The APSIM Maize Model

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

The model consists of:

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

Background: The Agricultural Production Systems sIMulator (APSIM) is a farming systems modelling framework that is being actively developed by the APSIM Initiative.

It is comprised of:

1. a set of biophysical models that capture the science and management of the system being modelled,
2. a software framework that allows these models to be coupled together to facilitate data exchange between the models,
3. a community of developers and users who work together, to share ideas, data and source code,
4. a data platform to enable this sharing and
5. a user interface to make it accessible to a broad range of users.

The literature contains numerous papers outlining the many uses of APSIM applied to diverse problem domains. In particular, Holzworth et al., 2014; Keating et al., 2003; McCown et al., 1996; McCown et al., 1995 have described earlier versions of APSIM in detail, outlining the key APSIM crop and soil process models and presented some examples of the capabilities of APSIM.
The APSIM Initiative has begun developing a next generation of APSIM (APSIM Next Generation) that is written from scratch and designed to run natively on Windows, LINUX and MAC OSX. The new framework incorporates the best of the APSIM 7.x framework with an improved supporting framework. The Plant Modelling Framework (a generic collection of plant building blocks) was ported from the existing APSIM to bring a rapid development pathway for plant models. The user interface paradigm has been kept the same as the existing APSIM version, but completely rewritten to support new application domains and the newer Plant Modelling Framework. The ability to describe experiments has been added which can also be used for rapidly building factorials of simulations. The ability to write C# scripts to control farm and paddock management has been retained. Finally, all simulation outputs are written to an SQLite database to make it easier and quicker to query, filter and graph outputs.

The model described in this documentation is for APSIM Next Generation.

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1 Introduction

The APSIM Maize model has been tested on a range of datasets from around the world to provide tests across a range of environmental conditions. Tests include ranges in plant population, nitrogen management and irrigation levels, as well as including historical datasets from Africa using cultivars developed during the 1960's, through to modern varieties grown in the American mid-West.
2 Model description

2.1 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 remains within an organ once it is partitioned there
- **Metabolic biomass** which generally remains within an organ but is able to be re-allocated when the organ senesces and may be re-translocated when demand is high relative to supply.
- **Non-structural biomass** which is partitioned to organs when supply is high relative to demand and is available for re-translocation to other organs whenever supply from uptake, fixation and re-allocation is lower than demand.

The process followed for biomass arbitration is shown in Figure 1. Arbitration responds to events broadcast daily by the central APSIM infrastructure:

1. **doPotentialPlantGrowth.** When this event is broadcast 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.** Non-structural 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.

2. **doPotentialPlantPartitioning.** On this event the Arbitrator first executes the DoDMSetup() method to establish the DM supplies and demands from each organ. 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() establish N supplies and Demands 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 the plants demand for N uptake from the soil (N Uptake Demand).

3. **doNutrientArbitration.** When this event is broadcast by the model framework 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.

4. **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.
Plant Arbitrator class (instance)

1. doPotentialPlantPartitioning
   - DoDMSetup()
   - DoPotentialDMAllocation()
   - DoNSetup()
   - DoNRallocation()
   - DoNUptakeAllocations()

2. doPotentialPlantPartitioning
   - Pass DM variables
   - Pass N Variables
   - N Uptake Demand

3. doNutrientArbitration
   - N Allocation to other plants
   - N Uptake demands from other plants

4. doActualPlantPartitioning
   - DoNFixation()
   - DoNRtranslocation()
   - DoActualDMallocation()

5. doActualPlantGrowth
   - Set Final N Allocation
   - Pass Final DM Allocation

Organ class (instance)

1. doPotentialPlantGrowth
   - DM properties
     - DM Demand
     - DM Realloc Supply
     - DM Photo Supply
     - DM Retrans Supply
     - DM Sink Capacity
     - Potential DM Alloc
   - Set potential DM allocation
   - Calculate N demand

2. N properties
   - N Realoc Supply
   - N Fixation Supply
   - N Retrans Supply
   - MaxNConc
   - MinNConc
   - N Demand

3. Biomass State Variables
   - Structural DM
   - Metabolic DM
   - NonStructural DM
   - Structural N
   - Metabolic N
   - NonStructural N
   - Organ Size

4. Allocation properties
   - DM Allocation
   - N Allocation
   - DM Realloc
   - N Realloc
   - DM Excess Alloc
   - N Uptake
   - DM Retransloc
   - N Retransloc

Soil Arbitrator class

- Allocate uptakes
- SetUpSupply&Demands
Figure 1. Schematic showing procedure for arbitration of biomass partitioning. Pink boxes are events that are broadcast each day by the model infrastructure and their numbering shows the order of procedure. Blue boxes are methods that are called when these events are broadcast. Orange boxes contain properties that make up the organ/arbitrator interface. Green boxes are organ specific properties.

Arbitration is performed in two passes for each of the biomass supply sources. On the first pass, structural and metabolic biomass is allocated to each organ based on their demand relative to the demand from all organs. On the second pass any remaining biomass is allocated to non-structural demands based on the organ's relative demand.

2.2 Phenology

This model simulates the development of the crop through successive developmental phases. Each phase is bound by distinct growth stages. Phases often require a target to be reached to signal movement to the next phase. Differences between cultivars are specified by changing the values of the default parameters shown below.

2.2.1 ThermalTime

\[ \text{ThermalTime} = \text{BaseThermalTime} \]

Where:

A value is calculated from the mean of 3-hourly estimates of air temperature based on daily max and min temperatures.

\[
\begin{align*}
  X & \quad Y \\
  0 & \quad 0 \\
  18 & \quad 10 \\
  26 & \quad 18 \\
  34 & \quad 26 \\
  44 & \quad 0
\end{align*}
\]

2.2.2 Germinating Phase

This phase goes from Sowing to Germination.

This model assumes that germination will be complete on any day after sowing if the extractable soil water is greater than zero.

2.2.3 Emerging Phase

This phase goes from Germination to Emergence.

This phase simulates time to emergence as a function of sowing depth. The ThermalTime Target from Sowing to Emergence is given by:

\[ \text{Target} = \text{SowingDepth} \times \text{ShootRate} + \text{ShootLag} \]

Where:

- \( \text{ShootRate} = 0.6 \) (deg day/mm),
- \( \text{ShootLag} = 55 \) (deg day),
and \( \text{SowingDepth} \) (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:

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

### 2.2.4 Juvenile Phase

This phase goes from Emergence to EndJuvenile.

It uses a ThermalTime Target to determine the duration between development Stages. ThermalTime is accumulated until the Target is met and remaining ThermalTime is forwarded to the next phase.

Target = 200 (deg day)

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

### 2.2.5 Photosensitive Phase

This phase goes from EndJuvenile to FloralInitiation.

It uses a ThermalTime Target to determine the duration between development Stages. ThermalTime is accumulated until the Target is met and remaining ThermalTime is forwarded to the next phase.

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

The photoperiod is likely to vary with individual maize cultivars. Therefore, the response shown here is indicative only. See the descriptions of individual cultivars for more detail on photoperiod responses used by the maize model.

Target is calculated as a function of [Phenology].Photoperiod

\[
\begin{array}{c|c}
X & Y \\
0 & 0 \\
12.5 & 0 \\
24 & 10 \\
\end{array}
\]

### 2.2.6 LeafAppearance Phase

This phase goes from FloralInitiation to FlagLeaf.

This phase extends from the end of the previous phase until the final main-stem leaf has finished expansion. The duration of this phase is determined by leaf appearance rate and the final main stem node number. As such, the model parameterisation of leaf appearance and final leaf number (set in the Structure object) are important for predicting the duration of the crop correctly.

### 2.2.7 FlagLeafToFlowering Phase

This phase goes from FlagLeaf to Flowering.

It uses a ThermalTime Target to determine the duration between development Stages. ThermalTime is accumulated until the Target is met and remaining ThermalTime is forwarded to the next phase.
Target = 50 (deg day)

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

2.2.8 FloweringToGrainFilling Phase

This phase goes from Flowering to StartGrainFill.

It uses a ThermalTime Target to determine the duration between development Stages. ThermalTime is accumulated until the Target is met and remaining ThermalTime is forwarded to the next phase.

Target = 120 (deg day)

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

2.2.9 GrainFilling Phase

This phase goes from StartGrainFill to EndGrainFill.

It uses a ThermalTime Target to determine the duration between development Stages. ThermalTime is accumulated until the Target is met and remaining ThermalTime is forwarded to the next phase.

Target = 550 (deg day)

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

2.2.10 Maturing Phase

This phase goes from EndGrainFill to Maturity.

It uses a ThermalTime Target to determine the duration between development Stages. ThermalTime is accumulated until the Target is met and remaining ThermalTime is forwarded to the next phase.

Target = 10 (deg day)

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

2.2.11 MaturityToHarvestRipe Phase

This phase goes from Maturity to HarvestRipe.

It uses a ThermalTime Target to determine the duration between development Stages. ThermalTime is accumulated until the Target is met and remaining ThermalTime is forwarded to the next phase.

Target = 10 (deg day)

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

2.2.12 ReadyForHarvesting Phase

This phase goes from HarvestRipe to Unused.

The end phase in phenology

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

2.2.13 Photoperiod

Returns the value of today's photoperiod calculated using the specified latitude and twilight sun angle threshold. If variable called ClimateControl.PhotoPeriod can be found this will be used instead.

Twilight = -6 (degrees)

2.2.14 FloweringDAS
A function is used to provide flowering date as days after sowing (DAS).

Before Flowering

\[ PreEventValue = 0 \]

On Flowering the value is set to:

\[ PostEventValue = [Phenology].DaysAfterSowing \]

### 2.2.15 MaturityDAS

A function is used to provide maturity date as days after sowing (DAS).

Before Maturity

\[ PreEventValue = 0 \]

On Maturity the value is set to:

\[ PostEventValue = [Phenology].DaysAfterSowing \]

### 2.3 Structure

The structure model calculates structural development of the plant. This includes the number of primordia, leaves, stems and nodes, as well as overall plant height.

\[ BranchingRate = 0 \text{ (/node)} \]

\[ zMainStemFinalNodeNumber = 15 \]

Though tillering is common in some maize varieties under certain agronomic conditions, no tillering is accounted for within this model. Therefore all branching has been parameterised out of the current maize model.

\[ ThermalTime = [Phenology].ThermalTime \]

The value of MainStemNodeAppearanceRate from Emergence to FlagLeaf is calculated as follows:

\[ Phyllochron \] is calculated as a function of \[ [Structure].LeafTipsAppeared \]

\[ \begin{array}{cc}
X & Y \\
1 & 30 \\
3.4 & 30 \\
4 & 42 \\
\end{array} \]

#### 2.3.1 HeightModel

Calculates the potential height increment and then multiplies it by the smallest of any childern functions (Child functions represent stress).

#### 2.3.1.1 PotentialHeight
PotentialHeight is calculated as a function of [Phenology].Stage

\[
\begin{array}{|c|c|}
\hline
\text{Stage} & \text{PotentialHeight} \\
\hline
3 & 20 \\
4 & 400 \\
5 & 450 \\
6 & 1700 \\
\hline
\end{array}
\]

2.3.1.2 WaterStress

WaterStress is calculated as a function of [Maize].WaterSupplyDemandRatio

\[
\begin{array}{|c|c|}
\hline
\text{WaterSupplyDemandRatio} & \text{WaterStress} \\
\hline
0 & 0 \\
0.6 & 1 \\
\hline
\end{array}
\]

2.3.2 BranchMortality

\[
\text{BranchMortality} = \text{ShadeInducedBranchMortality} + \text{DroughtInducedBranchMortality}
\]

Where:

\[
\begin{align*}
\text{ShadeInducedBranchMortality} &= 0 \\
\text{DroughtInducedBranchMortality} &= 0
\end{align*}
\]

MainStemFinalNodeNumber is the same as ValueToHold.Value until it reaches FloralInitiation stage when it fixes its value

2.3.2.1 ValueToHold

\[
\text{ValueToHold} = \text{PrimordiaAtEmergence} + \text{PrimordiaDuringJuvenilePhase}
\]

Where:

\[
\text{PrimordiaAtEmergence} = 6
\]
PrimordiaDuringJuvenilePhase = AddFunction / MeanPlastochron

Where:


The value of MeanPlastochron from Germination to Emergence is calculated as follows:

Constant = 15

The value of MeanPlastochron from Emergence to FlagLeaf is calculated as follows:

MeanPlastochron = AccumulatedPlastochron / Days

Where:

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

Plastochron = [Structure].MainStemNodeAppearanceRate x LeafTipsPerPrimordia

Where:

LeafTipsPerPrimordia = 0.5

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

Constant = 1

2.4 Grain

This organ uses a generic model for plant reproductive components. Yield is calculated from its components in terms of organ number and size (for example, grain number and grain size).

InitialGrainProportion = 0.05

MaximumPotentialGrainSize = 0.3 (g)

MaximumGrainsPerCob = 700 (number)

MinimumNConc = 0.008 (g/g)

Water content used to calculate a fresh weight.

WaterContent = 0.12 (g/g)

The value of DMDemandFunction from Flowering to StartGrainFill is calculated as follows:

Filling rate is calculated from grain number, a maximum mass to be filled and the duration of the filling process.

NumberFunction = [Grain].NumberFunction

FillingDuration = [Phenology].FloweringToGrainFilling.Target

ThermalTime = [Phenology].ThermalTime

PotentialSizeIncrement = [Grain].InitialGrainProportion x [Grain].MaximumPotentialGrainSize

The value of DMDemandFunction from StartGrainFill to EndGrainFill is calculated as follows:
Filling rate is calculated from grain number, a maximum mass to be filled and the duration of the filling process.

\[ NumberFunction = [Grain].NumberFunction \]

\[ FillingDuration = [Phenology].GrainFilling.Target \]

\[ ThermalTime = [Phenology].ThermalTime \]

\[ PotentialSizeIncrement = \text{ProportionLinearPhase} \times [Grain].MaximumPotentialGrainSize \]

Where:

\[ \text{ProportionLinearPhase} = 1 - [Grain].InitialGrainProportion \]

The value of MaximumNConc from Flowering to StartGrainFill is calculated as follows:

\[ InitialNconc = 0.05 \]

The value of MaximumNConc from StartGrainFill to EndGrainFill is calculated as follows:

\[ FinalNconc = 0.013 \]

The value of NFillingRate from Flowering to EndGrainFill is calculated as follows:

Filling rate is calculated from grain number, a maximum mass to be filled and the duration of the filling process.

\[ NumberFunction = [Grain].NumberFunction \]

\[ FillingDuration = [Phenology].FloweringToGrainFilling.Target + [Phenology].GrainFilling.Target \]

\[ ThermalTime = [Phenology].ThermalTime \]

\[ PotentialSizeIncrement = MaximumFinalNConc \times [Grain].MaximumPotentialGrainSize \]

Where:

\[ MaximumFinalNConc = 0.013 \]

### 2.4.1 NumberFunction

\[ NumberFunction = [MaximumGrainsPerCob] \times \text{GrowthRateFactor} \times [Maize].Population \]

Where:

\[ \text{GrowthRateFactor} \] is calculated as a function of \([\text{GrowthRateGrainDevelopment}]\)

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.55</td>
<td>0</td>
</tr>
<tr>
<td>3.3</td>
<td>0.6</td>
</tr>
<tr>
<td>6.6</td>
<td>1</td>
</tr>
<tr>
<td>10</td>
<td>1</td>
</tr>
</tbody>
</table>
2.4.2 YieldBuPerAcre

\[
\text{YieldBuPerAcre} = \text{[Grain].Live.Wt} \times 10^{-5} \times 56 \times 0.4536 \times 2.471
\]

2.4.3 GrowthGrainDevelopment

\text{GrowthGrainDevelopment} is a daily accumulation of the values of functions listed below between the FlagLeaf and StartGrainFill stages. Function values added to the accumulate total each day are:

\[
\text{DailyBiomassProduction} = \text{[Arbitrator].DMSupply}
\]

2.4.4 DaysGrainDevelopment

\text{DaysGrainDevelopment} is a daily accumulation of the values of functions listed below between the FlagLeaf and StartGrainFill stages. Function values added to the accumulate total each day are:

\[
\text{LengthOfADay} = 1 \text{ (days/day)}
\]

2.4.5 GrowthRateGrainDevelopment

\[
\text{GrowthRateGrainDevelopment} = \frac{\text{[GrowthGrainDevelopment]}}{\text{[DaysGrainDevelopment]}} / \text{[Maize].Population}
\]

2.4.6 BiomassRemovalDefaults

If a \textit{harvest} is performed and no fractions are specified then 100\% of grain biomass will be removed with none of it going to the surface organic matter pool.

If a \textit{cut} is performed and no fractions are specified then 100\% of grain biomass will be removed with none of it going to the surface organic matter pool.

If a \textit{prune} is performed and no fractions are specified then 80\% of grain biomass will be removed with all of it going to the surface organic matter pool.

If a \textit{graze} is performed and no fractions are specified then 80\% of grain biomass will be removed with 20\% of it going to the surface organic matter pool.

2.5 Root

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

\textbf{Root Growth}

Roots grow downward through the soil profile and rate is determined by \textit{RootFrontVelocity}. The \textit{RootFrontVelocity} is also influenced by the extension resistance posed by the soil, parameterised using the soil \textit{XF} value.

\textbf{Dry Matter Demands}

100\% of the dry matter (DM) demanded from the root is structural. The daily DM demand from root is calculated as a proportion of total DM supply using a \textit{PartitionFraction} function. The daily loss of roots is calculated using a \textit{SenescenceRate} function.

\textbf{Nitrogen Demands}

The daily structural N demand from root is the product of total DM demand and a nitrogen concentration of MinimumNConc\%.

\textbf{Nitrogen Uptake}
Potential N 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 mineral nitrogen in the layer, a factor controlling the rate of extraction (kNO$_3$ and kNH$_4$), the concentration of N (ppm) and a soil moisture factor which decreases as the soil dries. Nitrogen uptake demand is limited to the maximum of potential uptake and the plants N demand. Uptake N demand is then passed to the soil arbitrator which determines how much of their Nitrogen uptake demand each plant instance will be allowed to take up.

**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, and a factor controlling the rate of extraction (KL). The KL values are set in the soil and may be further modified by the crop via KLModifier, KNO3 and KN4.

No effect of soil water content on root growth is currently captured in the model.

\[
\text{SoilWaterEffect} = 1
\]

Maximum daily N uptake is set to an arbitrarily high value.

\[
\text{MaxDailyNUptake} = 20 \text{ (g/m2/d)}
\]

Jones and Kiniry (1986) used a constant root senescence fraction in the CERES-Maize model.

\[
\text{SenescenceRate} = 0.005 \text{ (/d)}
\]

\[
\text{StructuralFraction} = 1
\]

\[
\text{MaximumRootDepth} = 1000000 \text{ (0-1)}
\]

\[
\text{MaximumNConc} = 0.01 \text{ (g/g)}
\]

\[
\text{MinimumNConc} = 0.01 \text{ (g/g)}
\]

\[
\text{InitialDM} = 0.2 \text{ (g/plant)}
\]

\[
\text{SpecificRootLength} = 40 \text{ (m/g)}
\]

### 2.5.1 KLModifier

The parameter KL is described by Meinke et al (1993) to combine elements of soil conductivity (K) with root length (L) in determining root water uptake. Peake et al (2013) demonstrated that in maize KL varied with plant population through impacts on root length density. Here we adjust KL linearly with plant population.

KLModifier is calculated as a function of [Maize].Population

\[
\begin{array}{c|c}
X & Y \\
0 & 1 \\
10 & 1 \\
\end{array}
\]

\[
\text{KLModifier} = \frac{X}{Y} \text{ (m/g)}
\]
2.5.2 PartitionFraction

*PartitionFraction* is calculated as a function of *[Phenology].Stage*

\[
\begin{array}{c|c}
X & Y \\
0 & 0 \\
2.99 & 0 \\
3 & 0.2 \\
6 & 0.2 \\
7 & 0 \\
\end{array}
\]

2.5.3 RootFrontVelocity

*Hammer et al., 2009* used a constant extraction front velocity of 2.5cm per day in their analysis of historical maize yield trends in the US corn belt.

The value of RootFrontVelocity from *Germination to Flowering* is calculated as follows:

\[ \text{RootFrontVelocity} = 25 \text{ (mm/d)} \]

The value of RootFrontVelocity from *Flowering to Maturity* is calculated as follows:

\[ \text{RootFrontVelocity} = 0 \text{ (mm/d)} \]

2.5.4 NitrogenDemandSwitch

Returns a value of 1 if phenology is between start and end phases and otherwise a value of 0.

2.5.5 BiomassRemovalDefaults

If a *harvest* is performed and no fractions are specified then 20% of root biomass will be removed with all of it going to the surface organic matter pool.

If a *cut* is performed and no fractions are specified then 30% of root biomass will be removed with all of it going to the surface organic matter pool.

If a *prune* is performed and no fractions are specified then 10% of root biomass will be removed with all of it going to the surface organic matter pool.

If a *graze* is performed and no fractions are specified then 15% of root biomass will be removed with all of it going to the surface organic matter pool.

2.5.6 KNO3

*KNO3* is calculated as a function of *[Root].RootLengthDenisty*
2.5.7 KNH4

$KNH4$ is calculated as a function of $[Root].RootLengthDenisty$

2.5.8 NUptakeSWFactor

$NUptakeSWFactor$ is calculated as a function of $[Root].RWC$
2.6 Leaf

A generic leaf model

StructuralFraction = 0.7
Area = 380
Area = 0

2.6.1 CohortParameters

SenessingLeafRelativeSize = 1 (0-1)

2.6.1.1 MaxArea

Calculates the maximum leaf size (mm²/leaf) given its node position (Elings, 2000 - Agronomy Journal 92, 436-444)

Potential leaf area is calculated from leaf number using the approach of Keating and Wafula (1992). Individual leaf size is described using a bell-shaped curve, the parameters of which are derived from final leaf number.

2.6.1.1.1 LargestLeafPosition

\[ \text{LargestLeafPosition} = \text{[Structure].MainStemFinalNodeNumber} \times \text{RelativePositionOfLargestLeaf} \]

Where:

\[ \text{RelativePositionOfLargestLeaf} = 0.67 \]

2.6.1.1.2 AreaMax

AreaMax is calculated as a function of [Structure].MainStemFinalNodeNumber

\[
\begin{array}{cc}
X & Y \\
0 & 32530 \\
2 & 39259 \\
7 & 49659 \\
12 & 60000 \\
17 & 75000 \\
22 & 90000 \\
\end{array}
\]

2.6.1.1.3 Breadth

Breadth is calculated as a function of [Structure].MainStemFinalNodeNumber
2.6.1.2 CellDivisionStress

CellDivisionStress is calculated as a function of $[\text{Maize}.\text{WaterSupplyDemandRatio}]$

2.6.1.3 ExpansionStress

ExpansionStress is calculated as a function of $[\text{Maize}.\text{WaterSupplyDemandRatio}]$
2.6.1.4 GrowthDuration

*GrowthDuration* is calculated as a function of `[Structure].RelativeNodeAppearance`

<table>
<thead>
<tr>
<th>X</th>
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</thead>
<tbody>
<tr>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>0.3</td>
<td>200</td>
</tr>
<tr>
<td>0.5</td>
<td>250</td>
</tr>
<tr>
<td>1</td>
<td>100</td>
</tr>
</tbody>
</table>

2.6.1.5 LagDuration

*LagDuration* is calculated as a function of `[Structure].RelativeNodeAppearance`

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
</tr>
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<tbody>
<tr>
<td>0</td>
<td>300</td>
</tr>
<tr>
<td>0.3</td>
<td>300</td>
</tr>
<tr>
<td>0.5</td>
<td>650</td>
</tr>
</tbody>
</table>
2.6.1.6 SenescenceDuration

*SenescenceDuration* is calculated as a function of $[\text{Structure}.\text{RelativeNodeAppearance}]$.

![Graph showing SenescenceDuration as a function of RelativeNodeAppearance](image)

DetachmentLagDuration = 1000000
DetachmentDuration = 1000000

2.6.1.7 MaximumNConc

*MaximumNConc* is calculated as a function of $[\text{Structure}.\text{LeafTipsAppeared}]$.

![Graph showing MaximumNConc as a function of LeafTipsAppeared](image)

CriticalNConc = 0.015 (g/g)
MinimumNConc = 0.008 (g/g)

2.6.1.8 DroughtInducedSenAcceleration

*DroughtInducedSenAcceleration* = 1 + Stress

Where:

\[
\text{Stress} = \text{StressResponseCoefficient} \times \text{StressFactor}
\]

Where:

StressResponseCoefficient = 1
StressFactor is calculated as a function of \([\text{Maize}.\text{WaterSupplyDemandRatio}]\)

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0.5</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

2.6.1.9 SpecificLeafAreaMax

SpecificLeafAreaMax is calculated as a function of \([\text{Structure}.\text{LeafTipsAppeared}]\)

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>50000</td>
</tr>
<tr>
<td>9</td>
<td>25000</td>
</tr>
</tbody>
</table>

2.6.1.10 SpecificLeafAreaMin

SpecificLeafAreaMin is calculated as a function of \([\text{Structure}.\text{LeafTipsAppeared}]\)

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>8000</td>
</tr>
<tr>
<td>9</td>
<td>8000</td>
</tr>
</tbody>
</table>
StructuralFraction = 0.7
NonStructuralFraction = 0

2.6.1.11 ShadeInducedSenescenceRate

ShadeInducedSenescenceRate is calculated as a function of [Leaf.CohortCurrentRankCoverAbove]

\[
\begin{array}{cc}
X & Y \\
0  & 0 \\
0.7 & 0 \\
0.8 & 0 \\
0.96& 0 \\
0.99& 0 \\
\end{array}
\]

InitialNConc = 0 (g/g)

2.6.2 Photosynthesis

Biomass accumulation is the product of the amount 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. RUE is calculated from a potential value which is discounted using stress factors that account for plant nutrition (Fn), air temperature (Ft), vapour pressure deficit (Fvpd), water supply (Fw) and atmospheric CO2 concentration (Fco2).

\[RUE = 2\]

2.6.2.1 FT

FT is calculated as a function of average daily temperature weighted toward max temperature according to the specified MaximumTemperatureWeighting factor.

0.75 = 0.75
2.6.2.2 FVPD

FVPD is calculated as a function of $[Leaf].Photosynthesis.VPD$

$$
\begin{array}{c|c}
X & Y \\
0 & 0 \\
8 & 0 \\
15 & 1 \\
35 & 1 \\
50 & 0 \\
\end{array}
$$

2.6.2.3 FN

FN is calculated as a function of $[Leaf].Fn$

$$
\begin{array}{c|c}
X & Y \\
0 & 0.3 \\
1 & 1 \\
\end{array}
$$
2.6.2.4 FW

FW is calculated as a function of \([Leaf].Fw\)

2.6.2.5 FCO2

This model calculates CO2 Impact on RUE using the approach of Reyenga et al., 1999.

\[RadnInt = [Leaf].RadIntTot\]

2.6.3 ExtinctionCoeff

Extinction coefficient is specified in terms of a potential extinction coefficient which is then discounted during periods of water stress to account for the impact of leaf curling.

\[ExtinctionCoeff = PotentialExtinctionCoeff \times \text{WaterStressImpact}\]

Where:

\(PotentialExtinctionCoeff\) is calculated as a function of \([Maize].SowingData.RowSpacing\)

\[X \quad Y\]
\[0.2 \quad 0.7\]
\[0.5 \quad 0.5\]
\[1 \quad 0.4\]

\(WaterStressImpact\) is calculated as a function of \([Maize].WaterSupplyDemandRatio\)
2.6.4 FrostFraction

FrostFraction is calculated as a function of \([\text{Weather}.\text{MinT}]\):

\[
\text{FrostFraction} = \text{minimum}(\text{FT}, \text{FN}, \text{FVPD})
\]

Where:

\[
\begin{align*}
\text{FT} &= \text{[Leaf].Photosynthesis.FT} \\
\text{FN} &= \text{[Leaf].Photosynthesis.FN} \\
\text{FVPD} &= \text{[Leaf].Photosynthesis.FVPD}
\end{align*}
\]

2.6.5 FRGRFunction

FRGRFunction = minimum (FT, FN, FVPD)

2.6.6 BiomassRemovalDefaults

If a harvest is performed and no fractions are specified then 30% of leaf biomass will be removed with all of it going to the surface organic matter pool.

If a cut is performed and no fractions are specified then 80% of leaf biomass will be removed with none of it going to the surface organic matter pool.
If a prune is performed and no fractions are specified then 60% of leaf biomass will be removed with all of it going to the surface organic matter pool.

If a graze is performed and no fractions are specified then 70% of leaf biomass will be removed with 10% of it going to the surface organic matter pool.

2.7 Husk

This organ is simulated using a generic organ type.

**Dry Matter Demands** A given fraction of daily DM demand is determined to be structural and the remainder is non-structural.

**Dry Matter Supplies** A given fraction of Nonstructural DM is made available to the arbitrator as DMRetranlocationSupply.

**Nitrogen Demands** The daily nonstructural N demand is the product of Total DM demand and a Maximum N concentration less the structural N demand. The daily structural N demand is the product of Total DM demand and a Minimum N concentration. The Nitrogen demand switch is a multiplier applied to nitrogen demand so it can be turned off at certain phases.

**Nitrogen Supplies** As the organ senesces a fraction of senesced N is made available to the arbitrator as NReAllocationSupply. A fraction of nonstructural N is made available to the arbitrator as NRetranlocationSupply.

**Biomass Senescence and Detachment** Senescence is calculated as a proportion of the live dry matter. Detachment of biomass into the surface organic matter pool is calculated daily as a proportion of the dead DM.

**Canopy** The user can model the canopy by specifying either the LAI and an extinction coefficient, or by specifying the canopy cover directly. If the cover is specified, LAI is calculated using an inverted Beer-Lambert equation with the specified cover value.

The canopies values of Cover and LAI are passed to the MicroClimate module which uses the Penman Monteith equation to calculate potential evapotranspiration for each canopy and passes the value back to the crop. The effect of growth rate on transpiration is captured using the Fractional Growth Rate (FRGR) function which is parameterised as a function of temperature for the simple leaf.

\[
NReAllocationFactor = 0 \text{ (/d)}
\]

\[
NRetranlocationFactor = 0.1 \text{ (/d)}
\]

\[
MaximumNConc = 0.01 \text{ (g/g)}
\]

\[
StructuralFraction = 0.3 \text{ (g/g)}
\]

\[
SenescenceRate = 0 \text{ (/d)}
\]

\[
MinimumNConc = 0.01 \text{ (g/g)}
\]

\[
DMRetranlocationFactor = 0.1 \text{ (/d)}
\]

\[
InitialWtFunction = 0 \text{ (g/m^2)}
\]

\[
DetachmentRateFunction = 0 \text{ (/d)}
\]

2.7.1 DMDemandFunction

Demand is calculated from the product of growth rate, thermal time and population.

\[
ThermalTime = [Phenology].ThermalTime
\]

Stage when organ growth starts

\[
StartStage = 5.2
\]
ThermalTime duration of organ growth

\[ \text{GrowthDuration} = 120 \]

Size individual organs will grow to when fully supplied with DM

\[ \text{MaximumOrganWt} = 25 \]

\[ \text{OrganPopulation} = [\text{Rachis}. \text{CobNumber}] \]

\[ \text{SenescenceRate} = 0 \text{ (/d)} \]

### 2.7.1.1 ExpansionStress

ExpansionStress is calculated as a function of \([\text{Maize}. \text{WaterSupplyDemandRatio}]\):

\[
\begin{array}{c|c|c}
X & Y \\
0.3 & 0 \\
0.8 & 1 \\
\end{array}
\]

#### 2.7.2 BiomassRemovalDefaults

If a **harvest** is performed and no fractions are specified then 60% of husk biomass will be removed with 10% of it going to the surface organic matter pool.

If a **cut** is performed and no fractions are specified then 80% of husk biomass will be removed with none of it going to the surface organic matter pool.

If a **prune** is performed and no fractions are specified then 60% of husk biomass will be removed with all of it going to the surface organic matter pool.

If a **graze** is performed and no fractions are specified then 80% of husk biomass will be removed with 20% of it going to the surface organic matter pool.

### 2.8 Rachis

This organ is simulated using a generic organ type.

**Dry Matter Demands** A given fraction of daily DM demand is determined to be structural and the remainder is non-structural.

**Dry Matter Supplies** A given fraction of Nonstructural DM is made available to the arbitrator as DMReTranslocationSupply.

**Nitrogen Demands** The daily nonstructural N demand is the product of Total DM demand and a Maximum N concentration less the structural N demand. The daily structural N demand is the product of Total DM demand and a Minimum N concentration. The Nitrogen demand switch is a multiplier applied to nitrogen demand so it can be turned off at certain phases.
**Nitrogen Supplies** As the organ senesces a fraction of senesced N is made available to the arbitrator as NReallocationSupply. A fraction of nonstructural N is made available to the arbitrator as NRetranslocationSupply.

**Biomass Senescence and Detachment** Senescence is calculated as a proportion of the live dry matter. Detachment of biomass into the surface organic matter pool is calculated daily as a proportion of the dead DM.

**Canopy** The user can model the canopy by specifying either the LAI and an extinction coefficient, or by specifying the canopy cover directly. If the cover is specified, LAI is calculated using an inverted Beer-Lambert equation with the specified cover value.

The canopies values of Cover and LAI are passed to the MicroClimate module which uses the Penman Monteith equation to calculate potential evapotranspiration for each canopy and passes the value back to the crop. The effect of growth rate on transpiration is captured using the Fractional Growth Rate (FRGR) function which is parameterised as a function of temperature for the simple leaf.

- **NReallocationFactor** = 0 (/d)
- **NRetranslocationFactor** = 0.1 (/d)
- **MaximumNConc** = 0.008 (g/g)
- **StructuralFraction** = 1 (g/g)
- **SenescenceRate** = 0 (/d)
- **MinimumNConc** = 0.003 (g/g)
- **InitialWtFunction** = 0 (g/m^2)
- **DetachmentRateFunction** = 0 (/d)

### 2.8.1 CobNumber

\[ \text{CobNumber} = [\text{Structure}.\text{TotalStemPopn} \times \text{CobsPerStem}] \]

Where:  
\[ \text{CobsPerStem} = 1.1 \]

### 2.8.2 CobSize

\[ \text{CobSize} = [\text{Rachis}.\text{Live.Wt} / [\text{Rachis}.\text{CobNumber}]) \]

### 2.8.3 DMDemandFunction

Demand is calculated from the product of growth rate, thermal time and population.

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

Stage when organ growth starts

\[ \text{StartStage} = 5.5 \]

ThermalTime duration of organ growth

\[ \text{GrowthDuration} = 300 \]

Size individual organs will grow to when fully supplied with DM

\[ \text{MaximumOrganWt} = 23 \]

\[ \text{OrganPopulation} = [\text{Rachis}.\text{CobNumber}] \]

### 2.8.3.1 ExpansionStress
Expansion Stress is calculated as a function of \([\text{Maize}.\text{WaterSupplyDemandRatio}]\).

### 2.8.4 Expansion Stress

Expansion Stress is calculated as a function of \([\text{Maize}.\text{WaterSupplyDemandRatio}]\).

### 2.8.5 Biomass Removal Defaults

If a **harvest** is performed and no fractions are specified then 60% of rachis biomass will be removed with 10% of it going to the surface organic matter pool.

If a **cut** is performed and no fractions are specified then 80% of rachis biomass will be removed with none of it going to the surface organic matter pool.

If a **prune** is performed and no fractions are specified then 60% of rachis biomass will be removed with all of it going to the surface organic matter pool.

If a **graze** is performed and no fractions are specified then 80% of rachis biomass will be removed with 20% of it going to the surface organic matter pool.

### 2.9 Stem

This organ is simulated using a generic organ type.

**Dry Matter Demands** A given fraction of daily DM demand is determined to be structural and the remainder is non-structural.
Dry Matter Supplies  A given fraction of Nonstructural DM is made available to the arbitrator as DMReTranslocationSupply.

Nitrogen Demands  The daily nonstructural N demand is the product of Total DM demand and a Maximum N concentration less the structural N demand. The daily structural N demand is the product of Total DM demand and a Minimum N concentration. The Nitrogen demand switch is a multiplier applied to nitrogen demand so it can be turned off at certain phases.

Nitrogen Supplies  As the organ senesces a fraction of senesced N is made available to the arbitrator as NReallocationSupply. A fraction of nonstructural N is made available to the arbitrator as NRetranslocationSupply.

Biomass Senescence and Detachment  Senescence is calculated as a proportion of the live dry matter. Detachment of biomass into the surface organic matter pool is calculated daily as a proportion of the dead DM.

Canopy  The user can model the canopy by specifying either the LAI and an extinction coefficient, or by specifying the canopy cover directly. If the cover is specified, LAI is calculated using an inverted Beer-Lambert equation with the specified cover value.

The canopies values of Cover and LAI are passed to the MicroClimate module which uses the Penman Monteith equation to calculate potential evapotranspiration for each canopy and passes the value back to the crop. The effect of growth rate on transpiration is captured using the Fractional Growth Rate (FRGR) function which is parameterised as a function of temperature for the simple leaf.

\[
\text{StructuralFraction} = 0.7 \ (g/g)
\]

\[
\text{MinimumNConc} = 0.006 \ (g/g)
\]

\[
\text{NReallocationFactor} = 0 \ (/d)
\]

\[
\text{NRetranslocationFactor} = 0.5 \ (/d)
\]

\[
\text{DMRetranslocationFactor} = 0.1 \ (/d)
\]

\[
\text{InitialWtFunction} = 0 \ (g/m^2)
\]

\[
\text{DetachmentRateFunction} = 0 \ (/d)
\]

\[
\text{SenescenceRate} = 0 \ (/d)
\]

2.9.1 MaximumNConc

MaximumNConc is calculated as a function of [Structure].LeafTipsAppeared

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0.03</td>
</tr>
<tr>
<td>10</td>
<td>0.03</td>
</tr>
<tr>
<td>11</td>
<td>0.005</td>
</tr>
</tbody>
</table>

2.9.2 NitrogenDemandSwitch
Returns a value of 1 if phenology is between start and end phases and otherwise a value of 0.

2.9.3 DMDemandFunctionX

\[
\text{DMDemandFunctionX} = \text{minimum (PotentialDMAccumulation, HightLimitedDMAccumulation)}
\]

Where:

\[
\text{PotentialDMAccumulation} = \text{[Structure].DeltaTipNumber x [Structure].TotalStemPopn x PotentialInternodeWt}
\]

Where:

\[
\text{PotentialInternodeWt is calculated as a function of [Structure].RelativeNodeApperance}
\]

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>0.2</td>
<td>2</td>
</tr>
<tr>
<td>0.8</td>
<td>16</td>
</tr>
<tr>
<td>1</td>
<td>16</td>
</tr>
</tbody>
</table>

\[
\text{HightLimitedDMAccumulation} = \text{SpecificStemLengthMax x [Structure].TotalStemPopn x [Structure].HeightModel.DeltaHeight}
\]

Where:

\[
\text{SpecificStemLengthMax} = 0.1
\]

2.9.4 DMDemandFunction

the Partition Fraction Demand Function which returns the product of its PartitionFraction and the total DM supplied to the arbitrator by all organs

2.9.4.1 PartitionFraction

The value of PartitionFraction from Emergence to FloralInitiation is calculated as follows:

\[
\text{StemFraction} = 0.6
\]

The value of PartitionFraction from FloralInitiation to Flowering is calculated as follows:

\[
\text{StemFraction} = 0.82
\]

2.9.5 BiomassRemovalDefaults

If a harvest is performed and no fractions are specified then 60% of stem biomass will be removed with 10% of it going to the surface organic matter pool

If a cut is performed and no fractions are specified then 80% of stem biomass will be removed with none of it going to the surface organic matter pool
If a **prune** is performed and no fractions are specified then 60% of stem biomass will be removed with all of it going to the surface organic matter pool.

If a **graze** is performed and no fractions are specified then 80% of stem biomass will be removed with 20% of it going to the surface organic matter pool.

### 2.10 AboveGround

A composite biomass i.e. a biomass made up of 1 or more biomass objects. The AboveGround composite biomass object includes all organs occurring above the soil surface to allow output for total dry matter and Nutrient contents, including total structural, non-structural and metabolic pools.

### 2.11 BelowGround

A composite biomass i.e. a biomass made up of 1 or more biomass objects. The BelowGround composite biomass object includes all root biomass pools to allow output for total dry matter and Nutrient contents, including total structural, non-structural and metabolic pools.

### 2.12 Total

A composite biomass i.e. a biomass made up of 1 or more biomass objects. The Total composite biomass object includes all organs (above+below ground) to allow output for total dry matter and Nutrient contents, including total structural, non-structural and metabolic pools.

### 2.13 TotalLive

A composite biomass i.e. a biomass made up of 1 or more biomass objects. The TotalLive composite biomass object includes the Live pools of all organs (above+below ground) to allow output for total dry matter and Nutrient contents, including total structural, non-structural and metabolic pools.

### 2.14 TotalDead

A composite biomass i.e. a biomass made up of 1 or more biomass objects. The TotalDead composite biomass object includes the Dead pools of all organs (above+below ground) to allow output for total dry matter and Nutrient contents, including total structural, non-structural and metabolic pools.

### 2.15 EarLive

A composite biomass i.e. a biomass made up of 1 or more biomass objects. The EarLive composite biomass object includes the Live pools of all organs within the Ear to allow output for total dry matter and Nutrient contents, including total structural, non-structural and metabolic pools.

### 2.16 AboveGroundLive

A composite biomass i.e. a biomass made up of 1 or more biomass objects. The AboveGroundLive composite biomass object includes the Live pools of all organs occurring above the soil surface to allow output for total dry matter and Nutrient contents, including total structural, non-structural and metabolic pools.

### 2.17 AboveGroundDead

A composite biomass i.e. a biomass made up of 1 or more biomass objects. The AboveGroundDead composite biomass object includes the Dead pools of all organs occurring above the
soil surface to allow output for total dry matter and Nutrient contents, including total structural, non-structural and metabolic pools.

**Future Development requirements**

- Phenology not responding to stress events. Requires better data sets for quantifying the effects of water and nitrogen on leaf appearance and the timing of development stages.
- Phosphorus response
- Improved parameterisation of supply and demand for N and DM from organs and arbitration of these resources.
- Heat Stress responses in grain number
- More validation under a wider range of environments with more detailed datasets
- Seedling mortality
- Water demand (MicroClimate) needs validation

**2.18 Pioneer_39G12**

Cultivar class for holding cultivar overrides.

**2.19 Pioneer_3153**

Cultivar class for holding cultivar overrides.

**2.20 Katumani**

Cultivar class for holding cultivar overrides.

The variety Katumani Composite B was formed in 1966 and released in 1968 as part of the maize breeding work undertaken at the Katumani Research Station in Kenya which started in 1956. Katumani Composite B was an advanced generation of Katumani Synthetic V X Katumani Synthetic VI. It has slight photoperiod sensitivity and relatively small potential cob size.

**2.21 Makueni**

Cultivar class for holding cultivar overrides.

The variety Makueni Composite is a Kenyan variety with similar phenology but slightly higher cob size than Katumani composite.

**2.22 NSCM_41**

Cultivar class for holding cultivar overrides.

The variety NSCM_41 is a Zimbabwean early maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

**2.23 sc401**

Cultivar class for holding cultivar overrides.

The variety NSCM_41 is a Zimbabwean early maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

**2.24 r201**

Cultivar class for holding cultivar overrides.

The variety r201 is a Zimbabwean early maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

**2.25 sc501**
2.26 sr52

Cultivar class for holding cultivar overrides.

The variety sr52 is a Zimbabwean early-medium maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.27 Melkassa

Cultivar class for holding cultivar overrides.

The variety Melkassa is a local early-medium maturing Ethiopian variety.

2.28 r215

Cultivar class for holding cultivar overrides.

The variety r215 is a Zimbabwean early-medium maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.29 mh18

Cultivar class for holding cultivar overrides.

The variety mh18 is a Zimbabwean early-medium maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.30 CG4141

Cultivar class for holding cultivar overrides.

The variety CG4141 is a Zimbabwean early-medium maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.31 sc601

Cultivar class for holding cultivar overrides.

The variety sc601 is a Zimbabwean medium-late maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.32 sc625

Cultivar class for holding cultivar overrides.

The variety sc625 is a Zimbabwean medium-late maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.33 sc623

Cultivar class for holding cultivar overrides.

The variety sc623 is a Zimbabwean medium-late maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.34 mh12
Cultivar class for holding cultivar overrides.

The variety mh12 is a Malawian medium-late maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.35 mh16
Cultivar class for holding cultivar overrides.

The variety mh16 is a Malawian medium-late maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.36 mh17
Cultivar class for holding cultivar overrides.

The variety mh17 is a Malawian medium-late maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.37 mh19
Cultivar class for holding cultivar overrides.

The variety mh19 is a Malawian medium-late maturing hybrid. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.38 malawi_local
Cultivar class for holding cultivar overrides.

The variety malawi_local is a Malawian medium-late maturing local variety. Photoperiod response is taken from Ellis et al Crop Sci 32:1225 for SR52.

2.39 Dekalb_XL82
Cultivar class for holding cultivar overrides.

2.40 GH_5009
Cultivar class for holding cultivar overrides.

2.41 Hycorn_40
Cultivar class for holding cultivar overrides.

2.42 GH_5019WX
Cultivar class for holding cultivar overrides.

2.43 Laila
Cultivar class for holding cultivar overrides.

2.44 Pioneer_39V43
Cultivar class for holding cultivar overrides.

VShort duration variety released in New Zealand by Pioneer

2.45 Pioneer_34K77
Cultivar class for holding cultivar overrides.
VShort duration variety released in New Zealand by Pioneer

2.46 Pioneer_38H20
Cultivar class for holding cultivar overrides.

2.47 Pioneer_33M54
Cultivar class for holding cultivar overrides.

2.48 Hycorn_53
Cultivar class for holding cultivar overrides.
3 Validation

3.1 Africa

A selection of data from Kenya has been included from the work of KEATING et al., 1992. These include the trial originally labelled JMW2 by the original authors and was labelled Experiment 6 in KEATING et al., 1992. This trial includes maize (cultivar Katumani Composite B) sown at 5 populations (1.1, 2.2, 4.4, 6.6 and 8.8 plants/m²) under low (0 kg N/ha applied) and high (120 kgN/ha) fertiliser conditions during the Long Rains of 1988. This same experimental design was conducted at two locations, Katumani (1o 35’ S, 37o 14’ E) and Kiboko (2o 13’ S, 37o 43’ E). The trial was rainfed at Katumani but fully irrigated at Kiboko. Yields ranged from 2000 to 5400 kg/ha at Katumani and 1000 to 6000 kg/ha at Kiboko. There were strong population x nitrogen interactions at both sites. A second trial referred to as BMW1 or Experiment 1 in KEATING et al., 1992. A range of populations (2.0-6.5 plants/m²) and irrigation treatments (6-176 mm) where planted under high (80 kgN/ha) and low (0kgN/ha) fertiliser conditions at Katumani. Individual replicates are modeled separately due to variability in soil (depth to rock), establishment and irrigation application. Grain yields varied from 1600 to 8000 kg/ha.

Note. The BMW1 trial consists of data from unreplicated plots.

3.1.1 JMW2Katumani
3.1.2 JMW2Kiboko

GrainNo Population Response

GrainWt Population Response
3.1.3 BMW1

GrainNo Population Response

GrainSize Population Response

3.1.3 BMW1
**GrainWt**

- Formula: \( y = 0.80x + 146.25 \)
- \( r^2 = 0.48 \)
- \( n = 44 \)
- NSE = 0.04, ME = 84.53, MAE = 116.18
- RSR = 1.01, RMSD = 153.43

**Biomass**

- Formula: \( y = 0.87x + 140.12 \)
- \( r^2 = 0.69 \)
- \( n = 44 \)
- NSE = 0.63, ME = 38.88, MAE = 145.57
- RSR = 0.60, RMSD = 194.81
3.2 Australia
The data for two trials from near Katherine, Northern Territory, Australia, have been included from CARBERRY et al., 1989 and CARBERRY et al., 1991. These include two planting dates for the summer of 1983/1984 (labelled as K841, K842). At each planting date, cultivar Dekalb XL82 was sown at 4 populations (3, 5, 7, 9 plants/m\(^2\)) under low and high irrigation conditions. The low irrigation treatments only included preliminary applications to ensure crop establishment.

\[ y = 0.88x + 96.63, r^2 = 0.71, n = 46 \]
\[ \text{MSE} = 0.67, \text{MS} = 4.54, \text{MAE} = 110.92 \]
\[ \text{RSR} = 0.57, \text{RMSD} = 135.79 \]
Biomass

\[ y = 0.95x + 255.86, r^2 = 0.69, n = 34 \]
NSE = 0.95, ME = 181.89, MAE = 248.65
RSR = 0.79, RMSD = 305.53

FloweringDAS

\[ y = 0.86x + 11.09, r^2 = 0.84, n = 46 \]
NSE = 0.73, ME = 2.76, MAE = 3.76
RSR = 0.52, RMSD = 4.26
3.2.1 Angelo98

This data set has been published by Massignam et al., 2009. Three sowings were conducted at the CSIRO Cooper field station (27°34′S, 152°20′E), Gatton, Australia. The soil was a Lockyer clay loam for sowing 1 and 2 and a Hooper clay loam for sowing 3. Maize (Hycom53) was sown on three dates to provide a range of growing environments. Each sowing was provided with 3 rates of nitrogen. To ensure moisture was non-limiting, the plots were irrigated weekly by trickle irrigation, except when rainfall occurred. Plots were weeded regularly and insect pests and foliar diseases controlled as required.
3.2.2 Angelo99
3.2.3 Angelo00
3.3 USA
Testing of APSIM Maize, Soil Water, Soil Nitrogen, Manure, and Soil Temperature Modules in the Midwestern United States was undertaken by [Archontoulis et al. 2014] using APSIM version 7.4. A subset of these data has been chosen for testing of the maize model. Datasets involving application of compost have not been included so as to concentrate on tests of maize model performance, rather than overall soil organic matter dynamics.

3.3.1 Ames2006

3.3.1.1 Field
3.3.2 Ames2007

3.3.2.1 Field
3.4 New Zealand
Testing of APSIM Maize under New Zealand conditions to determine the performance of the model under temperate conditions with cool springs and mild summers. A range of trials have been conducted and are detailed below.

3.4.1 Lincoln2012

Lincoln2012 (Rain-Shelter Trail)

Testing of APSIM Maize under New Zealand conditions was undertaken using the data of Teixeira et al., 2014. This dataset includes the impact of three N (0 to 250 kg/ha N) and two water regimes (dryland and fully irrigated) using a rain-shelter structure. Observations include biomass growth and nitrogen content of individual organs, soil water contents, leaf area index, phenology and yield components. Total biomass ranged from 8000 kg/ha for dryland nil N crops to up to 28000 kg/ha for fully irrigated and N fertilised crops. Dryland crops recovered 25 percent less N from applied fertilizer than irrigated crops.

3.4.1.1 Graphs

AboveGroundWt
AboveGroundN

SoilWaterProfile
Grain Biomass

3.4.1.1 Canopy

LAI

3.4.2 Lincoln2010
Lincoln2010 (Leaf properties trial)

This trial was conducted to provide data for parametersising the Leaf Area model and is described in detail by Teixeira et al., 2011. Detailed measurements were conducted on leaf appearance and expansion with some measurements of biomass accumulation. Treatments of plus and minus Nitrogen were applied but there was sufficient N in the soil than N responses were very small.

3.4.3 HawksBay2010

3.4.3.1 Graphs

Combined Results

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

\[ y = 1.18x + 0.30, r^2 = 0.87, n = 74 \]
\[ NSE = 0.43, ME = 0.78, MAE = 0.79 \]
\[ RSR = 0.75, RMSD = 1.01 \]

Grain Number

\[ y = 0.91x + 243.71, r^2 = 0.85, n = 84 \]
\[ NSE = 0.84, ME = 63.94, MAE = 352.64 \]
\[ RSR = 0.89, RMSD = 479.55 \]
3.5 Statistics

3.5.1 Predicted vs. Observed

<table>
<thead>
<tr>
<th>Variable</th>
<th>n</th>
<th>Slope</th>
<th>Intercept</th>
<th>SEslope</th>
<th>SEinter</th>
<th>R2</th>
<th>RMSE</th>
<th>NSE</th>
<th>ME</th>
<th>MAE</th>
<th>RSR</th>
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<tr>
<td>Biomass</td>
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<td>1.295</td>
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<td>4.846</td>
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<td>-0.351</td>
<td>5.122</td>
<td>6.344</td>
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<tr>
<td>GPSM</td>
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<td>243.711</td>
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<td>479.548</td>
<td>0.843</td>
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<tr>
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<td>0.599</td>
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</tbody>
</table>
4 Sensibility Tests

4.1 Bugesera

Maize is grown in the Bugesera region of southern Rwanda in Central Africa. The region has a bimodal rainfall distribution which allows two plantings per year. For low input situations the maize yields should vary between 1 and 3 t/ha per crop. Under fertilised conditions the yield should increase up to 5 t/ha per crop.

![Yield CDF](image-url)
5 References


KEATING, BA, WAFULA, BM, WATIKI, JM, 1992. DEVELOPMENT OF A MODELING CAPABILITY FOR MAIZE IN SEMIARID EASTERN KENYA. ACIAR PROCEEDINGS SERIES, 26-33.


