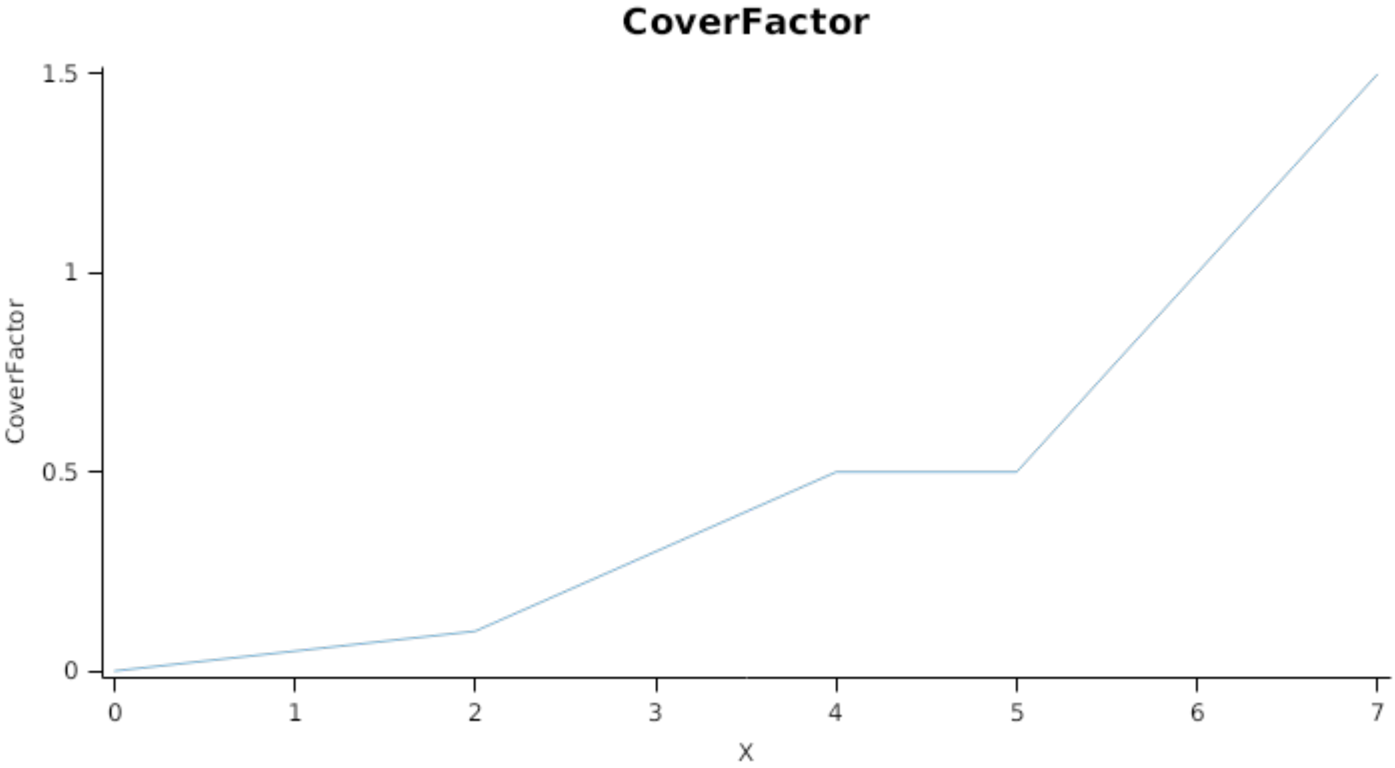
StageFactor is calculated using linear interpolation

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

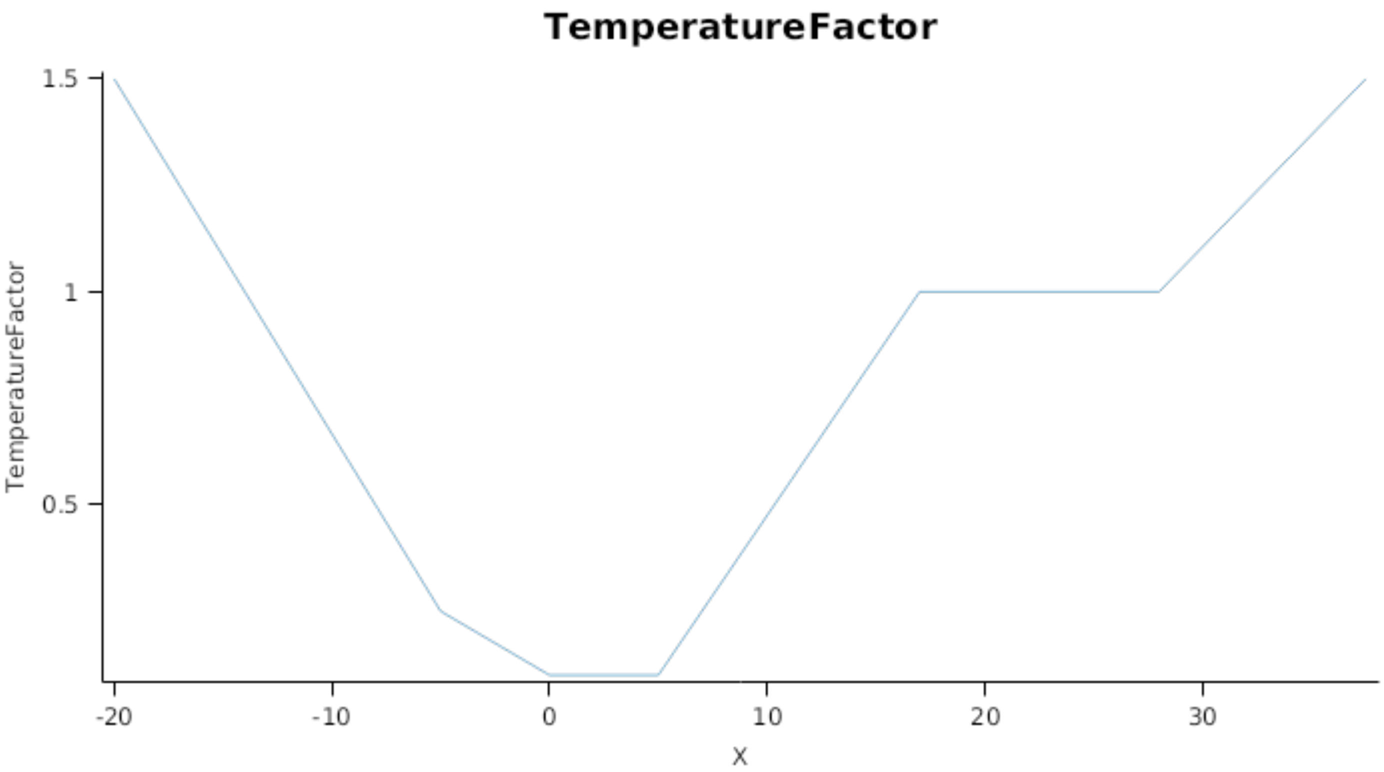
X	CoverFactor
0.0	0.0
2.0	0.1
4.0	0.5
5.0	0.5
7.0	1.5

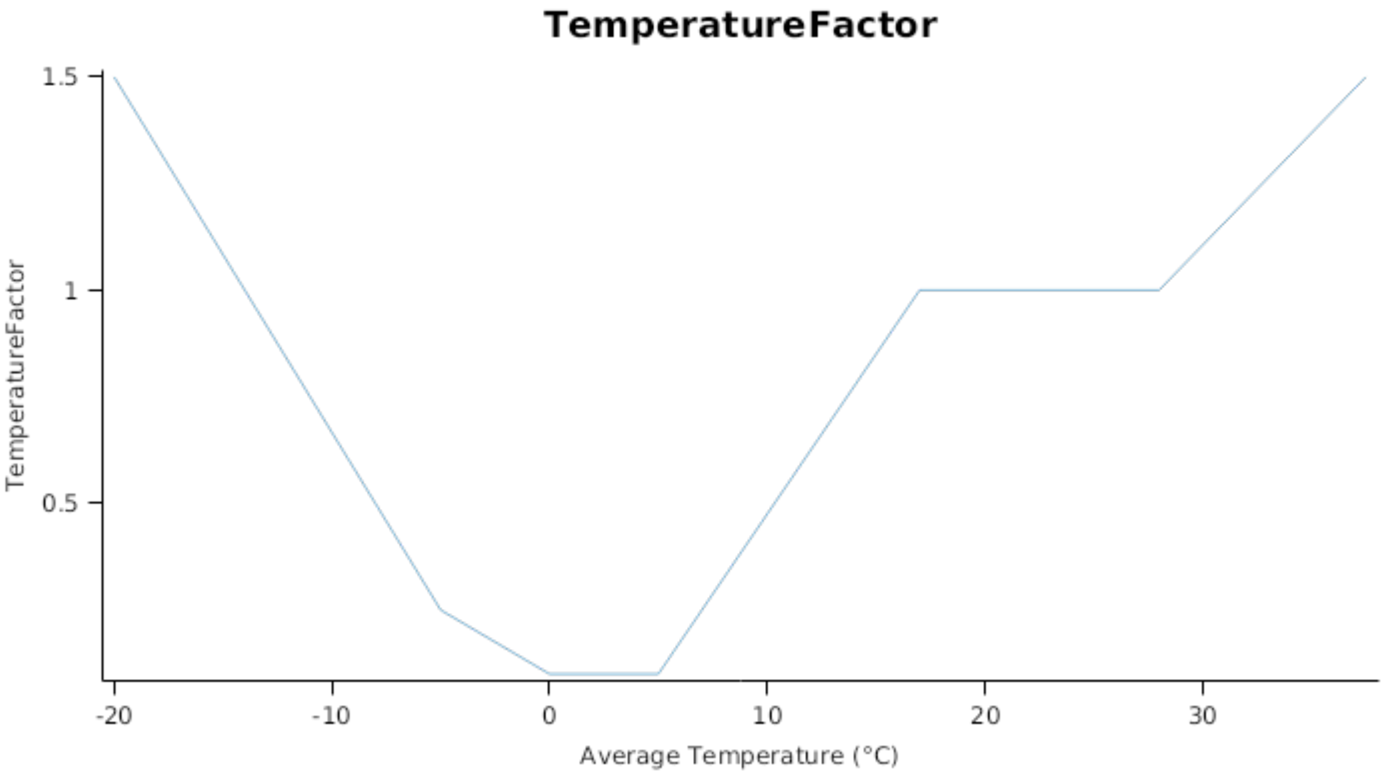


TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

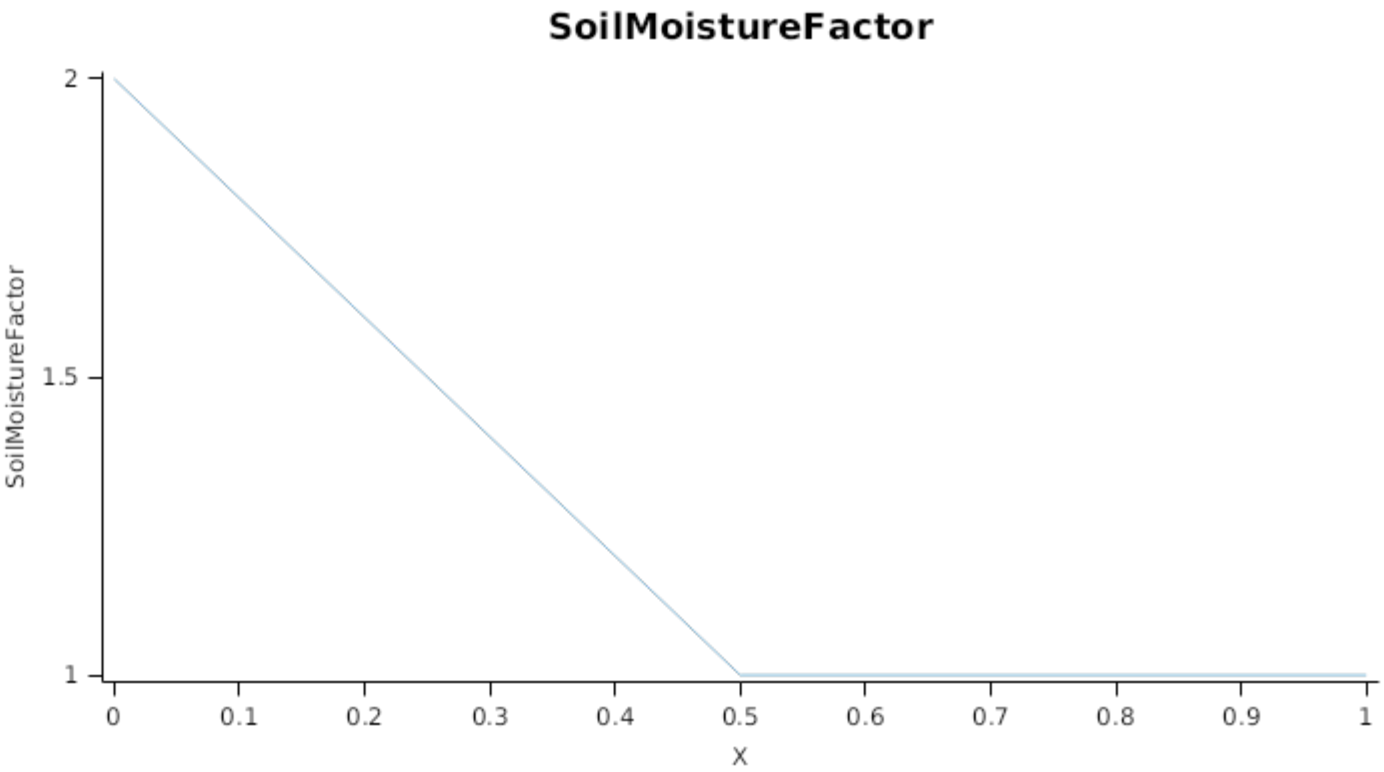
X	TemperatureFactor
-20.0	1.5
-5.0	0.2
0.0	0.1
5.0	0.1
17.0	1.0
28.0	1.0
37.5	1.5





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.

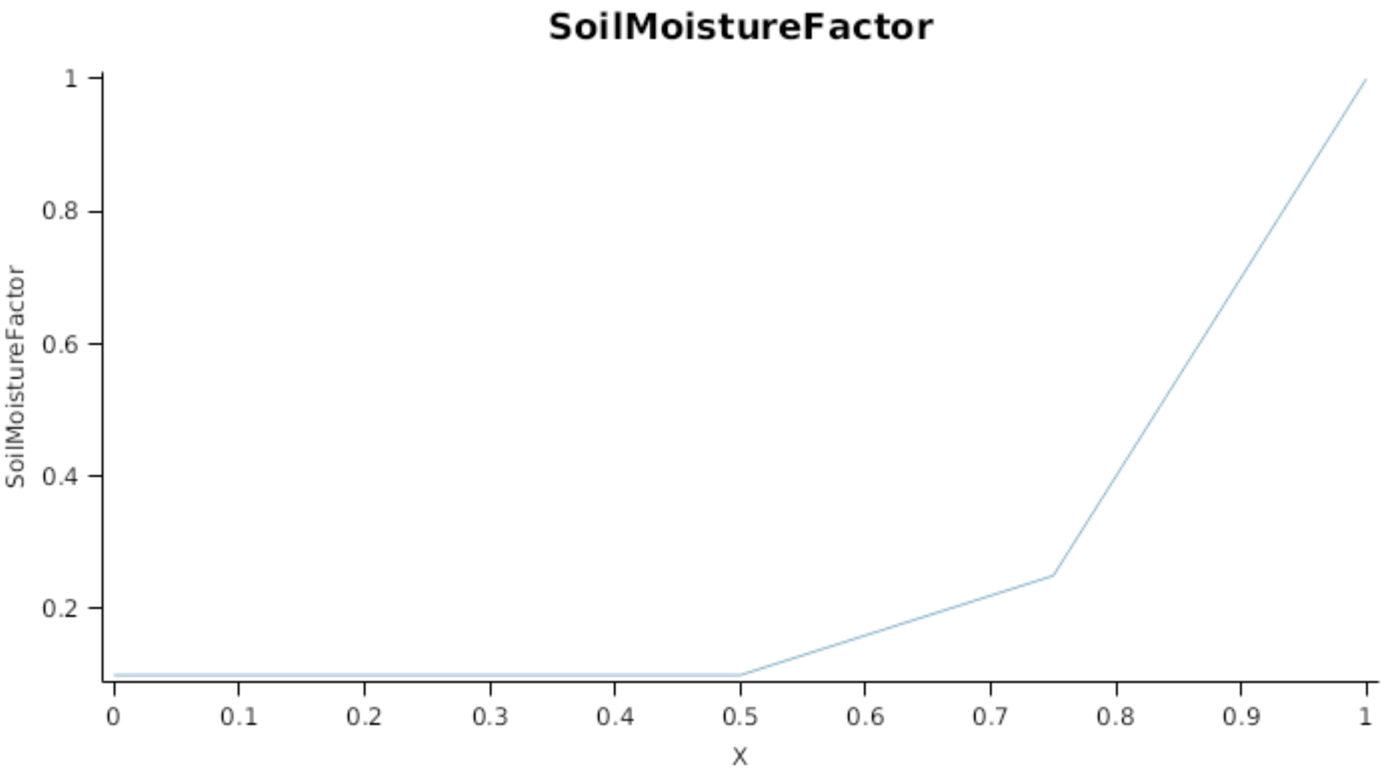
A generic relationship between detachment and soil moisture is assumed. It implies that under dry conditions the detachment rate decreases due to the lower level of activity of decomposing microorganisms.

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	50	50	0	0
Graze	50	30	10	10
Harvest	10	20	10	10
Prune	0	0	0	0

1.10 Stolon

1.10.1 Stolon

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.

The DM demands calculated here represent potential values, or a weighting factors, which are used by the OrganArbitrator to compute the allocated DM for all organs. The potential demand is computed as the sum of a *Base* and a *Deficit* demand. The *Base* demand is simply defined by the target proportion of leaf biomass, whereas the *Deficit* demand is defined by the difference between the actual and the targeted proportions. This approach is used to ensure promptly regrowth of aboveground organs after a defoliation; it relies in the assumption that a target biomass proportion for each organ exists. The *TargetBiomassProportion* is calculated based on a target shoot-to-root ratio and a biomass proportion for each organ above or below ground, these are defined elsewhere in this documentation and may vary with growth stage and environmental conditions.

Structural = *DMDemandFunction* x *StructuralFraction*

DMDemandFunction = *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 [Stolon].TargetBiomassProportion

DeficitBiomassDemand = Max(*Zero*, *Deficit*)

Where:

Zero = 0

Deficit = TargetBiomass - [Stolon].Live.Wt

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

StructuralFraction = 0.65 (g/g)

Metabolic = 0 (g/g)

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

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

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.

These N demands also represent potential values that are used by the OrganArbitrator to get the total plant N demand. This and any source of N in the plant are used to determine soil N demand, and eventually the actual amounts allocated to each pool in each organ.

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

Metabolic = MetabolicNconc x [Stolon].potentialDMAllocation.Structural

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

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

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

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

NitrogenDemandSwitch = [Stolon].nitrogenDemandSwitch

MaxNconc = [Stolon].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.10.4 N Concentration Thresholds

MinimumNConc = 0.02 (gN/gDM)

CriticalNConc = 0.025 (gN/gDM)

MaximumNConc = 0.03 (gN/gDM)

1.10.5 Dry Matter Supply

Stolon 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.

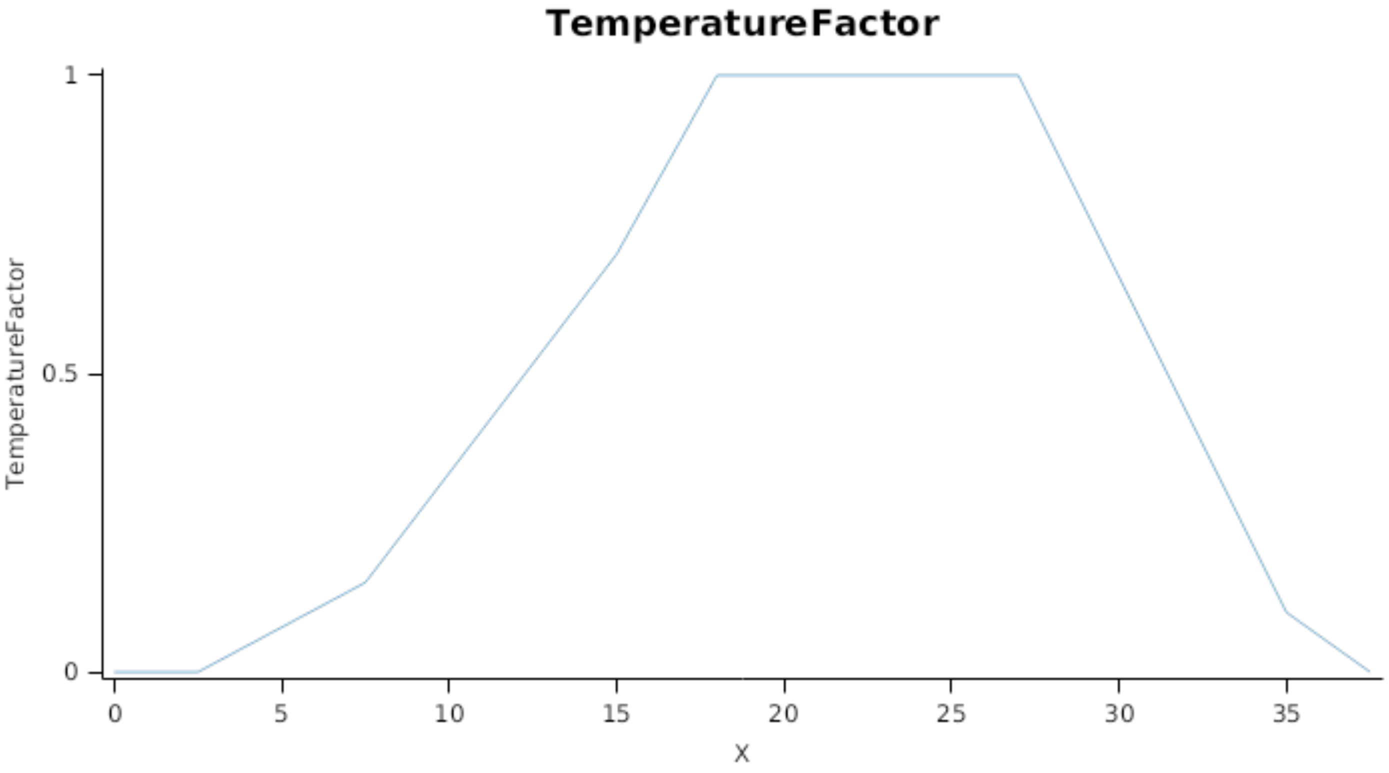
DMRetranslocationFactor = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor* x *PhotoPeriodFactor*

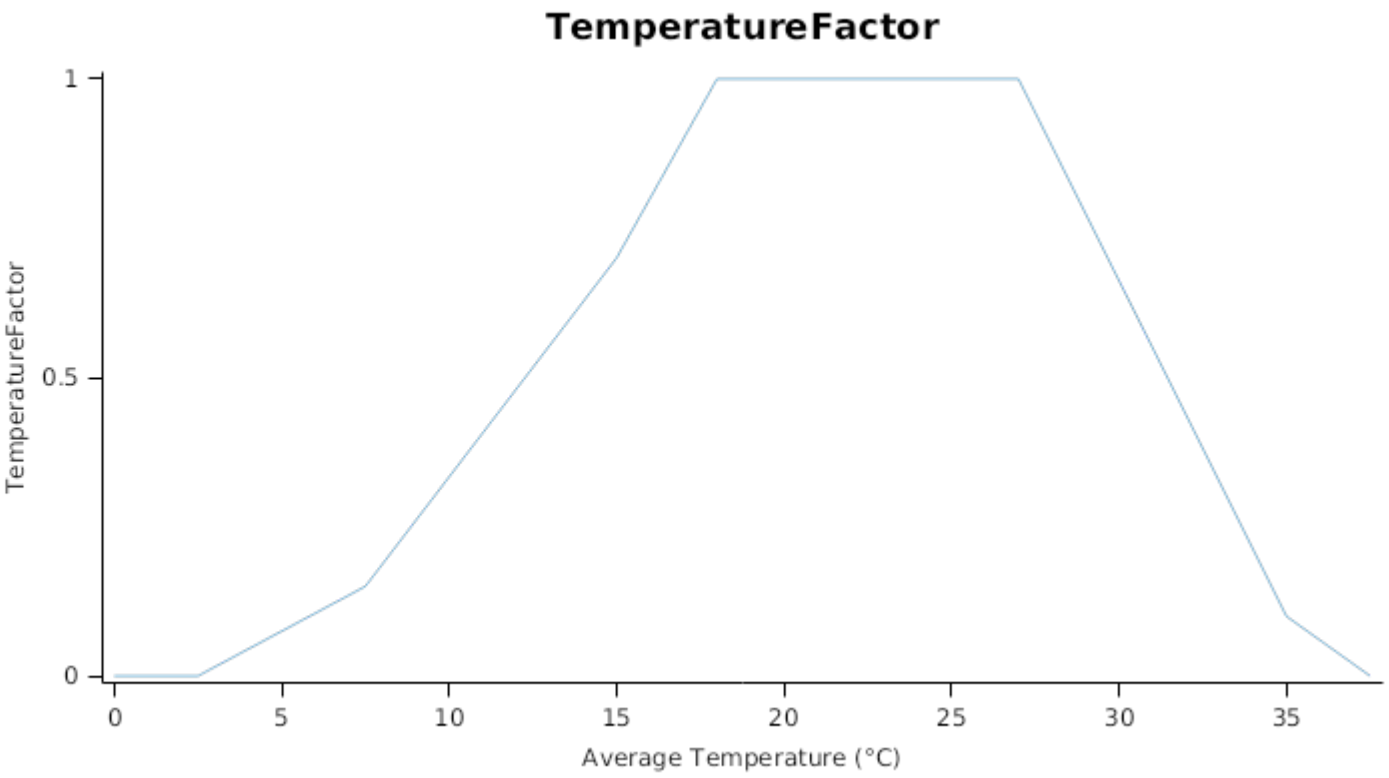
ReferenceRate = 0.05 (/day)

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

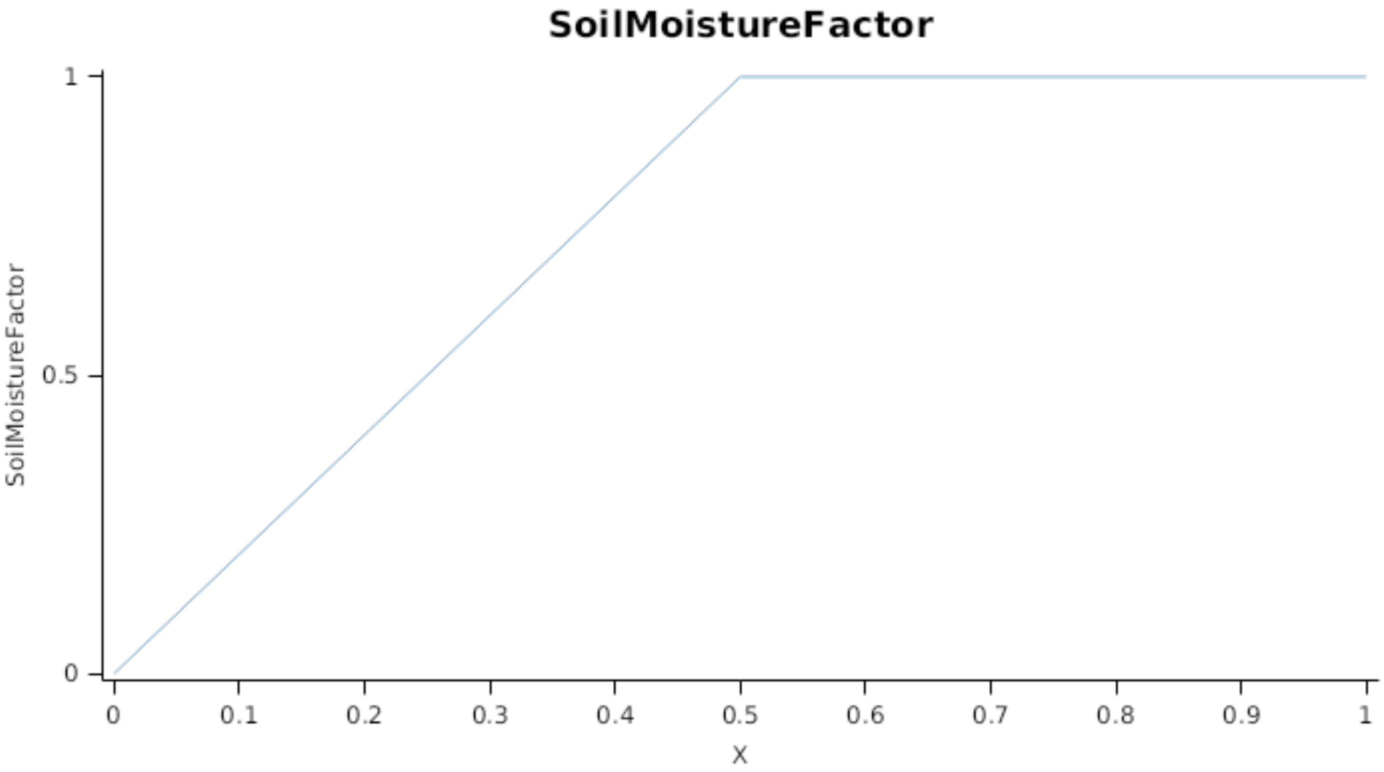
X	**TemperatureFactor**
0.0	0.0
2.5	0.0
7.5	0.1
15.0	0.7
18.0	1.0
27.0	1.0
35.0	0.1
37.5	0.0





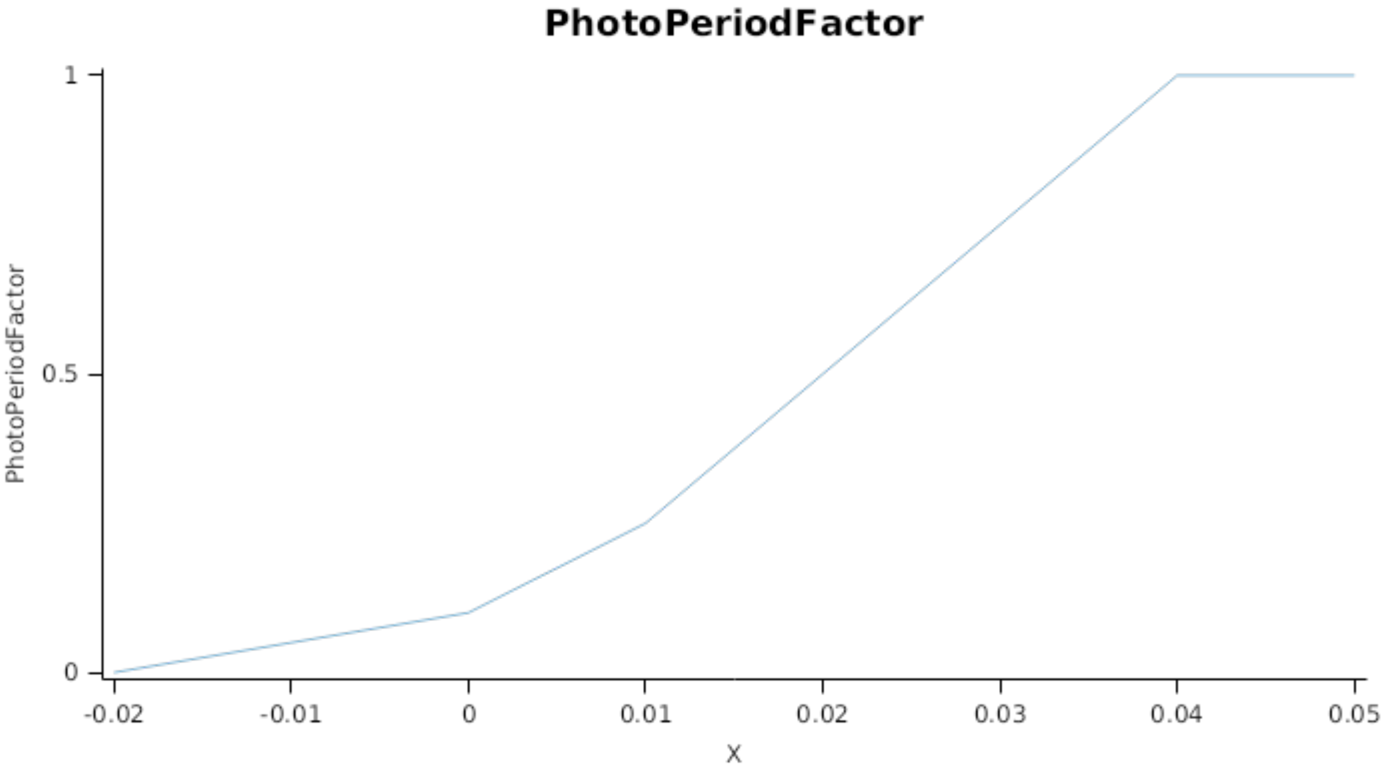
SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.0
0.5	1.0
1.0	1.0



PhotoPeriodFactor is calculated using linear interpolation

X	PhotoPeriodFactor
-0.0	0.0
-0.0	0.1
0.0	0.1
0.0	0.2
0.0	0.5
0.0	1.0
0.1	1.0



1.10.6 Nitrogen Supply

Stolon 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 *TemperatureFactor* x *SoilMoistureFactor* x *PhotoPeriodFactor*

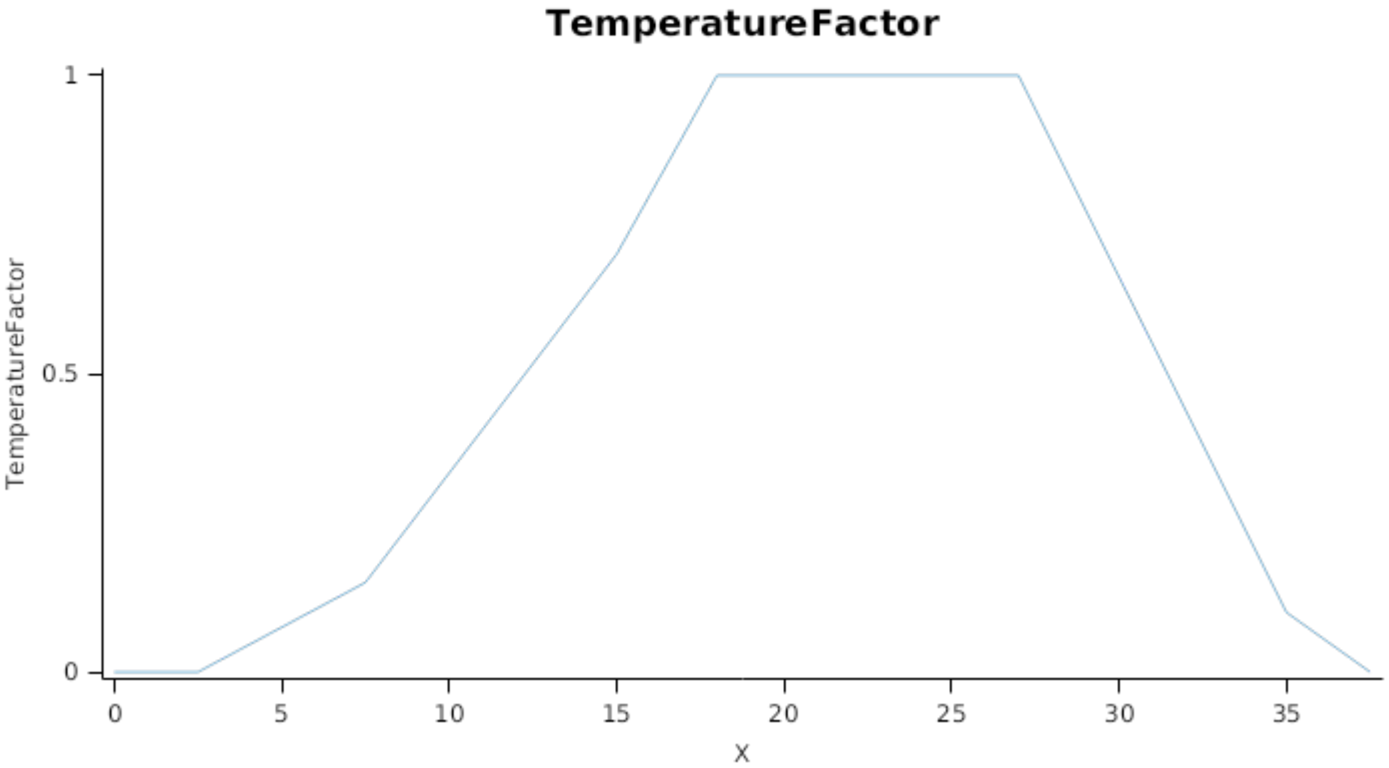
ReferenceRate = 0.1 (/day)

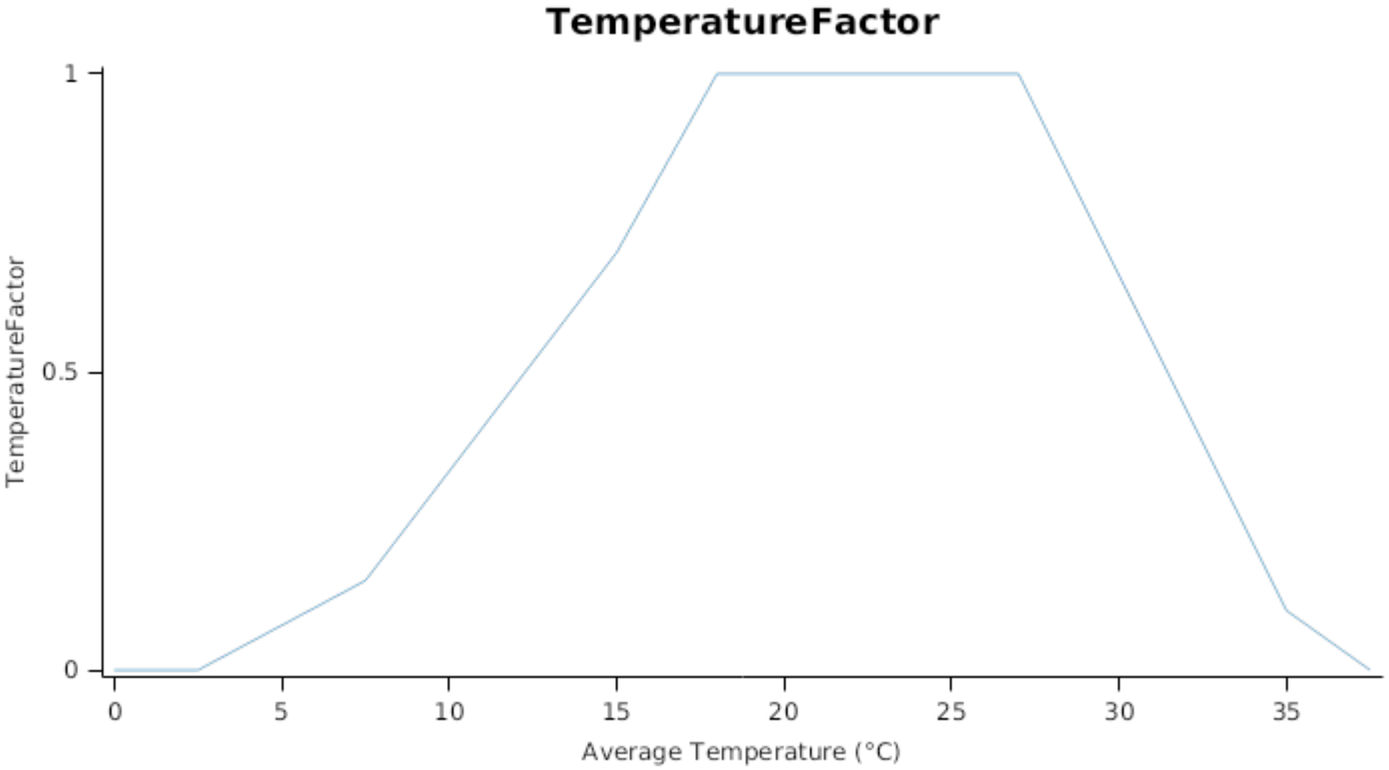
TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

X	TemperatureFactor
0.0	0.0
2.5	0.0

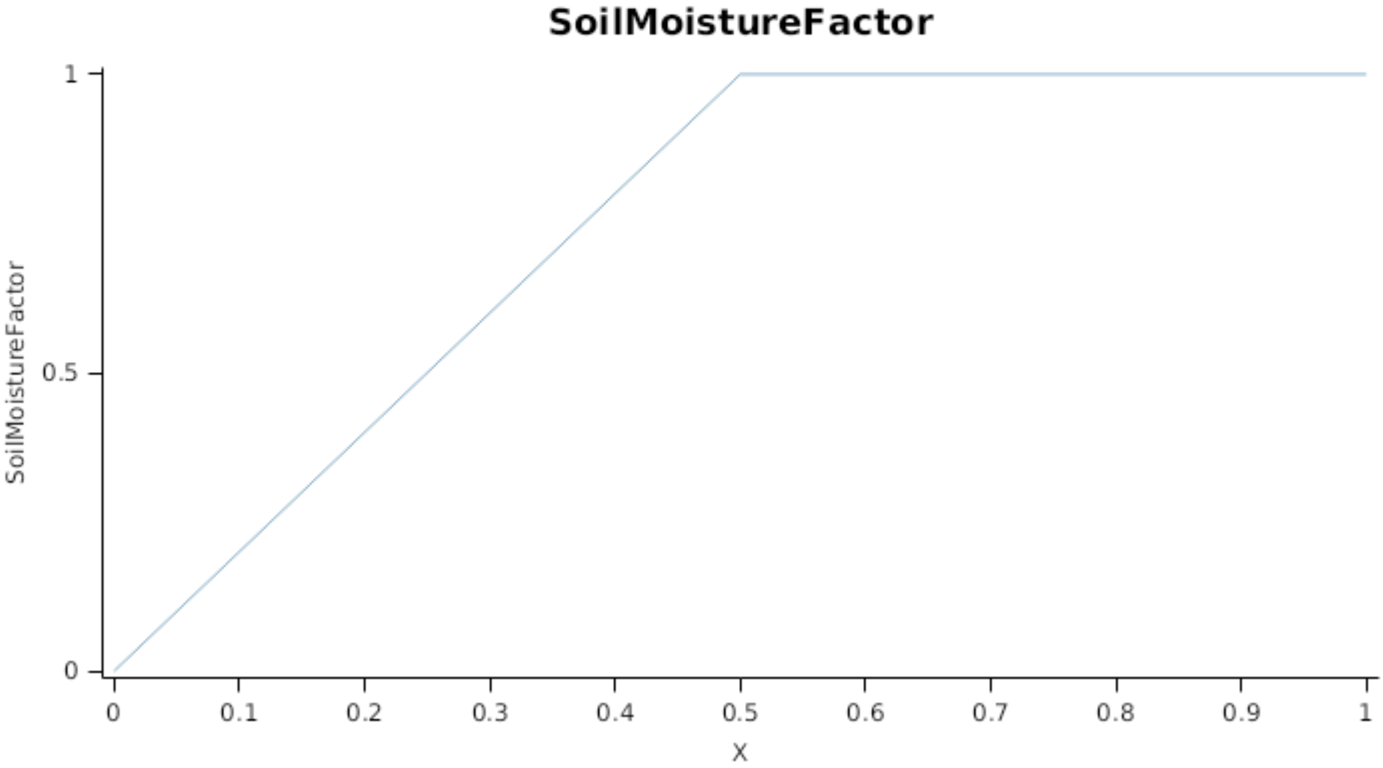
X	TemperatureFactor
7.5	0.1
15.0	0.7
18.0	1.0
27.0	1.0
35.0	0.1
37.5	0.0





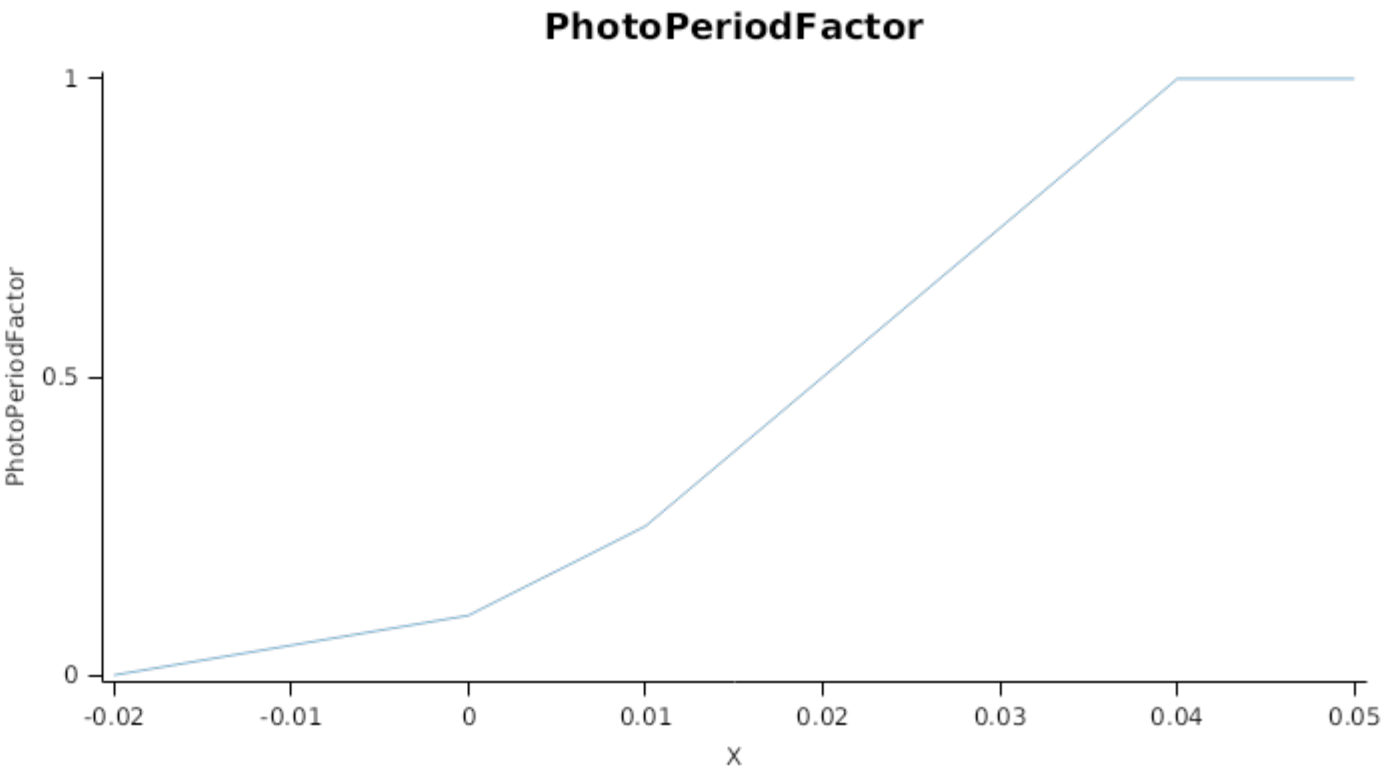
SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.0
0.5	1.0
1.0	1.0



PhotoPeriodFactor is calculated using linear interpolation

X	PhotoPeriodFactor
-0.0	0.0
-0.0	0.1
0.0	0.1
0.0	0.2
0.0	0.5
0.0	1.0
0.1	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.

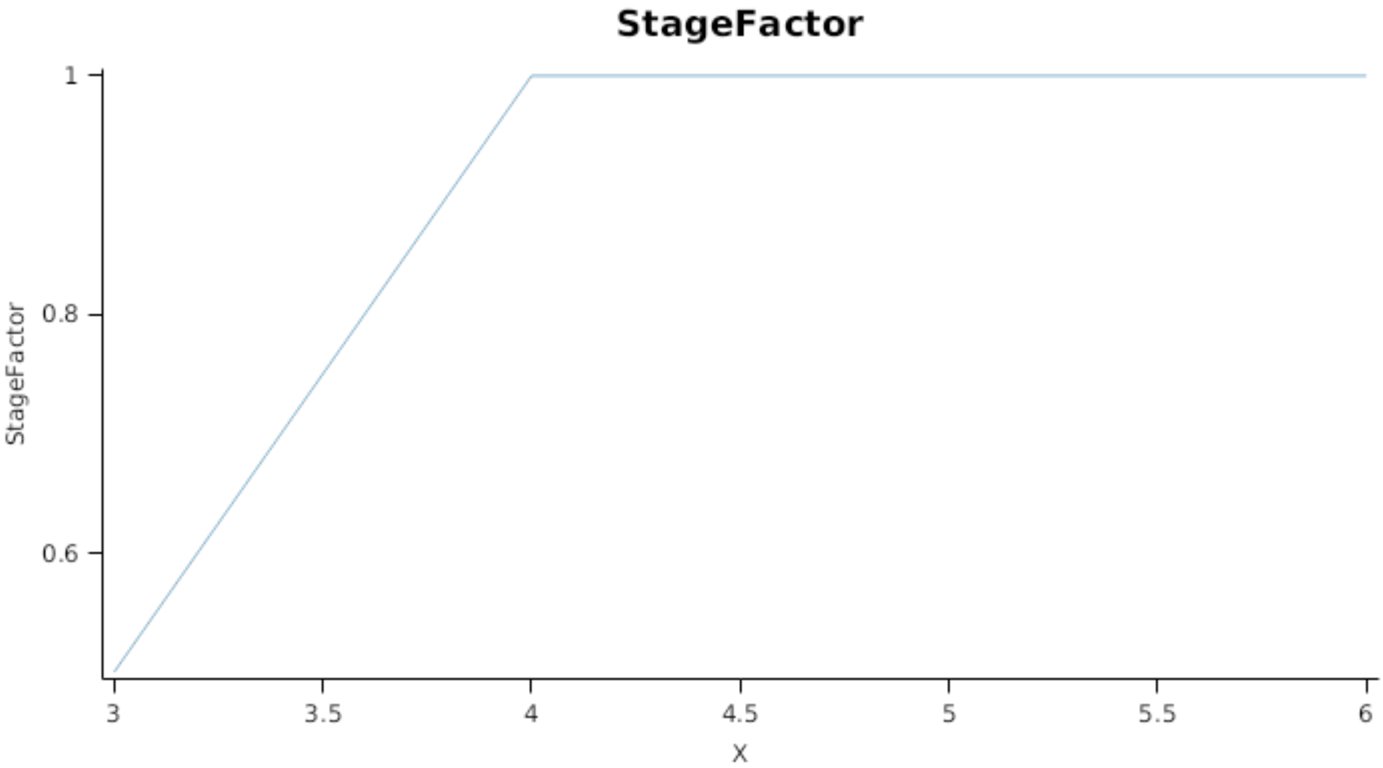
The reference senescence rate is adjusted using generic relationships to environmental factors, such as temperature and soil moisture. These are based on general knowledge from other plant models.

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

ReferenceRate = 0.01 (/day)

StageFactor is calculated using linear interpolation

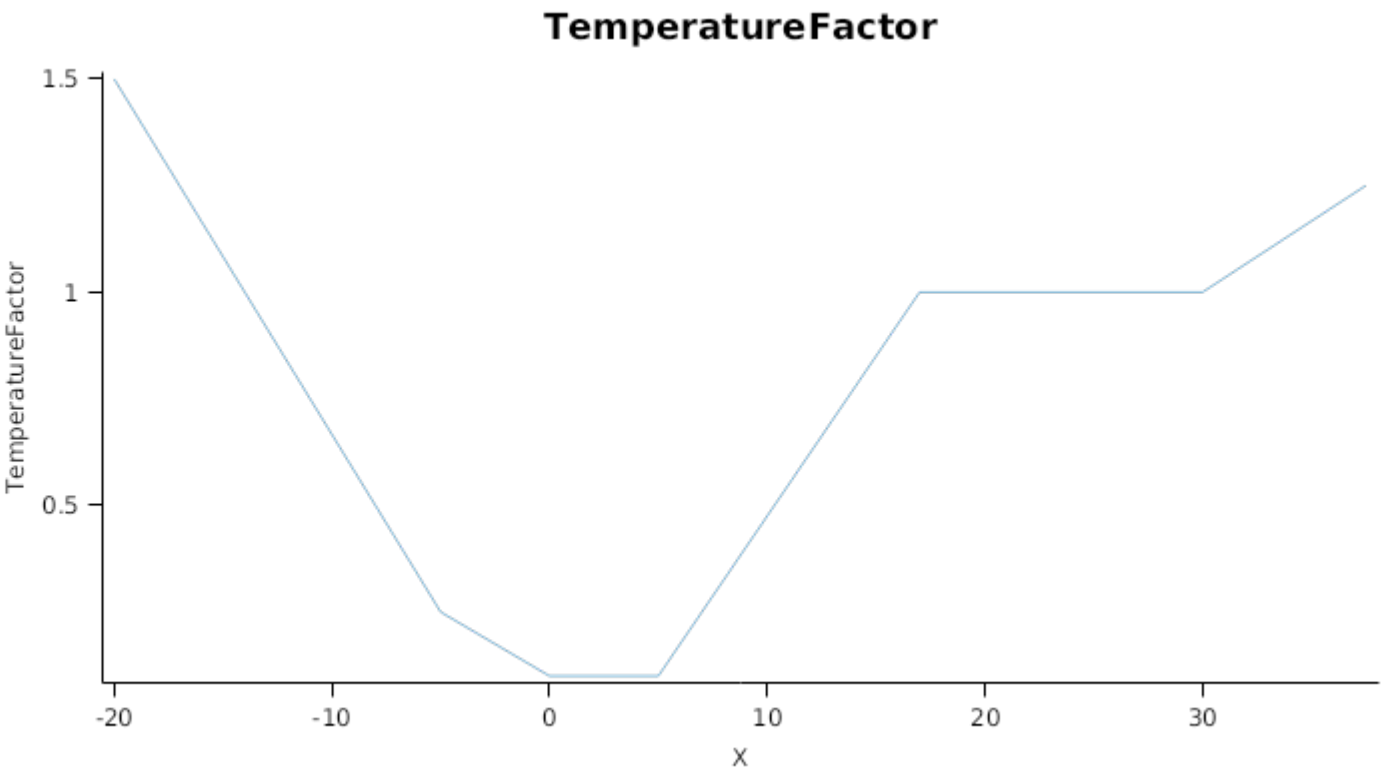
X	StageFactor
3.0	0.5
4.0	1.0
6.0	1.0

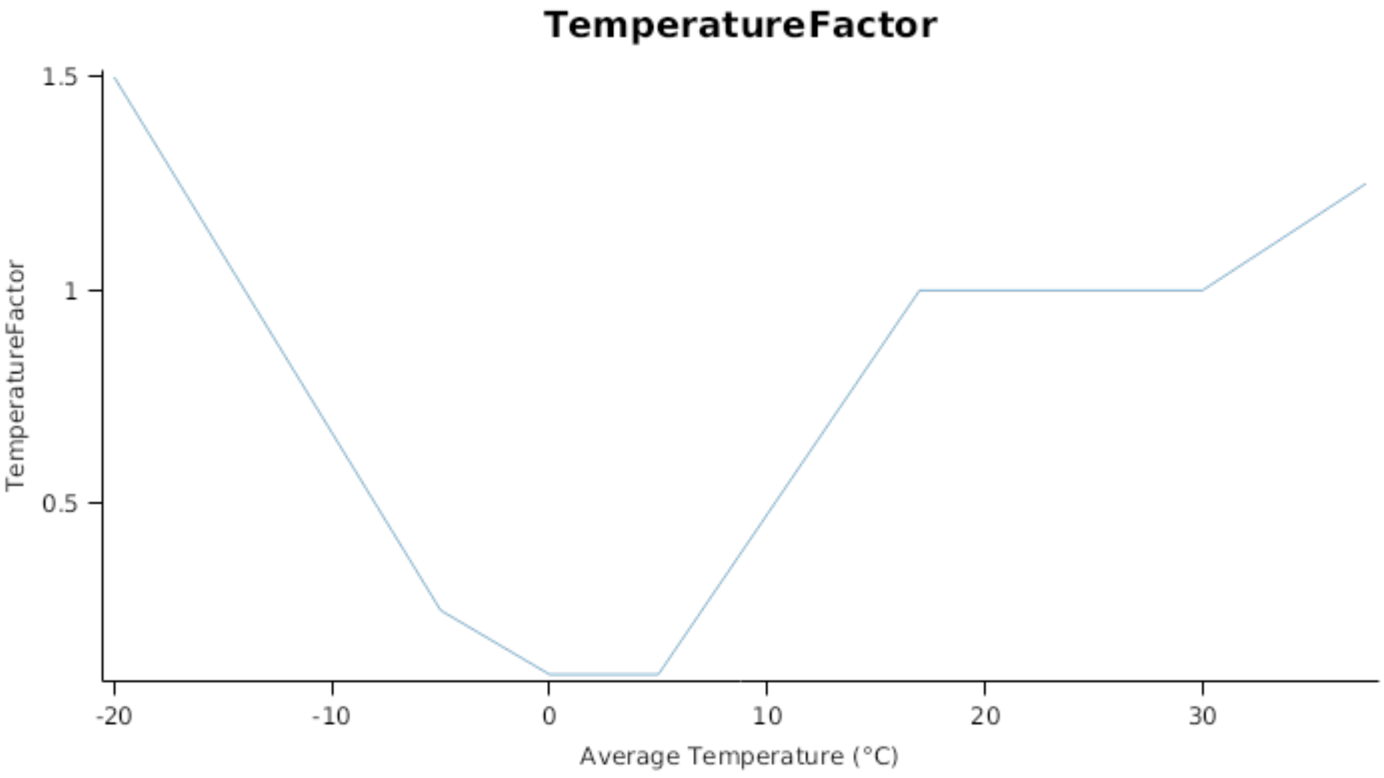


TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

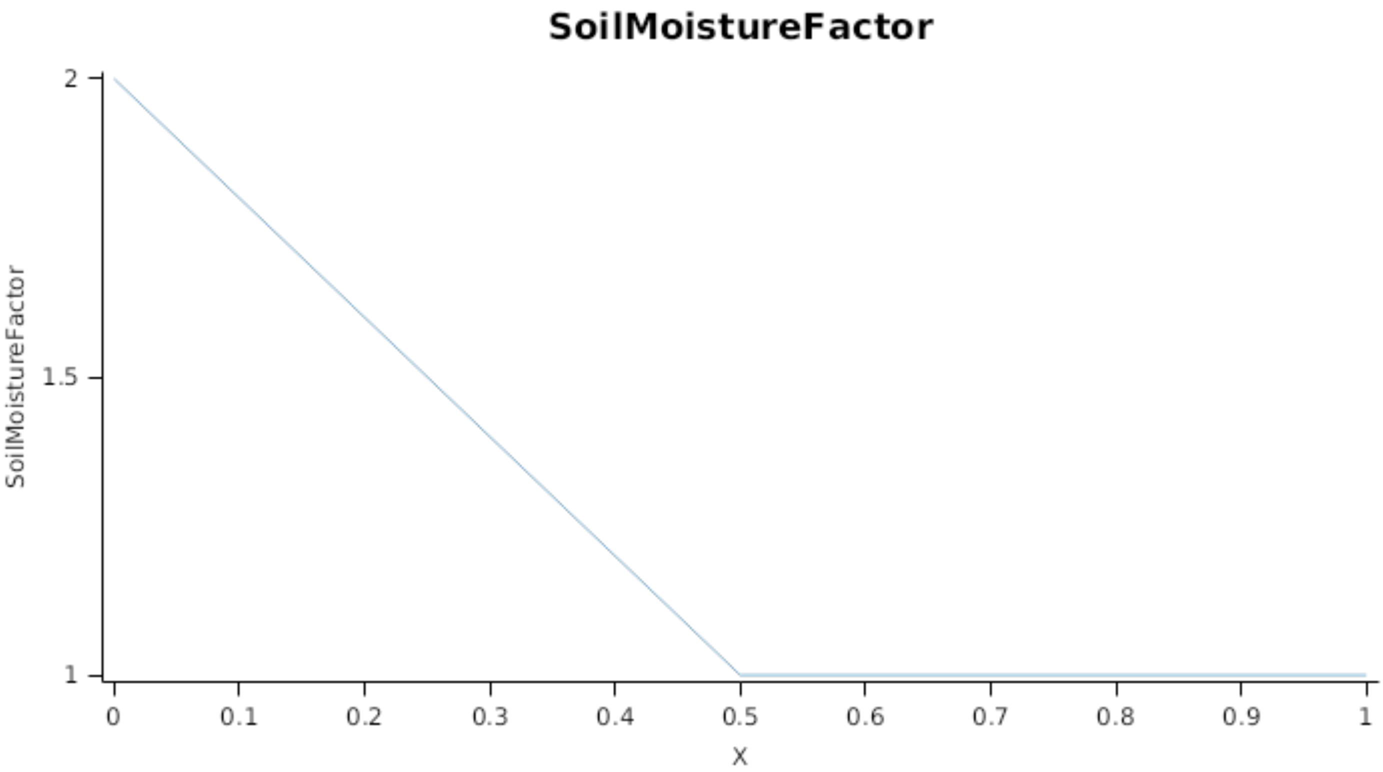
X	**TemperatureFactor**
-20.0	1.5
-5.0	0.2
0.0	0.1
5.0	0.1
17.0	1.0
30.0	1.0
37.5	1.2





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.

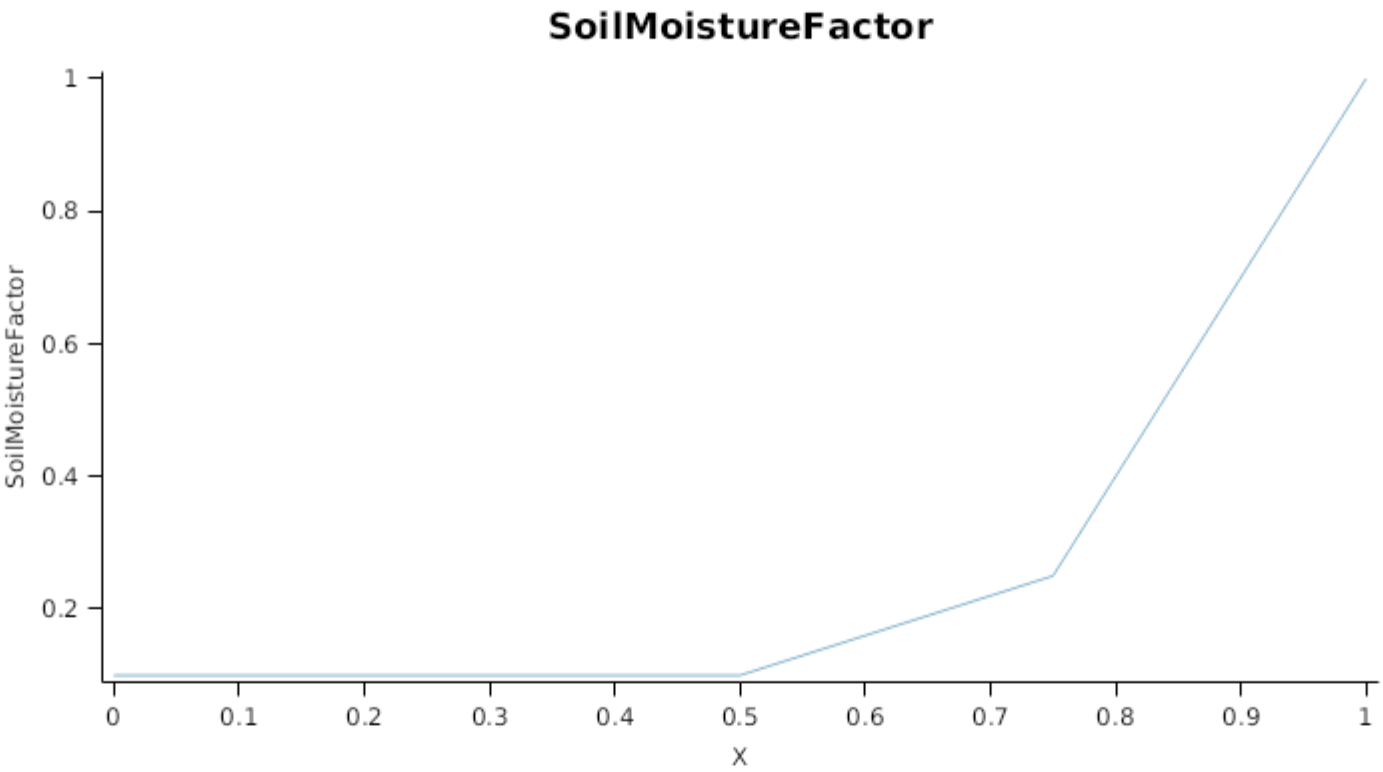
A generic relationship between detachment and soil moisture is assumed. It implies that under dry conditions the detachment rate decreases due to the lower level of activity of decomposing microorganisms.

DetachmentRateFunction = *ReferenceRate* x *SoilMoistureFactor* x *PhotoPeriodFactor*

ReferenceRate = 0.05 (/day)

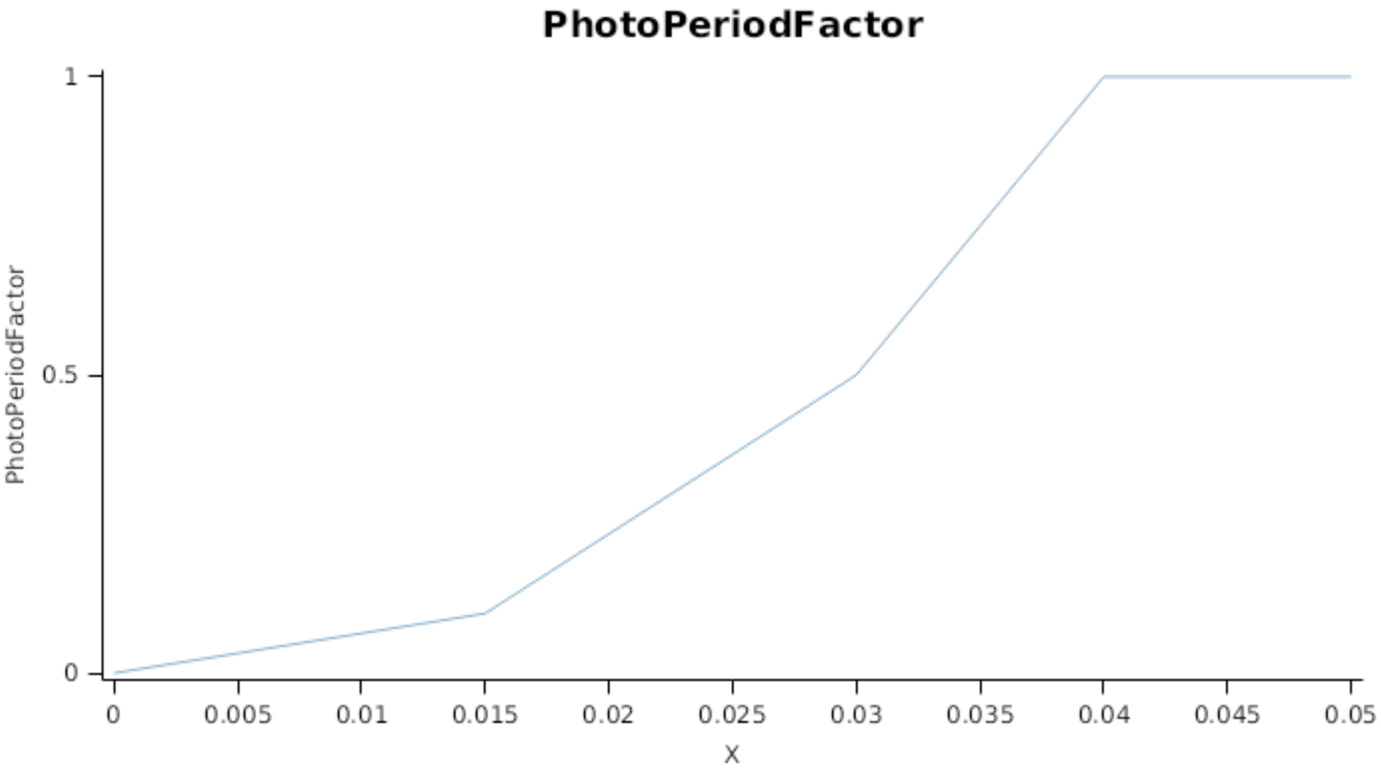
SoilMoistureFactor is calculated using linear interpolation

X	**SoilMoistureFactor**
0.0	0.1
0.5	0.1
0.8	0.2
1.0	1.0



PhotoPeriodFactor is calculated using linear interpolation

X	PhotoPeriodFactor
0.0	0.0
0.0	0.1
0.0	0.5
0.0	1.0
0.1	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	0	0	0	0
Graze	10	0	10	20
Harvest	0	0	0	0
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.

The DM demands calculated here represent potential values, or a weighting factors, which are used by the OrganArbitrator to compute the allocated DM for all organs. The potential demand is computed as the sum of a *Base* and a *Deficit* demand. The *Base* demand is simply defined by the target proportion of leaf biomass, whereas the *Deficit* demand is defined by the difference between the actual and the targeted proportions. This approach is used to ensure promptly regrowth of aboveground organs after a defoliation; it relies in the assumption that a target biomass proportion for each organ exists. The *TargetBiomassProportion* is calculated based on a target shoot-to-root ratio and a biomass proportion for each organ above or below ground, these are defined elsewhere in this documentation and may vary with growth stage and environmental conditions.

Structural = *DMDemandFunction* x *StructuralFraction*

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

Where:

Zero = 0

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

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

StructuralFraction = 1 (g/g)

Metabolic = 0 (g/g)

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.

These N demands also represent potential values that are used by the OrganArbitrator to get the total plant N demand. This and any source of N in the plant are used to determine soil N demand, and eventually the actual amounts allocated to each pool in each organ.

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

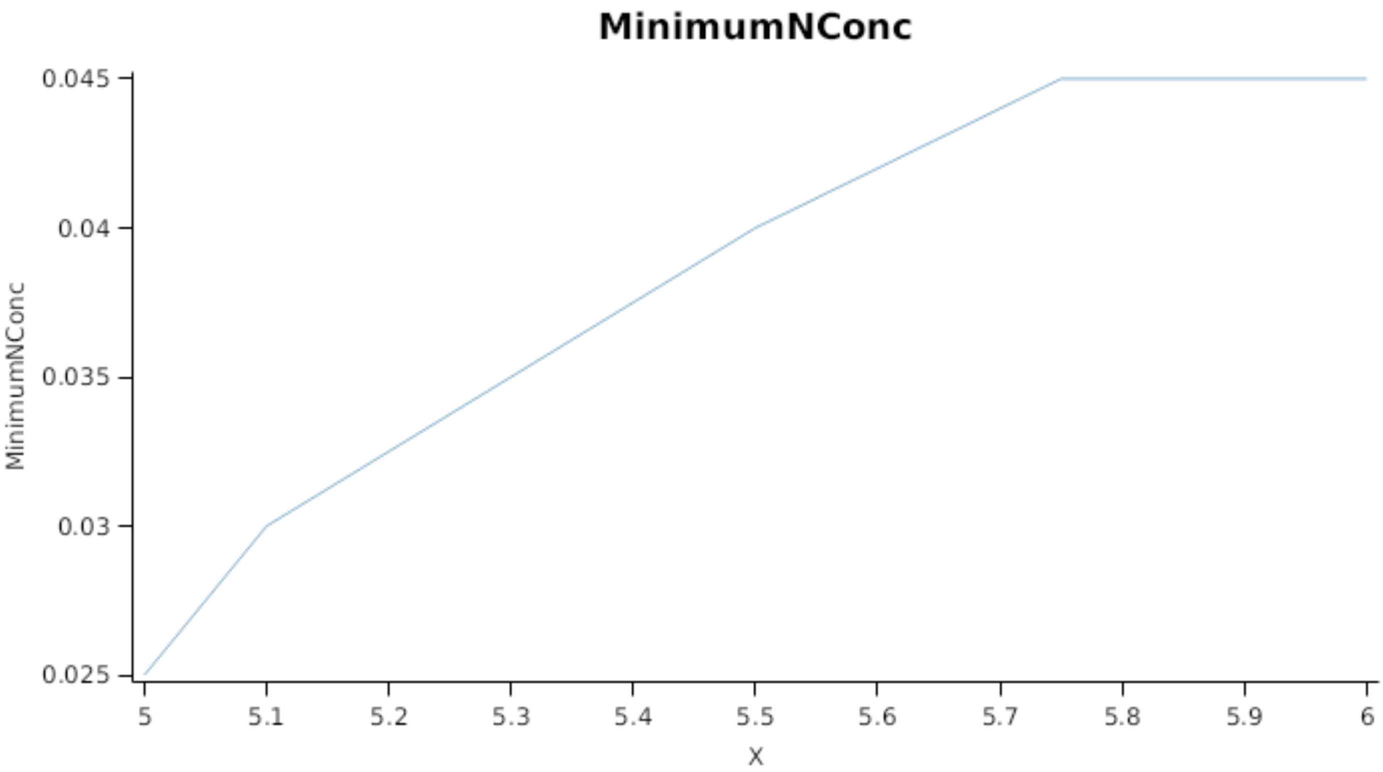
QMetabolicPriority = 1

QStoragePriority = 1

1.11.4 N Concentration Thresholds

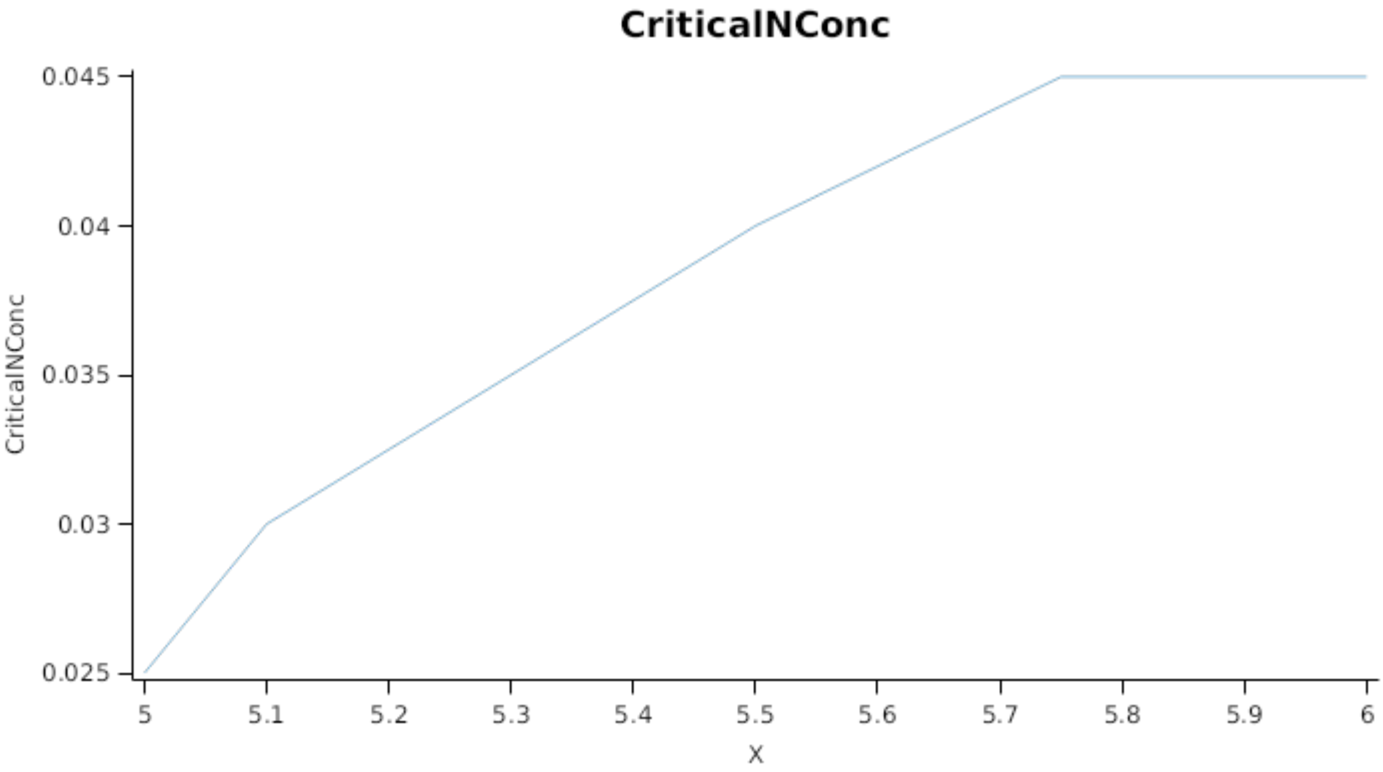
MinimumNConc is calculated using linear interpolation

X	**MinimumNConc**
5.0	0.0
5.1	0.0
5.5	0.0
5.8	0.0
6.0	0.0



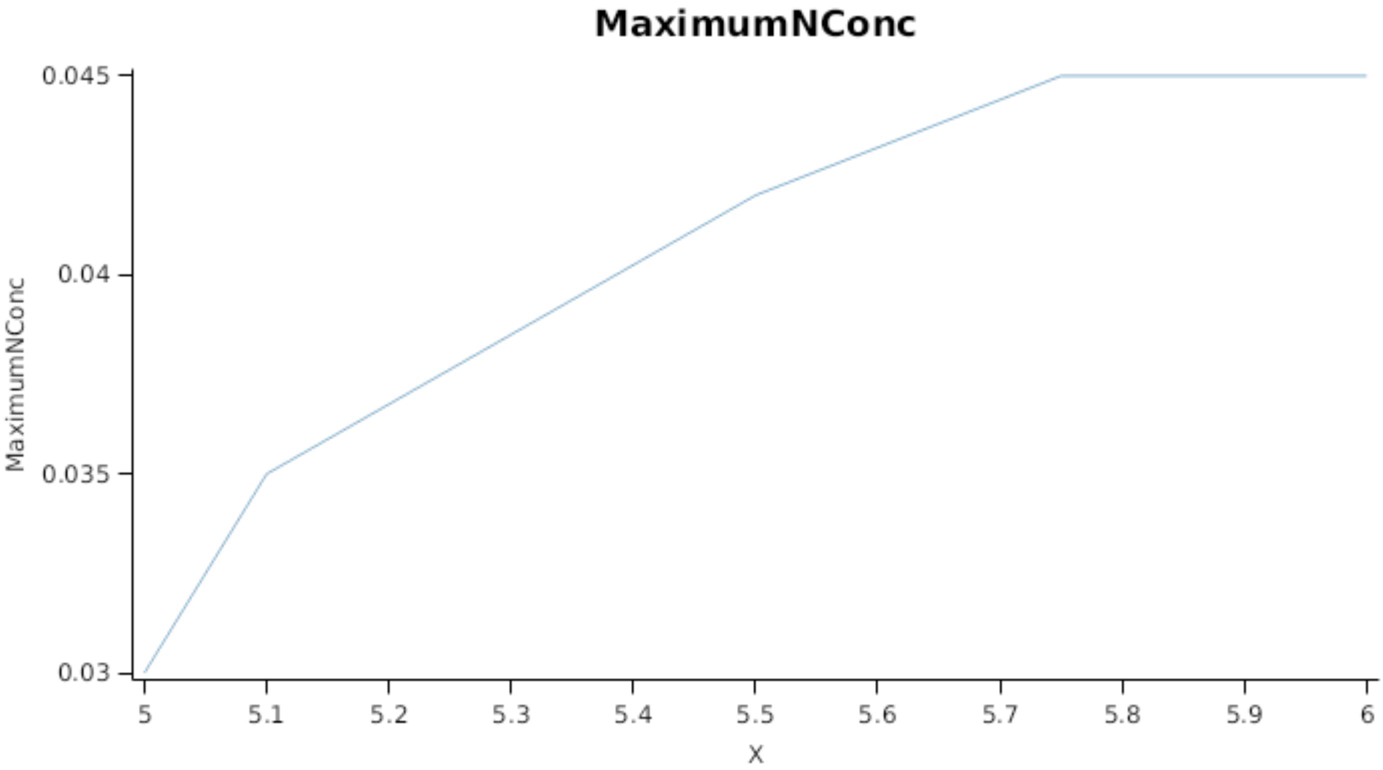
CriticalNConc is calculated using linear interpolation

X	CriticalNConc
5.0	0.0
5.1	0.0
5.5	0.0
5.8	0.0
6.0	0.0



MaximumNConc is calculated using linear interpolation

X	MaximumNConc
5.0	0.0
5.1	0.0
5.5	0.0
5.8	0.0
6.0	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.

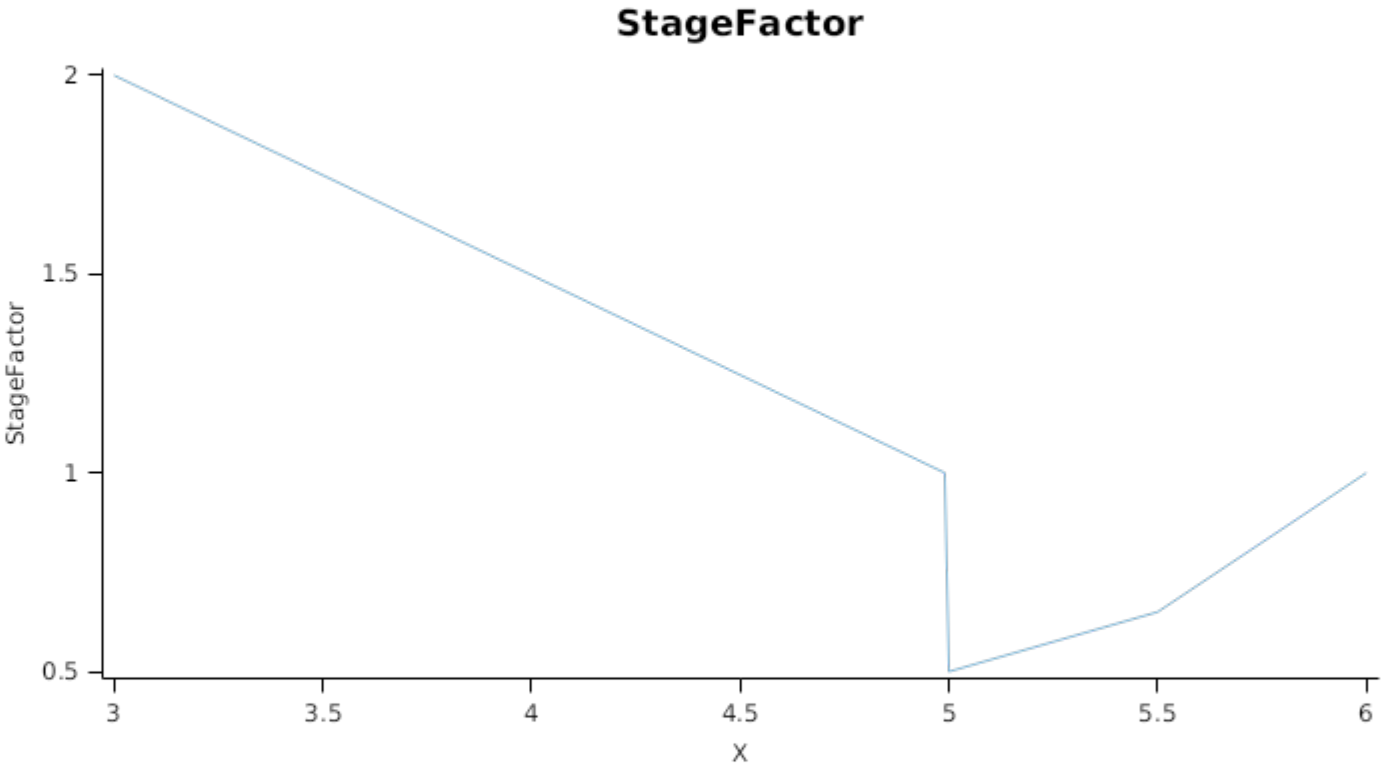
The reference senescence rate is adjusted using generic relationships to environmental factors, such as temperature and soil moisture. These are based on general knowledge from other plant models.

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

ReferenceRate = 0.1 (/day)

StageFactor is calculated using linear interpolation

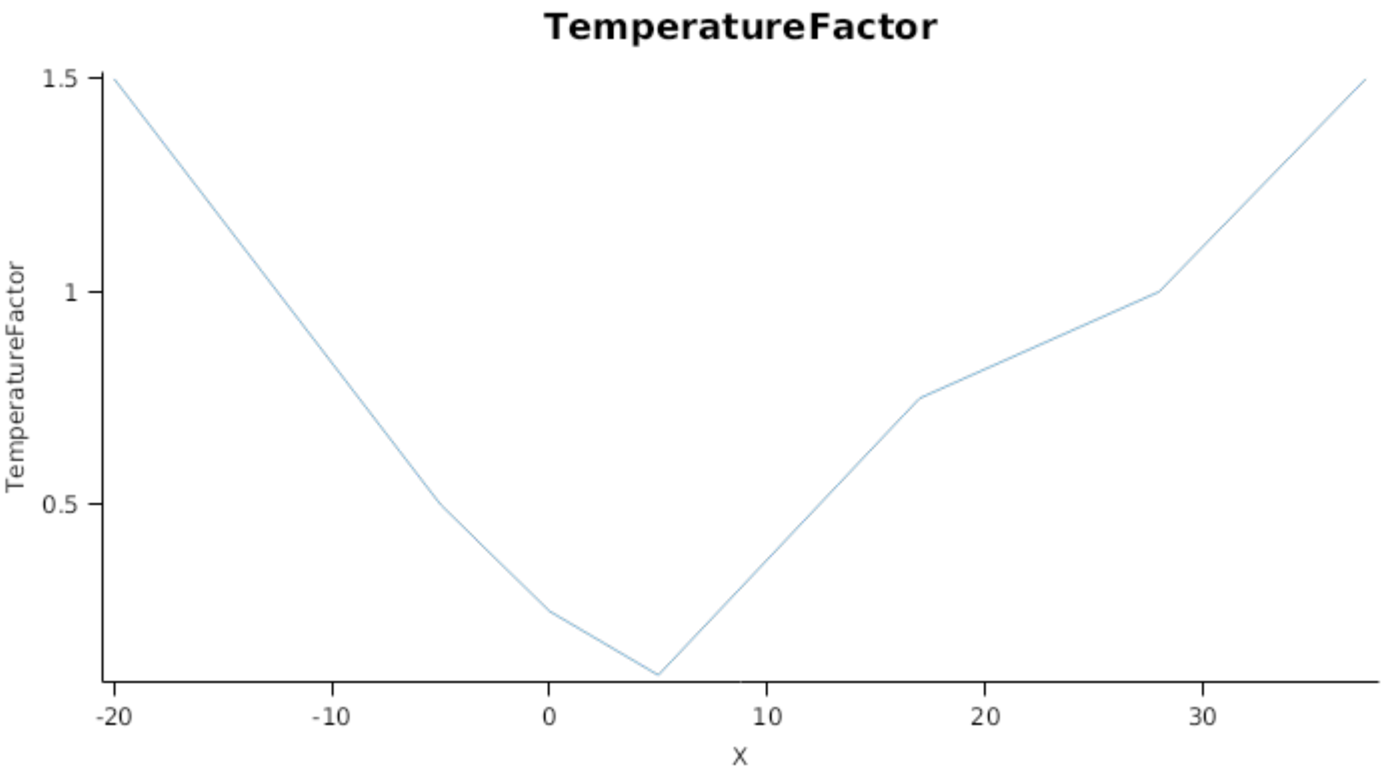
X	StageFactor
3.0	2.0
5.0	1.0
5.0	0.5
5.5	0.7
6.0	1.0

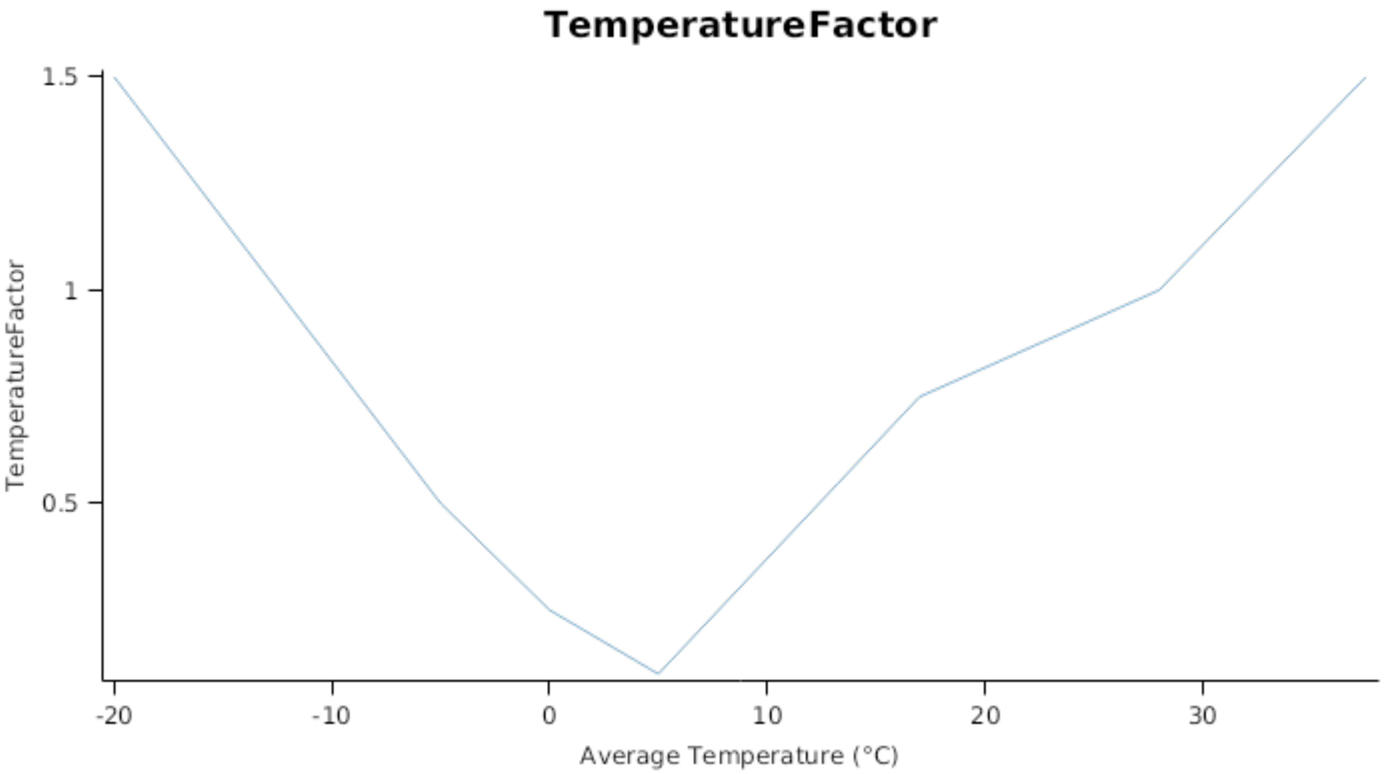


TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

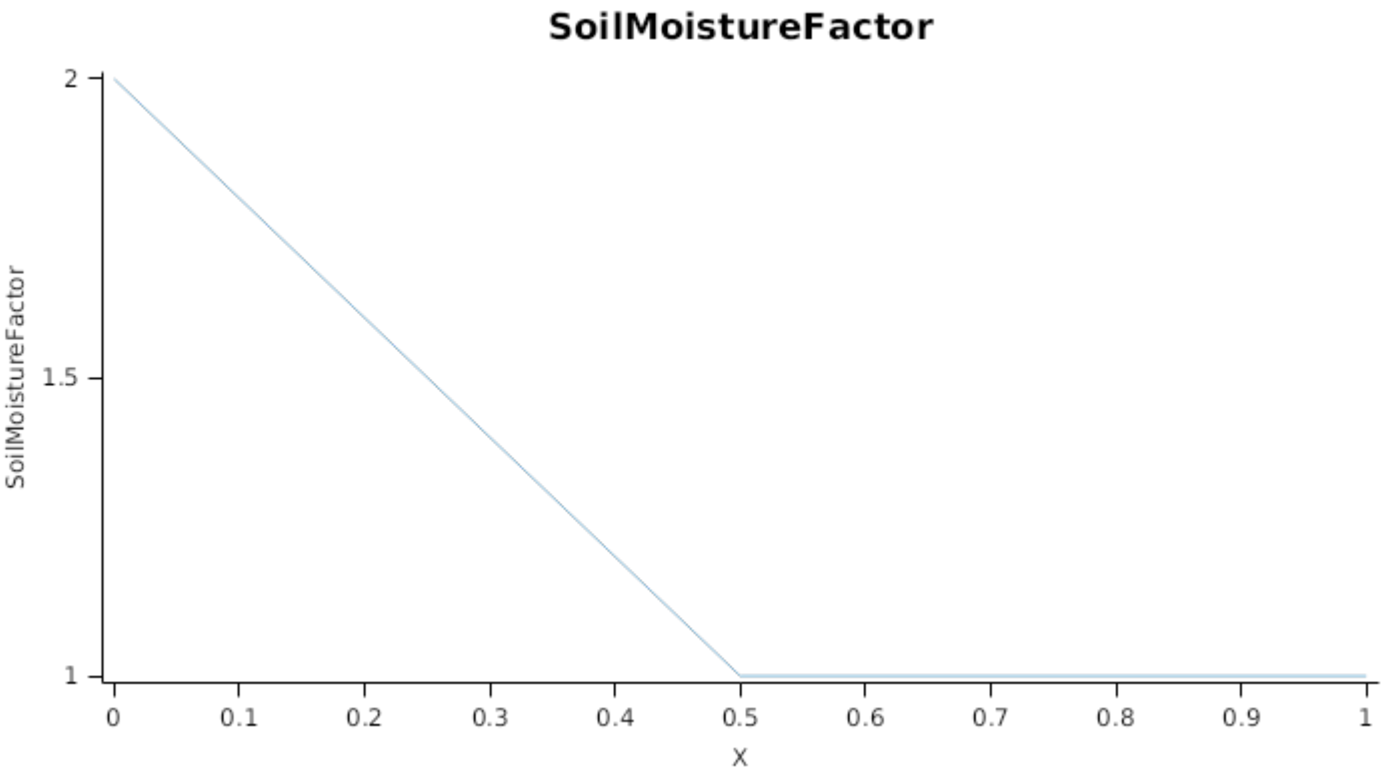
X	TemperatureFactor
-20.0	1.5
-5.0	0.5
0.0	0.2
5.0	0.1
17.0	0.8
28.0	1.0
37.5	1.5





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.

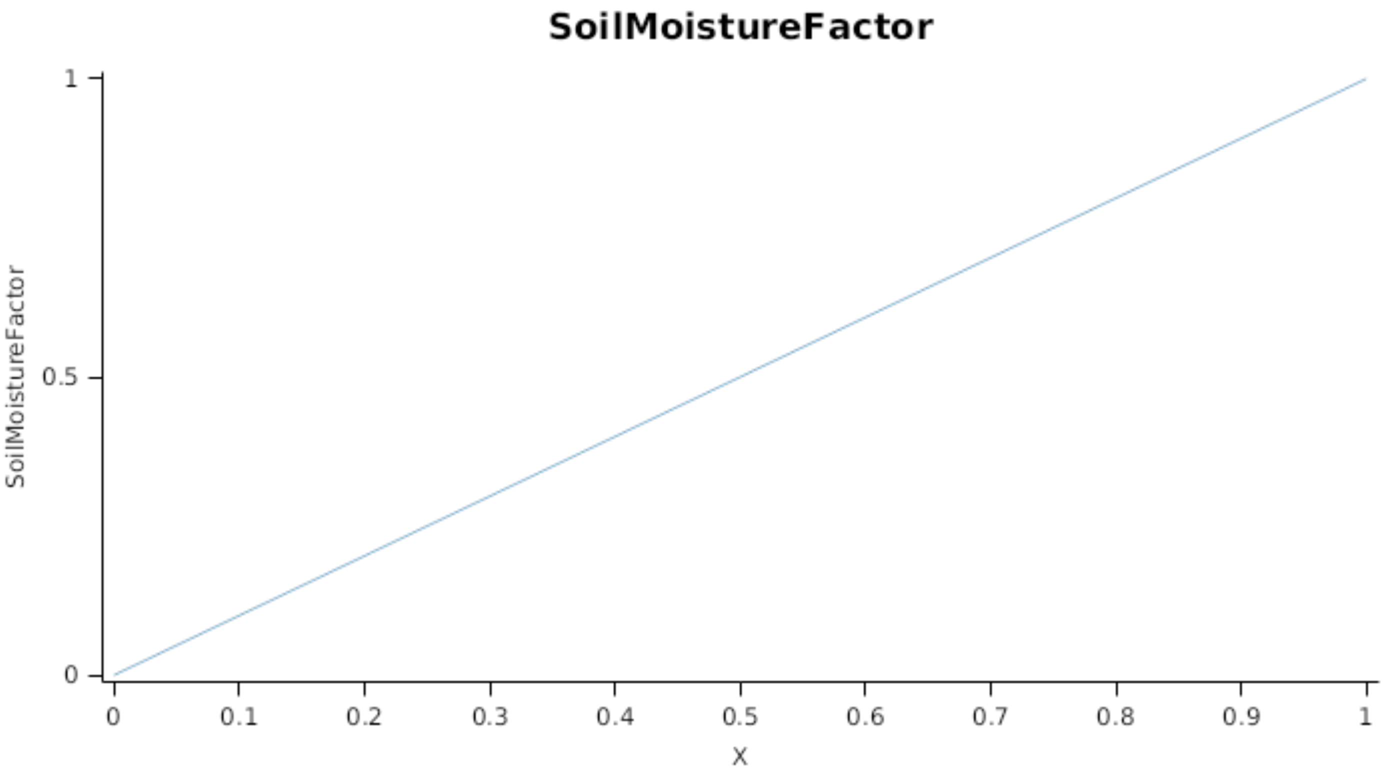
A generic relationship between detachment and soil moisture is assumed. It implies that under dry conditions the detachment rate decreases due to the lower level of activity of decomposing microorganisms.

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	80	60	0	0
Graze	60	20	20	30
Harvest	80	80	10	10
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.

The DM demands calculated here represent potential values, or a weighting factors, which are used by the OrganArbitrator to compute the allocated DM for all organs. The potential demand is computed as the sum of a *Base* and a *Deficit* demand. The *Base* demand is simply defined by the target proportion of leaf biomass, whereas the *Deficit* demand is defined by the difference between the actual and the targeted proportions. This approach is used to ensure promptly regrowth of aboveground organs after a defoliation; it relies in the assumption that a target biomass proportion for each organ exists. The *TargetBiomassProportion* is calculated based on a target shoot-to-root ratio and a biomass proportion for each organ above or below ground, these are defined elsewhere in this documentation and may vary with growth stage and environmental conditions.

Structural = *DMDemandFunction* x *StructuralFraction*

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

Where:

Zero = 0

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

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

TargetBelowGroundProp = 1 - [TargetAboveGroundFraction]

StructuralFraction = 1 (g/g)

Metabolic = 0 (g/g)

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.

These N demands also represent potential values that are used by the OrganArbitrator to get the total plant N demand. This and any source of N in the plant are used to determine soil N demand, and eventually the actual amounts allocated to each pool in each organ.

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 = 0.55 (gN/gDM)

MaximumNConc = 0.55 (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.

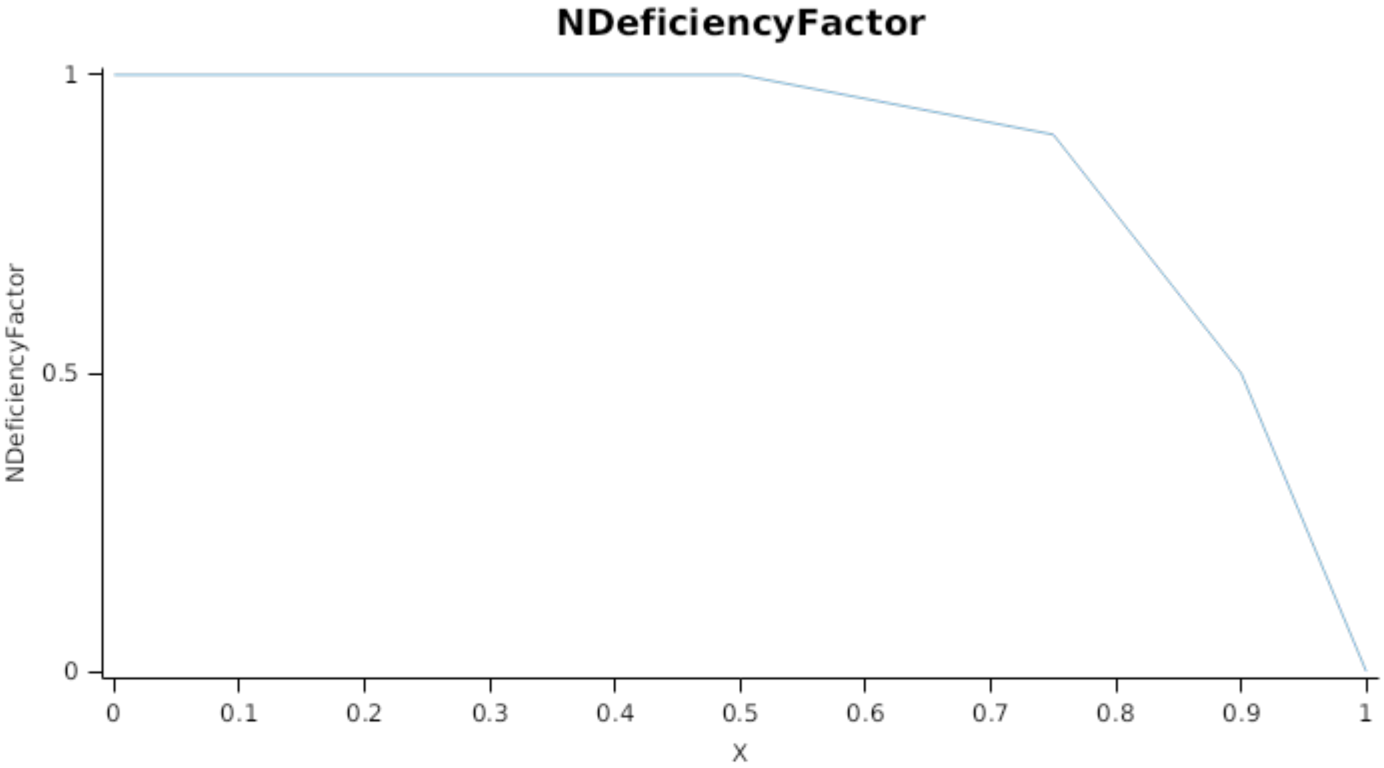
The rate of N fixation in nodules is highly regulated by the host plant, but in its basis it is defined by the presence and quantity of symbiont bacteria. The whiteclover model uses an approach whereby the basic fixation rate is directly proportional to the biomass of nodules (Rys et al., 1985; Ledgard et al., 1990; Hogh-Jensen et al., 2002; Russelle et al., 2008; Flora, 2013). This is then regulated by environmental factors and the plant itself (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 over the whole plant, with fixation rate being inversely proportional to the plant's N deficiency factor. The mechanism regulating N fixation is quite responsive, with fixation nearly ceasing soon after fertilisation or defoliation (e.g. Carroll et al., 1983; Russelle et al., 2008) and this is captured in the model by a prompt reduction of the N deficiency factor. By linking potential fixation to nodule's biomass, the model is also capable of describing both an upper limit for fixation (due to nodule growth being limited due to the competition for biomass among organs) and the temporal lag between the inception of N stress and an elevated N fixation rate (nodules need to grow before they can start fixing N).

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



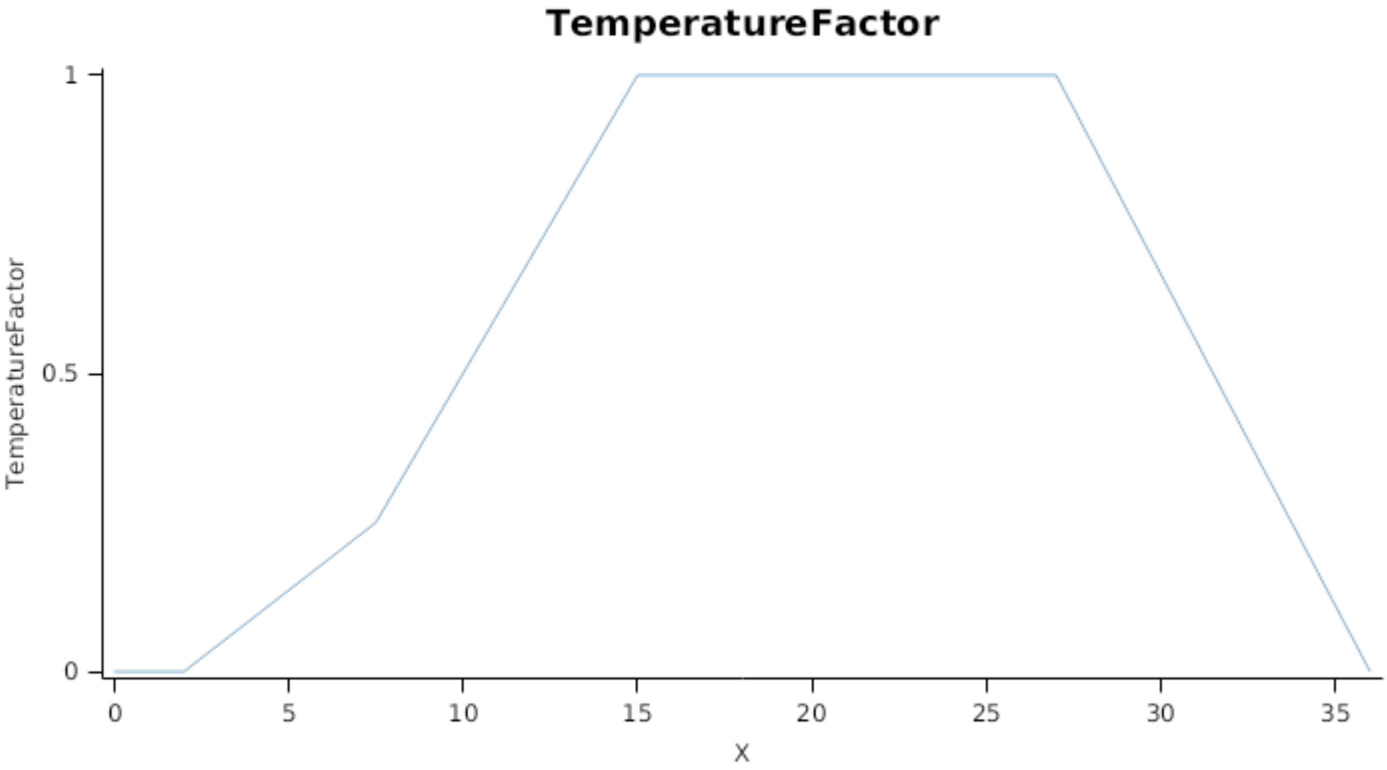
EnvironmentalFactor = Min(*TemperatureFactor*, *SoilMoistureFactor*)

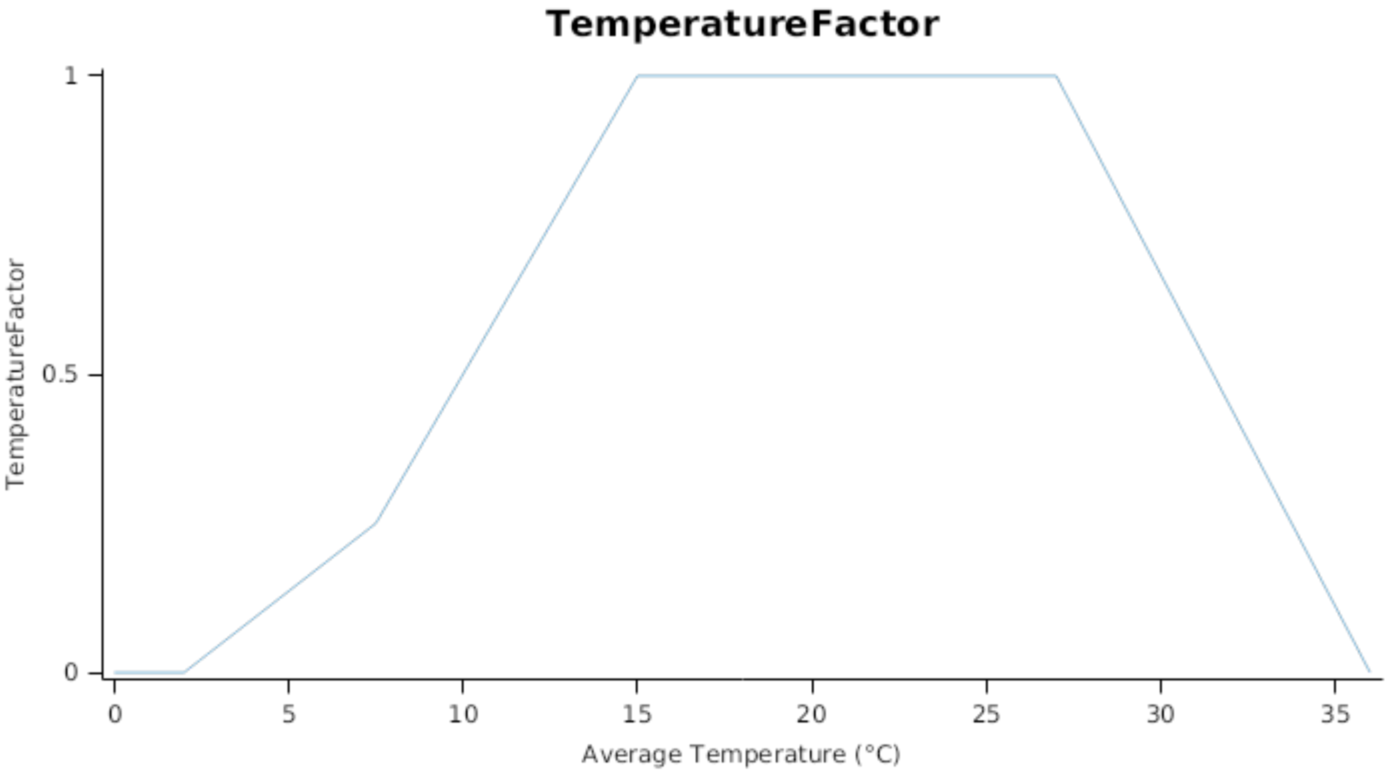
Where:

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

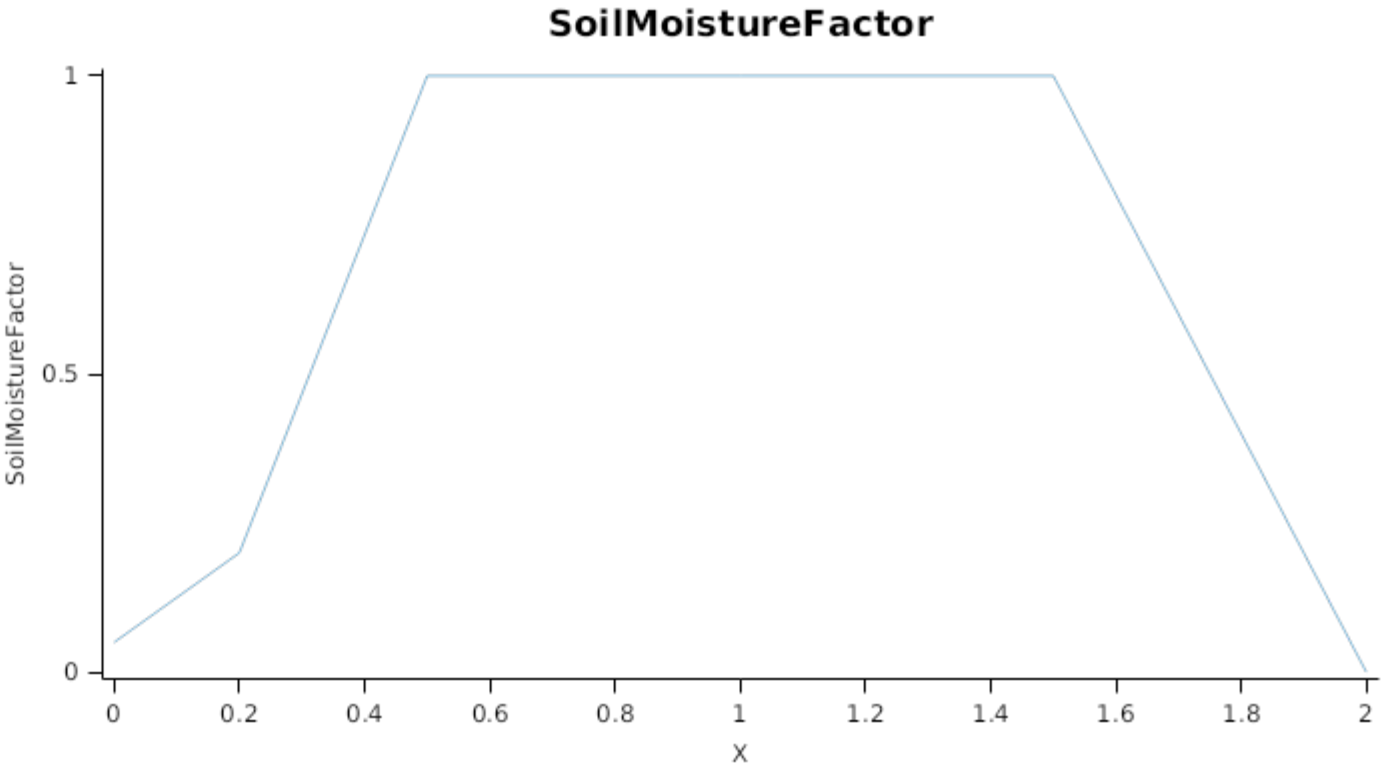
X	TemperatureFactor
0.0	0.0
2.0	0.0
7.5	0.2
15.0	1.0
27.0	1.0
36.0	0.0





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



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*

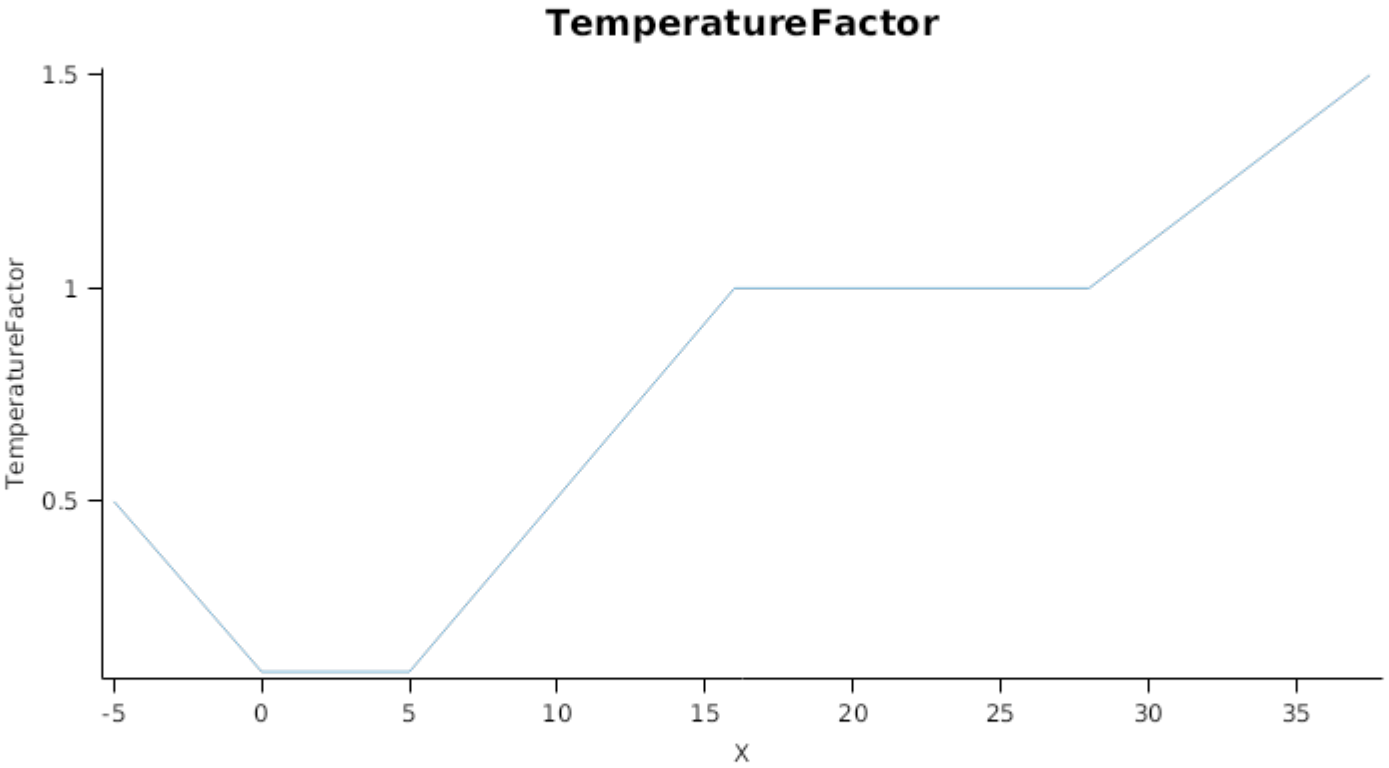
ReferenceRate = 0.005 (/day)

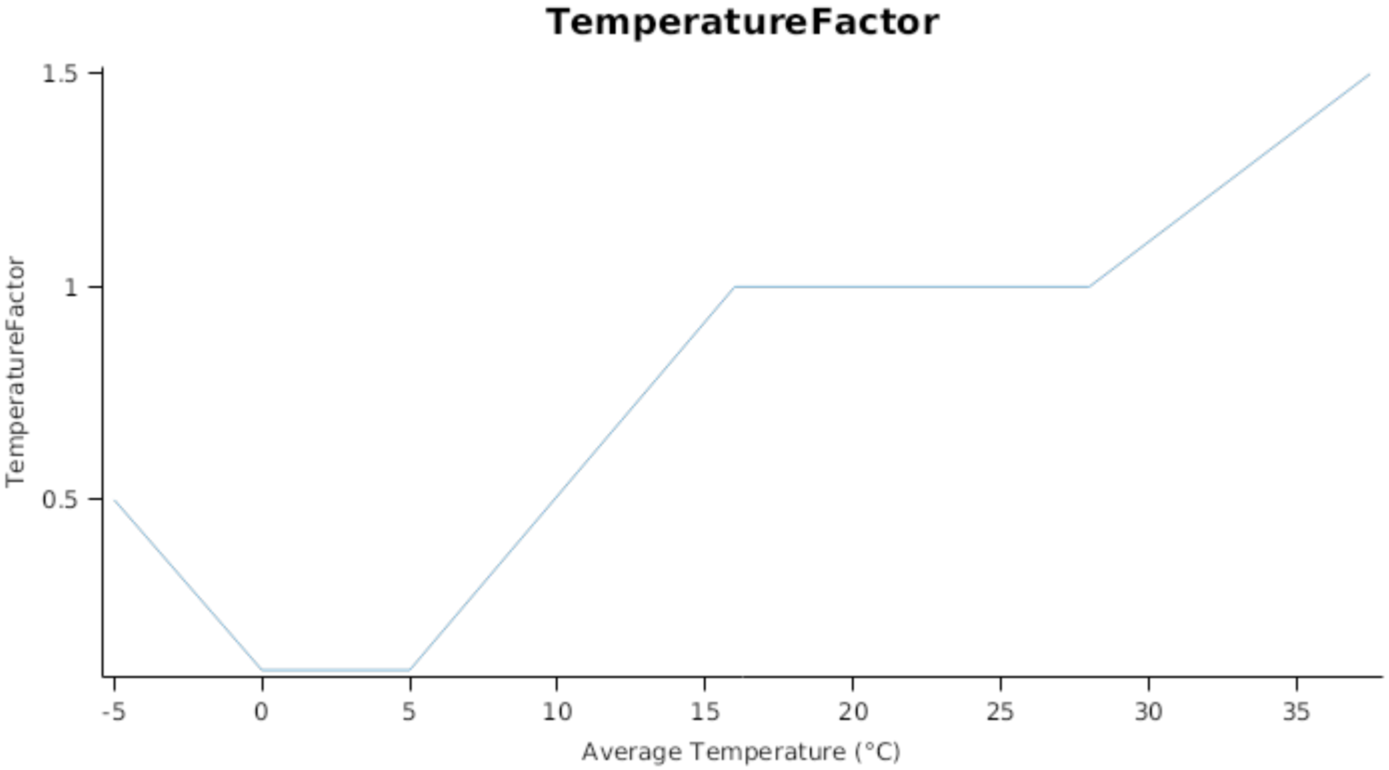
TemperatureFactor is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.

MaximumTemperatureWeighting = 0.5

X	**TemperatureFactor**
-5.0	0.5
0.0	0.1
5.0	0.1

X	TemperatureFactor
16.0	1.0
28.0	1.0
37.5	1.5

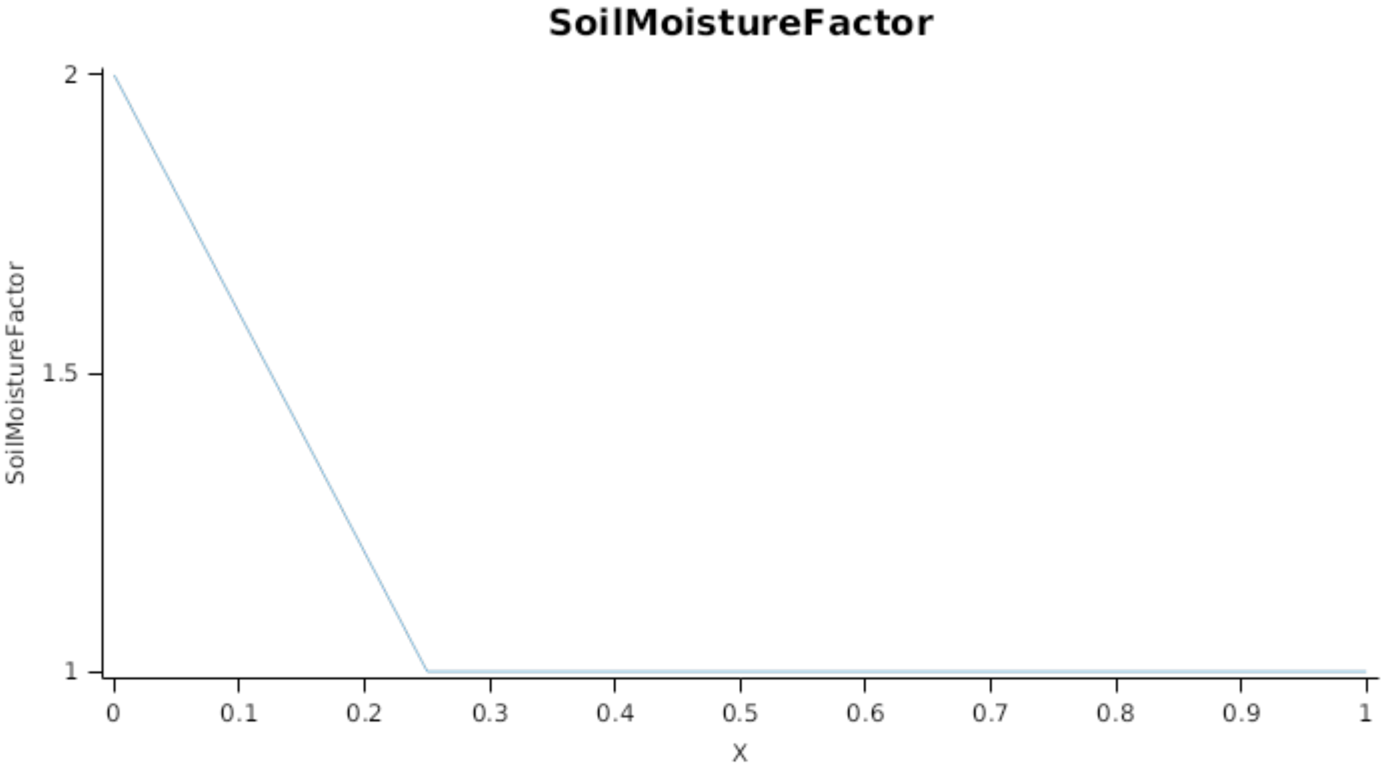




SoilMoistureFactor is calculated using linear interpolation

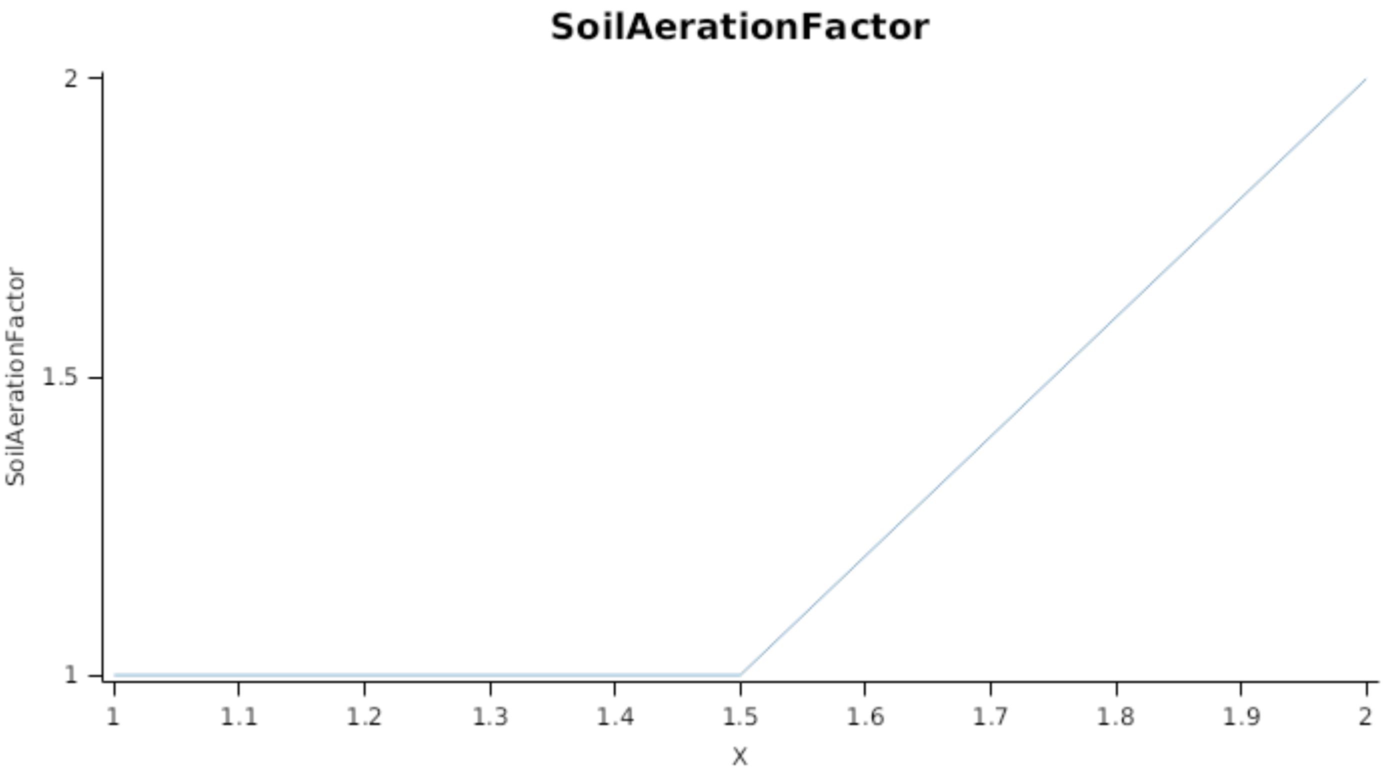
X	SoilMoistureFactor
0.0	2.0

X	SoilMoistureFactor
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
Cut	0	0	2	0
Graze	0	0	2	0
Harvest	0	0	2	0
Prune	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.

The DM demand as calculated here is a potential value, or a weighting factor, which is used by the OrganArbitrator to compute the allocated DM for all organs. The potential demand is computed as the sum of a base and a deficit demands. The base demand is simply defined by the target proportion of leaf biomass, whereas the deficit demand is defined by the difference between the actual and targeted proportions. This approach ensures promptly regrowth of aboveground organs after defoliation, but relies in the assumption that a target biomass proportion for each organ exist. The target proportion is calculated based on a target shoot-to-root ratio and then a biomass proportion for each organ, these are defined elsewhere in this documentation and may vary with growth stage and environmental conditions.

Structural = *DMDemandFunction* x *StructuralFraction*

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 = *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 = Max(*Zero*, *Deficit*)

Where:

Zero = 0

Deficit = TargetBiomass - [Taproot].Live.Wt

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

TargetBelowGroundProp = 1 - [TargetAboveGroundFraction]

StructuralFraction = 0.75 (g/g)

Metabolic = 0 (g/g)

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

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

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.

These N demands also represent potential values that are used by the OrganArbitrator to get the total plant N demand. This and any source of N in the plant are used to determine soil N demand, and eventually the actual amounts allocated to each pool in each organ.

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 = 0.03 (gN/gDM)

1.13.5 Dry Matter Supply

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

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

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.

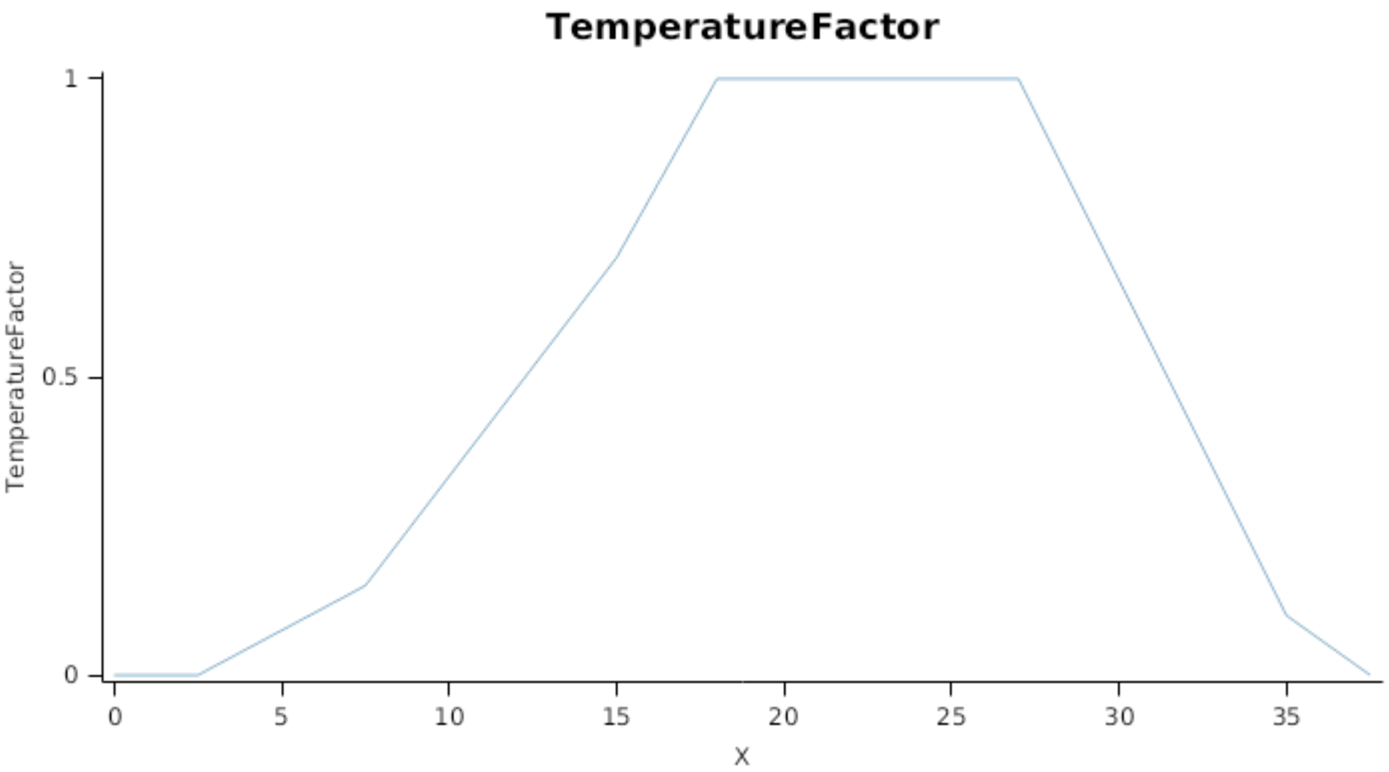
DMRetranslocationFactor = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor* x *PhotoPeriodFactor*

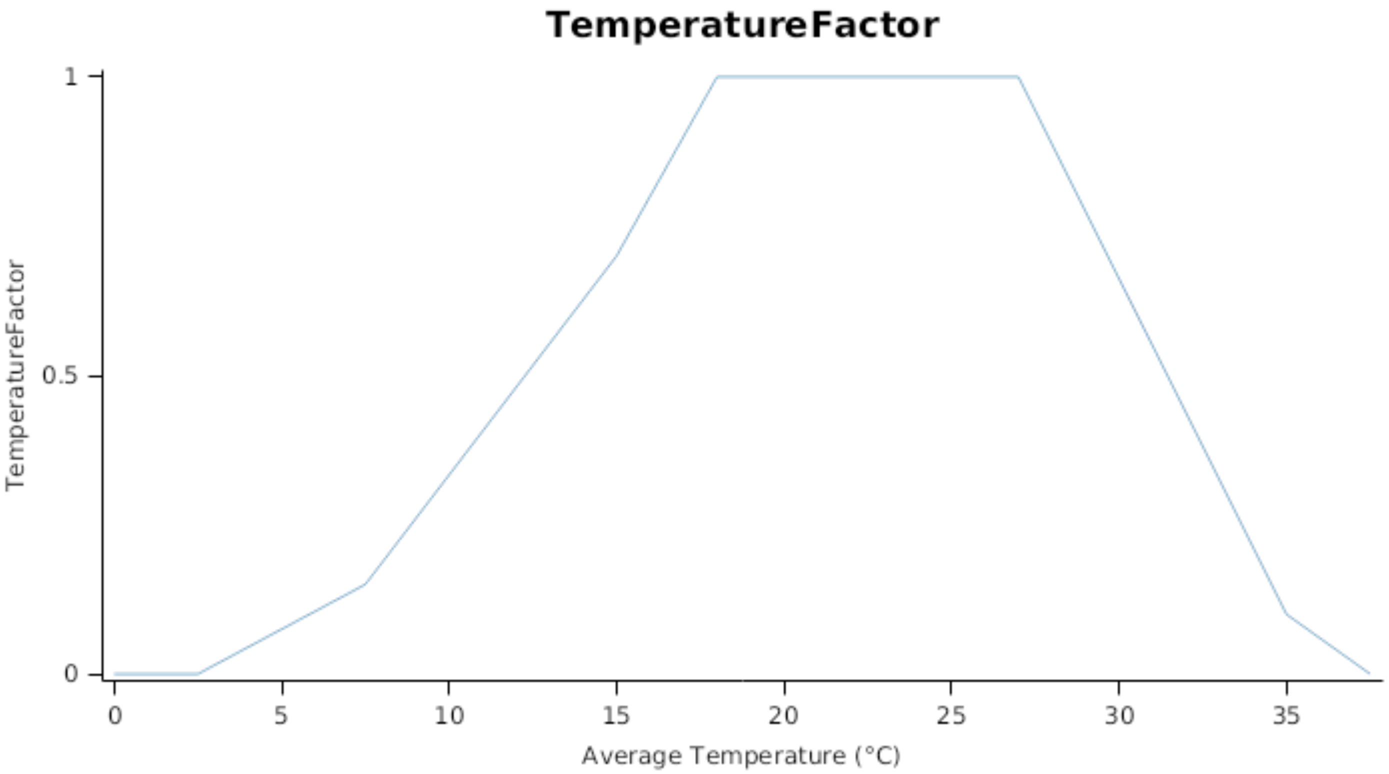
ReferenceRate = 0.05 (/day)

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

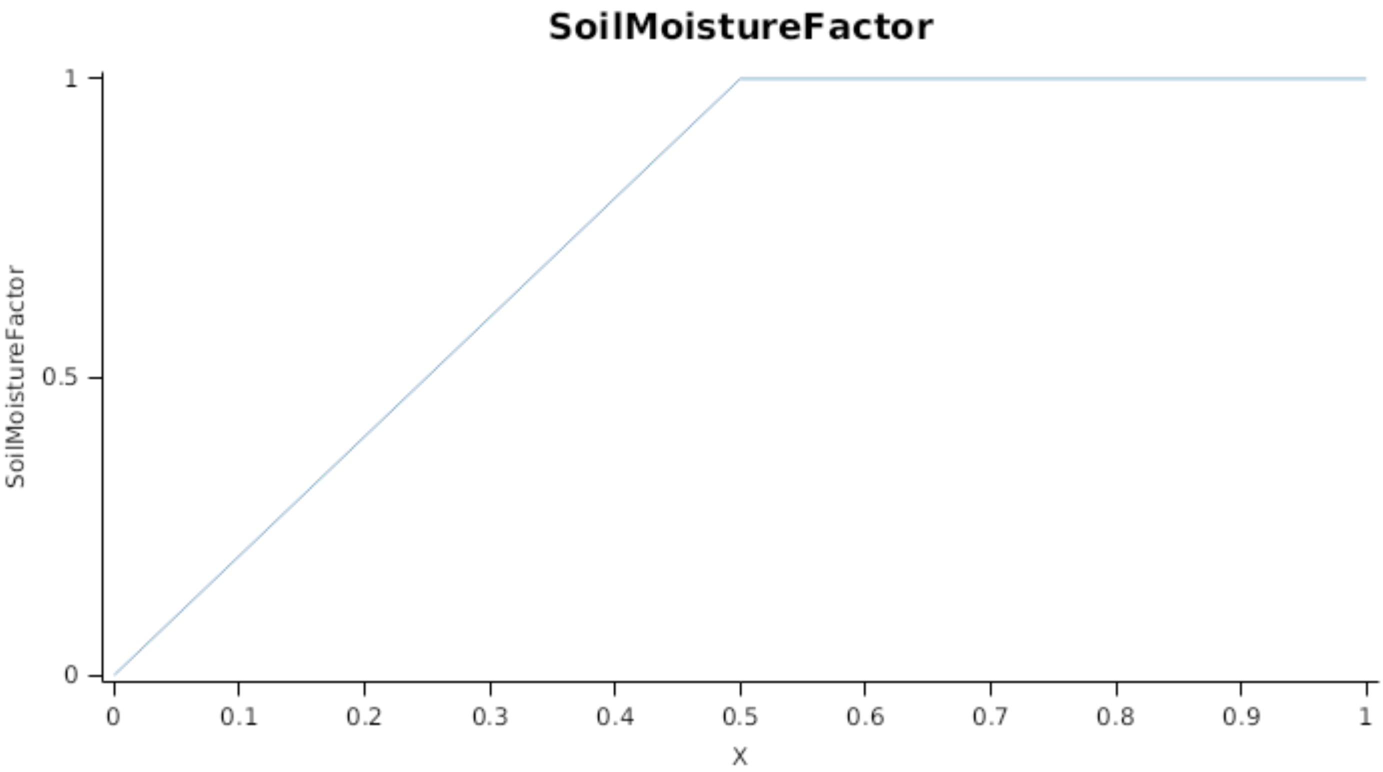
X	TemperatureFactor
0.0	0.0
2.5	0.0
7.5	0.1
15.0	0.7
18.0	1.0
27.0	1.0
35.0	0.1
37.5	0.0





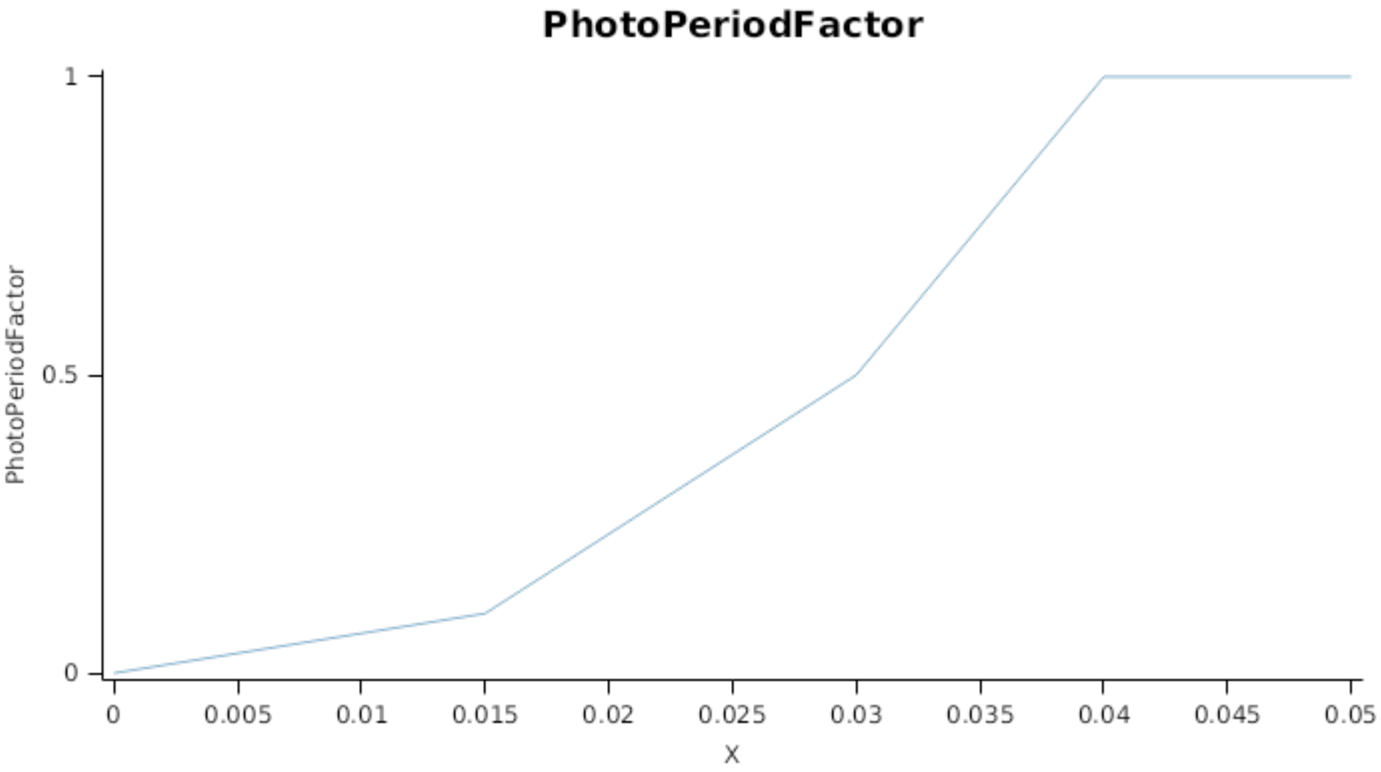
SoilMoistureFactor is calculated using linear interpolation

X	**SoilMoistureFactor**
0.0	0.0
0.5	1.0
1.0	1.0



PhotoPeriodFactor is calculated using linear interpolation

X	PhotoPeriodFactor
0.0	0.0
0.0	0.1
0.0	0.5
0.0	1.0
0.1	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.

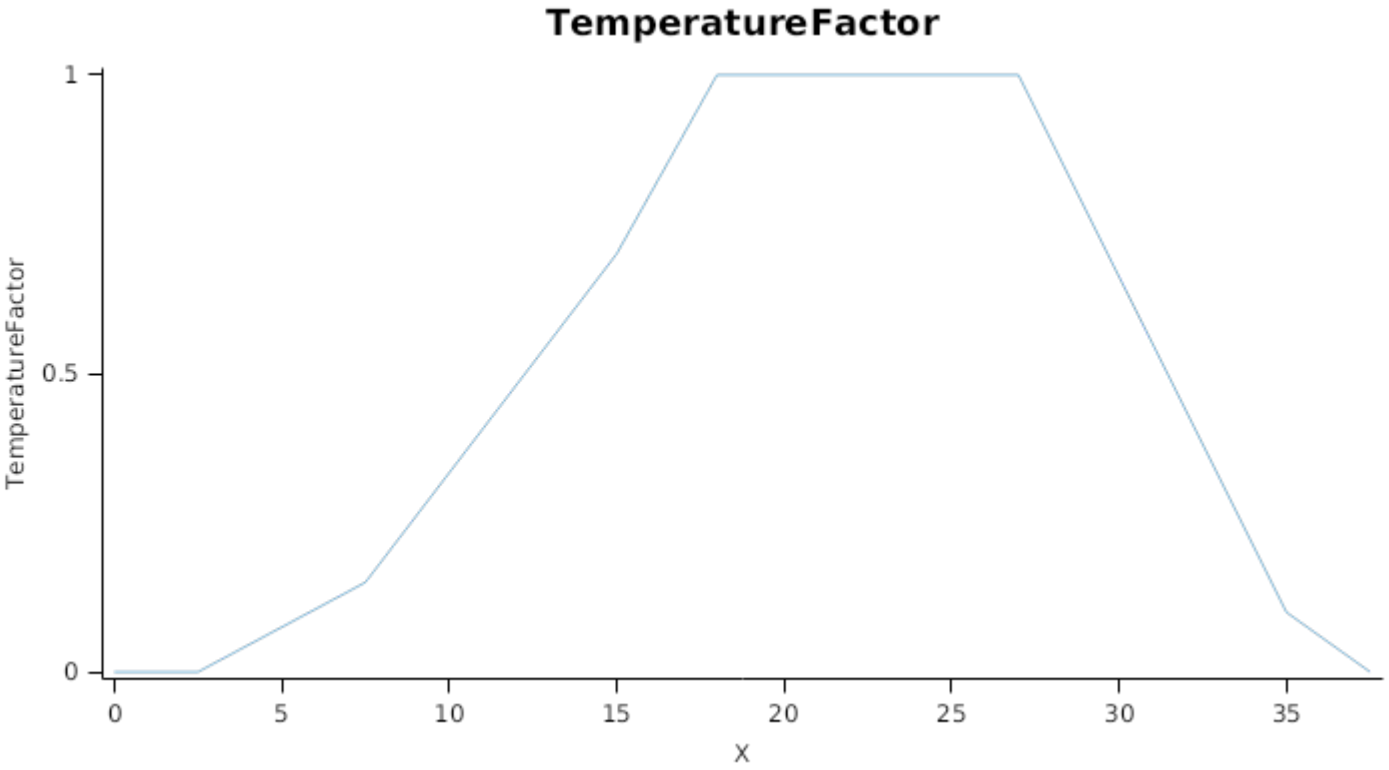
NRetranslocationFactor = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor* x *PhotoPeriodFactor*

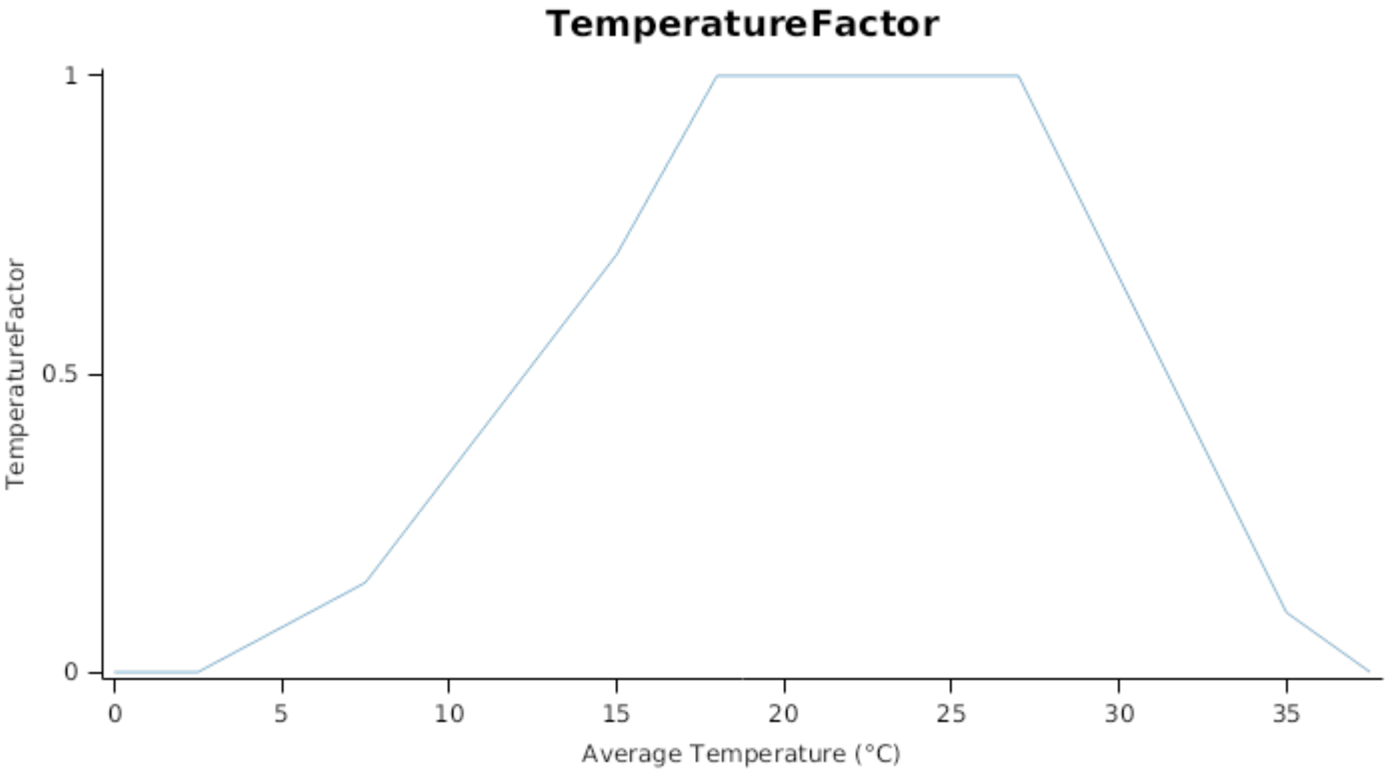
ReferenceRate = 0.1 (/day)

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

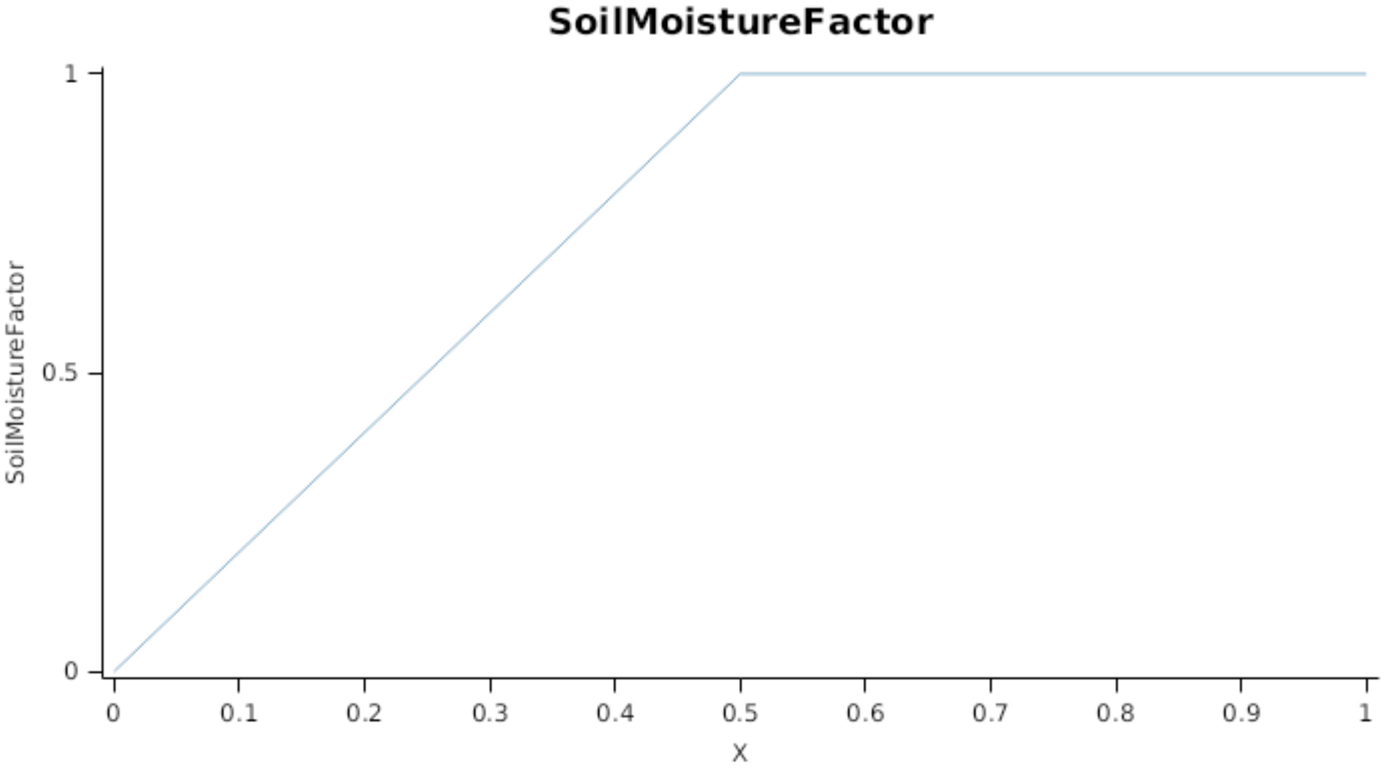
X	TemperatureFactor
0.0	0.0
2.5	0.0
7.5	0.1
15.0	0.7
18.0	1.0
27.0	1.0
35.0	0.1
37.5	0.0





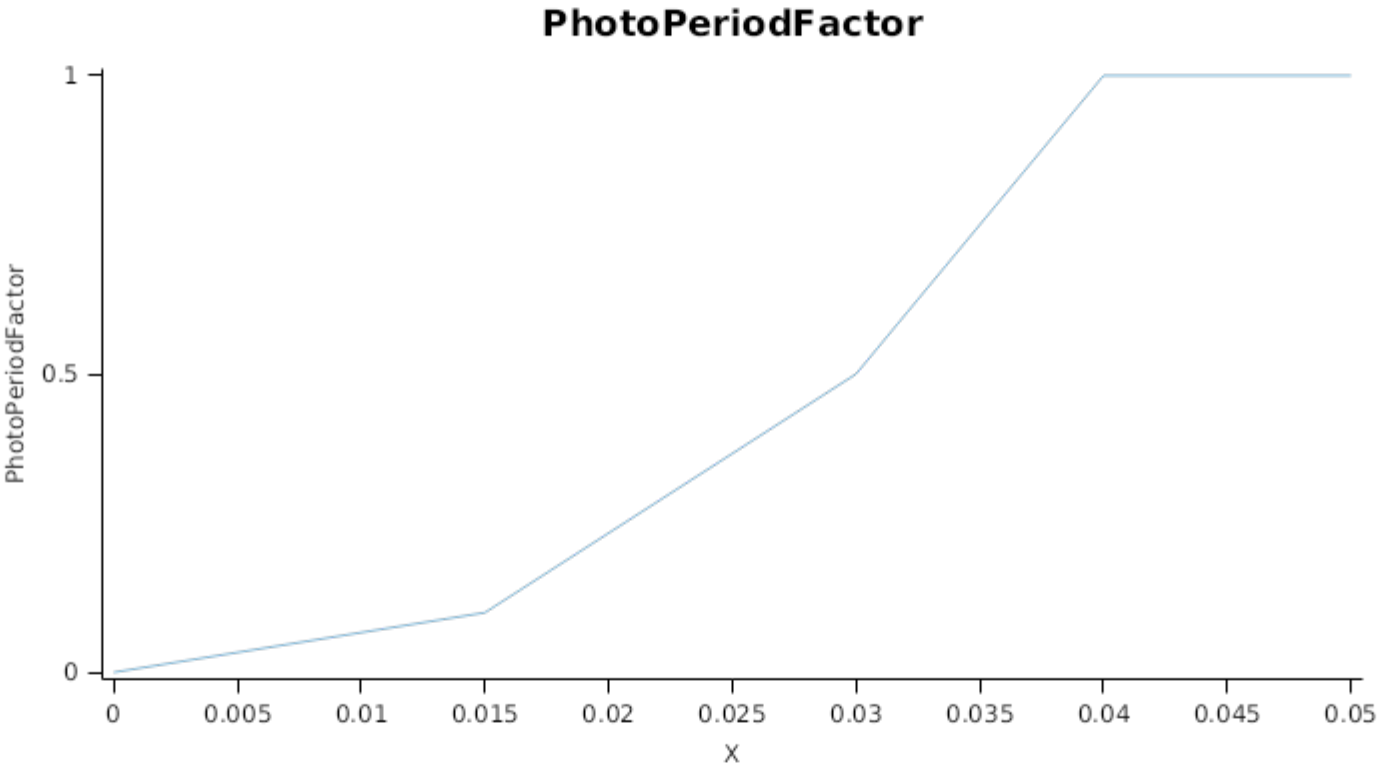
SoilMoistureFactor is calculated using linear interpolation

X	SoilMoistureFactor
0.0	0.0
0.5	1.0
1.0	1.0



PhotoPeriodFactor is calculated using linear interpolation

X	PhotoPeriodFactor
0.0	0.0
0.0	0.1
0.0	0.5
0.0	1.0
0.1	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.

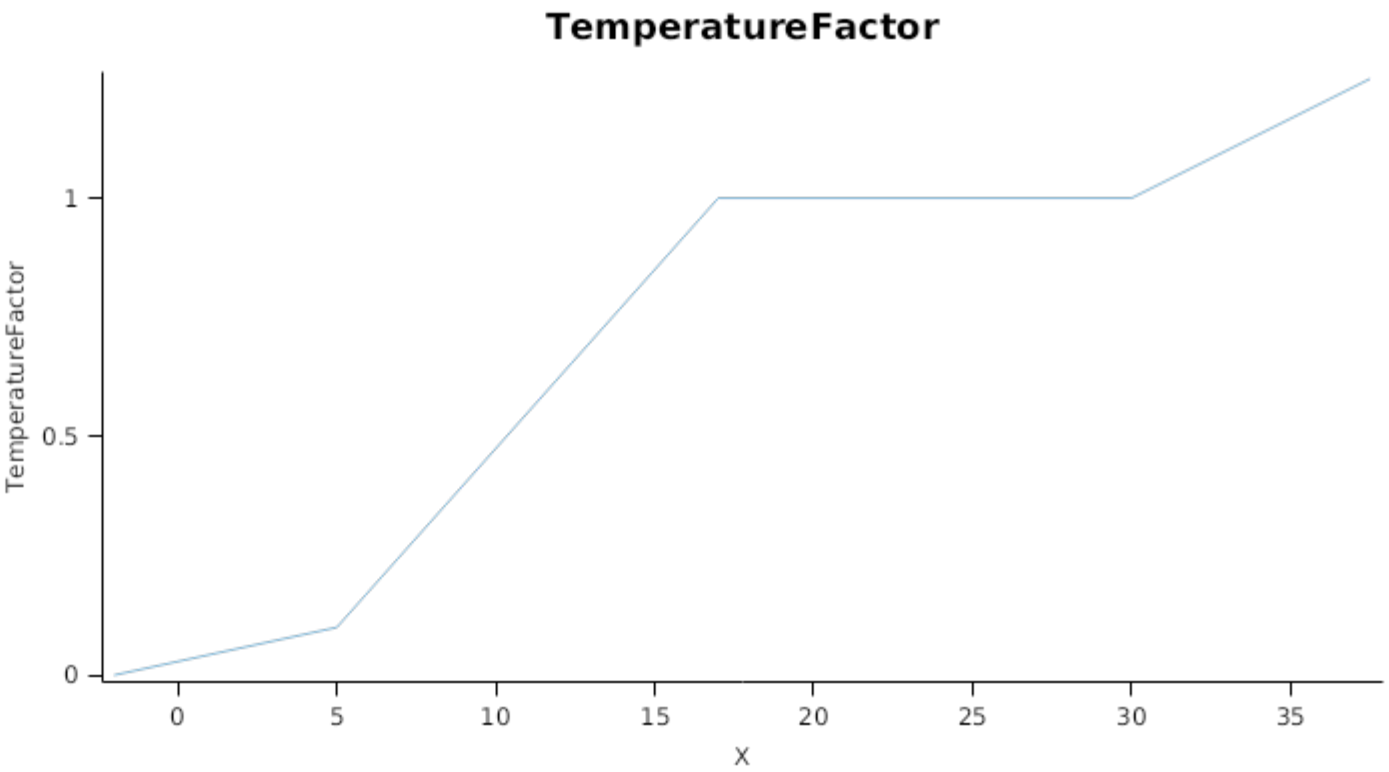
SenescenceRate = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor* x *SoilAerationFactor*

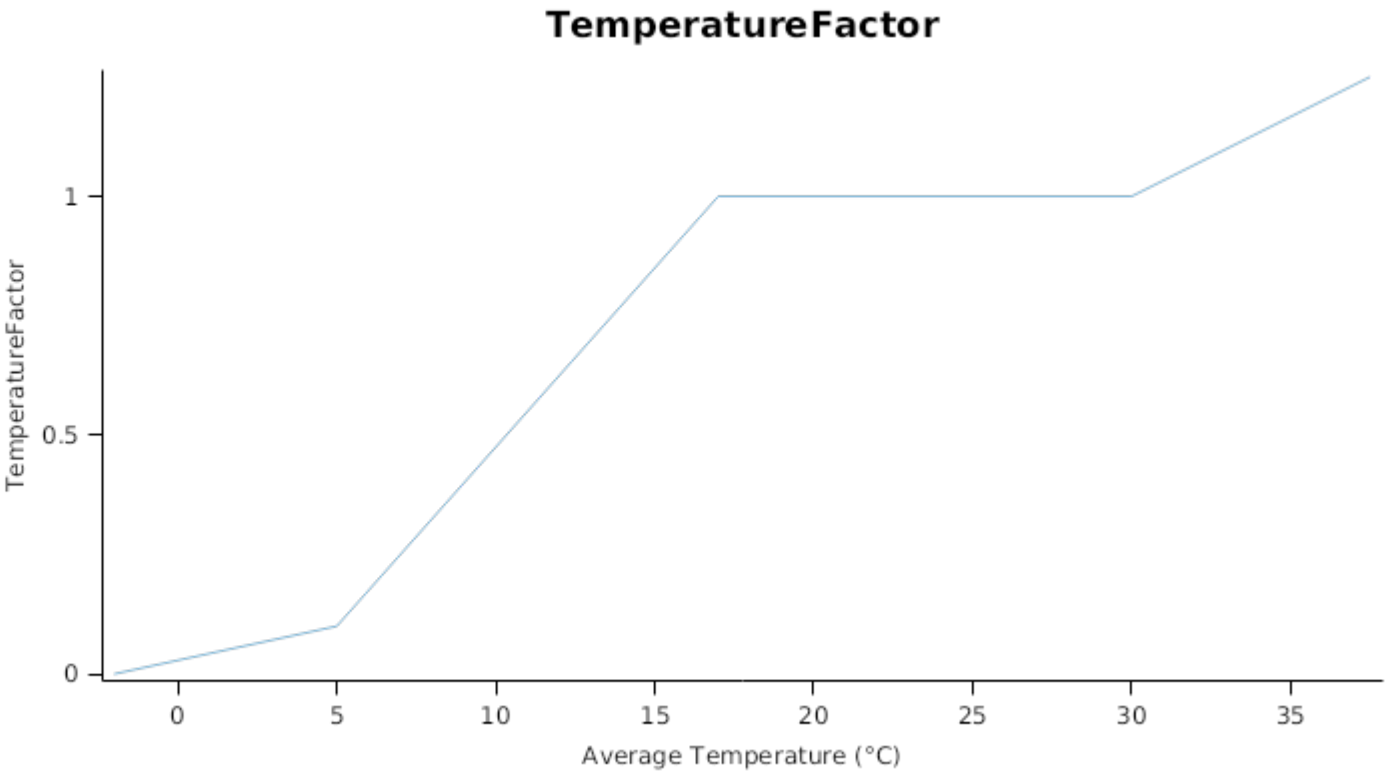
ReferenceRate = 0.01 (/day)

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

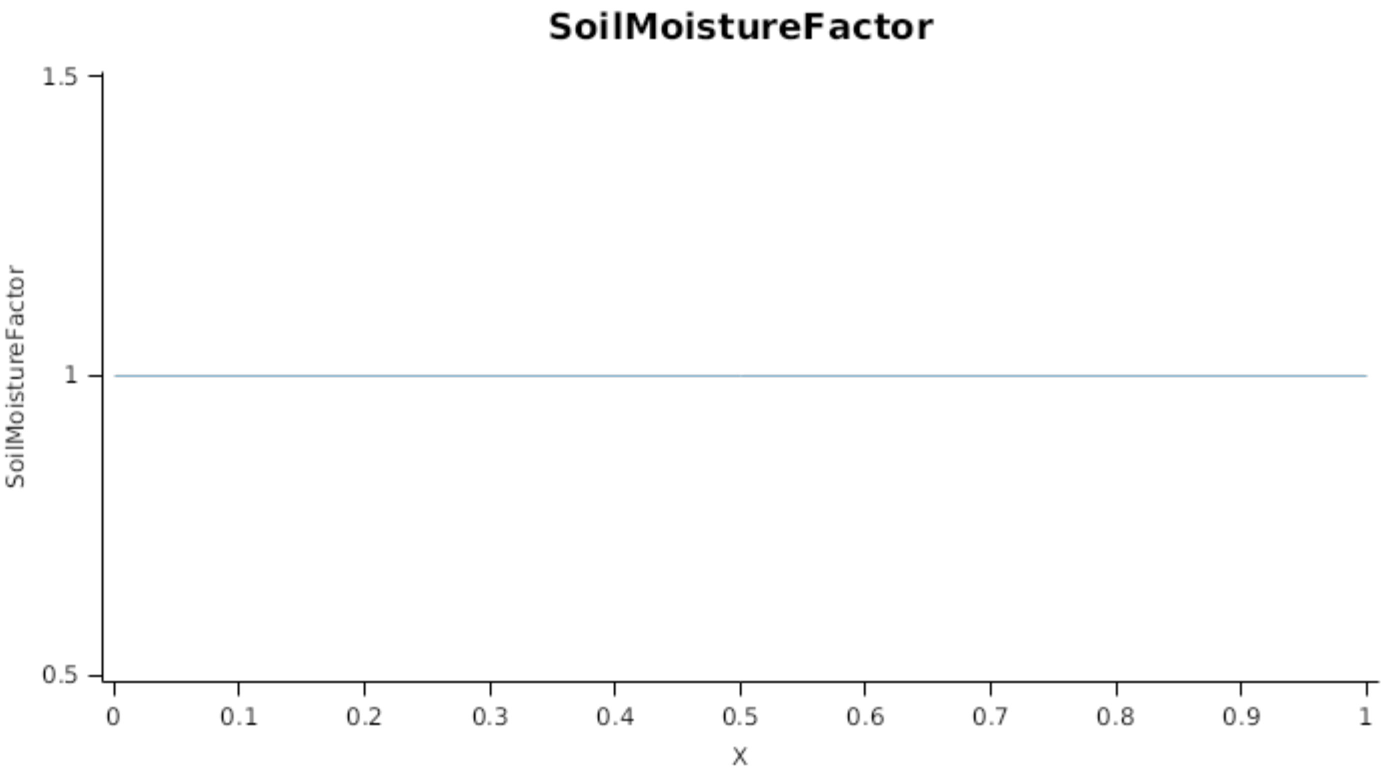
X	TemperatureFactor
-2.0	0.0
5.0	0.1
17.0	1.0
30.0	1.0
37.5	1.2





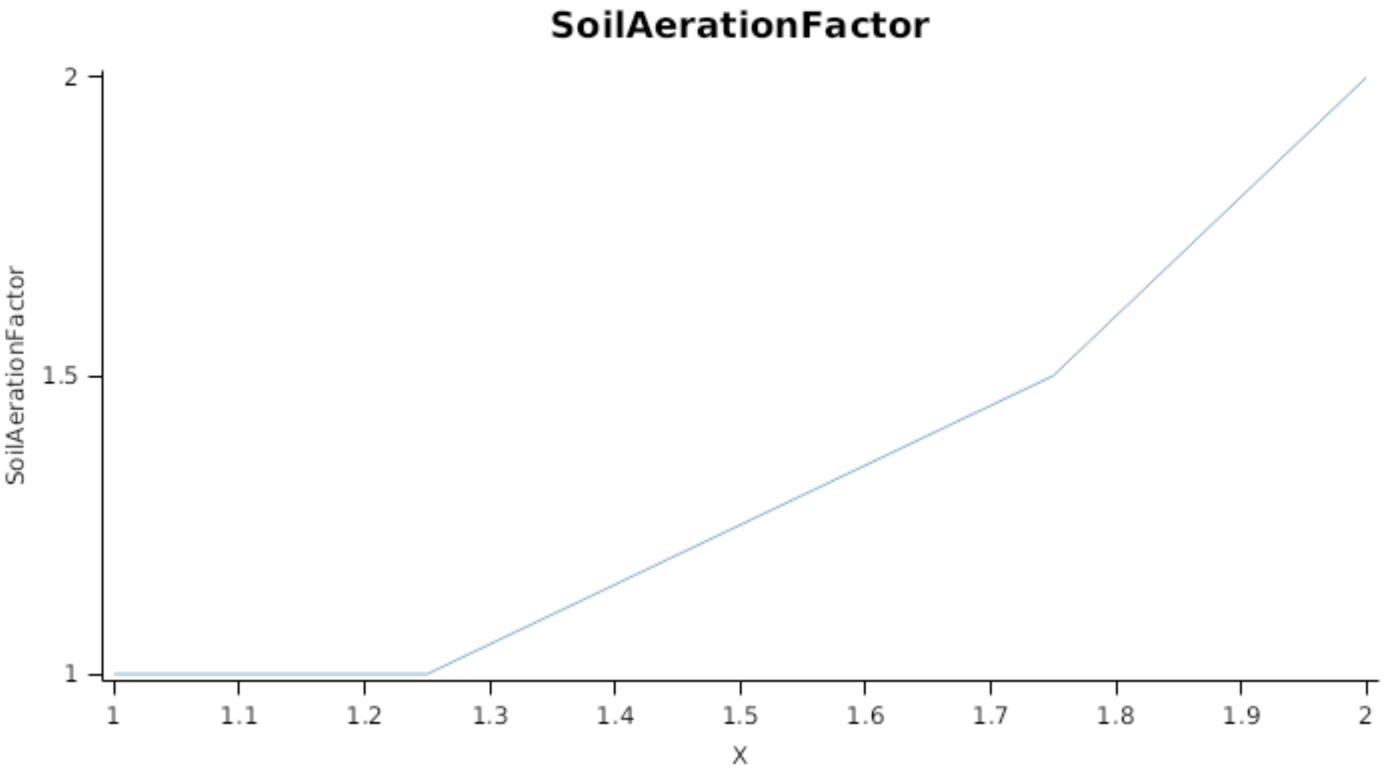
SoilMoistureFactor is calculated using linear interpolation

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	10	0
Graze	0	0	10	0
Harvest	0	0	10	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.

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

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

Root depth is also constrained by a maximum root depth.

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

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

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

$DMAllocated_i = TotalDMAllocated \times RAw_i / TotalRAw$

1.14.2 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 (gC/gDM)

MinimumNConc = 0.025 (gN/gDM)

CriticalNConc = 0.025 (gN/gDM)

MaximumNConc = 0.03 (gN/gDM)

DMConversionEfficiency = 1 (0-1)

MaintenanceRespirationFunction = 0 (0-1)

MaximumRootDepth = 750 (mm)

SpecificRootLength = 90 (m/g)

DMReallocationFactor = 1 (/day)

NReallocationFactor = 1 (/day)

RemobilisationCost = 0 (g/m^2)

MaxDailyNUptake = 10 (gN/m^2)

RootDepthStressFactor = 1

1.14.7 RootShape

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

1.14.8 Description

Note that this organs is parameterised to represents all the fine roots of the plant. The root organ is reponsible for uptake but can also supply both N and DM from its non-structural biomass, although this typically represents only a small contribution to plant growth and only happen upon senescence. The taproot organ is used for simulating biomass storage and remobilisation. The root depth increases through time, as described below, but currently it does not retreat in case of root depth, something that will have to be revisited in the future.

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 refers 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 nodules 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 = 0.8 (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.

The DM demand as calculated here is a potential value, or a weighting factor, which is used by the OrganArbitrator to compute the allocated DM for all organs. The potential demand is computed as the sum of a base and a deficit demands. The base demand is simply defined by the target proportion of leaf biomass, whereas the deficit demand is defined by the difference between the actual and targeted proportions. This approach ensures promptly regrowth of aboveground organs after defoliation, but relies in the assumption that a target biomass proportion for each organ exist. The target proportion is calculated based on a target shoot-to-root ratio and then a biomass proportion for each organ, these are defined elsewhere in this documentation and may vary with growth stage and environmental conditions.

Structural = *DMDemandFunction* x *StructuralFraction*

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

Where:

Zero = 0

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

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

TargetBelowGroundProp = 1 - [TargetAboveGroundFraction]

StructuralFraction = 1 (g/g)

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.

These N demands also represent potential values that are used by the OrganArbitrator to get the total plant N demand. This and any source of N in the plant are used to determine soil N demand, and eventually the actual amounts allocated to each pool in each organ.

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)

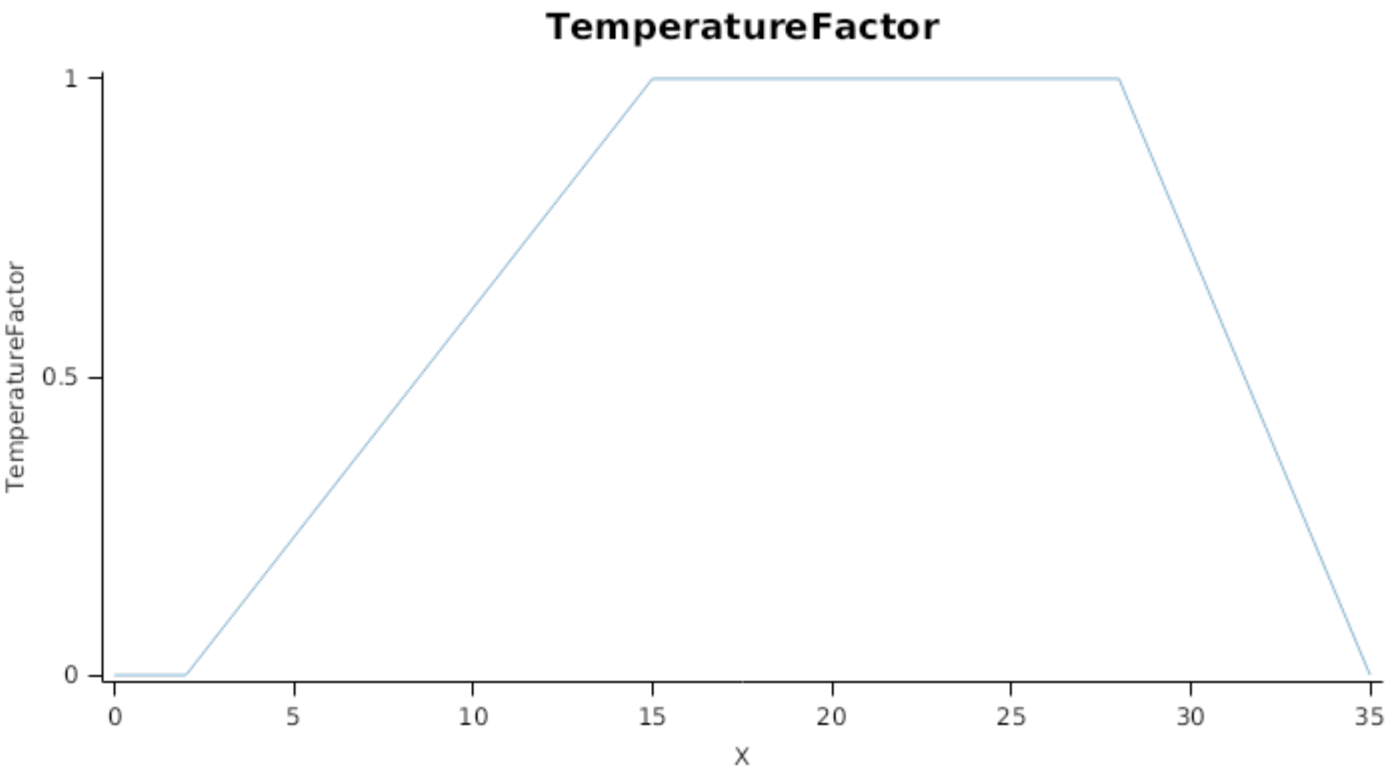
EnvironmentalFactor = Min(*TemperatureFactor*, *SoilMoistureFactor*, *SoilAerationFactor*)

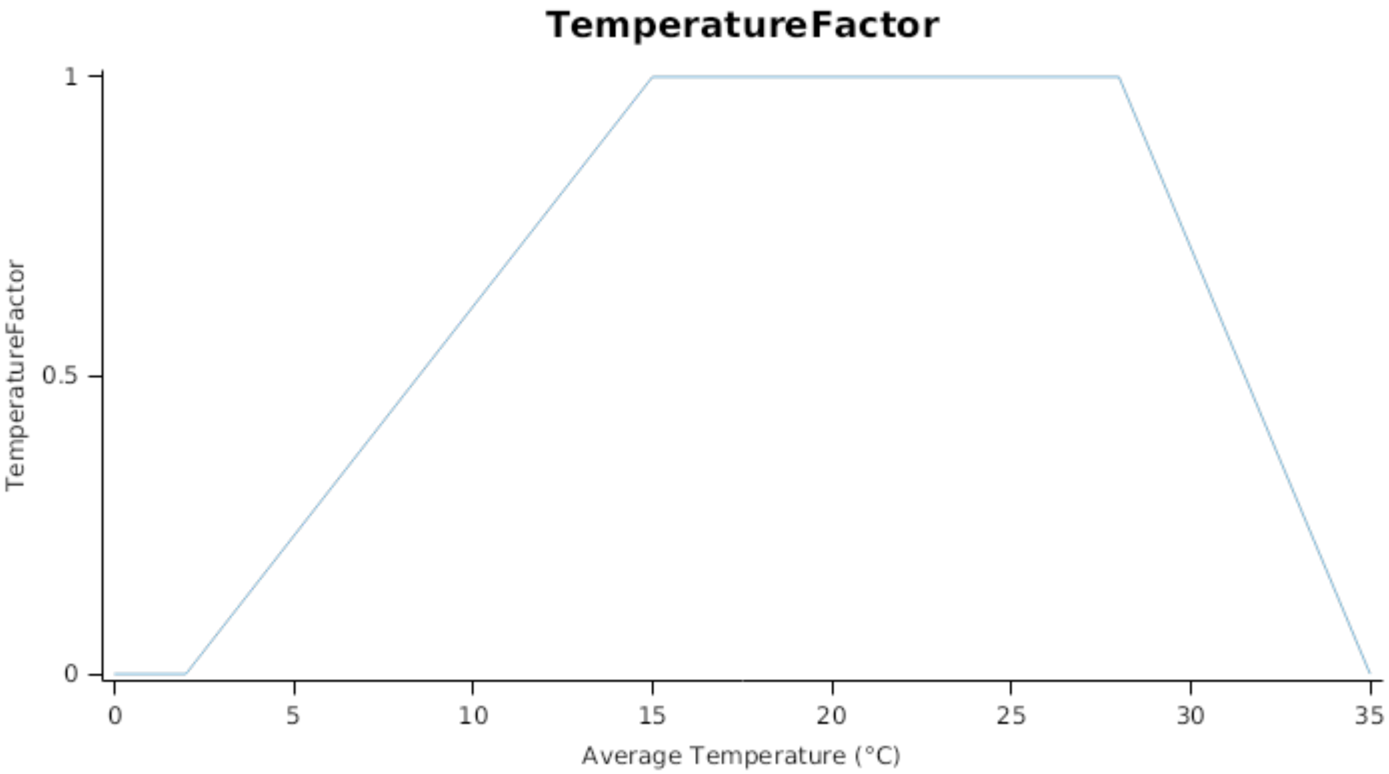
Where:

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)

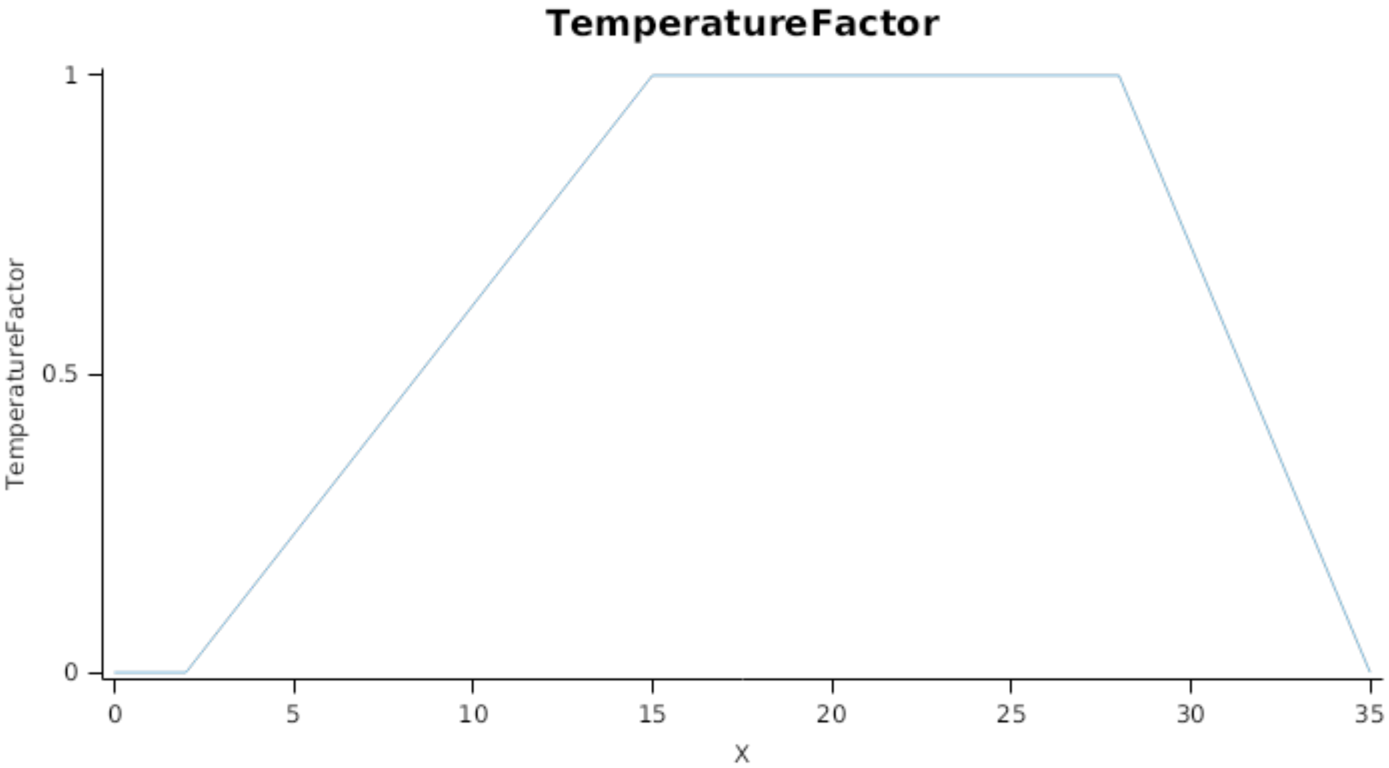
EnvironmentalFactor = Min(*TemperatureFactor*, *SoilMoistureFactor*, *SoilAerationFactor*)

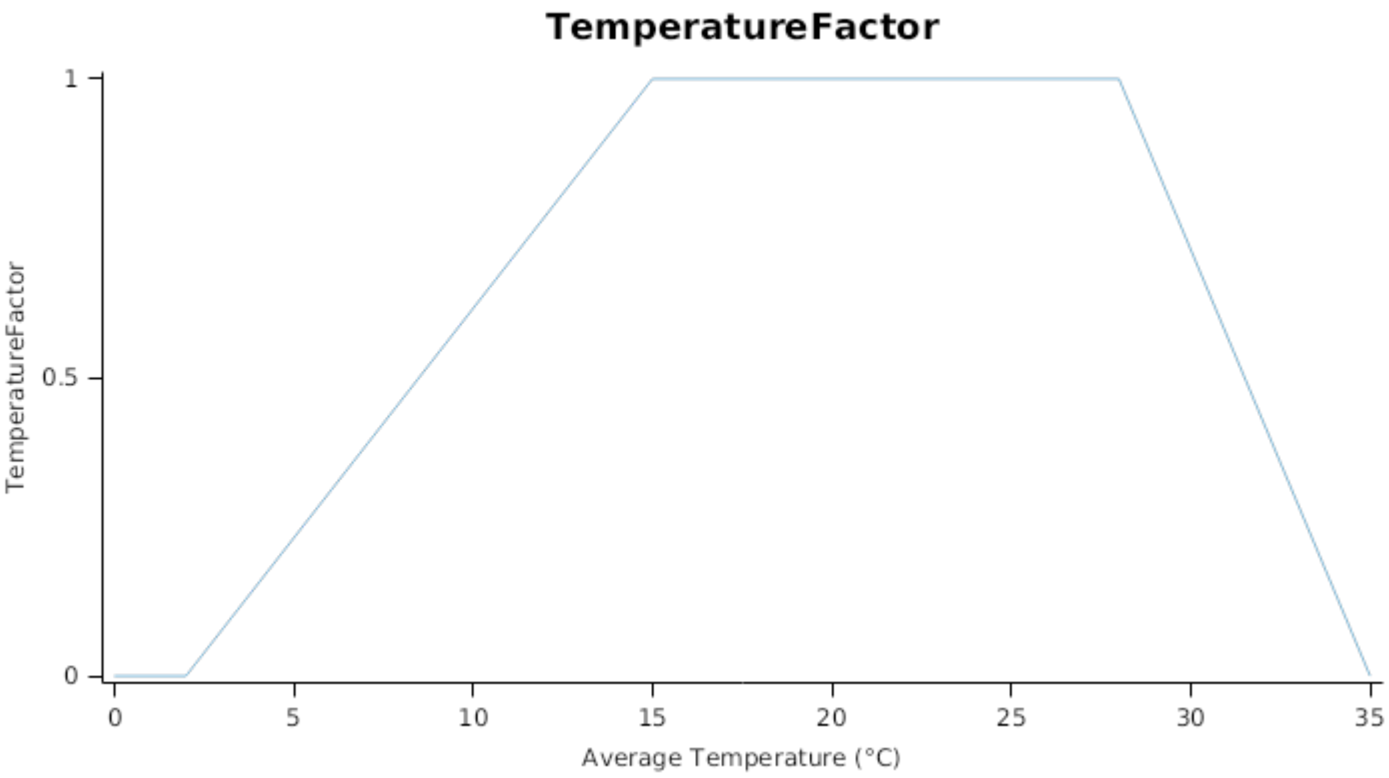
Where:

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.

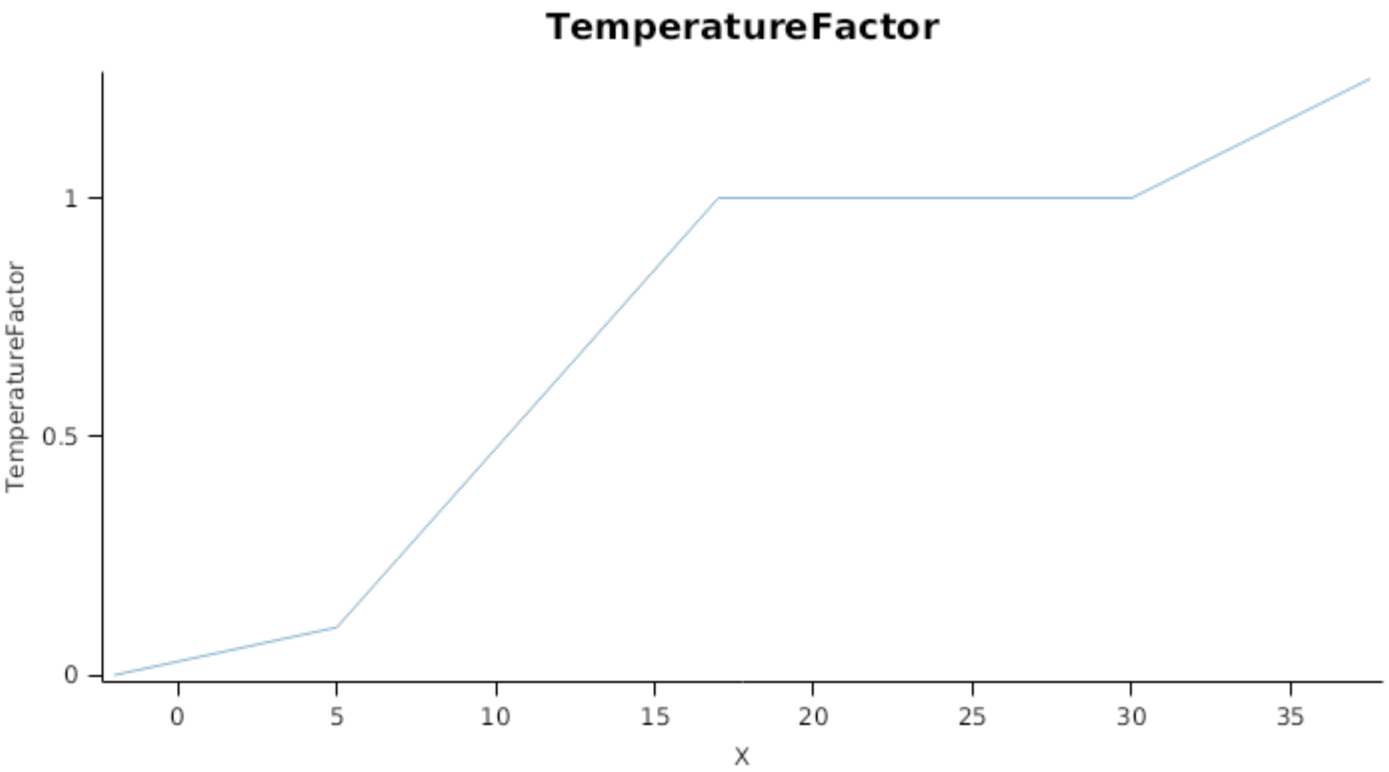
SenescenceRate = *ReferenceRate* x *TemperatureFactor* x *SoilMoistureFactor* x *SoilAerationFactor*

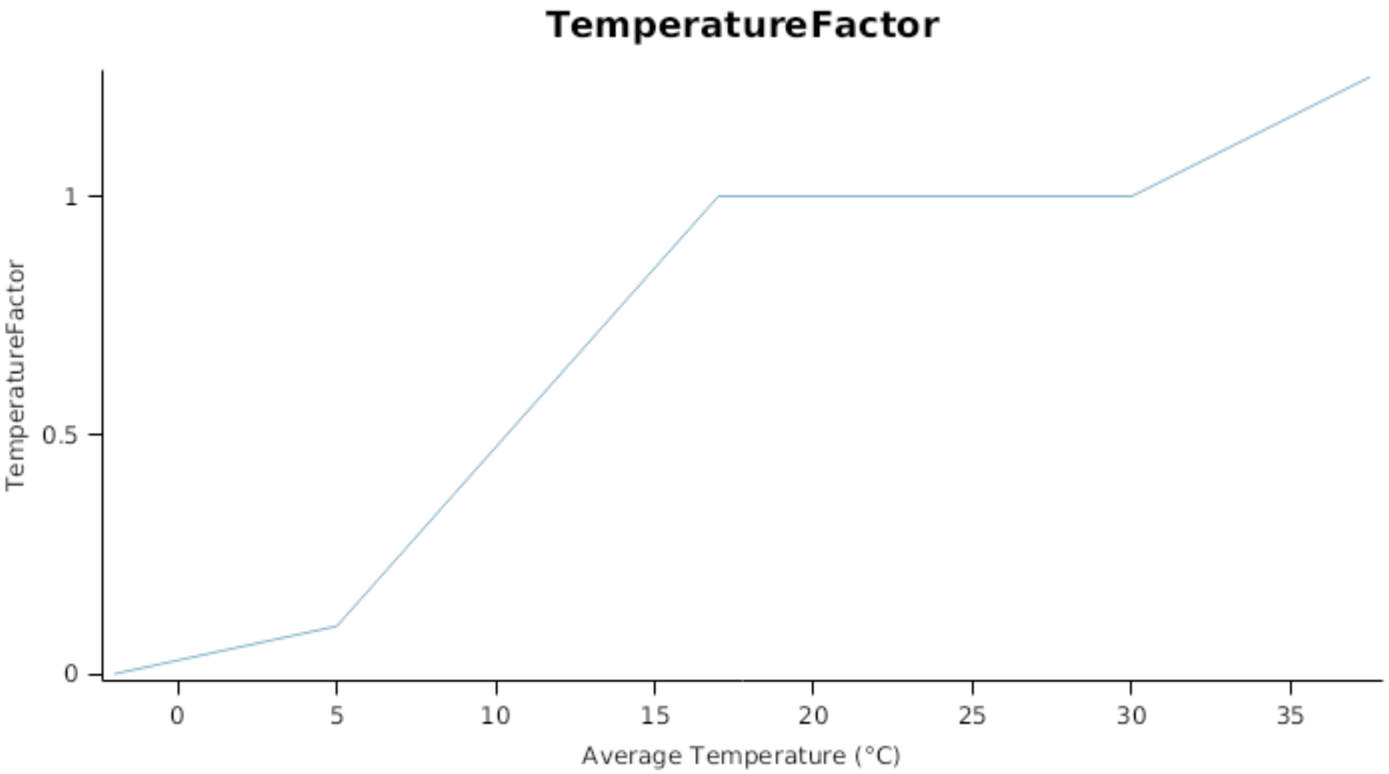
ReferenceRate = 0.02 (/day)

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

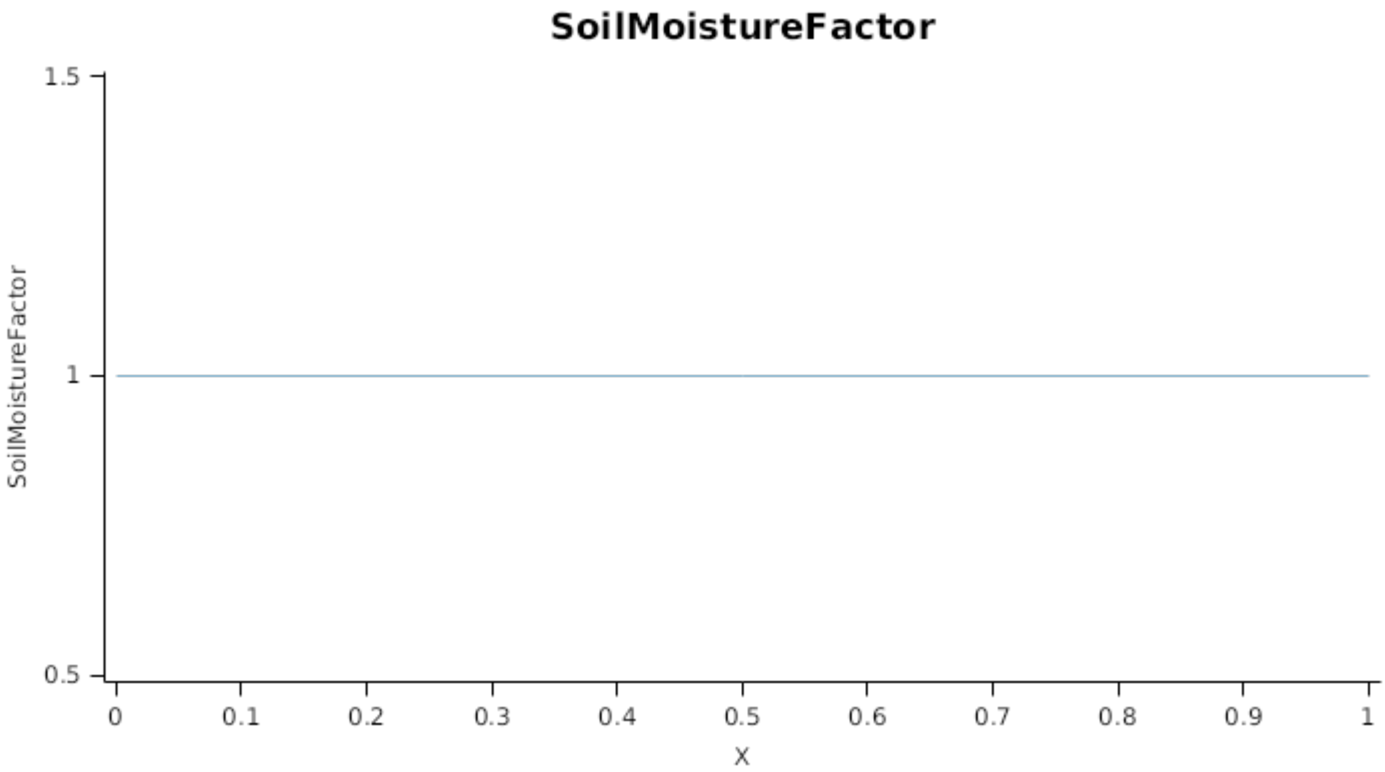
X	TemperatureFactor
-2.0	0.0
5.0	0.1
17.0	1.0
30.0	1.0
37.5	1.2





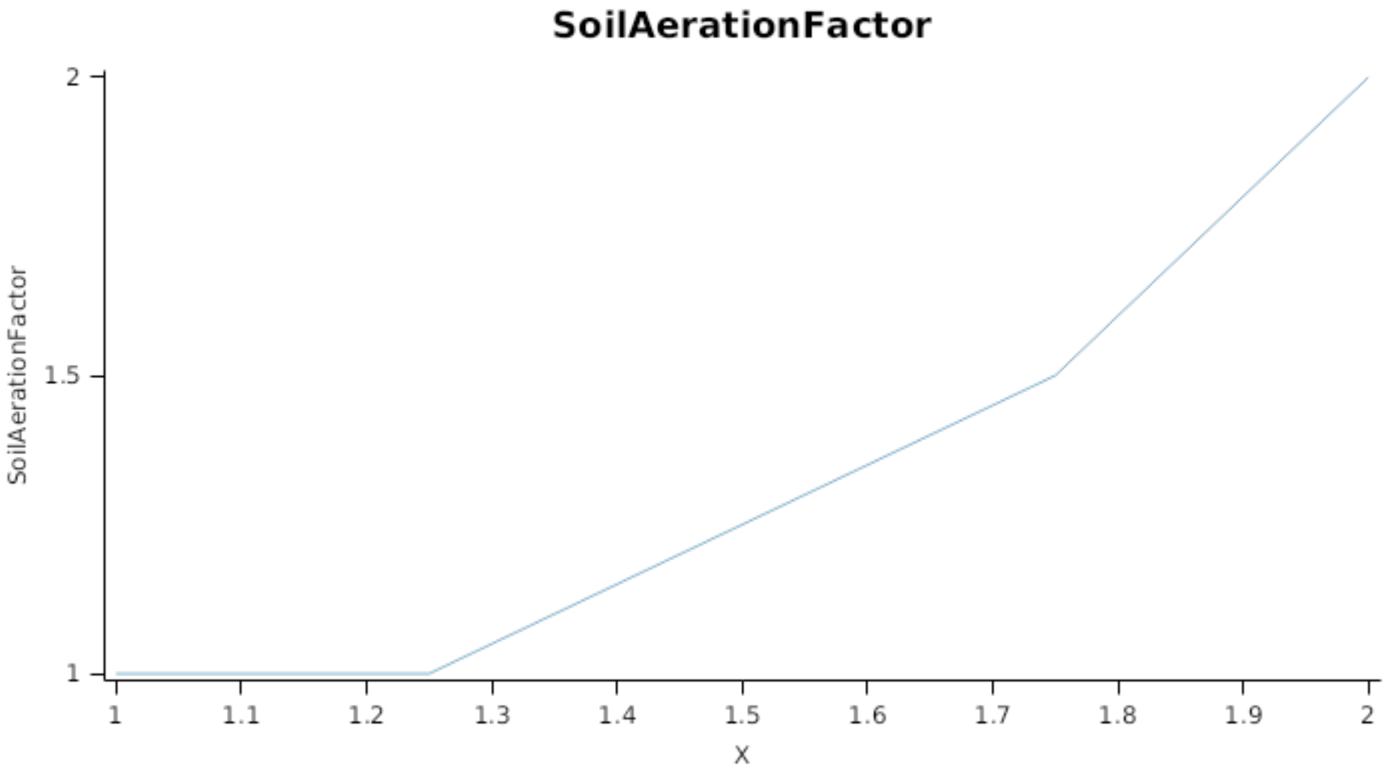
SoilMoistureFactor is calculated using linear interpolation

X	**SoilMoistureFactor**
0.0	1.0
0.5	1.0
1.0	1.0



SoilAerationFactor is calculated using linear interpolation

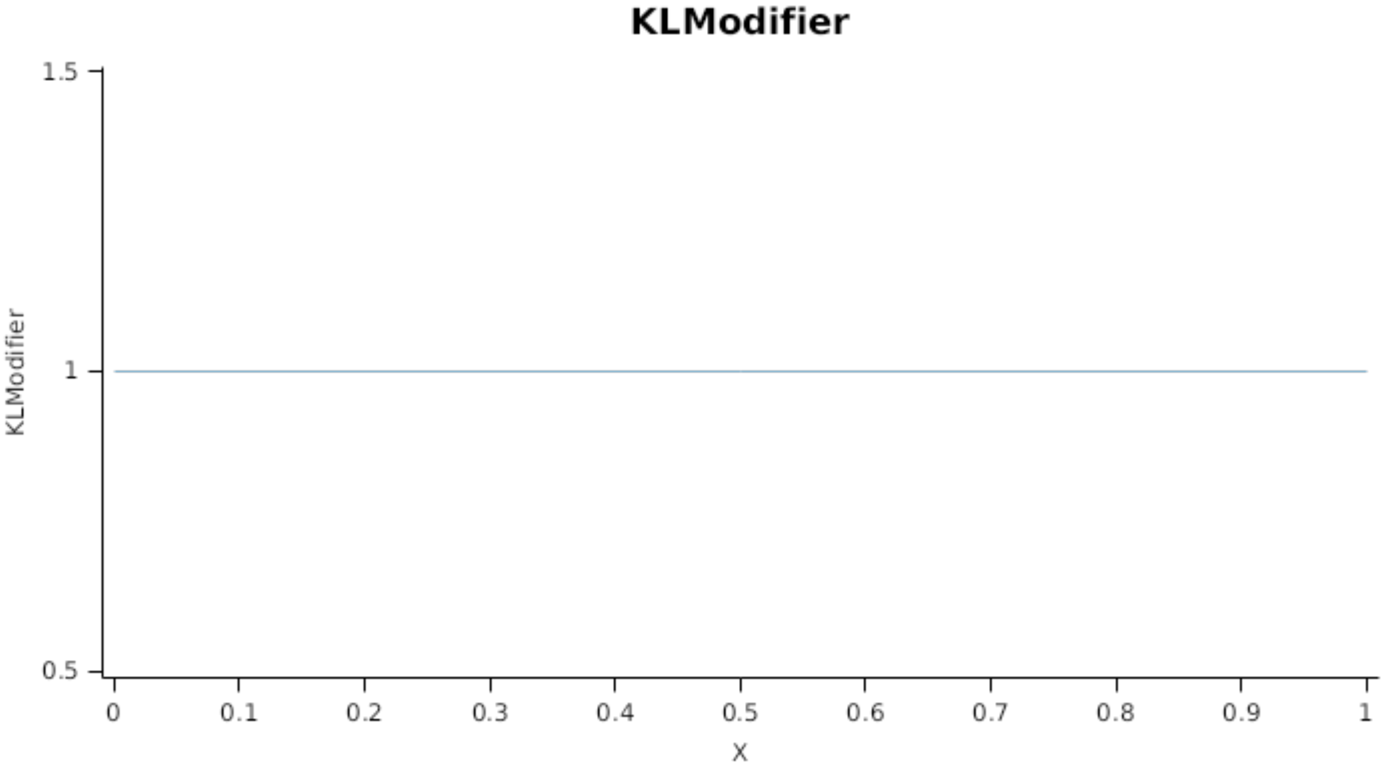
X	SoilAerationFactor
1.0	1.0
1.2	1.0
1.8	1.5
2.0	2.0



1.14.15 KLModifier

KLModifier is calculated using linear interpolation

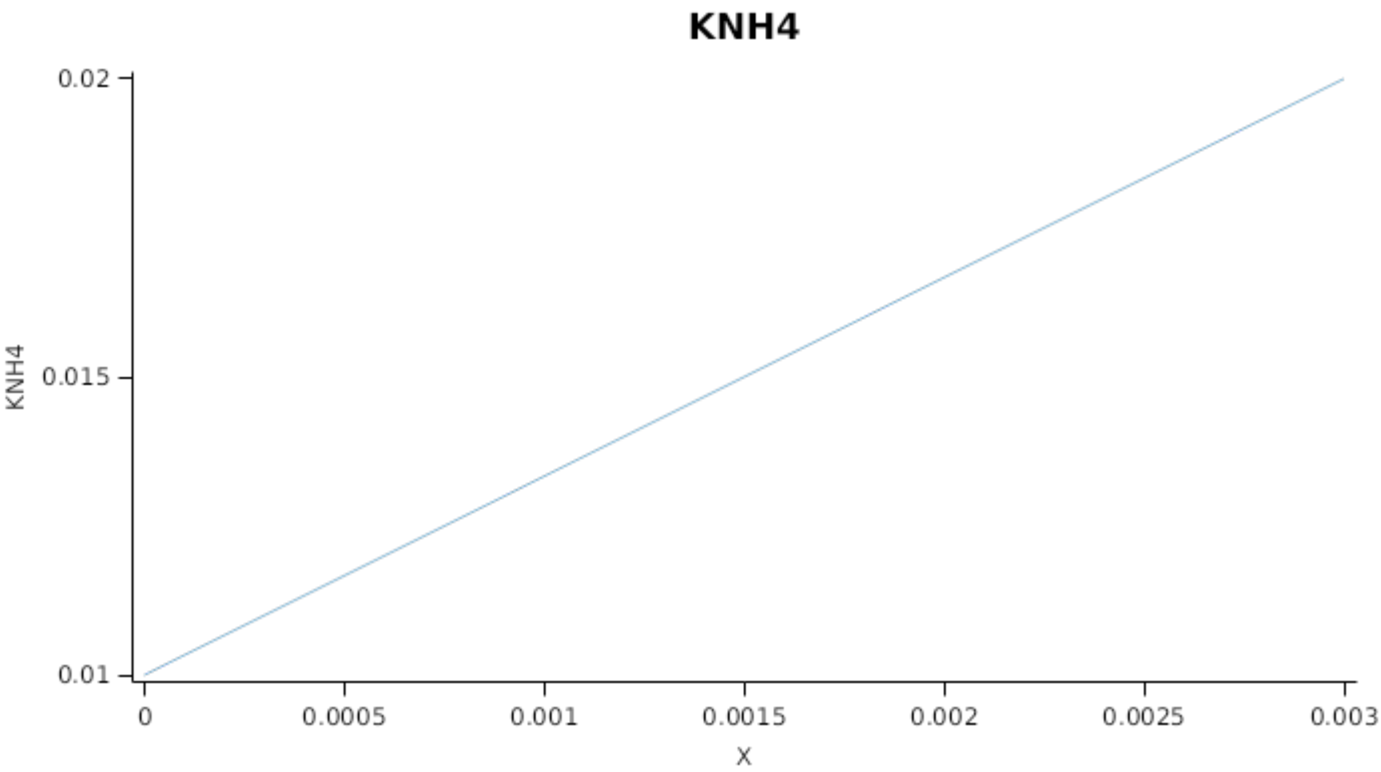
X	KLModifier
0.0	1.0
1.0	1.0



1.14.16 KNH4

KNH4 is calculated using linear interpolation

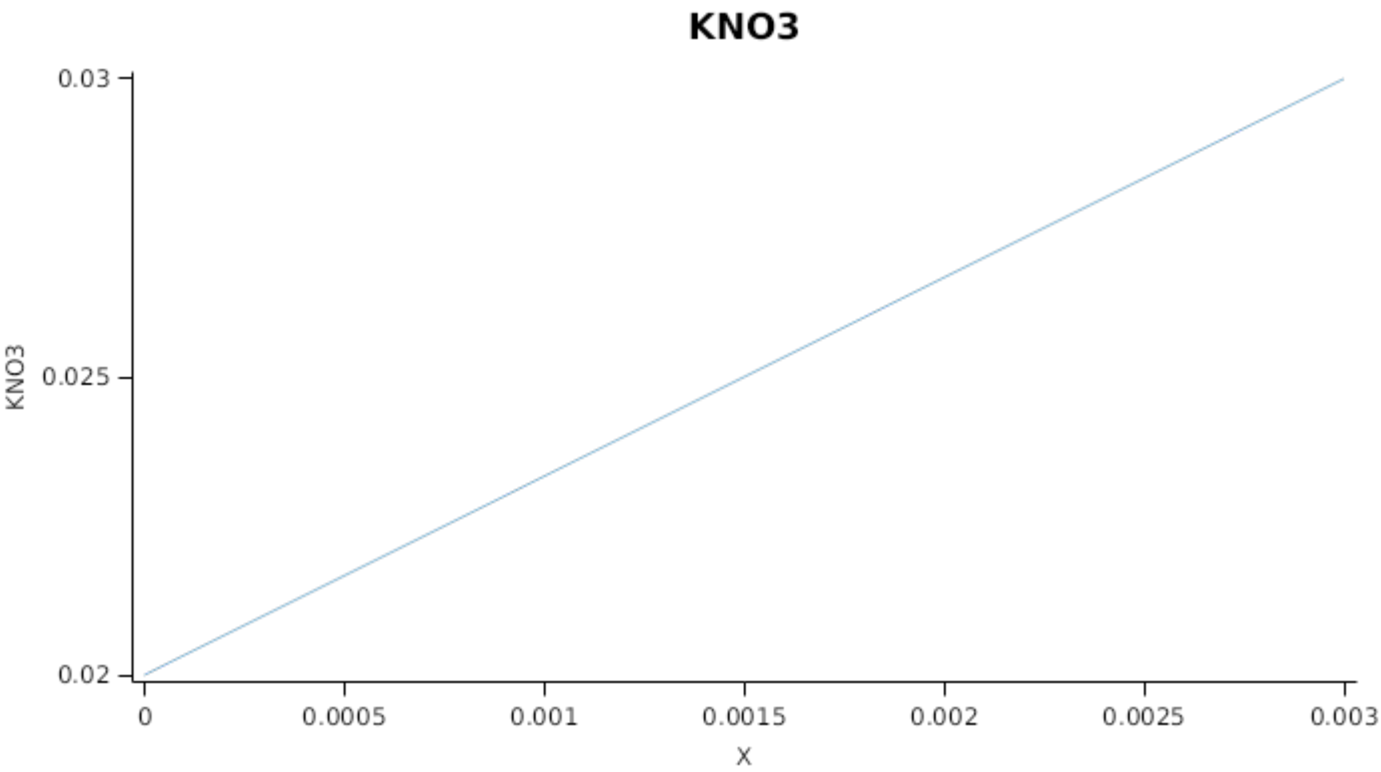
X	KNH4
0.0	0.0
0.0	0.0



1.14.17 KNO3

KNO3 is calculated using linear interpolation

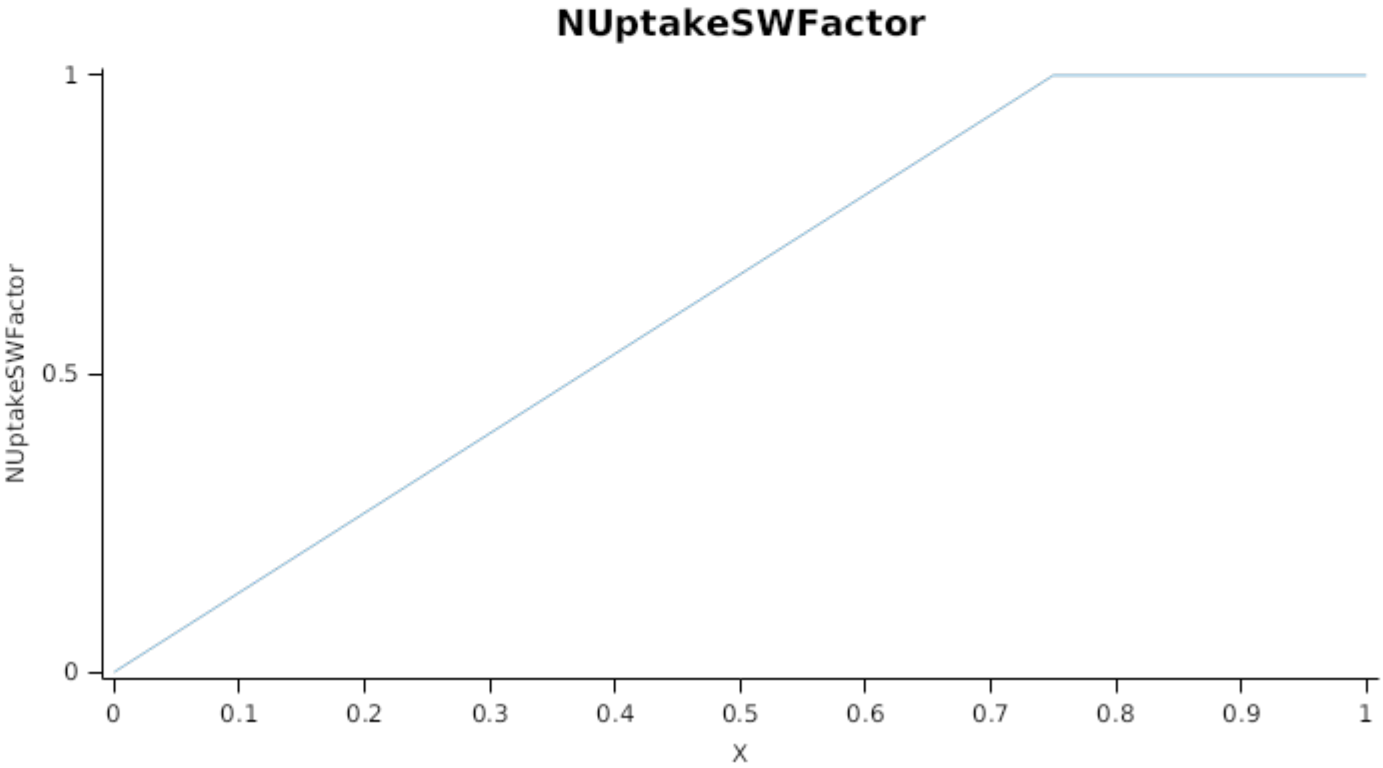
X	KNO3
0.0	0.0
0.0	0.0



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 white clover seeds varies between 0.5 and 0.8 g/1000 seeds (Thomas, 1987; Bissuel-Belaygue et al., 2002; 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
* Stolon
* 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
* Stolon
* 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
* Stolon
* 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
* Stolon
* 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
* Stolon
* 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
* Stolon
* 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 ratio 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 white clover show a considerable variability, with values between 1.5 to 8.0 for a wide range of conditions (Hart, 1987; Gourley et al., 1993; Almeida et al., 1999; de Neergaard et al., 2004; den Hollander et al., 2007; Murray, 2012; Crush et al., 2015). For typical enviromental conditions the data suggest a mean value around 2.5-3.5 for adult plants. This value can be affected by environmental conditions, with water or nutrient deficiency inducing greater root growth, while low light conditions lead to a higher allocation above ground. The current model does not explicitly consider these variations, this should be upgraded when more specific data becomes available.

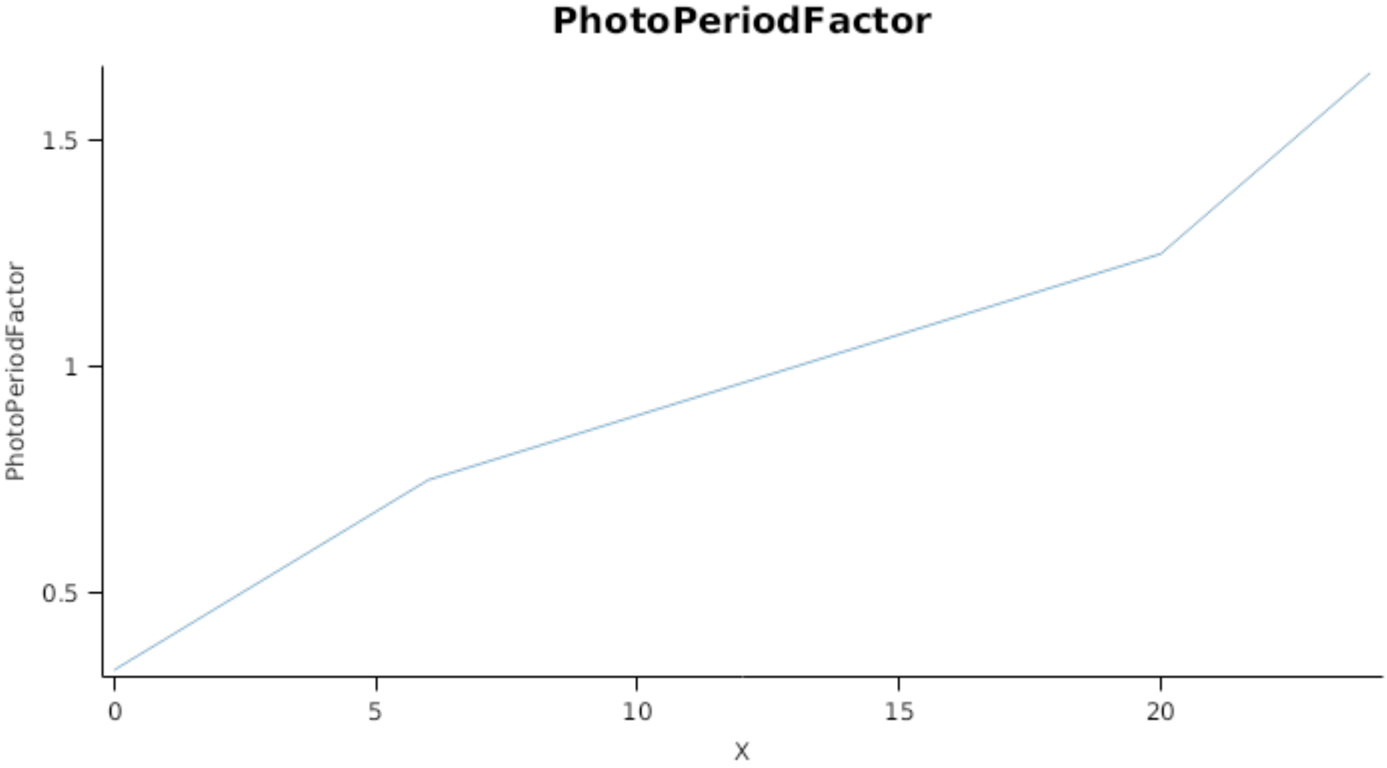
AllPhases has a value between Emergence and Ripening calculated as:

TargetSR = *MeanSR* x *PhotoPeriodFactor*

MeanSR = 3 (g/g)

PhotoPeriodFactor is calculated using linear interpolation

X	PhotoPeriodFactor
0.0	0.3
6.0	0.8
13.0	1.0
20.0	1.2
24.0	1.6



1.26 TargetAboveGroundFraction

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. This is in accord with the biomass allocation plasticity approach (e.g. Wilson, 1988; Levang-Brilz et al., 2002). The approach ensures that biomass allocation is shifted to the appropriate organs when the balance is disturbed, especially important for recovery after defoliation. Studies have show that white clover, unlike most plants, has a relatively fixed proportion of biomass above ground, even during reproductive phase (e.g. Thomas, 1980). The model uses the target shoot-to-root ratio to compute the proportion of biomass above ground (e.g. Johnson et al., 1987).

TargetAboveGroundFraction = [TargetShootRootRatio] / *TotalRatio*

TotalRatio = 1 + [TargetShootRootRatio]

1.27 Cultivars

1.27.1 Huia

Huia overrides the following properties:

1.27.2 Kopu

Kopu overrides the following properties:

[Phenology].ThermalTime.Response.X = 2.5,25,37.5

[Phenology].ThermalTime.Response.X = 0,22.5,0

[Leaf].Photosynthesis.FT.XYPairs.X = 0,2.5,7.5,15,18,27,35,37.5

[Leaf].TargetBiomassProportion.VegetativeInductive.TargetProportion.FixedValue = 0.45

[Leaf].Tallness.XYPairs.Y = 20,75,110,140,150

[Petiole].TargetBiomassProportion.VegetativeInductive.TargetProportion.ProportionToLeaves.FixedValue = 0.667

[Stolon].BiomassRemovalDefaults.Graze.FractionLiveToRemove = 0.2

[Taproot].TargetBiomassProportion.AllPhases.TargetProportion.BaseProportion.FixedValue = 0.1

[Root].MaximumRootDepth.FixedValue = 750

[Root].SpecificRootLength.FixedValue = 100

[TargetShootRootRatio].AllPhases.TargetSR.MeanSR.FixedValue = 3.0

1.27.3 Tahora

Tahora overrides the following properties:

[Phenology].ThermalTime.Response.X = 0,21,32

[Phenology].ThermalTime.Response.X = 0,21,0

[Leaf].Photosynthesis.FT.XYPairs.X = -1,0,5,12.5,15.5,24.5,32.5,35

[Leaf].TargetBiomassProportion.VegetativeInductive.TargetProportion.FixedValue = 0.4

[Leaf].Tallness.XYPairs.Y = 20,50,75,97.5,104

[Petiole].TargetBiomassProportion.VegetativeInductive.TargetProportion.ProportionToLeaves.FixedValue = 0.85

[Stolon].BiomassRemovalDefaults.Graze.FractionLiveToRemove = 0.05

[Taproot].TargetBiomassProportion.AllPhases.TargetProportion.BaseProportion.FixedValue = 0.05

[Root].MaximumRootDepth.FixedValue = 500

[Root].SpecificRootLength.FixedValue = 100

1.27.4 Apex

Apex overrides the following properties:

[Phenology].ThermalTime.Response.X = 2.5,25,37.5

[Phenology].ThermalTime.Response.X = 0,22.5,0

[Leaf].Photosynthesis.FT.XYPairs.X = 0,2.5,7.5,15,18,27,35,37.5

[Leaf].TargetBiomassProportion.VegetativeInductive.TargetProportion.FixedValue = 0.45

[Leaf].Tallness.XYPairs.Y = 20,65,100,130,135

[Petiole].TargetBiomassProportion.VegetativeInductive.TargetProportion.ProportionToLeaves.FixedValue = 0.7

[Stolon].BiomassRemovalDefaults.Graze.FractionLiveToRemove = 0.05

[Taproot].TargetBiomassProportion.AllPhases.TargetProportion.BaseProportion.FixedValue = 0.1

[Root].MaximumRootDepth.FixedValue = 950

[Root].SpecificRootLength.FixedValue = 100

1.28 MortalityRate

MortalityRate = 0

2 Validation

The performance of the white clover model is evaluated in simulations based on experiments conducted in New Zealand.

2.1 New Zealand

2.1.1 All data from New Zealand

##Discussion##

The results show that the model was able to capture the general growth pattern and the cumulative amounts of herbage harvested. Given the large uncertainties that measurements of plant biomass have, it is generally more appropriate to compare season cumulative values instead of values for individual measurements. The experimental results showed no significant effect of N fertilisation on biomass accumulation, which was expected as white clover can compensate for those variations through biological N fixation.
The values for N content were also highly variable, and they did show some response to fertilisation. The model results also shows similar response, but the general pattern was not we described by the model. The way the model computes demand and remobilisation of N seems to be a specific part of the model that still needs improvement.

List of experiments.

Experiment Name	Design (Number of Treatments)
FRNLLincoln	NRate (6)
FRNLRuakura	NRate (6)

2.1.2 FRNLLincoln

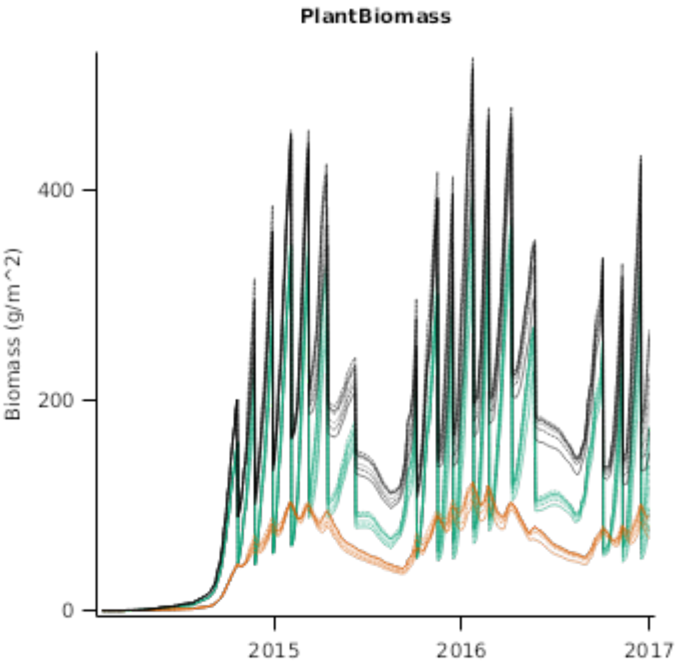
###Presentation###

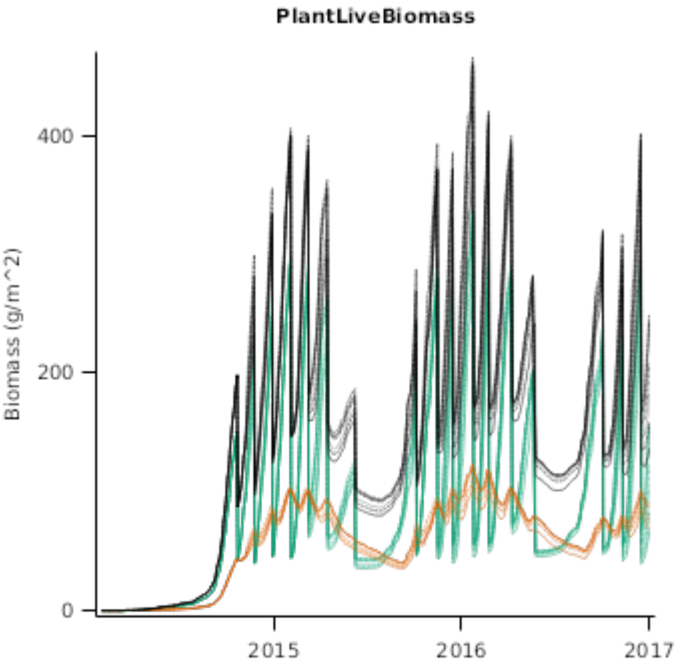
The simulation setup was based on a field trial performed at Lincoln University Research Dairy Farm, New Zealand, between 2014 and 2016. The experiment was part of the FRNL (Forages for Reduced Nitrogen Leaching) program (for more details see Martin et al., 2017). Here only plots with pure white clover are used.
The experiment consisted of six fertiliser treatments with four replicates. The nominal N rates were 0, 50, 100, 200, 350 and 500 kg/ha/yr, but the actual amounts applied varied as each application was linked to a defoliation event, the plan was to have 10 defoliation per year, but this was not possible, with seven events actually happening for white clover. The plots were mown at a height of about 4 cm and the harvested herbage was removed from the plots. The measurements comprised of dry matter yield and quality indicators (here herbage N content is used).
Data and general management of the experiment was supplied by Grant Edwards, Lincoln University.

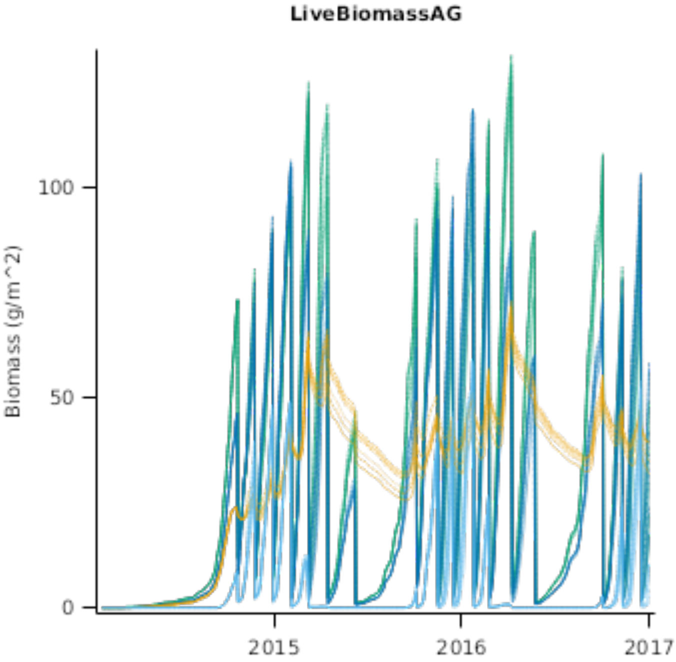
The soil at the experimental site was a Templeton fine sandy loam (an Immature Pallic soil, USDA: Udic Haplustept), the required parameters were inferred based on data from the New Zealand National Soils Database (Landcare Research). Weather data was obtained from nearby Broadfield weather station (NIWA).

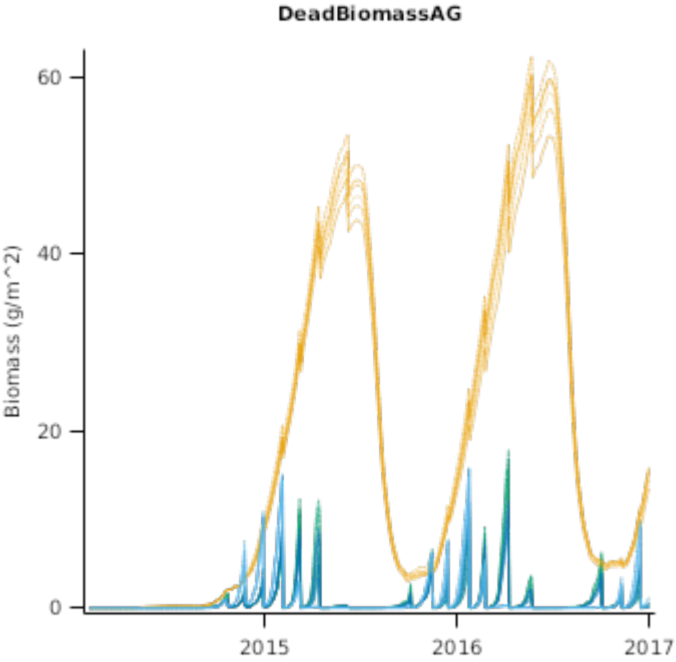
2.1.2.1 Results

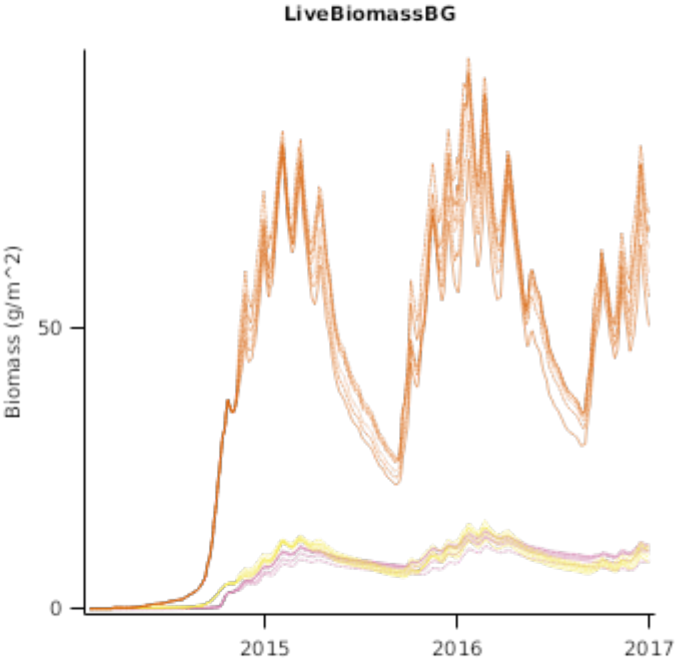
2.1.2.1.1 PlantDM

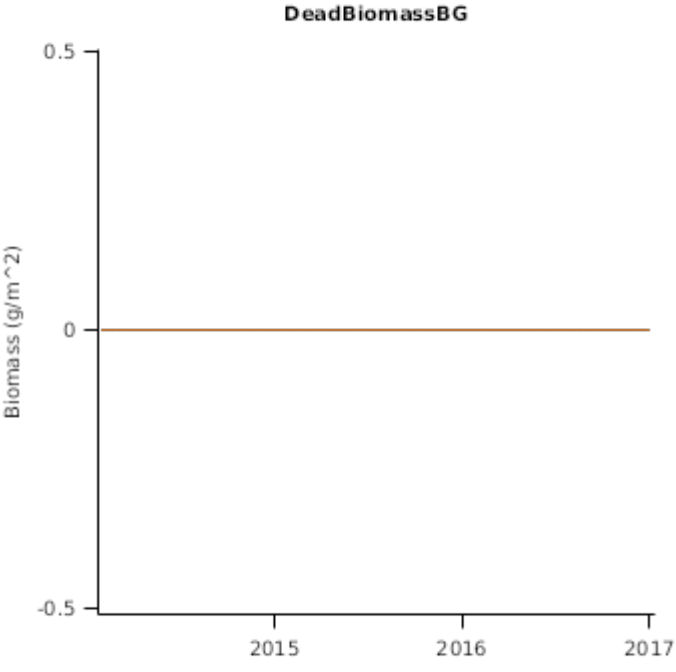

PlantBiomass


PlantLiveBiomass

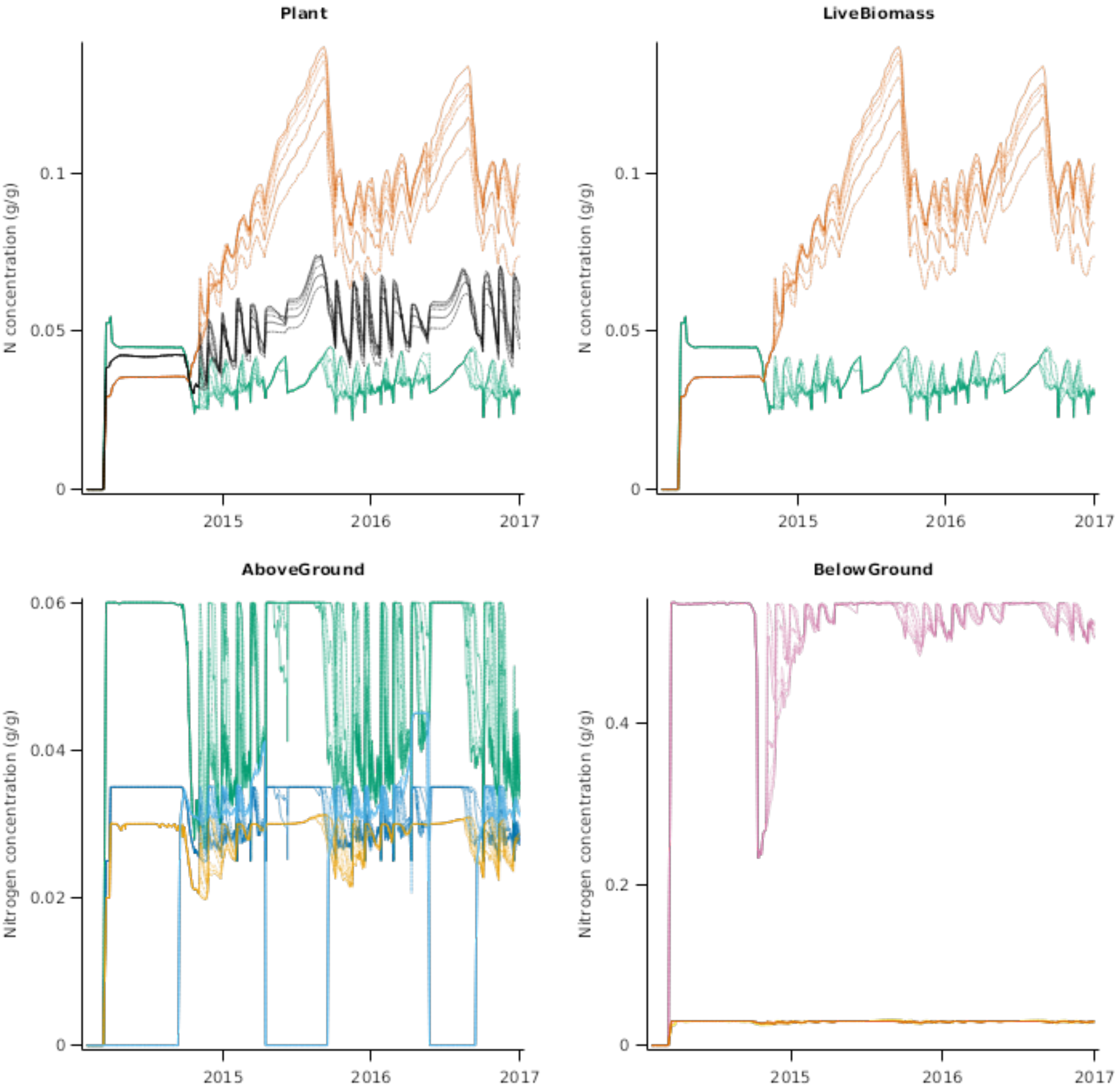

LiveBiomassAG


DeadBiomassAG

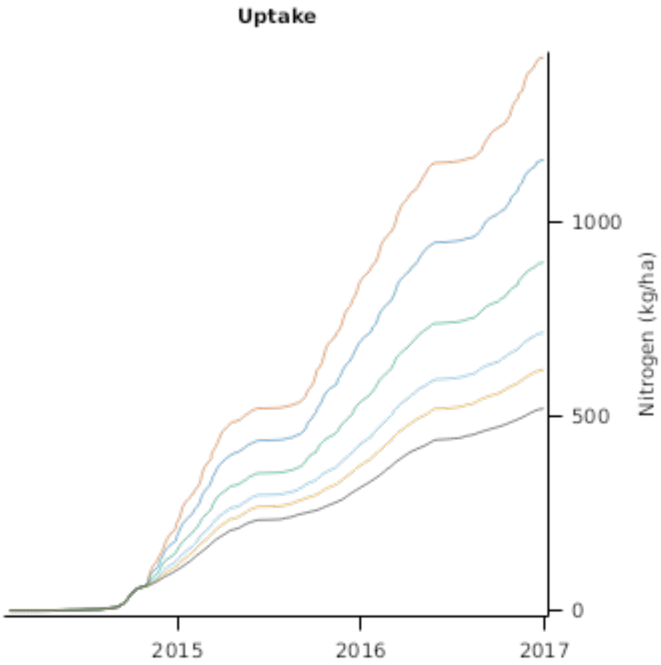

LiveBiomassBG

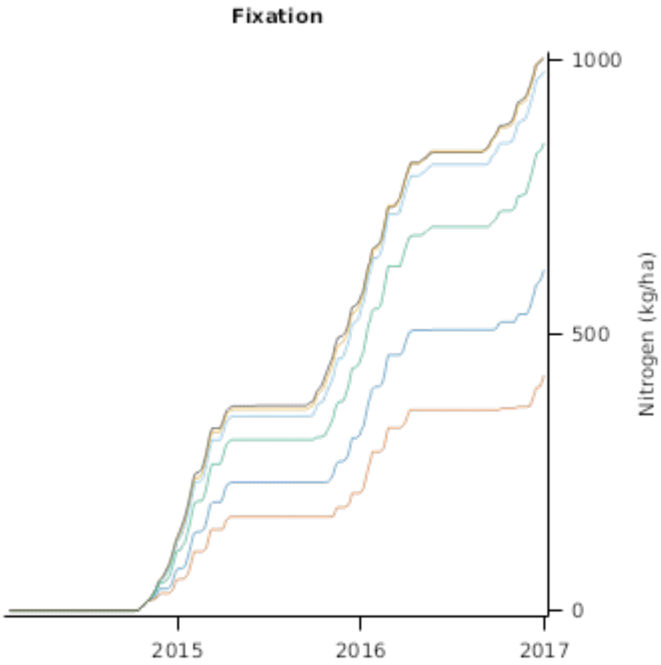

DeadBiomassBG

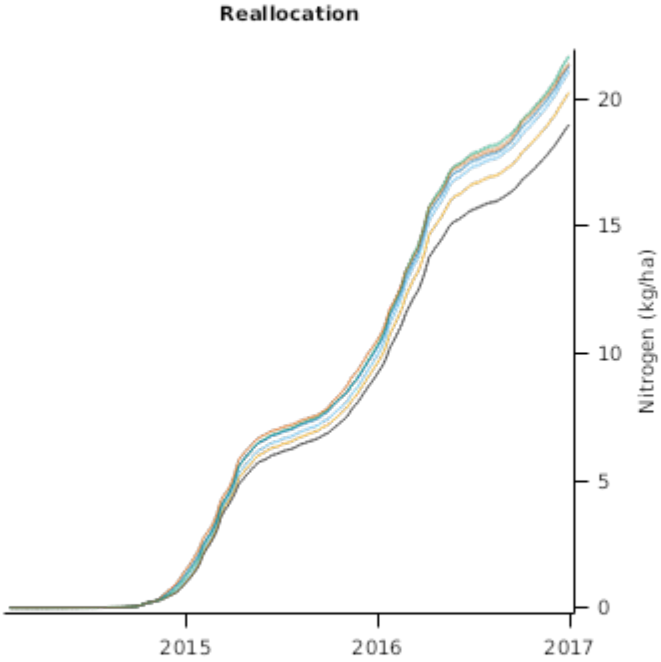
2.1.2.1.2 PlantNc

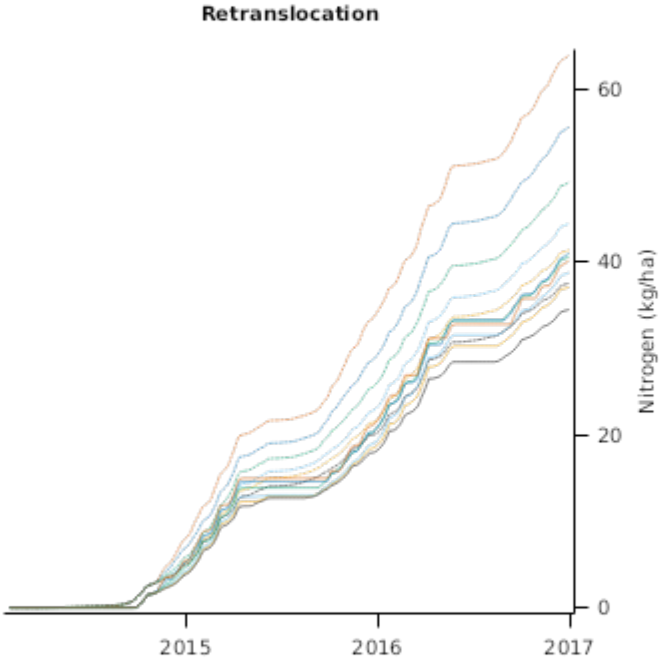


2.1.2.1.3 NSupply





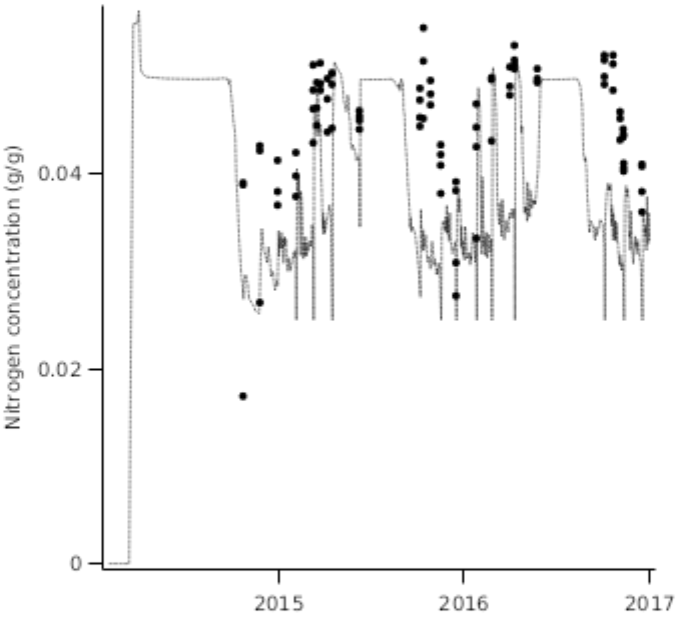




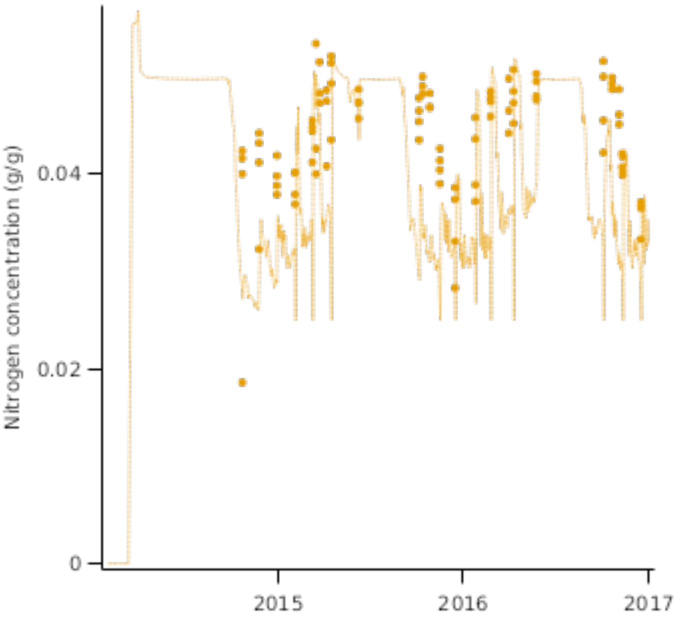
2.1.2.2 ObservedResults

2.1.2.2.1 Nconcentration

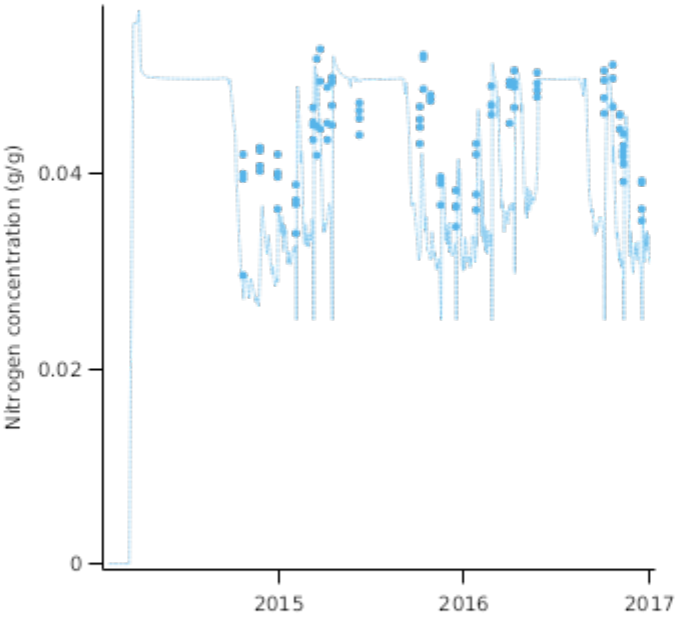
HerbageNc_R0



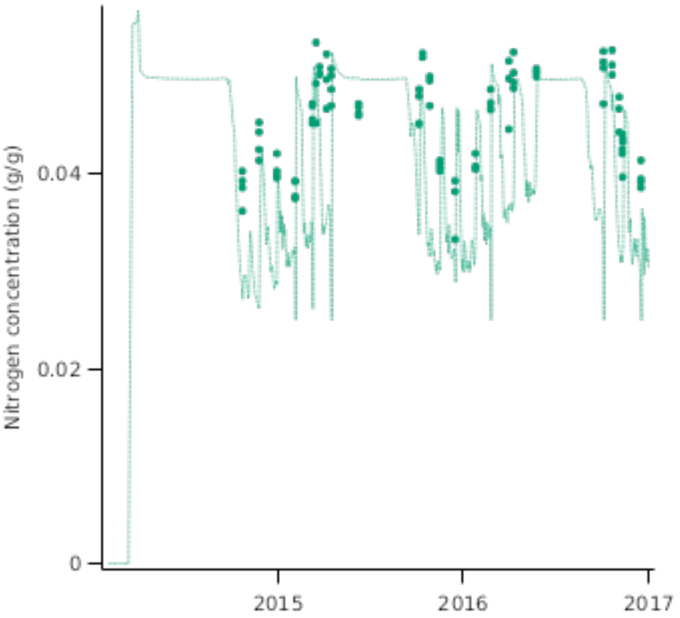
HerbageNc_R50



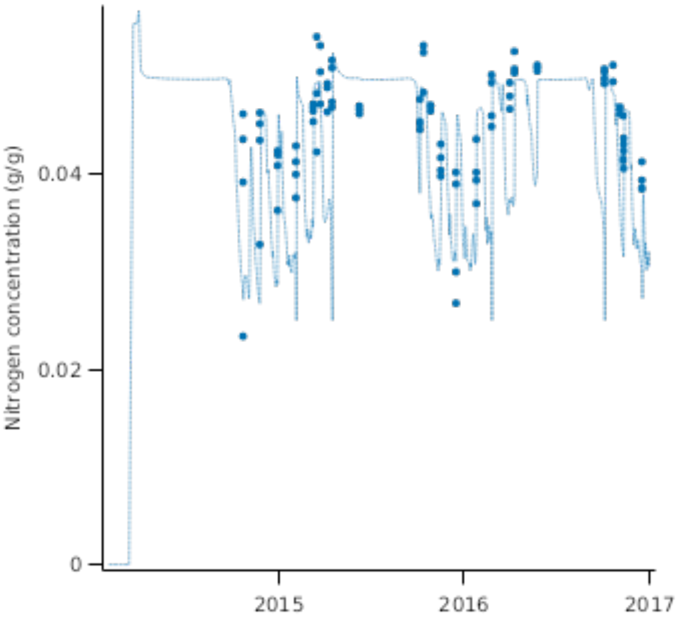
HerbageNc_R100



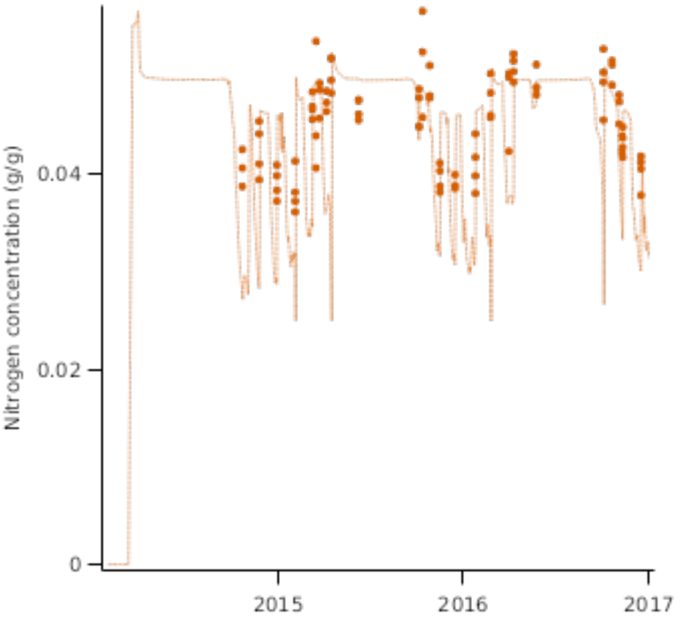
HerbageNc_R200



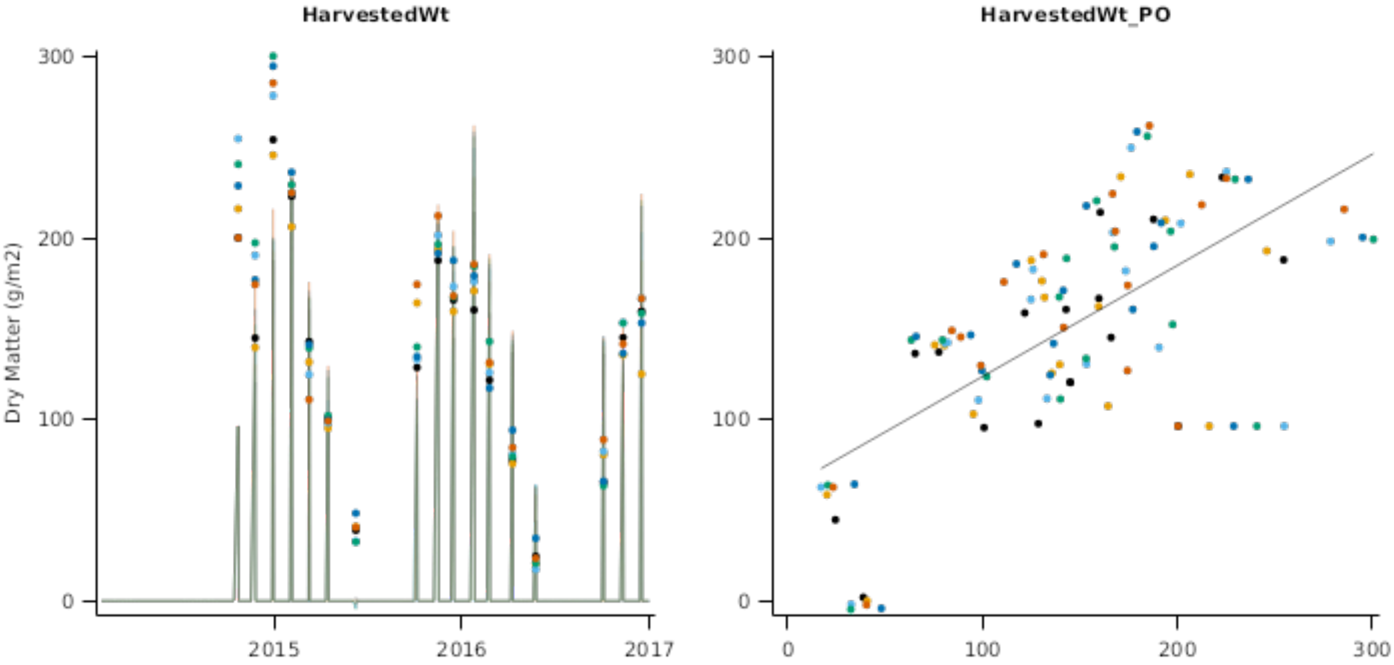
HerbageNc_R350

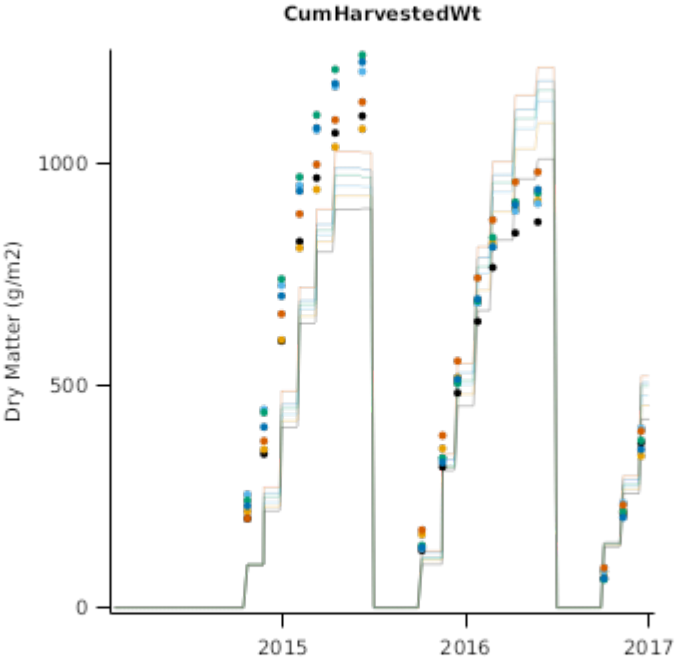


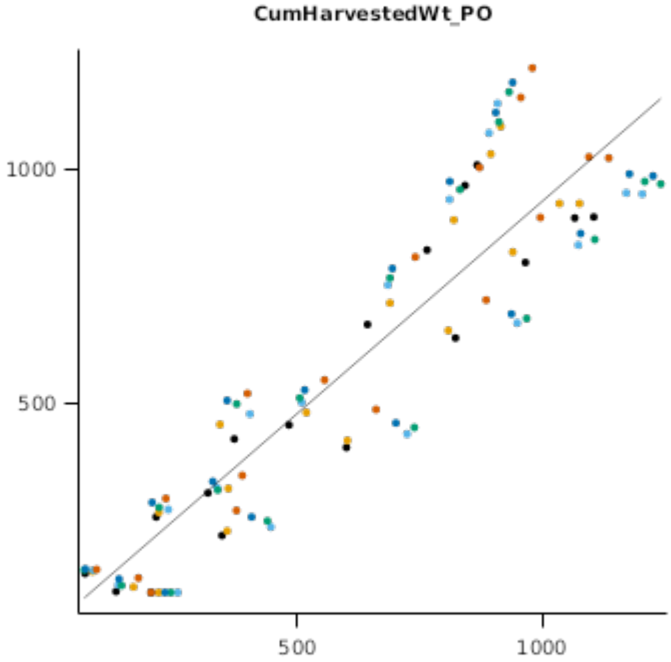
HerbageNc_R500

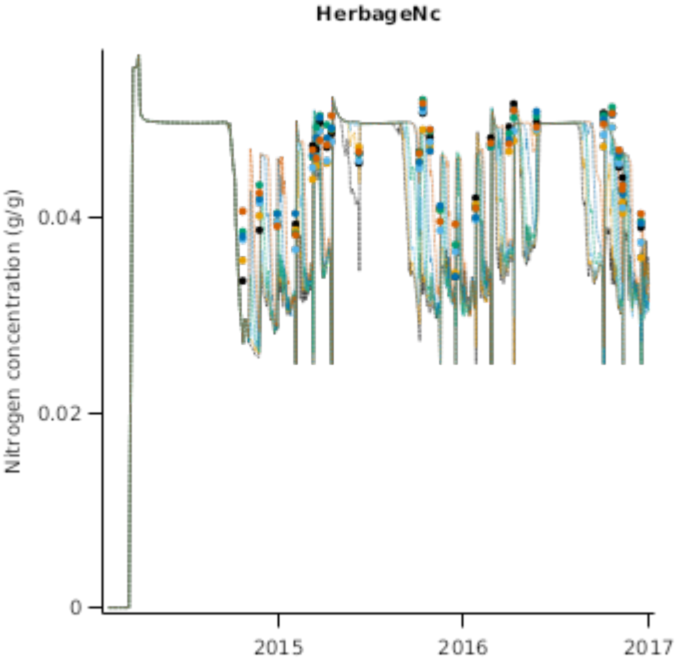


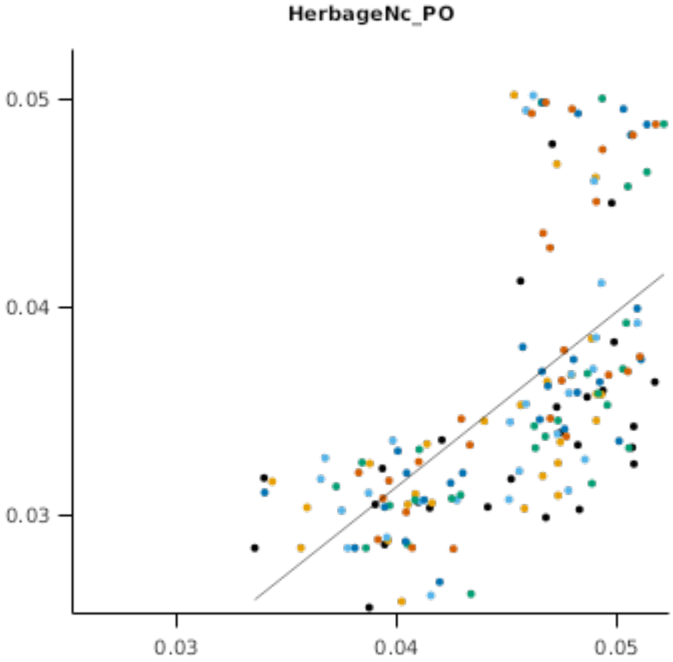
2.1.2.3 ObservedMeans

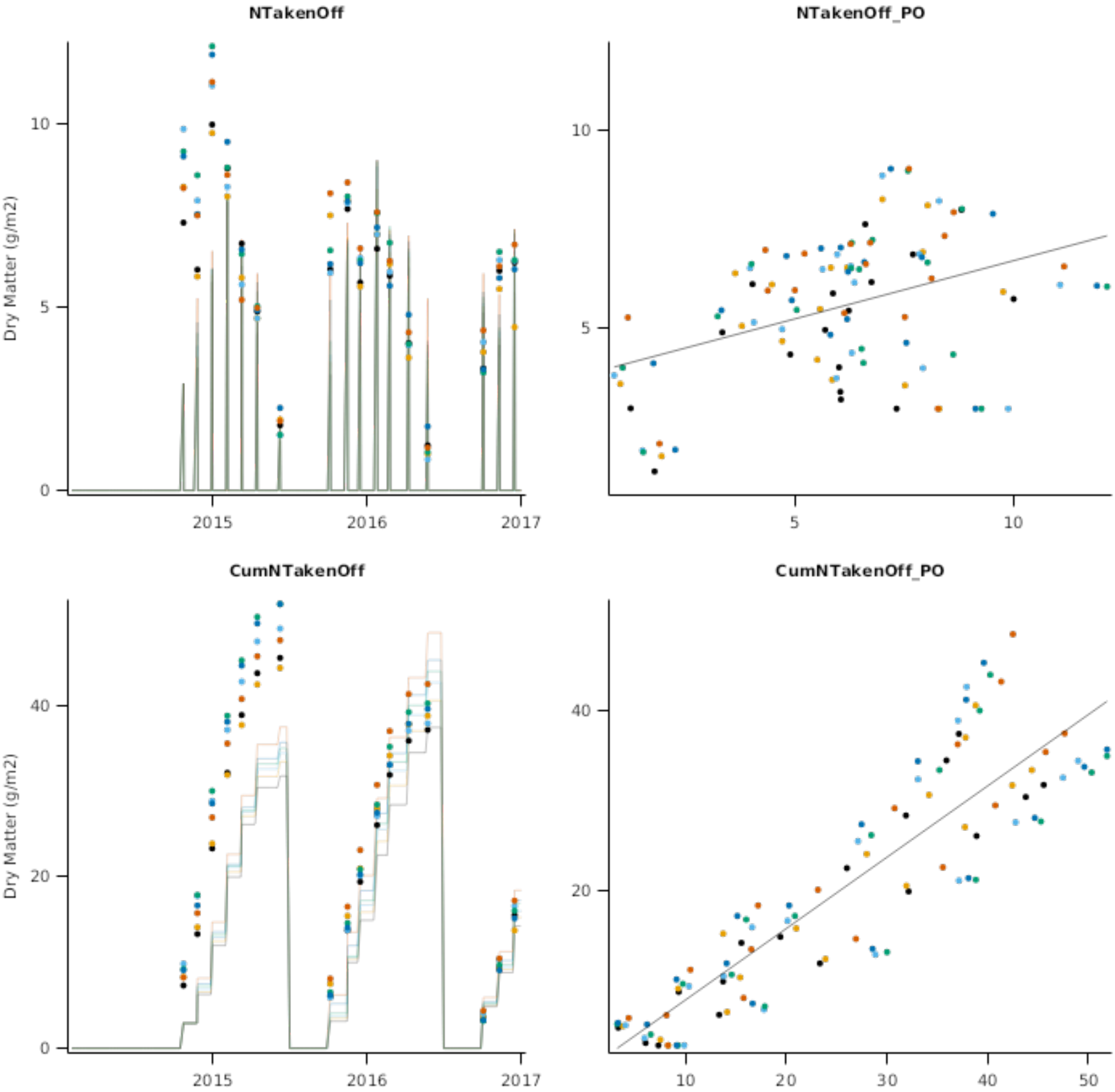



CumHarvestedWt
Dry Matter (g/m2)
0
500
1000
2015
2016
2017


CumHarvestedWt_PO
500
1000
500
1000


HerbageNc
Nitrogen concentration (g/g)
0
0.02
0.04
2015
2016
2017


HerbageNc_PO
0.03
0.04
0.05
0.03
0.04
0.05



NTakenOff

NTakenOff_PO

CumNTakenOff

CumNTakenOff_PO

2.1.3 FRNLRuakura

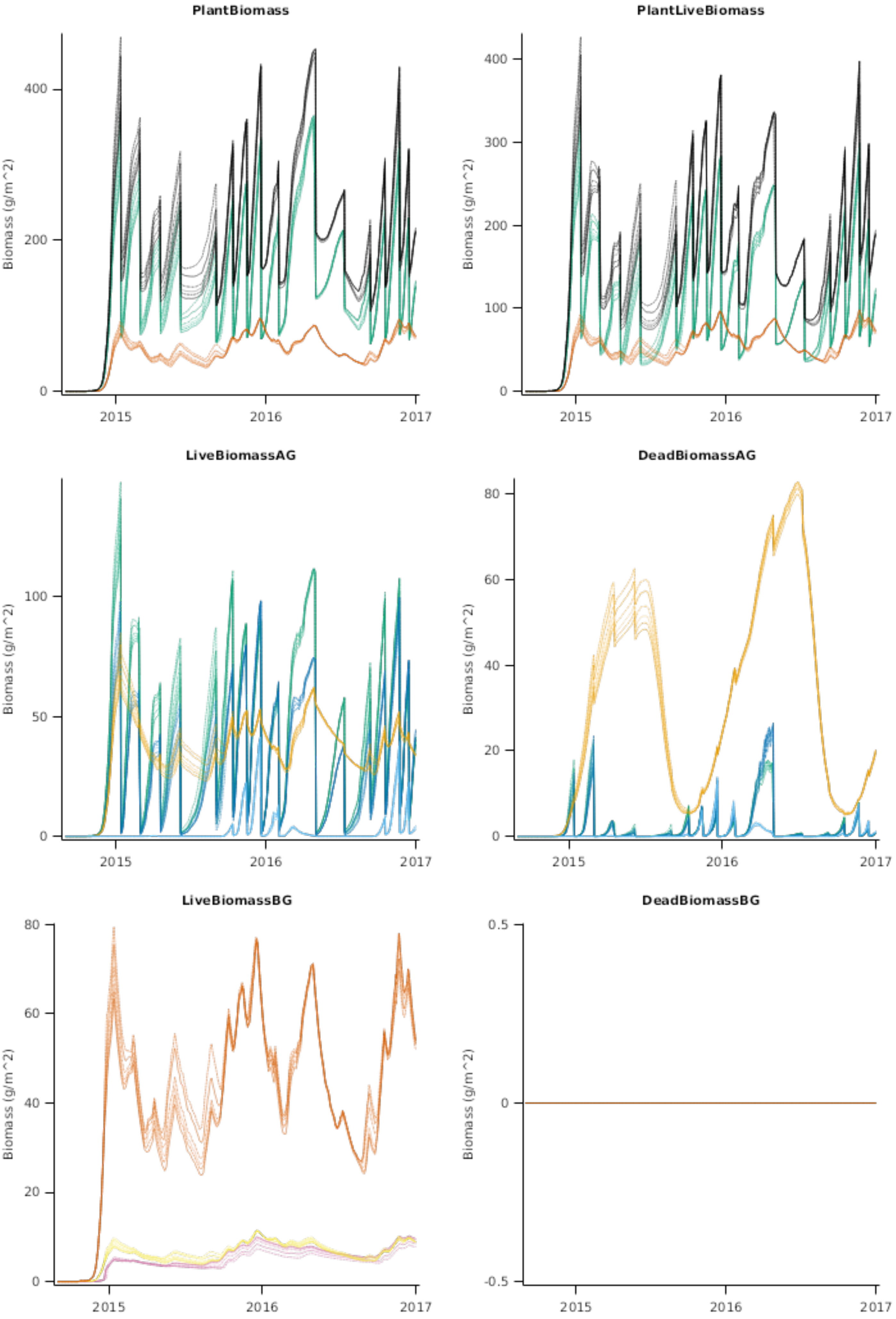
###Presentation###

This simulation setup was based on field trials performed at DairyNZ's Scott Farm, in Ruakura, New Zealand, between 2014 and 2016. The experiment was part of the FRNL (Forages for Reduced Nitrogen Leaching) program and the data is basically unpublished (references will be added when this come about). Here only plots with pure white clover are used. The experiment was set up with six fertiliser treatments and three replicates, with nominal N rates of 0, 50, 100, 200, 350 and 500 kg/ha/yr (actual rate varied). The swards were mown at a a height of approximately 4 cm and the herbage was removed from the plots. The measurements comprised of herbage yield and quality indicators (here N content is used). Observed data supplied by Grant Edwards, Lincoln University.

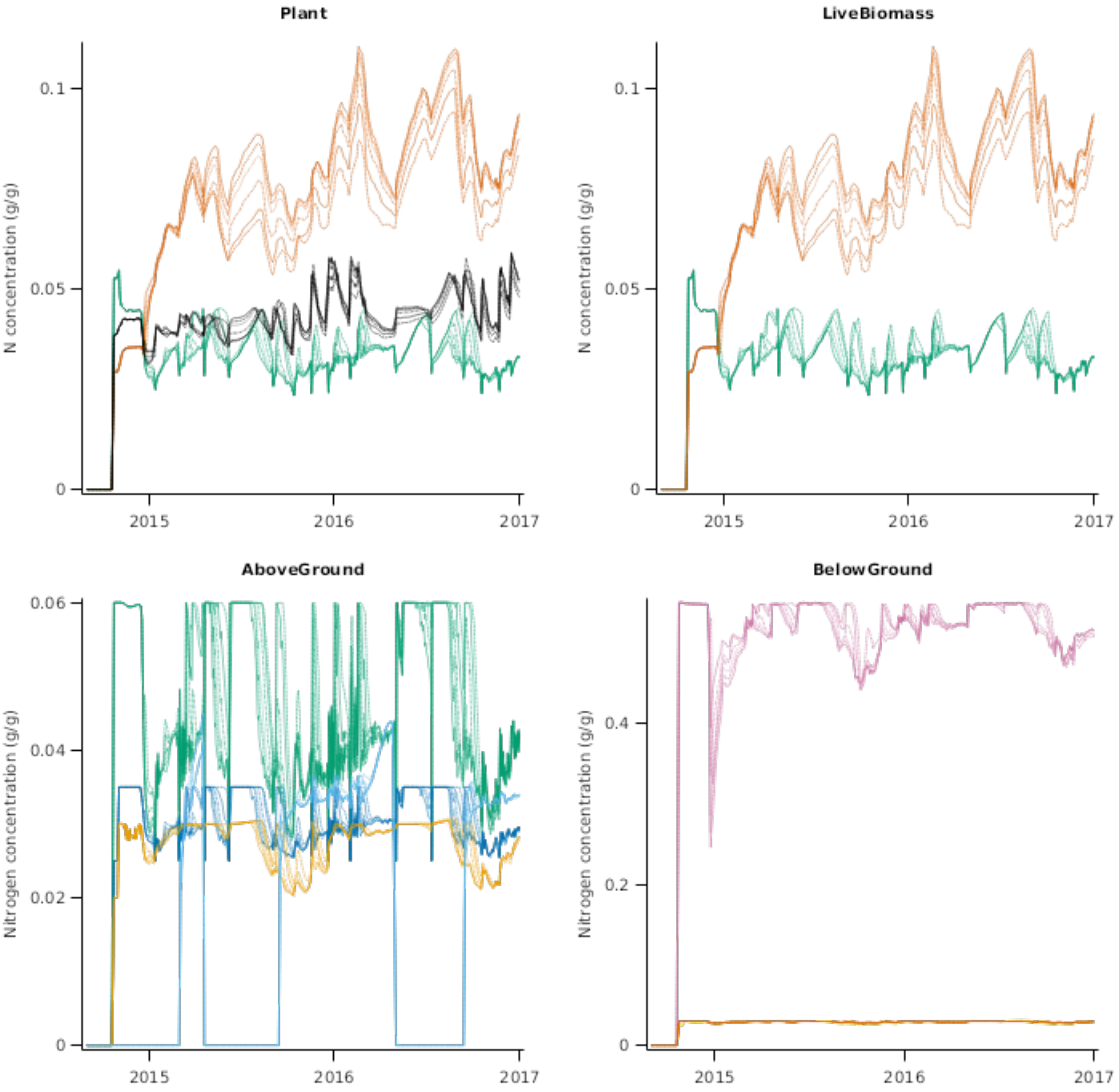
The soil at the experimental site was a Horotiu silt loam (an Orthic Allophanic soil; USDA: Typic Udivitrand), the parameters required were inferred using data from the New Zealand National Soils Database (Landcare Research). Weather data was obtained from nearby Ruakura weather station (NIWA).

2.1.3.1 Results

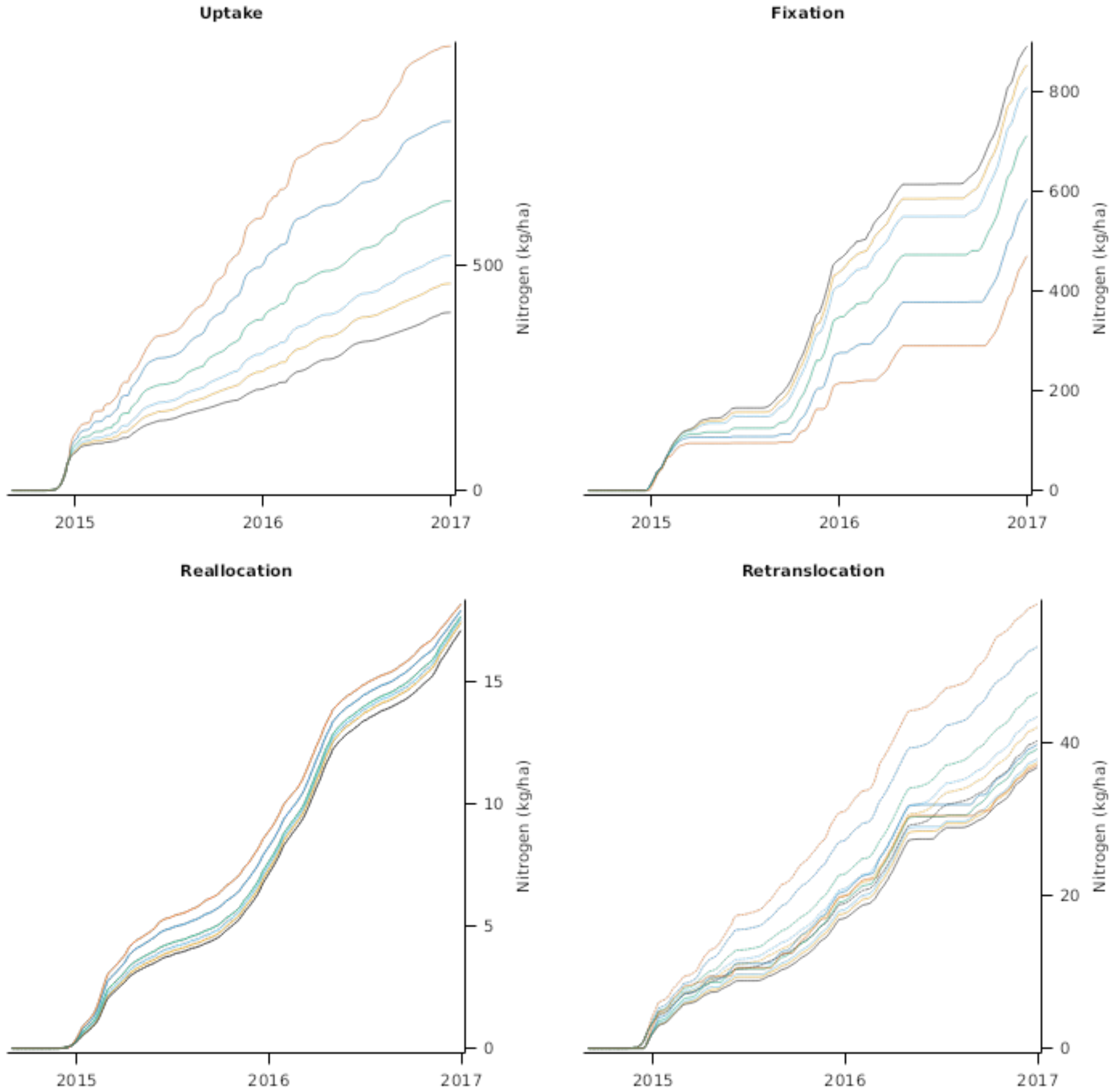
2.1.3.1.1 PlantDM


PlantBiomass
PlantLiveBiomass
LiveBiomassAG
DeadBiomassAG
LiveBiomassBG
DeadBiomassBG
Biomass (g/m^2)
0
200
400
100
300
50
20
40
60
80
0.5
-0.5
2015
2016
2017

2.1.3.1.2 PlantNc

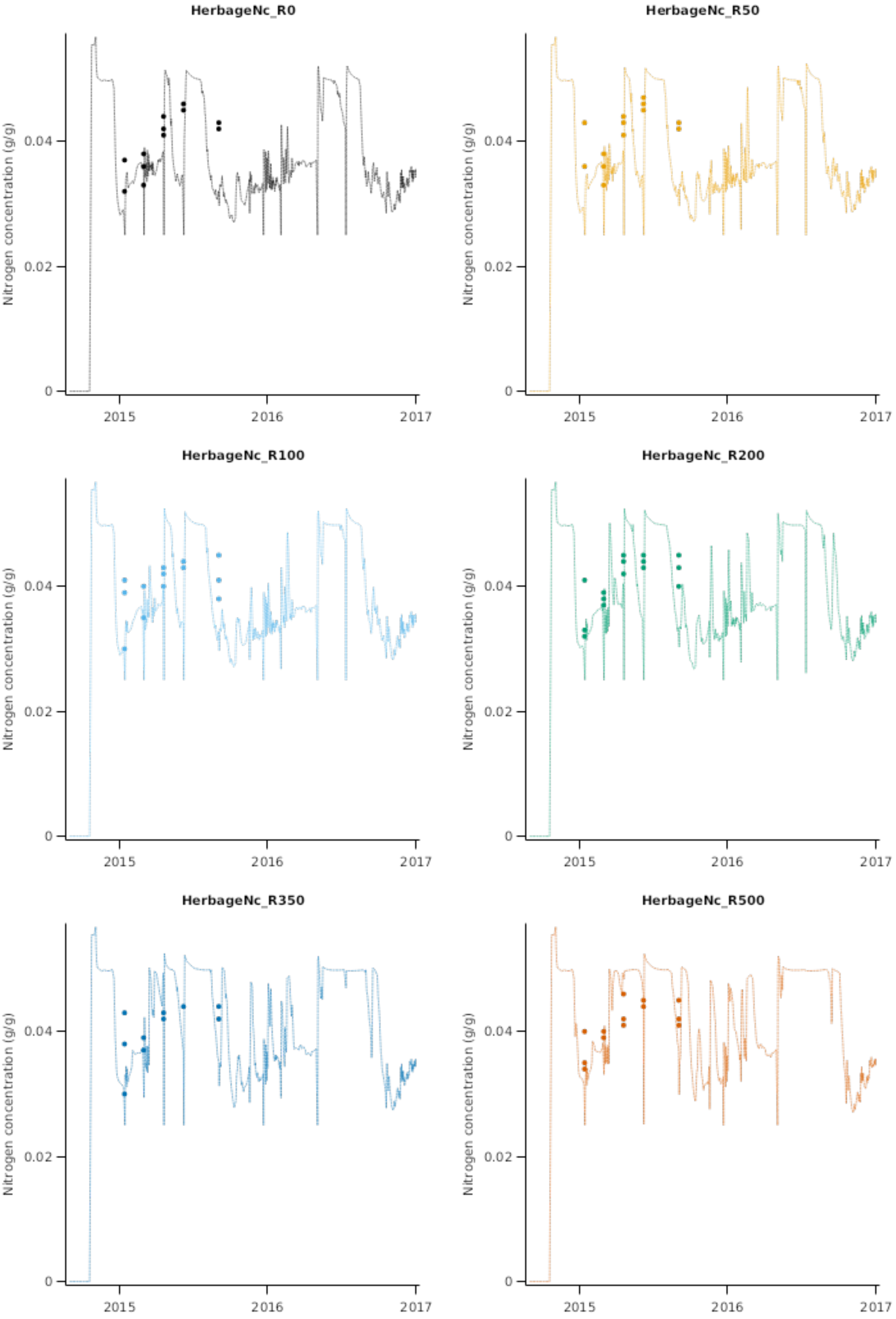


2.1.3.1.3 NSupply

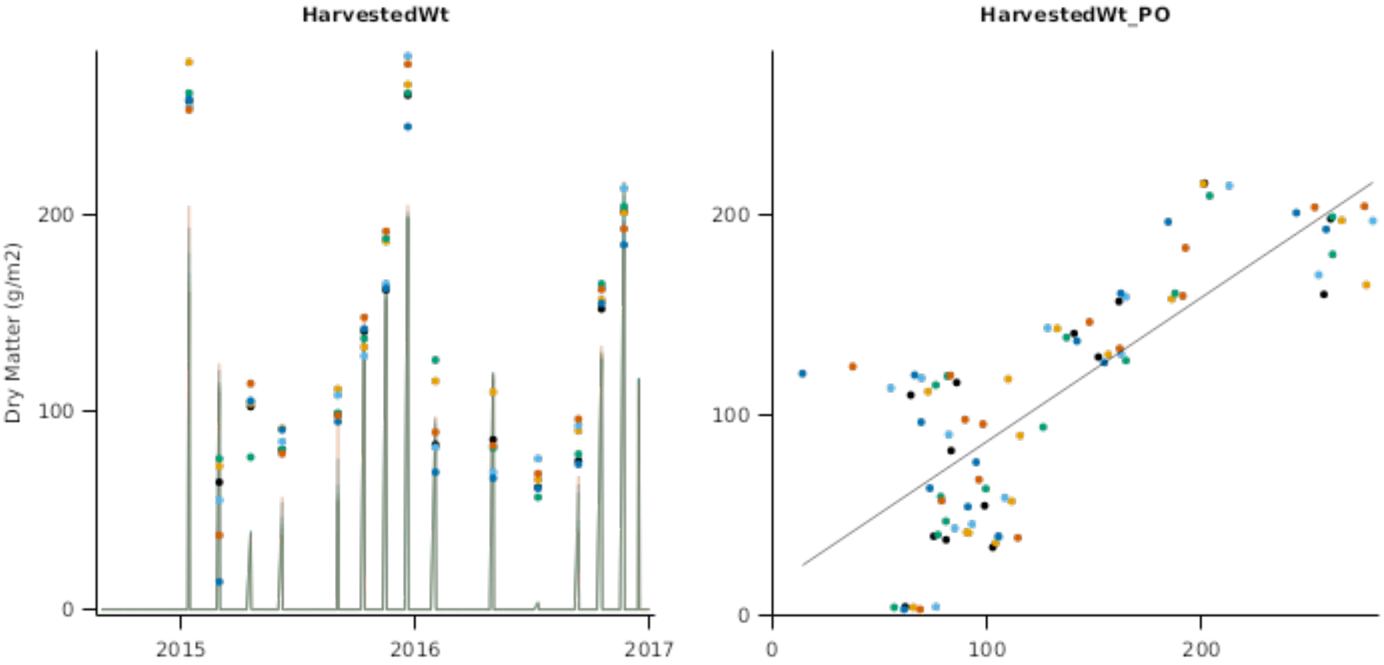


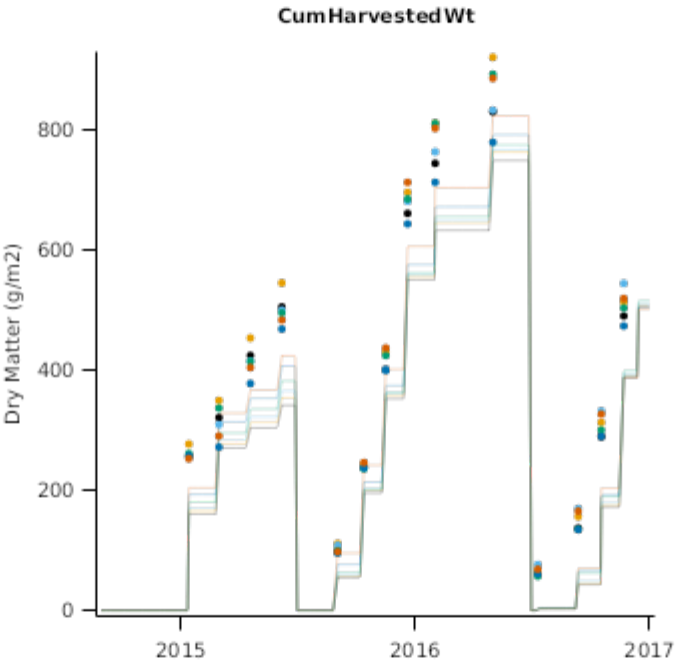
2.1.3.2 ObservedResults

2.1.3.2.1 Nconcentration

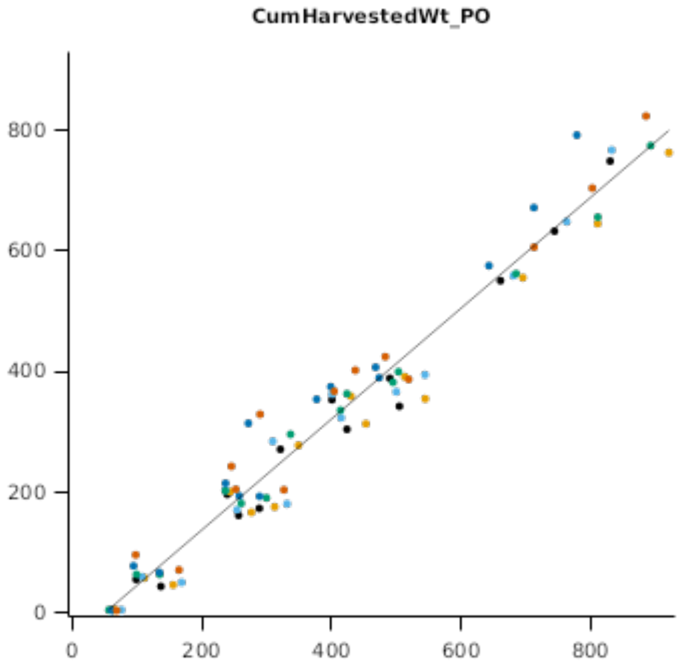

HerbageNc_R0
HerbageNc_R50
HerbageNc_R100
HerbageNc_R200
HerbageNc_R350
HerbageNc_R500
Nitrogen concentration (g/g)
0
0.02
0.04
2015
2016
2017

2.1.3.3 ObservedMeans

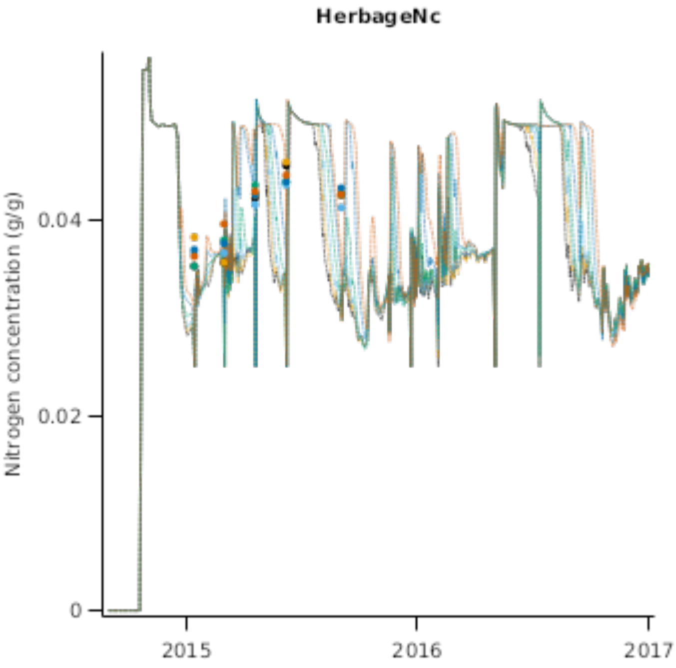




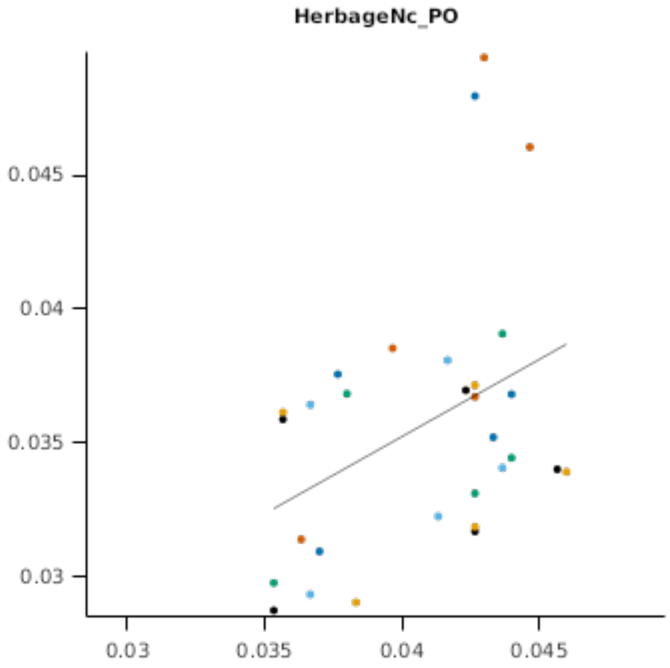
CumHarvestedWt



CumHarvestedWt_PO



HerbageNc



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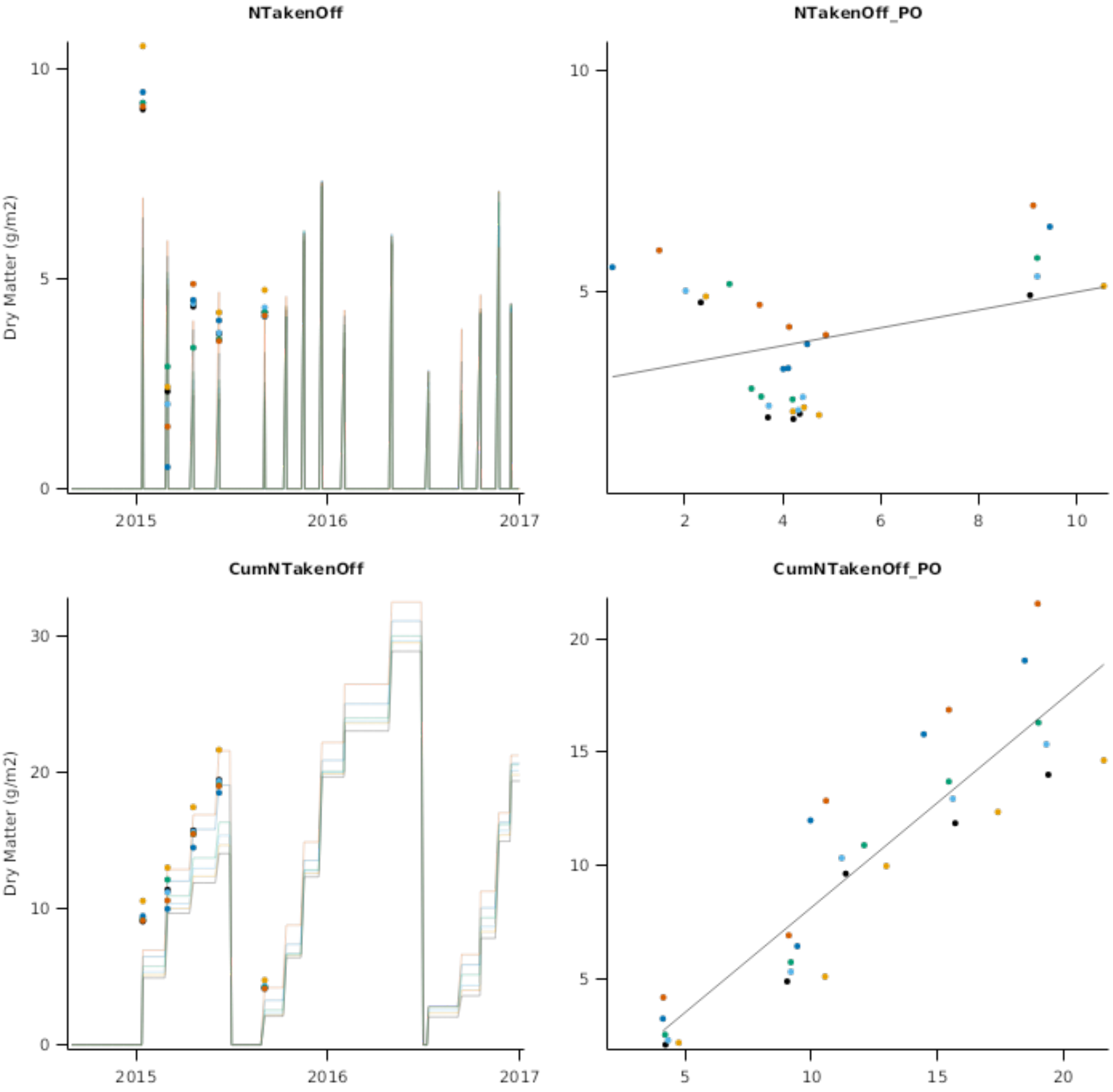

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