1 The APSIM Gliricidia Model

The model has been developed using the Plant Modelling Framework (PMF) of Brown et al., 2014. This new framework provides a library of plant organ and process submodels that can be coupled, at runtime, to construct a model in much the same way that models can be coupled to construct a simulation.This means that dynamic composition of lower level process and organ classes(e.g.photosynthesis, leaf) into larger constructions(e.g.maize, wheat, sorghum) can be achieved by the model developer without additional coding.

The model is constructed from the following list of software components. Details of the implementation and model parameterisation are provided in the following sections.

List of Plant Model Components.

Component Name	Component Type
MortalityRate	Models.Functions.Constant
Age	Models.Functions.AccumulateFunction
Phenology	Models.PMF.Phen.Phenology
Arbitrator	Models.PMF.OrganArbitrator
IndividualTreeLiveWt	Models.Functions.DivideFunction
Leaf	Models.PMF.Organs.PerennialLeaf
Root	Models.PMF.Organs.Root
Stem	Models.PMF.Organs.GenericOrgan
Nodule	Models.PMF.Organs.Nodule

1.1 MortalityRate

This model does not consider plant mortality.

MortalityRate = 0 (/d)

1.2 Age

Age = Accumulated *day* between emergence and old

Age is the age of the planting in years.

day = 1 / *DaysPerYear*

DaysPerYear = 365

1.3 Phenology

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

1.3.1 ThermalTime

This model uses standard days rather than a thermal time and so a value of 1 is used for each day.

ThermalTime = 1

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	Juvenile	Emergence	EndJuvenile
4	Mature	EndJuvenile	Maturity
5	Declining	Maturity	Old
6	Old	Old	Unused

1.3.2 Germinating

The phase goes from sowing to germination and assumes germination will be reached on the day after sowing or the first day thereafter when the extractable soil water at sowing depth is greater than zero.

1.3.3 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 = 0 (deg day/mm),

ShootLag = 1 (deg day),

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

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

ThermalTime = [Phenology].ThermalTime

1.3.4 Juvenile

This phase goes from emergence to endjuvenile.

The *Target* for completion is calculated as:

Target = 365 (oD)

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

Progression = 1

1.3.5 Mature

This phase goes from endjuvenile to maturity.

The *Target* for completion is calculated as:

Target = 1825 (oD)

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

Progression = 1

1.3.6 Declining

This phase goes from maturity to old.

The *Target* for completion is calculated as:

Target = 27010 (oD)

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

Progression = 1

1.3.7 Old

It is the end phase in phenology and the crop will sit, unchanging, in this phase until it is harvested or removed by other method

1.3.8 Constants

This model uses standard days rather than a thermal time and so a value of 1 is used for each day.

ThermalTime = 1

1.3.9 StageCode

1.3.9.1 StageCode

A value is linearly interpolated between phenological growth stages

1.4 Arbitrator

1.4.1 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.

1.5 AboveGround

1.5.1 AboveGround

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

AboveGround summarises the following biomass objects:

* Leaf
* Stem

1.6 BelowGround

1.6.1 BelowGround

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

BelowGround summarises the following biomass objects:

* Root

1.7 Total

1.7.1 Total

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

Total summarises the following biomass objects:

* Leaf
* Stem
* Root

1.8 TotalLive

1.8.1 TotalLive

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

TotalLive summarises the following biomass objects:

* Leaf
* Stem
* Root

1.9 IndividualTreeLiveWt

IndividualTreeLiveWt = [Gliricidia].TotalLive.Wt / [Gliricidia].Population

1.10 TotalDead

1.10.1 TotalDead

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

TotalDead summarises the following biomass objects:

* Leaf
* Stem
* Root

1.11 Leaf

This organ is parameterised using a simple leaf organ type which provides the core functions of intercepting radiation,

providing a photosynthesis supply and a transpiration demand. It also calculates the growth, senescence and detachment of leaves.

1.11.1 Constants

This model assumes that all senesced leaves detach immediately.

LaiDeadFunction = 0 ($m^2/m2$)

Value is taken from Harrington et al., 1995.

ExtinctionCoefficient = 0.57

MaximumNConc = 0.07

MinimumNConc = 0.03

NReallocationFactor = 0

DMConversionEfficiency = 1

This model assumes that all leaves detach upon senescence.

LeafDetachmentTime = 1

DMRetranslocationFactor = 0

NRetranslocationFactor = 0

LeafKillFraction = 0

MinimumLAI = 0.1

SpecificLeafAreaFunction = 0.01 (m^2/g)

CarbonConcentration = 0.4

Leaf cohorts age according to a simple aggregation of time (ie no accounting for differing rates of development with temperature or stress).

LeafDevelopmentRate = 1

1.11.2 InitialWtFunction

InitialWtFunction = InitialPlantWt x [Plant].Population

InitialPlantWt = 1 (g/plant)

1.11.3 Photosynthesis

Photosynthesis = RUE x FCO2 x [Leaf].RadiationIntercepted x [Leaf].Fw x [Leaf].FRGRFunction

Value of 1.06 g/MJ for above ground growth from Harrington et al., 1995 is increased to account for biomass partitioning to below-ground organs.

RUE = 1.2

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,

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

1.11.4 FRGRFunction

FRGRFunction = Min(*FRGRFunctionTemp*, *NitrogenStressFactor*)

Where:

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

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

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

X	FRGRFunctionTemp
5.0	0.0
15.0	1.0
32.0	1.0
42.0	0.0
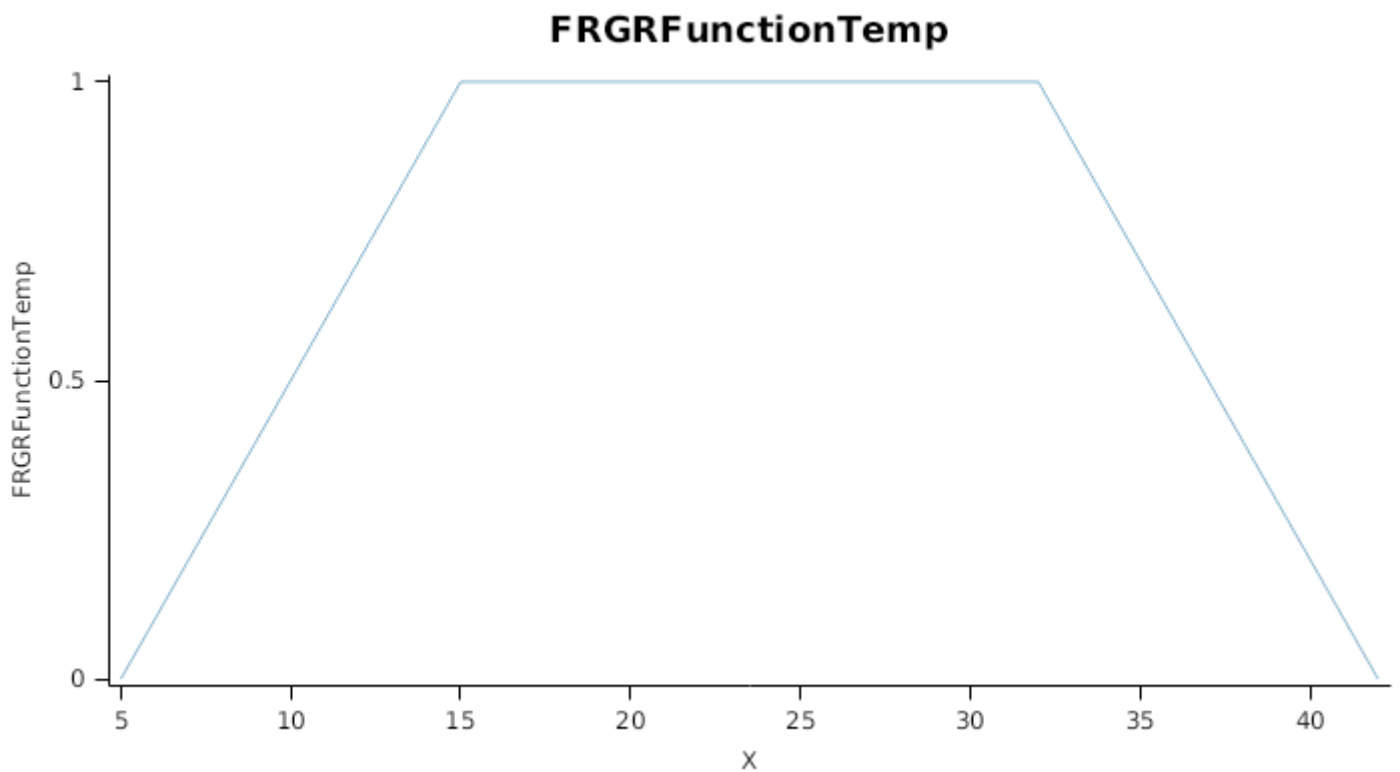
NitrogenStressFactor = [Leaf].Fn

1.11.5 ExtinctionCoefficientDead

ExtinctionCoefficientDead = [ExtinctionCoefficient]

1.11.6 HeightFunction

HeightFunction is calculated using linear interpolation

X	HeightFunction
60.0	250.0
2000.0	2500.0

HeightFunction
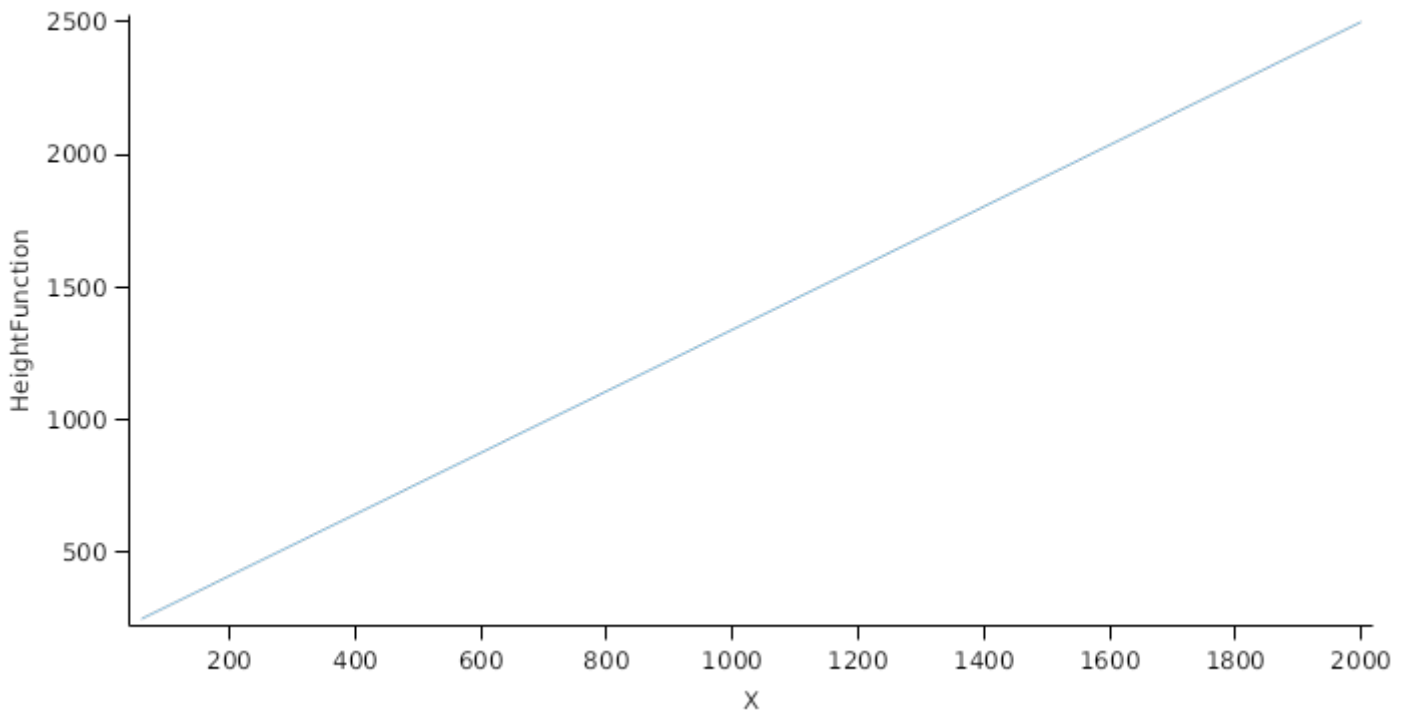
1.11.7 LeafResidenceTime

LeafResidenceTime is calculated using linear interpolation

X	LeafResidenceTime
5.0	1.0
10.0	120.0
15.0	184.0

LeafResidenceTime

1.11.8 BiomassRemovalDefaults

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

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	98	100
Cut	0	0	98	100
Prune	0	0	46	100
Graze	0	0	0	0
Thin	0	0	0	0

1.11.9 DMDemands

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

Structural = DMDemandFunction x *StructuralFraction*

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

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction = 0.29

StructuralFraction = 1

Metabolic = 0

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

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

1.11.10 NDemands

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

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

Metabolic = MetabolicNconc x [Leaf].potentialDMAllocation.Structural

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

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

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

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

MaxNconc = [Leaf].MaximumNConc

NitrogenDemandSwitch = 1

1.11.11 CO2internal

CO2internal = (163 - [IWeather].MeanT)/(5 - 0.1x[IWeather].MeanT)

1.11.12 StomatalConductanceCO2Modifier

StomatalConductanceCO2Modifier = [Leaf].Photosynthesis.FCO2 / *RelativeCO2Gradient*

RelativeCO2Gradient = ([IWeather].CO2 - [Leaf].CO2internal)/(350 - [Leaf].CO2internal)

1.12 Root

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

1.12.1 Growth

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

Root Depth Increase = RootFrontVelocity x XF_i x RootDepthStressFactor

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

Root depth is also constrained by a maximum root depth.

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

RAw_i = -$WaterUptake_i$ / $LiveRootWt_i$ x $LayerThickness_i$ x ProportionThroughLayer

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

$DMAllocated_i$ = TotalDMAllocated x RAw_i / TotalRAw

1.12.2 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.

1.12.3 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.

1.12.4 Nitrogen Uptake

Potential N uptake by the root system is calculated for each soil layer (i) that the roots have extended into. In each layer potential uptake is calculated as the product of the mineral nitrogen in the layer, a factor controlling the rate of extraction (kNO3 or kNH4), the concentration of N form (ppm), and a soil moisture factor (NUptakeSWFactor) which typically decreases as the soil dries. *NO3 uptake = $NO3_i$ x kNO3 x $NO3_{ppm, i}$ x NUptakeSWFactor* _NH4 uptake = $NH4_i$ x kNH4 x $NH4_{ppm, i}$ x NUptakeSWFactor_As can be seen from the above equations, the values of kNO3 and kNH4 equate to the potential fraction of each mineral N pool which can be taken up per day for wet soil when that pool has a concentration of 1 ppm.Nitrogen uptake demand is limited to the maximum daily potential uptake (MaxDailyNUptake) and the plant's N demand. The former provides a means to constrain N uptake to a maximum value observed in the field for the crop as a whole.The demand for soil N is then passed to the soil arbitrator which determines how much of the N uptake demandeach plant instance will be allowed to take up.

1.12.5 Water Uptake

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

1.12.6 Constants

RootFrontVelocity = 10

SenescenceRate = 0.005

MaximumNConc = 0.03

MinimumNConc = 0.01

MaxDailyNUptake = 6

MaximumRootDepth = 10000

This model does not account for any change in potential water uptake with plant development.

KLModifier = 1

This model does not account for any change in potential NO3 uptake with plant development.

KNO3 = 0.03

This model does not account for any change in potential NH4 uptake with plant development.

KNH4 = 0

SpecificRootLength = 100 (m/g)

DMConversionEfficiency = 1

MaintenanceRespirationFunction = 1

RemobilisationCost = 0

CarbonConcentration = 0.4

RootDepthStressFactor = 1

1.12.7 RootShape

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

1.12.8 NitrogenDemandSwitch

NitrogenDemandSwitch has a value between Emergence and Old calculated as:

Constant = 1

1.12.9 NUptakeSWFactor

NUptakeSWFactor is calculated using linear interpolation

X	NUptakeSWFactor
0.0	0.0
1.0	1.0

1.12.10 BiomassRemovalDefaults

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

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

1.12.11 DMDemands

1.12.11.1 DMDemands

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

Structural = DMDemandFunction x StructuralFraction

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

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction = 0.03

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

1.12.12 NDemands

1.12.12.1 NDemands

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

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

Metabolic = MetabolicNconc x [Root].potentialDMAllocation.Structural

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

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

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

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

NitrogenDemandSwitch = [Root].nitrogenDemandSwitch

MaxNconc = [Root].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.12.13 CriticalNConc

CriticalNConc = [Root].MinimumNConc

1.12.14 InitialWt

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

Structural = 5 (g/plant)

Metabolic = 0

Storage = 0

1.13 Stem

1.13.1 Stem

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

1.13.2 Dry Matter Demand

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

1.13.2.1 DMDemands

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

Structural = DMDemandFunction x *StructuralFraction*

This function calculated dry matter demand using plant allometry which is described using a simple power function (y=kX^p).

YValue = 0.0345 * XValue ^ 1.36

XValue = [AboveGround].Wt

YValue = [Stem].Live.Wt

StructuralFraction = 0.7 (g/g)

Metabolic = 0

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

StorageFraction = 1 - [Stem].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.

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

Metabolic = MetabolicNconc x [Stem].potentialDMAllocation.Structural

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

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

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

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

NitrogenDemandSwitch = [Stem].nitrogenDemandSwitch

MaxNconc = [Stem].maximumNconc

QStructuralPriority = 1

QMetabolicPriority = 1

QStoragePriority = 1

1.13.4 N Concentration Thresholds

MinimumNConc = 0.0014

CriticalNConc = [Stem].MinimumNConc

Value taken from Thomas et al., 1991.

MaximumNConc = 0.003

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

NitrogenDemandSwitch has a value between Emergence and Old calculated as:

Constant = 1

1.13.5 Dry Matter Supply

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

Stem does not retranslocate non-structural DM.

1.13.6 Nitrogen Supply

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

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

1.13.7 Senescence and Detachment

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

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

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

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	70	70
Cut	0	0	10	0
Prune	0	0	0	0
Graze	0	0	0	0
Thin	0	0	0	0

1.14 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.

1.14.1 Dry Matter Demand

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

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

Structural = DMDemandFunction x *StructuralFraction*

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

DMDemandFunction = PartitionFraction x [Arbitrator].DM.TotalFixationSupply

PartitionFraction = 0.05

StructuralFraction = 1 (g/g)

Metabolic = 0

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

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

1.14.2 Nitrogen Demand

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

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

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

Metabolic = MetabolicNconc x [Nodule].potentialDMAllocation.Structural

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

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

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

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

NitrogenDemandSwitch = [Nodule].nitrogenDemandSwitch

MaxNconc = [Nodule].maximumNconc

MinimumNConc = 0.03

CriticalNConc = [Nodule].MinimumNConc

MaximumNConc = 0.08

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

NitrogenDemandSwitch has a value between Emergence and Maturity calculated as:

Constant = 1

1.14.3 Dry Matter Supply

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

Nodule does not retranslocate non-structural DM.

1.14.4 Nitrogen Supply

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

Nodule does not retranslocate non-structural N.

FixationRate = 0.6 (g/m^2/d)

1.14.5 Senescence and Detachment

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

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

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

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

1.15 Gliricidia

Gliricidia overrides the following properties:

1.16 GliricidiaYoung

GliricidiaYoung overrides the following properties:

[Gliricidia].Stem.DMDemands.Structural.DMDemandFunction.Const=0.05

2 Validation

The Gliricidia model has been tested using datasets from Malawi, Guadeloupe and USA that cover a wide range of weather conditions, soil, and agronomic systems.

List of experiments.

Experiment Name	Design (Number of Treatments)
Hamakuapoko	Harvest (1)
Guadeloupe	Harvest (3)
GuadeloupeGodet	Harvest (3)
Makoka	N x Maize (6)

2.1 Hamakuapoko

This dataset measured above-ground biomass and leaf area, and calculated light interception, in a 2-year experiment on the island of Maui, Hawaii (Harrington et al., 1995). The soil was a silty clay classified as an Oxic Haplustoll, with a surface soil (0-15cm) pH of 5-2 (1:1 soil:water), 2-4% organic C, and 0-18% total N. The dry season from May to October receives one-third of the mean annual rainfall of 1200 mm. We used data only from the uncut treatment, as it was too hard to understand well enough the data for the coppice treatment.

2.1.1 Graphs

LAI

LightInterception
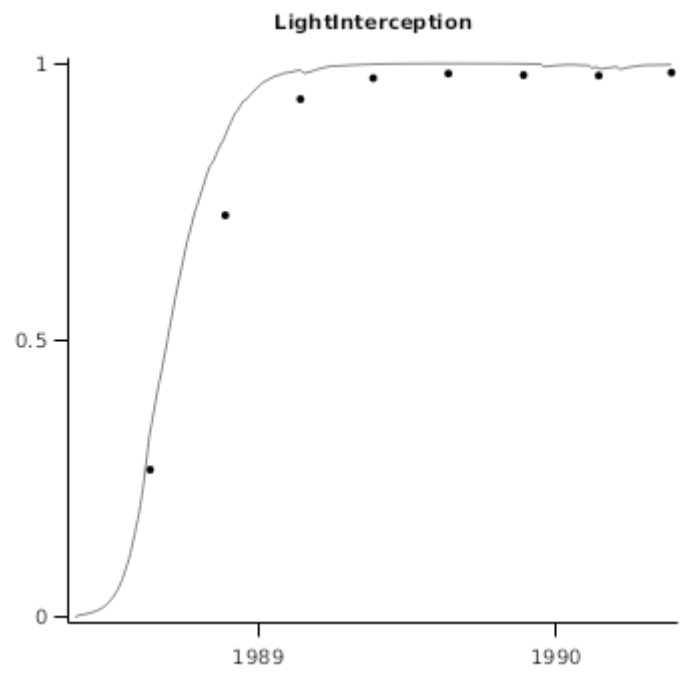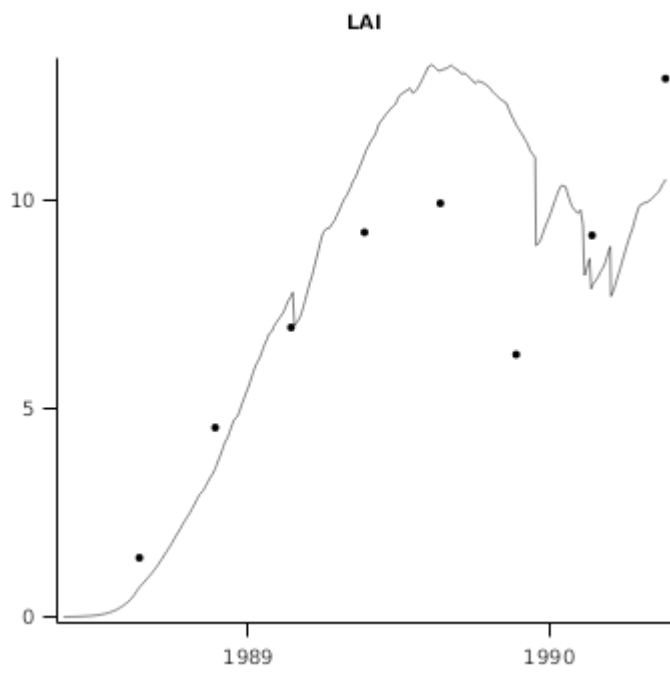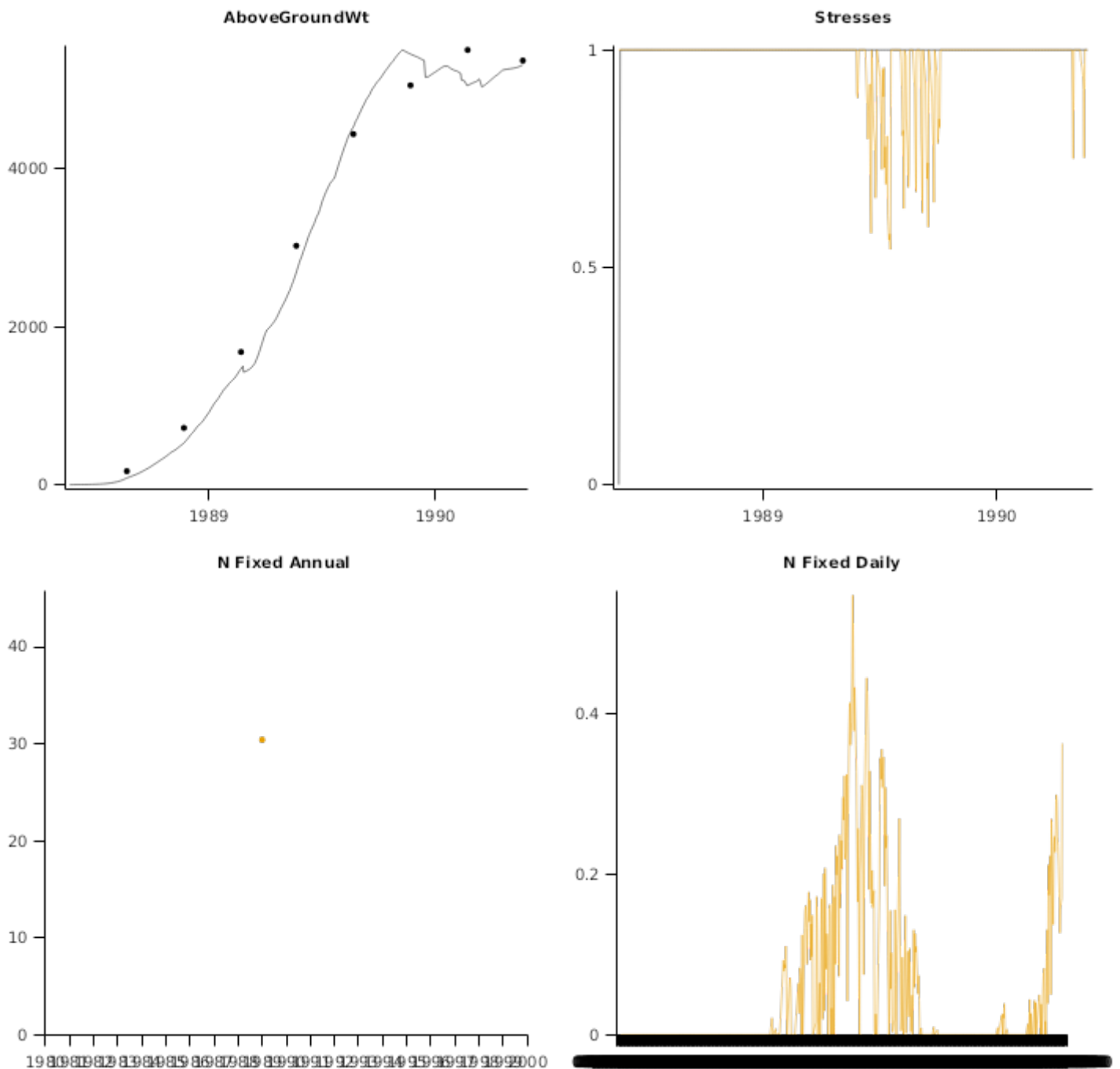
2.2 Guadeloupe

The study (Nygren et al., 2000, NYGREN et al., 1998, Garcia et al., 2001)was carried out at the experimental farm of the Antillean research centre of the Institut National de la Recherche Agronomique (INRA) in Prise d'Eau, Guadeloupe (16°12 N, 61°39 W, 125 m a.s.l.). The soils are alluvial Ultisols with low acidity and relatively high cation exchange capacity. The experiment was established in May 1993. Gliricidia sepium was planted using stakes cut from a near-by living fence. Between May 1993 and March 1995 the whole experiment was managed uniformly by means of partial prunings every 3–6 months according to the growth of trees, in order to avoid excessive shading of the grass layer. The experiment started 29th February, 1996, when the G. sepium trees were pruned completely. Three tree cutting regimes were then initiated: total removal of all leaves and branches above 0.5 m once a year, or every 6 months, and partial pruning every 2 months.

More frequent and severe cutting leads less biomass growth and biomass removed for residues (see Duguma et al., 1988 qualitatively simulated for the Makoka site as a sensibility test).

2.2.1 Graphs

Leaf Wt
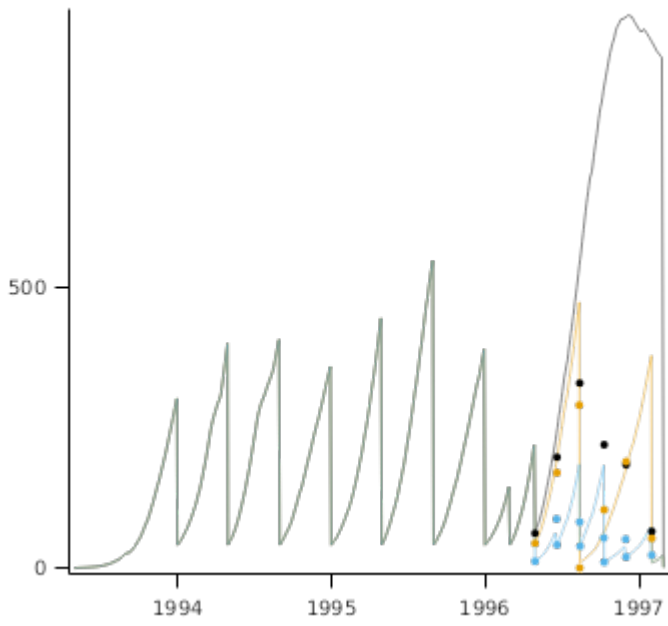
LAI
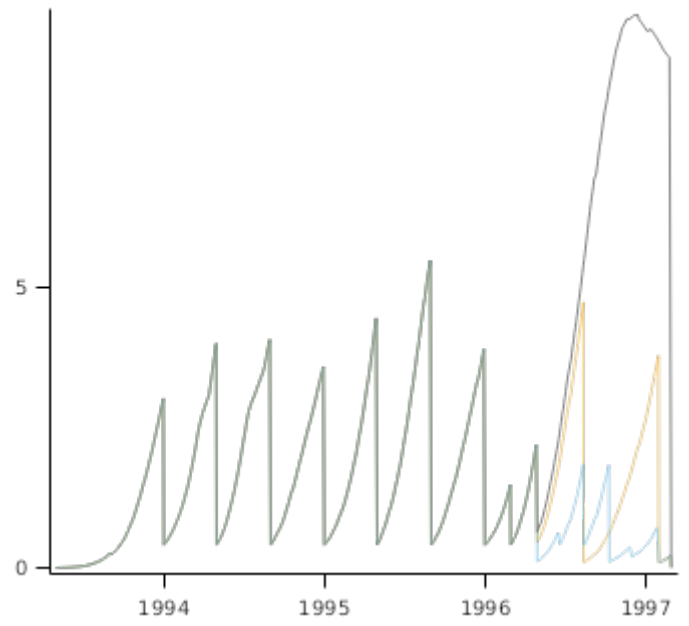
Stem Wt
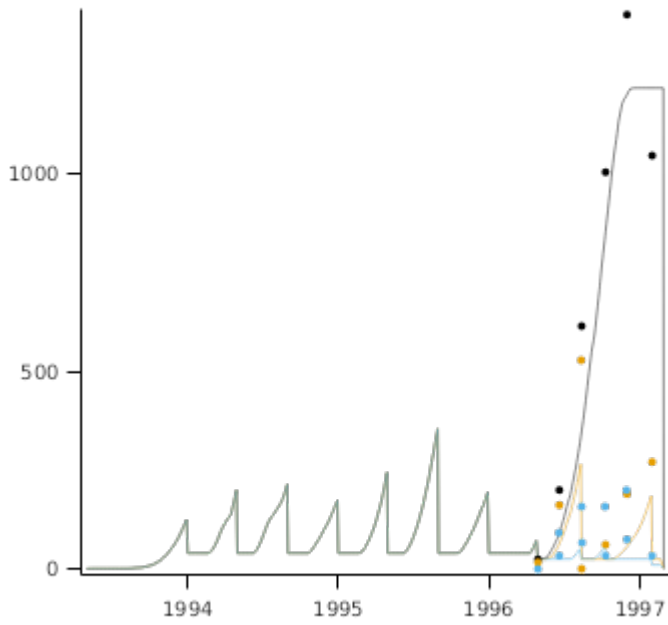
LitterFall
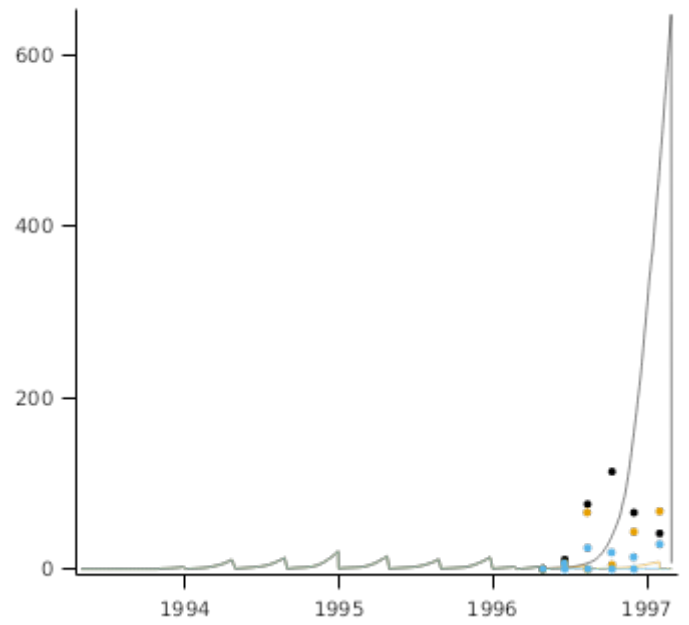
AboveGroundWt
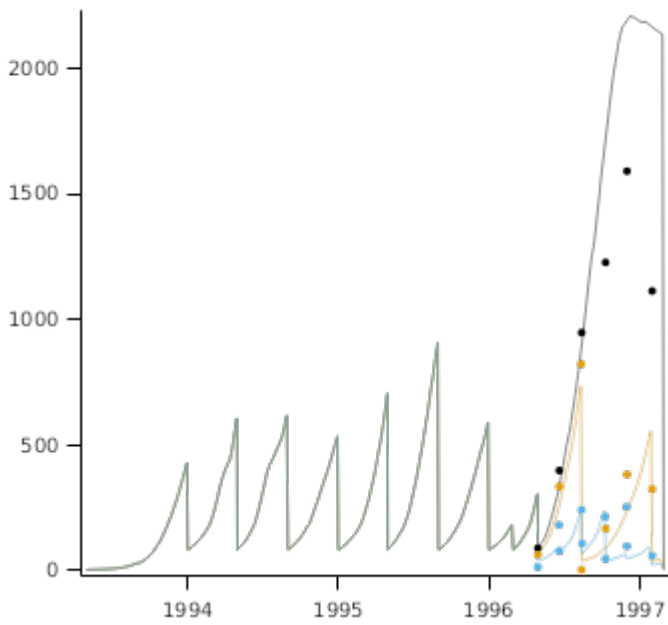
PreObs LeafWt
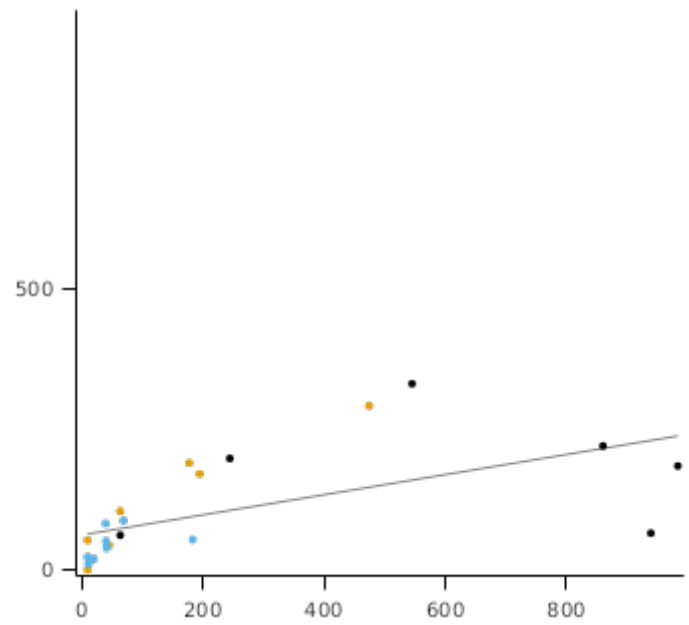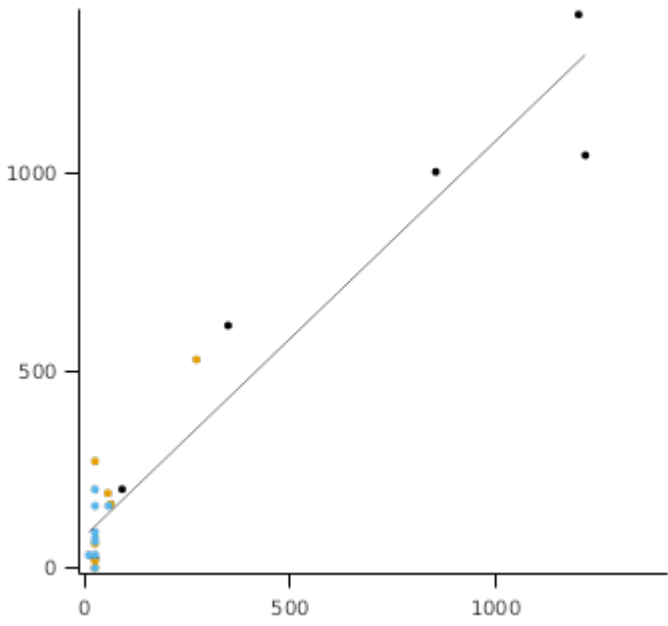
PreObs StemWt

PreObs AboveGroundWt
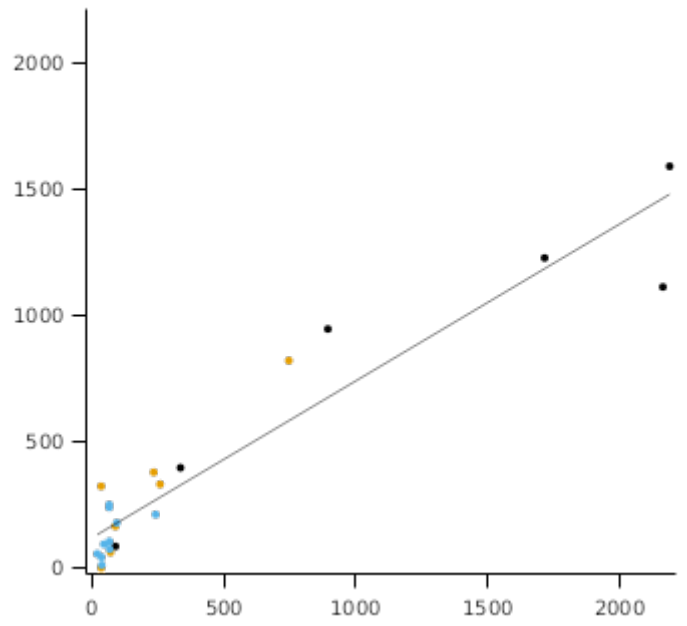
Leaf Wt1996to1997
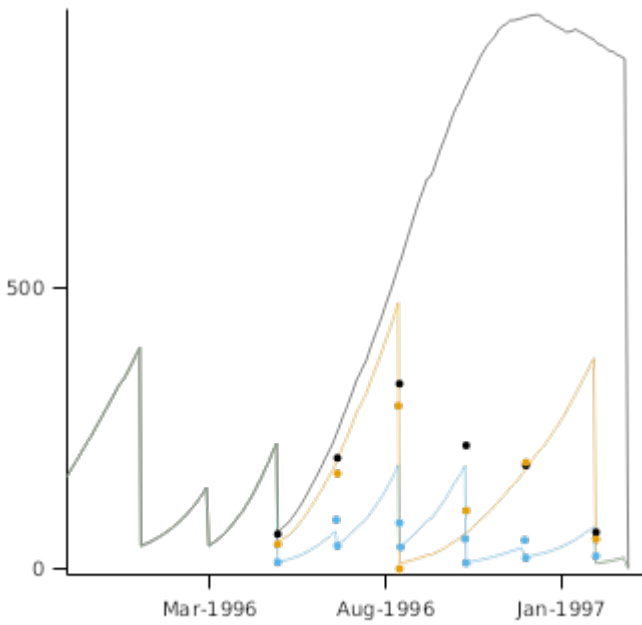
Stem Wt1996to1997
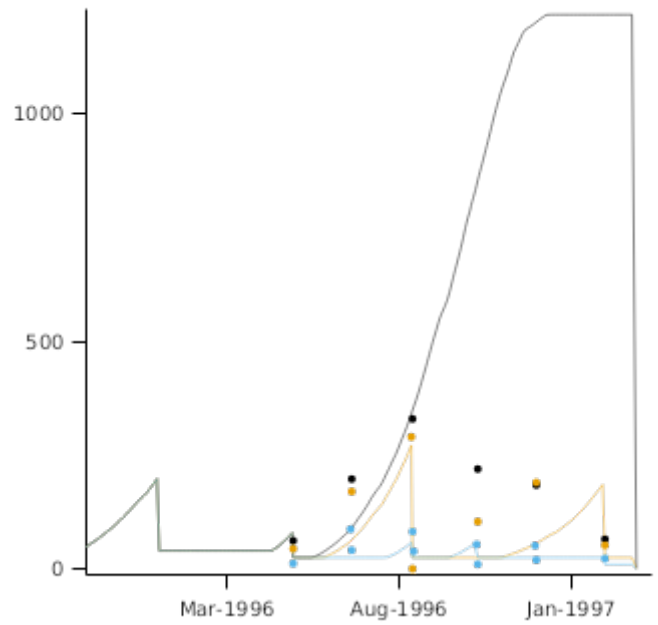
Stresses
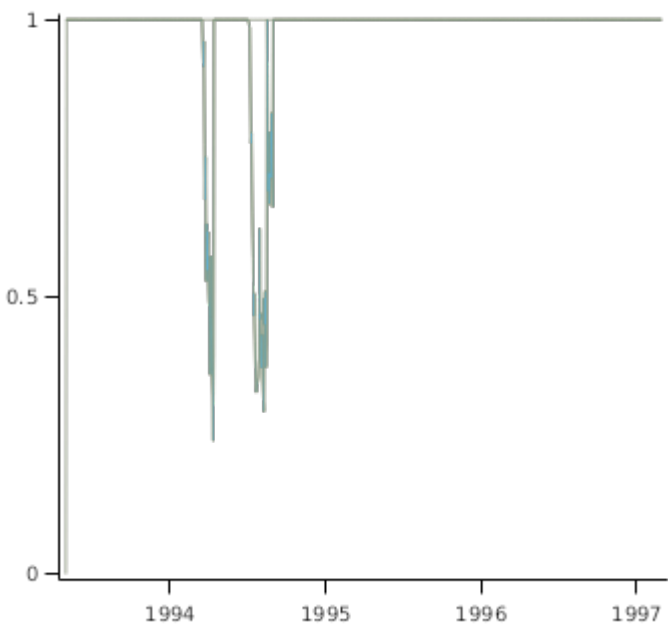
N Fixed Daily
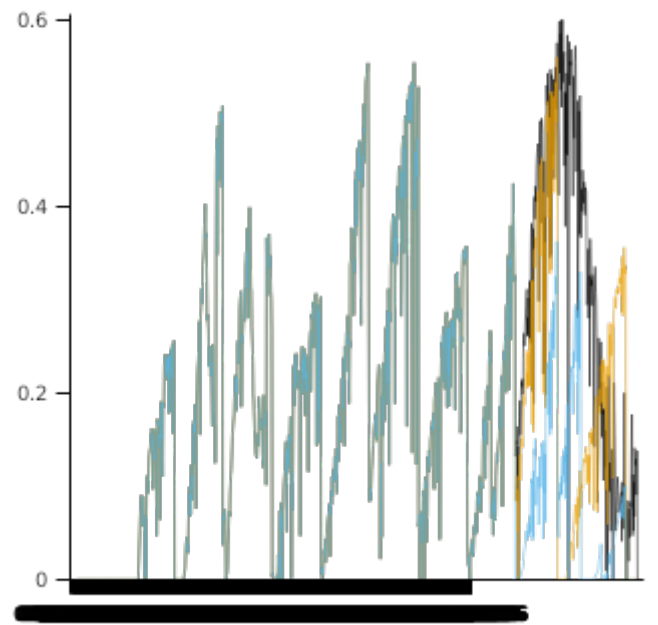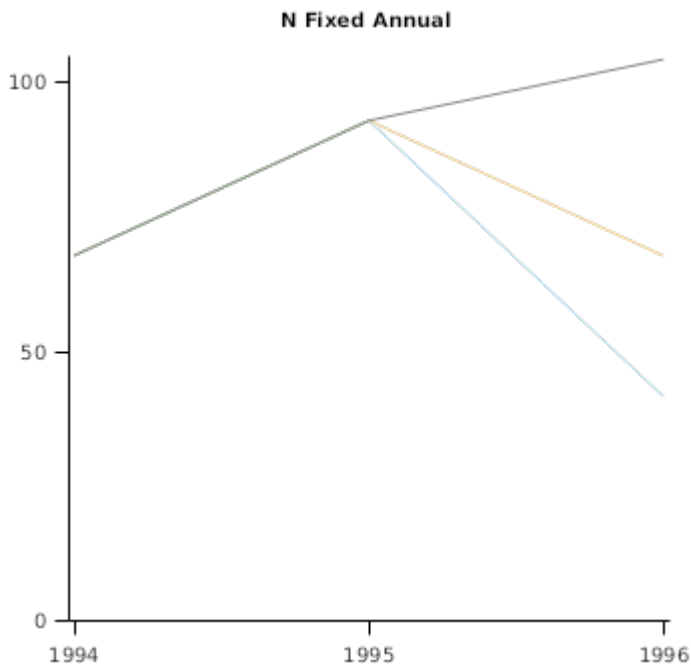
2.3 GuadeloupeGodet

The study (NYGREN et al., 2000, Cruz, 1997) was carried out at the experimental farm of the Antillean Research Centre of the Institut National de la Recherche Agronomique (INRA) in Godet, Guadeloupe (16°20 N, 61°30 W, 10 m a.s.l.). The soil is a slightly basic Vertisol with soil depth varying irregularly from 0.25 to 0.75 m. The climate is warm and subhumid. The experiment was established in May 1989 by planting G. sepium cuttings from a nearby living fence in natural D. aristatum grassland. Gliricidia sepium was pruned every 2–2.5 months with successive full (100%) and partial (20–30%) defoliations, and the pruning residues were removed from the site. On April 1, 1996, the G. sepium trees were pruned completely. Three tree cutting regimes were then initiated: total removal of all leaves and branches above 0.5 m once a year, or every 6 months, and partial pruning every 2 months. Dichantium aristatum was cut monthly and the cut grass removed from the site.

More frequent and severe cutting leads less biomass growth and biomass removed for residues. see Duguma et al., 1988 qualitatively simulated for the Makoka site as a sensibility test).

2.3.1 Graphs

Leaf Wt
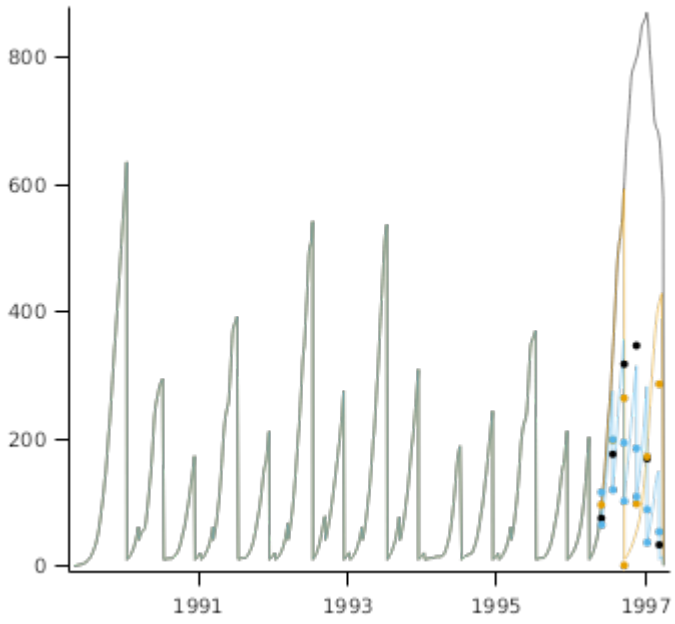
Stem Wt
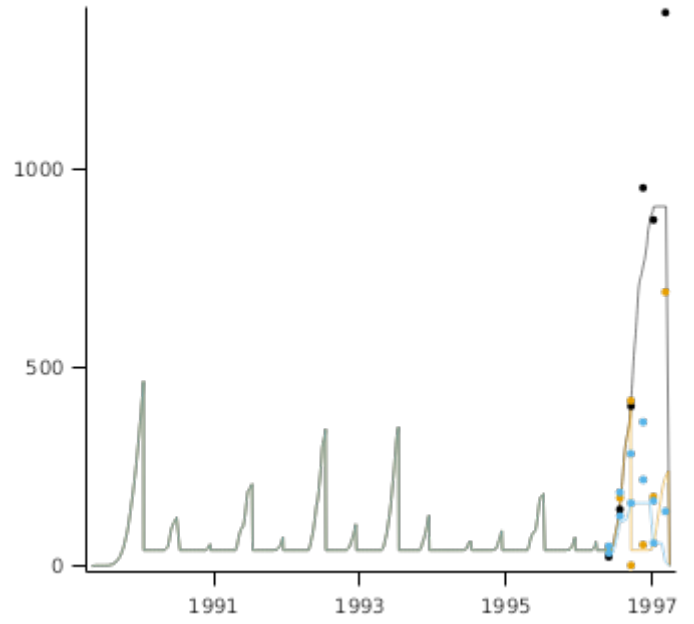
AboveGroundWt
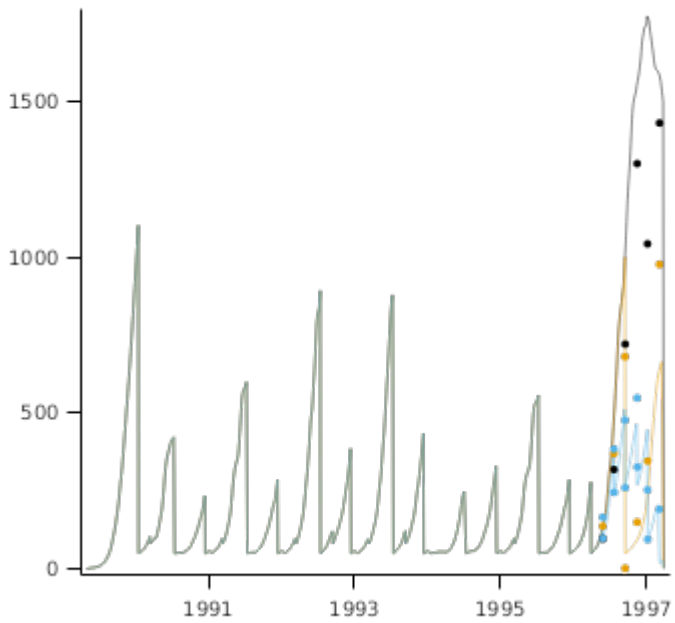
PreObs LeafWt
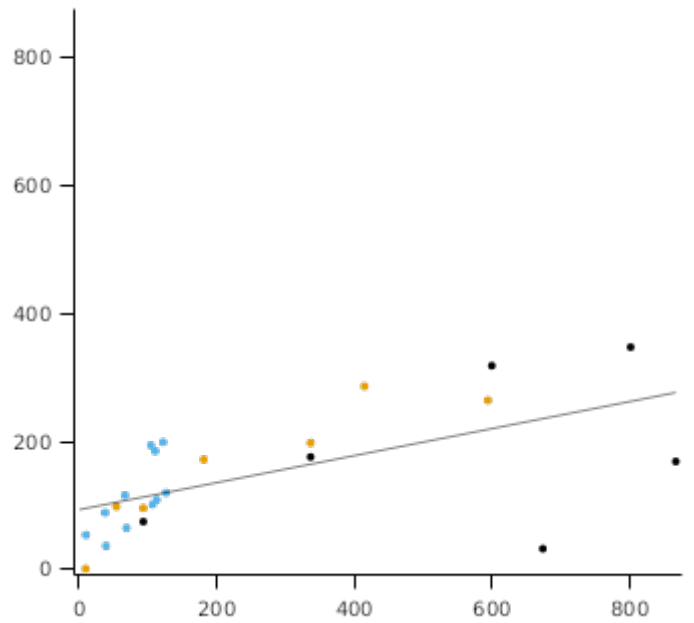
PreObs StemWt
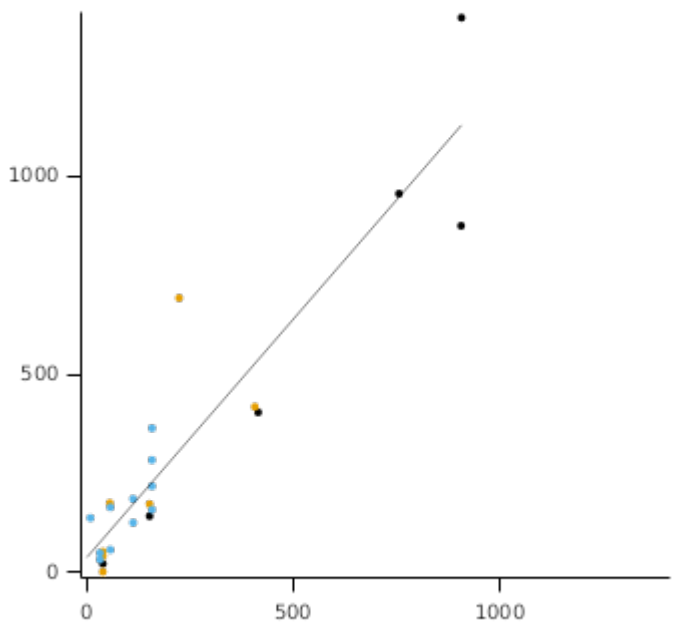
PreObs AboveGroundWt
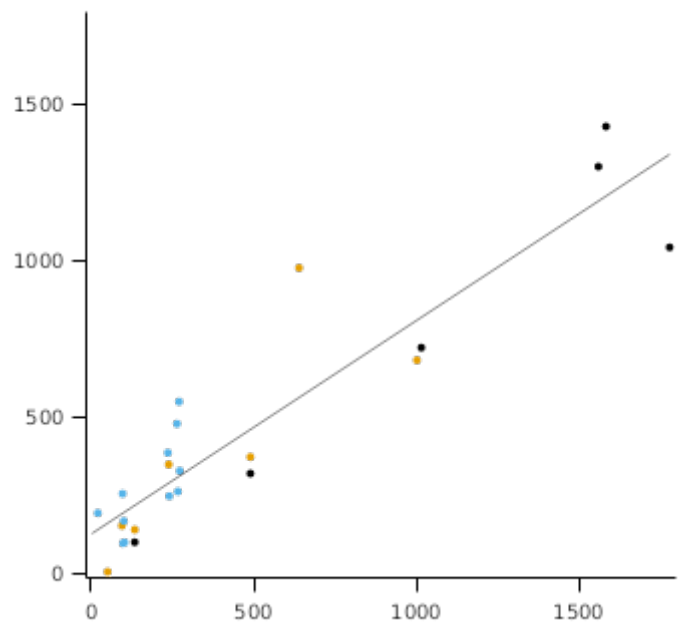
LAI
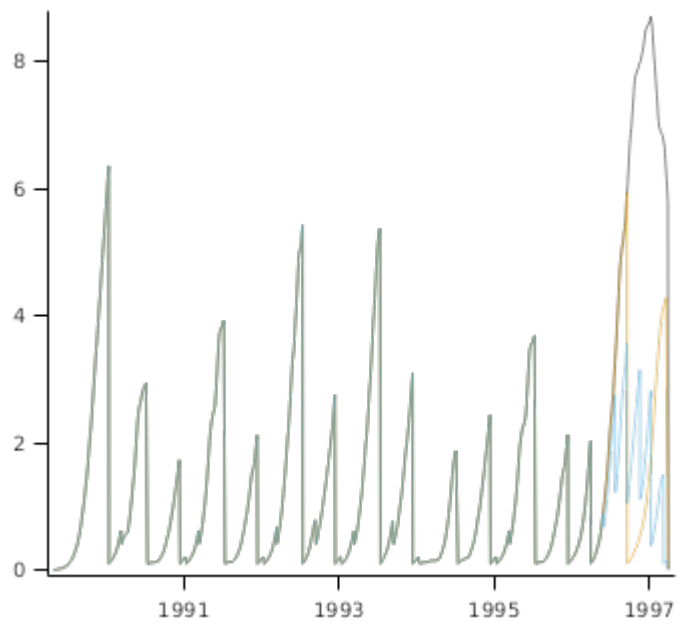
LeafRemovalWt
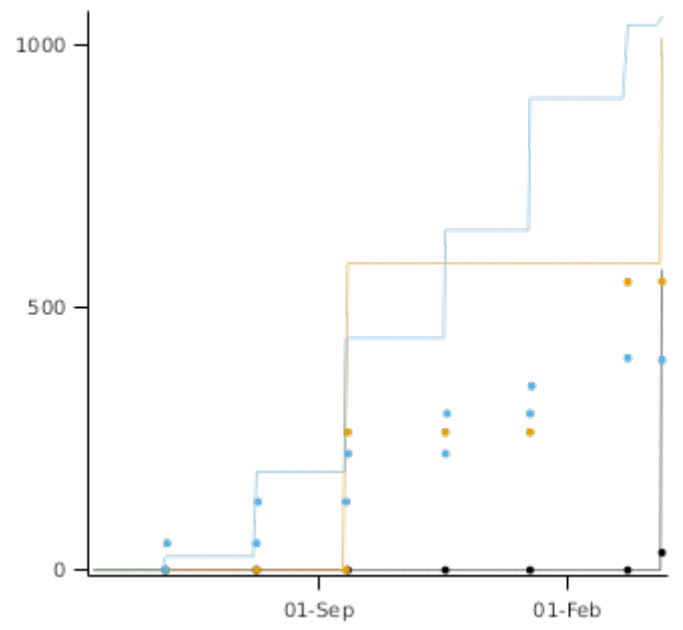
StemRemovalWt
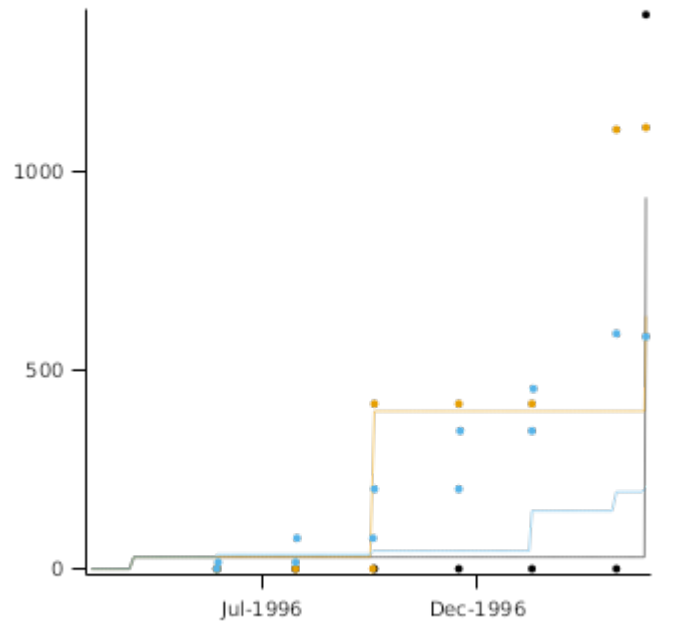
TotalRemovalWt

Stresses

N Fixed Daily

N Fixed Annual
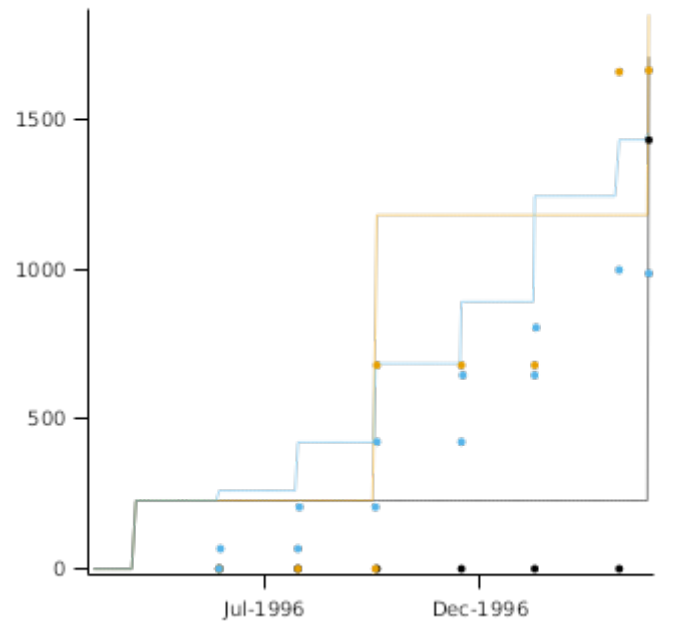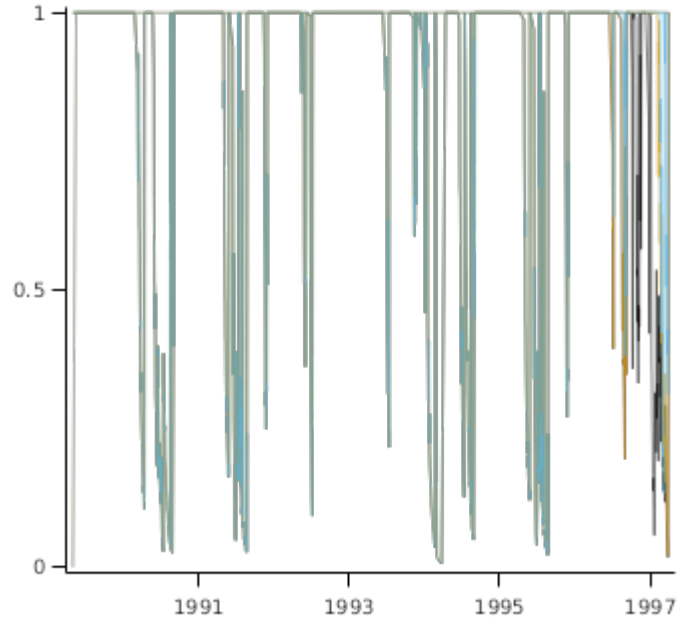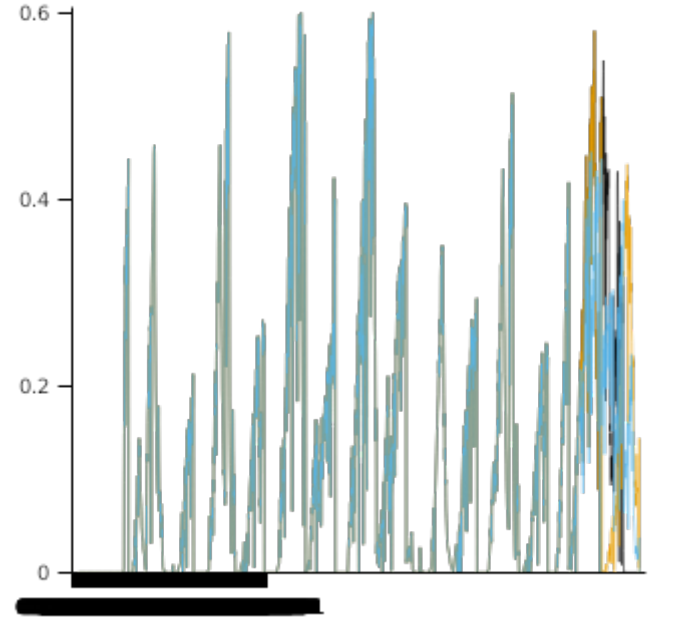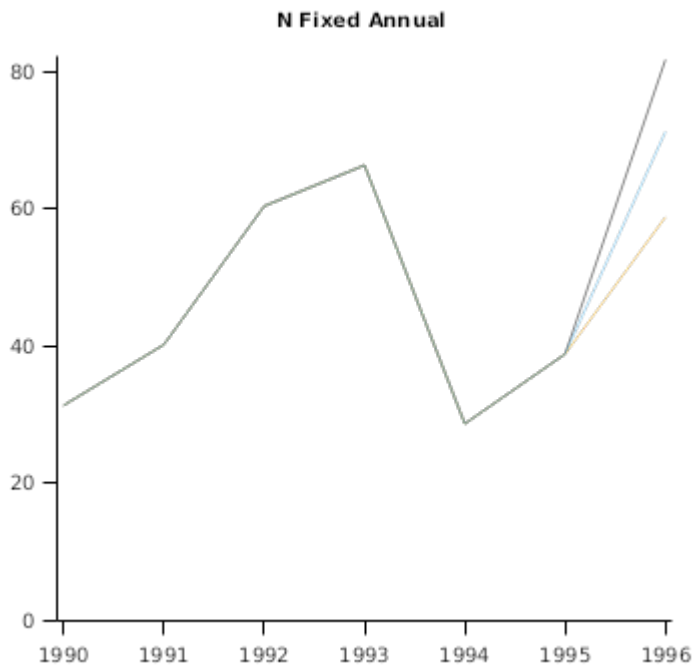
2.4 Makoka

This agroforestry experiment (Makumba et al., 2006, Makumba et al., 2007, Makumba et al., 2009, Akinnifesi et al., 2006, Akinnifesi et al., 2007, Akinnifesi et al., 2009, Mweta et al., 2007, Ikerra et al., 1999) was continuously cropped with maize between establishment in 1992 and final available measurementsa in 2004. The trial includes three rates of N fertiliser with and without Gliricidia sepium intercropping. The study was conducted at Makoka Agricultural Research Station near Zomba in Southern Malawi. The soil had 42% clay, 46% sand and 1.42 g/cm3 bulk density. The rainfall is unimodal with a mean rainfall of 937 mm. There was some P deficiency, demonstrated by a response to P fertilizer, so only the high P fertilizer treatment was simulated. There was also suspicion that P deficiency further developed quite later in the experiment.

Results indicated that, without Gliricidia, maize yield was low and decreased with time without N inputs. Gliricidia increased maize yields, but the effect took about 3 years to fully develop. N fertilization increased yields both with and without fertiliser. Annual trends reflected patterns of rainfall.

2.4.1 Graphs

Grain Yield all years
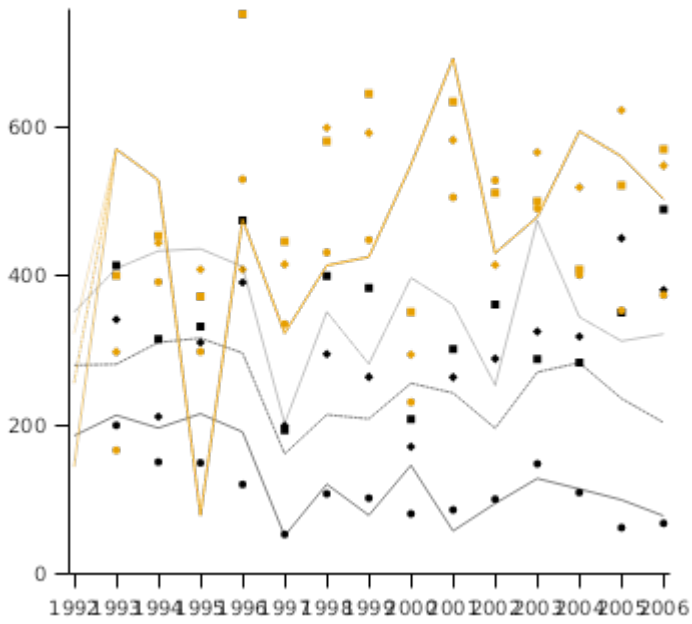
Grain Yield PvsO
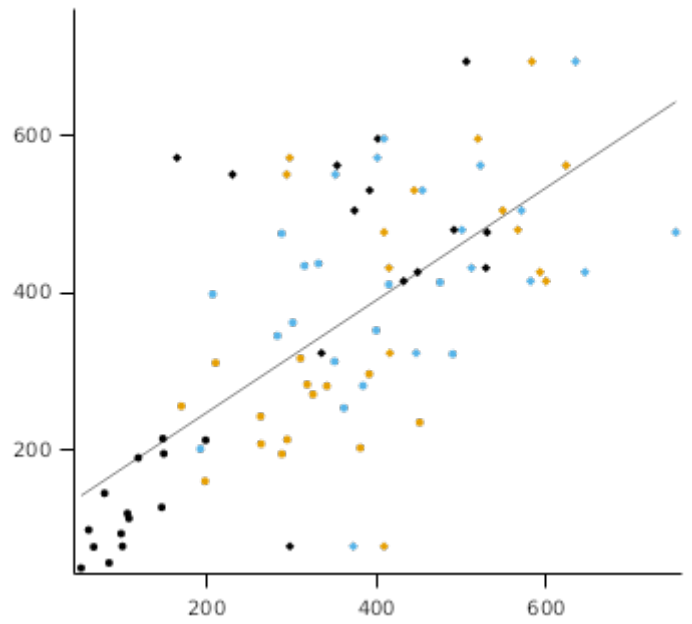
Maize AboveGroundWt vs Year
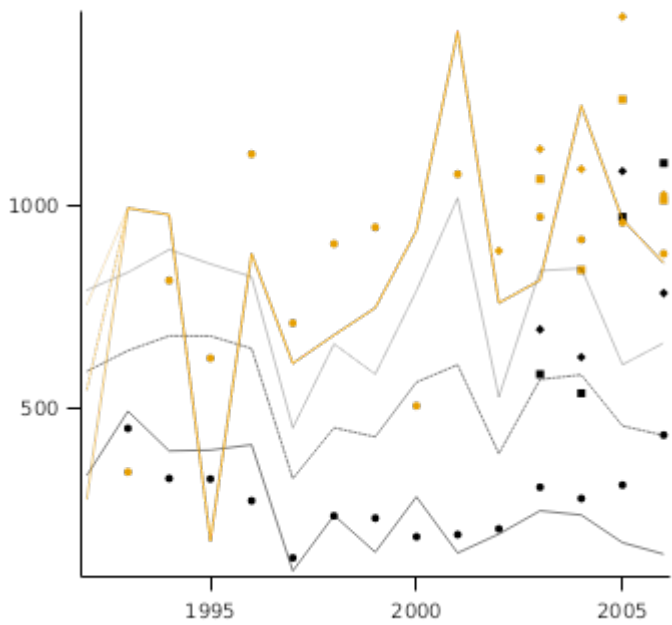
Maize AboveGroundWt PvsO
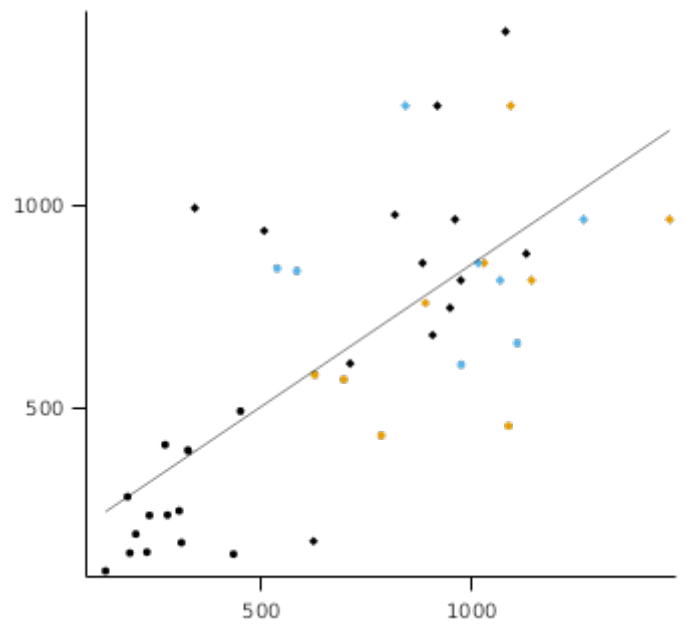
Maize Fn
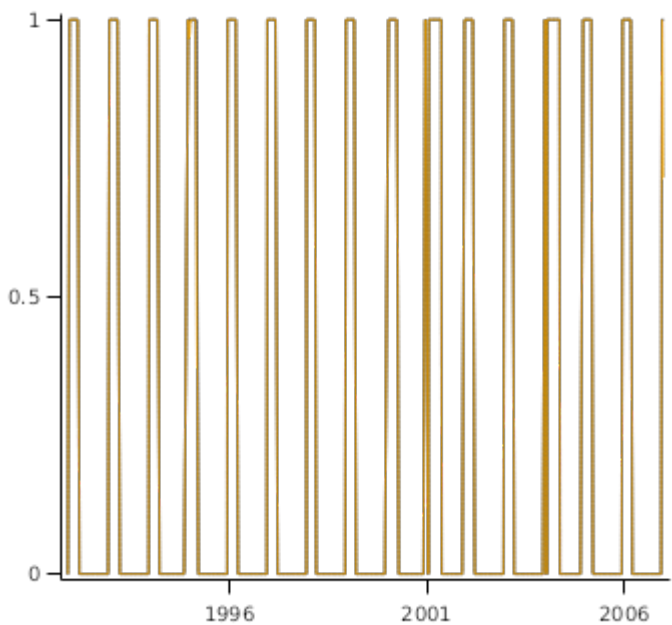
Maize Fw
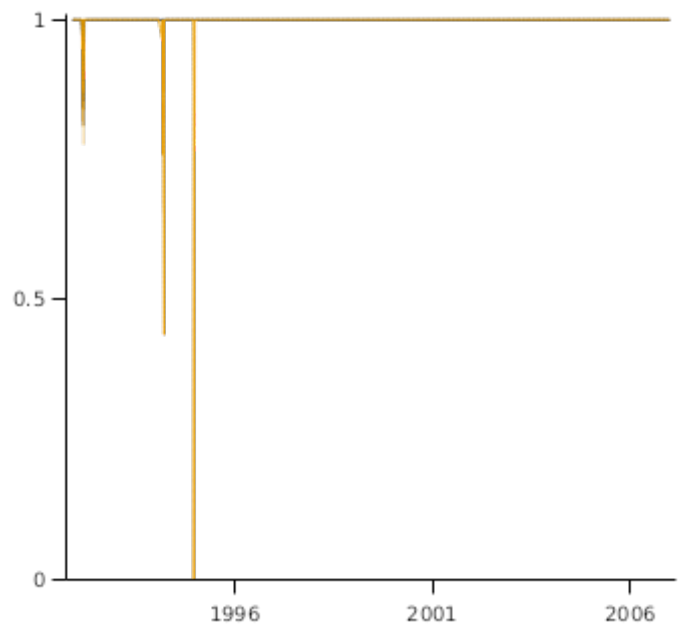
SurfaceMineralN vs Year
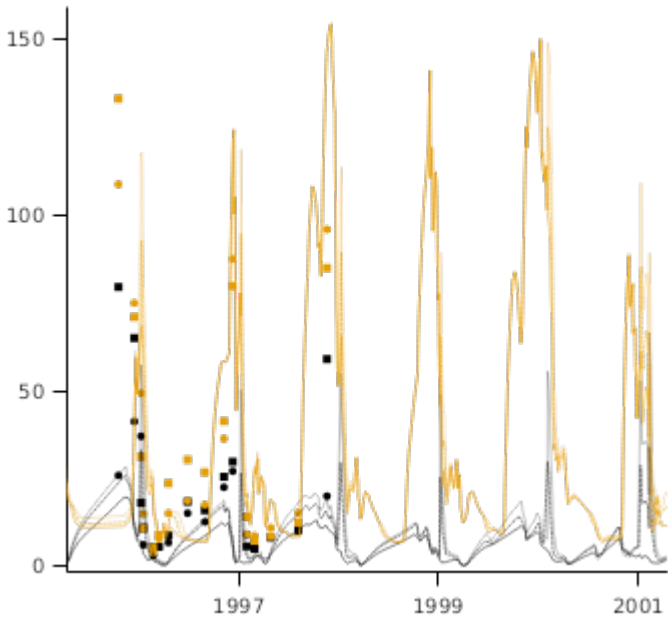
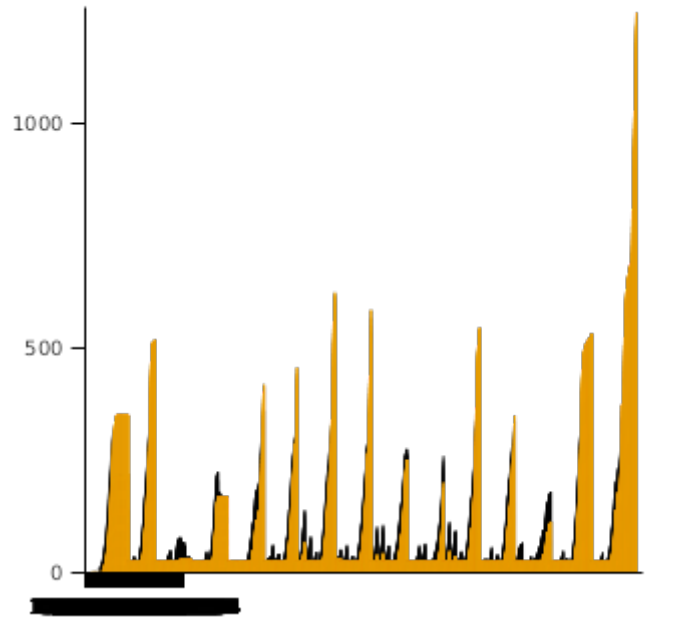**SurfaceMineralN PvsO**
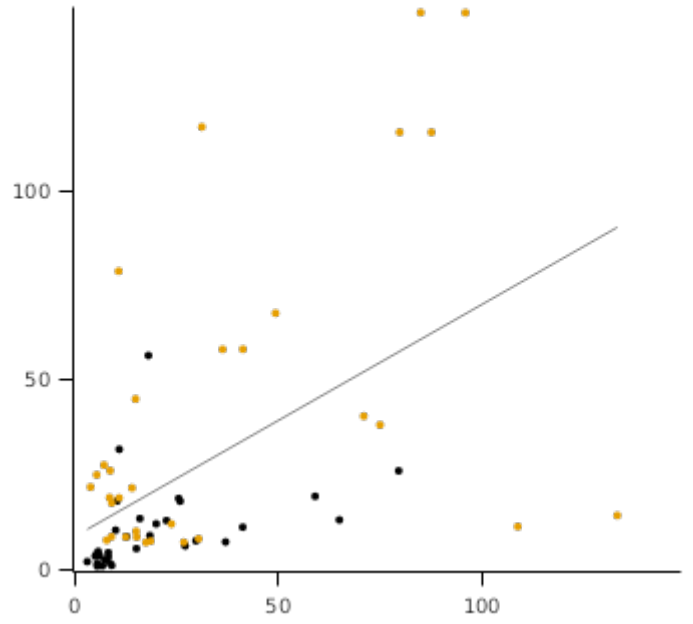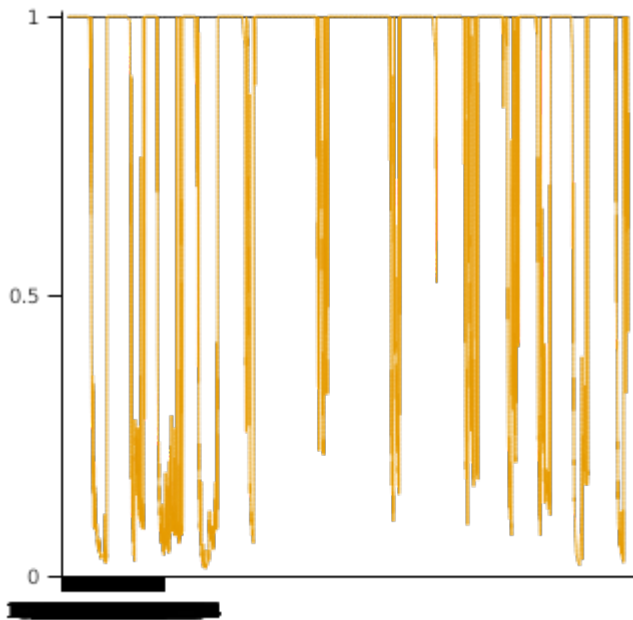
SuburfaceMineralN vs Year
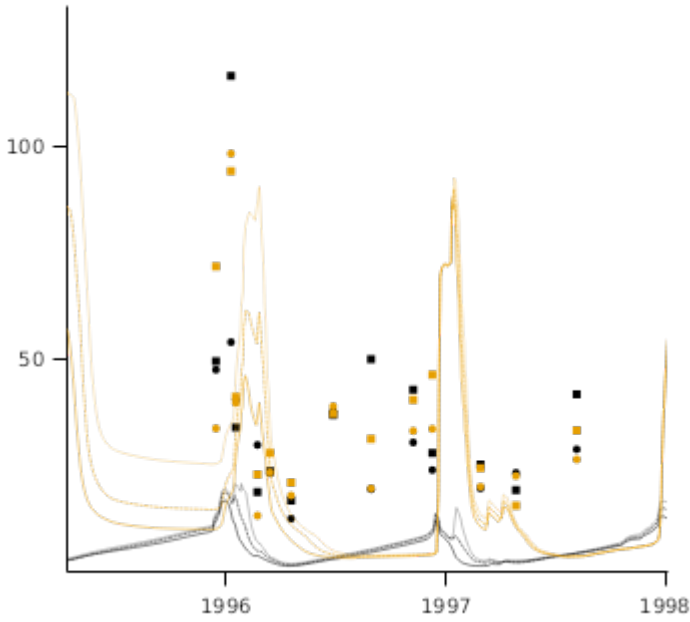
GrainSize PvsO
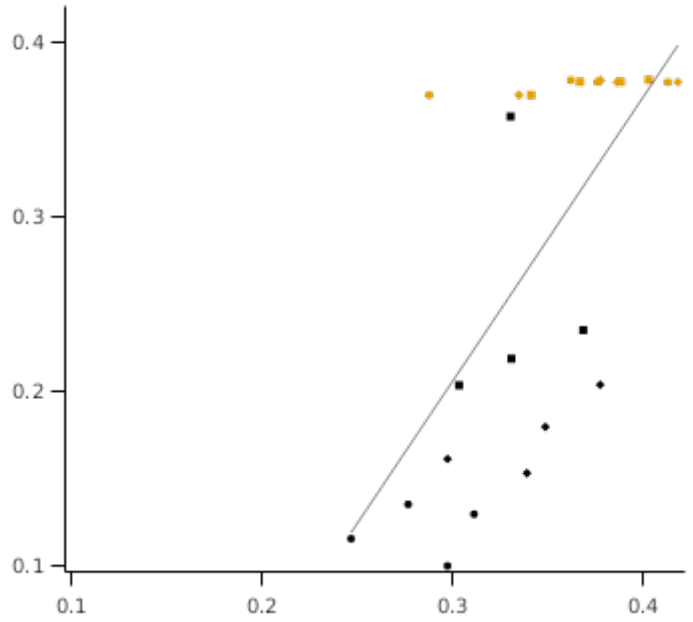
Grain No PvsO
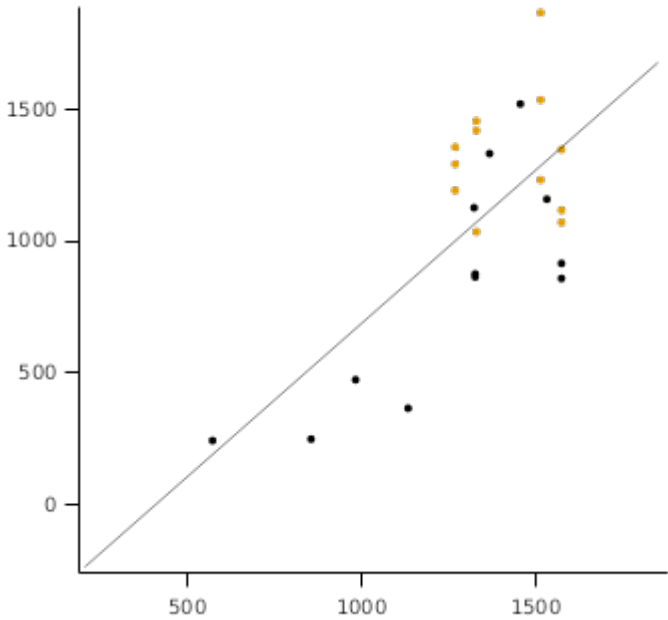
Gliricidia Wts

Gliricidia leafNconc
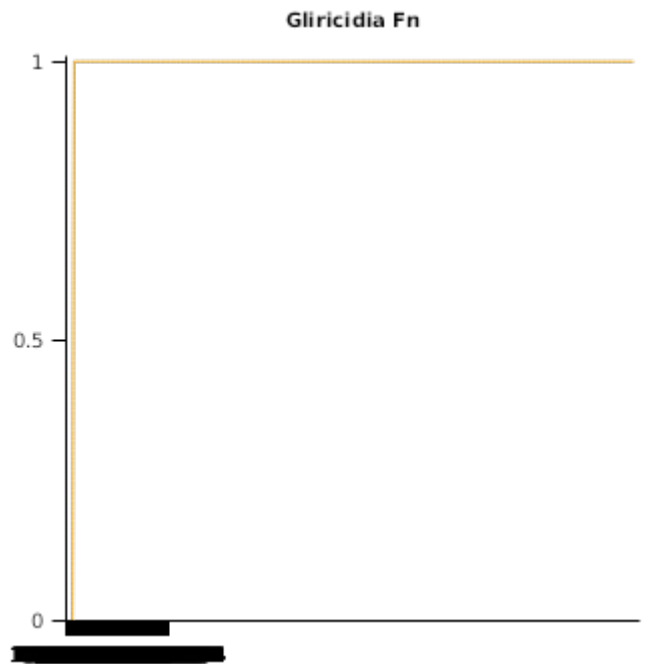
Gliricidia Fn

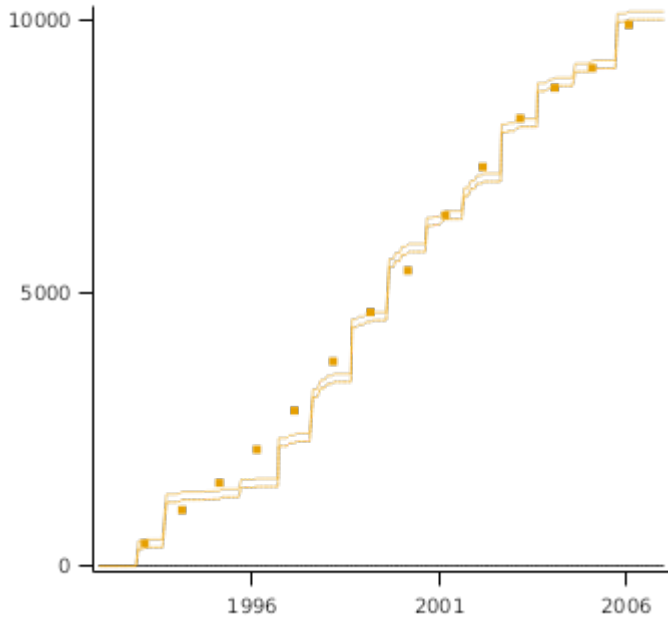**Gliricidia Fw**

N Fixed Daily
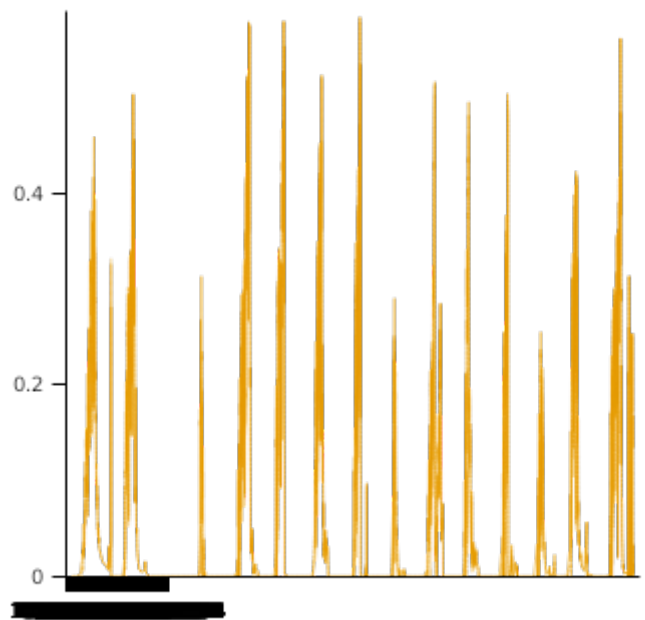
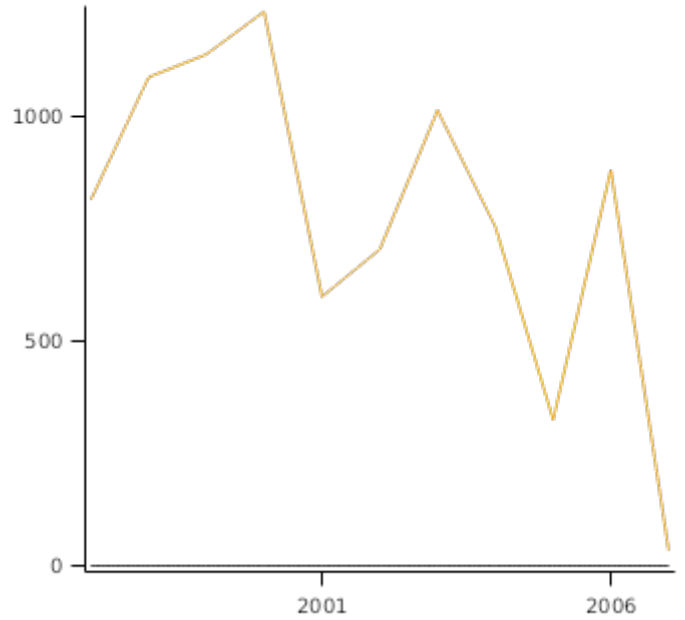**N Fixed Annual**
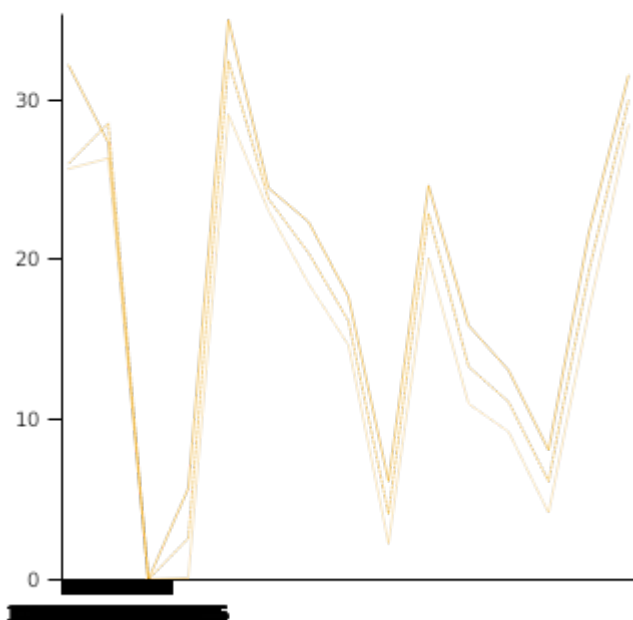
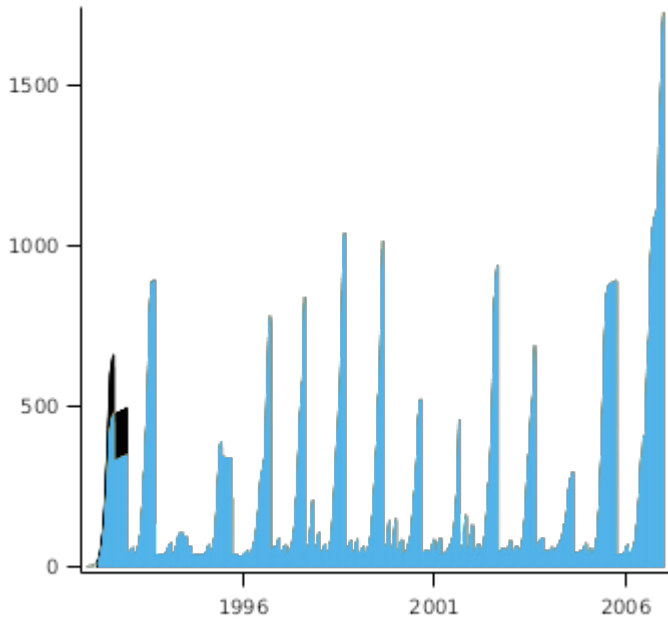**LeafRemovalWt**
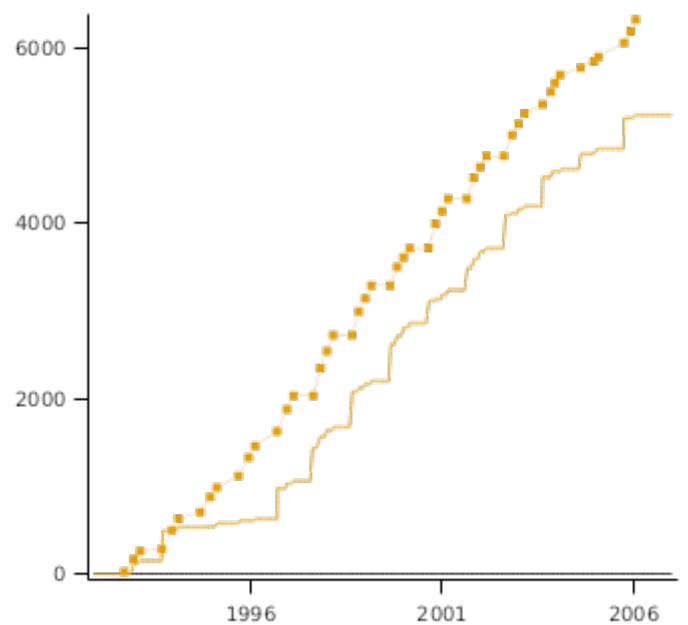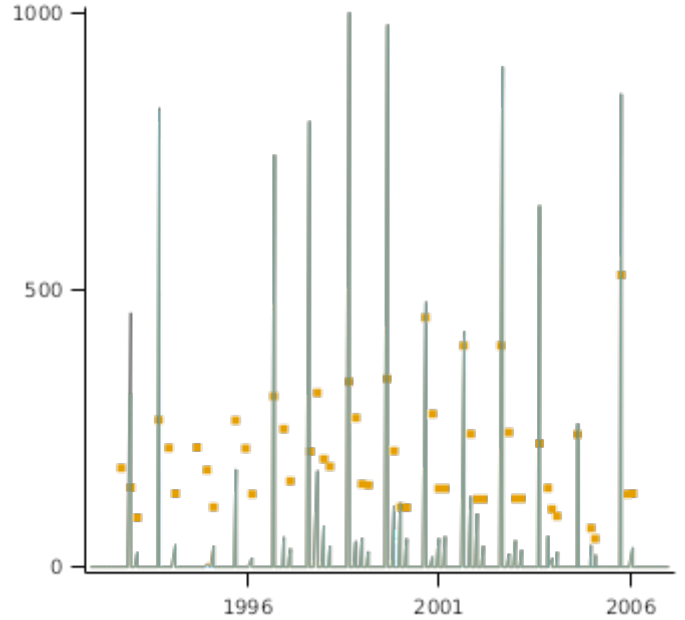
StemRemovalWt
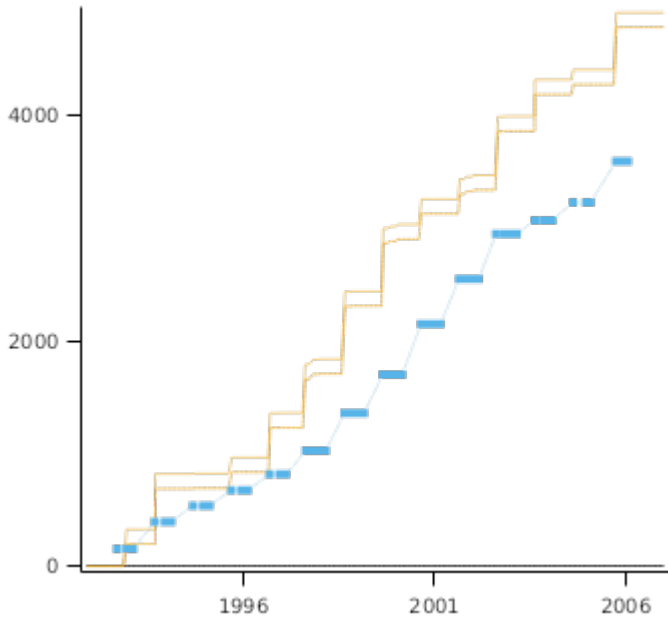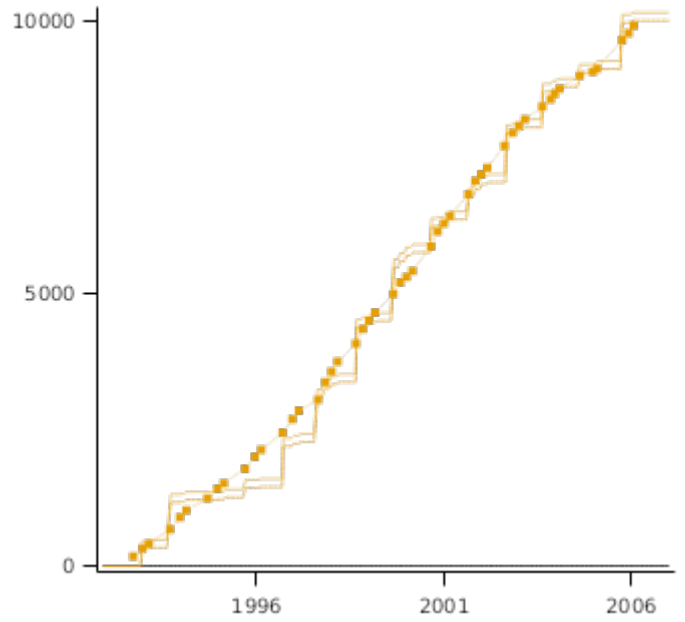
TotalRemovalWt
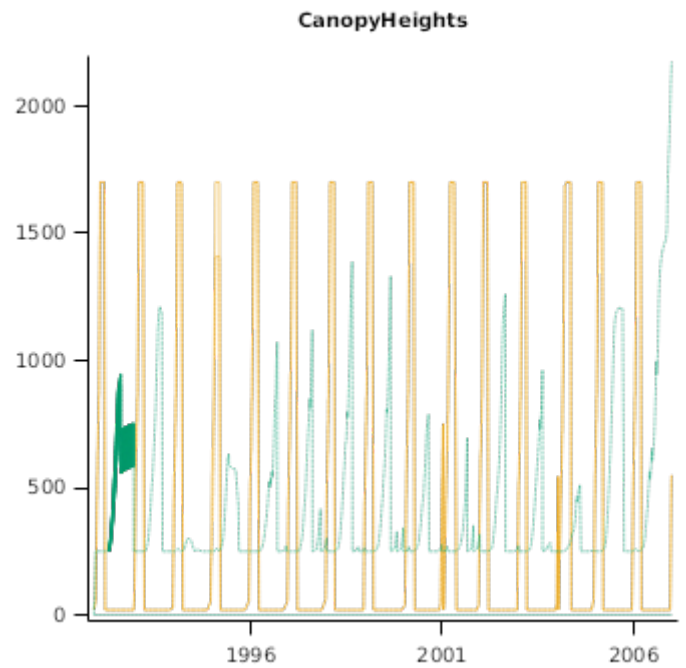
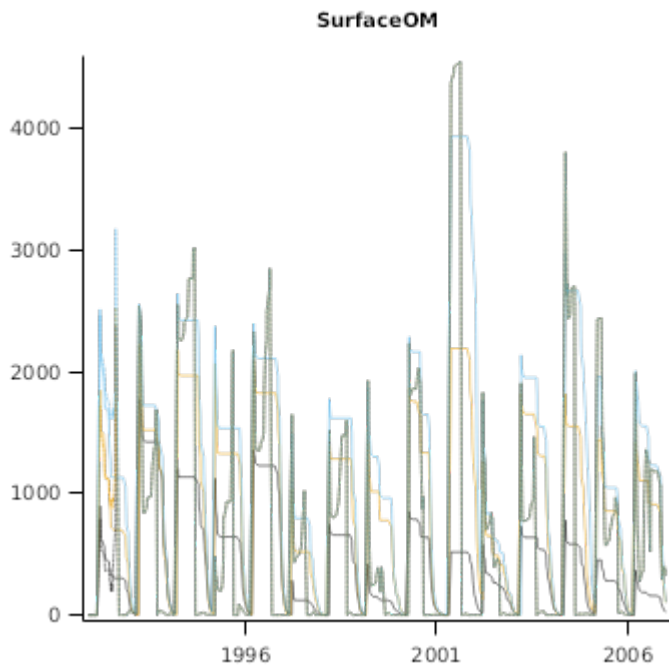**CumulativeTotalRemovalWt**

TotalRemovalWt Annual

Gliricidia AboveGroundWt

Gliricidia TotalRemovalWt vs Year

SurfaceOM

CanopyHeights
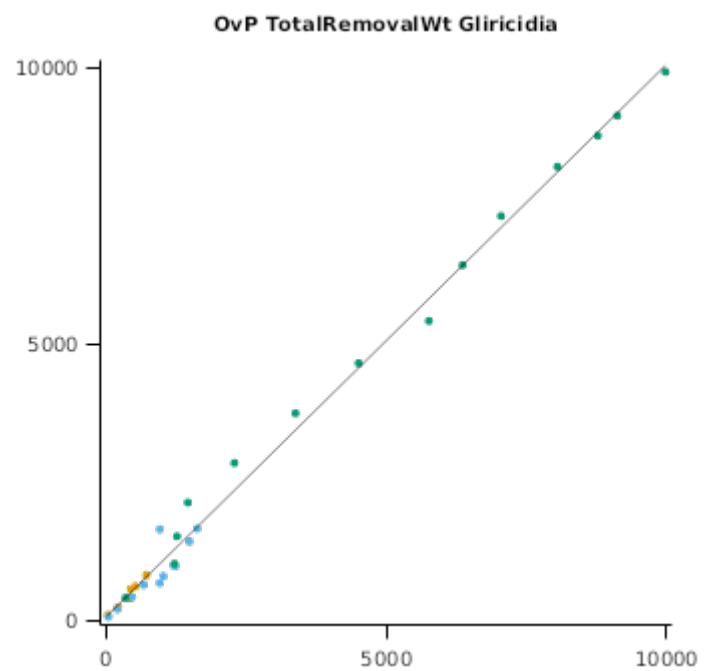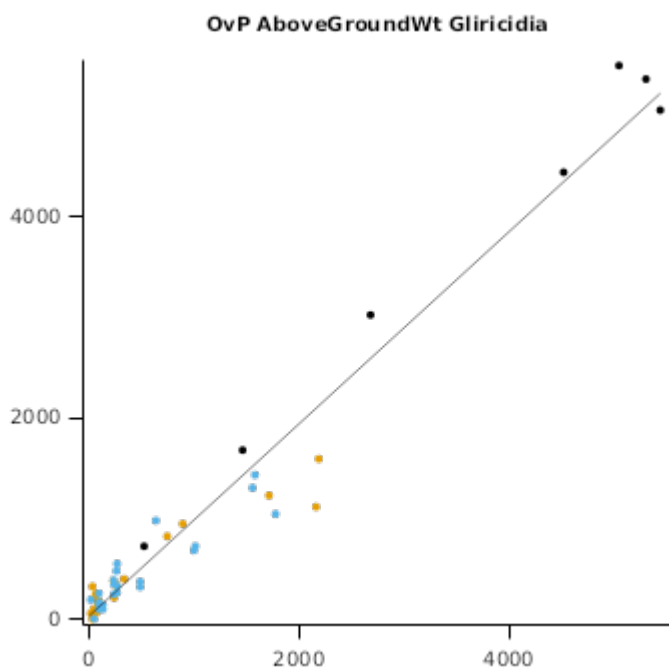
2.5 Combined Results

Combined results from all four sites indicates that the biomass growth of Gliricidia and amounts cut approximated those observed, which indicates that the Gliricidia model was adequate for these situations.

OvP AboveGroundWt Gliricidia

OvP TotalRemovalWt Gliricidia

3 Sensibility

3.1 StripCropping

This sensibility test checks that Gliricidia crops provide N supply to neighbouring maize crops in strip cropping situations. A simulation experiment has been constructed to simulate yield in Malawi. Yield response to Gliricidia was positive and was generally a little higher than to N ferilisation, and temporal variations were close to those for fertilised crops, as expected. However, under different conditions, N supply from residues or feriliser may not be sufficient in some wet years, and competition for water may reduce crop yield below fertilised sole crops in dry years. Finally, the benefits of the trees may take a few seasons to be realised.

Yield
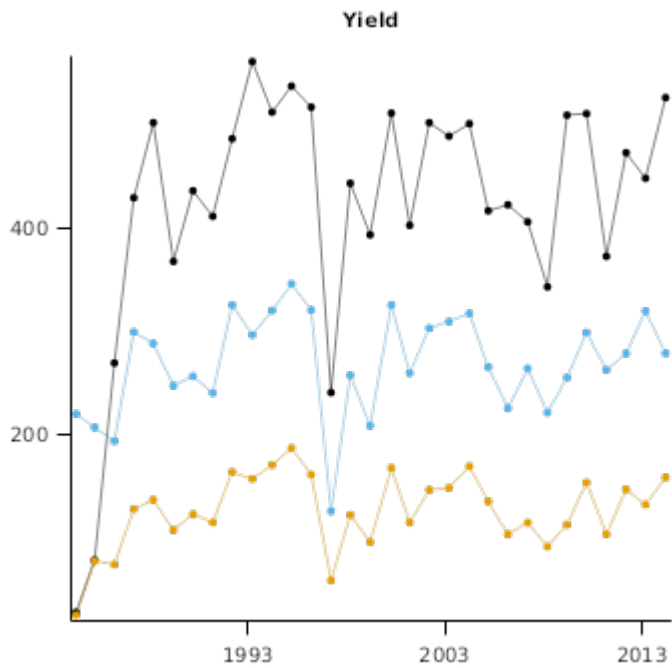
3.2 Temperature Response

The temperature requirements of Gliricidia sepium indicated by its distribution at native sites is for mean monthly temperatures in the range from approximately 21-29C (Simons et al., 1994). In addition we note: (1) Athanase Mukuralinda commented that gliricidia doesn't grow above about 1600 m in Rwanda, which occurs about half way along our Rwanda transect, and (2) There is a record of it growing on a transect up to 1000 m in Guatemala in its native range (Melchor-Marroqu\'\in et al., 1999). Gliricidia sheds leaves once night time temperatures fall below approximately 15C (Whiteman et al., 0), and the plant is susceptible to frosts unless pruned (Stewart J.L. et al., 1992). These tests should indicate a decrease in yield below an optimum average annual temperature, with negligible yield below about 19C.

List of experiments.

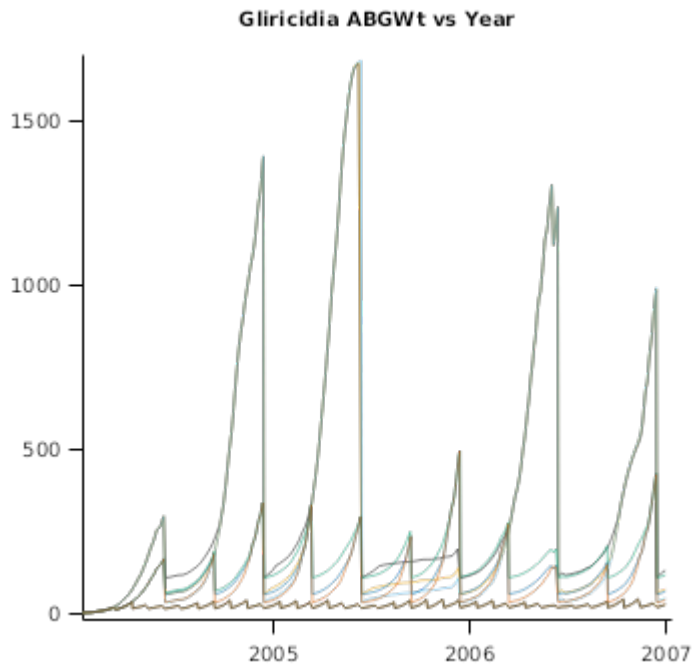| Experiment Name	Design (Number of Treatments)
GuatemalaTransect	Cell (8)
RwandaTransect	Cell (10)

Temperature Response
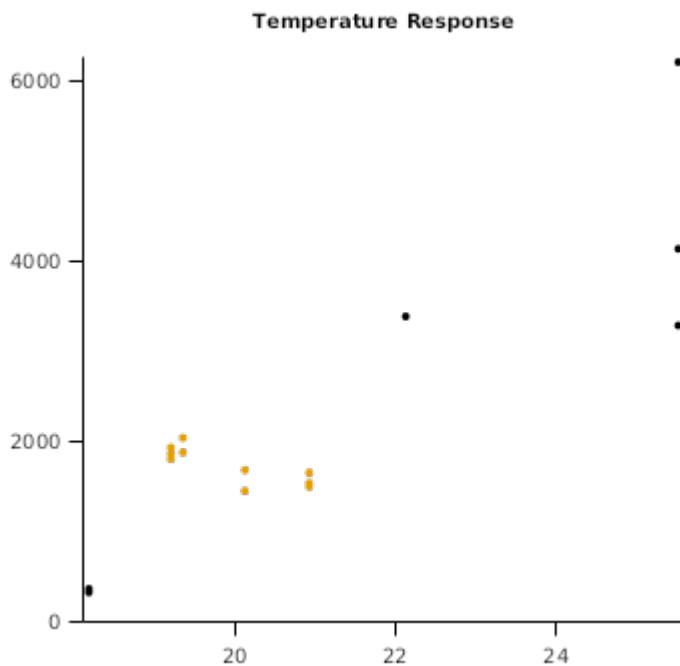
3.3 CuttingResponse

This sensibility test shows that biomass developoment is higher with a lower frequency of pruning and lower stump height of pruning, as showing in Duguma et al., 1988. This effect occurs because regrowth of shoots after pruning depends on carbohydrate remobilisation from roots and stumps. These reserves can be later replenished and added to once enough carbohydrate production and storage is reached in regrown shoots. This test applies these treatments to a hypothetical stand of gliricidia grown at the Makoka site in Malawi. In this test, cutting was done in factorial combinations of frequency (6-, 3-, and 1-monthly) and stump height (approximated by specifying the weight of stem remaining: 100 g, 50 g, or 25 g), while 10 g of leaf were left after pruning in all treatment combinations. These results may differ to those of Duguma et al., 1988 due to to the much warmer climate at Ibadan, Nigeria, compared to Makoka, Malawi, and weights of stump remaining (which was not reported by Duguma et al., 1988). Severe water stress was predicted to limit gliricidia growth in late 2005.

List of experiments.

Experiment Name	Design (Number of Treatments)
MakokaDuguma	Treat (9)

Gliricidia ABGWt vs Year

3.3.1 MakokaDuguma

Gliricidia Stem vs Year

Legend: F6H100, F6H50, F6H25, F3H100, F3H50, F3H25, F1H100, F1H50, F1H25
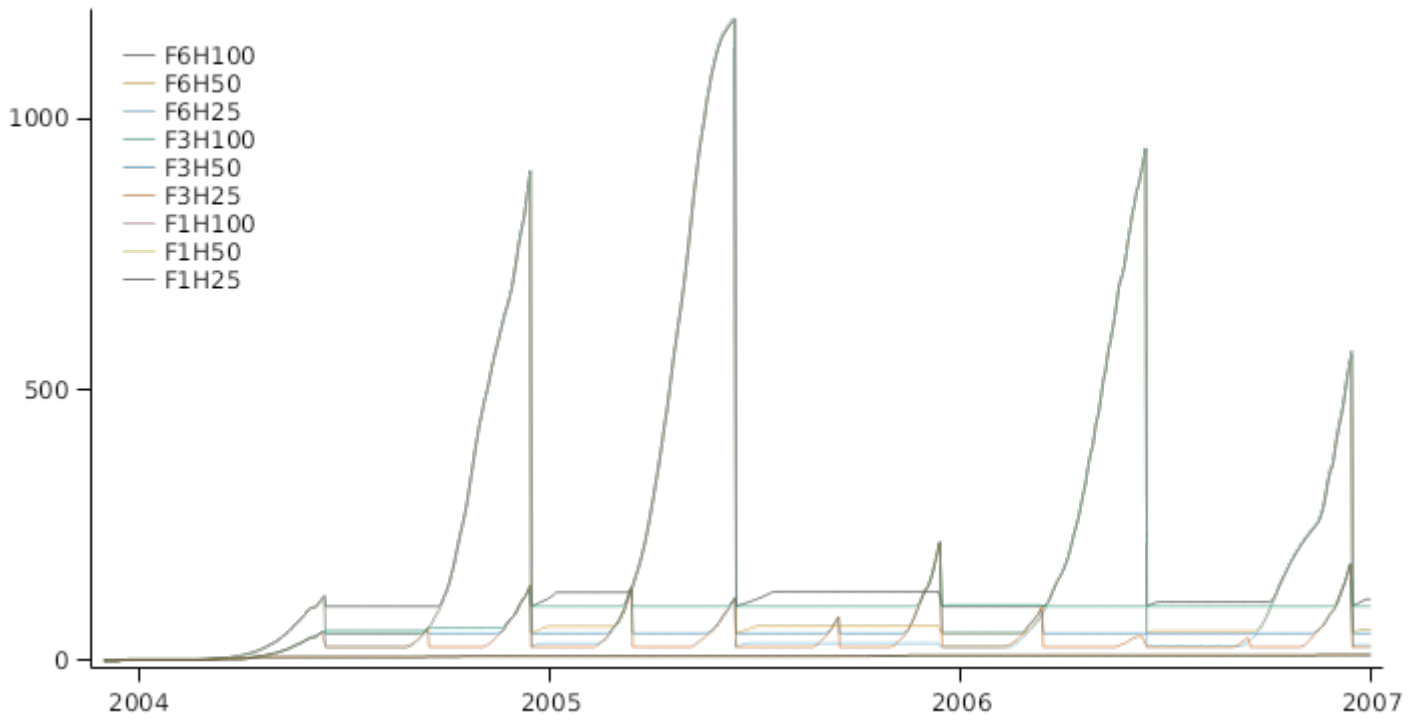
Gliricidia LeafWt vs Year

Legend: F6H100, F6H50, F6H25, F3H100, F3H50, F3H25, F1H100, F1H50, F1H25

Gliricidia Fw

Legend:
- F6H100
- F6H50
- F6H25
- F3H100
- F3H50
- F3H25
- F1H100
- F1H50
- F1H25

Gliricidia Fn

Legend:
- F6H100
- F6H50
- F6H25
- F3H100
- F3H50
- F3H25
- F1H100
- F1H50
- F1H25

N Fixed

Legend:
- F6H100
- F6H50
- F6H25
- F3H100
- F3H50
- F3H25
- F1H100
- F1H50
- F1H25

NFixedAnnual

Legend:
- F6H100
- F6H50
- F6H25
- F3H100
- F3H50
- F3H25
- F1H100
- F1H50
- F1H25
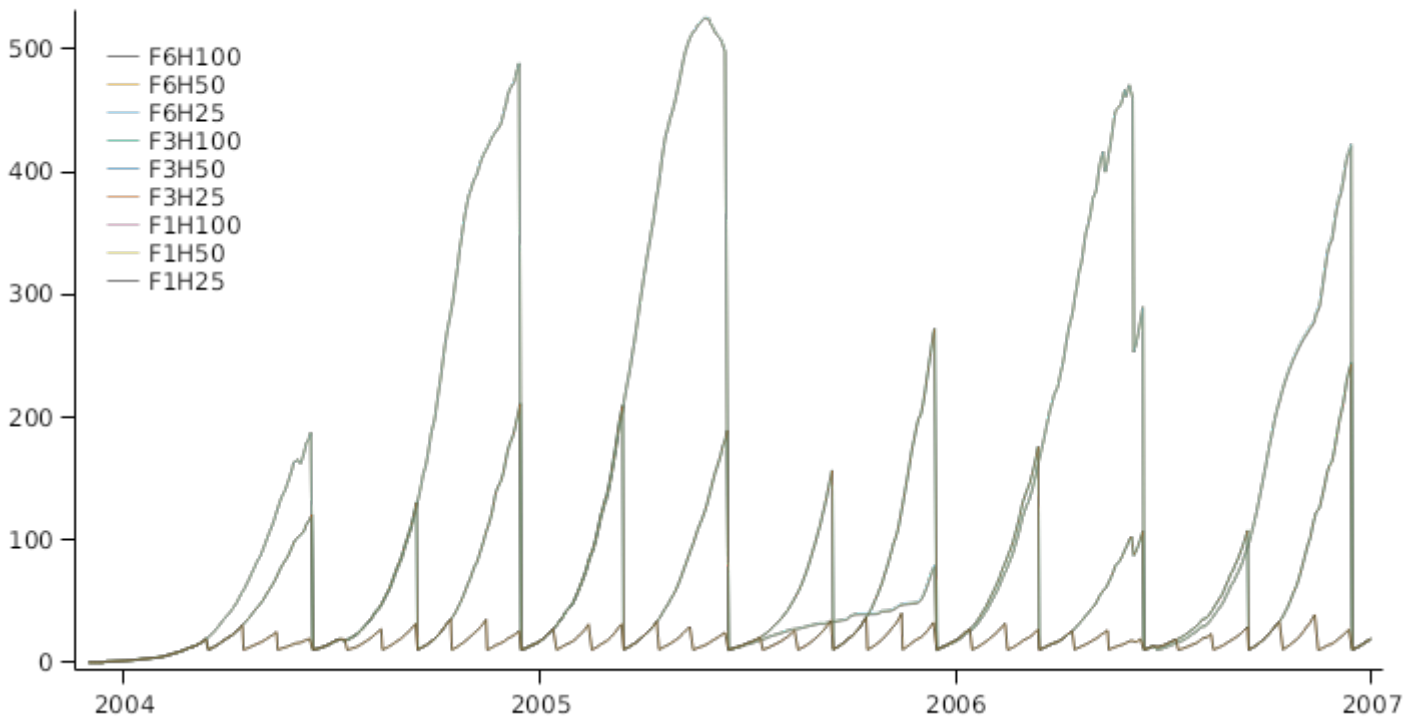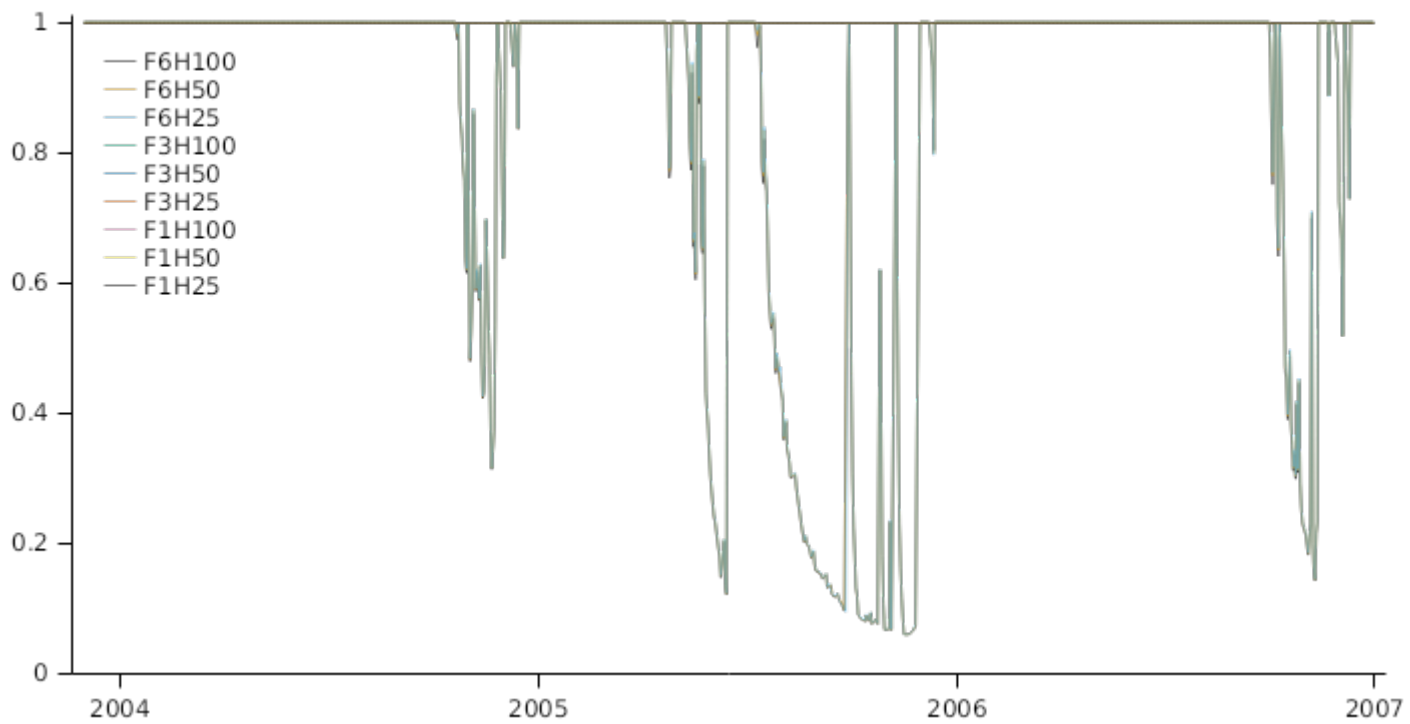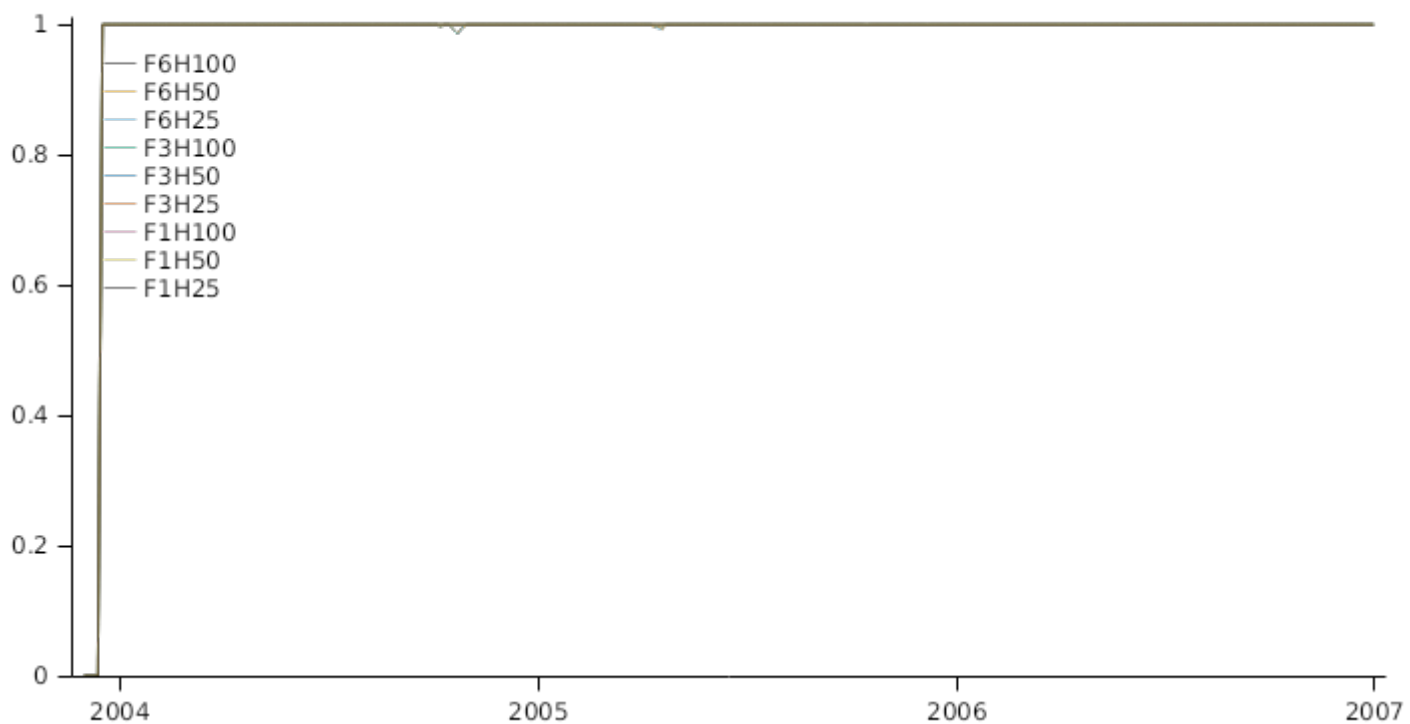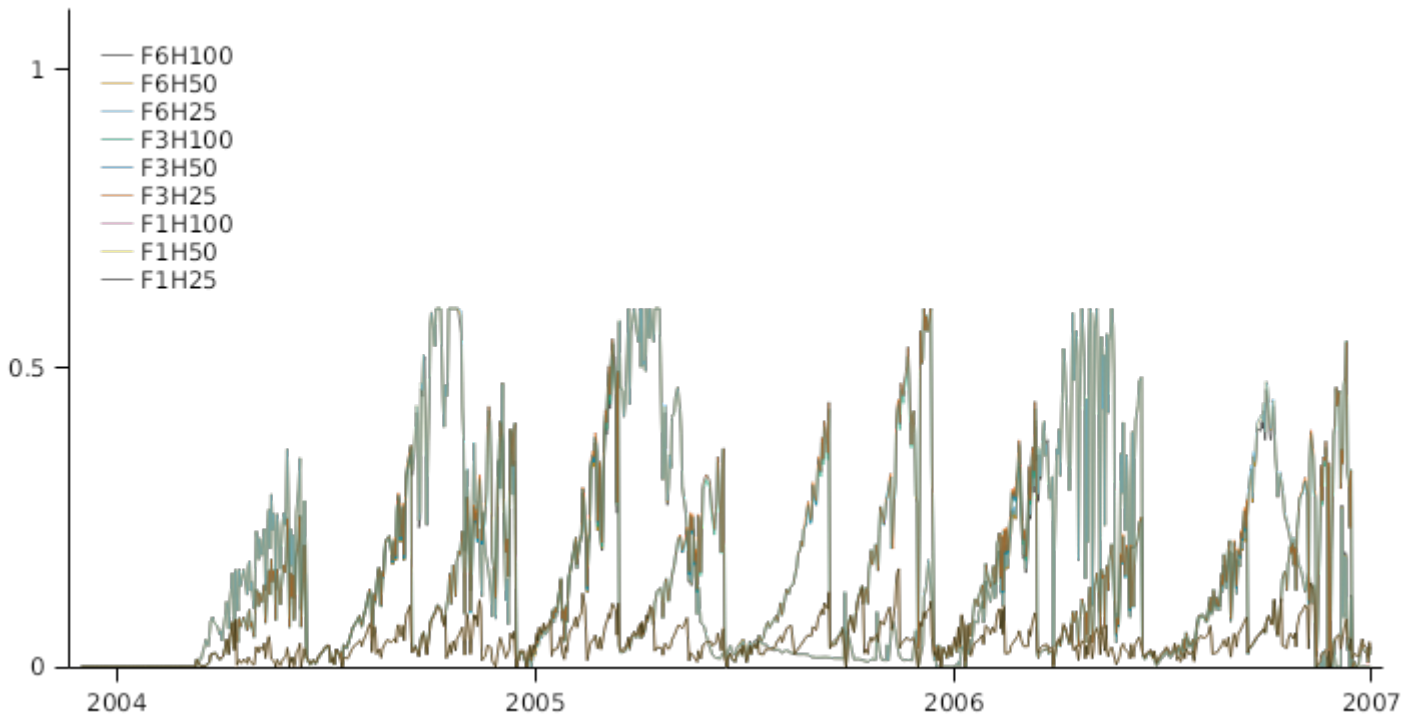
LAI

3.4 StockMassBalance

This sensibility test performs a livestock grazing mass balance check.

The MassBalanceCalculations script is intentionally before Stock in the simulation tree so that it will be called before the STOCK model does its calculati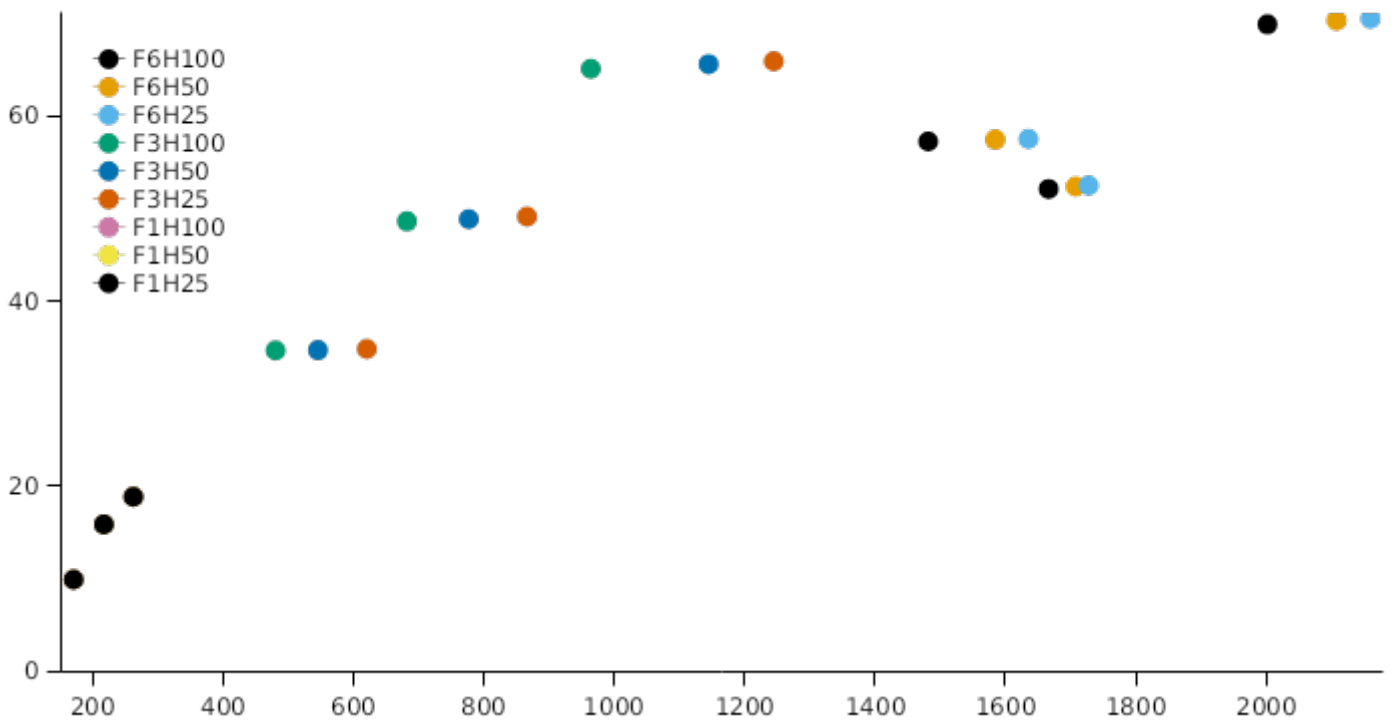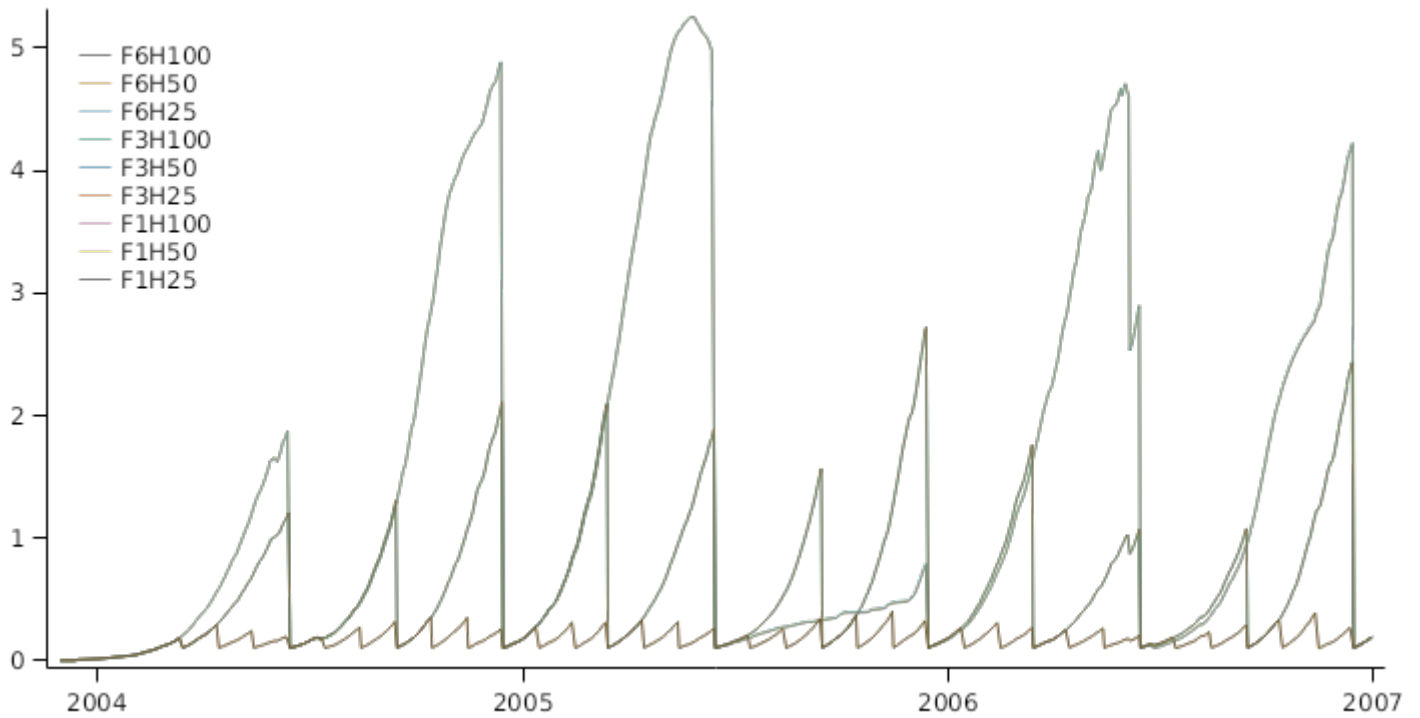ons for the day AND after the plant model has updated its biomass for the day. The script then stores the plant biomass before and after stock calculations its daily variables. It then calculates the amount of plant biomass removed:

```
PlantBiomassRemoved = PlantBiomassBeforeStock - PlantBiomassAfterStock;
```

It then subtracts the animal intake.

```
Lost = PlantBiomassRemoved - Intake;
```

The Lost variable (which is output) should always be zero. The script will throw an exception if this isn't the case.

The graph below shows the biomass removed from the plant is the same as the plant biomass consumed by the animal which results in a mass balance variable equal to zero.

Stock Plant Mass balance
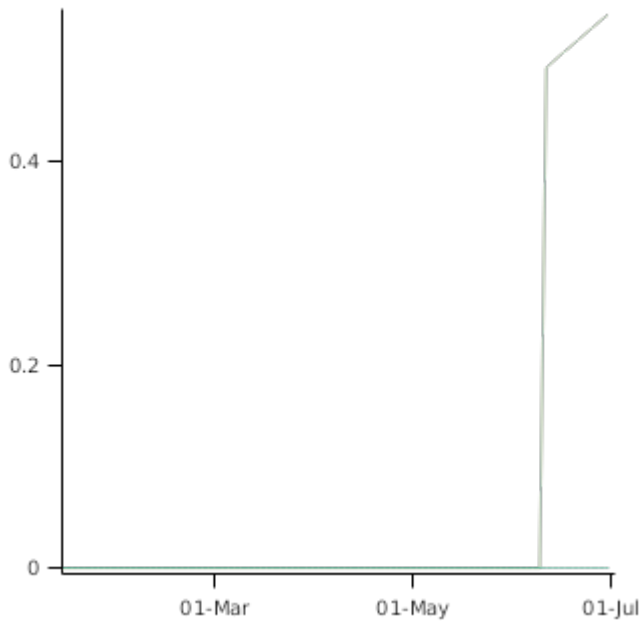
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