Documentation of APSIM-Wheat

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Chapter 1

Introduction

This documentation is based on the current version of APSIM-Wheat module with a few modifications in the next generation updated on 17-August-2017.

A simulation is setup to demo the relationship among traits based on the cv. Hartog with high nitrogen and irrigation management under 15TraitMod experiment. The values in the figures below could be variable in other environments.

This is only a documentation for Wheat model in next generation of APSIM with our own understanding.

The main contents include

- Detail description of science parts of APSIM-Wheat model
- Figures of default parameters
- Figures of general outputs

1.1 Contributors

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1.2 Conventions

1.2.1 Figures

Figures in the documentation are classified into two categories with different backgrounds, i.e. `Input` and `Output`. `Input` figures show default parameter values (not genotypic values) or dynamic parameter values (depending on the other status variables) in the APSIM Next Gen model. `Output` figures show reportable variables in the in the APSIM Next Gen model. The `Input` and `Output` variable names only show the last section (separated by full stop) or specified names to save spaces in the figures.

Most of figures use two time serial variables, i.e. `Stage` and `Accumulated thermal time since sowing`. However, only `Stage` is used if all values are constant (e.g. Fig. 7.8), or stage based input variables.

The key stages are displayed in all figures (Section 3.2) including `G` for stage 2 `Germination`, `T` for stage 4 `Terminal Spikelet`, `F` for stage 6 `Flowering`, `E` for stage 8 `End of Grain Filling`.

1.3 How to contribute?

This documentation is wrote by RMarkdown and bookdown. I suggest you firstly to read the introduction about RMarkdown and bookdown, then fork this repository into your github account. Feel free to submit a pull request and/or an issue if you notice any errors or have any comments.

The new document can be easily generated for any other simulations using following steps.

- Install the required software including R, RStudio, Bookdown and other depended packages.
- Fork or download all source codes from git repository.
- Replace your own simulation.apsimx under simulation subfolder. Your apsimx file should only have `ONE` simulation and include all report variables used in the report, which can be found in the report replacement of the existing apsimx file.
- Click `Build book` in the RStudio interface.

1.3.1 Retrieve fixed value

`get_fixed_value` function is used to retrieve `FixedValue` in APSIM Next Gen. The `path` argument is used to specify the full path to the node with class `FixedValue` using APSIM format which connects the names of all predecessors started from `Wheat`. For example, the code below is used to obtain value for `GrainsPerGramOfStem` with value 22.

```
get_fixed_value(g_pmf,
    path = 'Wheat.Grain.NumberFunction.GrainNumber.GrainsPerGramOfStem')
```

1.3.2 Add new figure

Figures are classified into `Input` and `Output` categories (Section 1.2). `div` tags in html are used to specify the category.

````
<div class="fig-input">
```{r chunk-label, fig.asp=1, fig.cap='A figure caption.'}
# add you codes here
```
</div>

<div class="fig-output">
```{r chunk-label, fig.asp=1, fig.cap='A figure caption.'}
# add you codes here
```
</div>
````

Two variables are exposed to global environment (`.GlobalEnv` in R), i.e. `g_pmf` for an `xml` object of the simulation file `_simulation/simulation.apsimx`, and `g_report` for a `data.frame` of the simulation output file. Variables `g_pmf` and `g_report` can be used in any places of the documentation.

A few `helper` functions are designed to plot figures, i.e. `plot_xypair` and `plot_report`.

`plot_xypair` is used to plot the `XYPairs` function in APSIM Next Gen. The `path` argument is used to specify the full path of a node with child `XYPairs` using APSIM format which connects the names of all predecessors

started from `Wheat` (e.g. `Wheat.Leaf.CohortParameters.MaxArea.AgeFactor`). `g_xlab` and `y_lab` can be used to specify the X and Y labels.

```
path <- 'Wheat.Leaf.CohortParameters.MaxArea.AgeFactor'
plot_xypair(g_pmf, path,
            x_lab'Growthing stage',
            y_lab = 'Multiplier of maximum leaf area')
```

`plot_report` is used to plot outputs of APSIM Next Gen for a single and multiple variables. Two types of X variables are predefined in the global environment (i.e. `g_xvar` for thermal time and stage; `g_xvar2` for stage only). `X` label is also defined in the global environment. These variables can be overwrote when the `plot_report` is called, but DO NOT add into global environment as other chunks use the default values.

```
g_xvar <- c('Wheat.Phenology.Stage',
           'Wheat.Phenology.AccumulateThermalTime')
g_xvar2 <- c('Wheat.Phenology.Stage')
g_xlab <- 'Accumulated thermal time or stage'
```

The argument `y_cols` is used to specify one and multiple variables in the APSIM report using `plot_report` function. Y label `y_lab` should be specified for each figure.

```
y_cols <- c('Wheat.Leaf.DMSupply.Fixation',
            'Wheat.Leaf.DMSupply.Retranslocation',
            'Wheat.Leaf.DMSupply.Reallocation')
plot_report(g_report, g_xvar, y_cols, x_lab = g_xlab,
            y_lab = 'Demand (g/d)', ncol = 3)
```

1.4 Software information

The R session information when compiling this book is shown below:

```
## R version 3.4.2 (2017-09-28)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 7 x64 (build 7601) Service Pack 1
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_Australia.1252  LC_CTYPE=English_Australia.1252
## [3] LC_MONETARY=English_Australia.1252 LC_NUMERIC=C
## [5] LC_TIME=English_Australia.1252
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  base
##
## other attached packages:
##  [1] bindrcpp_0.2     RSQLite_2.0      DiagrammeR_0.9.2 xml2_1.1.1
##  [5] assertive_0.3-5  dplyr_0.7.4      purrr_0.2.3      readr_1.1.1
##  [9] tidyr_0.7.1      tibble_1.3.4     ggplot2_2.2.1    tidyverse_1.1.1
## [13] magrittr_1.5     knitr_1.17
##
## loaded via a namespace (and not attached):
##  [1] viridis_0.4.0              httr_1.3.1
##  [3] bit64_0.9-7                viridisLite_0.2.0
##  [5] jsonlite_1.5               assertive.sets_0.0-3
```

```
##  [7] modelr_0.1.1               assertthat_0.2.0
##  [9] assertive.data_0.0-1       highr_0.6
## [11] blob_1.1.0                 cellranger_1.1.0
## [13] yaml_2.1.14                backports_1.1.1
## [15] lattice_0.20-35            glue_1.1.1
## [17] downloader_0.4             assertive.data.uk_0.0-1
## [19] assertive.matrices_0.0-1   digest_0.6.12
## [21] assertive.types_0.0-3      RColorBrewer_1.1-2
## [23] rvest_0.3.2                colorspace_1.3-2
## [25] htmltools_0.3.6            plyr_1.8.4
## [27] psych_1.7.8                XML_3.98-1.9
## [29] pkgconfig_2.0.1            broom_0.4.2
## [31] assertive.data.us_0.0-1    assertive.properties_0.0-4
## [33] assertive.reflection_0.0-4 haven_1.1.0
## [35] bookdown_0.5               scales_0.5.0
## [37] brew_1.0-6                 influenceR_0.1.0
## [39] assertive.code_0.0-1       lazyeval_0.2.0
## [41] mnormt_1.5-5               rgexf_0.15.3
## [43] readxl_1.0.0               assertive.strings_0.0-3
## [45] memoise_1.1.0              evaluate_0.10.1
## [47] methods_3.4.2              assertive.numbers_0.0-2
## [49] nlme_3.1-131               forcats_0.2.0
## [51] foreign_0.8-69             Rook_1.1-1
## [53] tools_3.4.2                hms_0.3
## [55] assertive.files_0.0-2      stringr_1.2.0
## [57] munsell_0.4.3              compiler_3.4.2
## [59] rlang_0.1.2                grid_3.4.2
## [61] rstudioapi_0.7             visNetwork_2.0.1
## [63] htmlwidgets_0.9            assertive.models_0.0-1
## [65] assertive.base_0.0-7       igraph_1.1.2
## [67] rmarkdown_1.6              gtable_0.2.0
## [69] codetools_0.2-15           DBI_0.7
## [71] assertive.datetimes_0.0-2  reshape2_1.4.2
## [73] R6_2.2.2                   gridExtra_2.3
## [75] lubridate_1.6.0            bit_1.1-12
## [77] bindr_0.1                  rprojroot_1.2
## [79] stringi_1.1.5              parallel_3.4.2
## [81] Rcpp_0.12.13
```

Chapter 2

Overview

The APSIM-Wheat model is based on a framework of the physiological determinants of crop growth and development (Hammer et al. 2016; Charles-Edwards 1982) and is focused at organ scale.

2.1 Organs

In the wheat module, wheat is divided into four components or parts: Grain, Root, Leaf, Spike and Stem. Leaf includes only leaf blades. Stem is defined in a functional rather than amorphological manner and includes plant stems, leaf sheaths. Head is divided into Grain and Spike (which correspond to spike without the grain).

2.2 Terminology

2.2.1 Phenology

- **Plastochron** The plastochron is commonly used as the thermal time between the appearance of successive leaf primordia on a shoot.
- **Phyllochron** The phyllochron is the thermal time it takes for successive leaves on a shoot to reach the same developmental stage.

2.2.2 Structure

- **Node (Phytomer)** A phytomer unit is defined as consisting of a leaf, and the associated axillary bud, node and internode.
- **Main stem** The first culm that emerges from the seeds is the main stem.
- **Tiller (Branch)** All remaining culms that emerges from main stem or other tillers (branches), are referred as tillers or branches.
- **Apex** A shoot apex is the terminal bud of plants that grows from 0.1-1.0 mm and consists of the apical meristem, developing leaves and the immediate surrounding leaf primordial. Each tiller has an apex which continuously developes new leaf.

2.2.3 Leaf

- **Leaf organ** is only included leaf blades excluding section under sheath, i.e. only parts of leaf blades to produce photosynthate.

- **Huan Index** is mainly concerned with the leaf production stage of development (Haun 1973). The length of each emerging leaf is expressed as a fraction of the length of the preceding fully emerged leaf. For example, a 3.2 indicates that three leaves are fully emerged, and a fourth leaf has emerged two-tenths of the length of the third.

Chapter 3

Phenology

3.1 Thermal time

The daily thermal time ΔTT is calculated using daily records of mean temperature (T) using a beta function (Wang and Engel 1998).

$$\Delta TT = T_{opt} \begin{cases} \frac{2(T-T_{min})^{\alpha}(T_{opt}-T_{min})^{\alpha}-(T-T_{min}^{2\alpha})}{(T_{opt}-T_{min})^{2\alpha}} & if \quad T_{min} \leqslant T \leqslant T_{max} \\ 0 \quad if \quad T < T_{min} \quad or \quad T > T_{max} \end{cases}$$

where, T_{min}, T_{opt} and T_{max} are the three cardinal temperatures for wheat development, which are 0, 27.5 and 40 °C, respectively. The parameter α is calculated by the following equation. THe daily mean temperature T is calculated as the average of daily minimum and maximum temperature.

$$\alpha = \frac{\ln(2)}{\ln \frac{(T_{max}-T_{min})}{T_{opt}-T_{min}}}$$

3.2 Stages and periods

The growth cycle of wheat is started from sowing and finished at harvest ripe.The whole cycle is separated into 10 stages and 10 phases. Wheat jumps into next stage or phase when certian conditions are statisfied (earliness "per se", vernalization and photoperiod).

Stage	Name	Description
1	Sowing	Sow seeds into field
2	Germination	Germination begins when the seed imbibes water from the soil and reaches 35 to 45 percent moisture on a dry weight basis
3	Emergence	The coleoptile extends to the soil surface
4	TerminalSpikelet	The terminal spikelet initial is formed
5	FlagLeaf	The appearance of flag leaf tip or ligule (??)
6	Flowering	The 50% plants are flowering in the field
7	StartGrainFill	Grain filling follows anthesis and refers to the period during which the kernel matures or ripens
8	EndGrainFill	Grain filling follows anthesis and refers to the period during which the kernel matures or ripens

Stage	Name	Description
9	Maturity	Grain dry weight reaches its maximum which is correlated to the absence of green color in the chaff or kernels
10	HarvestRipe	Wheat is ready for harvest

Each phase has a targer thermal time (earliness *per se*) and several impact factors to extend the growing period including vernalization, photoperiod, water, nitrogen stresses.

Name	Earliness per se	Vernalization	Photoperiod	Description
Germinating	NA	NA	NA	Depending on soil water in top layer
Emerging	$Lag + Rate * depth$	NA	NA	Depending on the sowing depth
Vegetative	NA	NA	NA	NA
StemElongation	NA	NA	NA	NA
EarlyReproductive	NA	NA	NA	NA
GrainDevelopment	NA	NA	NA	NA
GrainFilling	NA	NA	NA	NA
Maturing	NA	NA	NA	NA
Ripening	NA	NA	NA	NA
ReadyForHarvesting	NA	NA	NA	NA

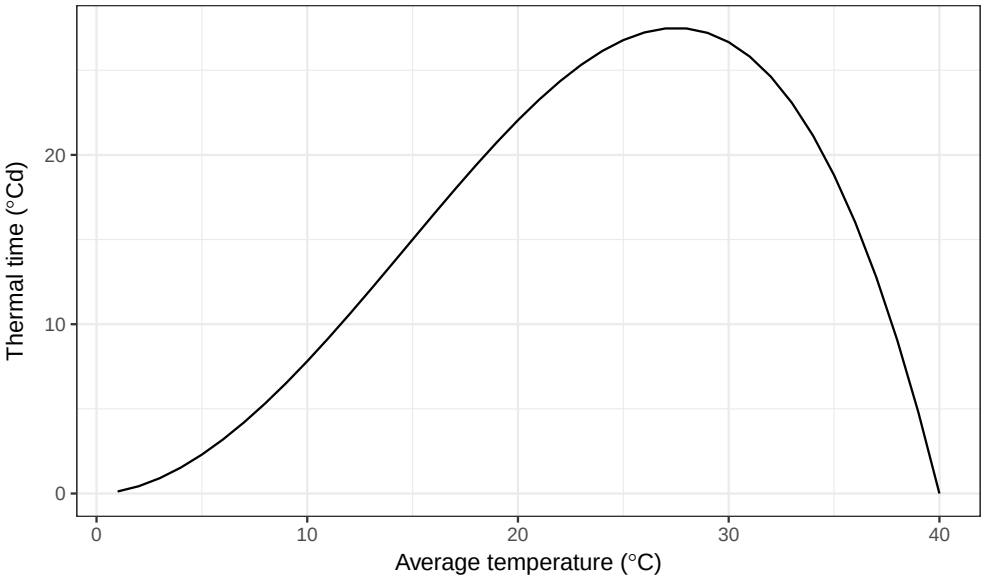

Figure 3.1: Temperature response of wheat development

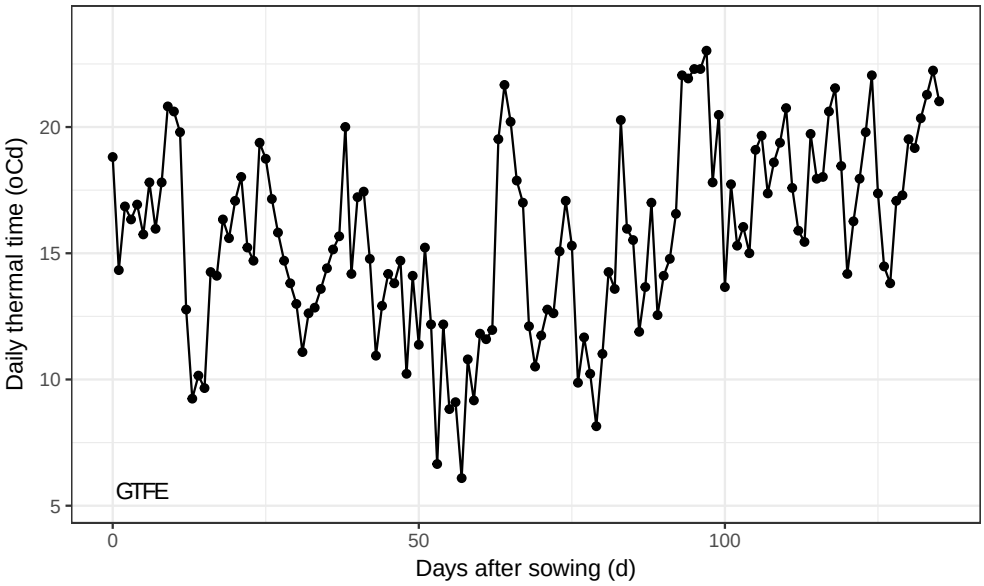

Figure 3.2: The daily thermal time calculated from the daily mean temperature

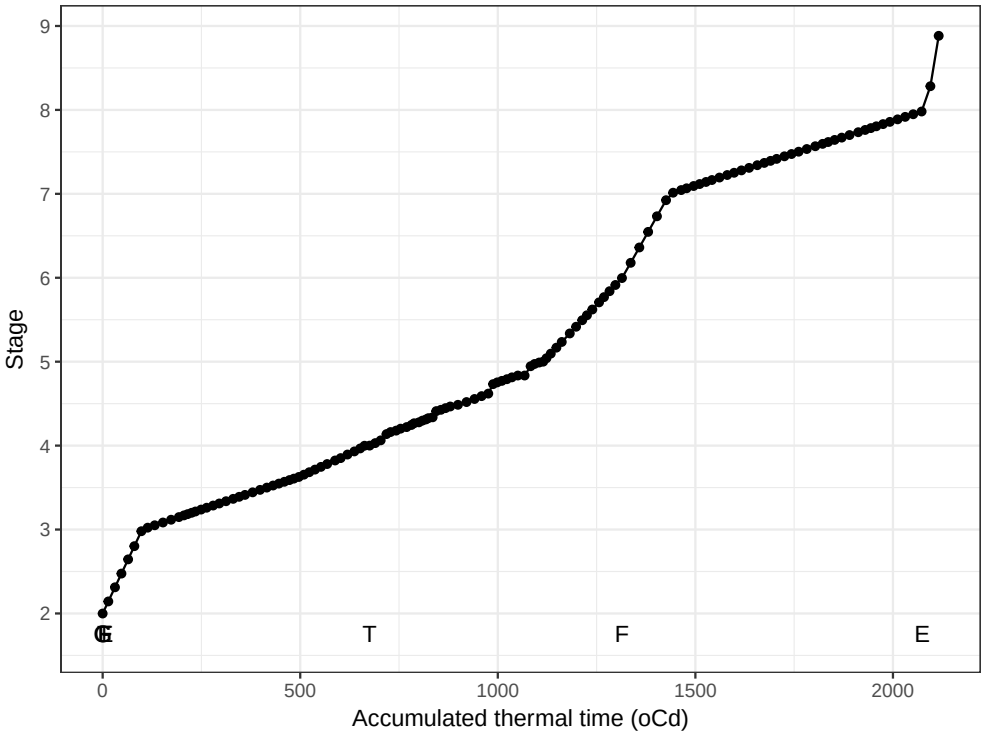

Figure 3.3: The growthing stage as a function of accumulated thermal time

Chapter 4

Structure

The development of wheat leaves and tillers are simulated with an apex model which is further developed from leaf cohort model (Brown et al. 2014). The basic assumptions include

1. The growth and development of a plant is controlled by apex. Only one apex is existed in a plant at emergence. Branching increases the total apex number of a plant. Apex death decreases the apex number, which are caused by several reasons including the carbon allocation, light intensity, natural death. The apex number is not necessary as an integer to simulate plant development in the population level.
2. The number of apex in a plant determines the number of the new leaves when initialization of a new cohort. The cohort size is fixed after initialization although attributes can be changed in the later stage.
3. The apexes are grouped by age and have the same age if they initialize at the same day. During development of new cohort, new apexes caused by branching develops into new tillers which have the same behaviours during the whole lift span (e.g. size, area, nitrogen, photosynthesis). The apex age equals to 1 when it initialize and increases by 1 when a new leaf cohort initializes. Each apex group has several attributes including size and age.

4. The leaves in a cohort also are distinguished and grouped by apex ages, which determines at the initialization of leaf cohort.
5. Death of branches or tillers only reduces the total number of apexes, not the size of existing cohorts. The apexes with youngest age are going to death first.

4.1 Phyllochron

The phyllochron is the intervening period between the sequential emergence of leaf tips on the main stem of a wheat (McMaster and Hunt 2003).

The non-linear reponse of temperature on phyllchron were observed by Friend et al. (1962) and Cao and Moss (1989). The soil temperature provided more accurately prediction of leaf development than air temperature (Jamieson et al. 1995). However, a simple linear reponse of phyllochron to air temperature works surprusingly well in predicting phyllochron for most field conditions (McMaster and Hunt 2003). If improvements are desired, the use of non-linear reponses and soil temperature shows promise (Jamieson et al. 1995; Yan and Hunt 1999). Consequently, we assume the linear reponse of air temperature on leaf appearance (phyllochorn).

The base phyllochron is a genotypic parameter with default value 120, but is chagned for most of cultivars. Based on (Jamieson et al. 1995), leaf appearance could be described by a base phyllochron determined between leaves 3 and 7 and a phyllochron that was 70% of base phyllochron for leaves < 3 and 140% of base phyllochroen for leaves > 7 (Fig. 4.1). The phyllochron also is adjusted by photoperiod [reference required] through increasing pholochron in the shorter day length (Fig. 4.2).

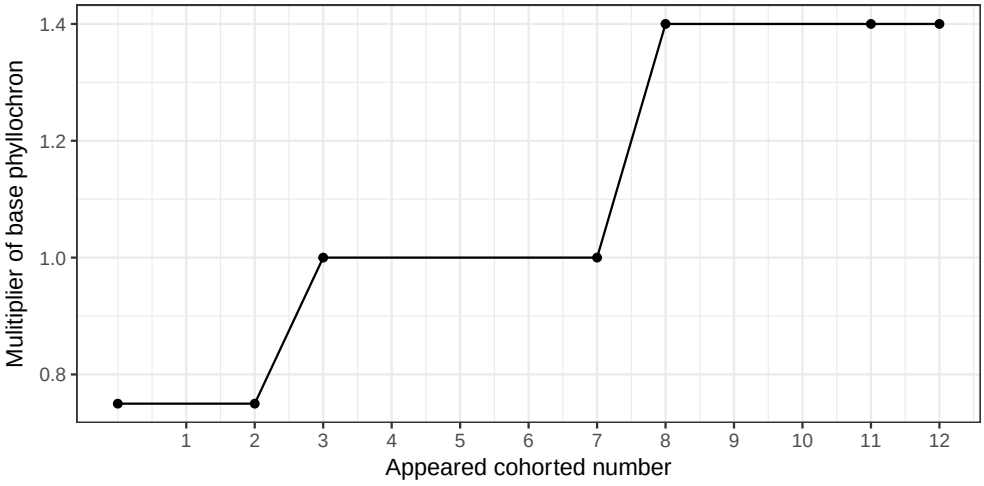

Figure 4.1: Phyllochron of leaf cohort is depending on the rank on the main stem

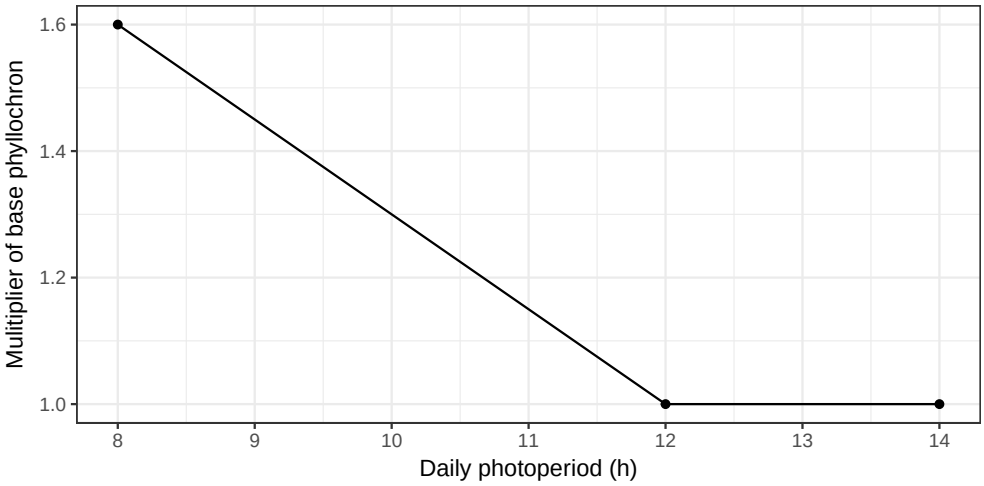

Figure 4.2: The multiplier of phyllochron which is effected by daily photoperiod length.

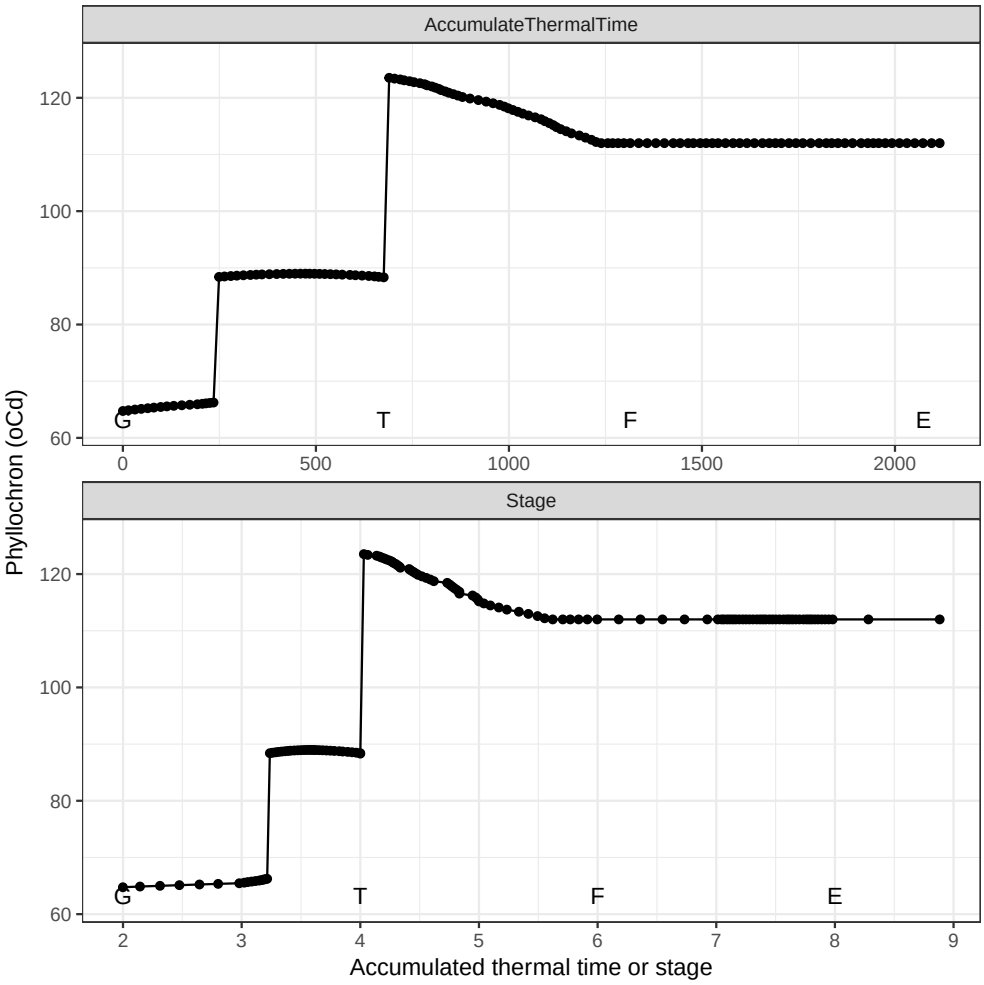

Figure 4.3: The actual phyllochron in the testing environment

Finally, the phyllochron is dynamically adjusted according to appeared cohort number and daily photoperiod (Fig. 4.3).

4.2 Final leaf number

Will be documented...

4.3 Initialization and appearance of leaf tips on main stem

At `Germination` stage, 2 new leaf cohorts or tips are initialized at the main stem. At `Emergence` stage, 1 leaf cohort or tip is appeared at the main stem, and 1 more leaf cohort is initialized. The potential appearance of leaf tip number ($N_{p,tip}$) is initialized as 1.

After `Emergence`, the potential appearance of tip number in the main stem ($N_{p,tip}$) is daily increased according to the daily phyllochron (Fig. 4.3) and thermal time (Section 3.1) until `Maturity` (Fig. 4.5 and 4.6. $N_{p,tip}$ should stop increasing when final leaf number is reached).

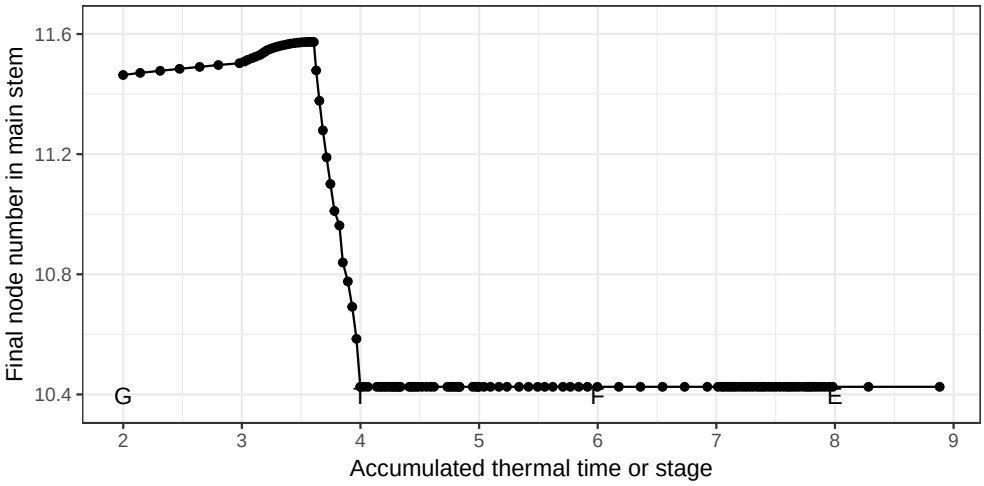

Figure 4.4: Final leaf number in main stem

$$\Delta N_{p,tip} = \frac{\Delta TT_t}{P_{phy}}$$

where, $N_{p,tip}$ is the daily increase of leaf tip number (Fig. 4.5), ΔTT_t is the daily thermal time, P_{phy} is the phyllochron calculated at today.

Potential appearance of tip number in main stem ($N_{p,tip}$) are summarized daily increases since `Emergence`, plus the appeared leaf tip at `Emergence` (1 for wheat model) (Fig. 4.6).

$$N_{p,tip} = \sum_{t=T_0}^{T} \Delta N_{p,tip} + 1$$

where, T_0 is day of `Emergence`. T is today. In the Structure model, the tip numbers are not calculated for branches or tillers, but only for main stem (Figure 4.6).

Before plant reaches the final leaf number (i.e. all leaves are initialized and appeared), a new leaf cohort is initialized and appeared when increases of $N_{p,tip}$ are more than 1 (Figure 4.5). Consequently, the rates of leaf initialization and appearance are same, except initialized tip number is more than 2 of appeared tip number.

Huan stage is exported as the output variable `LeafTipsAppeared`.

The fraction of final leaf is used to simulate the variation of final leaf number in a population. The fraction of leaf cohort is set as 1 for all leaf cohort, except the flag leaf which equal to decimal part of final leaf number (Fig. 4.4).

4.4 Tillering

At `Emergence`, the apex number equals to `1`. The apex number in a plant (A) is increased by branching (ΔA_B) and decreased by mortality (ΔA_M) in every day.

$$A = \sum_{i=1}^{N_{node}} (\Delta A_B - \Delta A_M)$$

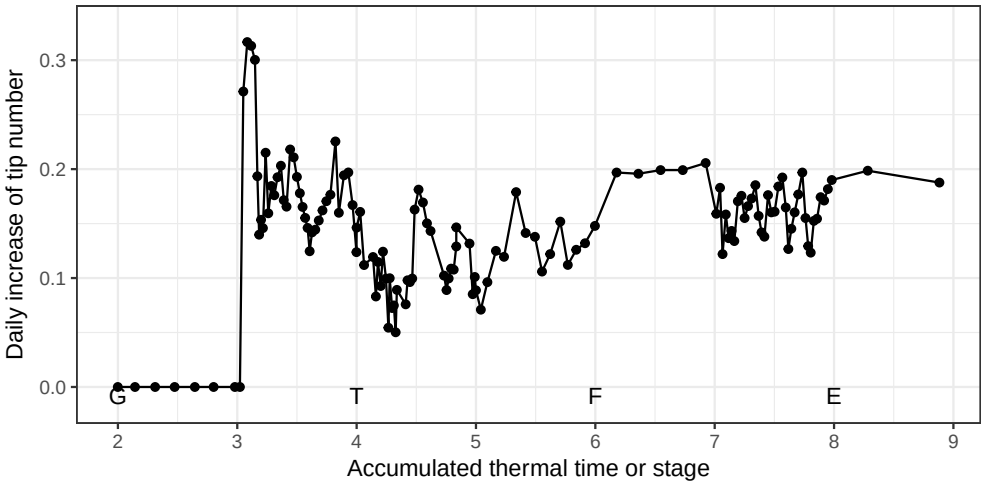

Figure 4.5: Daily increase of tip number in main stem. There is no point to consider increase of tip number after stage 4 (terminal spikelet), although model exports increase of tip number in the whole growth season

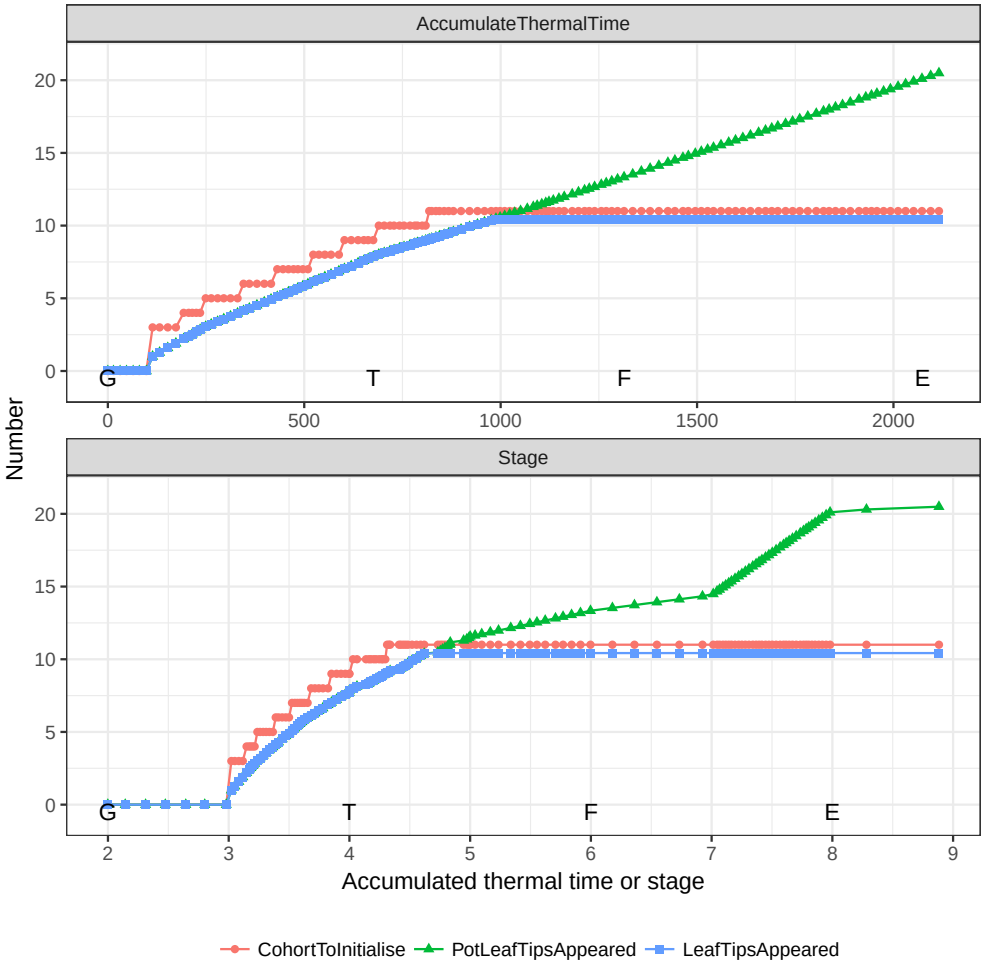

Figure 4.6: Tips number in main stem. The potential appeared tip number keeps increasing after flag leaf, which is only a model output and need to be fixed.

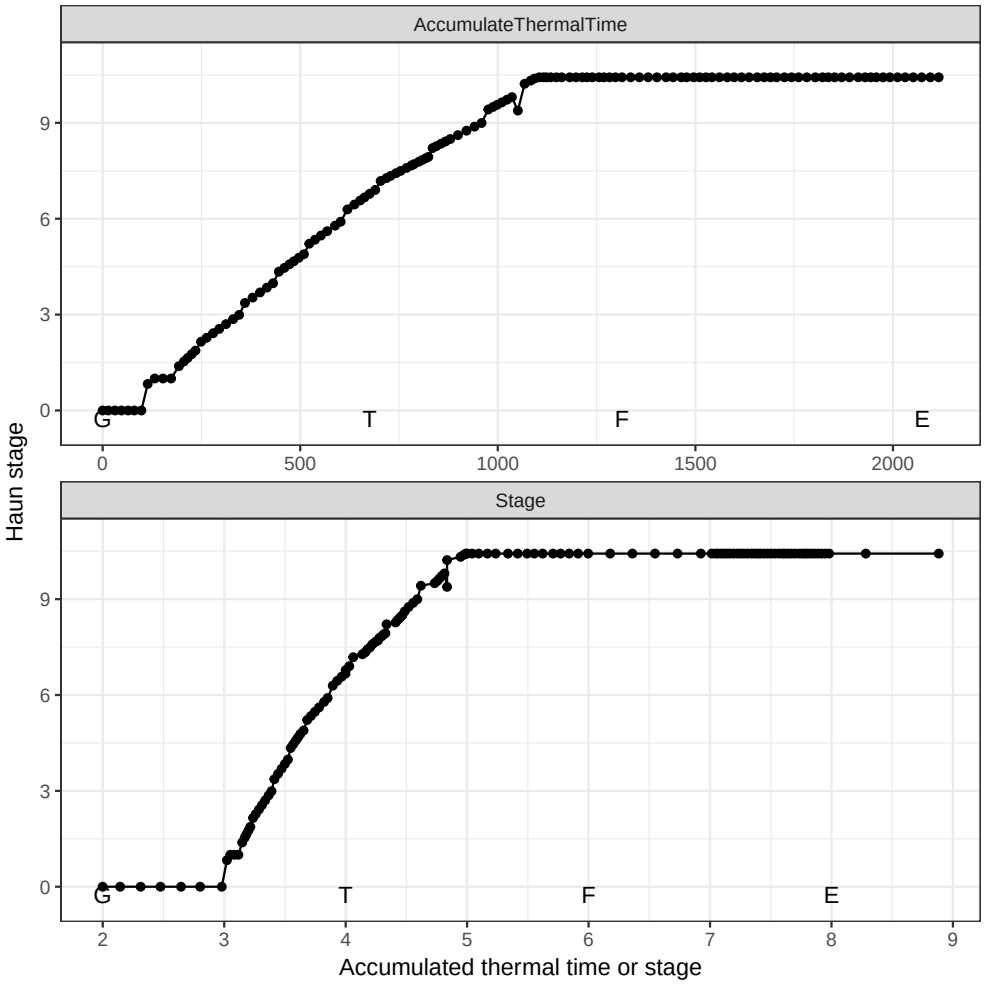

Figure 4.7: Haun stage in main stem

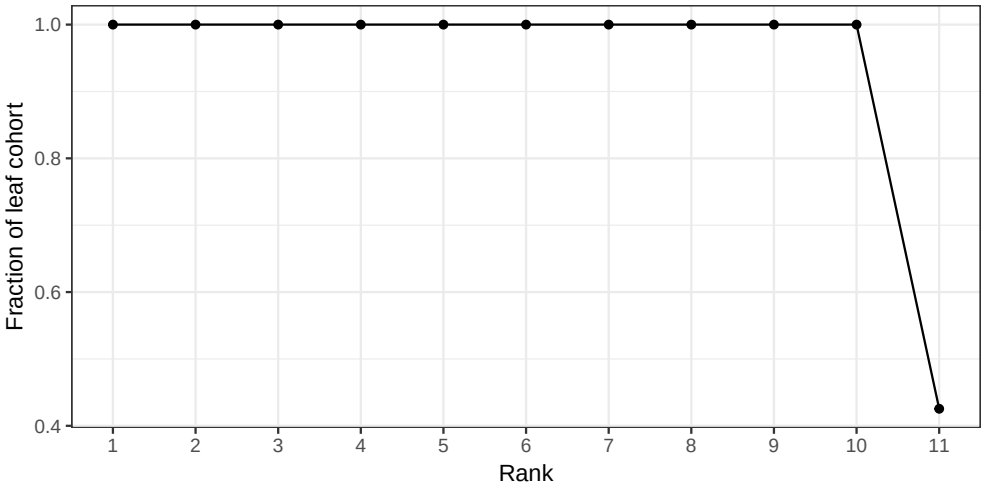

Figure 4.8: Fraction of leaf cohort

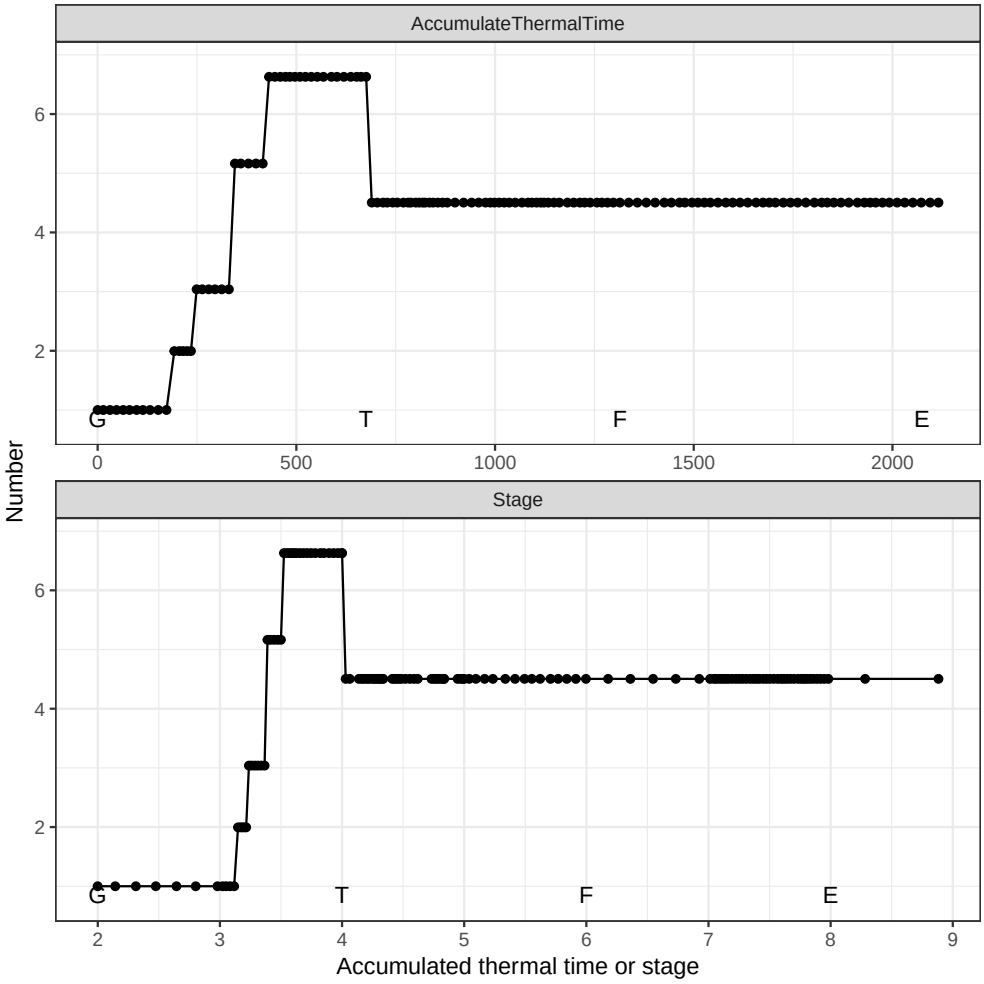

Figure 4.9: Apex number in the main stem

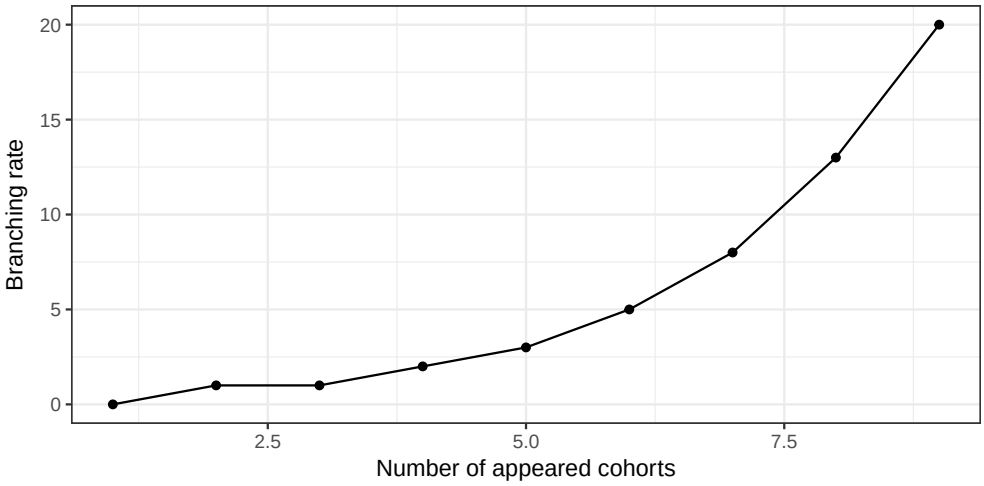

Figure 4.10: Potential branching rate of APSIM-Wheat as a function of appreared cohort number

4.4.1 Branching rate

The branching rate in a plant is specified by parameter BranchingRate (ΔA_B) and is calculated as potential branching rate (Fig. 4.10) and several stress factors (i.e. nitrogen stress, total coverage, and water stress). From stage Emergence to Terminal Spikelet (Section 3.2), the potential branching rate is defined as a function of number of appeared cohorts in the main stem (Figure 4.10) which follow the pattern of Fibonacci sequence. Beyond this period, the branching rate is set as zero.

Two stresses are defined in the APSIM-Wheat including nitrogen and WSC. A simple sensitivity analysis indicates the branching rate is too sensitive to WSC with default values (x = [0.1, 0.2]; y = [0, 1]). So, this feature is disabled for further analysis.

The nitrogen stress is calculated as a function of fraction of nitrogen supply relative to nitrogen demand which is exported from the Arbitrator module. Wheat module assumes no nitrogen stress when the nitrogen supply is bigger than 1.5 times of nitrogen demand (Figure 4.11). Nitrogen stress linearly increases when supply/demand ratio less then 1.5 (Reference required.)

Figure 4.13 shows the branching rate and total branching number in the test simulation without nitrogen stress on branching rate during branching period (from Emergence to Terminal Spikelet.

4.4.2 Mortality

Two types of mortality are considered in the apex model, i.e. smaller tiller at terminal spikelet and low growth rate. For any types of tiller mortality, the plant does not reduce the population of existing leaf cohort, but number of apex, then reduce the population size of new leaf cohort.

At the terminal spikelet, all tillers with less than 4 leaves are stopped to growth new leaves.

Branching mortality starts from the Flag leaf until Flowering which defines as a function of moving mean tiller growth rate (Figure 4.14. The mean tiller growth rate is calculated as the 5 days moving means of tiller growth rate, which is calculated by the daily biomass supply divides thermal time and total stem population. Reference required.

Figure 4.15 shows the mean tiller growth rate and the three factors to calculate it in the test simulation.

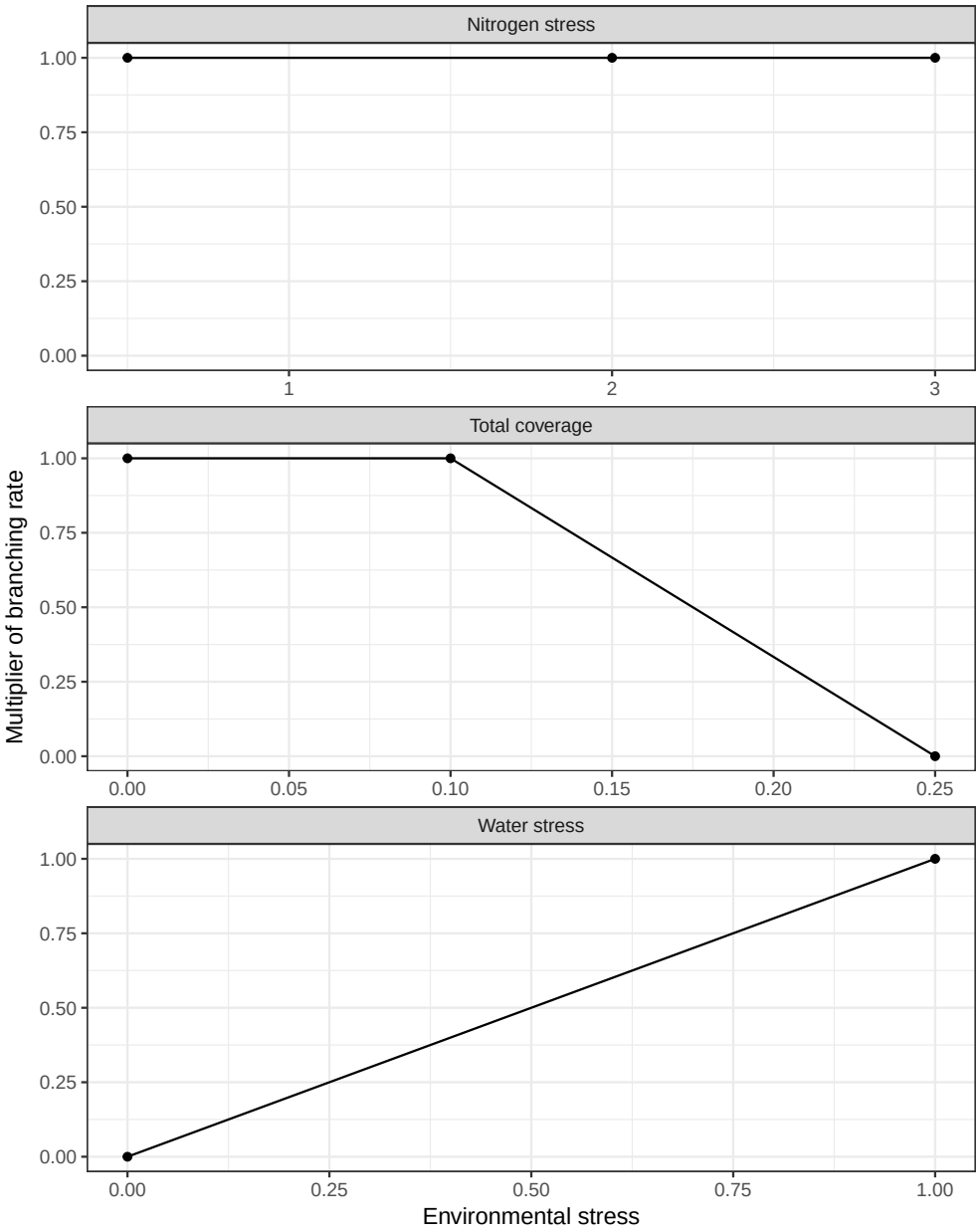

Figure 4.11: The factors to influence of branching rate (nitrogen stress, total coverage and water stress). The final multiplier of branching rate is the minimum values of the

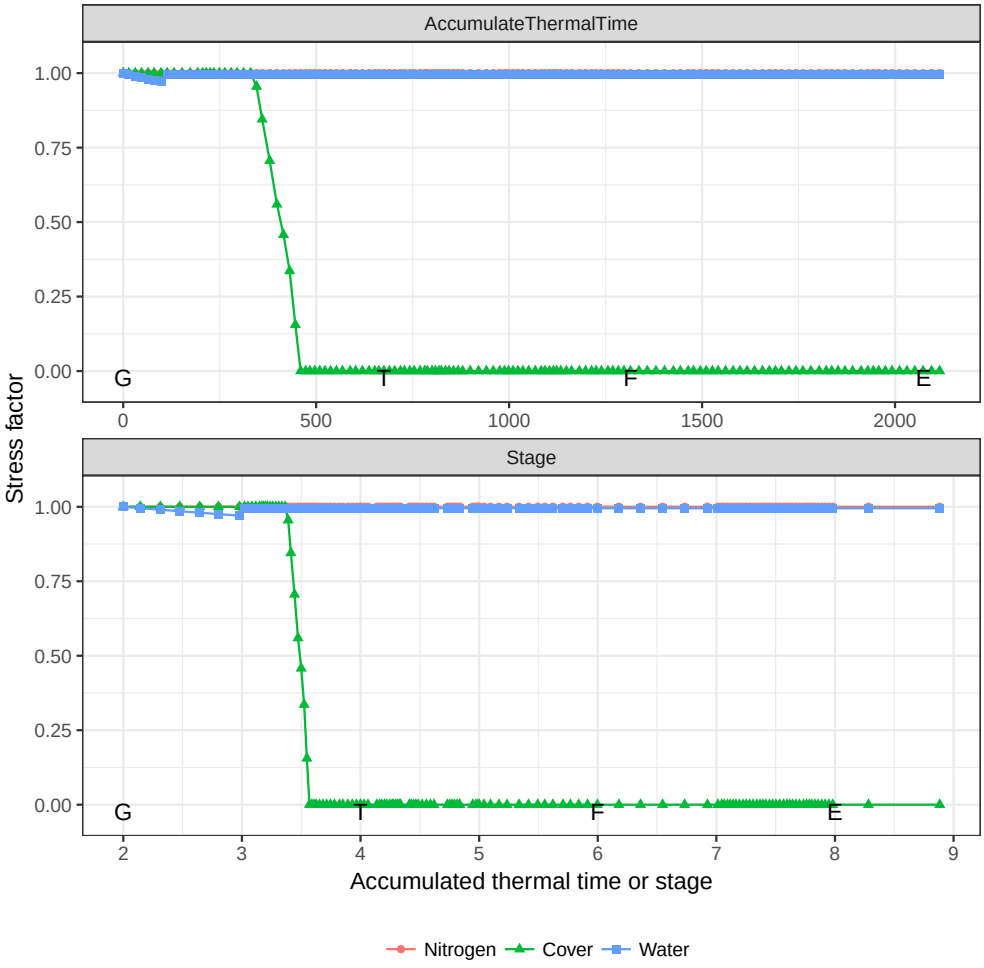

Figure 4.12: The stress factors for branching rate

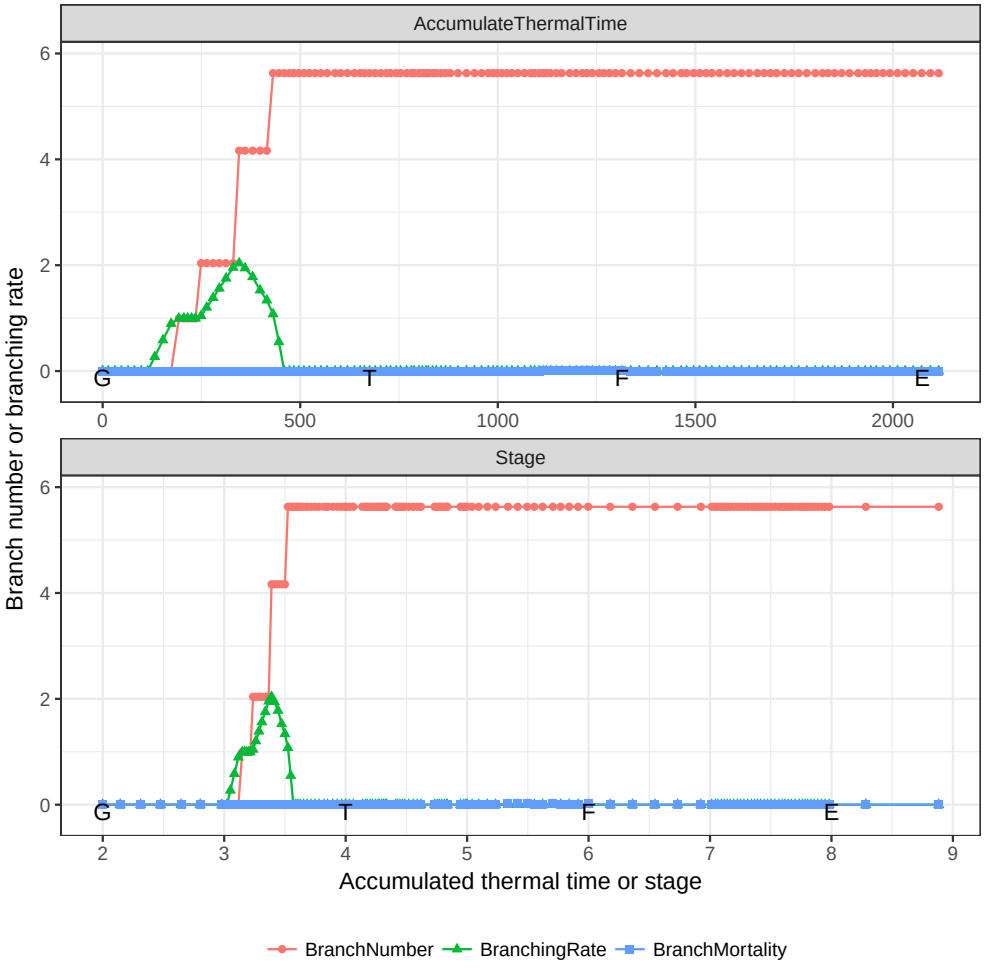

Figure 4.13: The branching rate and branch number for wheat

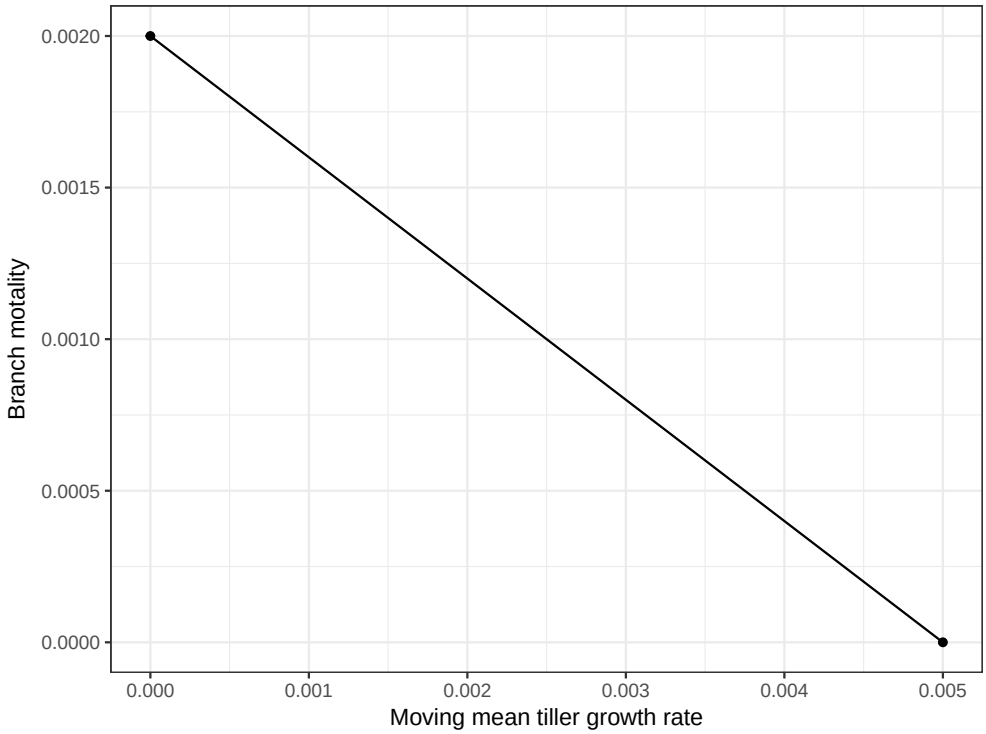

Figure 4.14: Tiller mortality as a function of moving mean tiller growth rate

4.5 Plant and Main-Stem Population

No plant mortality is considerred in the wheat model.

4.6 Canopy height

The canopy height (Fig. 4.21) is calculated as the potential height (Fig. 4.19) and adjusted by water stress (Fig. 4.20).

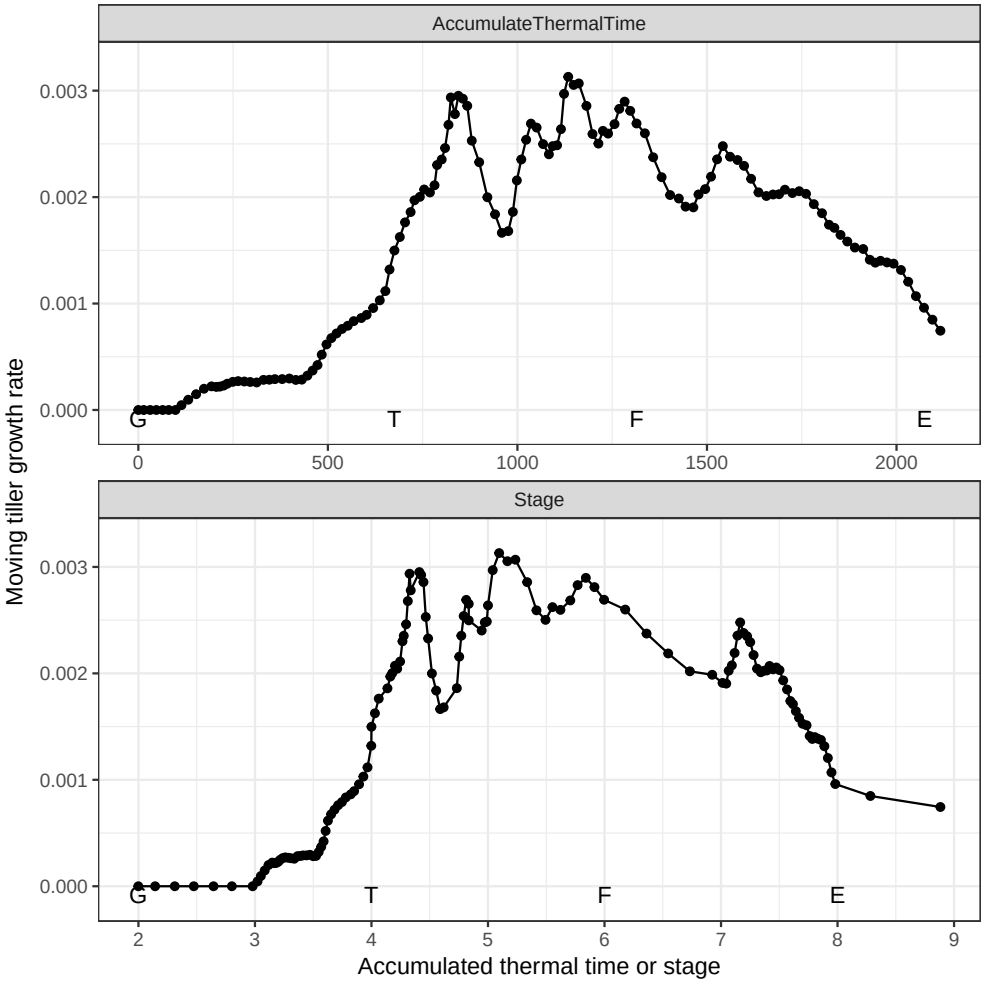

Figure 4.15: The moving tiller growth rate

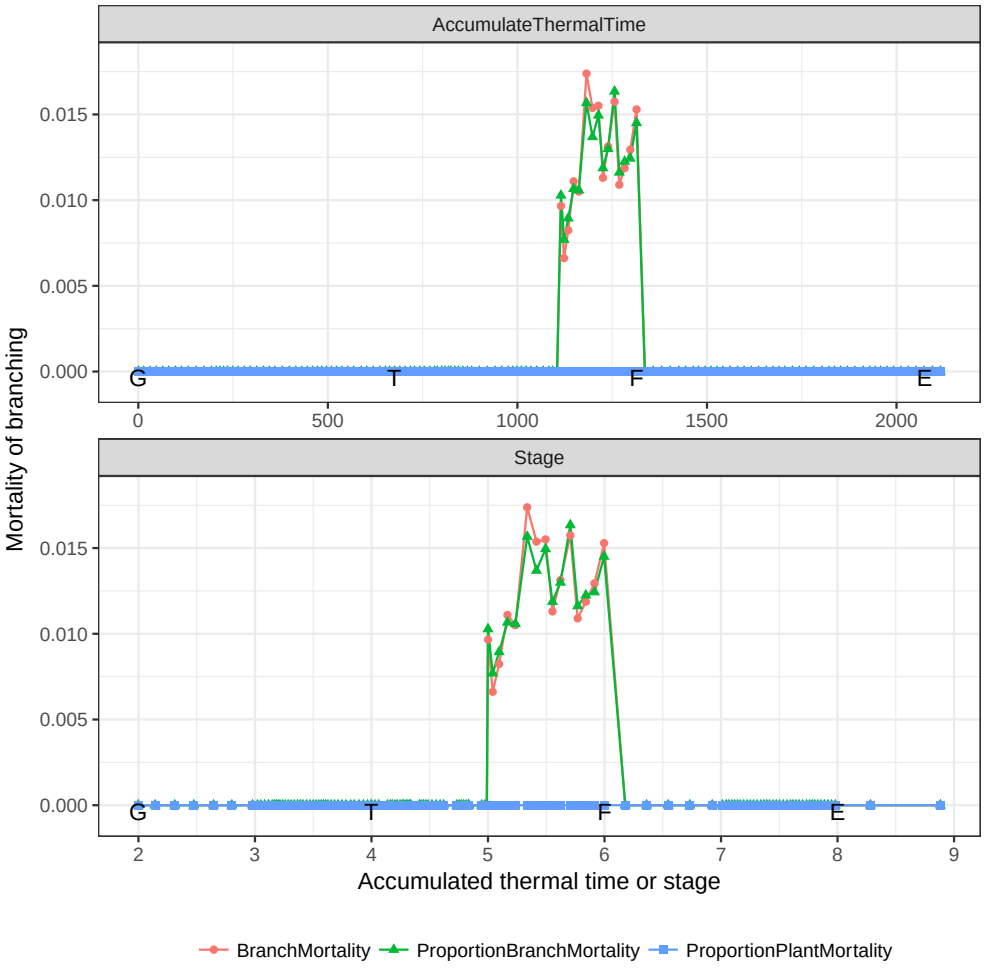

Figure 4.16: The mortality of tillers

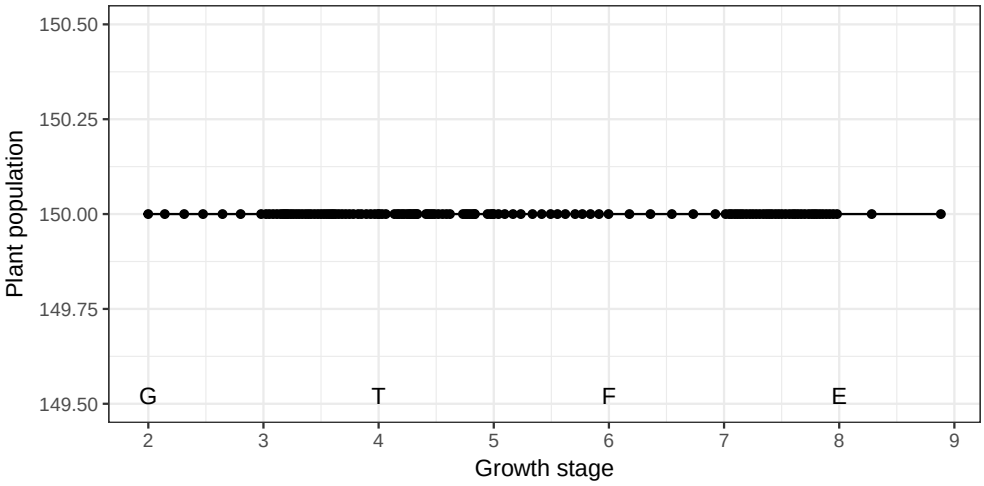

Figure 4.17: Plant population.

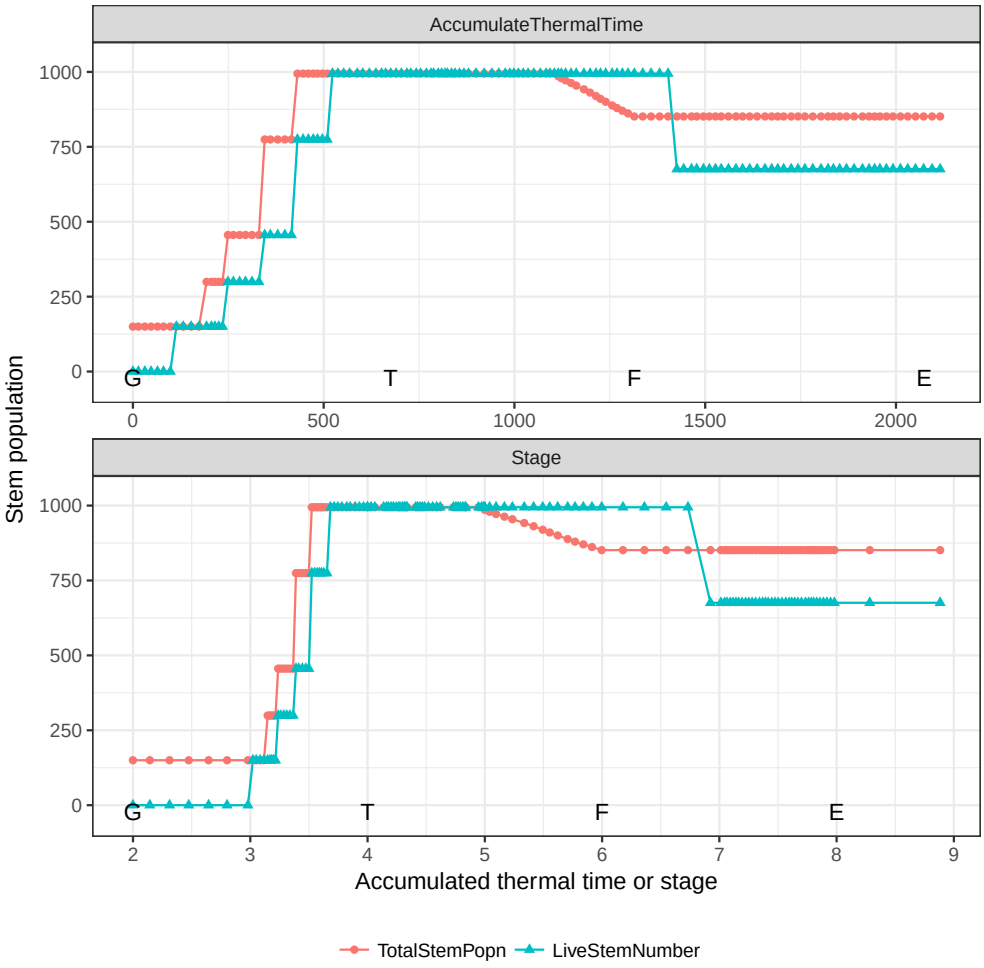

Figure 4.18: Total stem population and live stem number.

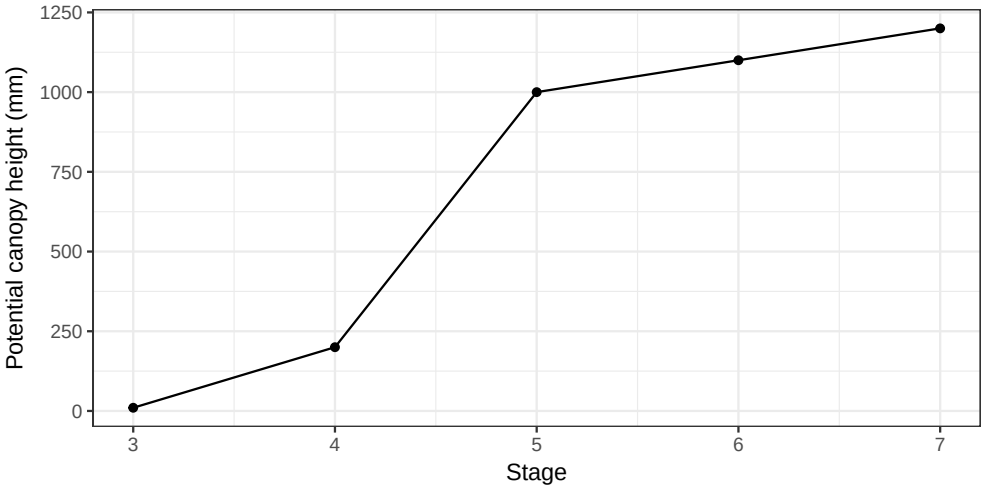

Figure 4.19: Potential canopy height

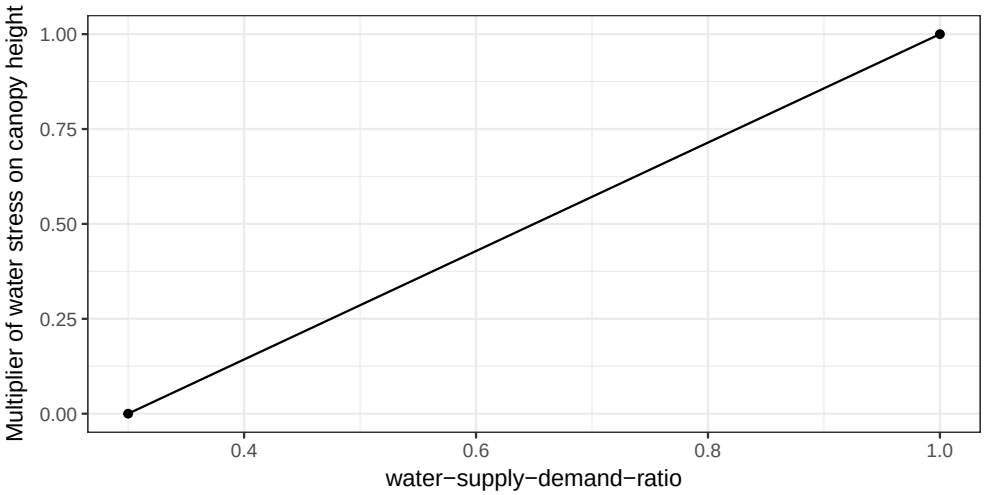

Figure 4.20: The impact of water stress on canopy height

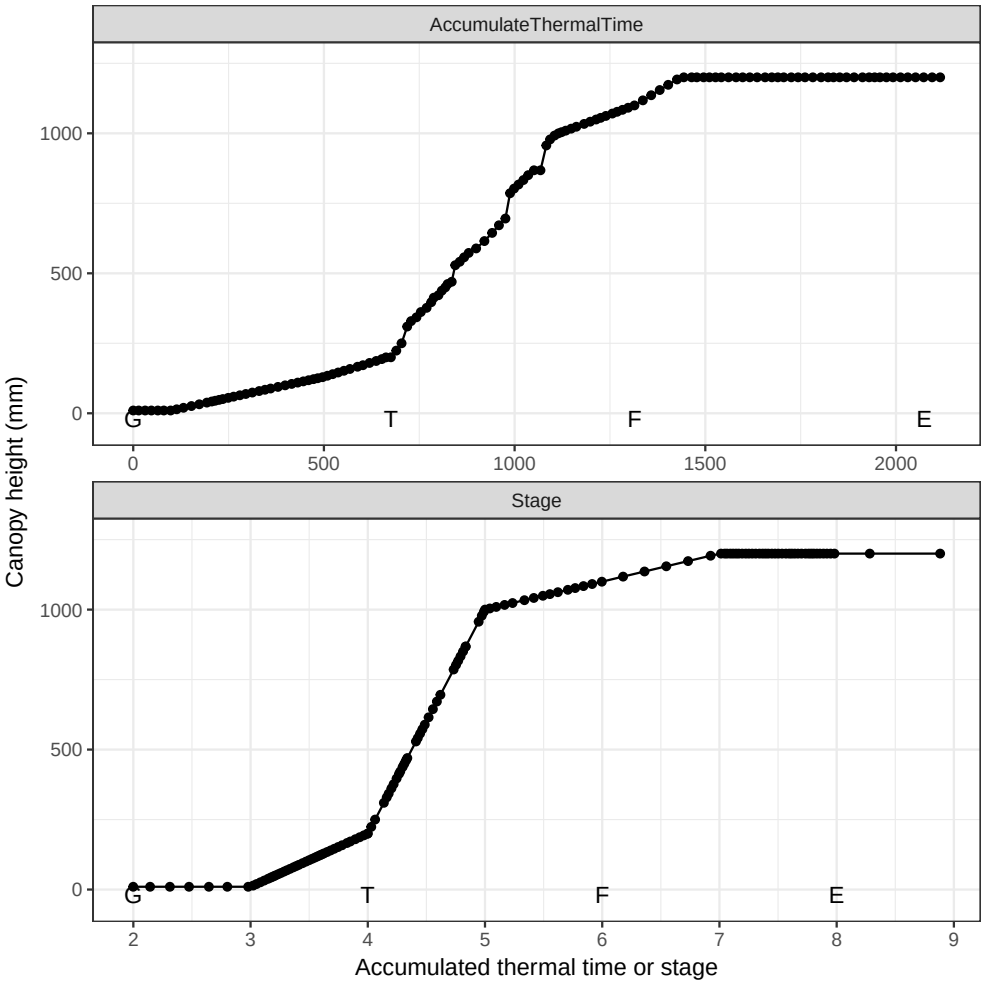

Figure 4.21: The simulated canopy height

Chapter 5

Biomass

The wheat is mainly source limited in APSIM-Wheat model.

The biomass and nitrogen of each organ is separated into two pools (i.e. `Live` and `Dead`). Each pool is separated into three components (i.e. `Structural`, `Metabolic`, `Storage`) (Brown et al. 2014).

- **Structural biomass and N** are essential for the growth of the organ. They remain within the organ once it has been allocated and are passed from Live to Dead pools as the organ senescence.
- **Metabolic biomass and N** are essential for growth and their concentration can influence the function of organs (e.g. photosynthetic efficiency of the leaf depends on Metabolic nitrogen content). Metabolic biomass and nitrogen may be reallocated (moved to another organ upon senescence of this organ) or retranslocated (moved to another organ at any time when supplies do not meet the structural and metabolic biomass demands of growing organs).
- **Storage biomass and N** are non-essential to the function of an organ. They will be allocated to an organ only when all other organs have received their Structural and Metabolic allocations and may be reallocated or retranslocated.

5.1 Supply

Biomass supplies are divided into three sources, i.e fixation (i.e. photosynthesis), retanslocation, reallocation (Table 5.1). The only source of fixation is organ `Leaf`. The sources of retanslocation include organs `Spike` and `Stem`. No reallocation is considered in the wheat model. See details in the organs about the dynamic of biomass supply.

Table 5.1: The source of biomass supply in all organs. X and - indicate the organ has and has not the source, respectively.

Organ	Fixation	Retranslocation	Reallocation
Grain	-	-	-
Root	-	-	-
Leaf	X	-	-
Spike	-	X	-
Stem	-	X	-

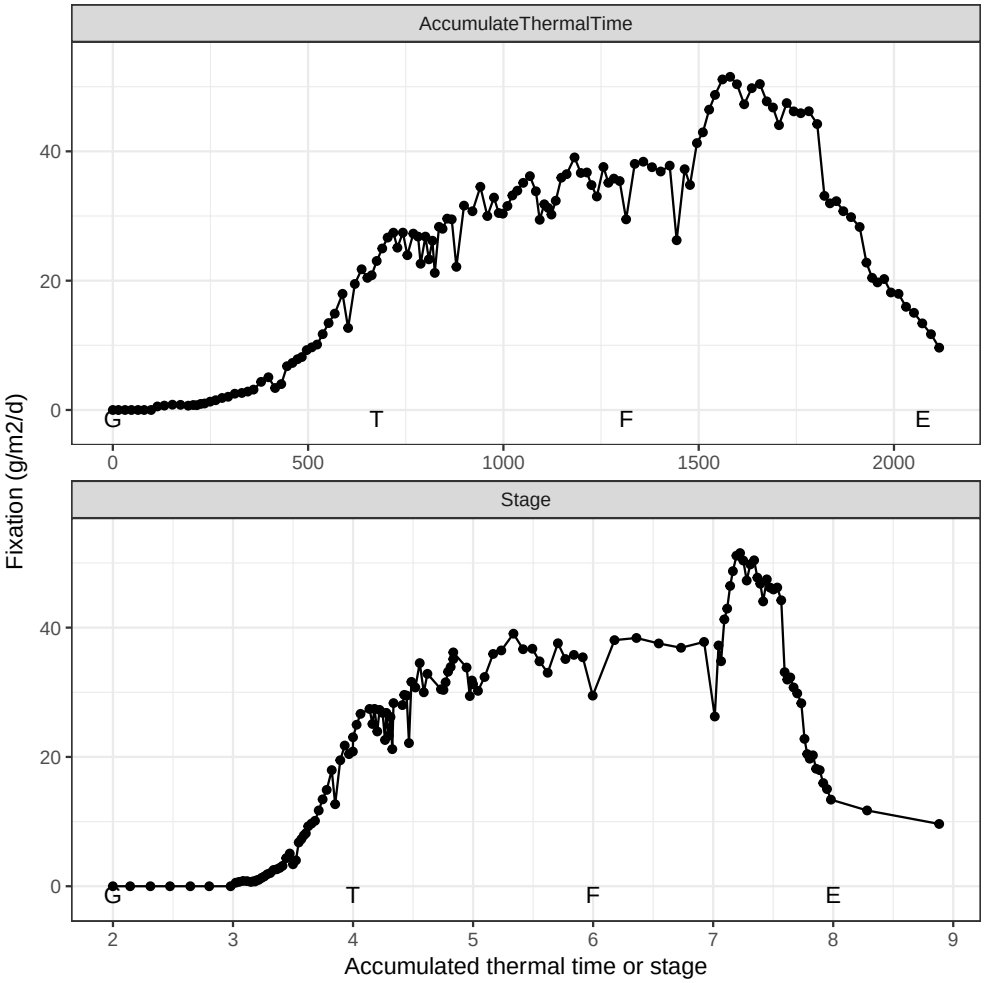

Figure 5.1: Biomass total supply from all organs

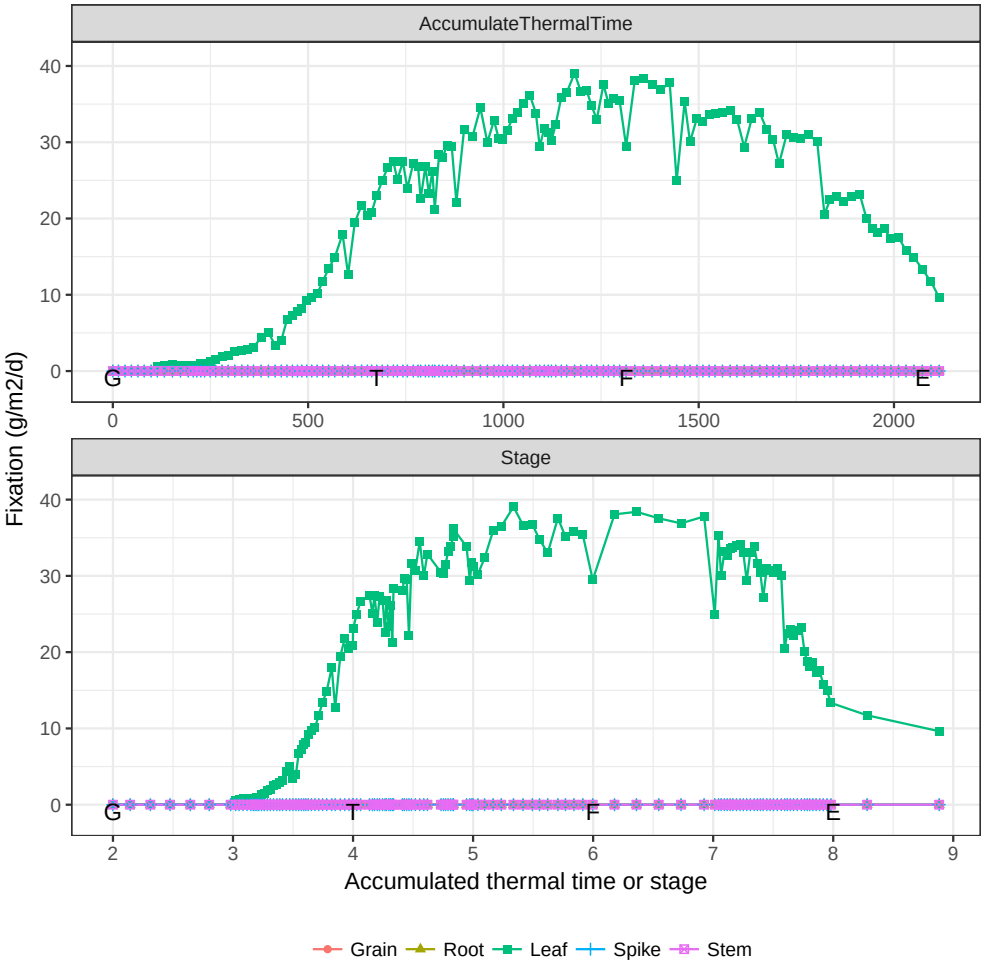

Figure 5.2: Biomass fixation from all organs

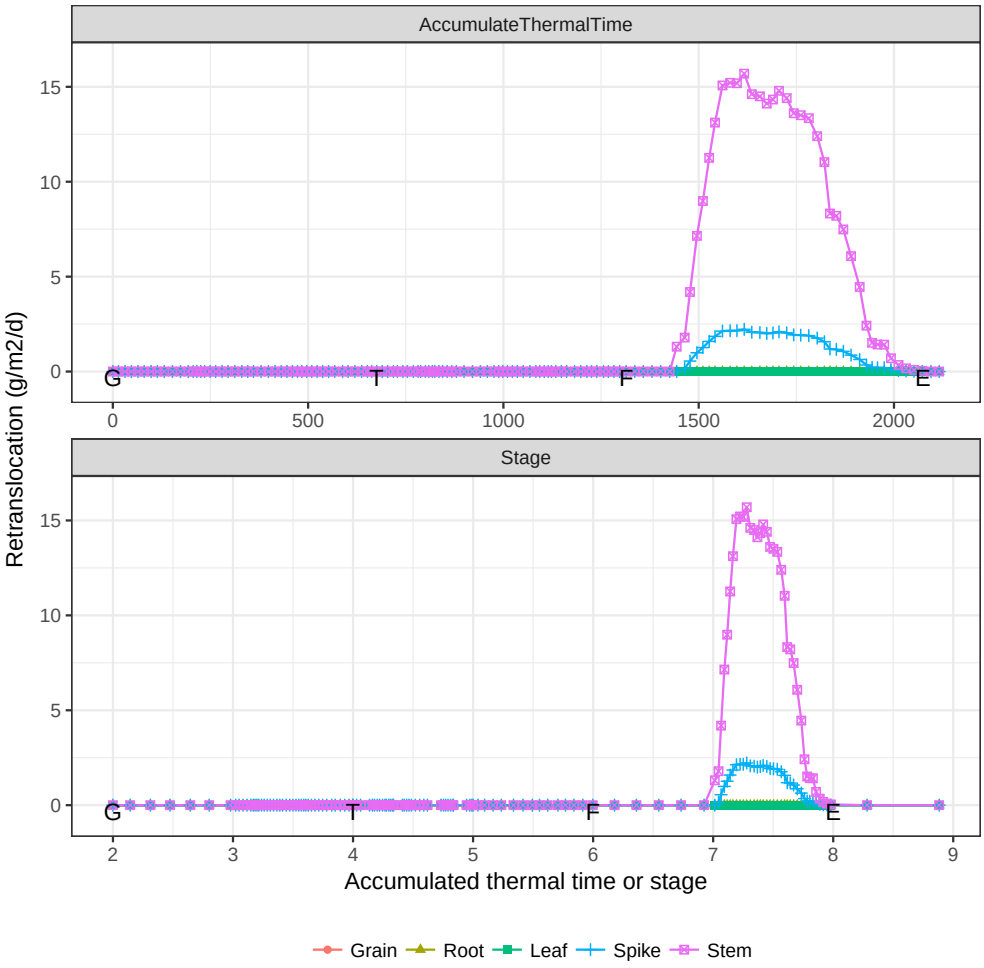

Figure 5.3: Biomass retranslocation from all organs

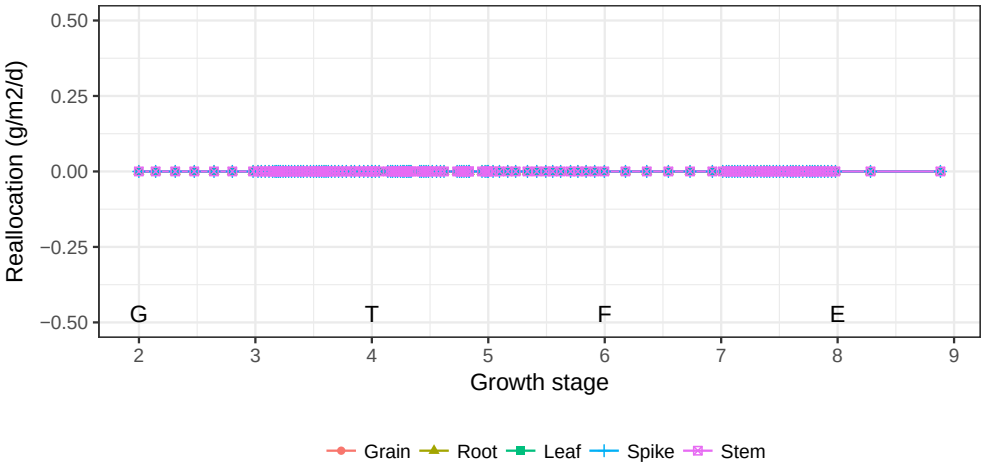

Figure 5.4: Biomass reallocation from all organs

Table 5.2: The three components of biomass in all organs. X and - indicate the organ has and has not the component, respectively.

Organ	Structural	Metabolic	Storage
Grain	X	-	-
Root	X	-	-
Leaf	X	X	-
Spike	X	-	X
Stem	X	-	X

Table 5.3: Biomass conversion efficiency for all organs.

Organ	Conversion efficiency
Grain	0.7067
Root	0.6925
Leaf	0.6853
Spike	0.7067
Stem	0.6600

5.2 Demand

Depending on the organ, not all components are considered (Table 5.2). `Structural` component is considered in all organs. `Metabolic` component is only considered in `Leaf` (Chapter 8). `Storage` component is only considered in `Stem` (Chapter 10) and `Spike` (Chapter 9).

`Stem` and `Root` demands determine as the fraction of daily `Fixation` (Fig. 10.3, and 7.9). The `Spike` demand determines as the head number and growth duration (Fig. 9.5).

5.3 Respiration

As the major roles of carbon balance of crop, respiration is separated into two components, i.e. growth and maintenance respiration (van Iersel and Seymour 2000; Chiariello, Mooney, and Williams 2000). van Iersel and Seymour (2000) described "growth respiration is referred as the amount of carbohydrates respired in a net gain in plant biomass. This includes the production of ATP and reductant for biosynthetic processes, transport processes, and nutrient uptake and reduction. Maintenance respiration is defined as the respiration needed to provide the energy for all plant processes that do not result in a net increase in plant dry matter, such as maintenance of ion gradients across membranes and the resynthesis of degraded organic compounds".

5.3.1 Growth respiration (Conversion efficiency))

The allocated biomass of an organ losses through growth respiration (i.e, 1 - Conversion efficiency). The growth respiration is applied to all components of an organ (i.e. structural, metabolic, storage).

5.3.2 Maintenance respiration

The maintenance respiration is required for metabolic and storage components (Table 5.2). The metabolic and storage components of `Live` pool is daily reduced according to a fraction which is used for maintenance respiration (Fig. 5.11). The maintenance fraction is calculated as reference maintenance fraction at 20 C and a beta function (Wang and Engel 1998) with three cardinal temperatures (i.e. minimum, optimal and

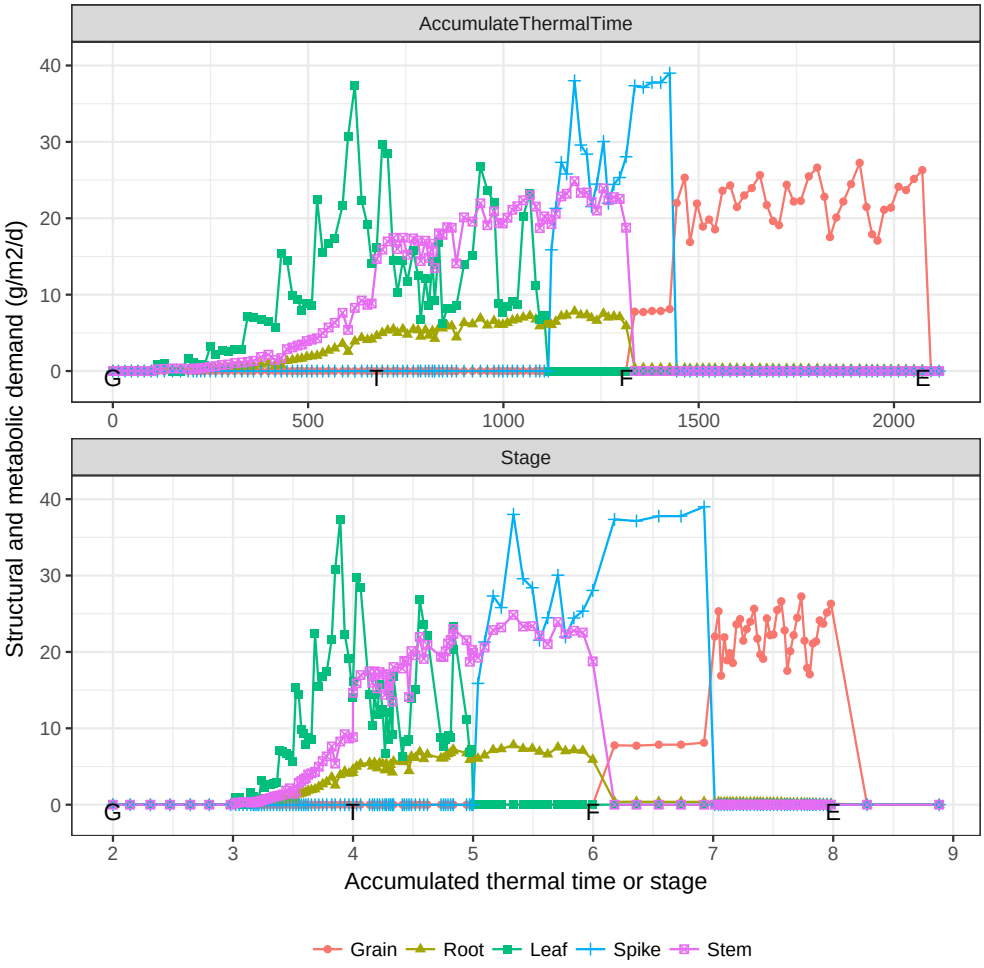

Figure 5.5: Total biomass demand for structural and metabolic from each organ

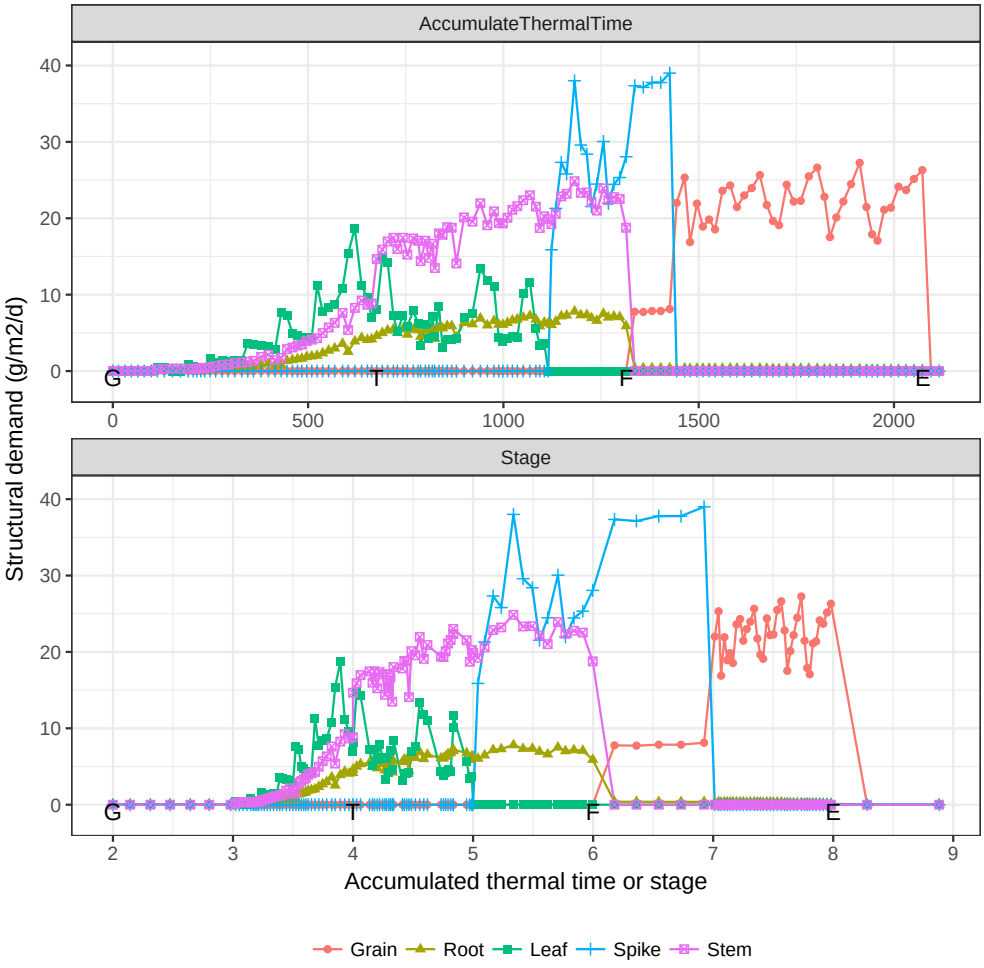

Figure 5.6: Biomass structural demand from all organs

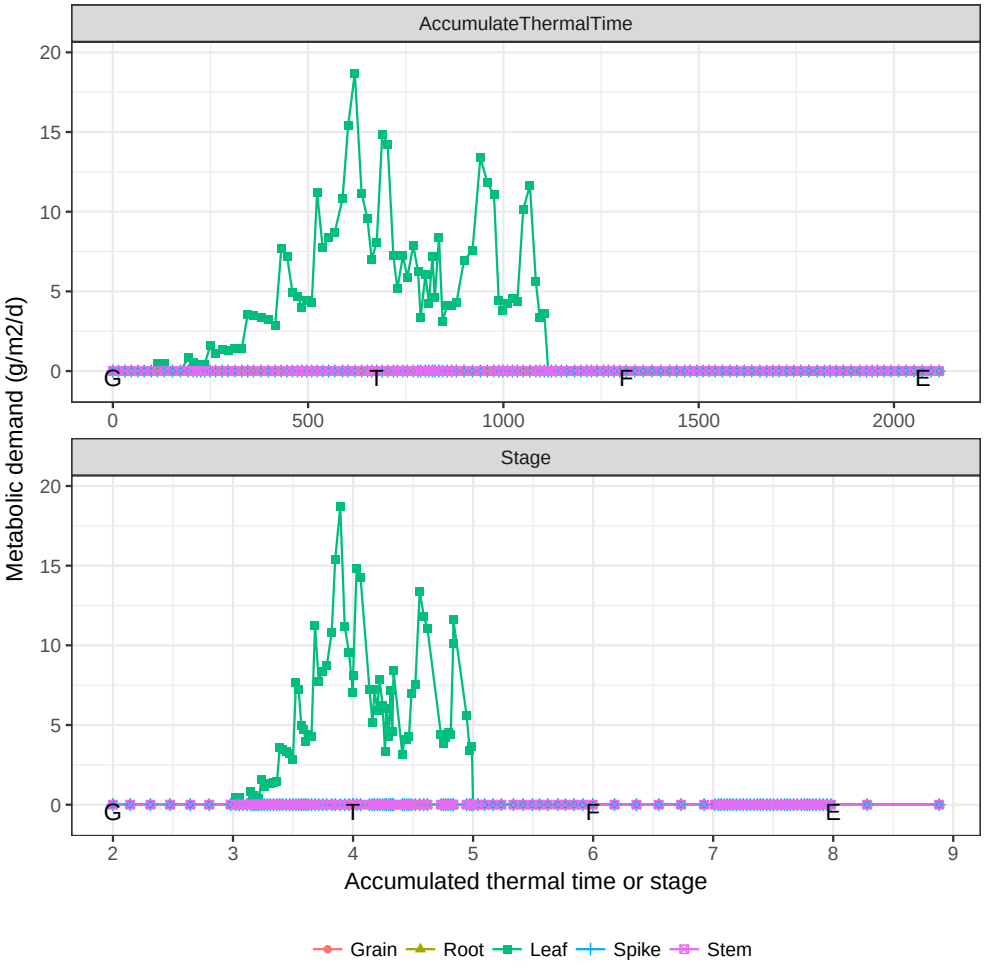

Figure 5.7: Biomass metabolic demand from all organs

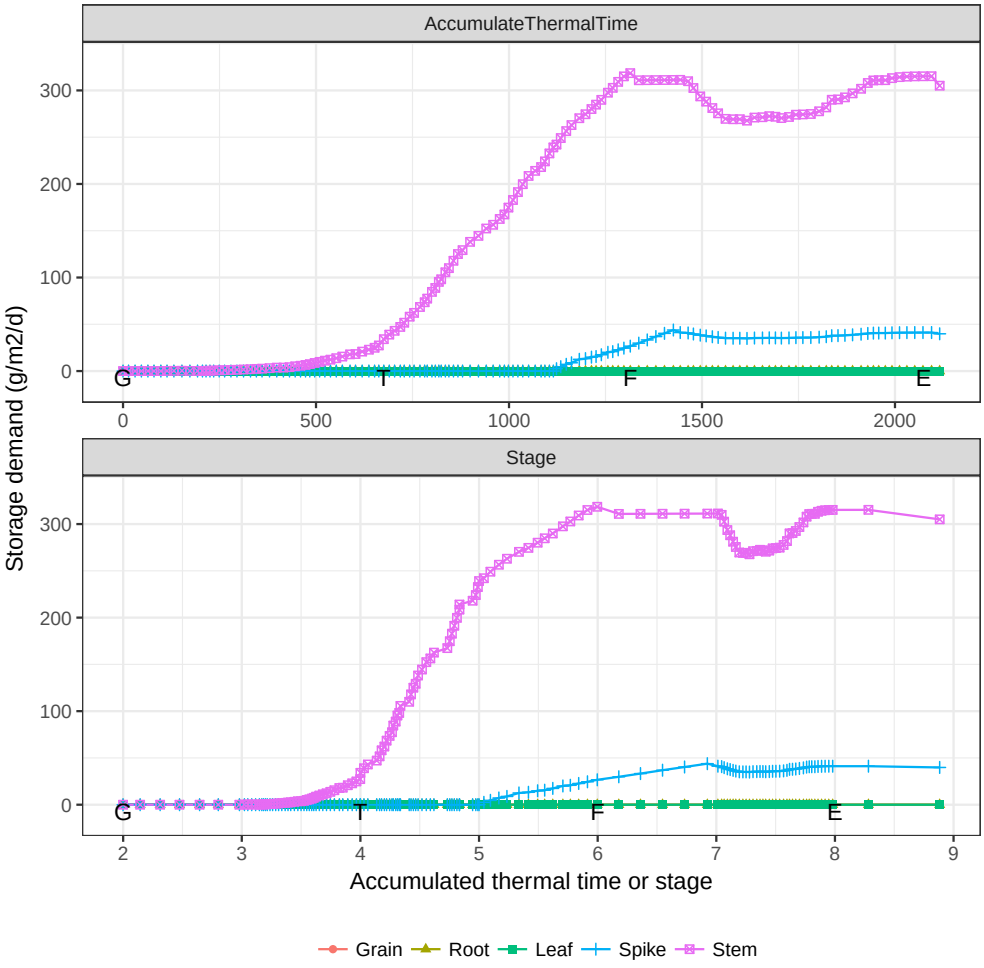

Figure 5.8: Biomass storage demand from all organs

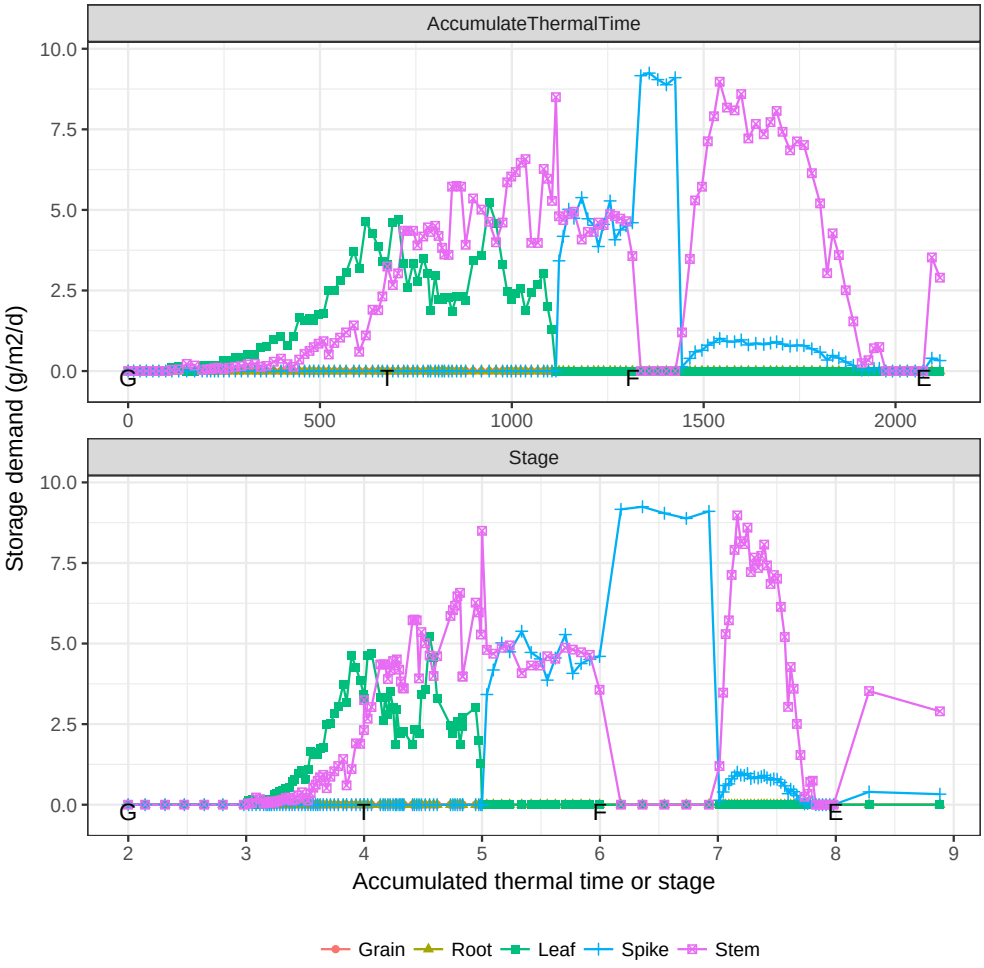

Figure 5.9: Growth respiration for all organs

Table 5.4: The parameter values of maintenance fractions for all organs. T_{min}, T_{opt} and T_{max} are the minimum, optimum and maximum temperatures in the Wang and Engle's beta equation. The W is the weighting of maximum temperature when calculats daily mean temperature. The T_{ref} and M_{20} are the reference temperature and fraction of maintenance fractions at reference temperature.

Organ	T_{min}	T_{opt}	T_{max}	T_{ref}	W	M_{20}
Grain	-50	48	60	20	0.5	0.01
Root	-50	48	60	20	0.5	0.02
Leaf	-50	48	60	20	0.5	0.03
Spike	-50	48	60	20	0.5	0.01
Stem	-50	48	60	20	0.5	0.02

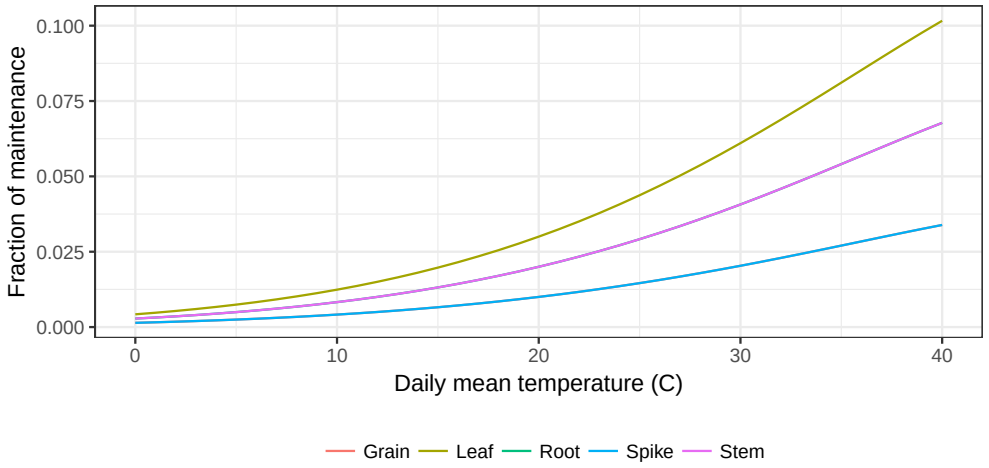

Figure 5.10: The response of maintenance respiration on daily average temperature with a beta function [@WangSimulationphenologicaldevelopment1998].

maximum temperatures). All organs have the same cardinal temperatures, but different maintenance fraction at 20C (Table 5.4). Finally, the actual maintenance fraction depends on the daily mean temperature (Fig. 5.11. `Leaf` and `Stem` have the major contributions to maintenance respiration (Fig. 5.12). Root and Grain don't have maintenance respiration (Fig. 5.12).

5.4 Biomass partitioning

The biomass partitions into structural and metabolic components firstly according to the relative demands. The remaining biomass allocates into storage according to the relative demands. The greatest storage demand of stem can store all remaining daily supply.

The daily supply is distributed into `Structural` and `Metabolic` components, then `Storage` component. The daily demand cannot be satisfied if the structural and metabolic demands are more than daily supply, then the allocated biomasses of all organs are proportionally reduced to match daily supply (Fig. 5.13). The extra daily supply is distributed into storage, i.e. `Stem` for wheat model, as the extreme higher storage demand for stem (Fig. 5.14).

The actual allocated biomass for each organ depends on the daily supply, relative structural and metabolic demand, and storage demands among all organs (Fig. 5.15, 5.16 and 5.17).

The daily biomass supply (Fig. 5.1) are consumed as growth respiration before partitioning into `Live` pool in

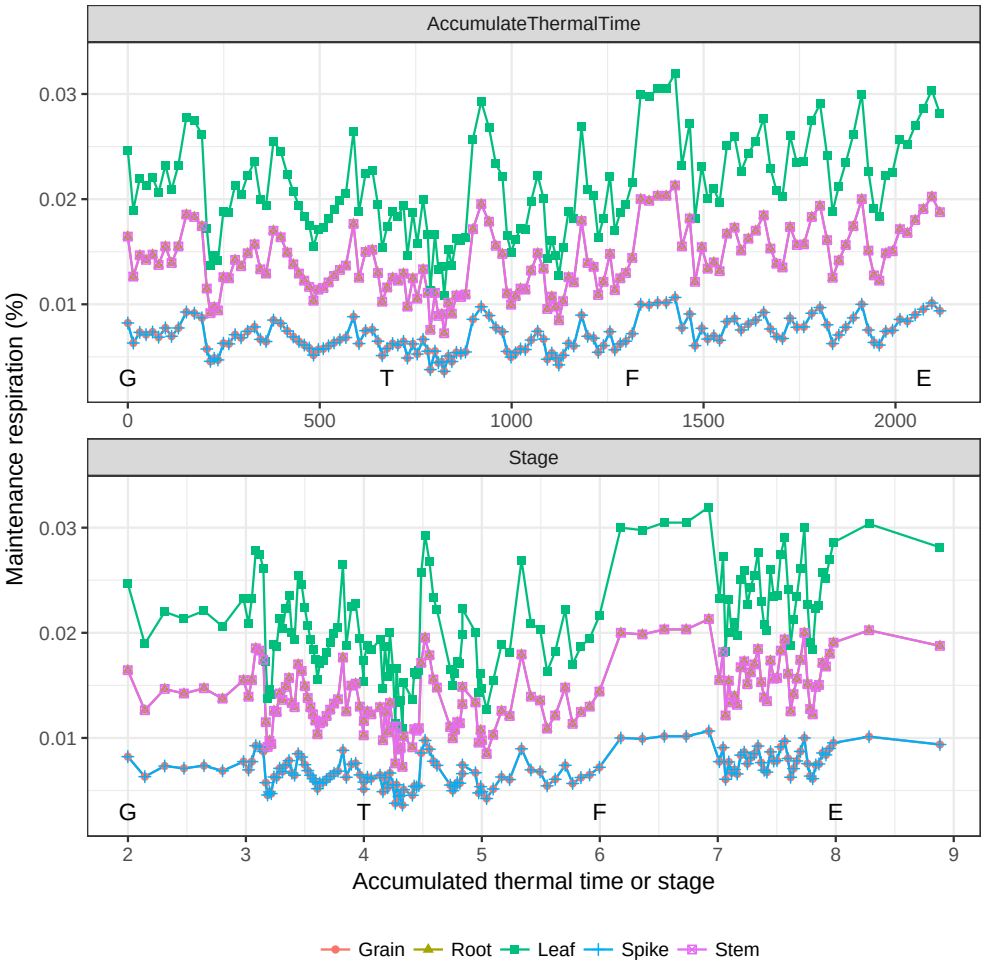

Figure 5.11: Daily fraction of maintenance respiration for all organs. The maintenance respirations of two groups of organs overlap each other (i.e. stem and root, spike and grain).

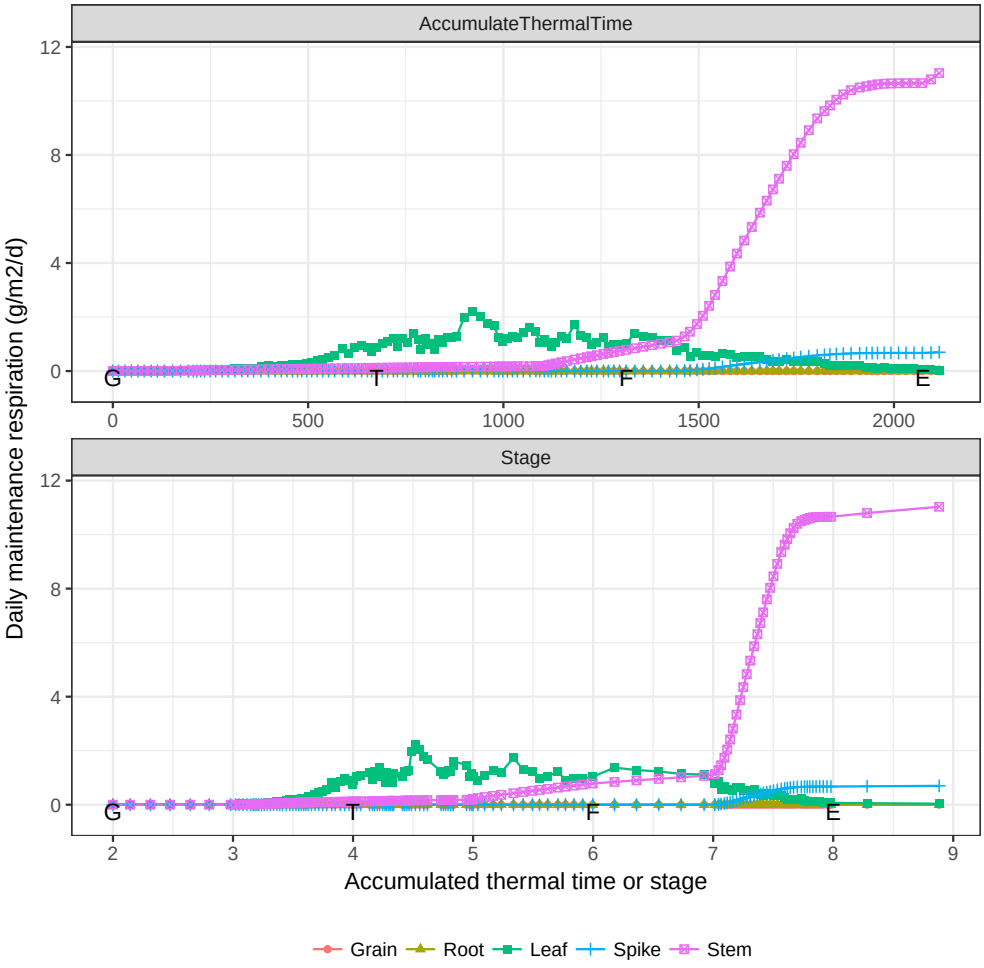

Figure 5.12: Daily maintenance respiration for all organs.

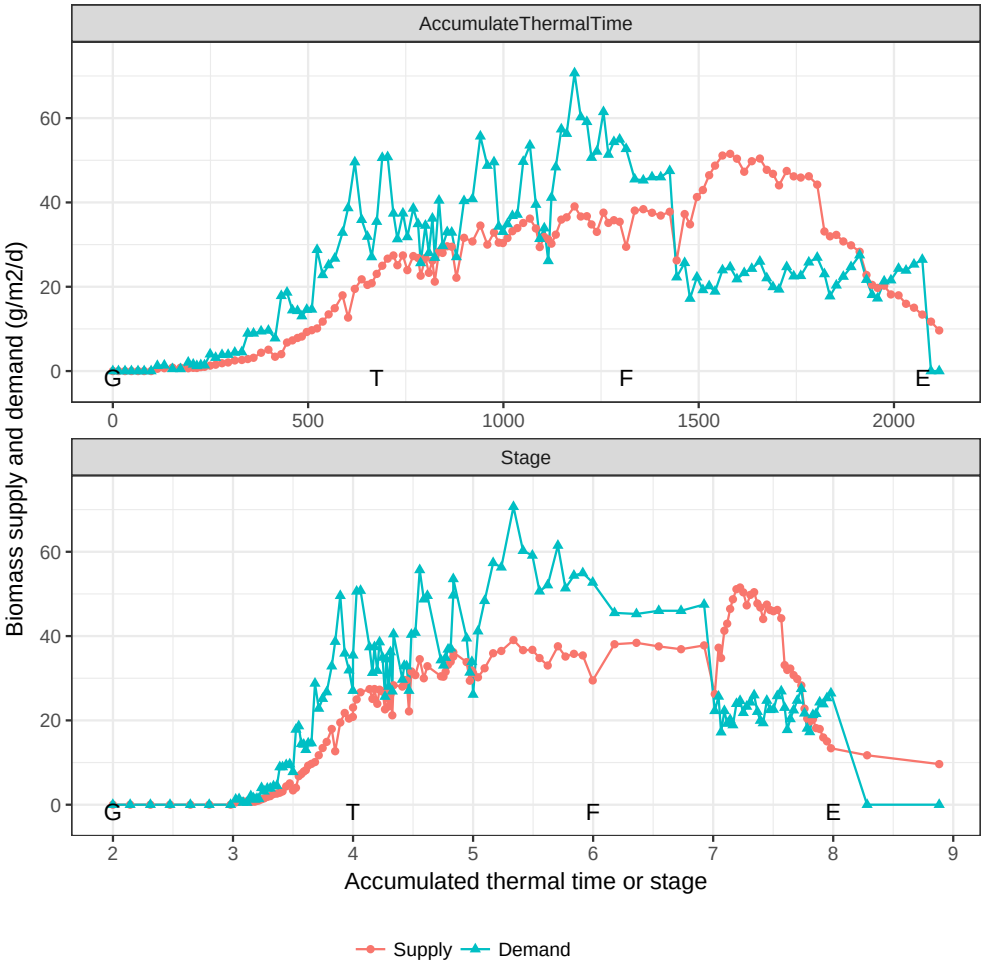

Figure 5.13: Daily biomass supply, and structural and metabolic demands for all organs.

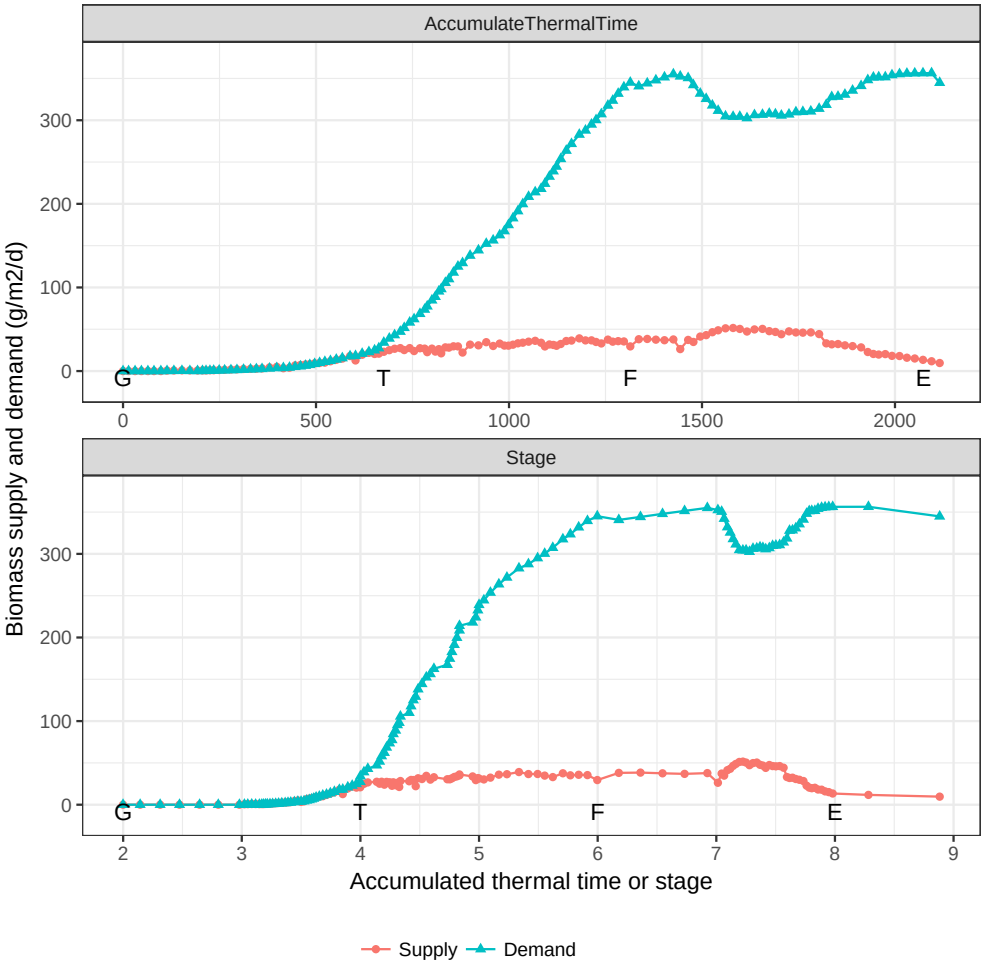

Figure 5.14: Daily biomass supply and storage demand for all organs

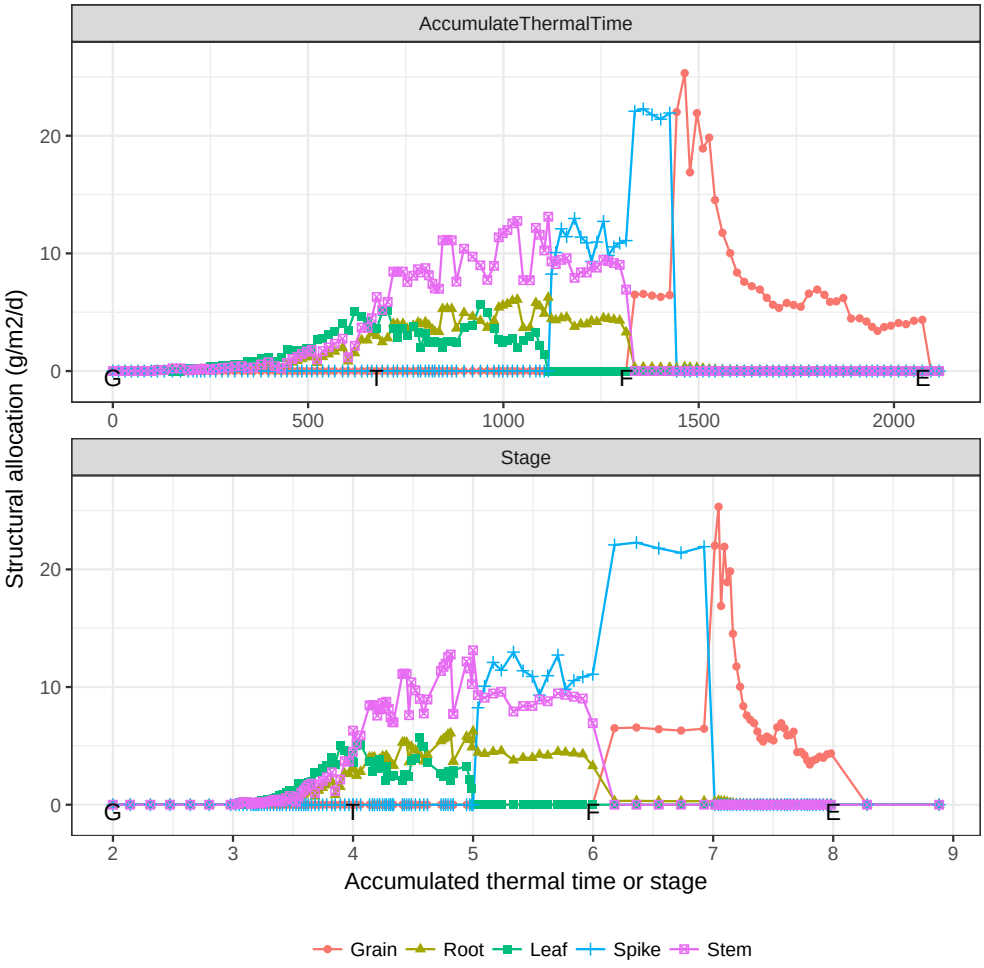

Figure 5.15: Biomass structural allocation from all organs

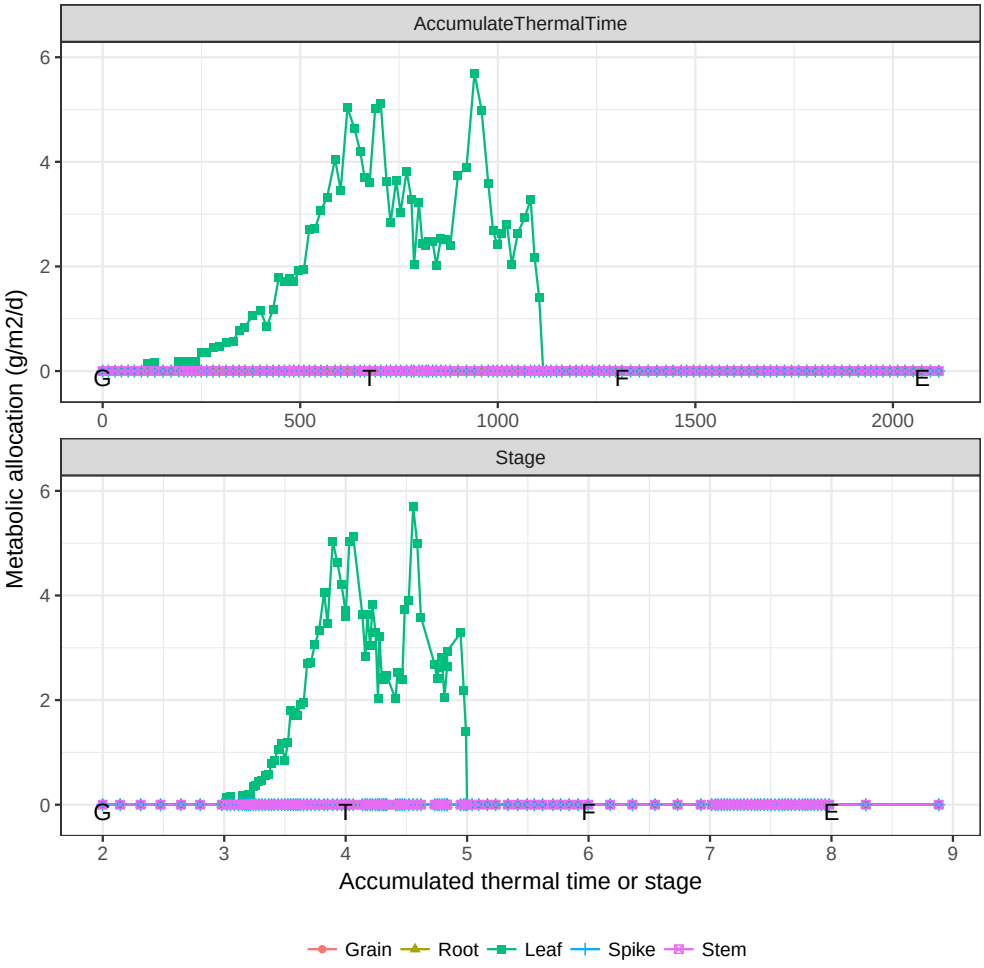

Figure 5.16: Biomass metabolic allocation from all organs

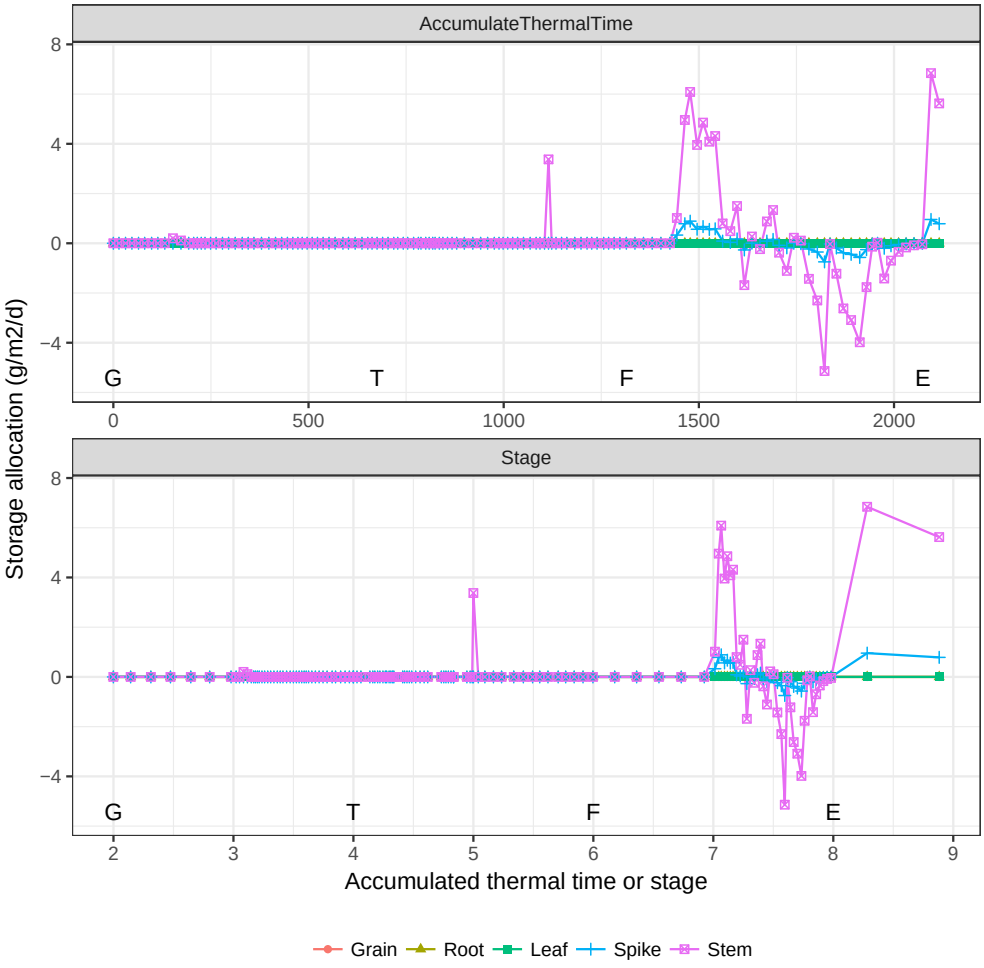

Figure 5.17: Biomass storage allocation from all organs

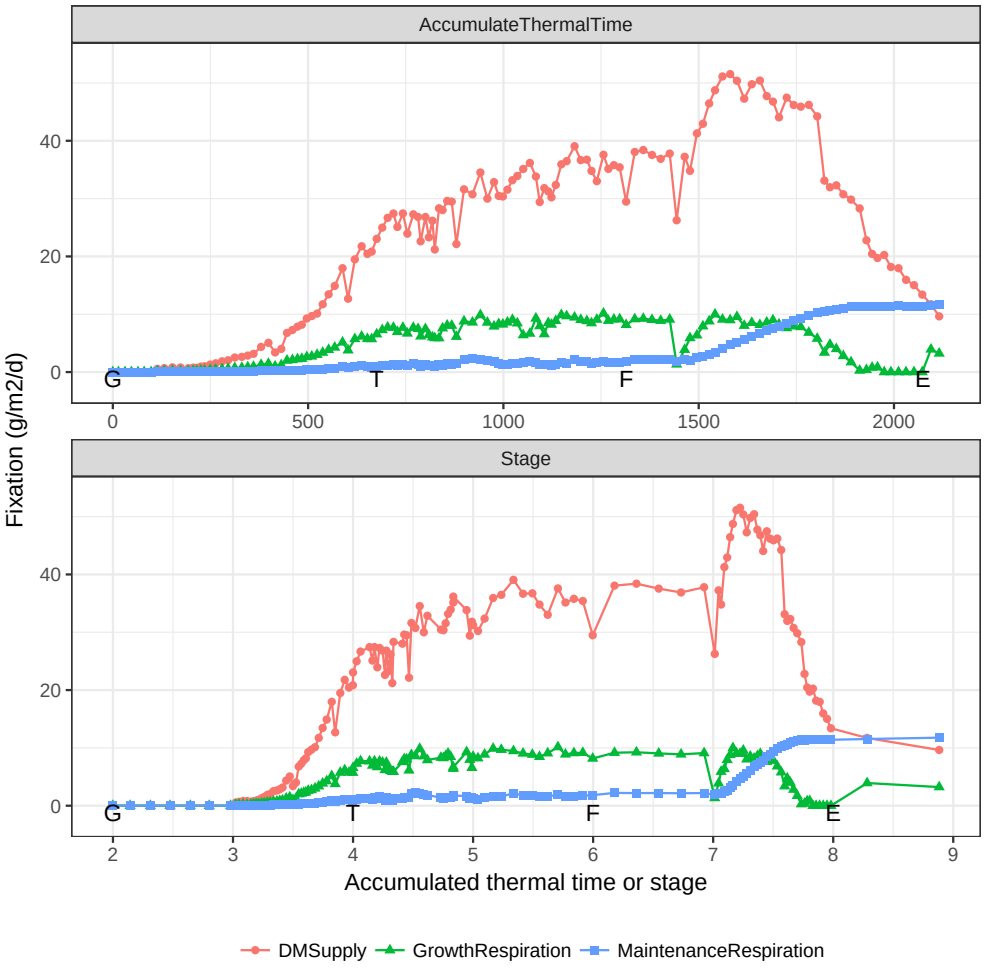

Figure 5.18: Daily biomass supply and respiration.

each organ, and consumed as daily maintenance respiration from `Live` pool in each organ (Fig. 5.18).

5.5 Biomass pool

All organs have the `Live` pool, but only `Leaf` has the `Dead` pool (Table 5.5).

Table 5.5: The live and dead groups of biomass in all organs. X and - indicate the organ has and has not the group, respectively.

Organ	Live	Dead
Grain	X	-
Root	X	-
Leaf	X	X
Spike	X	-
Stem	X	-

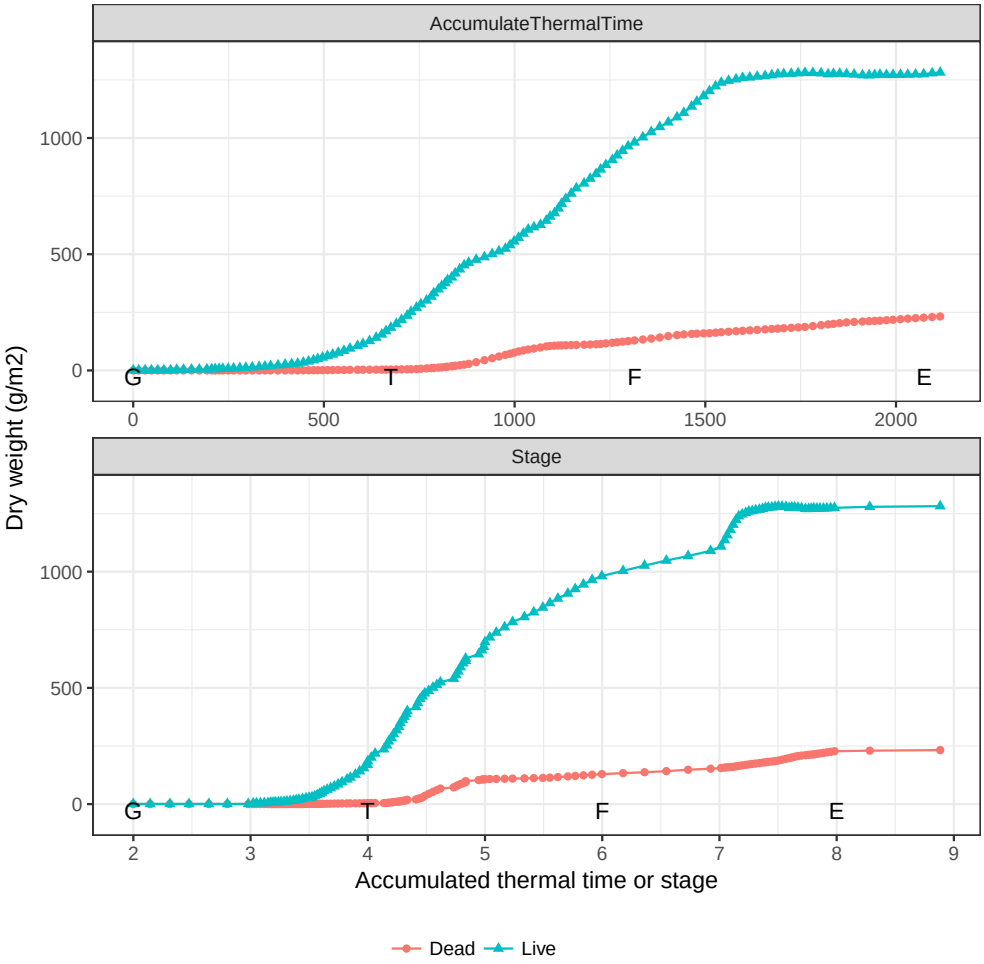

Figure 5.19: Dry weight of Live and Dead pools

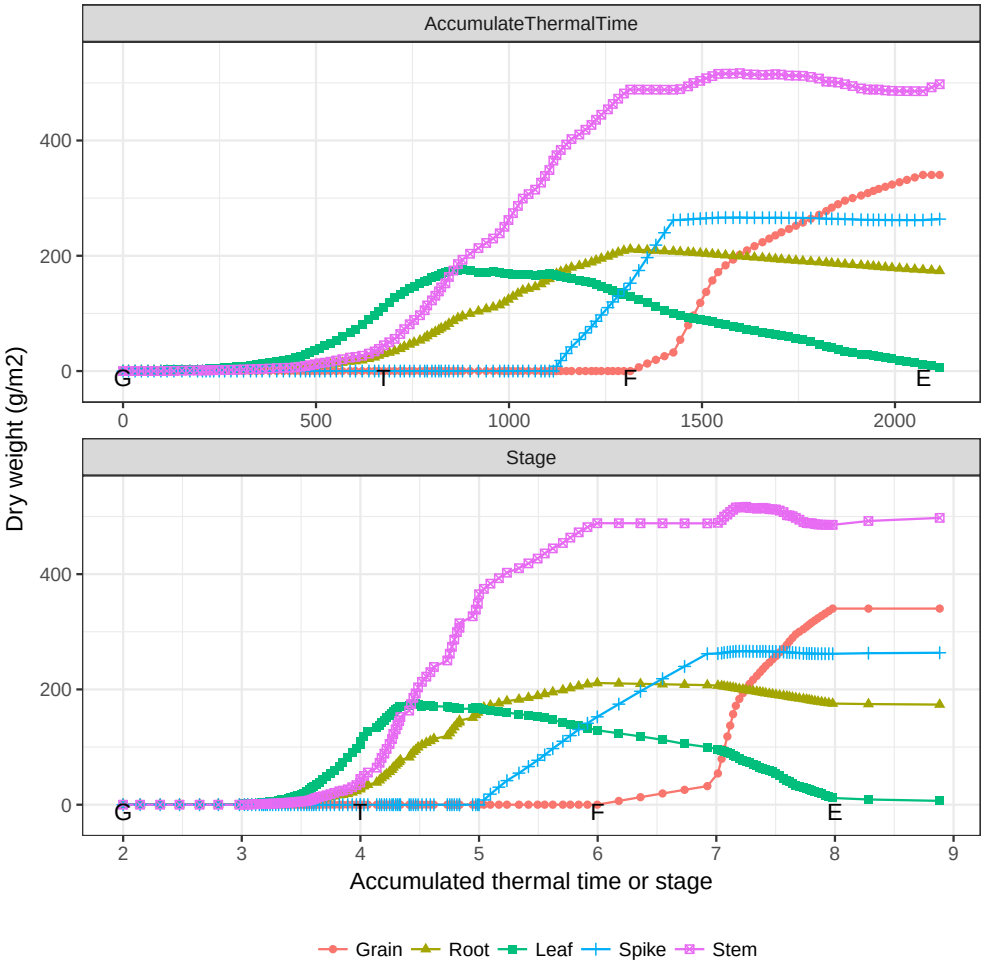

Figure 5.20: Dry weight of Live pool for all organs

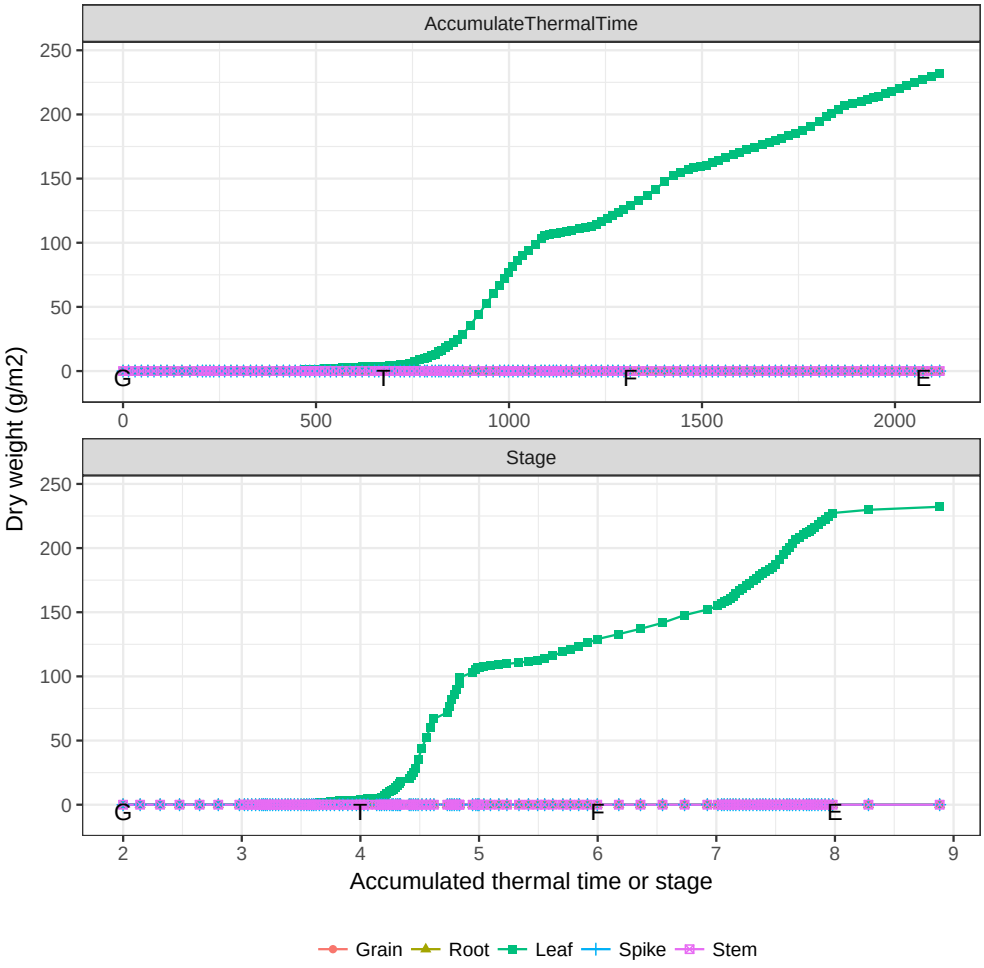

Figure 5.21: Dry weight of Dead pool for all organs

Chapter 6

Grain

6.1 Grain number

Grain number is correlated with stem [ref] and/or spike (Slafer, Andrade, and Satorre 1990; González, Slafer, and Miralles 2005) dry weight at anthesis.

The number of grains per plant (N_g) is determined by the `Stem` and `Spike` total biomass at `Flowering` (including `Live` and `Dead`).

$$N_g = R_g(W_{stem} + W_{spike})$$

where W_{stem} and W_{spike} are the stem and spkie total biomass at flowering, respectively. R_{g} is the grain number per gram stem and spike, with default value at 22 grain g-1.

6.2 Supply

No biomass supply is considered in the `Grain` organ (Fig. 6.1).

6.3 Demand

The grain demand is seperated into two periods (i.e. from `Flowering` to `StartGrainFill` and from `StartGrainFill` to `EndGrainFill`).

6.4 Biomass dynamic

`Grain` only considers the `Live` conponent, No `Dead` component.

6.4.1 Yield

The total grain weight at harvest can be considered as the final yield without moisture content in the grain. The normal range of moisture content in the grain is 10-15% with 12% as standard

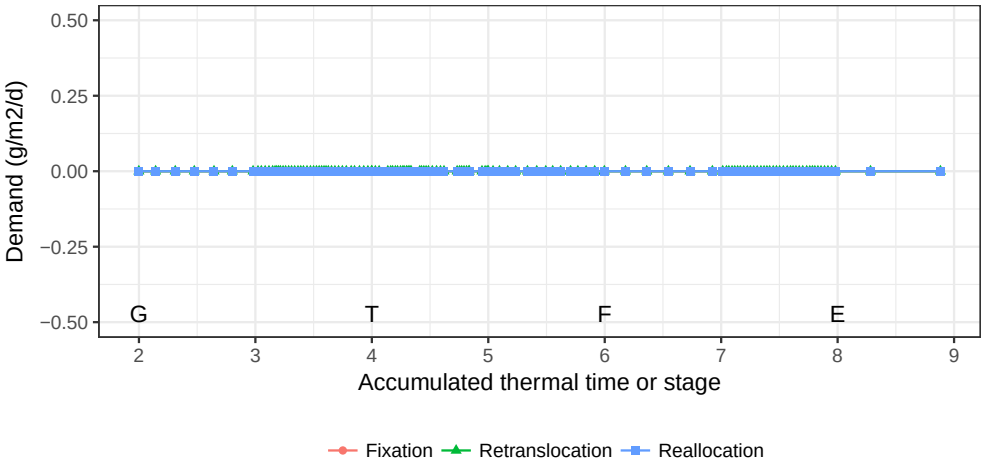

Figure 6.1: Biomass supply from grain

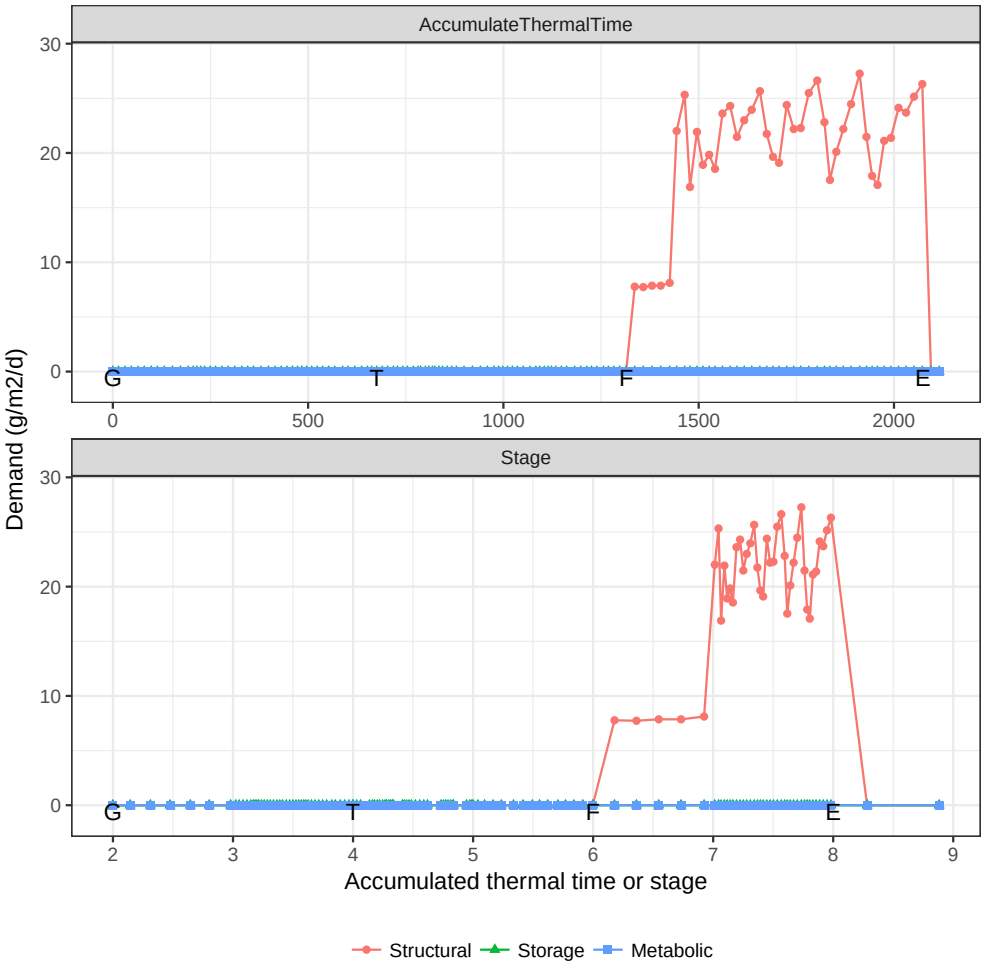

Figure 6.2: Biomass demand by grain

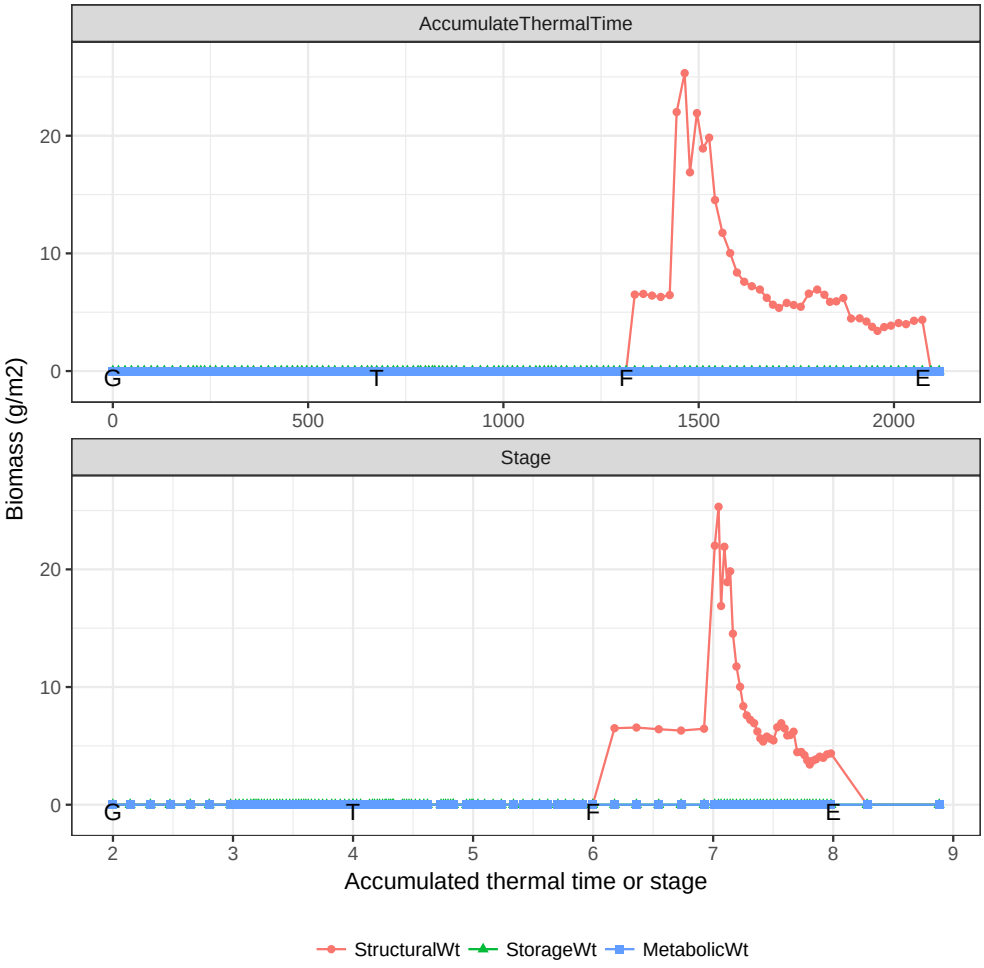

Figure 6.3: Actual allocated biomass for grain

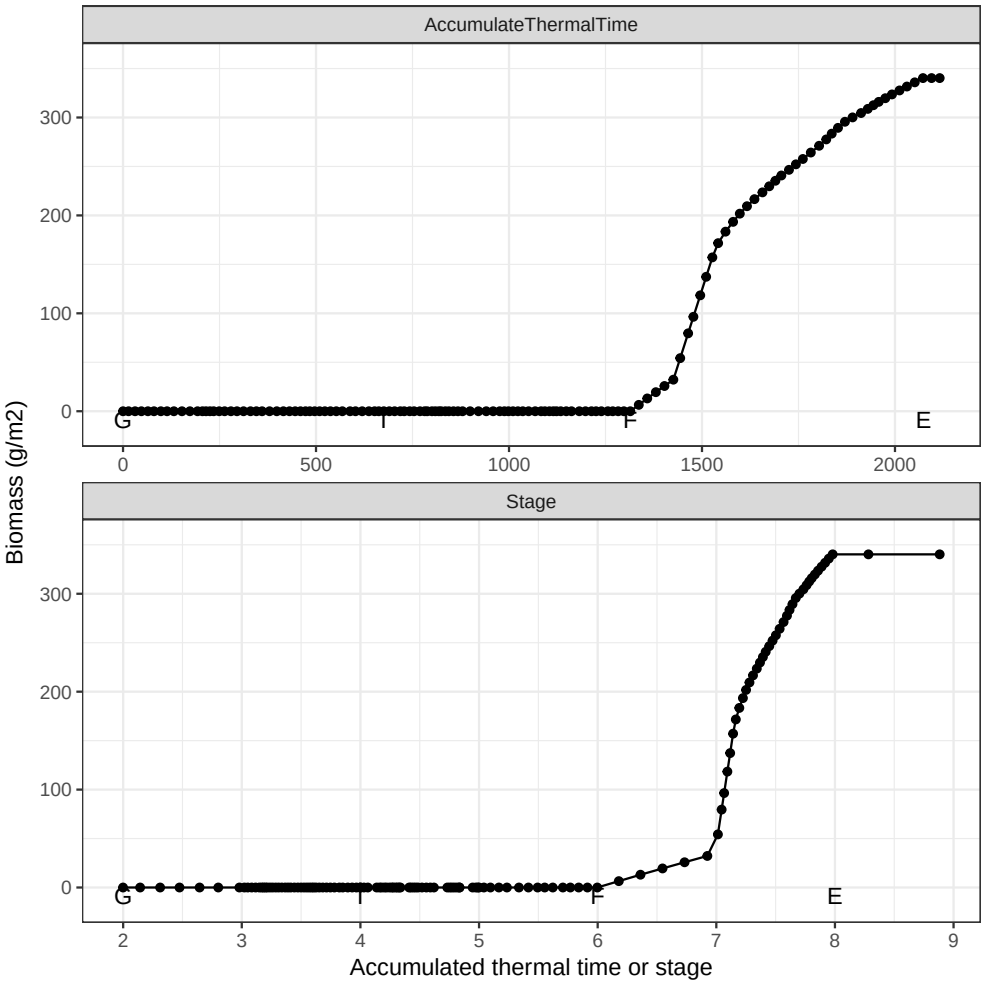

Figure 6.4: Dynamic of grain biomass (Total)

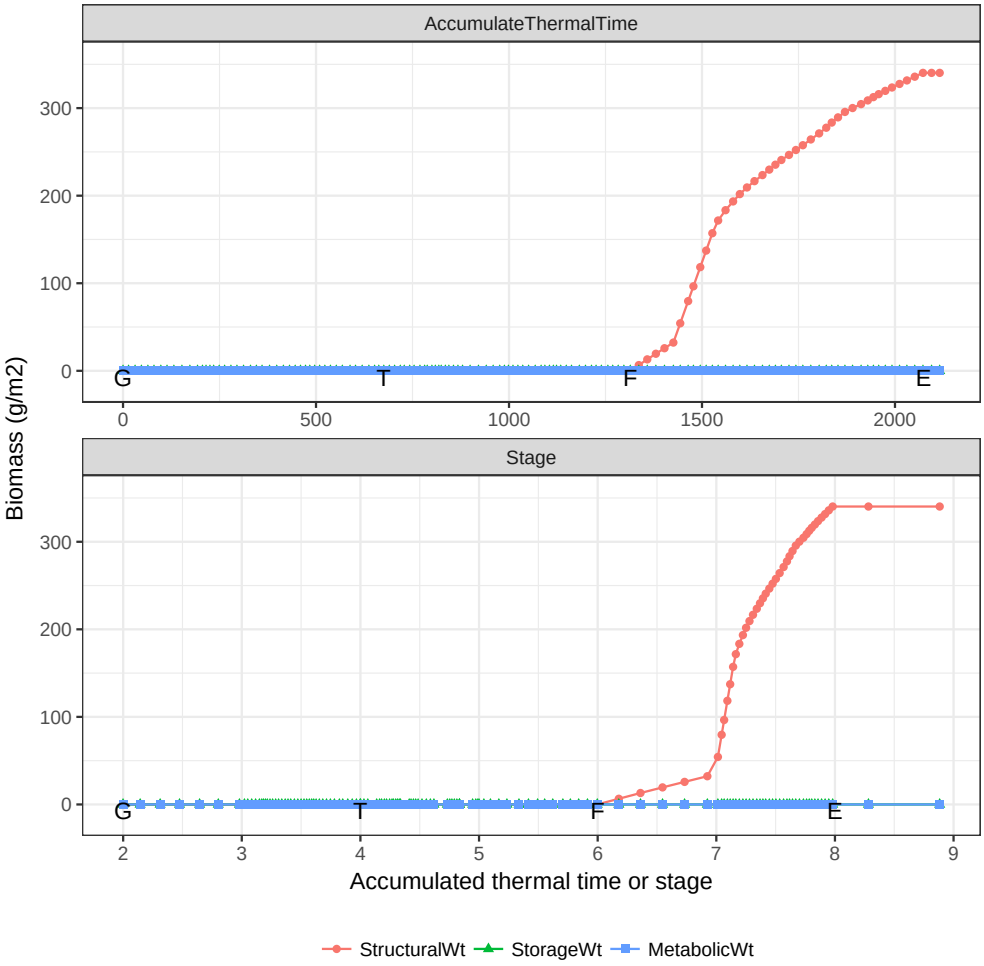

Figure 6.5: Dynamic of grain biomass (Live component)

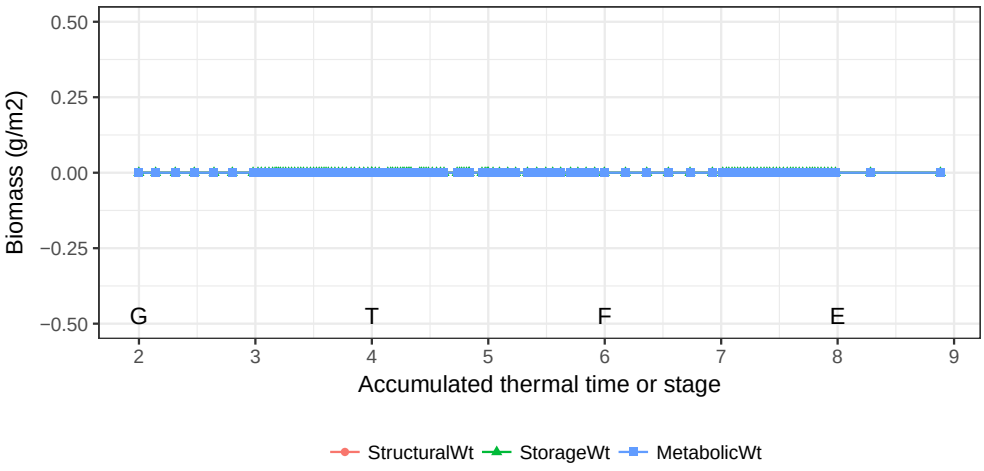

Figure 6.6: Dynamic of grain biomass (Dead component)

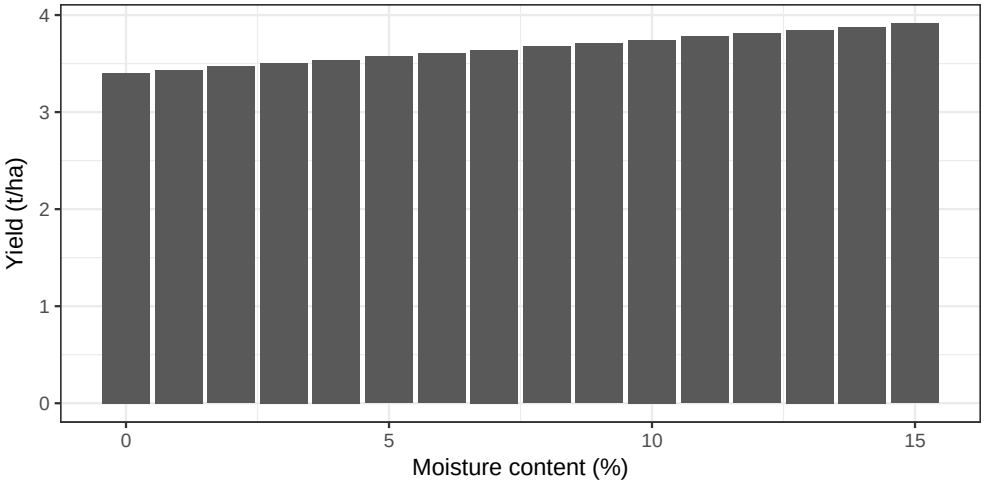

Figure 6.7: Final yield with different moisture content (t/ha).

Chapter 7

Root

Only `Structural` is considered in the three components of biomass for `Root`. The biomass allocation depending on the fraction of daily fixation (i.e. photosynthesis).

7.1 Root Growth

7.1.1 Root depth

Roots grow downwards through the soil profile, with initial depth determined by sowing depth and the growth rate determined by `RootFrontVelocity`, which is determined by potential root front velocity (5 mm/d for pre emergencee, and 20 mm/d for post-emergence, Fig. 7.1), and mofified (multification) by temperature (Fig. 7.2) and water stress (Fig. 7.4).

Soil water scale is A simple scale to convert soil water content into a value between 0 and 2 (i.e. from 0 to 1 when SW is between $LL15$ and DUL and from 1 to 2 when SW is between DUL and SAT, (Fig. 7.3)).

The multiplier of water stress on root front velocity depends on soil water scale which suppresses root growth when water scale is less than 0.25 (Fig. 7.4).

7.1.2 Root length

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

7.2 Supply

No biomass supply is considered in the `Root` organ (Fig. 7.8).

7.3 Demand

The daily biomass demand of `Root` is calculated as a fraction of daily fixation (i.e. photosynthesis) from Stage 3 (`Emergence`) to Stage 8 (`End of grain filling`). The fraction of root demand is 0.2 until `Flowering`

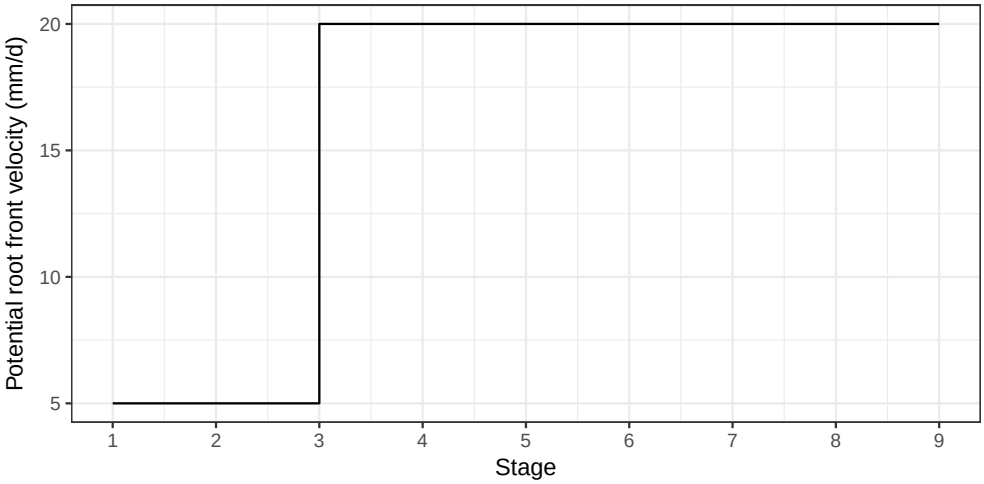

Figure 7.1: The potential root front velocity.

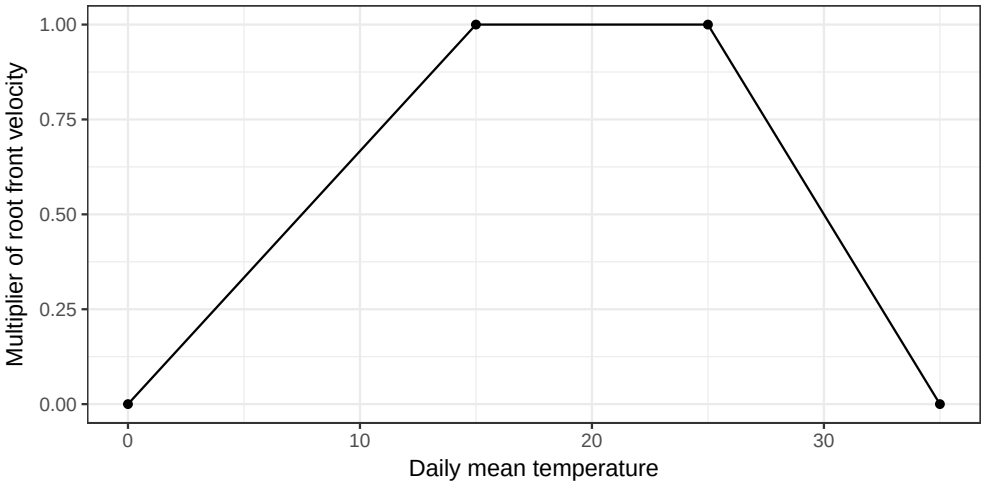

Figure 7.2: The temperature stress on root front velocity.

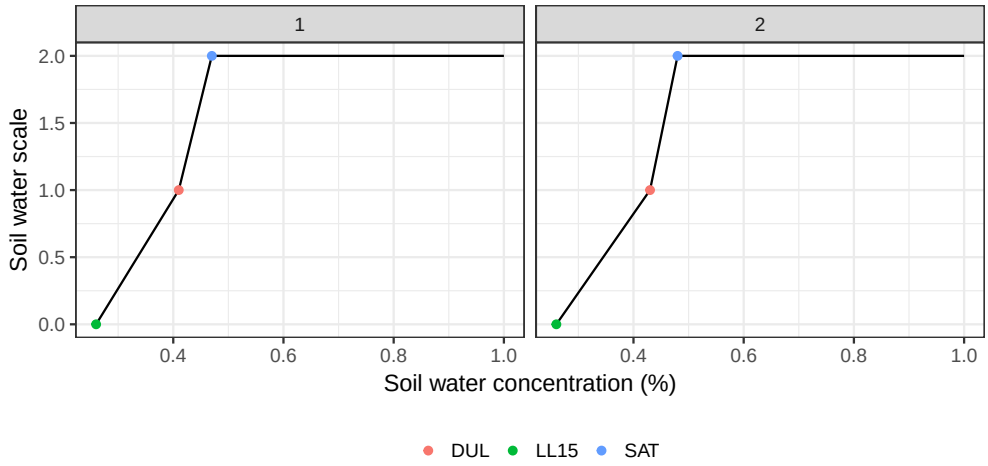

Figure 7.3: Response of soil water scale on soil water concentration in the top two layers of soil in the tested simulations.

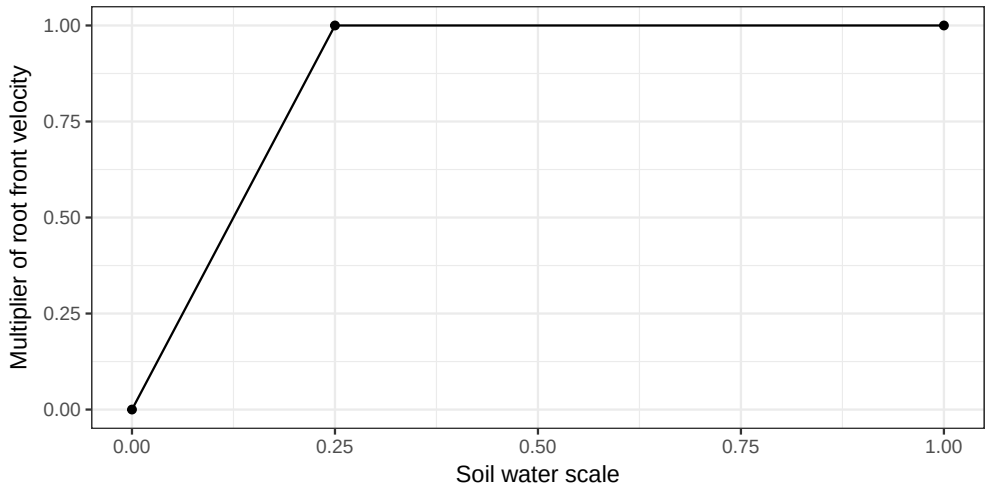

Figure 7.4: Soil water stress on root front velocity

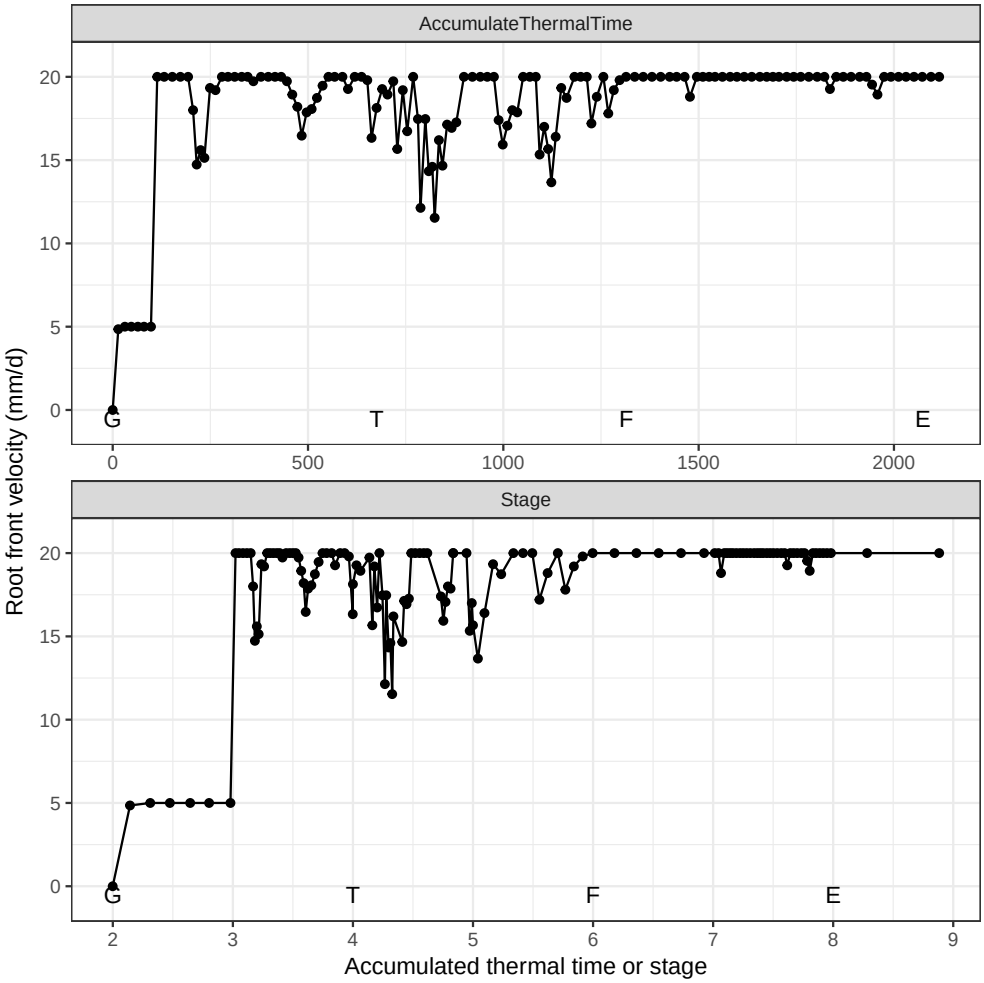

Figure 7.5: Root front velocity.

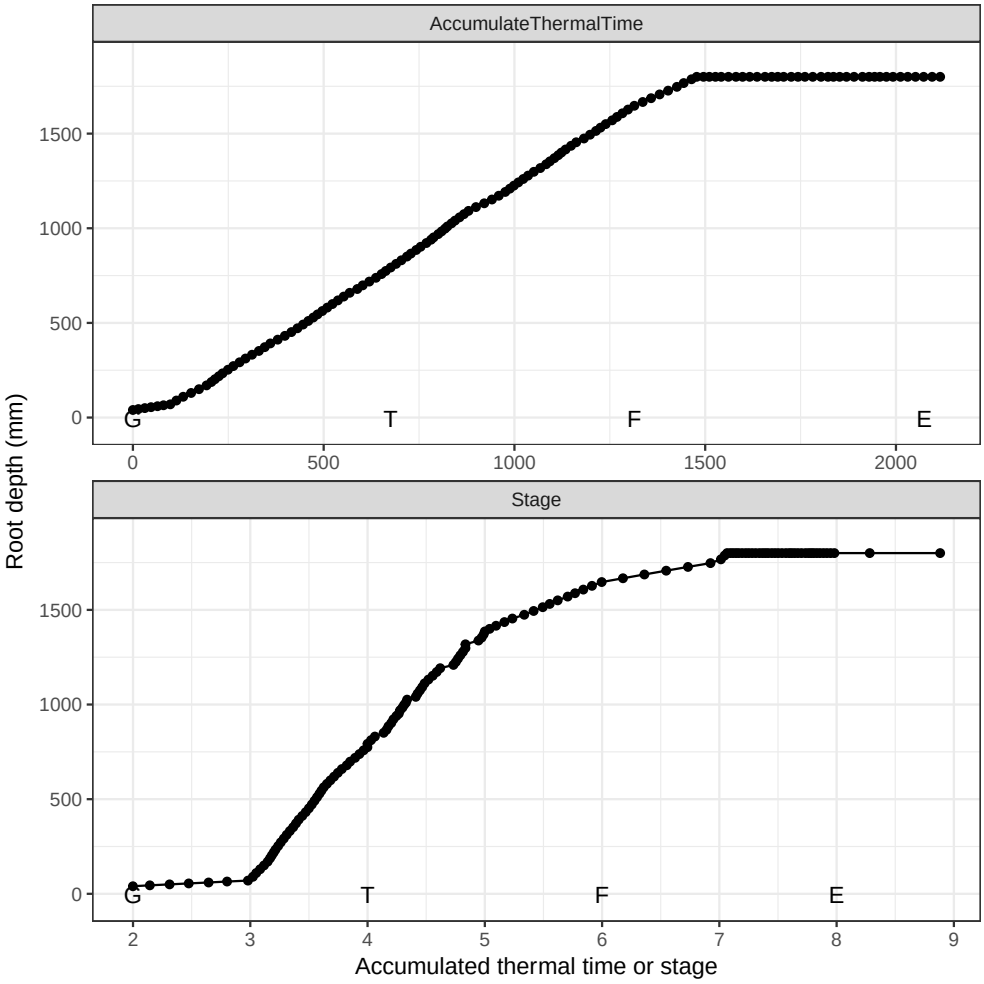

Figure 7.6: Root depth

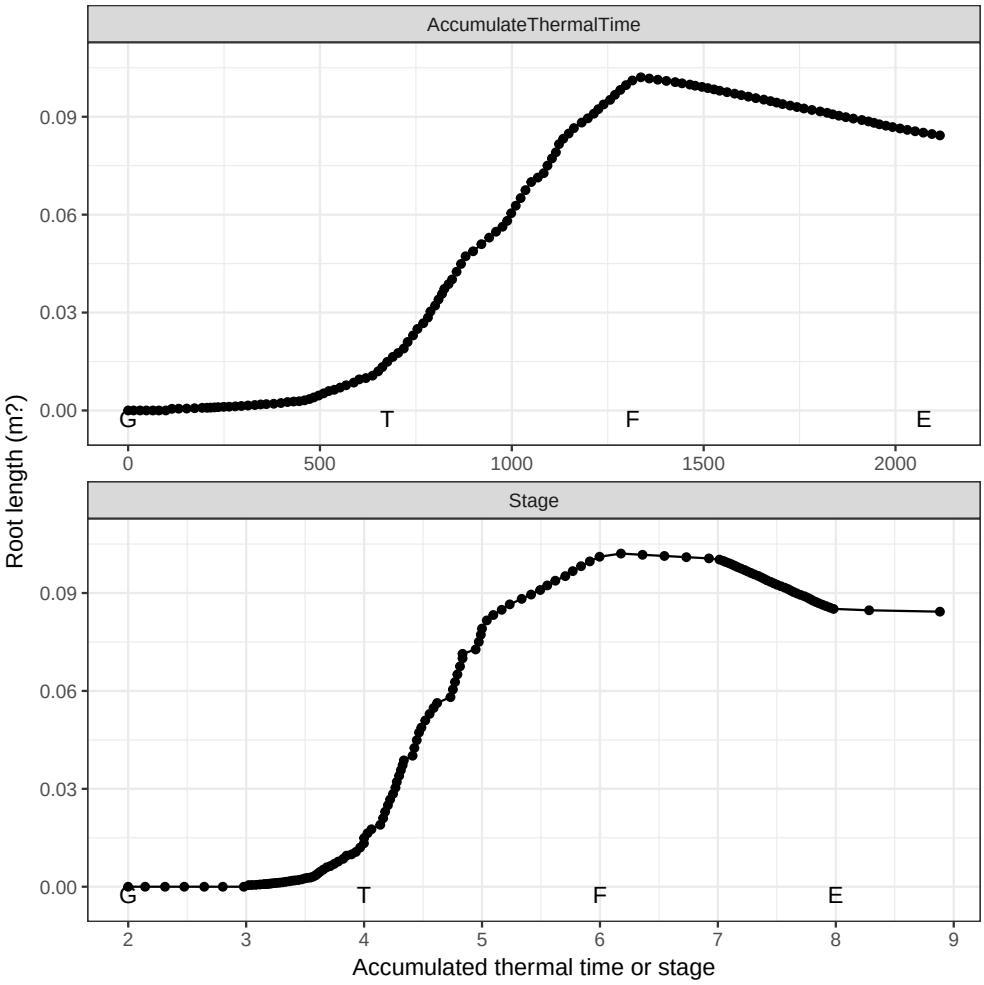

Figure 7.7: Root length

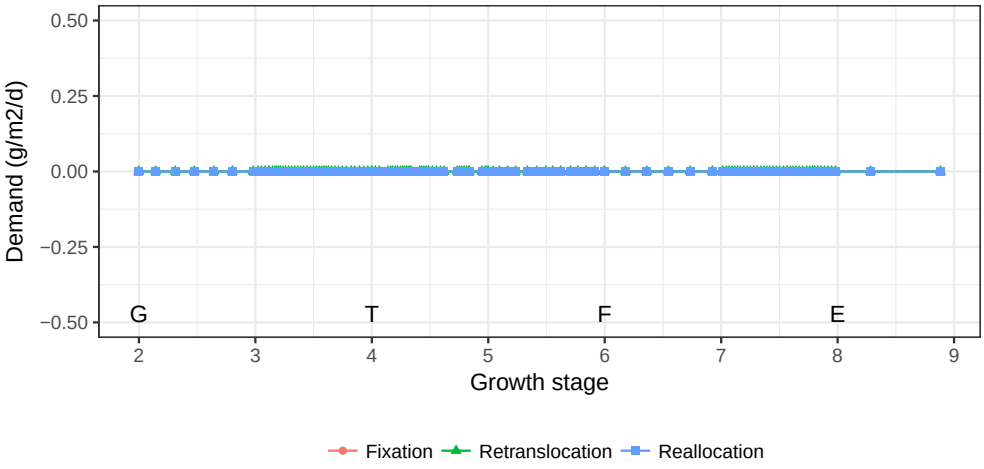

Figure 7.8: Biomass supply from root

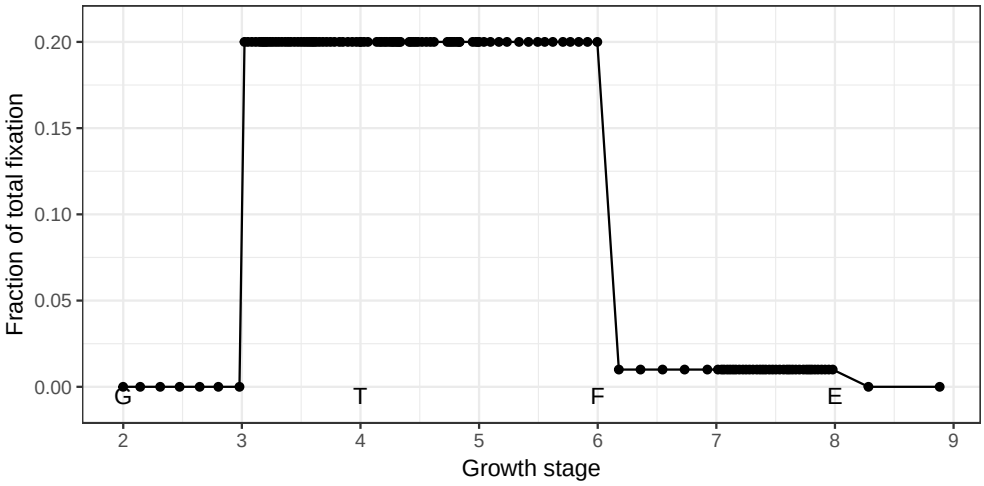

Figure 7.9: Fraction of root demand in the total fixation

`time`, then reduces into 0.02 until `End of grain filling` (Fig. 7.9). Only structural demand is considered in the `Root` organ (Fig. 7.10).

7.4 Biomass dynamic

The actual allocation (Fig. 7.11) is determined by the actual daily biomass supply (Fig. 5.1) which may be smaller than than biomass demand (Fig. 7.10).

The daily loss of roots is calculated using a SenescenceRate function (0.005 in the default value). All senescence material is automatically detached and added to the soil fresh organic matter (FOM) pool.

Finally `Root` biomass increases until `flowering time`, then gradually decreases as the senescence is more than allocation (Fig. 7.13). All biomass is allocated into `Live` component (Fig. 7.14), as the senescence `Root` immediately is detached and contributed into soil FOM (Fig. 7.15).

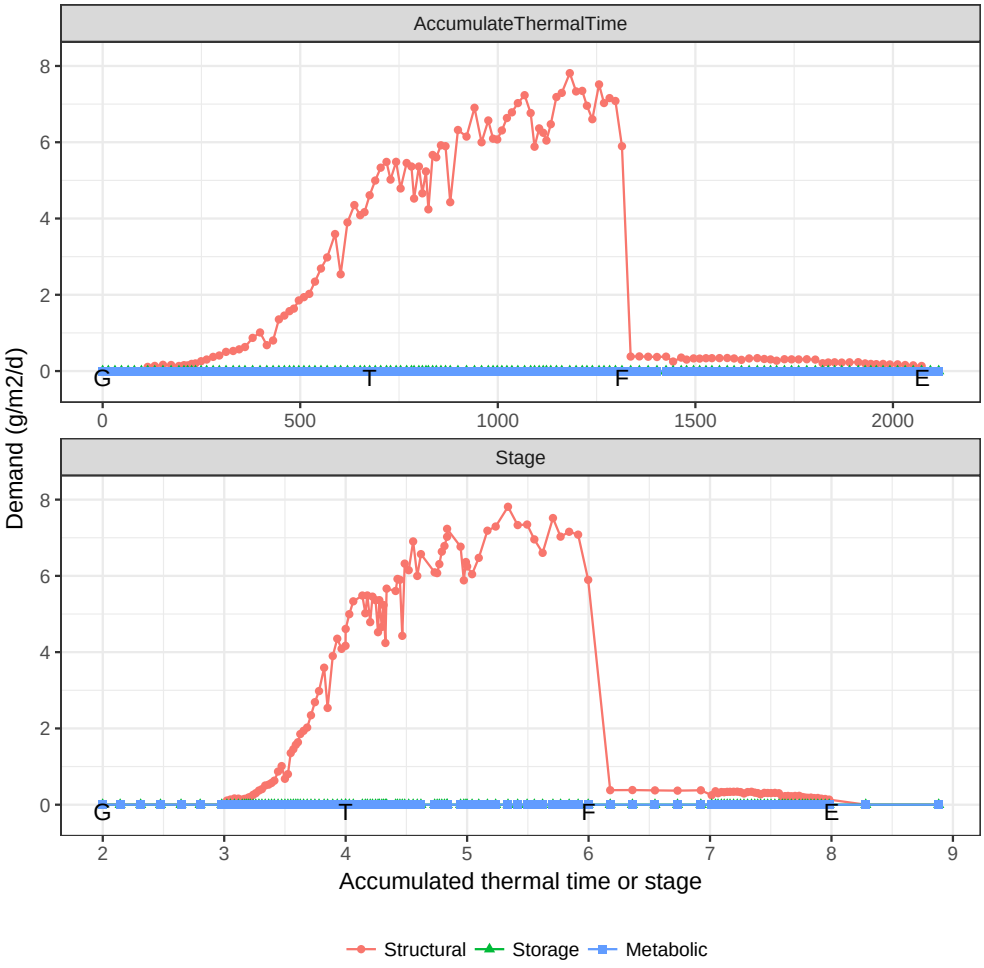

Figure 7.10: Biomass demand by root

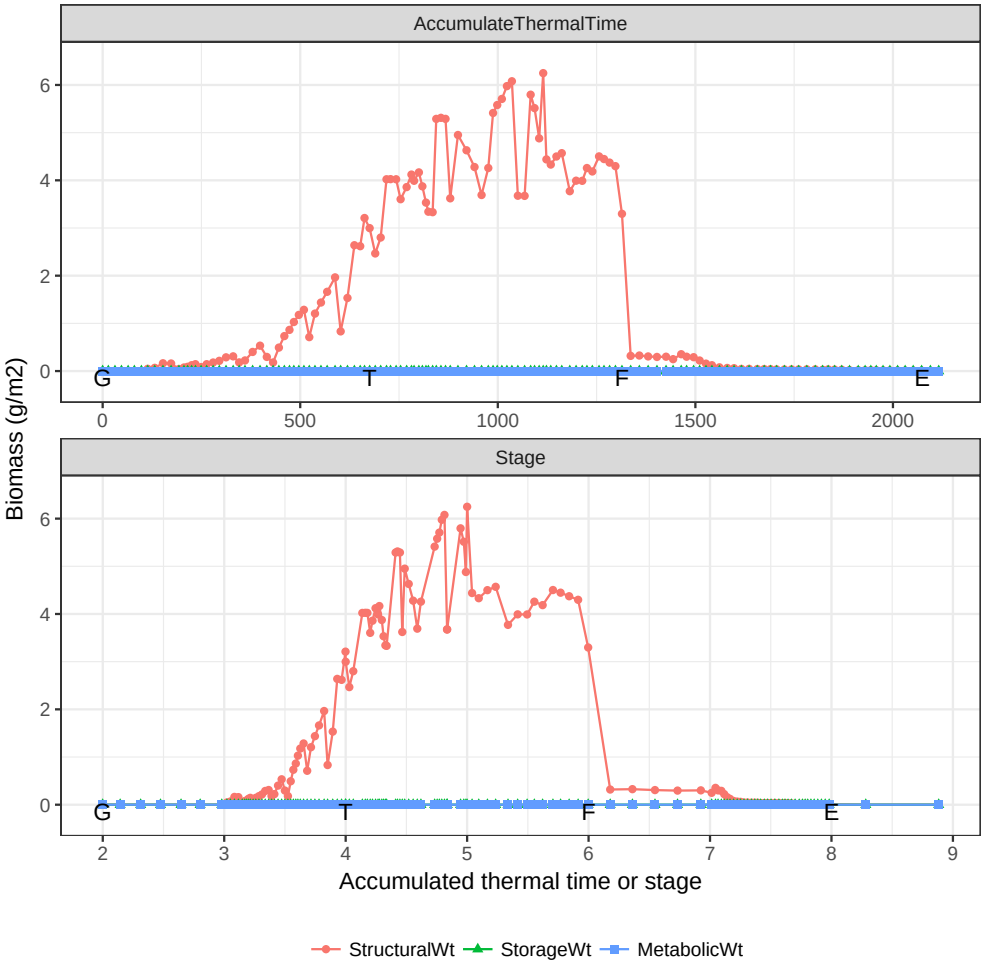

Figure 7.11: Actual allocated biomass for root

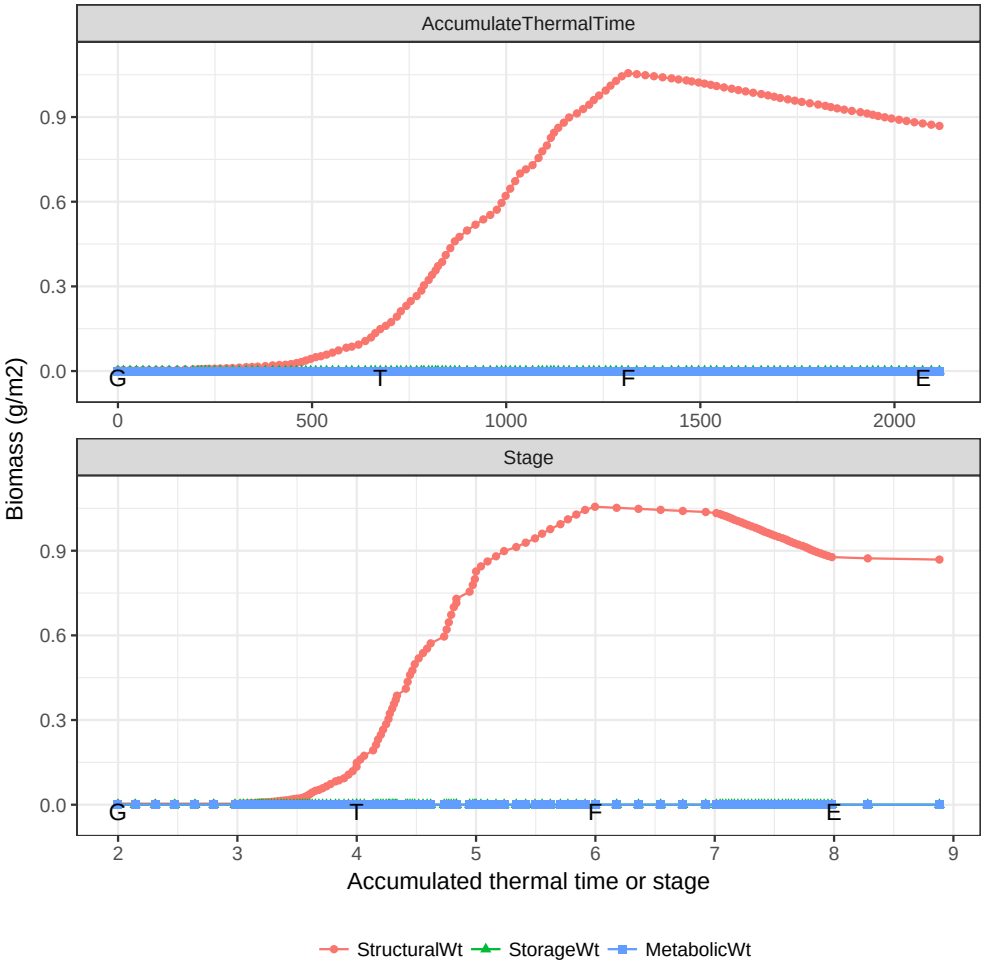

Figure 7.12: Detached biomass from root into soil organic.

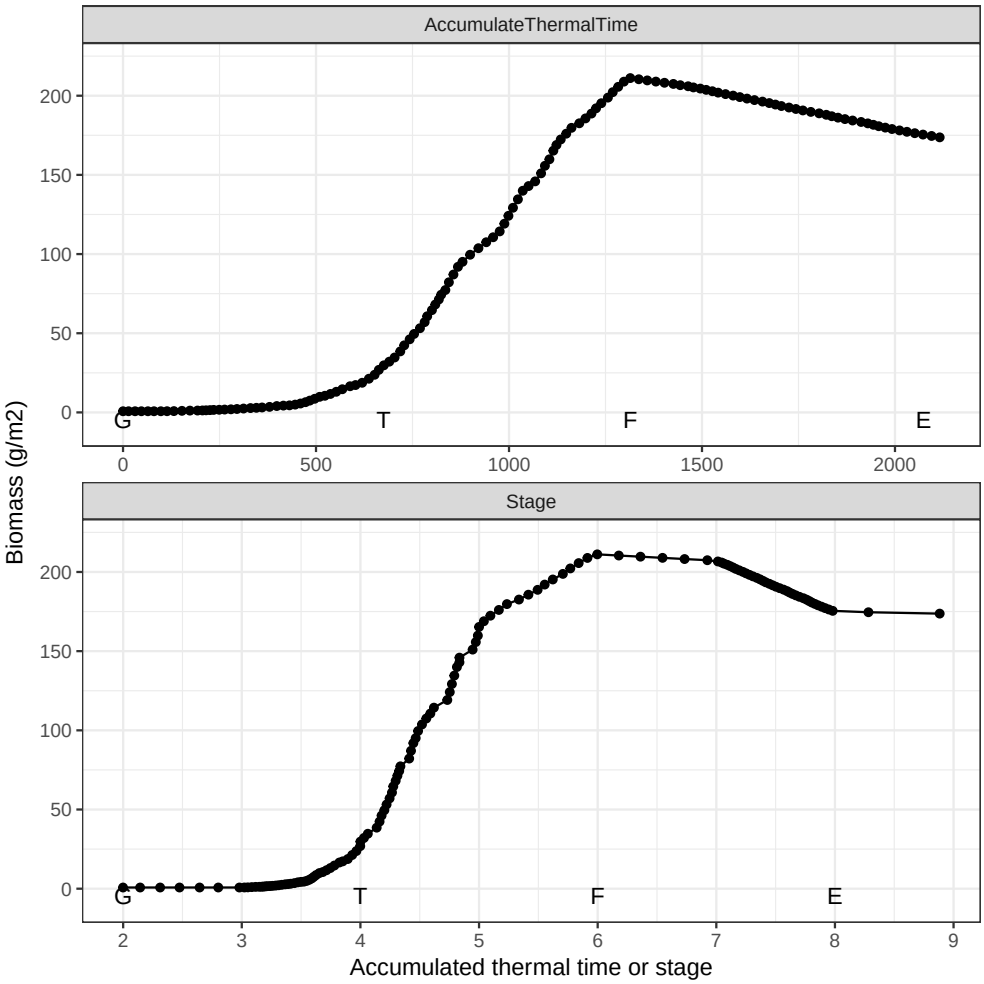

Figure 7.13: Dynamic of root biomass (Total)

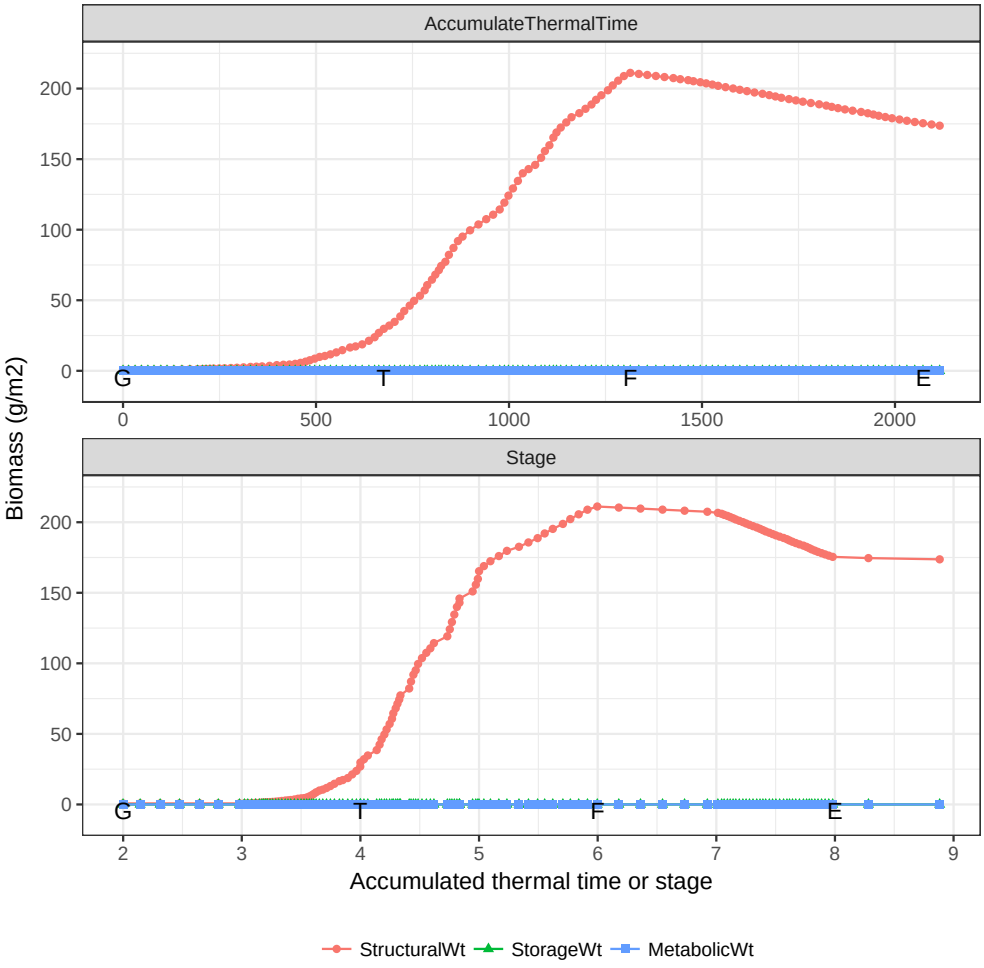

Figure 7.14: Dynamic of root biomass (Live component)

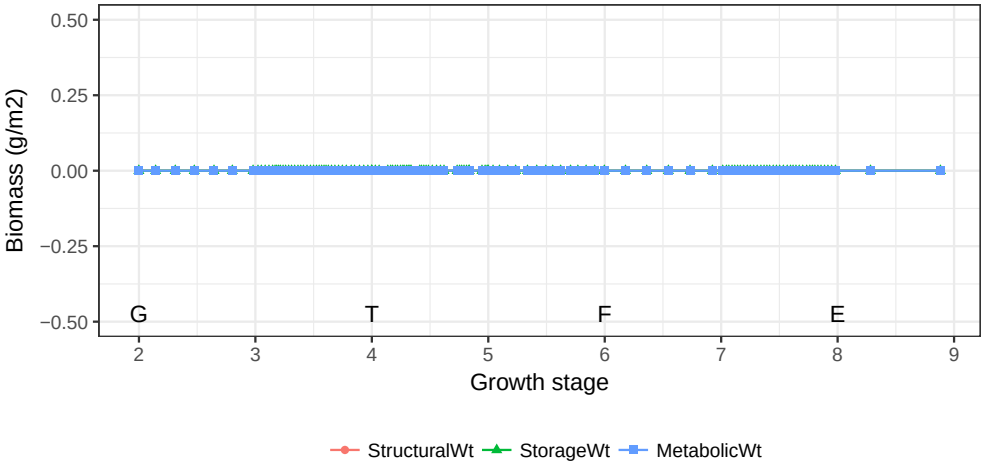

Figure 7.15: Dynamic of root biomass (Dead component)

Chapter 8

Leaf

The apex model is developed to simulate leaf dynamic based on leaf cohort model.

8.1 Life growth cycle

The growth cycle of leaf cohort is divided into 7 stages and 6 periods from `Initialized` to `Detached`. The length of each period depends on the `phylochron` during `Appearance` from `Initialized` to `Appeared` (fixed by 2 initial leaves at `Germination`). Other periods are configured by `CohortParameters` at `Appearance`, so that parameter values are determined by the values of status variables at the day of leaf cohort `Appearance` if they depend on other variables.

Several status variables are defined for each leaf cohort, which can be used in other modules to describe the current status of leaf cohort, i.e. `IsNotAppeared`, `IsGrowing`, `IsAlive`, `IsGreen`, `IsNotSenescing`, `Senescing`, `isFullyExpanded`, `ShouldBeDead`, `IsAppeared` and `IsInitialised`.

8.1.1 leaf age

The age of leaf cohort is defined as the thermal time after appearance, (i.e. keep zero after initialization). As the default values of `DetachmentLagDuration` and `DetachmentDuration` are set as `1000000` °Cd, the cohort age keeps increasing until growth stage `ReadyForHarvesting`. The age of first leaf cohort starts from 200 °Cd.

8.1.2 Leaf initialization and appearance

At `Germination`, 2 new leaf cohorts are initialized with initial leaf area 200, 0 mm^2. The inital leaf area simulates seed biomass or embryo size.

At `Emergence` stage, 1 leaf cohort is appeared at the main stem, and 1 new leaf cohort is initialized.

After `Emergence` and before plant reaches the final leaf number (i.e. all leaves are initialized and appeared), a new leaf cohort initialises and an existing leaf cohot appears when increases of potential appearance of tip number are more than 1 (Figure 4.5). Consequently, the rates of leaf initialization and appearance are same, except initialized tip number is more than 2 of appeared tip number (Fig. 8.2).

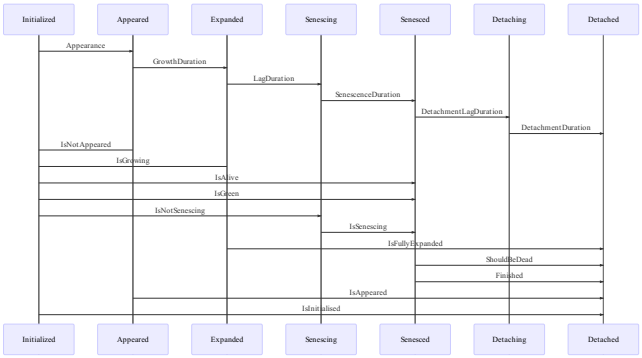

Figure 8.1: The life cycle of a leaf cohort.

8.1.3 Leaf growth and senescing

Growth (expansion) duration

Leaf expansion of cohort i starts from appearance of leaf tip i, i.e. the expansion of leaf cohort in the sheath is ignored which does not contribute to green leaf or leaf area index. The growth duration of spring wheat is close to one phylochron as the synchronization of leaf blade and sheath (Skinner and Nelson 1995). The growth duration is set as 1.3 phyllochron in default. The growth duration is adjusted for fraction of flag leaf (Fig. 4.8) to simulate the variation of final leaf number in a population.

Lag duration

Lag duration (full functional duration) is defined as 4 phyllochrons for leaf appeared during vegetative period (from `Emergence` to `TerminalSpikelet`) and adjusted by leaf age. For leaf cohort appeared during stem elongation period (from `TerminalSpikelet` to `FlagLeaf`), the lag duration equals to total length from stage `FlagLeaf` to stage `EndGrainFill` minus 3 phyllochron (`senescence duration`), i.e. flag leaf is completely death at the stage `EndGrainFill`.

Senescene duration

Senescence duration is defined as 3 phyllochrons in default.

As the variation of phyllochron (Fig. 4.3), the growth, lag and senescence durations also change by cohort rank (Fig. 8.3). The growth duration of flag leaf is shorter than secondary leaf as the fraction of flag leaf.

Figures 8.4 and 8.5 shows the number of leaf cohorts changing status including expanding and senescing and at certain status including expanded, green, and dead, respectively.

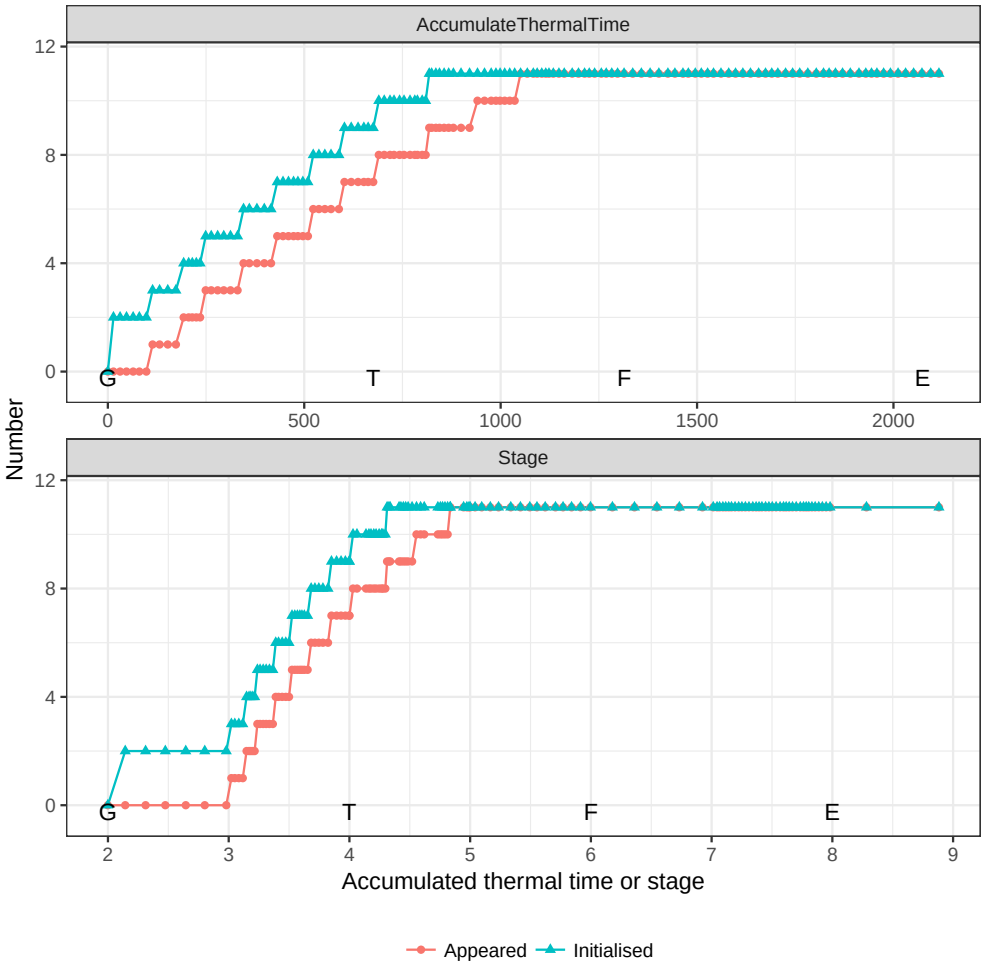

Figure 8.2: The initialized and appeared leaf cohort number in the main stem

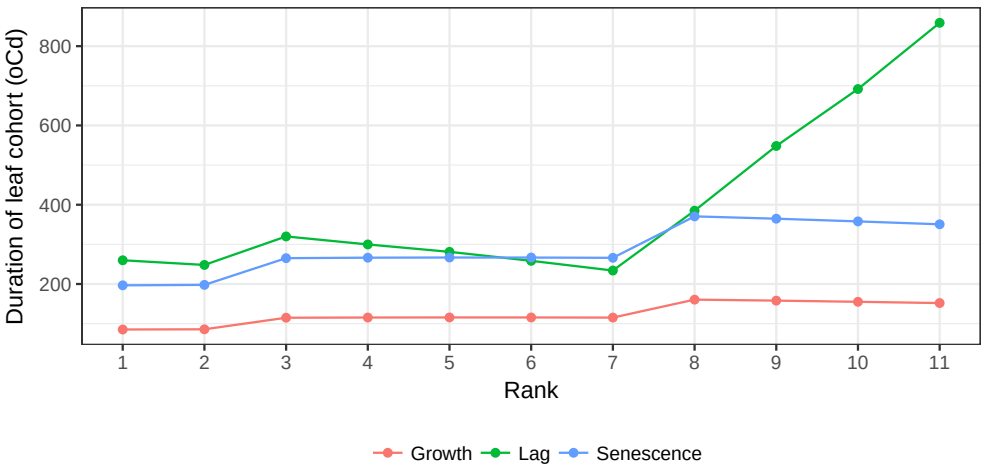

Figure 8.3: Senescene duration of leaf cohort which is determined at appearance of leaf cohort. The black dots indicate the appearances of leaf cohorts

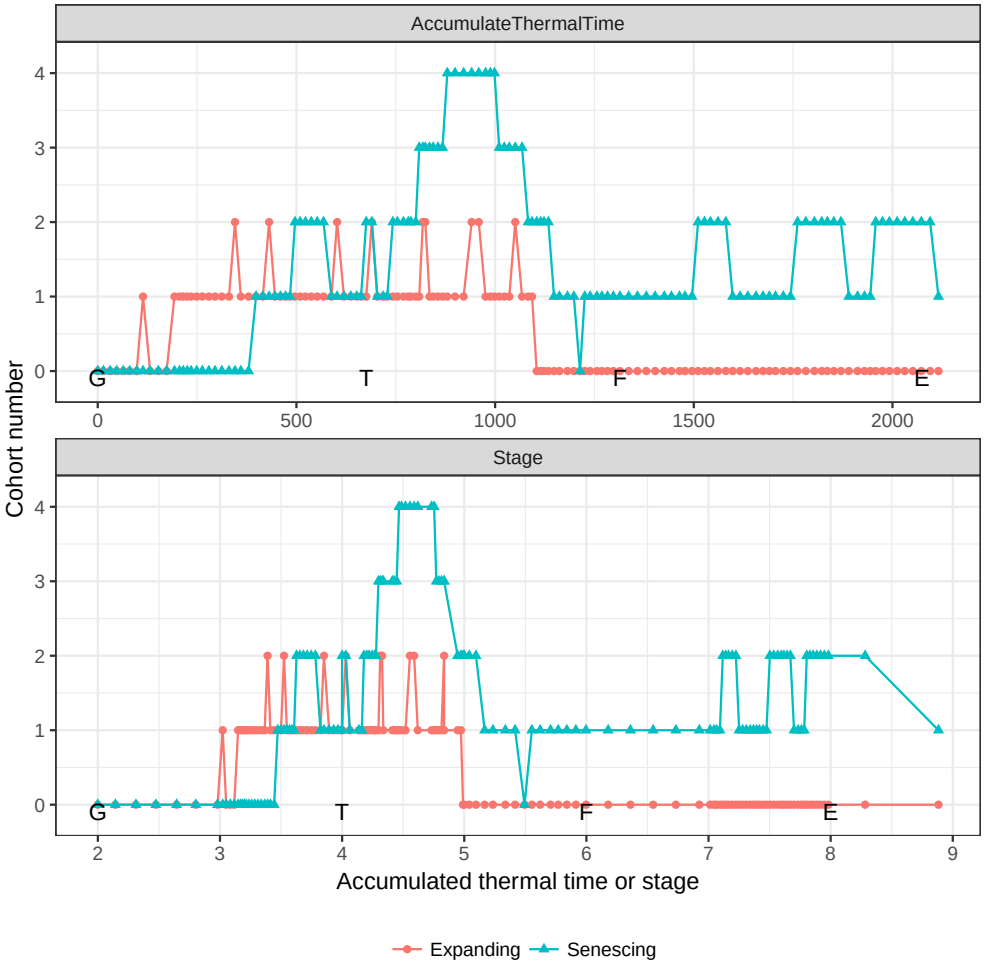

Figure 8.4: The number of leaf cohort with certain status including expanding and senescing

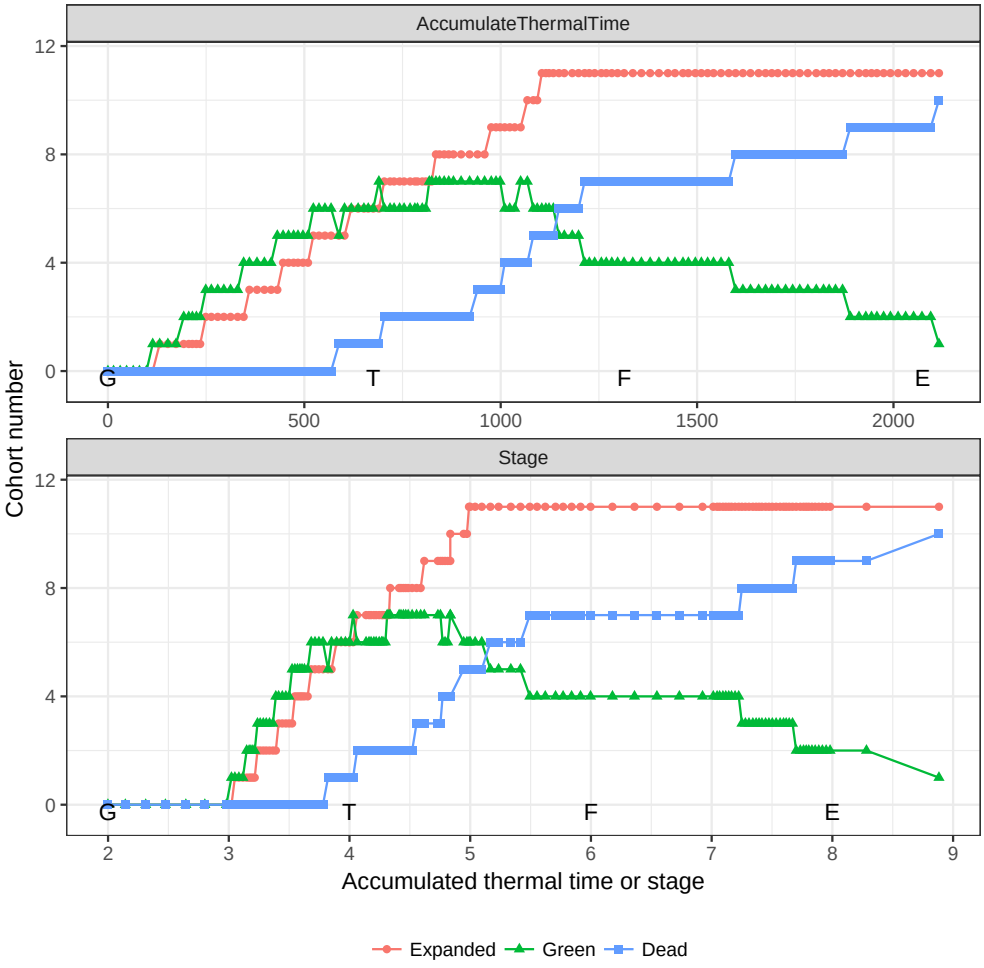

Figure 8.5: The number of leaf cohort with certain status including expanded, green, dead

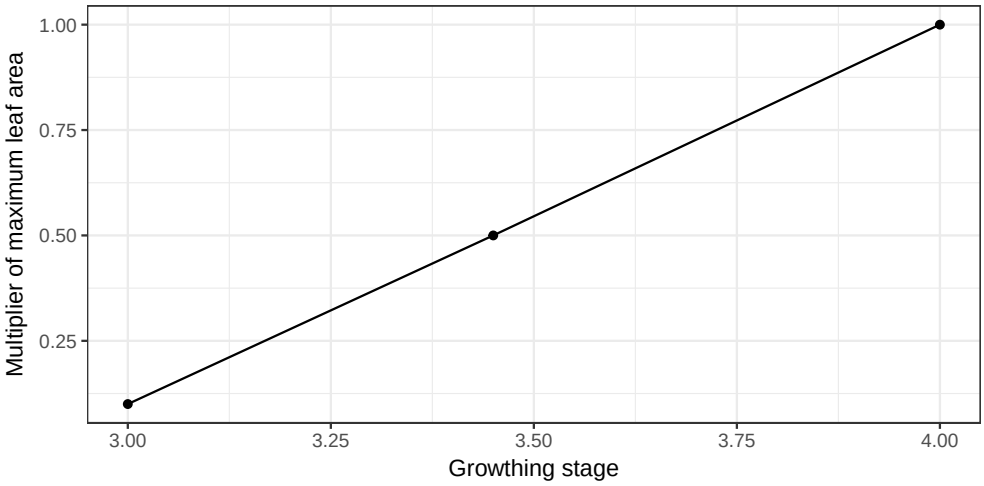

Figure 8.6: Multiplier of maximum leaf area as a function of growthing stage

8.1.4 Detachment lag and detachment durations

Detachment lag and detachment durations for leaf cohort are set as a big value `1000000` which assumes no detachment in wheat leaf. Actually all leaves are detached at `Harvesting` event.

8.2 Leaf area

During the growth (expanding) duration of each cohort (Fig. 8.4), the daily increase of leaf area is detemined by the minimum increases by water (ΔA_{water}) and carbon (ΔA_{carbon}) constrained leaf area.

8.2.1 Maximum (potential) leaf area

The maximum leaf area of each leaf cohort is determined by potential maximum leaf area and reduced by cell division stress from `Initialization` to `Appearance`.

The potential maximum leaf areas by rank are specified by two parameters the maximum leaf area in all leaves (`AreaLargestLeaves` with default value 2600 mm^2) and an age factor (Fig. 8.6). The age factor is assumed leaf areas are linearly increasing from stage `Emergence` to `TerminalSpikelet`, and all leaves appeared after stage `TerminalSpikelet` have the same maximum leaf area (Fig. 8.7).

The stress factor of cell division is the minimum multipliers of water stress and nitrogen stresses (Fig. 8.8). Multipliers of water stress (Fig. 8.9) is a function of water supply and demand ratio (Fig. 11.1). Multipliers of nitrogen stress (Fig. 8.10) is a function of ratio of functional nitrogen (Fig. 8.30).

Stress of cell division is averaged by cell division stress factors from `Initialization` to `Appearance`, then reduces the potential maximum leaf area (Fig. 8.11). The actual maximum leaf area of flag leaf can be much smaller than other leaves as the fraction of final leaf to simulate the variation of final leaf number in a population (Fig. 4.8).

8.2.2 Potential expansion of leaf cohort

The potential leaf area is increased following a logistic equation as a function of thermal time after leaf appearance. The shape of logistic equation is determiend by parameter `LeafSizeShapeParameter` with

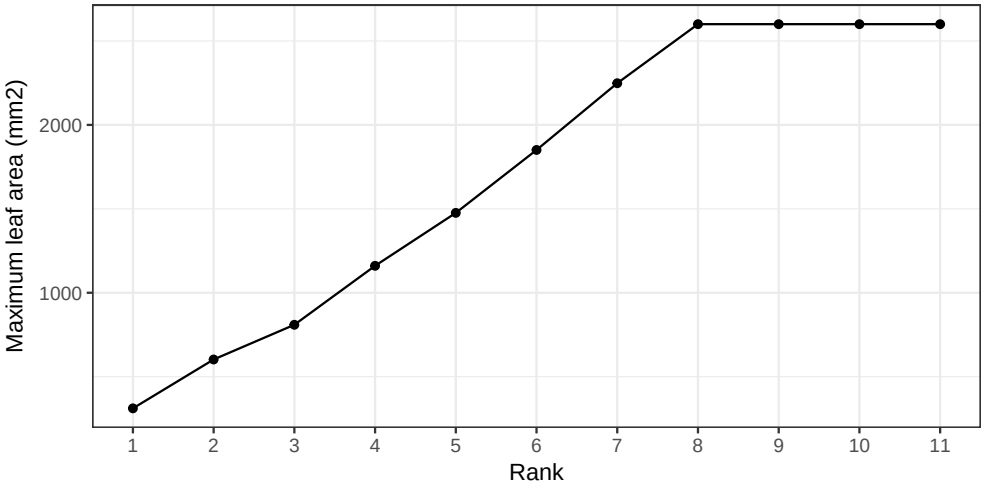

Figure 8.7: Maximum leaf area by leaf rank

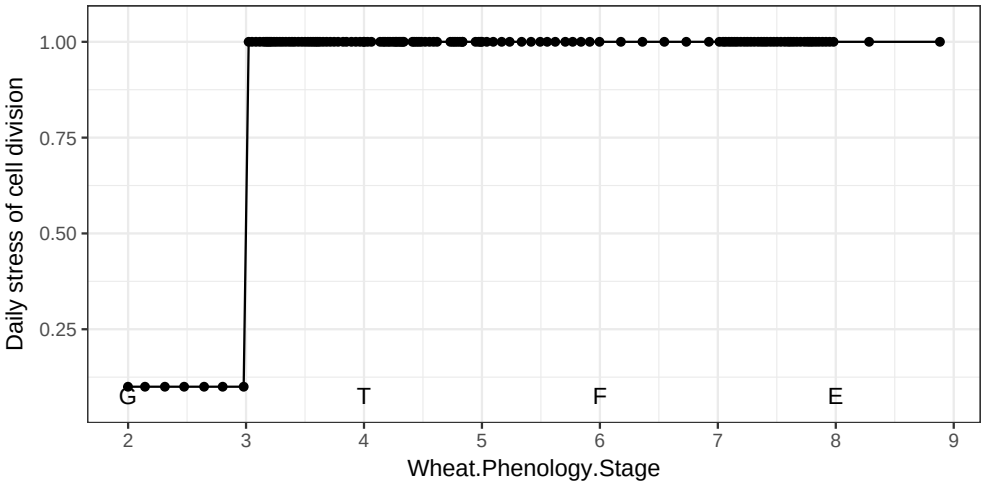

Figure 8.8: Daily stress of cell division

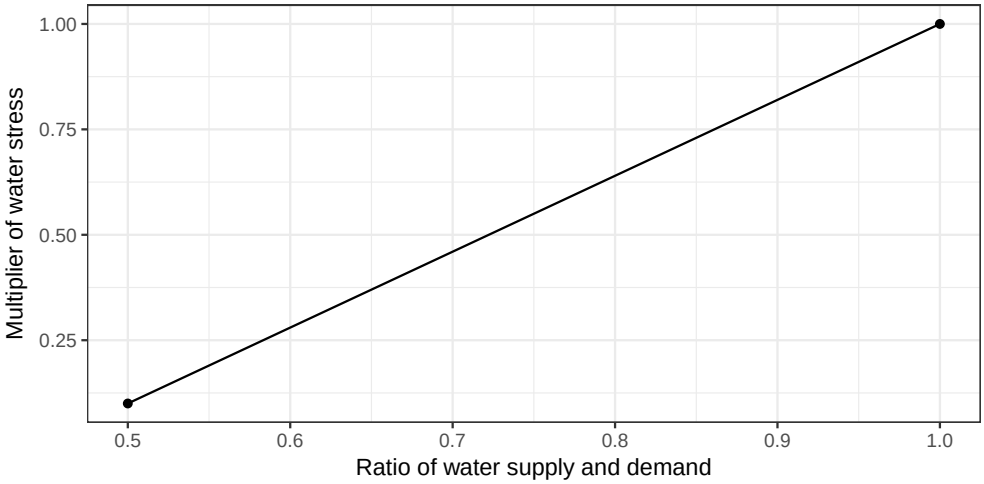

Figure 8.9: Multiplier of water stress on cell division

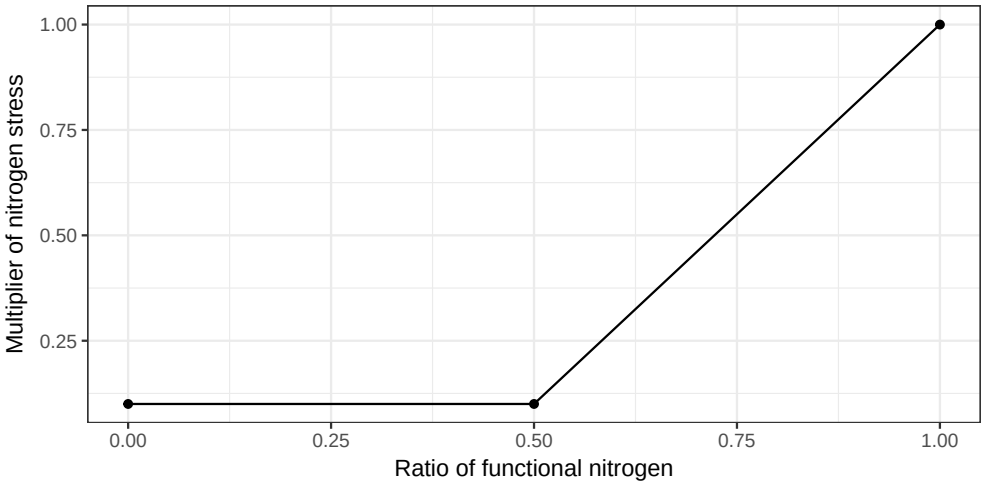

Figure 8.10: Multiplier of nitrogen stress on cell division

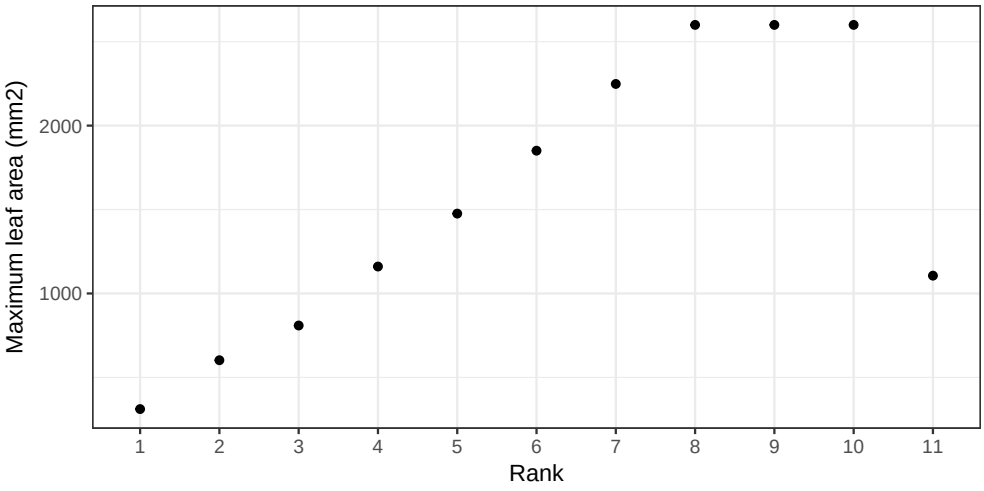

Figure 8.11: Actual maximum area of leaf cohorts by leaf rank.

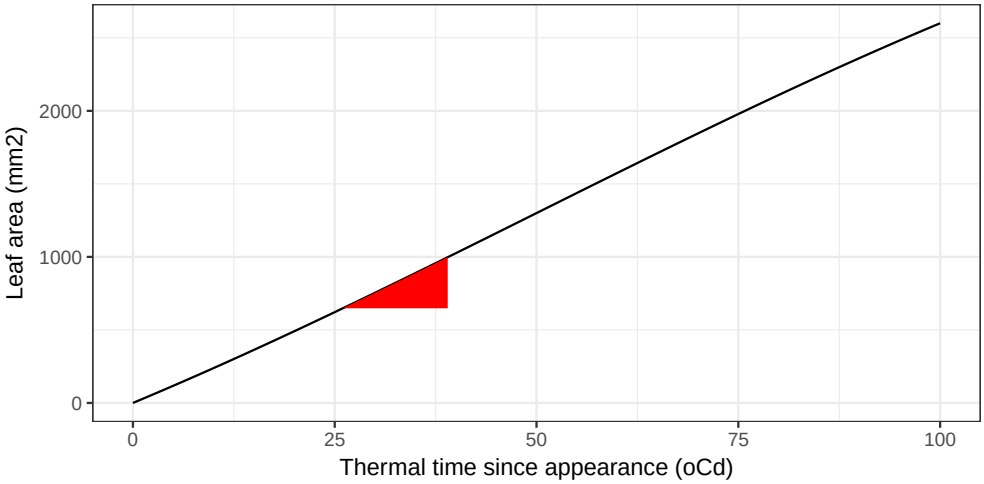

Figure 8.12: The size function of leaf area development. The maximum leaf area sets as 2600 mm2

default value 0.3 (Fig. 8.12). The daily potential increase of leaf area is the difference of size function in today and previous (e.g. the height of red area in Fig. 8.12).

8.2.3 Water constrained leaf area

The water constrained leaf area equals to the daily potential increase of leaf area which reduced by `ExpansionStress` (Fig. 8.13) which is a minimum value among temperature, water and nitrogen stresses (Fig. 8.14). Temperature stress is related with daily mean temperature; water stress is related with water tension factor in root; nitrogen stress related with fraction of functional nitrogen in leaf (Fig. 8.30).

8.2.4 Carbon constrained leaf area

The leaf area also constrained by the daily allocated cardon (biomass) including structural and metabolic in the leaf cohort [ref], then multiplies maximum specific leaf area for the biggest expansion (Fig. 8.18).

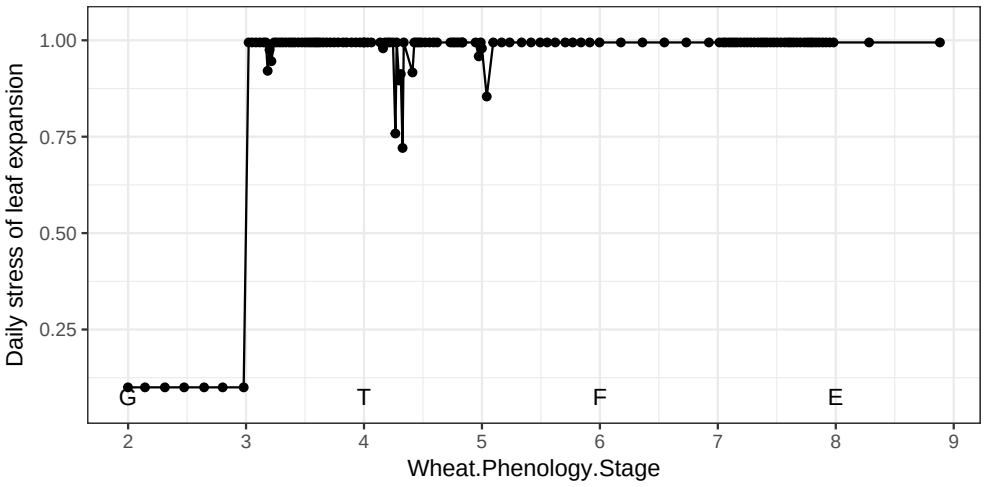

Figure 8.13: Daily stress of leaf expansion

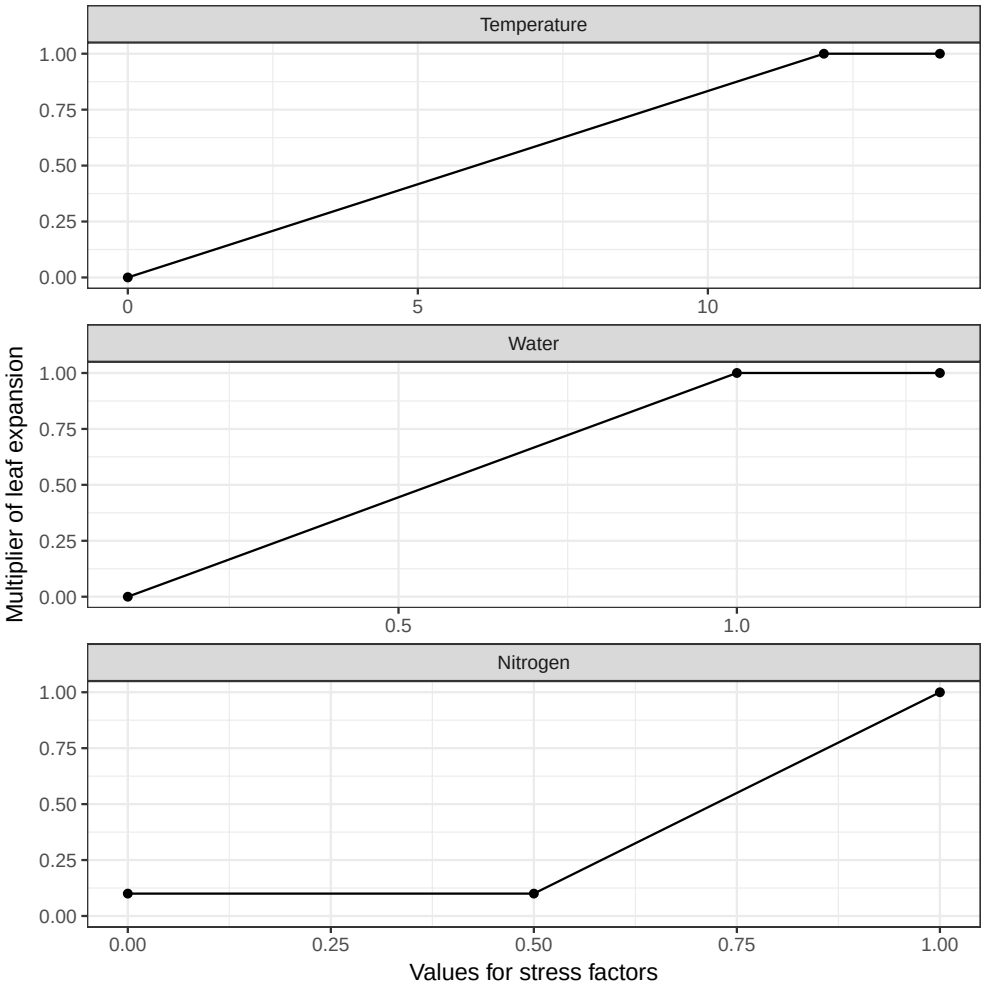

Figure 8.14: Multiplier of temperature stress on leaf expansion. Temperature stress is related with daily mean temperature. Water stress is related with water tension factor in root. Nitrogen stress is related with ratio of functional nitrogen.

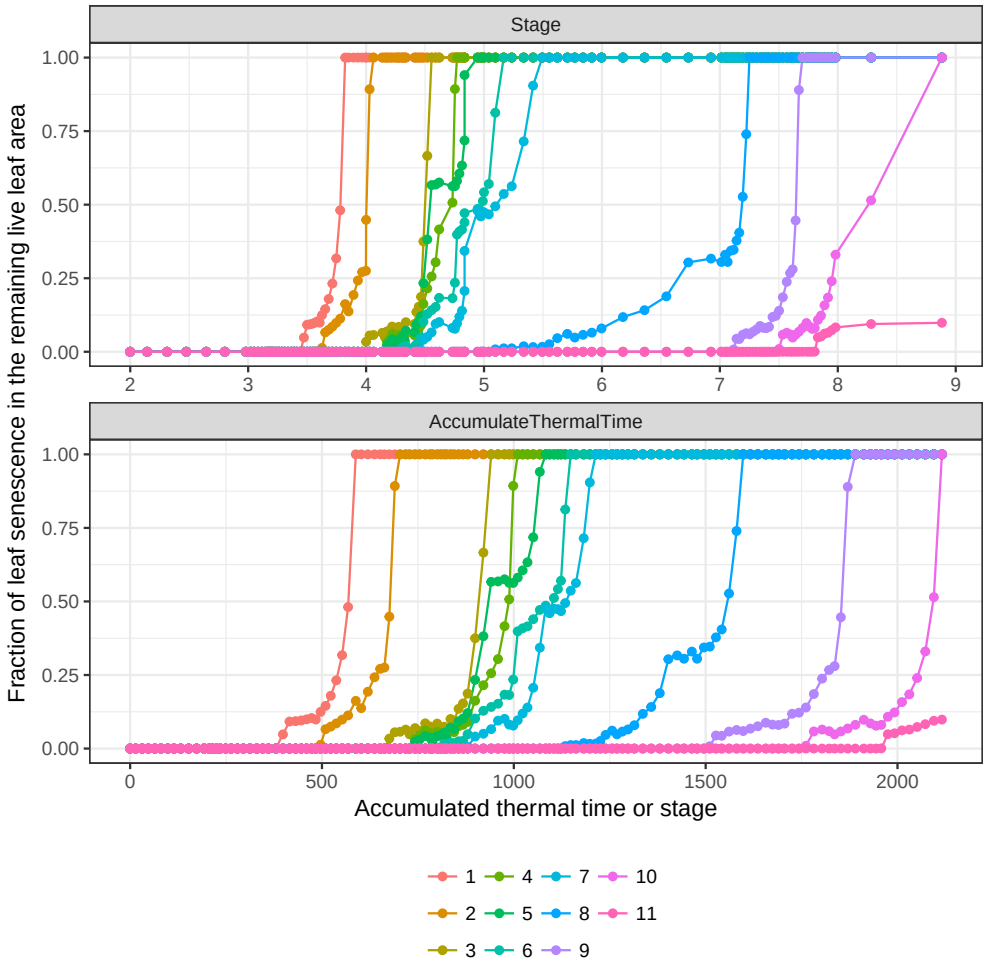

Figure 8.15: Fraction of leaf senescence by leaf cohort in the remaining live leaf area.

The actual daily increase of leaf area is the minimum of water and carbon constrained leaf area.

8.2.5 Leaf senescence

During the period of leaf senescene, the daily fraction of leaf senescence is linearly related with thermal time.

8.2.6 Leaf area index and ground coverage

Leaf area index (LAI) are calculated for green leaf (LAI_g), dead leaf (LAI_d), and total leaf (LAI_t) (Fig. 8.16).

Ground coverage also are calculated for green leaf (C_g), dead leaf (C_d), and total leaf (C_t) from LAI and extinction coefficient for green leaf (k_g) and dead leaf (k_d).

$$C_g = C_{max}(1 - \exp(-k_g \frac{\text{LAI}_g}{C_{max}}))$$

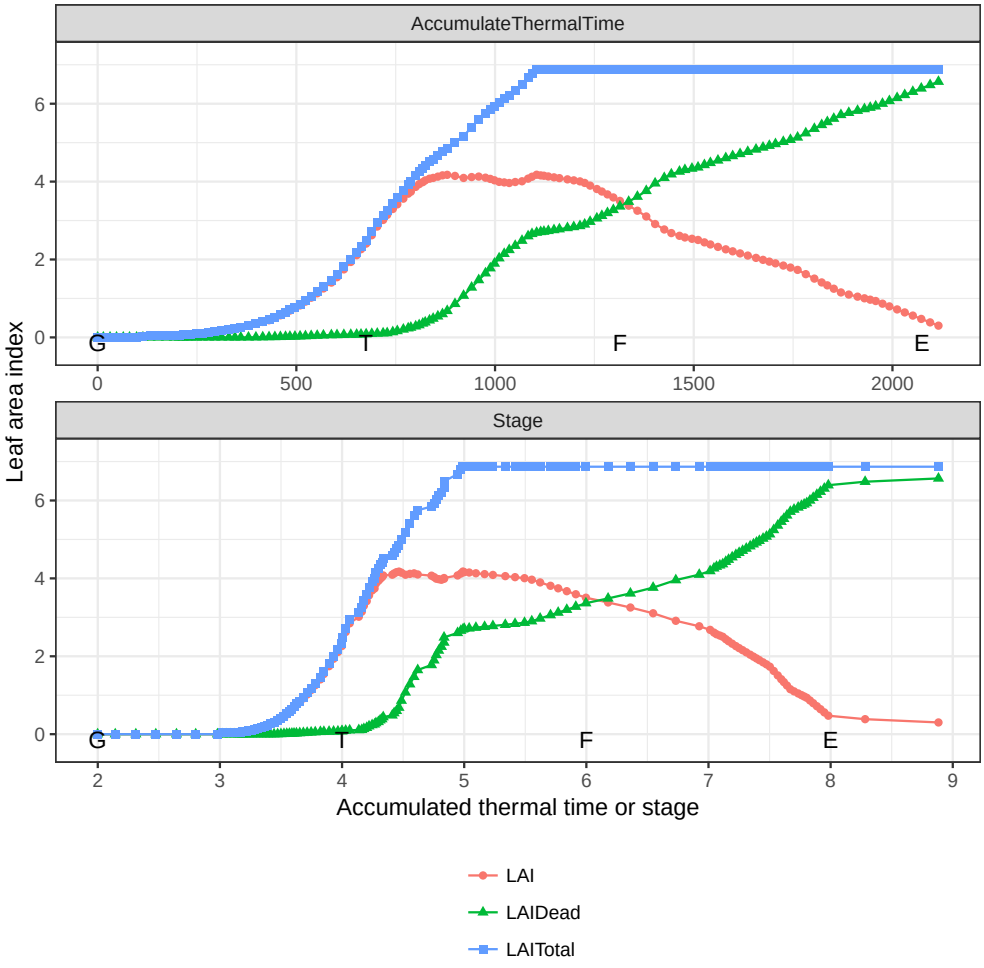

Figure 8.16: Leaf area index

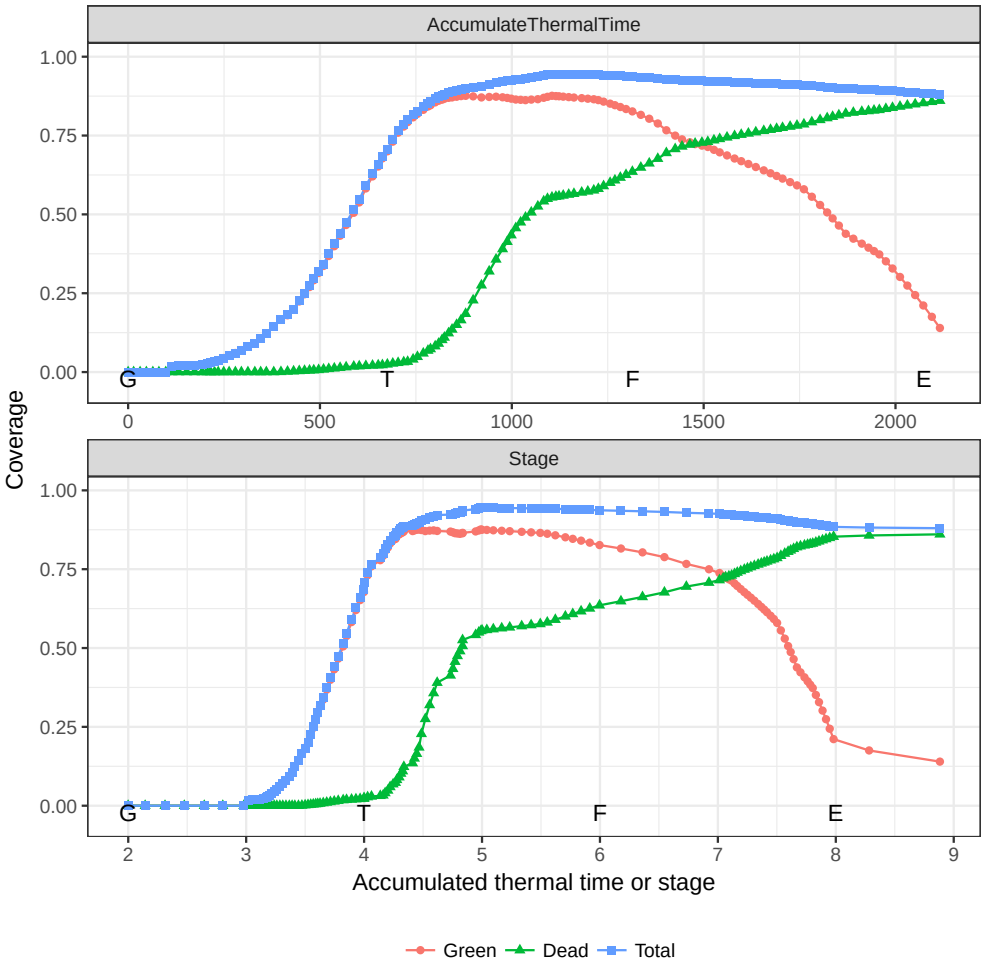

Figure 8.17: Coverage

As the default value of maximum coverage (C_{max}) is 1, the function is reduced to

$$C_g = 1 - \exp(-k_g \mathrm{LAI}_g)$$

The similar equation is used for dead coverage.

$$C_d = 1 - \exp(-k_d \mathrm{LAI}_d)$$

Total coverage (C_t) is calculated from coverage of green and dead leaves.

$$C_t = 1 - (1 - C_g)(1 - C_d)$$

The extinction coefficient for dead leaf (k_d) is defined as 0.3. The extinction coefficient for green leaf (k_g) is calculated by parameter `ExtinctionCoeff` with default value 0.5.

Specific leaf area The minimum and maximum specific leaf areas are defined in the `CohortParameters` (Fig. 8.18), which related with fraction of functional nitrogen (Fig. 8.30) and stage, respectively.

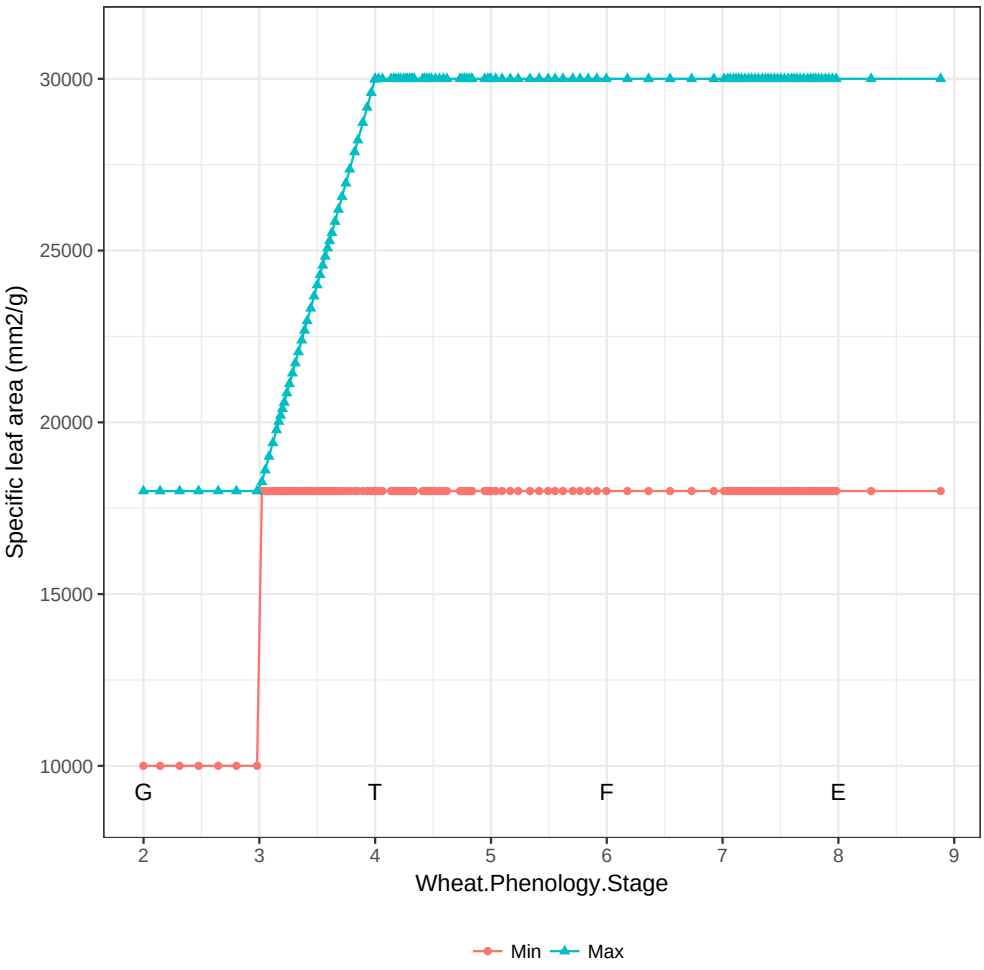

Figure 8.18: Maximum and minimum specific leaf area.

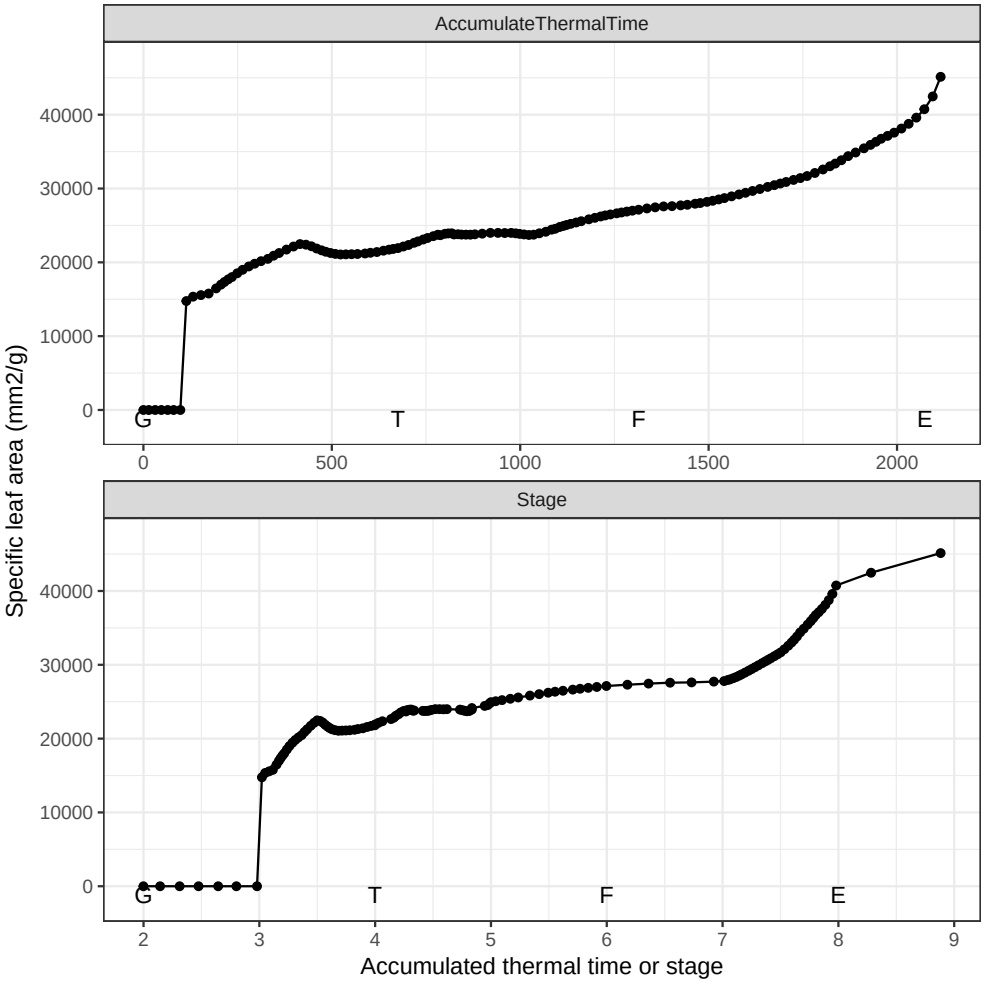

Figure 8.19: Specific leaf area

8.3 Supply

In `Leaf` organ, the biomass supply only sources from `Fixation` (i.e. photosynthesis, Fig. 8.23). Three photosynthesis models are implemented in the APSIM next generation,

8.3.1 Radiation use efficiency model

The radiation-limited dry-biomass accumulation (ΔQ_r) is calculated by the intercepted radiation (I), radiation use efficiency (RUE).

$$\Delta Q_r = I \times RUE$$

Radiation interception

Radiation interception is calculated from the leaf area index (LAI, m^2 m^{-2}) and the extinction coefficient (k) (Monsi and Saeki 2005).

$$I = I_0(1 - \exp(-k \times LAI)$$

where I_0 is the total radiation at the top of the canopy (MJ) which is directly imported from weather records. Extinction coefficient (k) set as a constant value 0.5.

Actual radiation use efficiency

The actual RUE (g MJ^{-1}) is calculated as the potential RUE (RUE_p) and several reduction factors, including plant nutrition ($F_{n,\ photo}$), air temperature($F_{t,\ photo}$), vapour pressure deficit (F_{vpd}), water supply (F_w) and atmospheric CO2 concentration (F_{co2}).

$$RUE = RUE_p \times \min\left(F_{t,\ photo}, F_{n,\ photo}, F_{VPD}\right) \times F_W \times F_{CO2}$$

The potential RUE (RUE_p) has a default value 1.5.

The temperature factor (F_t) is calculated as a function of average daily temperature weighted toward maximum temperature according to the specified `MaximumTemperatureWeighting` factor (W_{maxt}) with default value 0.75.

$$F_{t,\ photo} = h_{t,\ photo}[W_{maxt}T_{max} + (1 - W_{maxt})T_{min}]$$

The plant nutrition factor is determined by the ratio of functional nitrogen in leaf (Fig. 8.30) and the multiplier of nitrogen stress (Fig. 8.21).

Water stress factor

F_W quantifies water stress and is calculated as Leaf.Transpiration/Leaf.WaterDemand, where Leaf.Transpiration is the minimum of Leaf.WaterDemand and Root.WaterUptake

CO_2 factor is calculated by a function of environmental CO_2 concentration (C, ppm; $C > 350$ ppm) and daily mean temperature ($T_{mean} < 50$°C) as published by Reyenga et al. (1999)

$$f_c = \frac{(C - C_i)(350 + 2C_i)}{(C + 2C_i)(350 - C_i)}$$

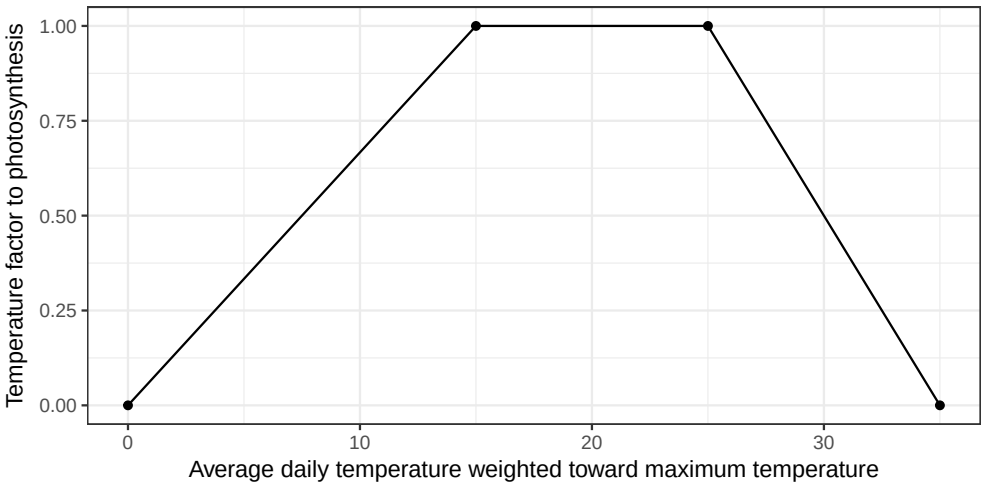

Figure 8.20: The temperature factor which influences radiation use efficiency

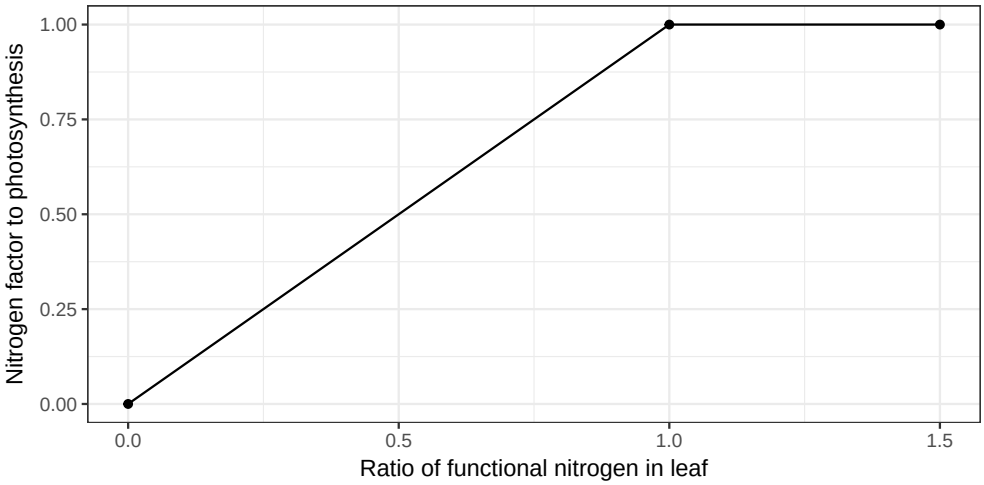

Figure 8.21: The nitrogen factor which influences radiation use efficiency

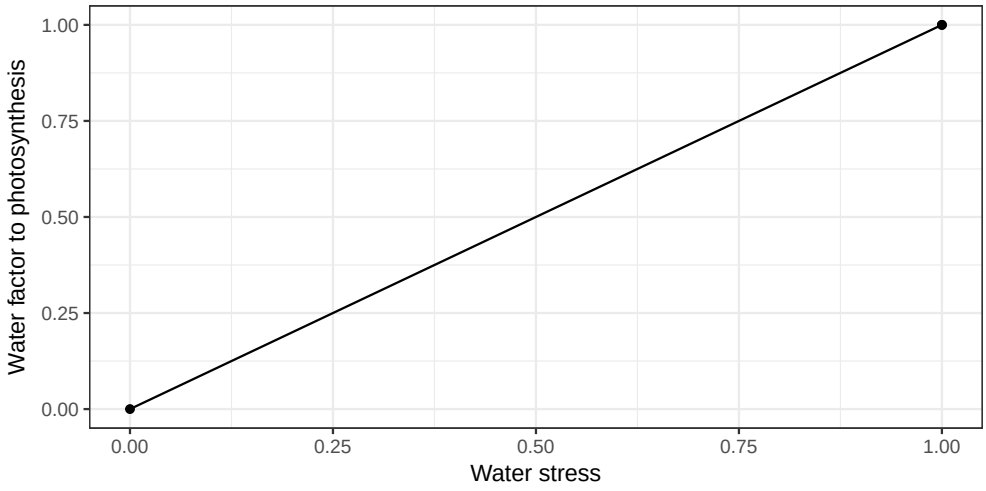

Figure 8.22: The water factor which influences radiation use efficiency

where C_i is the temperature dependent CO_2 compensation point (ppm) and is derived from the following function.

$$C_i = \frac{163 - T_{mean}}{5 - 0.1T_{mean}}$$

8.3.2 WE's photosynthesis model

8.3.3 Layered Canopy Photosynthesis Model with Transpiration (or DCaPS)

8.4 Demand

The leaf demand is summarised for all leaf cohorts in the expanding period (Figs 8.1 and 8.4), so that there is no leaf demand after `FlagLeaf`. No `Storage` demand is considered in the leaf organ. As the structural fraction is defined as 0.5, the structural and metabolic demands have the same values in the whole life cycle.

The daily demand (D_{leaf}) is the minimum between potential leaf area (ΔA_p, Section 8.2.2) and water stressed (ΔA_w, Section 8.2.3) leaf area.

$$D_{leaf} = \min(\frac{\Delta A_p}{(\mathrm{SLA}_{max} + \mathrm{SLA}_{min})/2}, \frac{\Delta A_w}{\mathrm{SLA}_{min}})$$

where, SLA_{min} and SLA_{max} are the minimum and maximum specific leaf areas, respectively (Fig. 8.18).

8.5 Biomass dynamic

8.6 Nitrogen

8.6.1 Functional nitrogen

Ratio of leaf functional nitrogen ($f_{N,leaf}$) quantifys the nitrogen stress status of the plant and represents the concentration of metabolic N relative the maximum potentil metabolic N content of the leaf.

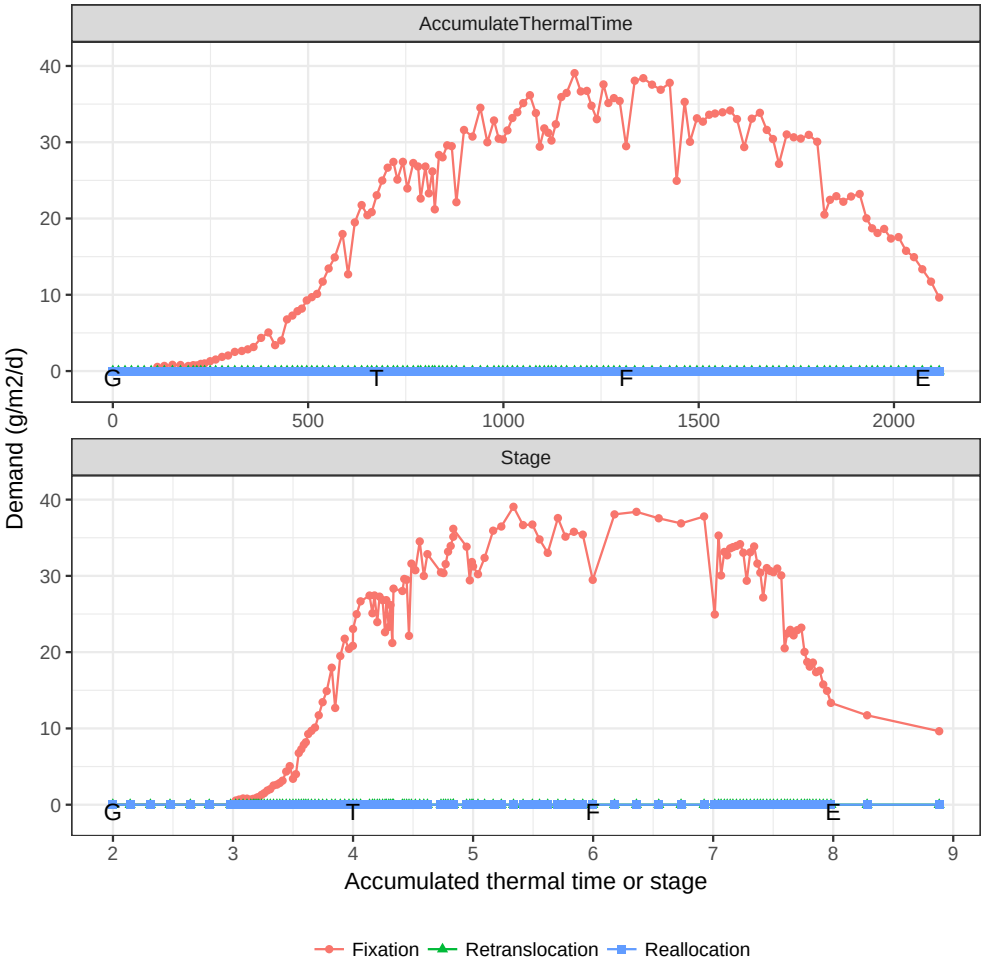

Figure 8.23: Biomass supply from leaf

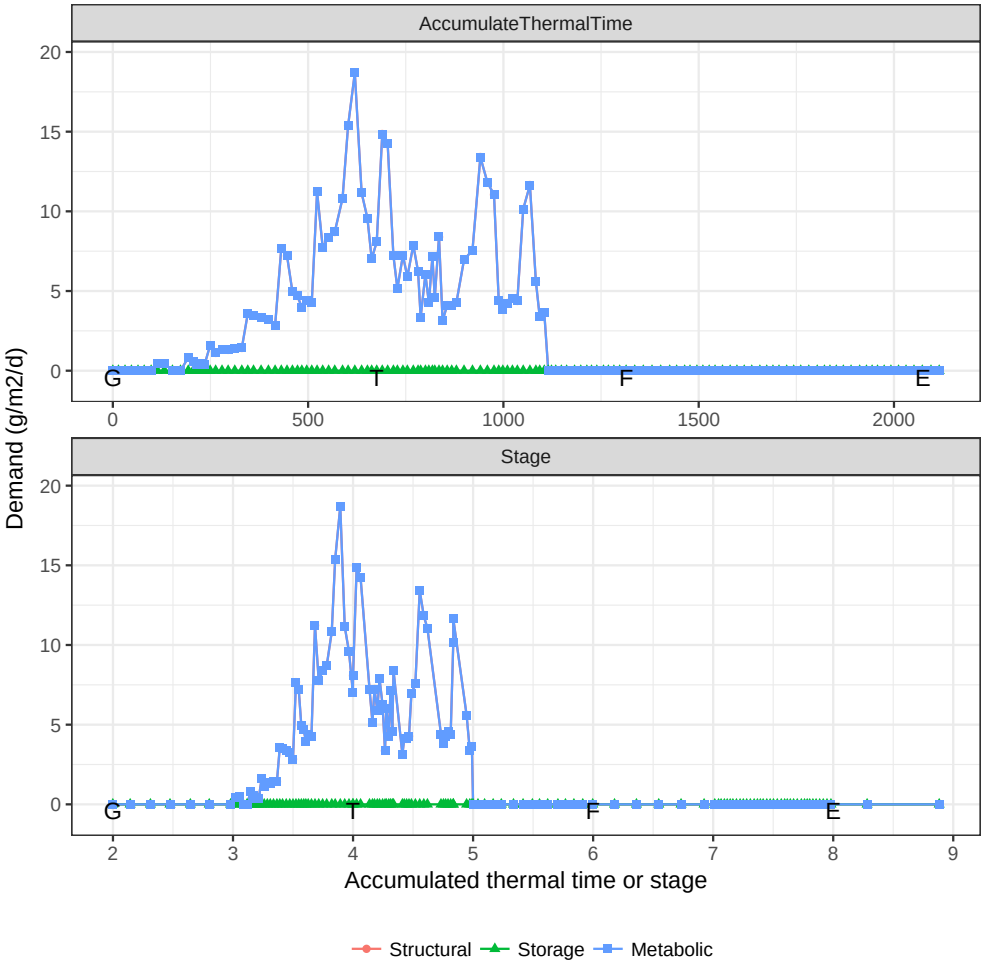

Figure 8.24: Biomass demand by leaf. The structural and metabolic demands overlap each other as the structural fraction is defined as 0.5.

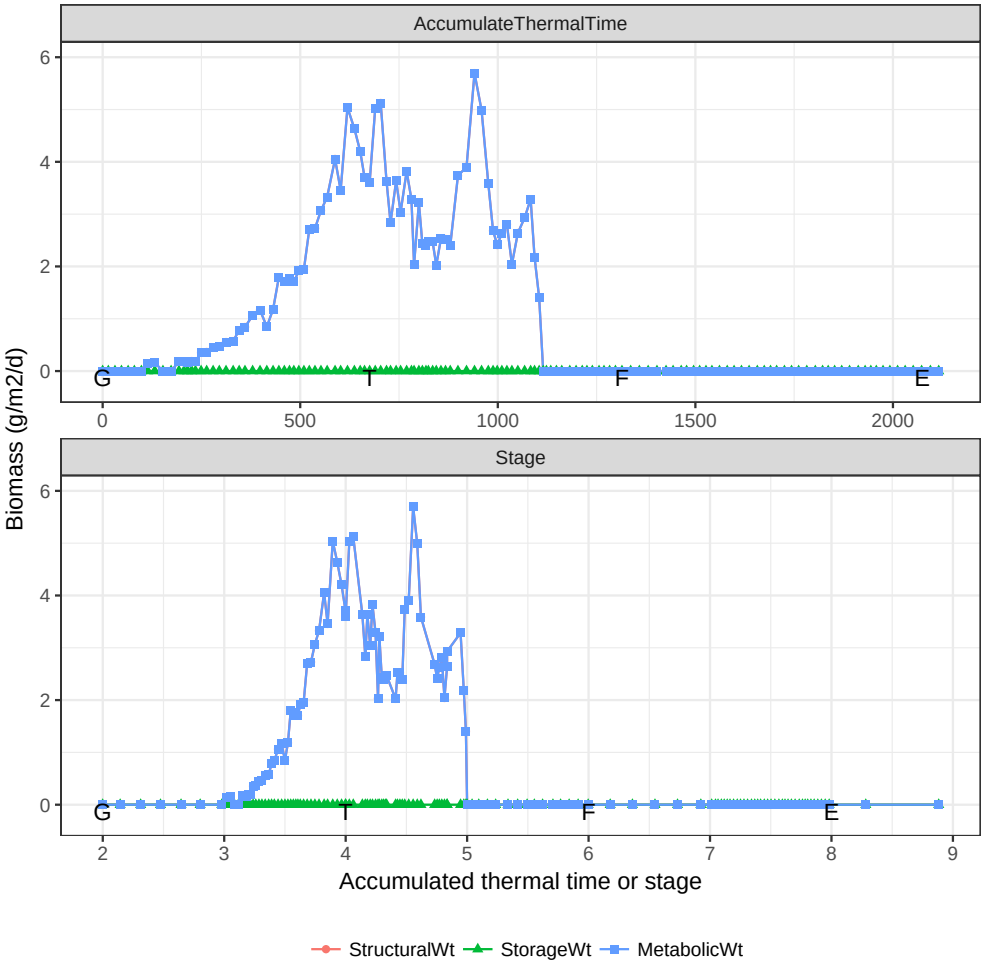

Figure 8.25: Actual allocated biomass for leaf

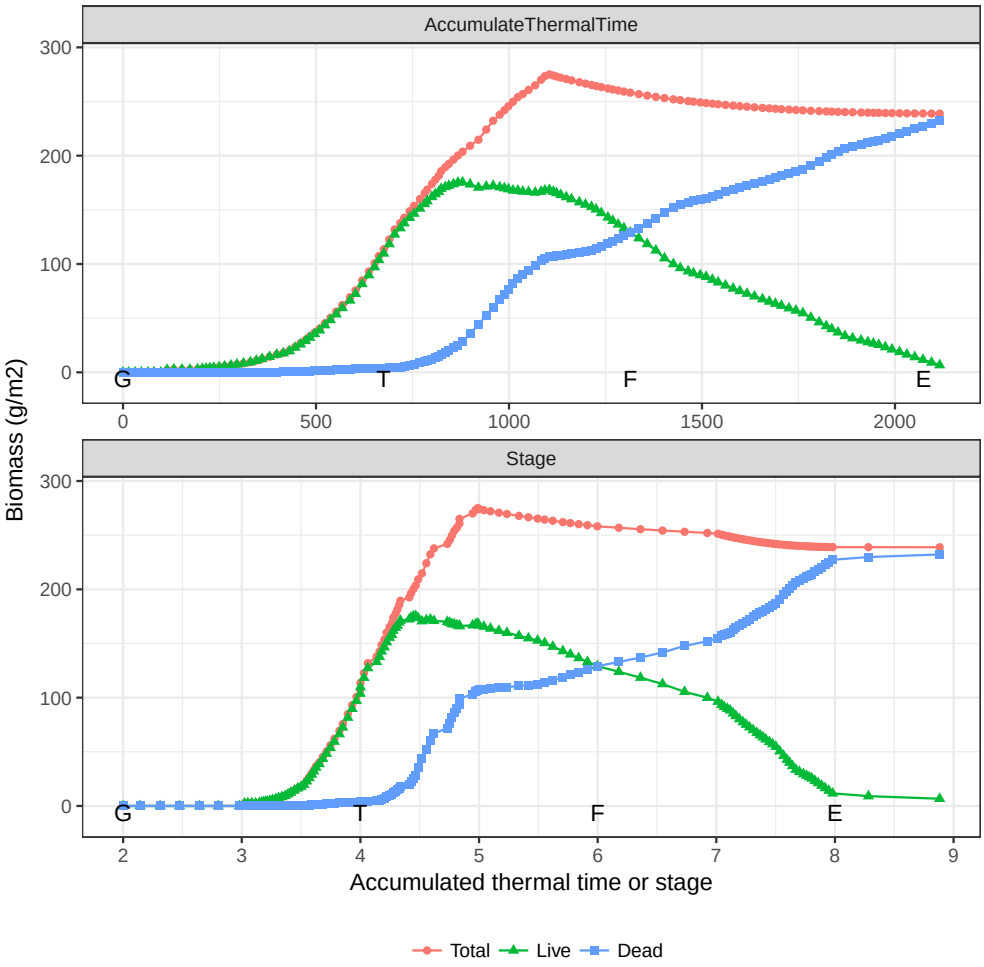

Figure 8.26: Dynamic of leaf biomass (Total)

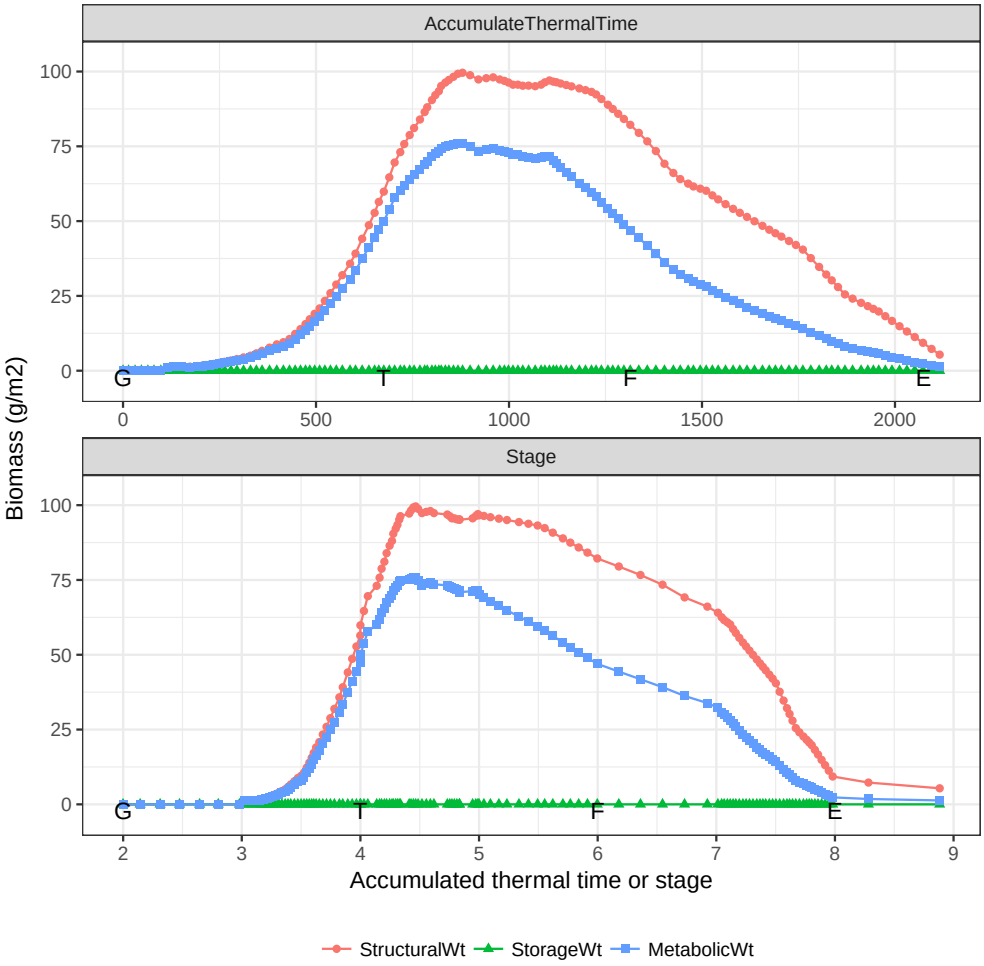

Figure 8.27: Dynamic of leaf biomass (Live component). The structural and metabolic weights overlap each other as the structural fraction is defined as 0.5.

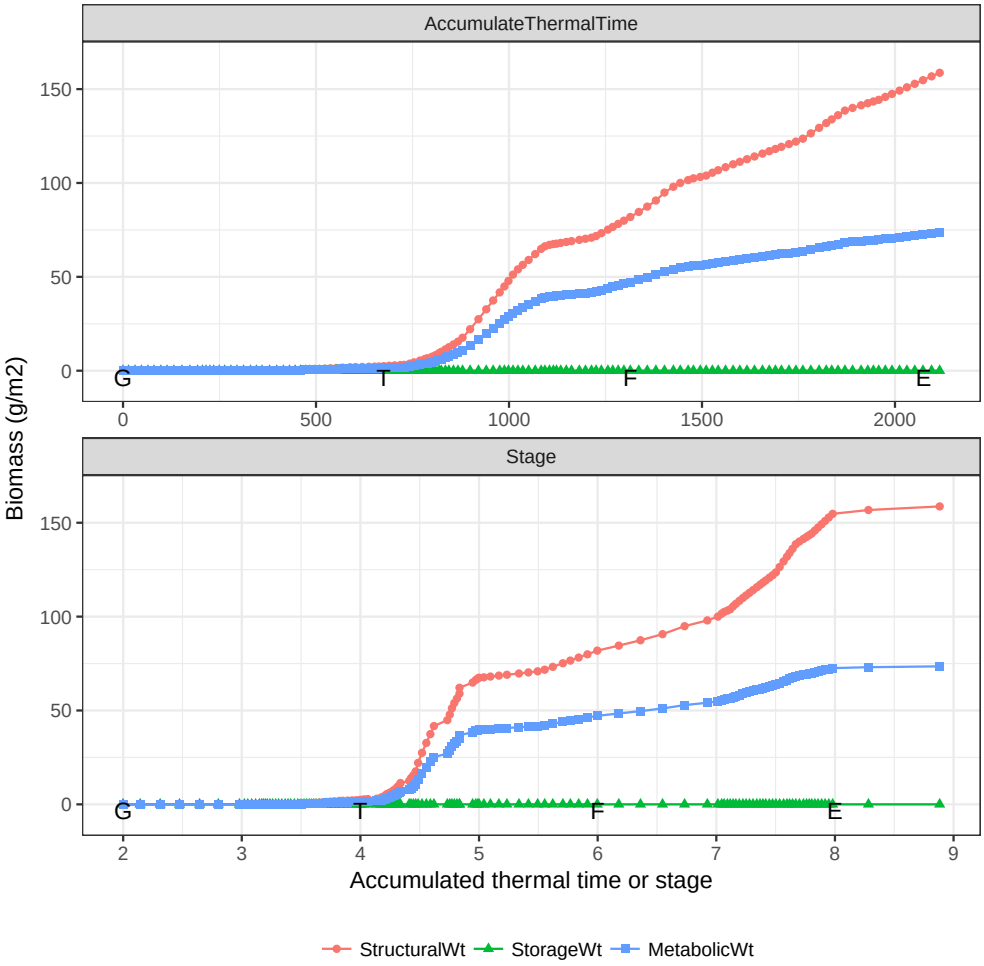

Figure 8.28: Dynamic of leaf biomass (Dead component). The structural and metabolic weights overlap each other as the structural fraction is defined as 0.5.

$$f_{N,\,photo} = R_{N,\,photo}\frac{C_N - C_{N,\,min}}{C_{N,\,crit} - C_{N,\,min}}$$

where C_N is the nitrogen concentration of `Leaf` parts; $R_{N,\,expan}$ is multiplier for nitrogen deficit effect on phenology which is specified by `N_fact_photo` in the wheat.xml and default value is 1.5.

```
if (CohortParameters == null)
    return 1;


double f;
double functionalNConc = (CohortParameters.CriticalNConc.Value() -
                          CohortParameters.MinimumNConc.Value() * CohortParameters.StructuralFraction.Va
                         (1 / (1 - CohortParameters.StructuralFraction.Value()));
if (functionalNConc <= 0)
    f = 1;
else
    f = Math.Max(0.0, Math.Min(Live.MetabolicNConc / functionalNConc, 1.0));

return f;
```

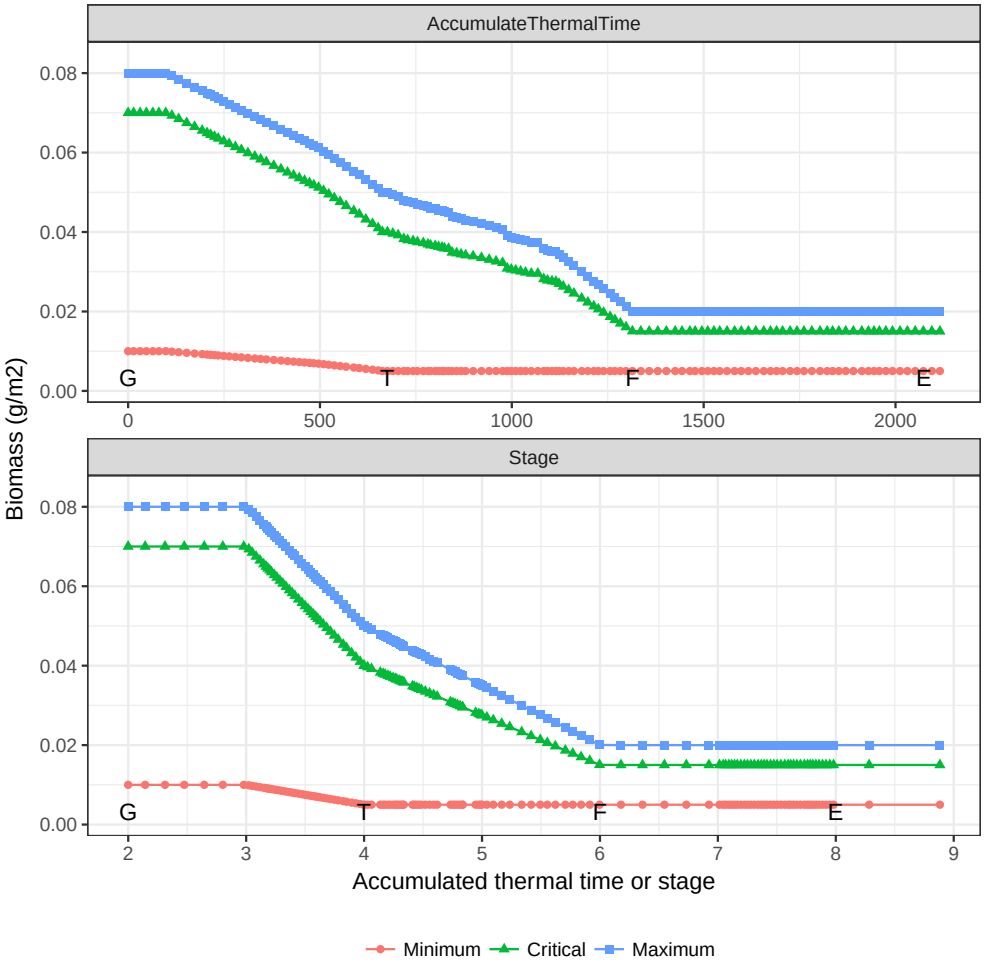

Figure 8.29: Actual allocated biomass for leaf

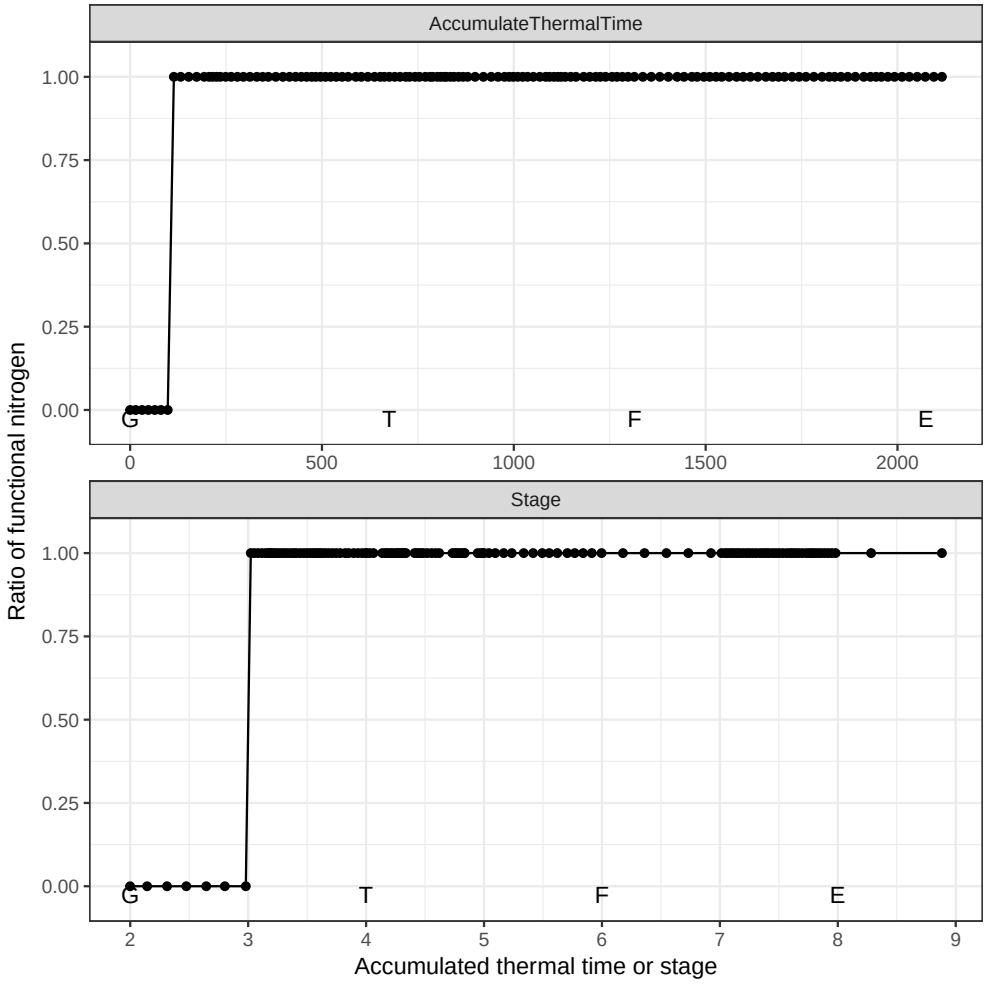

Figure 8.30: Ratio of functional nitrogen

Chapter 9

Spike

`Spike` provides biomass through retranslocation, requires biomass depending on the population and potential spike weight. The biomass is allocated into two components, i..e `Structural` and `Storage`. No `Metabolic` is considered.

9.1 Supply

In `Spike`, the biomass supply only sources from retranslocation (Fig. 9.2). Daily retranslocation is the proportion of current storage ($W_{spike,storage}$). The default value of proportion is 0.5 since `StartGrainFill`, i.e. retranslocatable biomsss is 50% during grain filling (Fig. 9.1).

9.2 Demand

The Structural demand of `Spike` ($D_{spike,structural}$) is determined by the population based demand function since Stage 5 (`FlagLeaf`) to Stage 7 (`StartGrainFill`). The structural demand includes the growth respiration.

$$D_{spike,structural} = \Delta TT \times N_{head} \frac{W_{max,grain}}{T_{growth}} \times F_{spike,structure}/C_{spike,efficiency}$$

where ΔTT is the daily thermal time in the phenology module (Fig. 3.2); N_{head} is the head number per unit area, i.e. stem population (Fig. 4.17); $W_{max,grain}$ is the potential weight per spike (g) with default value 0.5; T_{growth} is the growth duration of spike (TT, the thermal time target from `FlagLeaf` to `StartGrainFill`). As the target of `EarlyReproductive` is sensitive to photoperiod (Section 3.2), the growth duration can be changed during spike development depending on the photoperiod (Fig. 9.3). The head number, growth duration and potential spike weight are defined as potential spike weight including the structural and storage conponents and the growth respiration.

$F_{spike,structure}$ is the structura fraction of `Spike` with default value 0.9 (Fig. 9.4). $C_{spike,efficiency}$ is the conversion efficiency of `Spike`, i.e. the efficiency of alloction biomass converted into structural carbon (growth respiration). $C_{efficiency}$ has the default value 0.7067 (Fig. @(fig:spike-stucture-fraction)) and is counted befor allocation.

Storage demand is to fill the non-structural components (i.e. storage for `Spike`). Current structural biomass and structural demand are used to calculate the potential total biomass of `Spike` (structural plus storage). The difference of potental total biomas and current biomass are the storage demand. Storage demand also include the growth respiration.

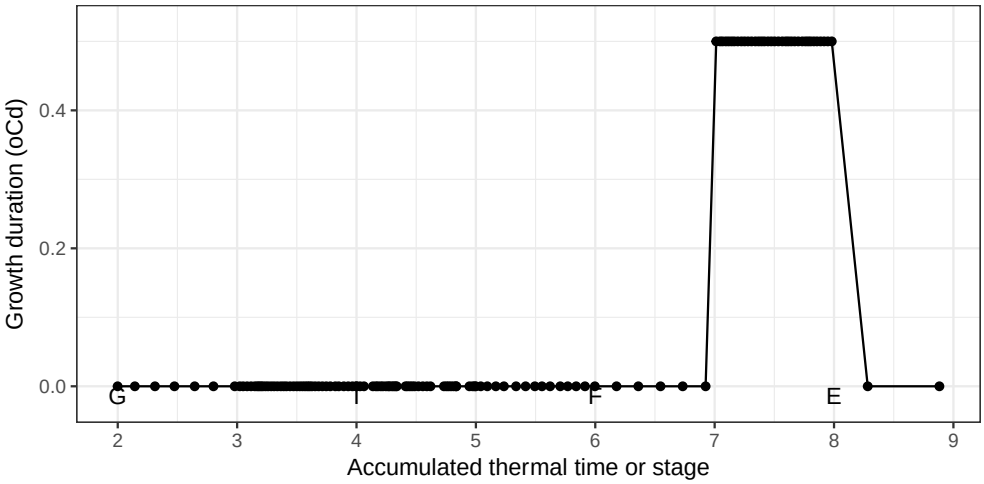

Figure 9.1: Growth duration of spike development

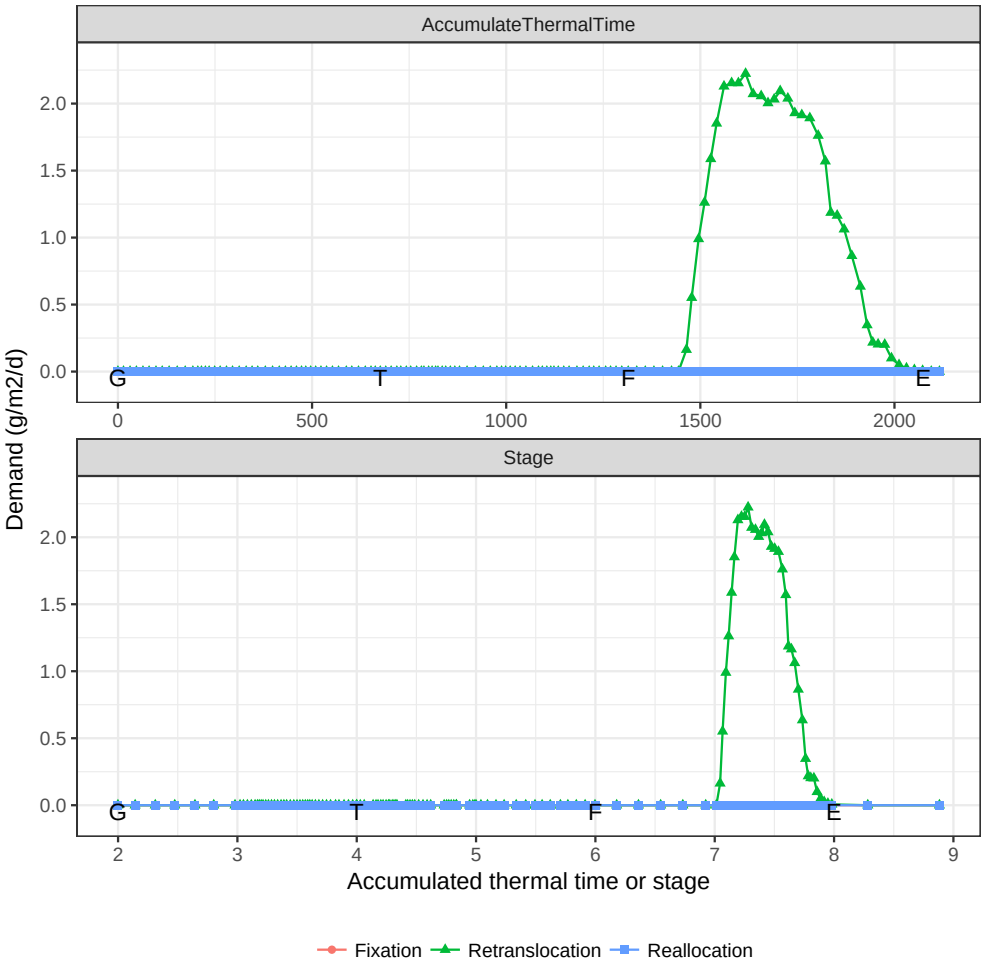

Figure 9.2: Biomass supply from spike

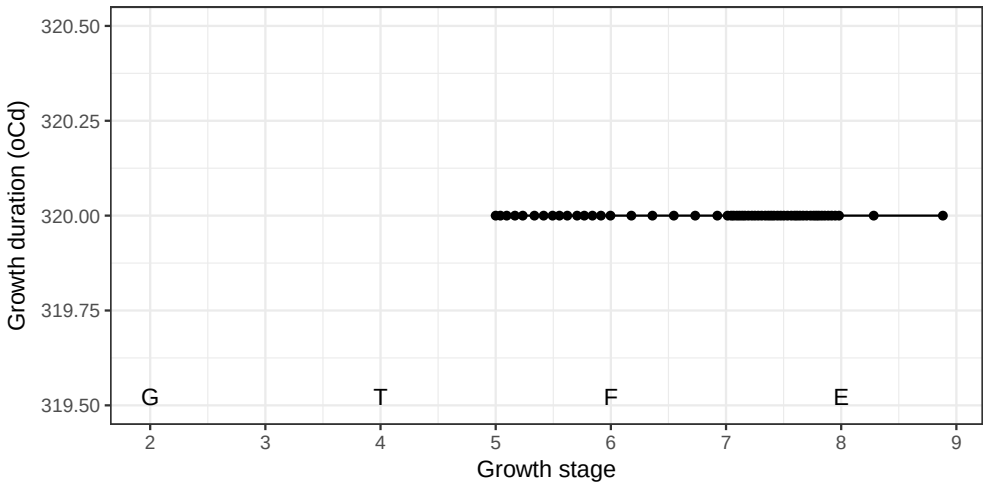

Figure 9.3: Growth duration of spike development

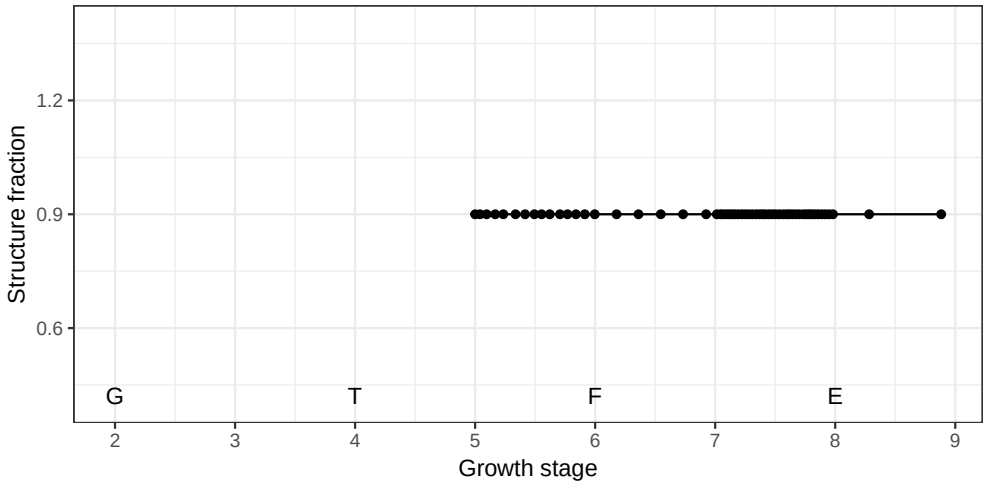

Figure 9.4: Growth duration of spike development

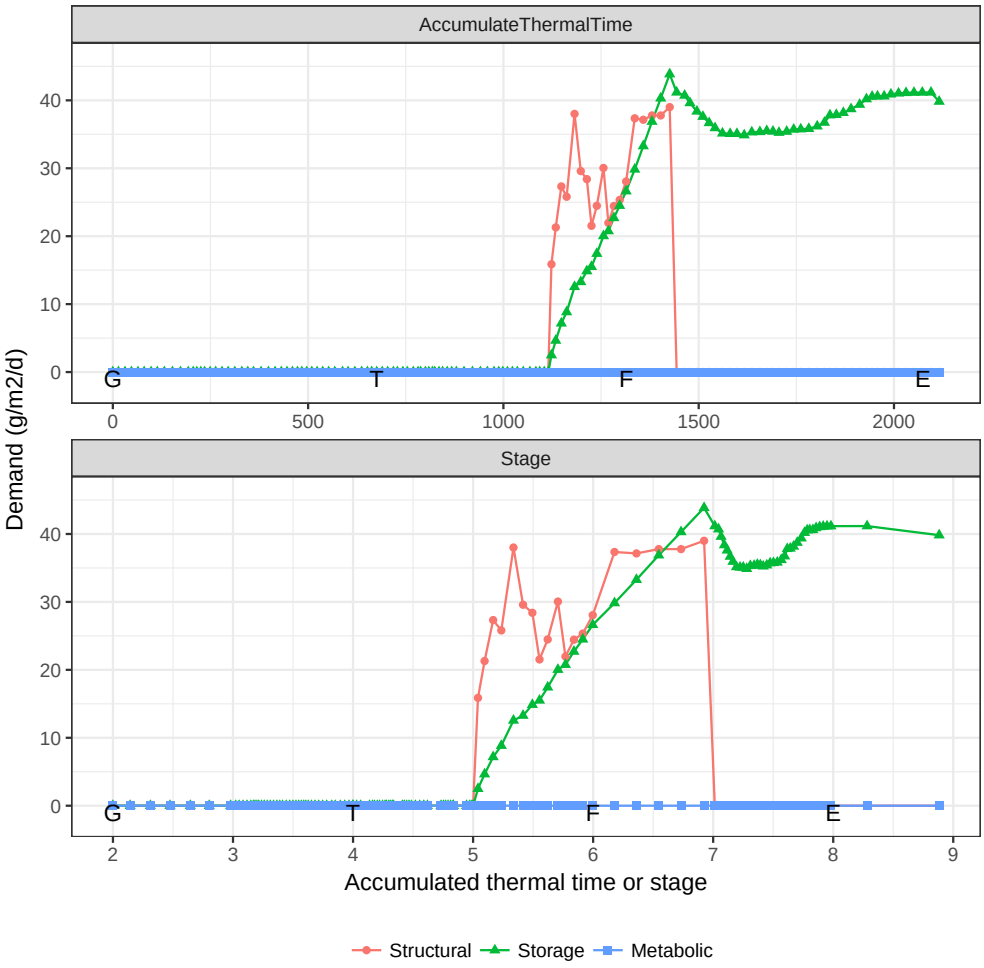

Figure 9.5: Biomass demand by spike

$$D_{spike,storage} = \frac{(W_{spike,structural} + D_{spike,structural})/F_{spike,structure} - W_{spike,structural} + W_{spike,storage} + D_{spike,structural}}{C_{spike,efficiency}}$$

No metabolic demand is calculated for `Spike`.

The figure below shows the demands of `Spike` in the test simulation (Fig. @(fig:spike-demand)).

9.3 Biomass dynamic

The actual allocation reflects the increase of structural component, and retranslocation of storage component (Fig. 9.6). `Spike` only considers the `Live` biomass (Fig. 9.8, no `Dead` biomass (Fig. 9.9).

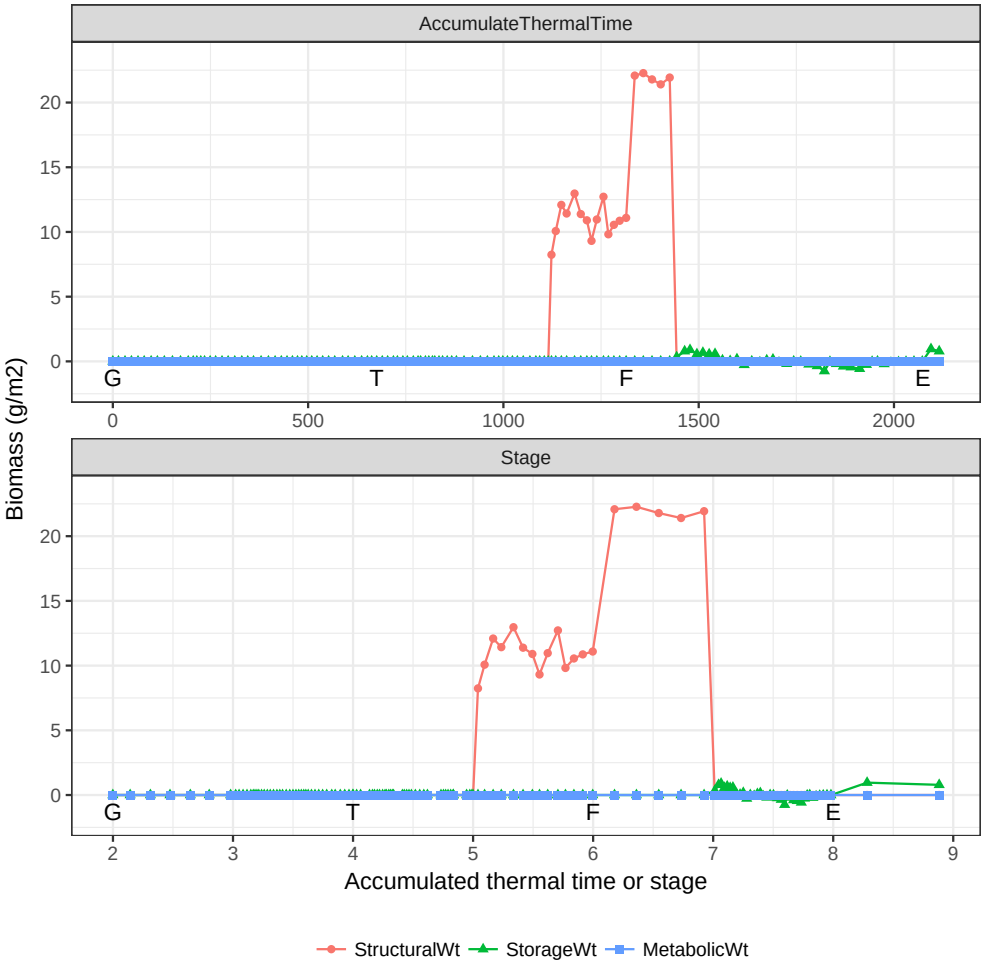

Figure 9.6: Actual allocated biomass for spike

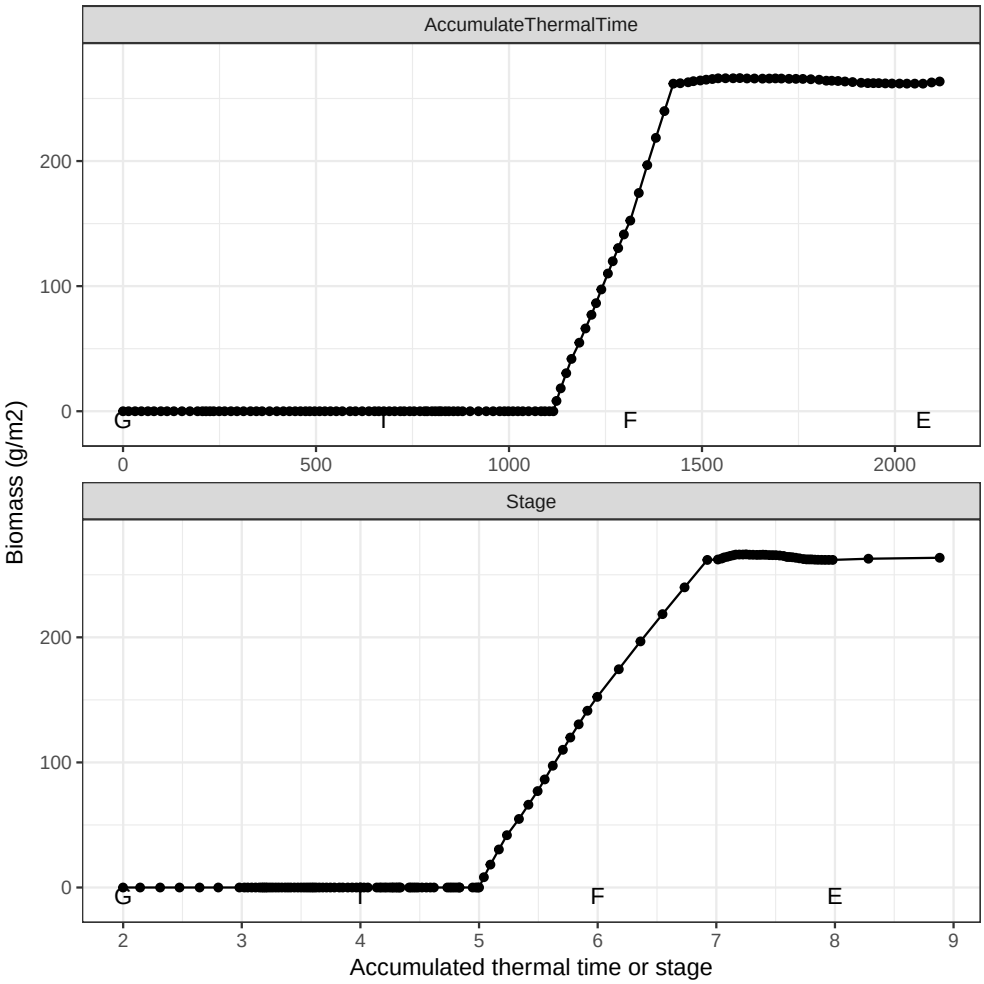

Figure 9.7: Dynamic of spike biomass (Total)

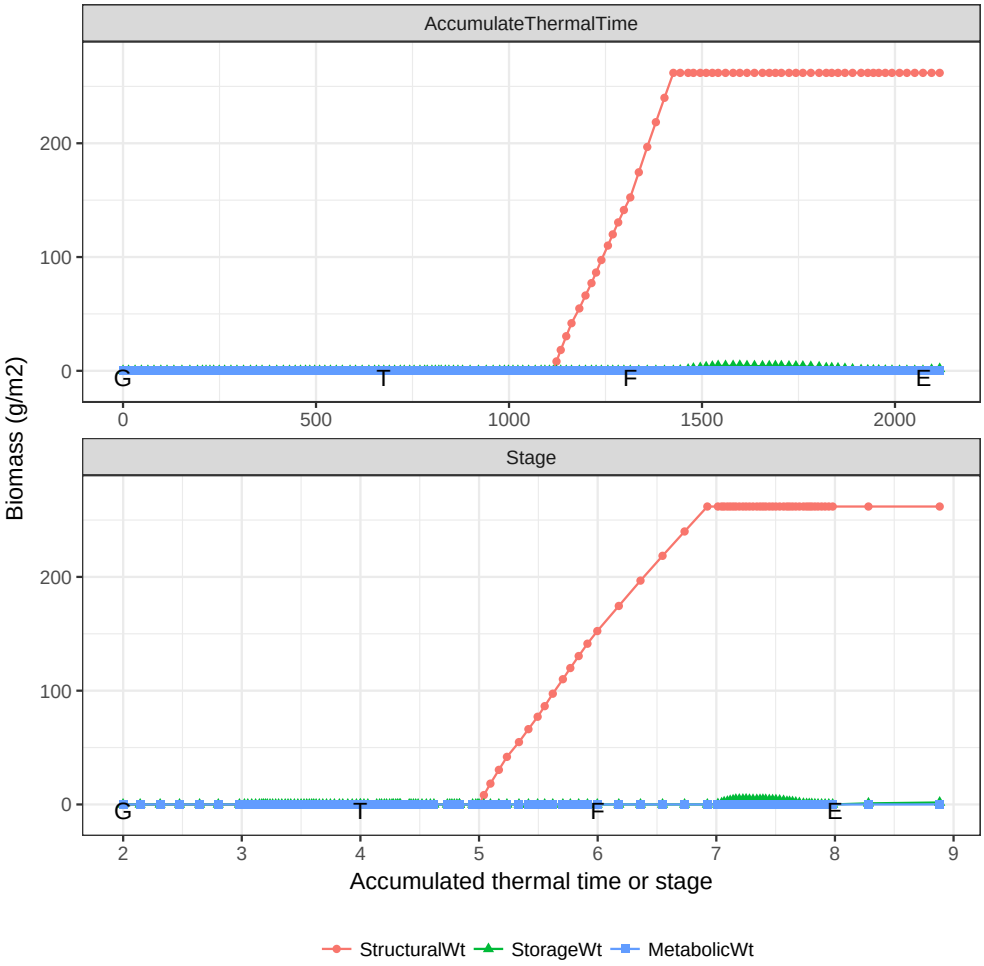

Figure 9.8: Dynamic of spike biomass (Live component)

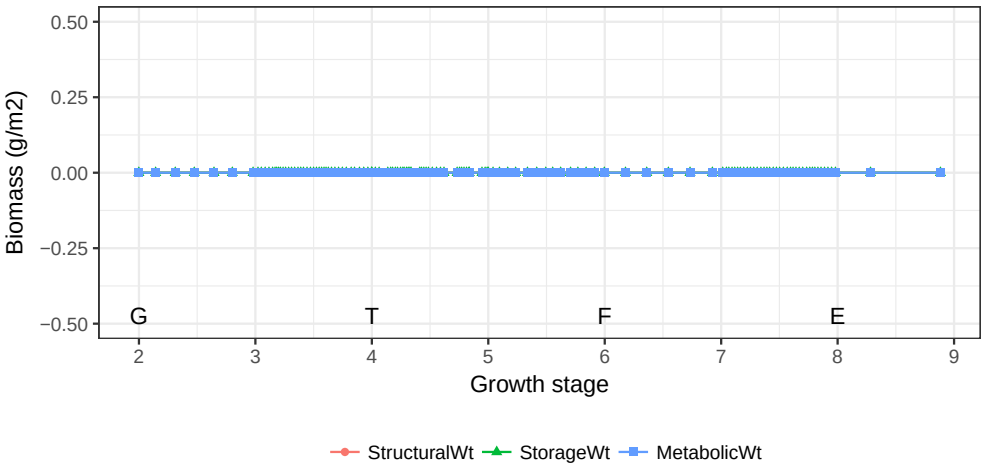

Figure 9.9: Dynamic of spike biomass (Dead component)

Chapter 10

Stem

`Stem` provides biomass through retranslocation, requires biomass a proportion of daily fixation (i.e. photosynthesis in `Leaf`). The biomass is allocated into two components, i..e `Structural` and `Storage`. No `Metabolic` is considered.

10.1 Supply

In `Stem`, the biomass supply only sources from retranslocation (Fig. 10.2). Daily retranslocation is the proportion of current storage ($W_{stem,storage}$). The default value of proportion is 0.5 since `StartGrainFill`, i.e. retranslocatable biomsss is 50% during grain filling (Fig. 10.1).

10.2 Demand

The daily biomass demand of `Stem` is calculated as a fraction of daily fixation (i.e. photosynthesis) from Stage 3 (`Emergence`) to Stage 6 (`Flowering time`) (Fig. 10.3) and increases at Stage 4 (`Terminal spikelet`) (Fig. 10.3). After `Flowering time`, no biomass allocated into stem (Fig. 10.4).

10.3 Biomass dynamic

The actual allocation reflects the increase of structural component, and retranslocation of storage component (Fig. 10.5). `Stem` only considers the `Live` biomass (Fig. 10.7, no `Dead` biomass (Fig. 10.8).

10.4 Water soluble carbohydrate

Water soluble carbohydrates (WSC) are sugars such as fructans, sucrose, glucose and fructose which are accumulated in the stem as reserves.

In APSIM Next Gen, the WSC of stem is defined as the ratio of storage and total weights in the `Live` pool of stem.

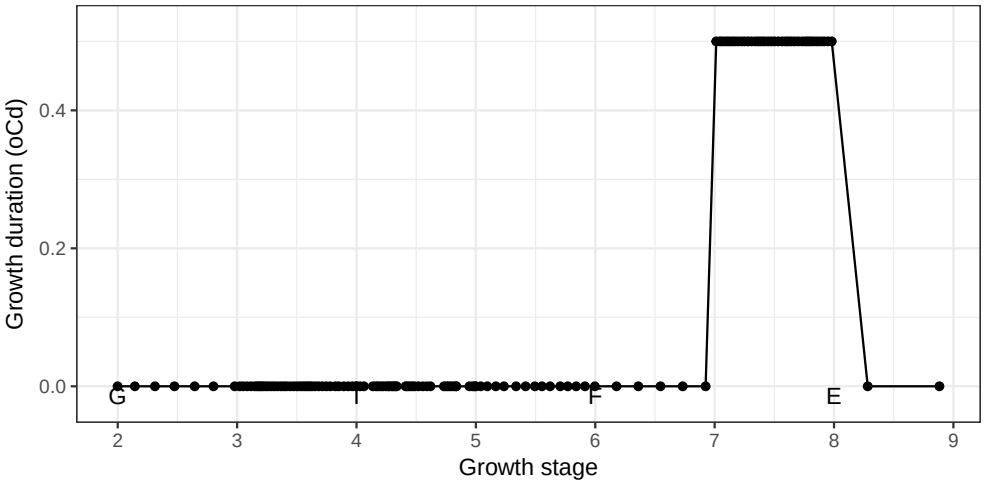

Figure 10.1: Growth duration of stem development

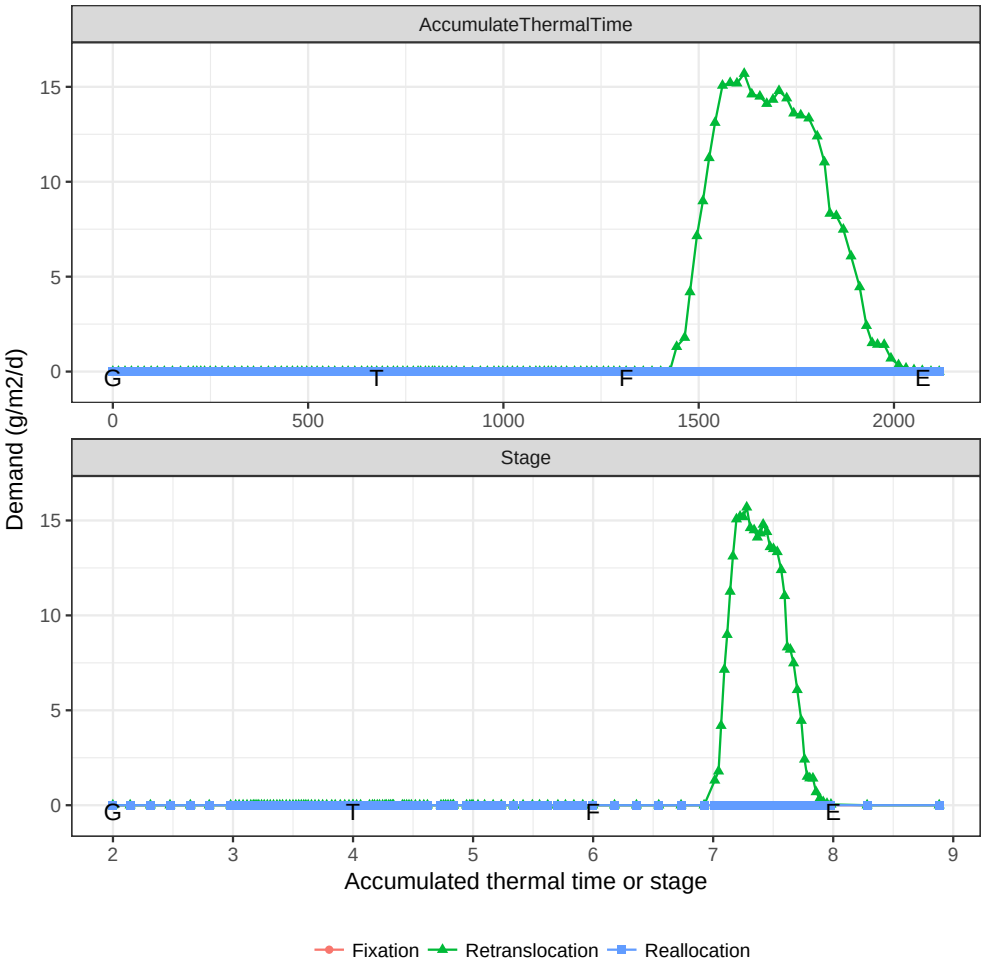

Figure 10.2: Biomass supply from stem

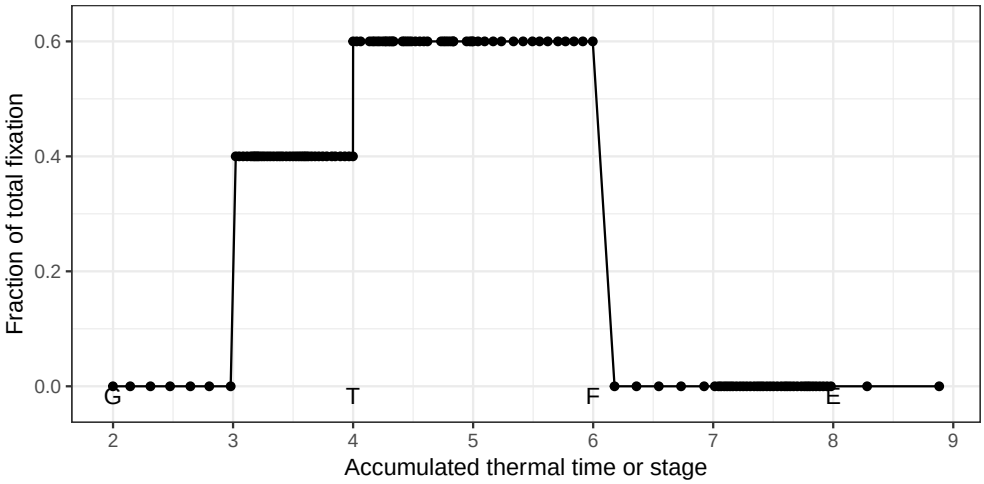

Figure 10.3: Fraction of stem demand in the total fixation

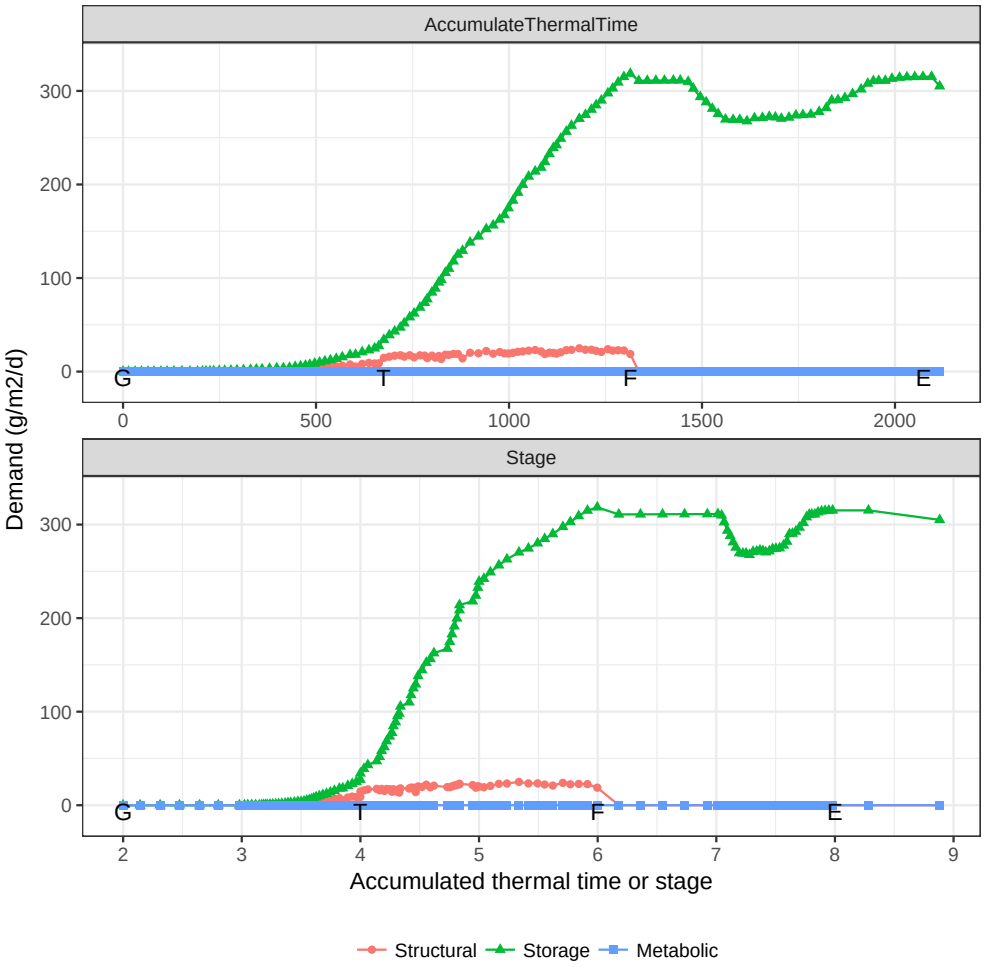

Figure 10.4: Biomass demand by stem

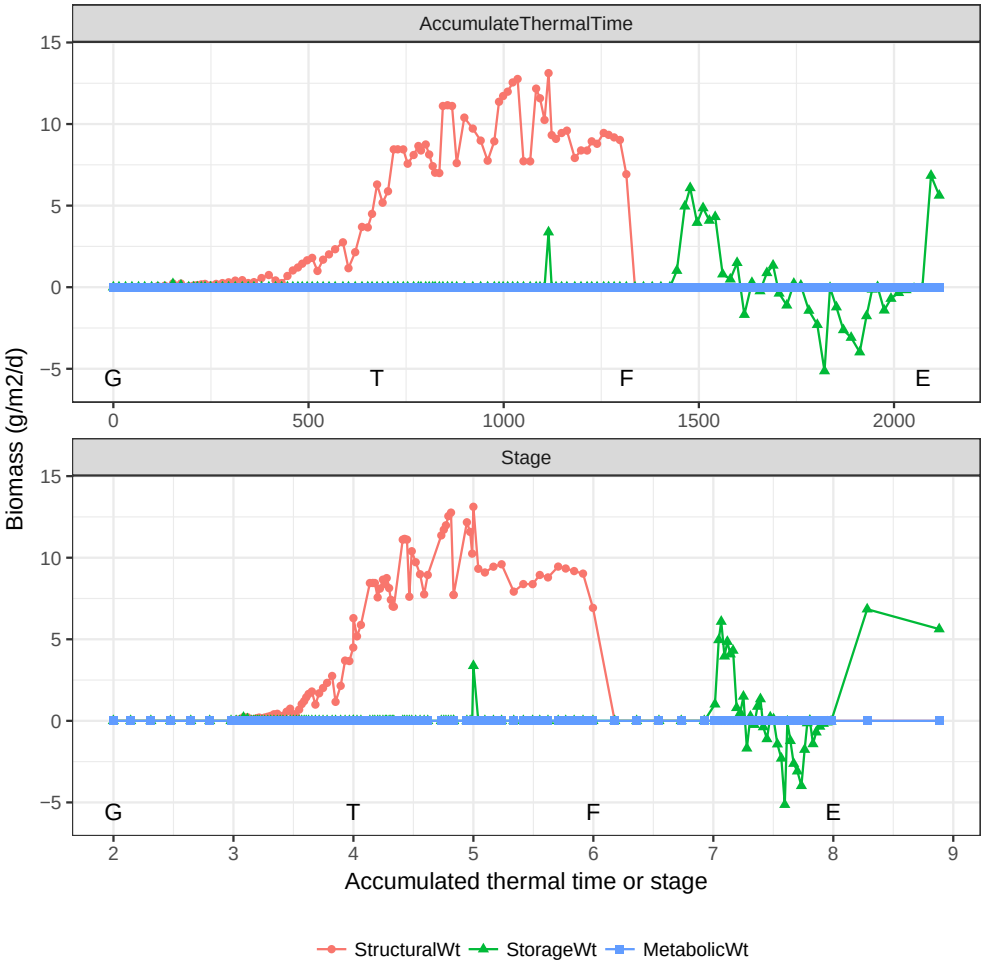

Figure 10.5: Actual allocated biomass for stem

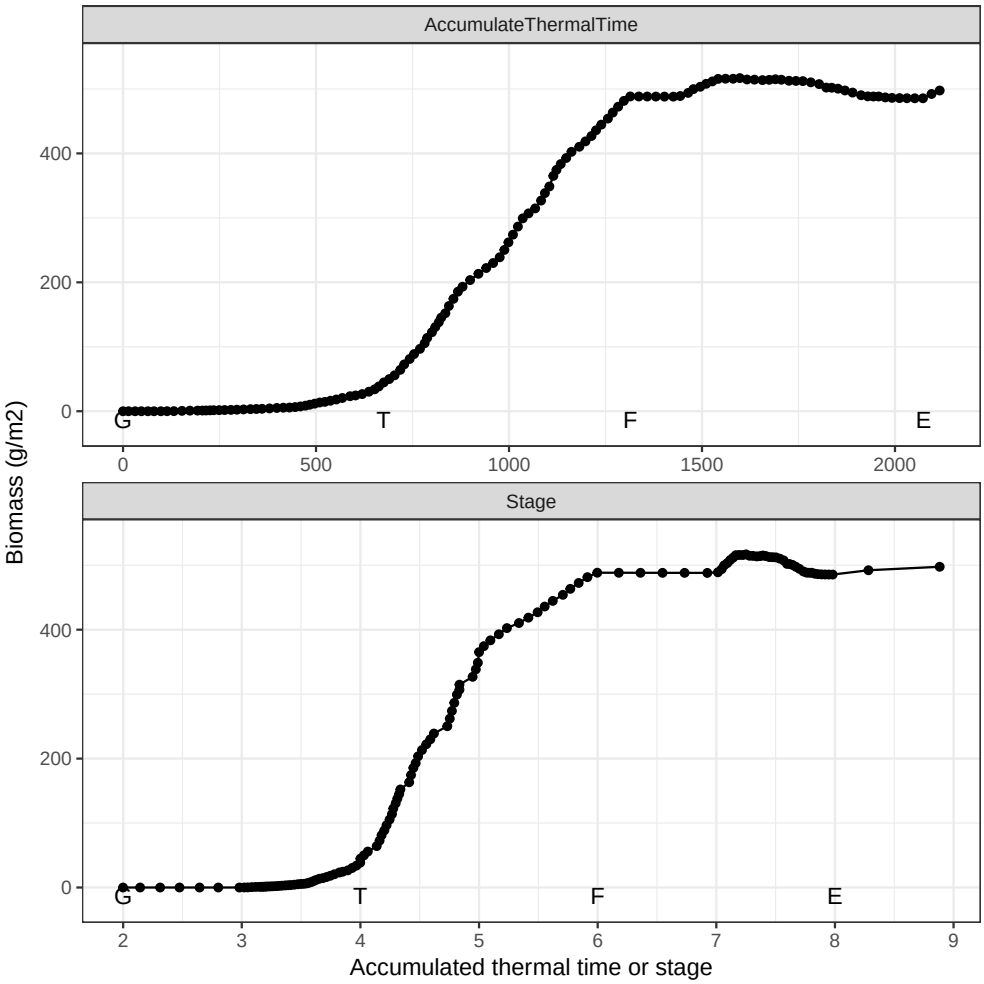

Figure 10.6: Dynamic of stem biomass (Total)

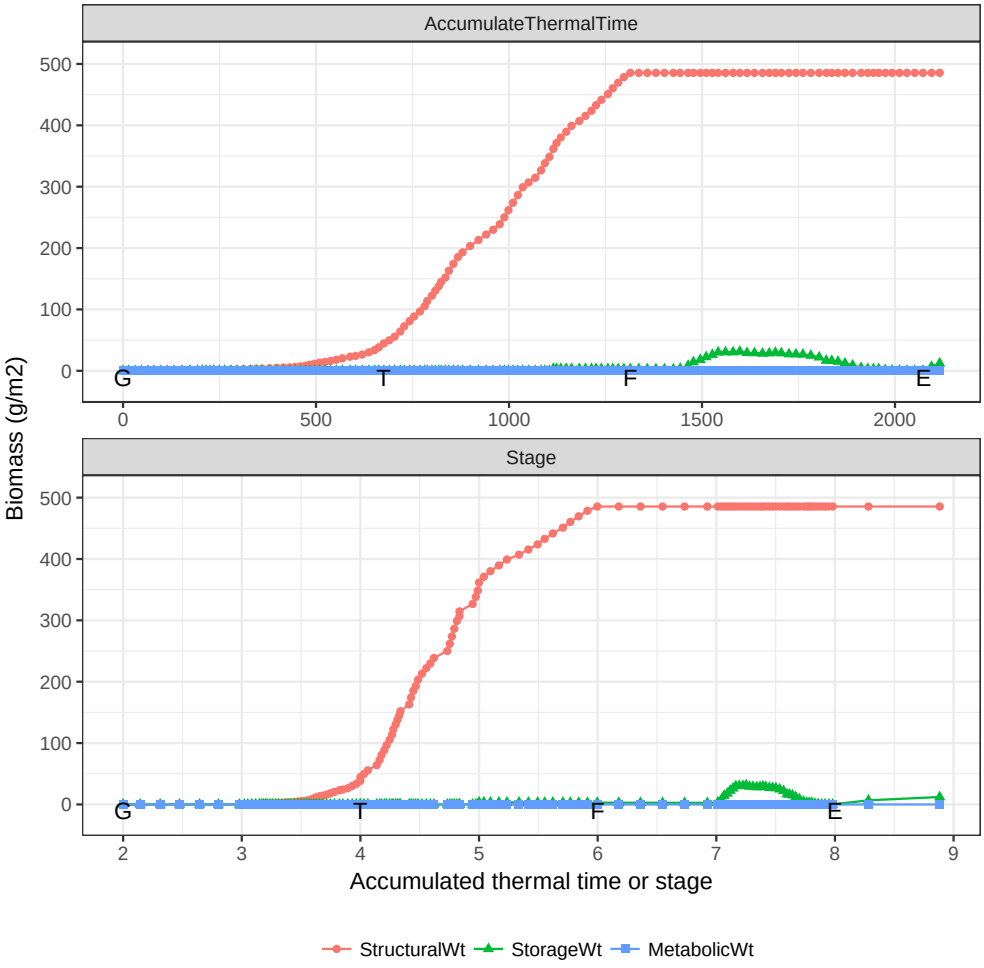

Figure 10.7: Dynamic of stem biomass (Live component)

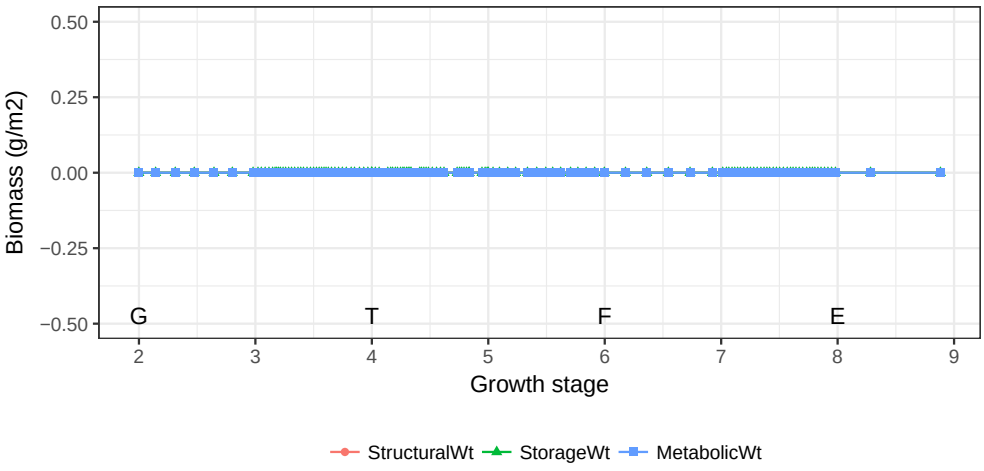

Figure 10.8: Dynamic of stem biomass (Dead component)

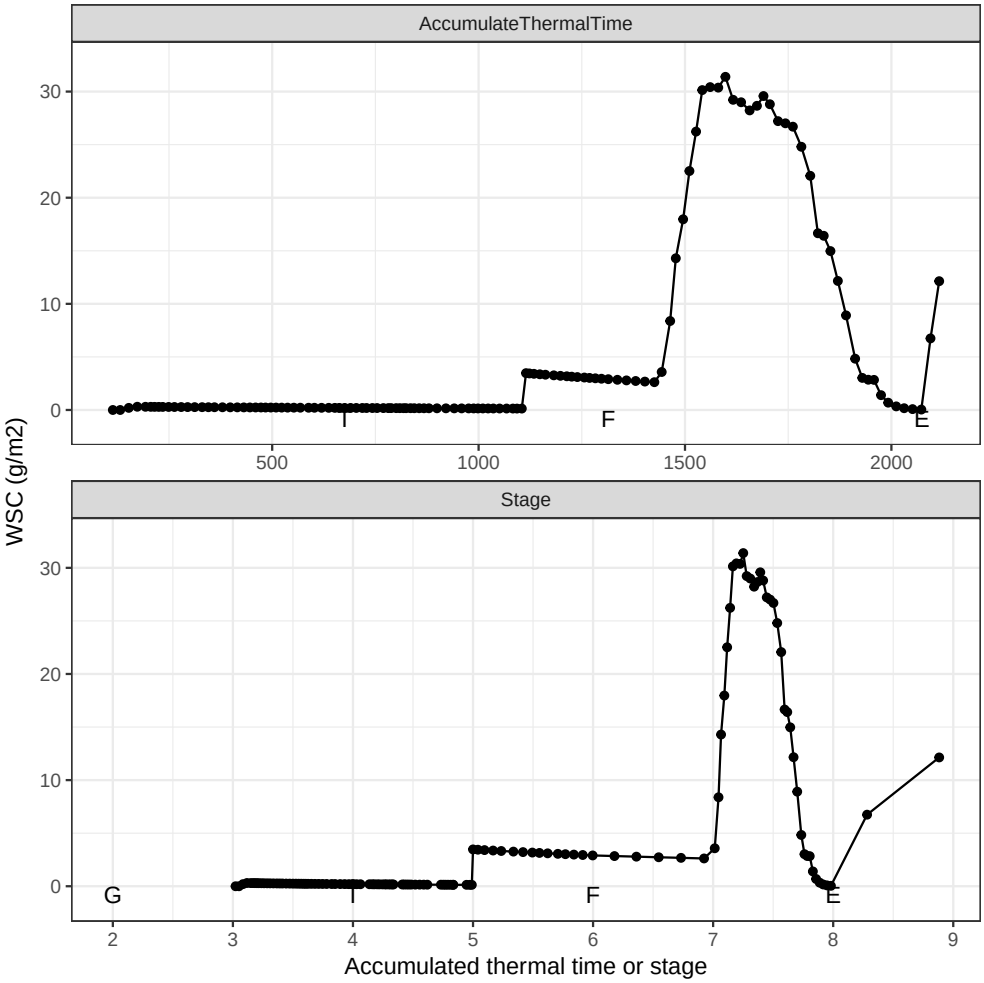

Figure 10.9: Water soluble carbohydrate in stem.

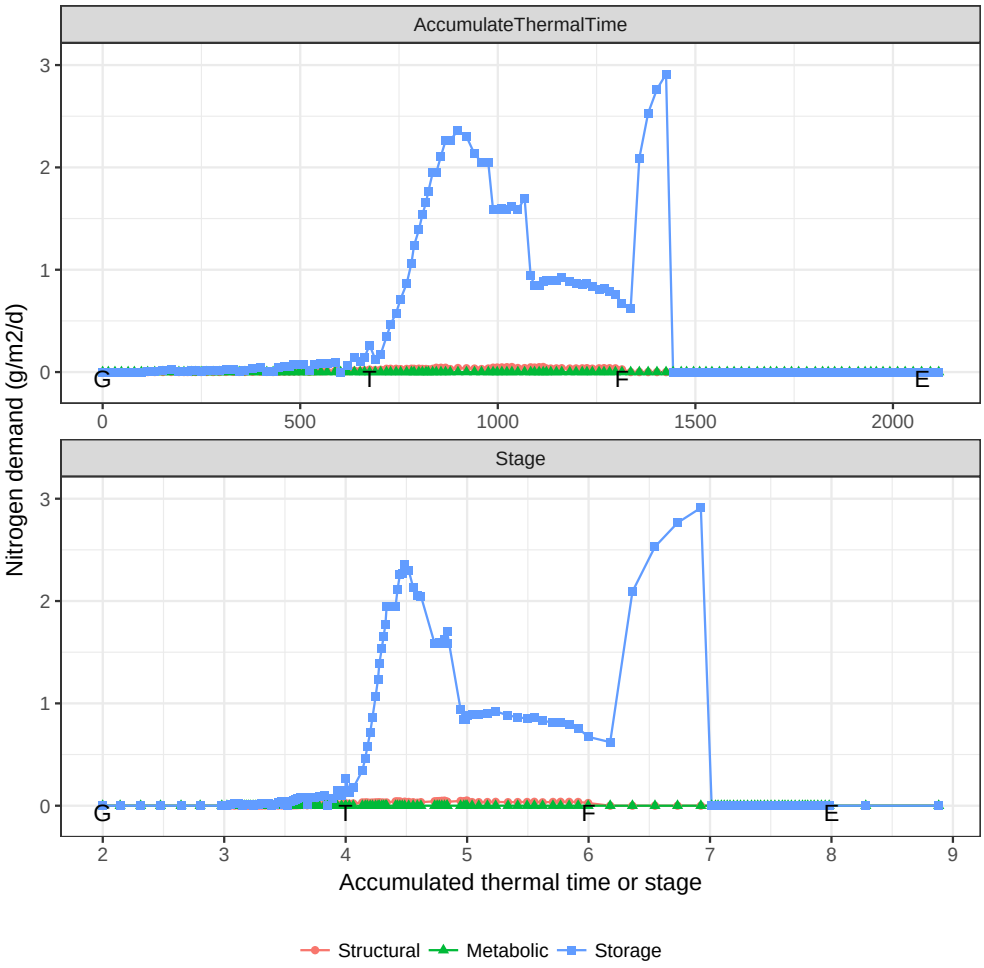

Figure 10.10: The stem nitrogen demand for all components

10.5 Nitrogen

10.5.1 Demand

10.5.2 Supply

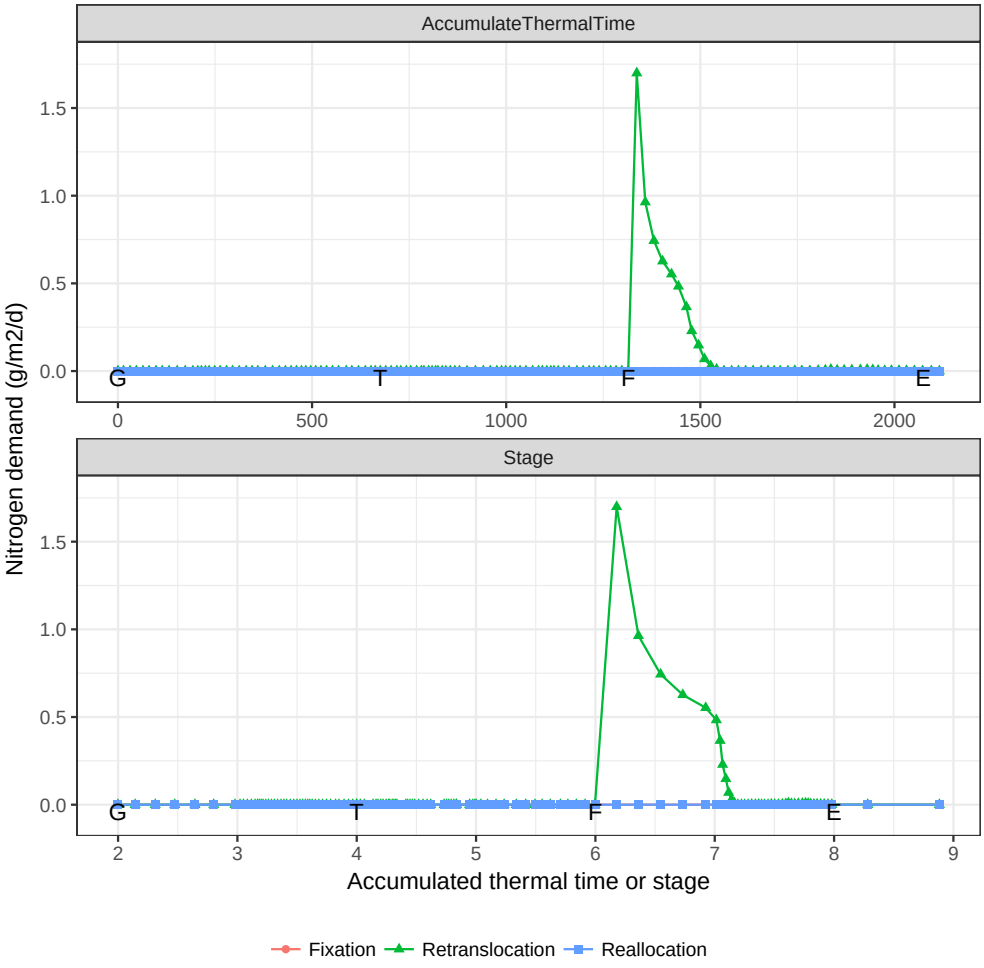

Figure 10.11: The stem nitrogen supply for all components

Chapter 11

Water

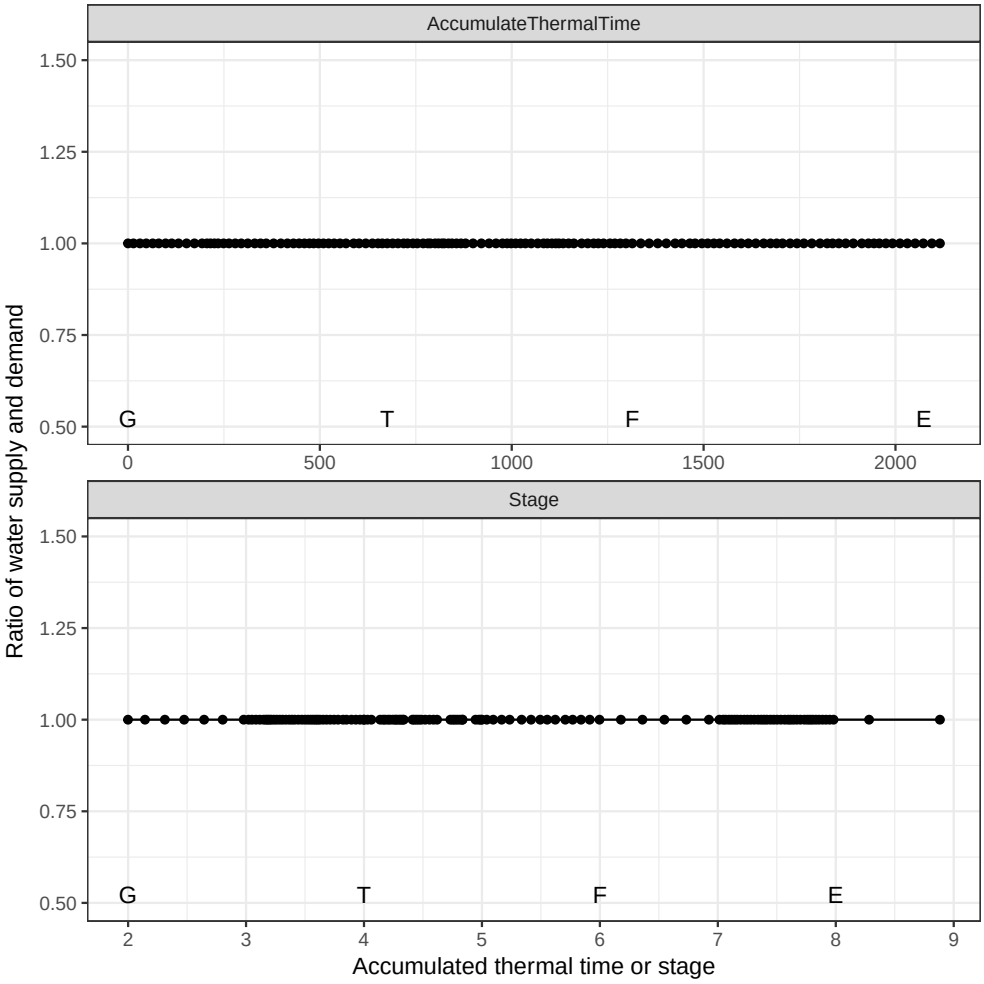

Figure 11.1: Coverage

Chapter 12

Nitrogen

12.1 Demand

12.2 Supply

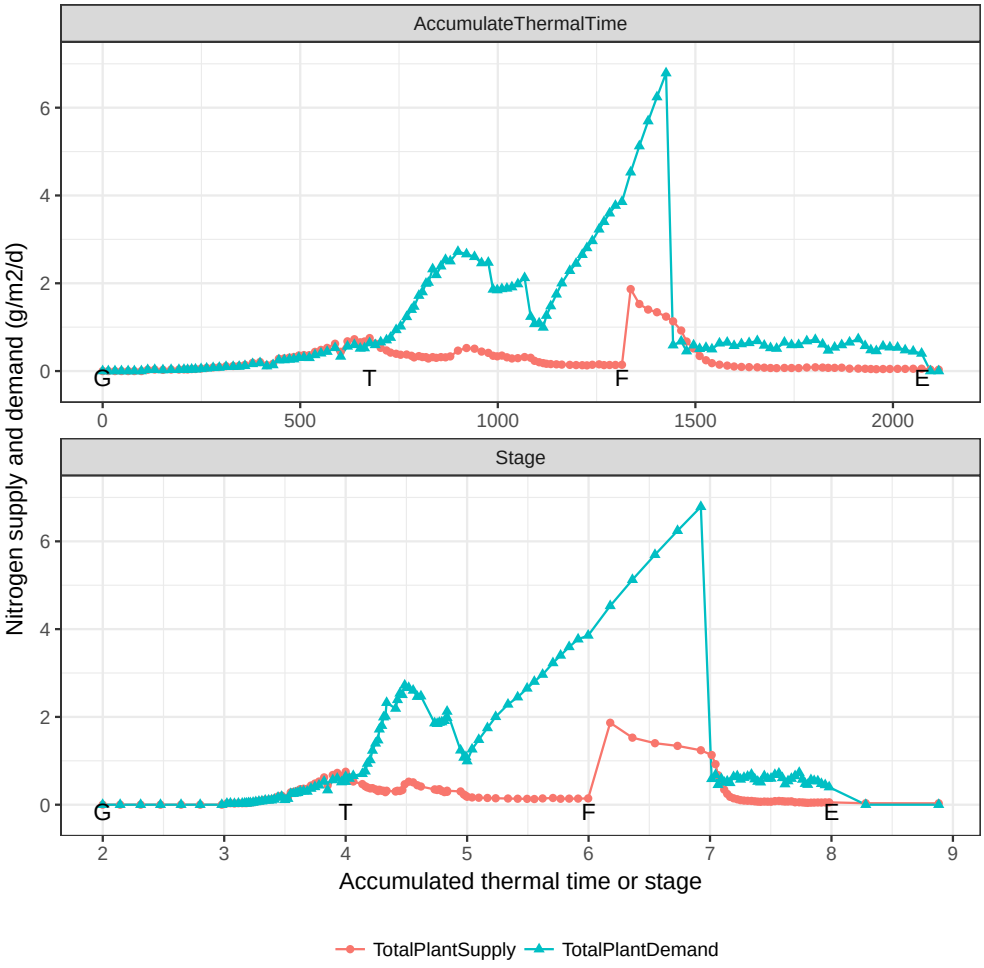

Figure 12.1: The plant total nitrogen demand and supply

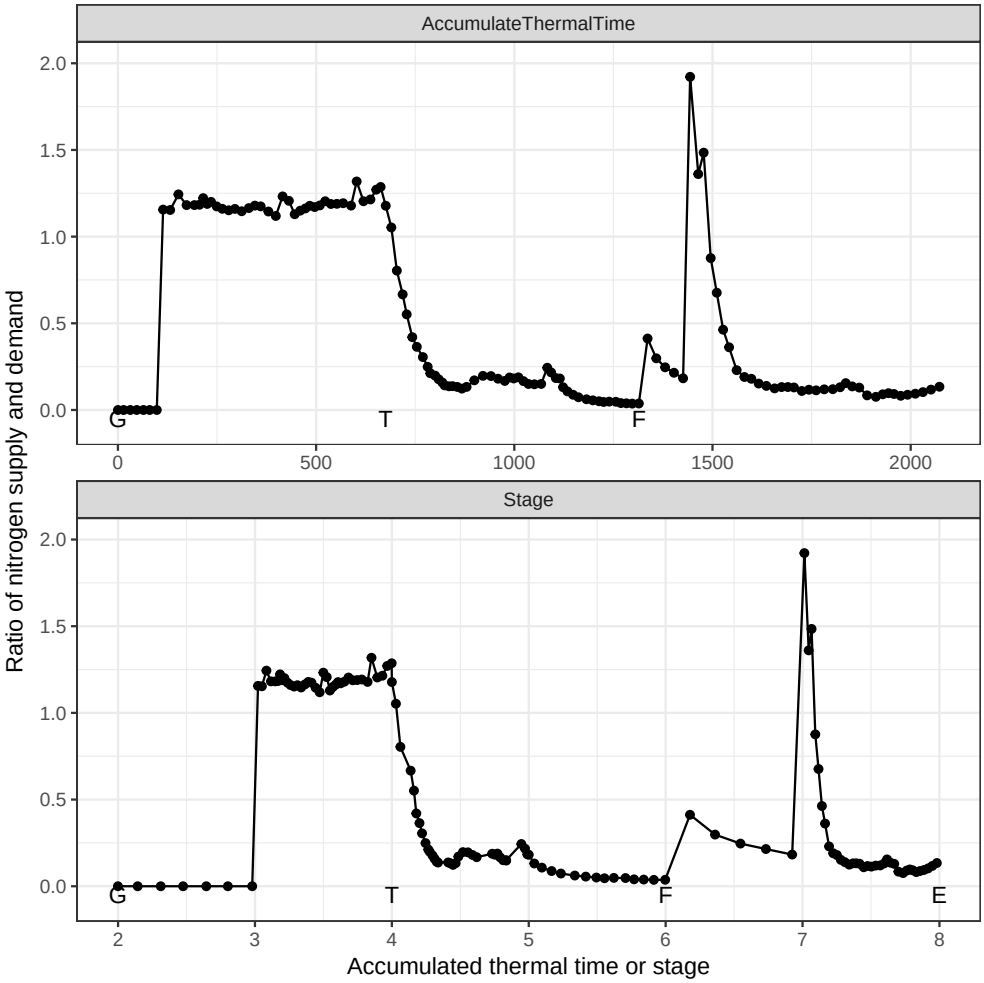

Figure 12.2: The fraction of nitrogen supply relative to nitrogen demand

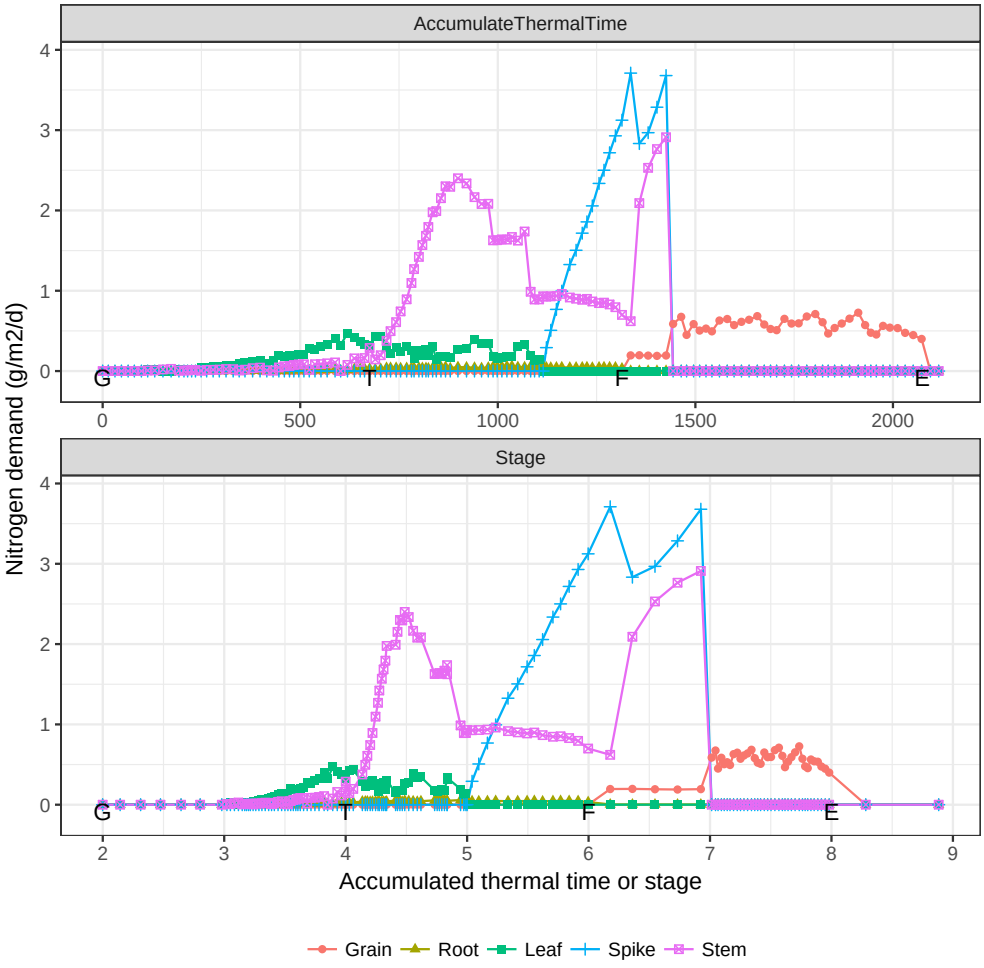

Figure 12.3: The plant nitrogen demand for all organs

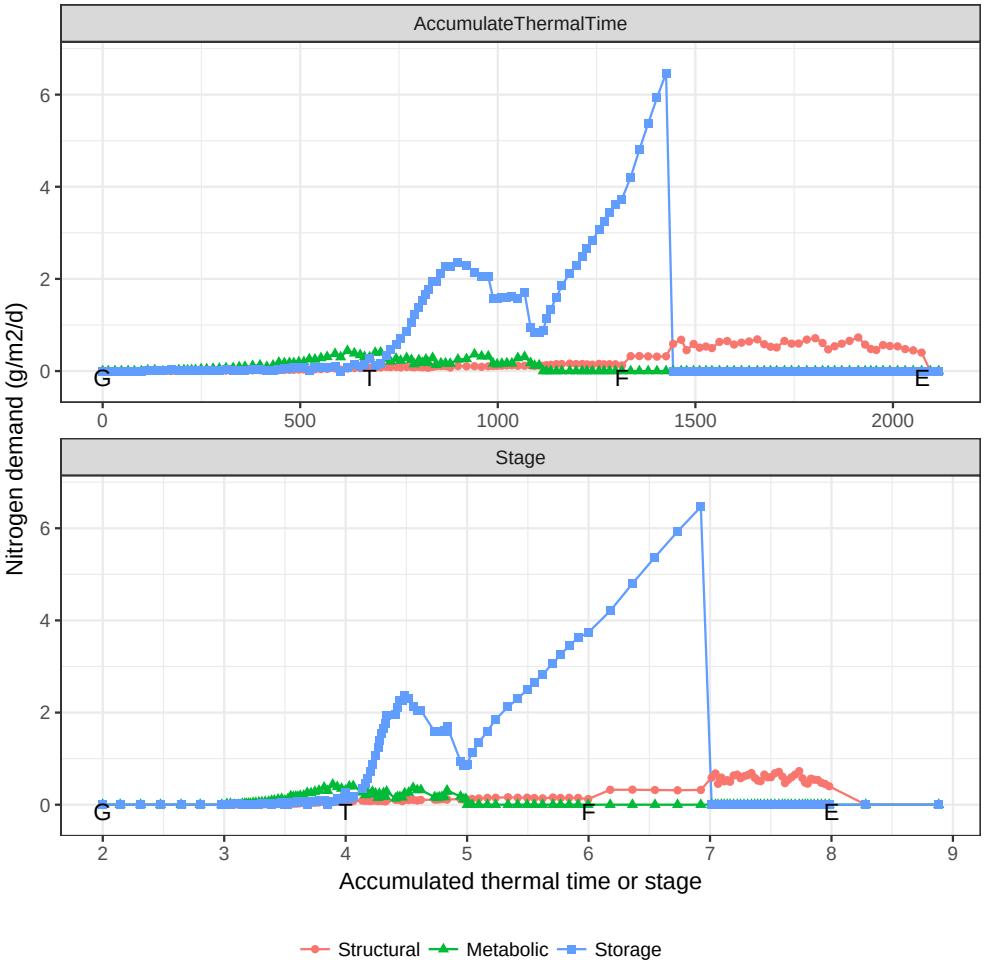

Figure 12.4: The plant nitrogen demand for all components

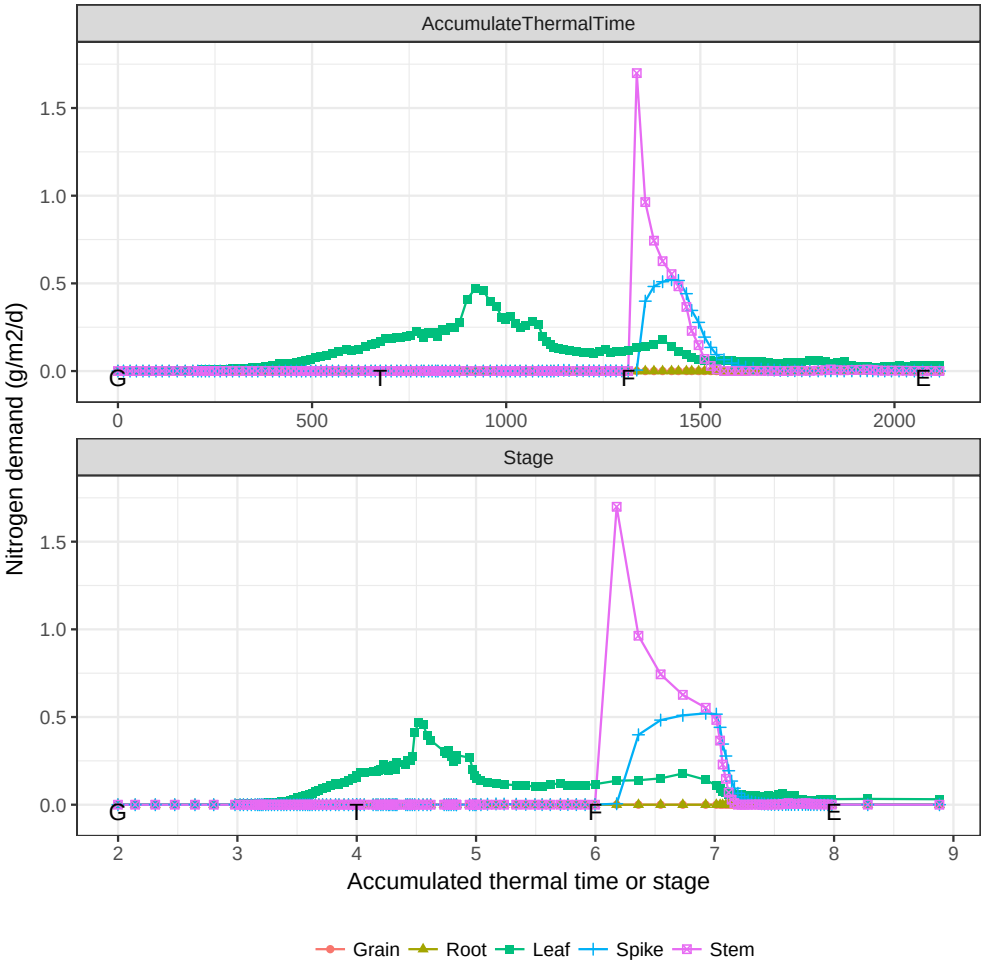

Figure 12.5: The plant nitrogen supply for all organs

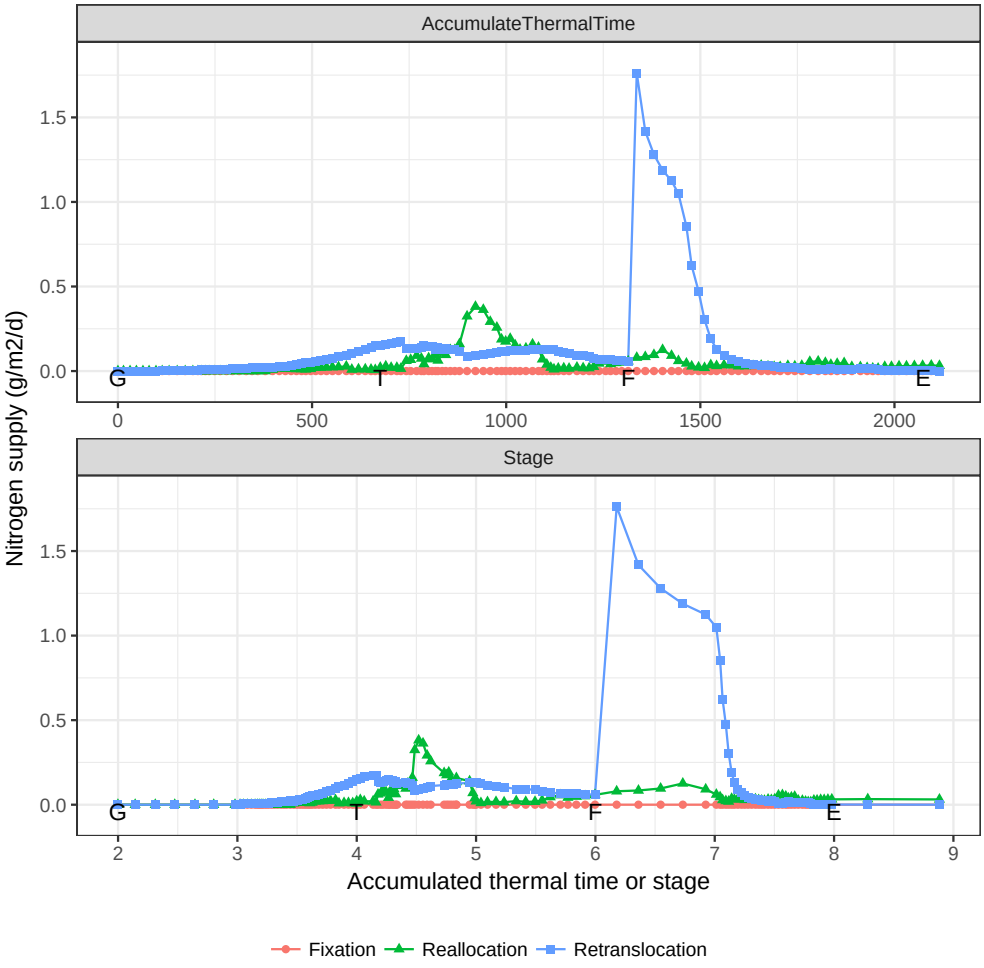

Figure 12.6: The plant nitrogen supply for all components

Chapter 13

Variable

The input and output variables are listed in this chapter and linked to the figures and tables.

13.1 Input

13.2 Output

Table 13.1: The input variables which are used in this documentation. The prefix of 'Wheat.' is removed from all variables.

Input	Reference
Grain.DMConversionEfficiency	Table \@ref(tab:biomass-conversio
Grain.MaintenanceRespirationFunction.MaintenanceFractionAt20C	Table \@ref(tab:biomass-wefunctor
Grain.MaintenanceRespirationFunction.WangEngelTempFunction	Table \@ref(tab:biomass-wefunctor
Leaf.CohortParameters.CellDivisionStress.NitrogenStressEffect	Fig. \@ref(fig:leaf-cell-division-nitr
Leaf.CohortParameters.CellDivisionStress.WaterStressEffect	Fig. \@ref(fig:leaf-cell-division-wat
Leaf.CohortParameters.ExpansionStress.NitrogenStressEffect	Fig. \@ref(fig:leaf-expansion-stress
Leaf.CohortParameters.ExpansionStress.TemperatureEffect	Fig. \@ref(fig:leaf-expansion-stress
Leaf.CohortParameters.ExpansionStress.WaterStressEffect	Fig. \@ref(fig:leaf-expansion-stress
Leaf.CohortParameters.MaxArea.AgeFactor	Fig. \@ref(fig:leaf-maximum-area-a
Leaf.DMConversionEfficiency	Table \@ref(tab:biomass-conversio
Leaf.MaintenanceRespirationFunction.MaintenanceFractionAt20C	Table \@ref(tab:biomass-wefunctor
Leaf.MaintenanceRespirationFunction.WangEngelTempFunction	Table \@ref(tab:biomass-wefunctor
Leaf.Photosynthesis_RUE.FN	Fig. \@ref(fig:leaf-rue-fn)
Leaf.Photosynthesis_RUE.FT	Fig. \@ref(fig:biomass-ft)
Leaf.Photosynthesis_RUE.FW	Fig. \@ref(fig:leaf-rue-fw)
Root.DMConversionEfficiency	Table \@ref(tab:biomass-conversio
Root.MaintenanceRespirationFunction.MaintenanceFractionAt20C	Table \@ref(tab:biomass-wefunctor
Root.MaintenanceRespirationFunction.WangEngelTempFunction	Table \@ref(tab:biomass-wefunctor
Root.RootFrontVelocity.TemperatureFactor	Fig. \@ref(fig:root-front-velocity-te
Root.RootFrontVelocity.WaterFactor	Fig. \@ref(fig:root-front-velocity-w
Spike.DMConversionEfficiency	Table \@ref(tab:biomass-conversio
Spike.MaintenanceRespirationFunction.MaintenanceFractionAt20C	Table \@ref(tab:biomass-wefunctor
Spike.MaintenanceRespirationFunction.WangEngelTempFunction	Table \@ref(tab:biomass-wefunctor
Stem.DMConversionEfficiency	Table \@ref(tab:biomass-conversio
Stem.MaintenanceRespirationFunction.MaintenanceFractionAt20C	Table \@ref(tab:biomass-wefunctor
Stem.MaintenanceRespirationFunction.WangEngelTempFunction	Table \@ref(tab:biomass-wefunctor
Structure.BranchingRate.PotentialBranchingRate.Vegetative.PotentialBranchingRate	Fig. \@ref(fig:str-branching-rate)
Structure.BranchingRate.StressFactors.CoverEffect	Fig. \@ref(fig:str-branching-factor)
Structure.BranchingRate.StressFactors.NitrogenEffect	Fig. \@ref(fig:str-branching-factor)
Structure.BranchingRate.StressFactors.WaterStressEffect	Fig. \@ref(fig:str-branching-factor)
Structure.BranchMortality.MortalityPhase.Mortality.MortalityPerDegDay	Fig. \@ref(fig:str-mortality-growth
Structure.HeightModel.PotentialHeight	Fig. \@ref(fig:str-potential-height)
Structure.HeightModel.WaterStress	Fig. \@ref(fig:str-height-water-stre
Structure.Phyllochron.LeafStageFactor	Fig. \@ref(fig:str-phyllochron-age)
Structure.Phyllochron.PhotoPeriodEffect	Fig. \@ref(fig:str-phyllochron-ppd)

Table 13.2: The output variables which are used in this documentation. The prefix of 'Wheat.' is removed from all variables.

Output	Reference
Arbitrator.FN	Fig. \@ref(fig:nitrogen-fn)
Arbitrator.N.TotalPlantDemand	Fig. \@ref(fig:nitrogen-demand-supply)
Arbitrator.N.TotalPlantSupply	Fig. \@ref(fig:nitrogen-demand-supply)
DMDemand.SM.Grain	Fig. \@ref(fig:biomass-demand-organ)
DMDemand.SM.Leaf	Fig. \@ref(fig:biomass-demand-organ)
DMDemand.SM.Root	Fig. \@ref(fig:biomass-demand-organ)
DMDemand.SM.Spike	Fig. \@ref(fig:biomass-demand-organ)
DMDemand.SM.Stem	Fig. \@ref(fig:biomass-demand-organ)
DMDemand.Storage	Fig. \@ref(fig:biomass-supply-demand-sto)
DMDemand.StructuralMetabolic	Fig. \@ref(fig:biomass-supply-demand-str-met)
DMSupply	Fig. \@ref(fig:biomass-supply-total), \@ref(fig:biomass-supply-
Grain.Allocated.MetabolicWt	Fig. \@ref(fig:biomass-allocated-metabolic), \@ref(fig:grain-all
Grain.Allocated.StorageWt	Fig. \@ref(fig:biomass-allocated-storage), \@ref(fig:grain-alloca
Grain.Allocated.StructuralWt	Fig. \@ref(fig:biomass-allocated-structural), \@ref(fig:grain-all
Grain.Dead.MetabolicWt	Fig. \@ref(fig:grain-dead)
Grain.Dead.StorageWt	Fig. \@ref(fig:grain-dead)
Grain.Dead.StructuralWt	Fig. \@ref(fig:grain-dead)
Grain.DeadWt	Fig. \@ref(fig:biomass-dead-weight)
Grain.DMDemand.Metabolic	Fig. \@ref(fig:biomass-demand-metabolic), \@ref(fig:grain-dem
Grain.DMDemand.Storage	Fig. \@ref(fig:biomass-demand-storage), \@ref(fig:grain-deman
Grain.DMDemand.Structural	Fig. \@ref(fig:biomass-demand-structural), \@ref(fig:grain-dem
Grain.DMSupply.Fixation	Fig. \@ref(fig:biomass-supply-fixation), \@ref(fig:grain-supply)
Grain.DMSupply.Reallocation	Fig. \@ref(fig:biomass-supply-reallocation), \@ref(fig:grain-sup
Grain.DMSupply.Retranslocation	Fig. \@ref(fig:biomass-supply-retranslocation), \@ref(fig:grain-
Grain.GrowthRespiration	Fig. \@ref(fig:biomass-growth-respiration)
Grain.Live.MetabolicWt	Fig. \@ref(fig:grain-live)
Grain.Live.StorageWt	Fig. \@ref(fig:grain-live)
Grain.Live.StructuralWt	Fig. \@ref(fig:grain-live)
Grain.LiveWt	Fig. \@ref(fig:biomass-live-weight)
Grain.MaintenanceRespiration	Fig. \@ref(fig:biomass-maintenance-respiration)
Grain.MaintenanceRespirationFunction	Fig. \@ref(fig:biomass-maintenance-respiration-fraction)
Grain.NDemand.Total	Fig. \@ref(fig:nitrogen-demand-organ)
Grain.NSupply.Total	Fig. \@ref(fig:nitrogen-supply-organ)
GrainWt	Fig. \@ref(fig:grain-weight)
GrowthRespiration	Fig. \@ref(fig:biomass-denstiny)
Leaf.Allocated.MetabolicWt	Fig. \@ref(fig:biomass-allocated-metabolic), \@ref(fig:leaf-alloc
Leaf.Allocated.StorageWt	Fig. \@ref(fig:biomass-allocated-storage), \@ref(fig:leaf-allocat
Leaf.Allocated.StructuralWt	Fig. \@ref(fig:biomass-allocated-structural), \@ref(fig:leaf-alloc
Leaf.AppearedCohortNo	Fig. \@ref(fig:leaf-cohort-number)
Leaf.CohortParameters.CellDivisionStress	Fig. \@ref(fig:leaf-cell-division-daily)
Leaf.CohortParameters.CriticalNConc	Fig. \@ref(fig:leaf-nconc)
Leaf.CohortParameters.ExpansionStress	Fig. \@ref(fig:leaf-expansion-daily)
Leaf.CohortParameters.GrowthDuration	Fig. \@ref(fig:leaf-duration)
Leaf.CohortParameters.LagDuration	Fig. \@ref(fig:leaf-duration)
Leaf.CohortParameters.MaxArea	Fig. \@ref(fig:leaf-maximum-area)
Leaf.CohortParameters.MaximumNConc	Fig. \@ref(fig:leaf-nconc)
Leaf.CohortParameters.MinimumNConc	Fig. \@ref(fig:leaf-nconc)
Leaf.CohortParameters.SenescenceDuration	Fig. \@ref(fig:leaf-duration)
Leaf.CohortParameters.SpecificLeafAreaMax	Fig. \@ref(fig:leaf-sla)
Leaf.CohortParameters.SpecificLeafAreaMin	Fig. \@ref(fig:leaf-sla)
Leaf.CoverDead	Fig. \@ref(fig:leaf-cover)
Leaf.CoverGreen	Fig. \@ref(fig:leaf-cover)
Leaf.CoverTotal	Fig. \@ref(fig:leaf-cover)
Leaf.Dead.MetabolicWt	Fig. \@ref(fig:leaf-dead)

Chapter 14

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