

## 1. Purpose of Component

The PASTURE component encapsulates the GRAZPLAN pasture model. An earlier version of the model is described in:

Moore, A.D., Donnelly, J.R. and Freer, M. (1997). GRAZPLAN: Decision support systems for Australian grazing enterprises. III. Pasture growth and soil moisture submodels and the GrassGro DSS. *Agricultural Systems* **55**, 535-582.

The pasture model can also be used as a simple residue decomposition model by other plant models (e.g. crop models). This permits grazing of the residues.

## 2. Initialisation Properties

The initialisation property set is nearly completely optional. The intent is to allow the user to specify a minimal information set as well as a maximally detailed initialisation. Genotypic parameters are not provided through initialisation values; they are stored in separate parameter files.

The pasture model is configurable in different modes for handling soil fertility:

- “Simple” mode is a slight extension of the fertility-scalar approach used in the GrassGro decision support tool. The fertility scalar may be provided at initialisation and will also be subscribed to as an optional variable at each timestep.
- In “nitrogen” mode, the full plant nitrogen model will be activated.
- If the plant phosphorus and sulphur models are to be activated, so must the nitrogen model.

The following initialisations handle parameterisation and configuration of the model:

Property	Type	Required?	Units	Description
<i>param_file</i>	string	No		Name of the pasture parameter file. Default behaviour is to use a default pasture parameter set that is compiled into PASTURE.DLL.
<i>species</i>	string	Yes		Name of the pasture species for which parameters are to be used.
<i>nutrients</i>	string	No		Determines which of the plant nutrient submodels to activate. Feasible values are: Null “Simple” nutrient mode “N” Nitrogen submodel only “NP” Nitrogen & phosphorus submodels “NS” Nitrogen & sulphur submodels “NPS” All three plant nutrients The value is case-insensitive.
<i>fertility</i>	double	No	0-1	“Fertility scalar”. Only meaningful in “simple” mode. Default is 1.0.
<i>layers</i>	double[ ]	No	mm	Depth of each soil layer referenced in specifying root and seed pools. Must be given if soil profiles for root or seed pools are given; otherwise the profile depths will be requested (as <i>layers</i> ) from the rest of the simulation.
<i>max_rtdep</i>	double	No	mm	Maximum rooting depth. The default value is calculated from soil bulk density and sand content.

The following initialisations give initial values of state variables:

Variable	Type	Required?	Units	Description
<i>lagged_day_t</i>	double	No	°C	Lagged daytime temperature. Default value is -999.9, which denotes that the value of daytime temperature in the first time step should be used.
<i>phenology</i>	double	No	–	Value denoting the phenological stage of the species, as follows: 0-1 Vernalizing. The fractional part denotes the vernalization index. 1-2 Vegetative. The fractional part denotes degree-days since the vegetative phase began (0.0001 per degree-day). 2-3 Reproductive. The fractional part denotes degree-days since the reproductive phase began (0.0001 per degree-day). 3-4 Summer-dormant perennials. The fractional part denotes days since dormancy began (0.001 per day). 4.0 Senescent annuals. 5-6 Spraytopped. The fractional part denotes effective degree-days since the reproductive phase began (0.0001 per degree-day). 6.0 Winter-dormant perennials. The value must denote a feasible stage for the particular species.
<i>flower_len</i>	double	No	d	Current maximum length of the flowering period. Ignored if the species is modelled with no seed pools or the phenological stage is not reproductive. Default depends on the phenological stage.
<i>flower_time</i>	double	No	d	Time since the start of flowering. Default depends on the phenological stage.
<i>senc_index</i>	double	No	d	Number of preceding days of “dry” conditions. Only meaningful if the pasture population is vulnerable to senescence. Default value is 0.
<i>dorm_index</i>	double	No	d	Number of preceding days of “cool, moist” conditions. Only meaningful if the pasture population is summer-dormant. Default value is 0.
<i>dorm_t</i>	double	No	°C	Lagged mean temperature used in summer-dormancy calculations. Default value is -999.9, which denotes that the value of mean temperature in the first time step should be used.
<i>extinct_coeff</i>	double[3]	No	–	Apparent extinction coefficients of seedlings, established plants and senescing plants.

Variable	Type	Required?	Units	Description
<i>green</i>	record[ ]	No		Each element specifies the state of a cohort of green (living) herbage:
<i>:status</i>	string			• Feasible values are “seedling”, “established” or “senescing”.
<i>:herbage</i>	record[ ]			• Specifies initial state of above-ground herbage pools:
<i>:dmd</i>	double[ ]		0-1	- Class boundaries for the dry matter digestibility (DMD) classes to which the other fields refer.
<i>:weight</i>	double[ ]		kg/ha	- Tissue mass in each DMD class.
<i>:n_conc</i>	double[ ]		g/g	- Nitrogen concentration of each DMD class. Only meaningful if <i>nutrients</i> includes N.
<i>:p_conc</i>	double[ ]		g/g	- Phosphorus concentration of each DMD class. Only meaningful if <i>nutrients</i> includes P.
<i>:s_conc</i>	double[ ]		g/g	- Sulphur concentration of each DMD class. Only meaningful if <i>nutrients</i> includes S.
<i>:root_wt</i>	double[ ][ ]		kg/ha	• Mass of roots. The first index denotes a root age class (1=effective roots, 2=old roots); if only one sub-array is given, it is taken to be total root mass. The second index denotes a soil layer (defined by the <i>layers</i> property). If only a single value is given in a sub-array, mass will be distributed over all soil layers to the current rooting depth, using a near-exponential distribution.
<i>:rt_dep</i>	double		mm	• Current rooting depth of the cohort.
<i>:estab_index</i>	double		0,1.0- $K_{Z1}$	• Establishment index. Only meaningful if <i>status</i> = “seedling”.
<i>:stress_index</i>	double		0.0-1.0	• Stress index. Only meaningful if <i>status</i> = “seedling”.
<i>:stem_reloc</i>	double		kg/ha	• Maximum amount of stem tissue to be relocated to seed. Only meaningful if (a) the species is modelled as having seeds, (b) <i>status</i> = “established” or “senescing” and (c) the phenological stage is reproductive or senescent. Default depends on the above conditions.
<i>:frosts</i>	integer		–	• Number of frosts experienced by this herbage cohort during its lifetime.
<i>dry</i>	record[ ]	No		Each element specifies the state of a cohort of dry herbage (standing dead or litter):
<i>:status</i>	string			• Feasible values are “dead” or “litter”.
<i>:herbage</i>	record[ ]			• Definition is the same as <i>green:herbage</i> .
<i>seeds</i>	record	No		Mass of seeds in each soil layer.
<i>:soft_unripe</i>	double[ ]		kg/ha	• Mass of soft, unripe seeds. If only a single element is given, all seeds are placed in the first soil layer.
<i>:soft_ripe</i>	double[ ]		kg/ha	• Mass of soft, ripe seeds. If only a single element is given, all seeds are placed in the first soil layer.
<i>:hard_unripe</i>	double[ ]		kg/ha	• Mass of hard, unripe seeds. If only a single element is given, all seeds are placed in the first soil layer.
<i>:hard_ripe</i>	double[ ]		kg/ha	• Mass of hard, ripe seeds. If only a single element is given, all seeds are placed in the first soil layer.
<i>seed_dorm_time</i>	double	No	d	Time since commencement of embryo dormancy. Only meaningful if unripe seeds are present. Default is 0.0.
<i>germ_index</i>	double	No	d	Germination index. Only meaningful if the species is modelled with seed pools. Default is 0.0.
<i>kl</i>	single[ ]	No	d <sup>-1</sup>	Rate parameter for the optional Monteith water uptake submodel.
<i>ll</i>	single[ ]	No	mm/mm	Minimum water content parameter for the optional Monteith water uptake submodel.

- Further rules apply when providing values for *green[:herbage]* or *dry[:herbage]*:
  - ⇒ The *herbage* field must have zero, one or two elements. If there is one element, it denotes the total (shoot) pool; if there are two elements, they denote leaf and stem.
  - ⇒ If the *dmd* sub-field has more than one element, then the *weight* sub-field must have one fewer elements. *weight[1]* denotes the mass of tissue with DMD in the range from *dmd[1]* to *dmd[2]*, and so on.
  - ⇒ If a single value (i.e. an array of length 1) is provided for the *dmd* sub-field, it denotes the average DMD of all shoot/leaf/stem (depending on context). In this case, the corresponding *weight* sub-field must have a single element, which denotes the total weight of shoot/leaf/stem.
  - ⇒ The lengths of the *n\_conc*, *p\_conc* and/or *s\_conc* sub-fields must be either the same as the *weight* sub-field, one or zero. If the length is same as the weight field, each value gives the nutrient concentration of the corresponding DMD class. If the length is one, the value denotes the average nutrient concentration. If the array is empty, a species-specific set of default nutrient concentrations is used.

### 3. Subscribed events – sequenced

#### 3.1. *init\_step*

Default sequencing: 100

Zeroes various cumulated quantities (e.g. herbage removal). Acquires the green mass, green area index and cover of other plants and computes totals for the field.

#### 3.2. *do\_pasture\_water*

Default sequencing: 4000

Computes demand for soil water.

#### 3.3. *do\_pasture\_growth*

Default sequencing: 6000

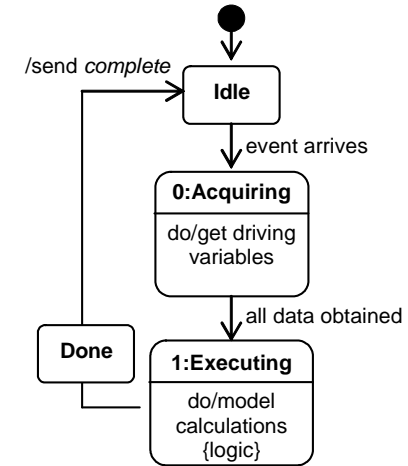
Computes rates of development, growth and digestibility change of the species. Updates phenology state variables.

#### 3.4. *end\_step*

Default sequencing: 9000

Obtains and computes removal of herbage by livestock. Obtains and adds residue inputs from other plant models. Updates remaining state variables.

All events follow the same state diagram:



#### 4. Subscribed events - other

##### 4.1. *sow*

Adds a given amount of seed of the species. The new seed is assumed to be immediately germinable. In species that are modelled as not having seed pools, the sown material is added as established plants.

Parameter	Type	Units	Description
<i>rate</i>	double	kg/ha	Amount of seed sown

##### 4.2. *spraytop*

This event causes the pasture to mimic the effects of spraying with glyphosate. It has no parameters.

##### 4.3. *cultivate*

Kills the nominated proportion of the sward and incorporates the newly-dead material, along with the nominated proportion of dead, litter and seeds, into the soil.

Parameter	Type	Units	Description
<i>depth</i>	double	mm	Depth of cultivation.
<i>propn_incorp</i>	double	-	Proportion of surface herbage incorporated into the soil.
<i>propn_mixed</i>	double	-	Proportion of soil in each soil layer that is mixed across the cultivation depth (the remainder remains in its original layer).

##### 4.4. *cut*

Removes all herbage down to a nominated threshold and makes it available for storage as hay.

Parameter	Type	Units	Description
<i>cut_height</i>	double	mm	Height of cutting.
<i>gathered</i>	double	-	Proportion of cut forage gathered in (the remainder becomes litter).
<i>dmd_loss</i>	double	-	Loss of DMD during cutting, drying and storage.
<i>dm_content</i>	double	kg/kg	Dry matter content when stored.

##### 4.5. *kill*

Kills the nominated proportions of herbage (including roots) and seeds. When killed, green herbage becomes standing dead and roots become residues.

Parameter	Type	Units	Description
<i>propn_herbage</i>	double	-	Proportion of herbage to be killed
<i>propn_seed</i>	double	-	Proportion of seeds to be killed

4.6. *burn*

Simulates the effect of a fire; equivalent to a *kill* event followed by removal of a proportion of the herbage. Surviving, killed and already-dead herbage are removed in equal proportions.

Parameter	Type	Units	Description
<i>kill_plants</i>	double	-	Proportion of herbage killed by the fire.
<i>kill_seed</i>	double	-	Proportion of seeds killed by the fire.
<i>propn_unburnt</i>	double	-	Proportion of herbage (green & dead) that remains after the fire has passed.

4.7. *remove\_herbage*

Removes plant shoots and seeds. This event is published by the Stock component and may also be published by other components.

Parameter	Type	Units	Description
<i>herbage</i>	double[ ]	kg/ha	Mass of shoots removed in each of 5 digestibility classes.
<i>seed</i>	double[ ]	kg/ha	Mass of unripe and ripe seeds removed.

4.8. *add\_residue*

Adds standing dead or litter.

Parameter	Type	Units	Description
<i>name</i>	string		Species name. Addition of residues only takes place if <i>name</i> matches the <i>species</i> property.
<i>standing</i>	boolean		TRUE if standing dead, FALSE if litter.
<i>part</i>	string		Valid values are “leaf” or “stem”.
<i>weight</i>	double	kg/ha	Mass (as DM) of residues to be added.
<i>n</i>	double	kg/ha	Mass of nitrogen in residues.
<i>p</i>	double	kg/ha	Mass of phosphorus in residues.
<i>s</i>	double	kg/ha	Mass of sulphur in residues.
<i>ash_alk</i>	double	mol/ha	Ash alkalinity in residues.
<i>dmd</i>	double		DM digestibility of residues.

4.9. *crop\_chopped*

Adds dry herbage. The allocation between standing dead and litter is determined.

Parameter	Type	Units	Description
<i>croptype</i>	string		Species name. Addition of residues only takes place if <i>name</i> matches the <i>species</i> property.
<i>dm_type</i>	string[ ]		List of plant part. Values of ‘leaf’ are assigned to leaf residues, values of ‘root’ are ignored, and the remainder are allocated as stem residues.
<i>dlt_crop_dm</i>	single[ ]	kg/ha	Mass (as DM) of each plant part to be added.
<i>dlt_dm_n</i>	single[ ]	kg/ha	Mass of nitrogen in residues of each plant part.

---

Parameter	Type	Units	Description
<i>dlt_dm_p</i>	single[ ]	kg/ha	Mass of phosphorus in residues of each plant part.
<i>fraction_to_residue</i>	single[ ]	-	Proportion of each plant part to be added to the herbage pools.

---



## 5. Published events

### 5.1. *on\_conserve*

Reports the amount and quality of conserved forage produced by a *cut* event.

Published in response to a *cut* event.

Parameter	Type	Units	Description
<i>fresh_wt</i>	double	kg	Mass of conserved forage
<i>dm_content</i>	double	kg/kg	Dry matter content
<i>dmd</i>	double	-	Dry matter digestibility
<i>n_conc</i>	double	kg/kg	Crude protein content
<i>p_conc</i>	double	kg/kg	P content
<i>s_conc</i>	double	kg/kg	S content
<i>ash_alk</i>	double	mol/kg	Ash alkalinity

### 5.2. *on\_mass\_change*

Signals a change in herbage mass to the remainder of the simulation.

No parameters.

Published in response to *sow*, *spraytop*, *cultivate*, *add\_residue*, *crop\_chopped*, *cut*, *kill*, and *burn* events.

### 5.3. *add\_fom*

Used to transfer residue (fresh organic matter) inputs to a soil organic matter model. A single destination module is identified by the Pasture module based on the simulation structure.

Published in response to the *end\_step* event.

Parameter	Type	Units	Description
<i>fom_types</i>	string[ ]		Contains 'pasture_root', 'pasture_leaf', and 'pasture_stem'.
<i>layers</i>	double[ ]	mm	Thickness of each soil layer to which the elements of <i>fom</i> apply.
<i>fom</i>	record[ ][ ]		The first index denotes soil layers; the second index denotes inputs of different quality within each layer.
: <i>weight</i>	double	kg/ha	Mass (as DM) of residues to be added.
: <i>n</i>	double	kg/ha	Mass of nitrogen in residues.
: <i>p</i>	double	kg/ha	Mass of phosphorus in residues.
: <i>s</i>	double	kg/ha	Mass of sulphur in residues.
: <i>ash_alk</i>	double	mol/ha	Ash alkalinity in residues.

## 6. Driving properties

Property	Type	Units	Event:State	Number	Description
<i>bd_layer</i>	record		initialisation	1	Soil bulk density profile.
: <i>layers</i>	double[ ]	mm			
: <i>bd</i>	double[ ]	Mg/m <sup>3</sup>			
<i>dul_layer</i>	record		initialisation	1	Profile of water content at drained upper limit.
: <i>layers</i>	double[ ]	mm			
: <i>value</i>	double[ ]	mm/mm			
<i>latitude</i>	double	deg	initialisation	1	Latitude (south is negative).
<i>ll15_layer</i>	record		initialisation	1	Profile of water content at (soil) lower limit.
: <i>layers</i>	double[ ]	mm			
: <i>value</i>	double[ ]	mm/mm			
<i>sand_layer</i>	record		initialisation	1	Sand content profile.
: <i>layers</i>	double[ ]	mm			
: <i>value</i>	double[ ]	kg/kg			
<i>cover_tot</i>	double	m <sup>2</sup> /m <sup>2</sup>	<i>init_step</i> :0	0+	Total cover of co-occurring plant species.
<i>gai</i>	double	m <sup>2</sup> /m <sup>2</sup>	<i>init_step</i> :0	0+	Green area index of co-occurring plant species.
<i>dai</i>	double	m <sup>2</sup> /m <sup>2</sup>	<i>init_step</i> :0	0+	Dead area index of co-occurring plant species.
<i>green_dm</i>	double	kg/ha	<i>init_step</i> :0	0+	Green shoot mass of co-occurring plant species.
<i>co2_ppm</i>	double	mg/kg	<i>do_pasture_water</i> :0	0-1	Atmospheric [CO <sub>2</sub> ].
<i>eo</i>	double	mm	<i>do_pasture_water</i> :0	1	Reference evapotranspiration.
<i>light_profile</i>	record		<i>do_pasture_water</i> :0	0-1	Light interception profiles of plant populations interacting with this module.
: <i>interception</i>	record[ ]				• Interception by each plant population.
: <i>population</i>	integer4				• Module ID of the plant population
: <i>element</i>	record[ ]				• Set of sub-canopies within the plant population
: <i>name</i>	string				• Name of the sub-canopy
: <i>layer</i>	record[ ]				• Interception profile of this sub-canopy
: <i>thickness</i>	single	m			• Thickness (depth) of a canopy layer (first layer topmost)
: <i>amount</i>	single	MJ/m <sup>2</sup>			• Radiation intercepted by this sub-canopy in this layer
: <i>intensity</i>	single	W/m <sup>2</sup>			• Average light intensity in this canopy layer
: <i>transmission</i>	single	MJ/m <sup>2</sup>			• Amount of light not intercepted
<i>surf_evap</i>	double	mm	<i>do_pasture_water</i> :0	0-1	Evaporation rate of free surface water (including water intercepted on herbage). Default value is 0.0.
<i>sw_layer</i>	record		<i>do_pasture_water</i> :0	0-1	Soil water content profile.

Property	Type	Units	Event:State	Number	Description
: <i>layers</i>	double[ ]	mm			
: <i>value</i>	double[ ]	mm/mm			
<i>fert_scalar</i>	double	-	<i>do_pasture_growth:0</i>	0-1	“Fertility scalar”. Default is the value of <i>fertility</i> . Only used when <i>nutrients=</i> ”.
<i>intercepted</i>	double	mm	<i>do_pasture_growth:0</i>	0-1	Precipitation intercepted by herbage. Default is 0.0.
<i>ph_layer</i>	record		<i>do_pasture_growth:0</i>	0-1	Soil pH profile. Default value is 7.0 in all layers.
: <i>layers</i>	double[ ]	mm			
: <i>value</i>	double[ ]	-			
<i>soil_fract</i>	record[ ]		<i>do_pasture_growth:0</i>	0-1	Proportion of the soil volume occupied by roots of plant populations.
: <i>population</i>	integer				• Module ID of a plant population
: <i>element</i>	record[ ]				• Set of sub-populations for which soil occupancy is calculated separately.
: <i>name</i>	string				• Name of the sub-population
: <i>layer</i>	record[ ]				• Set of soil layers over which uptake is calculated (surface layer first)
: <i>thickness</i>	single	mm			• Thickness (depth) of the soil layer
: <i>fract</i>	single	-			• Fraction of soil volume in this layer occupied by roots of this sub-population.
<i>soil_nh4</i>	record		<i>do_pasture_growth:0</i>	0-1	Soil ammonium availability.
: <i>layers</i>	double[ ]	mm			• Thickness of each soil layer.
: <i>nutrient</i>	record[ ]				• Nutrient availabilities in one or more sub-divisions of the field area
: <i>area_fract</i>	double	-			○ Fraction of the field area in this sub-division
: <i>soln_conc</i>	double[ ]	mg/l			○ Solution nutrient concentration in this sub-division (as element)
: <i>avail_nutr</i>	double[ ]	kg/ha			○ Total mass of nutrient available for uptake (as element)
<i>soil_no3</i>	— as for <i>soil_nh4</i> —		<i>do_pasture_growth:0</i>	0-1	Soil nitrate availability.
<i>soil_pox</i>	— as for <i>soil_nh4</i> —		<i>do_pasture_growth:0</i>	0-1	Soil phosphate availability.
<i>soil_so4</i>	— as for <i>soil_nh4</i> —		<i>do_pasture_growth:0</i>	0-1	Soil sulphate availability.
<i>time</i>	record		<i>do_pasture_growth:0</i>	1	Current time step
: <i>startDay</i>	integer4	d			
: <i>startSec</i>	integer4	s			
: <i>startSecPart</i>	double	s			
: <i>endDay</i>	integer4	d			
: <i>endSec</i>	integer4	s			
: <i>endSecPart</i>	double	s			
<i>trampling</i>	double	kg/ha	<i>do_pasture_growth:0</i>	0+	Stocking rate factor used to determine fall of standing dead. Read as mass of grazers per unit area. Default is 0.0.

Property	Type	Units	Event:State	Number	Description
<i>water_uptake</i>	record[ ]		<i>do_pasture_growth:0</i>	0-1	Water uptake by plant populations interacting with this module.
: <i>population</i>	integer				• Module ID of a plant population
: <i>element</i>	record[ ]				• Set of sub-populations for which water uptake is calculated separately
: <i>name</i>	string				• Name of the sub-population
: <i>layer</i>	record[ ]				• Set of soil layers over which uptake is calculated (surface layer first)
: <i>thickness</i>	single	mm			• Thickness (depth) of the soil layer
: <i>amount</i>	single	kg/m <sup>2</sup>			• Water uptake from this layer by this sub-population
<i>weather</i>	record		<i>do_pasture_growth:0</i>	1	Weather record.
: <i>maxt</i>	double	°C			
: <i>mint</i>	double	°C			
: <i>rain</i>	double	mm			
: <i>snow</i>	double	mm			
: <i>radn</i>	double	MJ/m <sup>2</sup>			
: <i>vpd</i>	double	kPa			
: <i>wind</i>	double	m/s			
<i>area</i>	double	ha	<i>cut:0</i>	0-1	Area of the field containing the pasture
<i>harvest_height</i>	double	mm	<i>crop_chopped:0</i>	0-1	Height at which incoming residues were harvested. Default is 0.0.

If the following properties are not found, then alternative properties are subscribed to instead:

Property	Alternative	Type	Units	Event:State	Number	Description
<i>bd_layer</i>	<i>bd</i>	double[ ]	Mg/m <sup>3</sup>	initialisation	1	Soil bulk density.
<i>bd_layer</i>	<i>dlayer</i>	double[ ]	mm	initialisation	1	Thickness of each soil layer.
<i>dul_layer</i>	<i>dul</i>	double[ ]	mm/mm	initialisation	1	Water content at drained upper limit.
<i>ll15_layer</i>	<i>ll15</i>	double[ ]	mm/mm	initialisation	1	Water content at (soil) lower limit.
<i>sand_layer</i>	<i>sand</i>	double[ ]	kg/kg	initialisation	1	Sand content of each soil layer.
<i>sw_layer</i>	<i>sw</i>	double[ ]	mm/mm	<i>do_pasture_water:0</i>	1	
<i>ph_layer</i>	<i>ph</i>	double[ ]	-	<i>do_pasture_growth:0</i>	0-1	Soil pH profile. The default value is 7.0.
<i>soil_nh4</i>	<i>nh4ppm</i>	double[ ]	mg/kg	<i>do_pasture_growth:0</i>	0-1	Soil ammonium-N concentration.
<i>soil_no3</i>	<i>no3ppm</i>	double[ ]	mg/kg	<i>do_pasture_growth:0</i>	0-1	Soil nitrate-N concentration.
<i>weather</i>	<i>maxt</i>	double	°C	<i>do_pasture_growth:0</i>	1	Maximum air temperature.
<i>weather</i>	<i>mint</i>	double	°C	<i>do_pasture_growth:0</i>	1	Minimum air temperature.
<i>weather</i>	<i>rain</i>	double	mm	<i>do_pasture_growth:0</i>	1	Precipitation in all forms other than snow.
<i>weather</i>	<i>radn</i>	double	MJ/m <sup>2</sup>	<i>do_pasture_growth:0</i>	1	Total solar radiation.
<i>weather</i>	<i>vpd</i>	double	kPa	<i>do_pasture_growth:0</i>	1	Vapour pressure deficit.

## 7. Owned properties

All initialisation properties are readable. In addition, the following owned properties are available:

### (a) Standard properties

Property	Type	Units	Description
<i>name</i>	string		Fully-qualified name of the component.
<i>type</i>	string		Value is “Pasture”
<i>version</i>	string		Value is “1.2”
<i>author</i>	string		Value is “CSIRO Plant Industry”
<i>active</i>	Boolean		Denotes whether or not the component is active
<i>state</i>	string		SDML description of the current state

### (b) Component-specific properties

Property	Type	Units	Description
<i>assimilation</i>	double	kg/ha/d	Gross whole-plant assimilation rate.
<i>avail_cp</i>	double	g/g	Average crude protein content of herbage available for grazing.
<i>avail_dm</i>	double	kg/ha	Total dry weight of herbage available for grazing.
<i>avail_dm_q</i>	double[ ]	kg/ha	Dry weight of herbage available for grazing in each digestibility class.
<i>avail_dmd</i>	double	g/g	Average DM digestibility of herbage available for grazing.
<i>avail_dry</i>	double	kg/ha	Weight of dry (standing dead+litter) herbage available for grazing.
<i>avail_green</i>	double	kg/ha	Weight of green (seedling+established+senescing) herbage available for grazing.
<i>canopy</i>	record[ ]		Canopy characteristics of a child APSIM-Plant module. The array has one member per sub-canopy.
: <i>name</i>	string		• Name of the sub-canopy.
: <i>plant_type</i>	string		• Classification of the sub-canopy.
: <i>layer</i>	record[ ]		• Array of canopy layers (topmost layer first).
: <i>thickness</i>	single	m	• Thickness of the canopy layer.
: <i>area_index</i>	single	m <sup>2</sup> /m <sup>2</sup>	• Area index of this sub-canopy within this layer.
: <i>cover_green</i>	single	-	• Projective cover of green biomass of this sub-canopy within this layer.
: <i>cover_total</i>	single	-	• Projective cover of all biomass of this sub-canopy within this layer.
<i>cover_green</i>	double	m <sup>2</sup> /m <sup>2</sup>	Green cover.
<i>cover_tot</i>	double	m <sup>2</sup> /m <sup>2</sup>	Total cover.
<i>dai</i>	double	m <sup>2</sup> /m <sup>2</sup>	Dead area index.
<i>dead_cp</i>	double	g/g	Average crude protein content of standing dead herbage.
<i>dead_dm</i>	double	kg/ha	Total dry weight of standing dead herbage.
<i>dead_dm_q</i>	double[ ]	kg/ha	Dry weight of standing dead herbage in each digestibility class.
<i>dead_dmd</i>	double	g/g	Average DM digestibility of standing dead herbage.
<i>dead_n</i>	double	g/g	Average nitrogen content of standing dead herbage.

Property	Type	Units	Description
<i>dead_p</i>	double	g/g	Average phosphorus content of standing dead herbage.
<i>dead_s</i>	double	g/g	Average sulphur content of standing dead herbage.
<i>death_rate</i>	double[ ][ ]	kg/ha/d	Rate of death of green herbage from each of leaf/stem (1 <sup>st</sup> index) x DMD class (2 <sup>nd</sup> index; 1=DMD 80-85%, 12=DMD 35-40%). Does not include defoliation or death due to <i>kill</i> , <i>cultivate</i> or <i>cut</i> events
<i>defoliation</i>	double[ ][ ][ ]	kg/ha	Amount of herbage defoliated from each of green/standing dead/litter (1 <sup>st</sup> index) x leaf/stem (2 <sup>nd</sup> index) x DMD class (3 <sup>rd</sup> index; 1=DMD 80-85%, 12=DMD 35-40%)
<i>dry_cp</i>	double	g/g	Average crude protein content of dry herbage (standing dead+litter).
<i>dry_dm</i>	double	kg/ha	Total dry weight of dry herbage.
<i>dry_dm_q</i>	double[ ]	kg/ha	Dry weight of dry herbage in each digestibility class.
<i>dry_dmd</i>	double	g/g	Average DM digestibility of dry herbage.
<i>dry_n</i>	double	g/g	Average nitrogen content of dry herbage.
<i>dry_p</i>	double	g/g	Average phosphorus content of dry herbage.
<i>dry_s</i>	double	g/g	Average sulphur content of dry herbage.
<i>eff_root_dm</i>	double	kg/ha	Total dry weight of effective roots.
<i>eff_root_dm_dep</i>	double[ ]	kg/ha	Dry weight of effective roots in each soil layer.
<i>est_index</i>	double	-	Weighted average value of the establishment index for seedlings.
<i>estab_cp</i>	double	g/g	Average crude protein content of herbage of established plants.
<i>estab_dm</i>	double	kg/ha	Total dry weight of herbage of established plants.
<i>estab_dm_q</i>	double[ ]	kg/ha	Dry weight of herbage of established plants in each digestibility class.
<i>estab_dmd</i>	double	g/g	Average DM digestibility of herbage of established plants.
<i>estab_n</i>	double	g/g	Average nitrogen content of herbage of established plants.
<i>estab_p</i>	double	g/g	Average phosphorus content of herbage of established plants.
<i>estab_s</i>	double	g/g	Average sulphur content of herbage of established plants.
<i>fall_rate</i>	double[ ][ ]	kg/ha/d	Rate of fall of standing dead herbage from each of leaf/stem (1 <sup>st</sup> index) x DMD class (2 <sup>nd</sup> index; 1=DMD 80-85%, 12=DMD 35-40%)
<i>gai</i>	double	m <sup>2</sup> /m <sup>2</sup>	Green area index.
<i>glf_gai</i>	double	-	Light interception growth-limiting factor.
<i>glf_nitr</i>	double	-	Nitrogen growth-limiting factor.
<i>glf_nutr</i>	double	-	Nutrient growth-limiting factor.
<i>glf_phos</i>	double	-	Phosphorus growth-limiting factor.
<i>glf_sm</i>	double	-	Soil moisture growth-limiting factor.
<i>glf_sulf</i>	double	-	Sulphur growth-limiting factor.
<i>glf_tmp</i>	double	-	Temperature growth-limiting factor.
<i>glf_vpd</i>	double	-	VPD growth-limiting factor.
<i>glf_wl</i>	double	-	Waterlogging growth-limiting factor.
<i>green_bd</i>	double	kg/m <sup>3</sup>	Herbage bulk density of green shoots
<i>green_cp</i>	double	g/g	Average crude protein content of green herbage (seedlings+established+senescing).

Property	Type	Units	Description
<i>green_dm</i>	double	kg/ha	Total dry weight of green herbage.
<i>green_dm_q</i>	double[ ]	kg/ha	Dry weight of green herbage in each digestibility class.
<i>green_dmd</i>	double	g/g	Average DM digestibility of green herbage.
<i>green_n</i>	double	g/g	Average nitrogen content of green herbage.
<i>green_p</i>	double	g/g	Average phosphorus content of green herbage.
<i>green_s</i>	double	g/g	Average sulphur content of green herbage.
<i>growth</i>	double	kg/ha/d	Daily shoot growth rate.
<i>height</i>	double	mm	Average height of the pasture.
<i>incorp_rate</i>	double[ ][ ]	kg/ha/d	Rate of incorporation of litter from each of leaf/stem (1 <sup>st</sup> index) x DMD class (2 <sup>nd</sup> index; 1=DMD 80-85%, 12=DMD 35-40%)
<i>killed</i>	double[ ]	kg/ha	Amount of death of green herbage as a result of <i>kill</i> or <i>cultivate</i> events from each of leaf & stem
<i>leachate</i>	record		Mass of organic nutrients leached from dead pasture & litter by rainfall
<i>: n</i>	double	kg/ha	• Nitrogen in leachate.
<i>: p</i>	double	kg/ha	• Phosphorus in leachate.
<i>: s</i>	double	kg/ha	• Sulphur in leachate.
<i>leaf_cp</i>	double	g/g	Average crude protein content of all leaves.
<i>leaf_dm</i>	double	kg/ha	Total dry weight of all leaves.
<i>leaf_dm_q</i>	double[ ]	kg/ha	Dry weight of all leaves in each digestibility class.
<i>leaf_dmd</i>	double	g/g	Average DM digestibility of all leaves.
<i>leaf_n</i>	double	g/g	Average nitrogen content of all leaves.
<i>leaf_p</i>	double	g/g	Average phosphorus content of all leaves.
<i>leaf_residues</i>	record		Dry weight and quality of leaf residues incorporated into the soil in this time step.
<i>: weight</i>	double	kg/ha	• Dry weight of residues.
<i>: n</i>	double	kg/ha	• Nitrogen in residues.
<i>: p</i>	double	kg/ha	• Phosphorus in residues.
<i>: s</i>	double	kg/ha	• Sulphur in residues.
<i>: ash_alk</i>	double	mol/ha	• Ash alkalinity in residues.
<i>leaf_s</i>	double	g/g	Average sulphur content of all leaves.
<i>litter_cp</i>	double	g/g	Average crude protein content of litter.
<i>litter_dm</i>	double	kg/ha	Total dry weight of litter.
<i>litter_dm_q</i>	double[ ]	kg/ha	Dry weight of herbage of litter in each digestibility class.
<i>litter_dmd</i>	double	g/g	Average DM digestibility of litter.
<i>litter_n</i>	double	g/g	Average nitrogen content of litter.
<i>litter_p</i>	double	g/g	Average phosphorus content of litter.
<i>litter_s</i>	double	g/g	Average sulphur content of litter.
<i>n_fixed</i>	double	kg/ha/d	Nitrogen fixation rate.
<i>n_gas_loss</i>	double	kg/ha/d	Rate of volatilization of tissue N into the atmosphere

Property	Type	Units	Description
<i>nh4_uptake</i>	record[ ]		Ammonium-N uptake from each soil layer.
: <i>thickness</i>	single	mm	• Thickness of a soil layer (first member of the array is the surface layer).
: <i>amount</i>	single	kg/ha	• Ammonium-N uptake by the plant population from this layer.
<i>no3_uptake</i>	record[ ]		Nitrate-N uptake from each soil layer.
: <i>thickness</i>	single	mm	• Thickness of a soil layer (first member of the array is the surface layer).
: <i>amount</i>	single	kg/ha	• Nitrate-N uptake by the plant population from this layer.
<i>npp</i>	double	kg/ha/d	Whole-plant net primary productivity.
<i>pheno_horizon</i>	double[ ]	-	Relative height of two “horizons” affecting the impact of defoliation on phenology
<i>plant2stock</i>	record		Description of the pasture for use by the ruminant model.
: <i>herbage</i>	record[ ]		
: <i>dm</i>	double	kg/ha	
: <i>dmd</i>	double	-	
: <i>cp_conc</i>	double	kg/kg	
: <i>p_conc</i>	double	kg/kg	
: <i>s_conc</i>	double	kg/kg	
: <i>prot_dg</i>	double	kg/kg	
: <i>ash_alk</i>	double	mol/kg	
: <i>height_ratio</i>	double	-	
: <i>propn_green</i>	double	-	
: <i>legume</i>	double	-	
: <i>select_factor</i>	double	-	
: <i>seed</i>	record[ ]		
: <i>dm</i>	double	kg/ha	
: <i>dmd</i>	double	-	
: <i>cp_conc</i>	double	kg/kg	
: <i>p_conc</i>	double	kg/kg	
: <i>s_conc</i>	double	kg/kg	
: <i>prot_dg</i>	double	kg/kg	
: <i>ash_alk</i>	double	mol/kg	
: <i>height_ratio</i>	double	-	
: <i>seed_class</i>	integer4[ ]		
<i>pox_uptake</i>	record[ ]		Phosphate-P uptake from each soil layer.
: <i>thickness</i>	single	mm	• Thickness of a soil layer (first member of the array is the surface layer).
: <i>amount</i>	single	kg/ha	• Phosphate-P uptake by the plant population from this layer.
<i>residue_cover</i>	double	m <sup>2</sup> /m <sup>2</sup>	Cover of standing dead and litter.



Property	Type	Units	Description
<i>residues</i>	record[ ]		Dry weight and quality of residues incorporated into the soil in this time step (one member per soil layer).
: <i>weight</i>	double	kg/ha	• Dry weight of residues.
: <i>n</i>	double	kg/ha	• Nitrogen in residues.
: <i>p</i>	double	kg/ha	• Phosphorus in residues.
: <i>s</i>	double	kg/ha	• Sulphur in residues.
: <i>ash_alk</i>	double	mol/ha	• Ash alkalinity in residues.
<i>respiration</i>	double	kg/ha/d	Whole-plant respiration rate, in dry weight equivalent terms.
<i>rlv</i>	double[ ]	mm/mm <sup>3</sup>	Length density of effective roots in each soil layer.
<i>root_dm</i>	double	kg/ha	Total dry weight of all roots.
<i>root_dm_dep</i>	double[ ]	kg/ha	Dry weight of all roots in each soil layer.
<i>root_n</i>	double	g/g	Average nitrogen content of all roots.
<i>root_n_dep</i>	double[ ]	kg/ha	Average nitrogen content of roots in each soil layer.
<i>root_p</i>	double	g/g	Average phosphorus content of all roots.
<i>root_p_dep</i>	double[ ]	kg/ha	Average phosphorus content of roots in each soil layer.
<i>root_radius</i>	double	mm	Average radius of all roots.
<i>root_residues</i>	record[ ]		Dry weight and quality of root residues incorporated into the soil in this time step (one member per soil layer).
: <i>weight</i>	double	kg/ha	• Dry weight of residues.
: <i>n</i>	double	kg/ha	• Nitrogen in residues.
: <i>p</i>	double	kg/ha	• Phosphorus in residues.
: <i>s</i>	double	kg/ha	• Sulphur in residues.
: <i>ash_alk</i>	double	mol/ha	• Ash alkalinity in residues.
<i>root_s</i>	double	g/g	Average sulphur content of all roots.
<i>root_s_dep</i>	double[ ]	kg/ha	Average sulphur content of roots in each soil layer.
<i>rtdep</i>	double	mm	Current depth of the rooting front.
<i>seed_cp</i>	double	g/g	Average crude protein content of seeds.
<i>seed_dm</i>	double	kg/ha	Total dry weight of seeds in all soil layers.
<i>seed_n</i>	double	g/g	Average nitrogen content of seeds.
<i>seed_p</i>	double	g/g	Average phosphorus content of seeds.
<i>seed_s</i>	double	g/g	Average sulphur content of seeds.
<i>seedl_cp</i>	double	g/g	Average crude protein content of seedlings.
<i>seedl_dm</i>	double	kg/ha	Total dry weight of seedlings.
<i>seedl_dm_q</i>	double[ ]	kg/ha	Dry weight of herbage of seedlings in each digestibility class.
<i>seedl_dmd</i>	double	g/g	Average DM digestibility of seedlings.
<i>seedl_n</i>	double	g/g	Average nitrogen content of seedlings.
<i>seedl_p</i>	double	g/g	Average phosphorus content of seedlings.
<i>seedl_s</i>	double	g/g	Average sulphur content of seedlings.
<i>senc_cp</i>	double	g/g	Average crude protein content of herbage of senescing plants.

Property	Type	Units	Description
<i>senc_dm</i>	double	kg/ha	Total dry weight of herbage of senescing plants.
<i>senc_dm_q</i>	double[ ]	kg/ha	Dry weight of herbage of senescing plants in each digestibility class.
<i>senc_dmd</i>	double	g/g	Average DM digestibility of herbage of senescing plants.
<i>senc_n</i>	double	g/g	Average nitrogen content of herbage of senescing plants.
<i>senc_p</i>	double	g/g	Average phosphorus content of herbage of senescing plants.
<i>senc_s</i>	double	g/g	Average sulphur content of herbage of senescing plants.
<i>shoot_cp</i>	double	g/g	Average crude protein content of all herbage.
<i>shoot_dm</i>	double	kg/ha	Total dry weight of all herbage.
<i>shoot_dm_q</i>	double[ ]	kg/ha	Dry weight of all herbage in each digestibility class.
<i>shoot_dmd</i>	double	g/g	Average DM digestibility of all herbage.
<i>shoot_n</i>	double	g/g	Average nitrogen content of all herbage.
<i>shoot_npp</i>	double	kg/ha/d	Net primary productivity of shoots.
<i>shoot_p</i>	double	g/g	Average phosphorus content of all herbage.
<i>shoot_s</i>	double	g/g	Average sulphur content of all herbage.
<i>so4_uptake</i>	record[ ]		Sulphate-S uptake from each soil layer.
: <i>thickness</i>	single	mm	• Thickness of a soil layer (first member of the array is the surface layer).
: <i>amount</i>	single	kg/ha	• Sulphate-S uptake by the plant population from this layer.
<i>stem_cp</i>	double	g/g	Average crude protein content of all stems.
<i>stem_dm</i>	double	kg/ha	Total dry weight of all stems.
<i>stem_dm_q</i>	double[ ]	kg/ha	Dry weight of all stems in each digestibility class.
<i>stem_dmd</i>	double	g/g	Average DM digestibility of all stems.
<i>stem_n</i>	double	g/g	Average nitrogen content of all stems.
<i>stem_p</i>	double	g/g	Average phosphorus content of all stems.
<i>stem_residues</i>	record		Dry weight and quality of stem residues incorporated into the soil in this time step.
: <i>weight</i>	double	kg/ha	• Dry weight of residues.
: <i>n</i>	double	kg/ha	• Nitrogen in residues.
: <i>p</i>	double	kg/ha	• Phosphorus in residues.
: <i>s</i>	double	kg/ha	• Sulphur in residues.
: <i>ash_alk</i>	double	mol/ha	• Ash alkalinity in residues.
<i>stem_s</i>	double	g/g	Average sulphur content of all stems.
<i>stress_index</i>	double	-	Weighted average value of the seedling stress index.
<i>sw_uptake</i>	double[ ]	mm	Water uptake from each soil layer.
<i>uptake_nh4</i>	double[ ]	kg/ha/d	Ammonium-N uptake from each soil layer
<i>uptake_no3</i>	double[ ]	kg/ha/d	Nitrate-N uptake from each soil layer
<i>uptake_pox</i>	double[ ]	kg/ha/d	Phosphate-P uptake from each soil layer
<i>uptake_so4</i>	double[ ]	kg/ha/d	Sulphate-S uptake from each soil layer

Property	Type	Units	Description
<i>water_info</i>	record[ ]		Water demand and supply attributes of a child APSIM-Plant module (one member per sub-population).
: <i>name</i>	string		• Name of the sub-population.
: <i>plant_type</i>	string		• Classification of the sub-population.
: <i>demand</i>	single	kg/m <sup>2</sup>	• Soil water demand of this sub-population..
: <i>layer</i>	record[ ]		• Array of soil layers (surface layer first).
: <i>thickness</i>	single	mm	• Thickness of the soil layer.
: <i>max_supply</i>	single	kg/m <sup>2</sup>	• Maximum supply of soil water to this sub-population from this layer.
: <i>rld</i>	single	mm/mm <sup>3</sup>	• Root length density of this sub-population in this layer.
: <i>radius</i>	single	mm	• Mean radius of soots of this sub-population in this layer.
<i>water_params</i>	double[ ]		Parameters used by the Paddock component to determine water uptake.

## Configuration Details

Title: Pasture Component Description  
 Created by: A.D. Moore  
 Modified by: A.D. Moore  
 Processor: Microsoft Word 2002  
 Printed: 20 Jul 2010

## Revision History

Version	Date	Changes
0.1	27 Nov 1997	First draft
0.2	8 Dec 1997	Revised to have all init variables as simple arrays. Mappings to TSward and TSwardInits included in document
0.3	21 Jun 2000	<i>dmd</i> variable added; section on interpreting TPastureInits added.
0.4	27 June 2001	Updated to conform to final protocol. Implementation details removed.
0.5	25 Nov 2003	Updated to conform to the revised implementation of the pasture and water uptake models
1.0	20 April 2006	<i>fom_added</i> → <i>add_fom</i> ; <i>residue_added</i> → <i>add_residue</i>
1.1	17 Dec 2006	Updated to reflect changes to resource allocation interface. <i>kl</i> and <i>ll</i> added.
1.2	20 Feb 2007	<i>burn</i> event added
1.3	25 Mar 2009	<i>defoliation</i> , <i>death_rate</i> , <i>fall_rate</i> , <i>incorp_rate</i> and <i>killed</i> properties added

## Document Distribution Policy

All versions: To be distributed in PDF format with FarmWi\$e, the Pasture+Paddock component package and component-developer packages.