



1 The APSIM Canola Model

1.1 The APSIM Canola Model

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

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

1.2 Plant Model Components

| Component Name | Component Type |
|-------------------|-------------------------------------|
| Arbitrator | Models.PMF.OrganArbitrator |
| Phenology | Models.PMF.Phen.Phenology |
| Root | Models.PMF.Organs.Root |
| Leaf | Models.PMF.Organs.SimpleLeaf |
| Grain | Models.PMF.Organs.ReproductiveOrgan |
| Stem | Models.PMF.Organs.GenericOrgan |
| Shell | Models.PMF.Organs.GenericOrgan |
| MortalityRate | Models.Functions.Constant |
| SeedMortalityRate | Models.Functions.Constant |

1.3 Composite Biomass

| Component Name | Component Type |
|-----------------|-----------------------------|
| Pod | Models.PMF.CompositeBiomass |
| AboveGround | Models.PMF.CompositeBiomass |
| AboveGroundLive | Models.PMF.CompositeBiomass |
| BelowGround | Models.PMF.CompositeBiomass |
| Total | Models.PMF.CompositeBiomass |
| TotalLive | Models.PMF.CompositeBiomass |
| TotalDead | Models.PMF.CompositeBiomass |

1.4 Cultivars

| Cultivar Name | Alternative Name(s) |
|---------------|---------------------|
| GenericWinter | GenericWinter |

| Cultivar Name | Alternative Name(s) |
|----------------------|----------------------------|
| GenericEarly | GenericEarly |
| GenericLate | GenericLate |
| 43C80_CL | 43C80_CL |
| 44Y84_CL | 44Y84_CL |
| 44Y87_CL | 44Y87_CL |
| 44Y89_CL | 44Y89_CL |
| 44Y90_CL | 44Y90_CL |
| 45Y25_RR | 45Y25_RR |
| 45Y86_CL | 45Y86_CL |
| 45Y88_CL | 45Y88_CL |
| 45Y91_CL | 45Y91_CL |
| 46Y78 | 46Y78 |
| Arazzo | Arazzo |
| Archer | Archer |
| ATR_Bonito | ATR_Bonito |
| ATR_Gem | ATR_Gem |
| ATR_Marlin | ATR_Marlin |
| ATR_Stingray | ATR_Stingray |
| ATR_Wahoo | ATR_Wahoo |
| Crusher_TT | Crusher_TT |
| AV_Garnet | AV_Garnet |
| AV_Zircon | AV_Zircon |
| CB_Taurus | CB_Taurus |
| CB_Telfer | CB_Telfer |
| CBI_306 | CBI_306 |
| CSCH_01 | CSCH_01 |
| CSCH_02 | CSCH_02 |
| Drum_triazine | Drum_triazine |
| Dunkeld | Dunkeld |
| Grouse | Grouse |
| GT50_RR | GT50_RR |
| Hyola42 | Hyola42 |
| Hyola450_TT | Hyola450_TT |
| Hyola559_TT | Hyola559_TT |

| Cultivar Name | Alternative Name(s) |
|-------------------|-----------------------------|
| Hyola575_CL | Hyola575_CL,Hyola_575_CL_GT |
| Hyola577_CL | Hyola577_CL |
| Hyola600_RR | Hyola600_RR |
| Hyola635_CL | Hyola635_CL |
| Hyola650_TT | Hyola650_TT |
| Hyola725_RT | Hyola725_RT |
| Hyola750_TT | Hyola750_TT |
| Hyola970_CL | Hyola970_CL |
| Hyola971_CL | Hyola971_CL |
| IH30_RR | IH30_RR |
| IVT4510 | IVT4510 |
| K50055 | K50055 |
| K50058 | K50058 |
| Karoo_triazine | Karoo_triazine |
| Monty | Monty |
| NS_Diamond | NS_Diamond |
| NX953 | NX953 |
| Oscar | Oscar |
| Pinnacle_triazine | Pinnacle_triazine,Pinnacle |
| Range | Range |
| Sensation | Sensation |
| SF_Brazzil | SF_Brazzil |
| SF_Edimax | SF_Edimax |
| Victory_7001_CL | Victory_7001_CL |

1.5 Child Components

1.5.1 Arbitrator

The Arbitrator class determines the allocation of dry matter (DM) and Nitrogen between each of the organs in the crop model. Each organ can have up to three different pools of biomass:

- * **Structural biomass** which is essential for growth and remains within the organ once it is allocated there.
- * **Metabolic biomass** which generally remains within an organ but is able to be re allocated when the organ senesces and may be retranslocated when demand is high relative to supply.
- * **Storage biomass** which is partitioned to organs when supply is high relative to demand and is available for retranslocation to other organs whenever supply from uptake, fixation, or re allocation is lower than demand.

The process followed for biomass arbitration is shown in the figure below. Arbitration calculations are triggered by a series of events (shown below) that are raised every day. For these calculations, at each step the Arbitrator exchange information with each organ, so the basic computations of demand and supply are done at the organ level, using their specific parameters.

1. **doPotentialPlantGrowth**. When this event occurs, each organ class executes code to determine their potential

growth, biomass supplies and demands. In addition to demands for structural, non structural and metabolic biomass (DM and N) each organ may have the following biomass supplies:

- * **Fixation supply.** From photosynthesis (DM) or symbiotic fixation (N)
- * **Uptake supply.** Typically uptake of N from the soil by the roots but could also be uptake by other organs (eg foliage application of N).
- * **Retranslocation supply.** Storage biomass that may be moved from organs to meet demands of other organs.
- * **Reallocation supply.** Biomass that can be moved from senescing organs to meet the demands of other organs.

1. **doPotentialPlantPartitioning.** On this event the Arbitrator first executes the DoDMSetup() method to gather the DM supplies and demands from each organ, these values are computed at the organ level. It then executes the DoPotentialDMAAllocation() method which works out how much biomass each organ would be allocated assuming N supply is not limiting and sends these allocations to the organs. Each organ then uses their potential DM allocation to determine their N demand (how much N is needed to produce that much DM) and the arbitrator calls DoNSetup() to gather the N supplies and demands from each organ and begin N arbitration. Firstly DoNReallocation() is called to redistribute N that the plant has available from senescing organs. After this step any unmet N demand is considered as plant demand for N uptake from the soil (N Uptake Demand).

2. **doNutrientArbitration.** When this event occurs, the soil arbitrator gets the N uptake demands from each plant (where multiple plants are growing in competition) and their potential uptake from the soil and determines how much of their demand that the soil is able to provide. This value is then passed back to each plant instance as their Nuptake and doNUptakeAllocation() is called to distribute this N between organs.

3. **doActualPlantPartitioning.** On this event the arbitrator call DoNRetranslocation() and DoNFixation() to satisfy any unmet N demands from these sources. Finally, DoActualDMAAllocation is called where DM allocations to each organ are reduced if the N allocation is insufficient to achieve the organs minimum N concentration and final allocations are sent to organs.

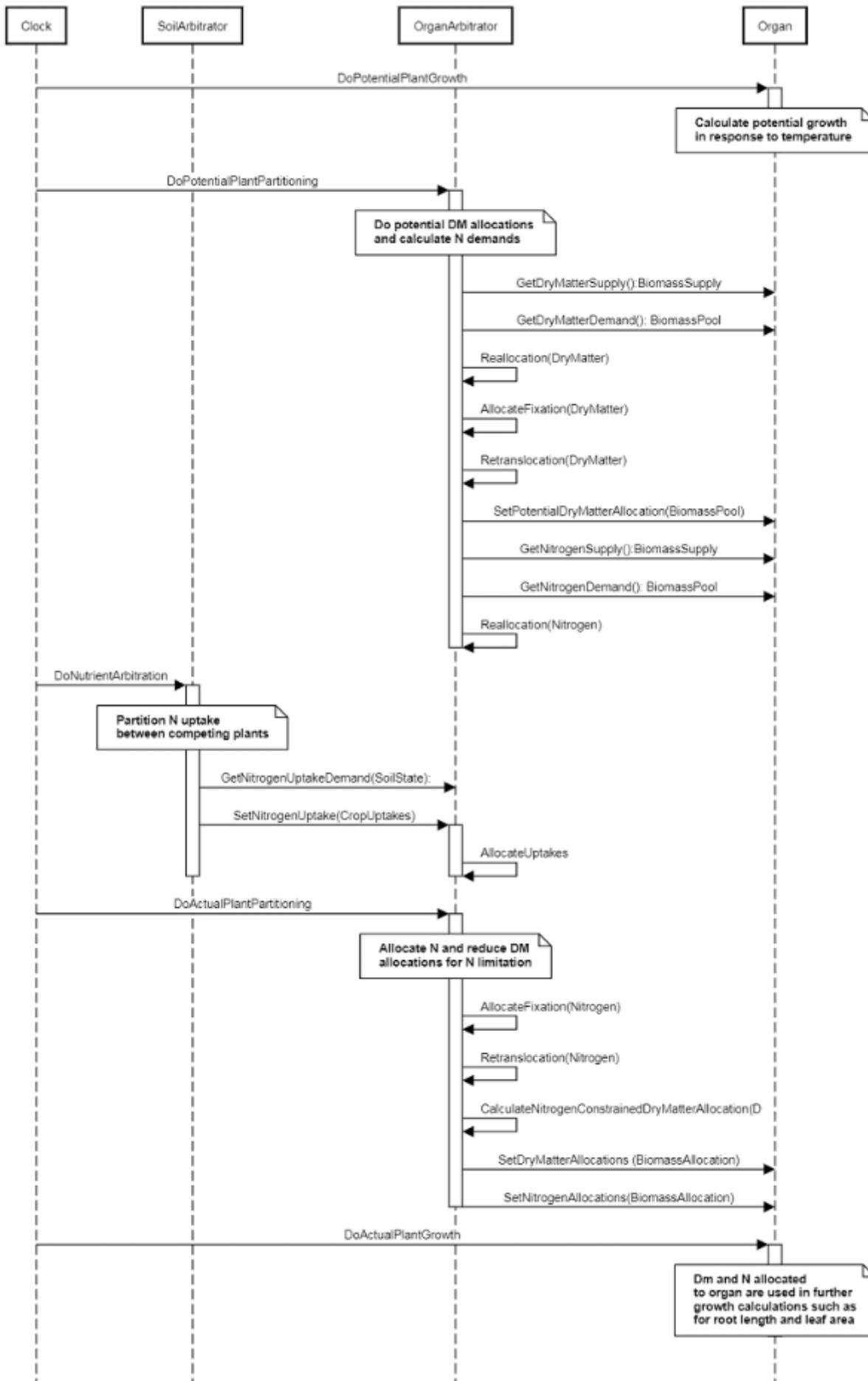


Figure 1: Schematic showing the procedure for arbitration of biomass partitioning. Pink boxes represent events that occur every day and their numbering shows the order of calculations. Blue boxes represent the methods that are called when these events occur. Orange boxes contain properties that make up the organ/arbitrator interface. Green boxes are organ specific properties.

1.5.2 Phenology

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

1.5.3 Root

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

1.5.4 Leaf

This organ is simulated using a SimpleLeaf organ type. It provides the core functions of intercepting radiation, producing biomass through photosynthesis, and determining the plant's transpiration demand. The model also calculates the growth, senescence, and detachment of leaves. SimpleLeaf does not distinguish leaf cohorts by age or position in the canopy.

Radiation interception and transpiration demand are computed by the MicroClimate model. This model takes into account competition between different plants when more than one is present in the simulation. The values of canopy Cover, LAI, and plant Height (as defined below) are passed daily by SimpleLeaf to the MicroClimate model. MicroClimate uses an implementation of the Beer Lambert equation to compute light interception and the Penman Monteith equation to calculate potential evapotranspiration.

These values are then given back to SimpleLeaf which uses them to calculate photosynthesis and soil water demand.

SimpleLeaf has two options to define the canopy: the user can either supply a function describing LAI or a function describing canopy cover directly. From either of these functions SimpleLeaf can obtain the other property using the Beer Lambert equation with the specified value of extinction coefficient. The effect of growth rate on transpiration is captured by the Fractional Growth Rate (FRGR) function, which is passed to the MicroClimate model.

1.5.5 Grain

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

1.5.6 Stem

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

1.5.7 Shell

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

1.5.8 MortalityRate

A constant function (name=value)

1.5.9 SeedMortalityRate

A constant function (name=value)

2 Validation

A test dataset has been developed to test the APSIM Canola model for a range of environmental (soil and climate) conditions, management options (sowing dates, populations, nitrogen rates, irrigation) and genetic backgrounds (different regions, cultivar types). These tests have been grouped into experiments focusing on phenological development or growth and resource use. Graphs of model performance are provided for yield, biomass production, canopy development, phenological development, water and nitrogen uptake, and grain yield components.

2.1 Map



2.2 Phenology Experiments

2.2.1 OCP Phenology

GRDC funded Optimised Canola Profitability project had experiments at Gatton in 2015, and Gatton and Canberra in 2016 and 2017 which consisted of 3 to 5 sowing dates [Whish et al., 2020](#). In 2016 and 2017 photoperiod treatments (daylength extension with lights) were also applied. Experiments were in the field in single rows of 1-3.5m in length and row spacing of 50cm. Plants were well watered and supplied with nutrients and were removed after flowering. The total number of cultivars included across the 5 experiments was 37, with each cultivar being included 4 to 28 combinations of location, year, TOS, and photoperiod (most cultivars between 13 and 18 combinations). Data collected: plant growth stage and leaf number was recorded 2 to 3 x weekly between emergence and flowering for 8 plants in each plot. Data was summarised as average sowing, emergence, floral initiation, green bud, flowering date for each cultivar/treatment.

Contact Jeremy Whish, Julianne Lilley (CSIRO)

2.2.1.1 List of experiments

| Experiment Name | Design (Number of Treatments) |
|-----------------|-------------------------------|
| Gatton2015 | TOS x Cv x PP (90) |
| Gatton2016 | TOS x Cv x PP (228) |
| Gatton2017 | TOS x Cv x PP (132) |
| Canberra2016 | TOS x Cv x PP (252) |

| Experiment Name | Design (Number of Treatments) |
|-----------------|-------------------------------|
| Canberra2017 | TOS x Cv x PP (198) |

2.2.2 Omics Phenology

GRDC funded "CSP1901-002RTX: Optimising Canola Production in Diverse Australian Growing Environments" project had experiments at Gatton in 2019, 2020, Boorowa 2019, 2021, Cummins 2020, 2021, York 2020, 2021 which consisted of 2-4 sowing dates. Project aimed to use field observations and transcriptomic and genomic data to establish a genetic phenology model. This project assesses G x E effects on phenological traits (including flowering time) in a diverse set of modern Australian and globally important canola varieties (~350) across key growing environments and regions relevant to the Australian industry (14 combinations of site, year and TOS), as well as three controlled environments.

Data collected: plant growth stage and leaf number was recorded 2 to 3 x weekly between emergence and flowering for 4 plants in each plot. Data was summarised as average sowing, emergence, floral initiation, green bud, flowering date for each cultivar/treatment.

Contact Jeremy Whish, Julianne Lilley (CSIRO)

2.2.2.1 List of experiments

| Experiment Name | Design (Number of Treatments) |
|-----------------|-------------------------------|
| Gatton2019 | TOS x Cv (28) |
| Gatton2020 | TOS x Cv (18) |
| Boorowa2019 | TOS x Cv (24) |
| Cummins2020 | TOS x Cv (18) |
| York2020 | TOS x Cv (18) |

2.3 Growth Experiments

2.3.1 Kojonup

2.3.1.1 List of experiments

| Experiment Name | Design (Number of Treatments) |
|-----------------|-------------------------------|
| Kojonup2013 | Cv x Fert (18) |
| Kojonup2014 | Cv x Fert (20) |

2.3.2 Cunderdin

2.3.2.1 List of experiments

| Experiment Name | Design (Number of Treatments) |
|-----------------|-------------------------------|
| Cunderdin2013 | Cv x Fert (36) |
| Cunderdin2014 | Cv x Fert (20) |

2.3.3 Wagga

2.3.3.1 List of experiments

| Experiment Name | Design (Number of Treatments) |
|-----------------|-------------------------------|
| Wagga2008 | Cv x Treat (12) |

2.3.3.2 Wagga2008

McCormick et al 2012. irrigated experiment, 3 cultivars, 3 densities, grazed and ungrazed

2.3.4 Harden

2.3.4.1 List of experiments

| Experiment Name | Design (Number of Treatments) |
|-----------------|-------------------------------|
| Harden1999 | Cv (1) |

2.3.5 Greenthorpe

2.3.5.1 List of experiments

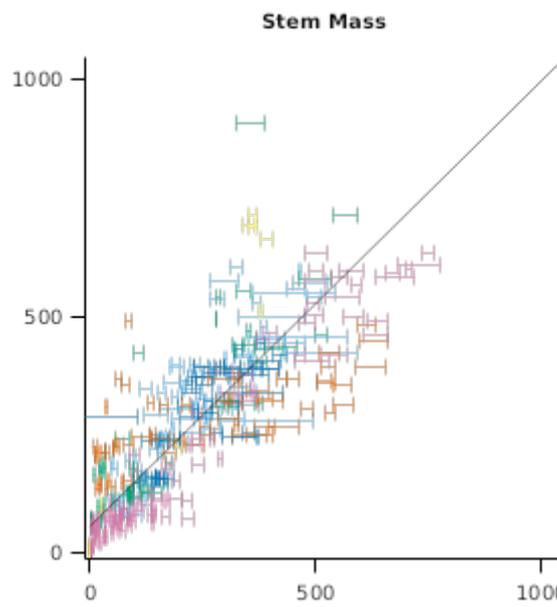
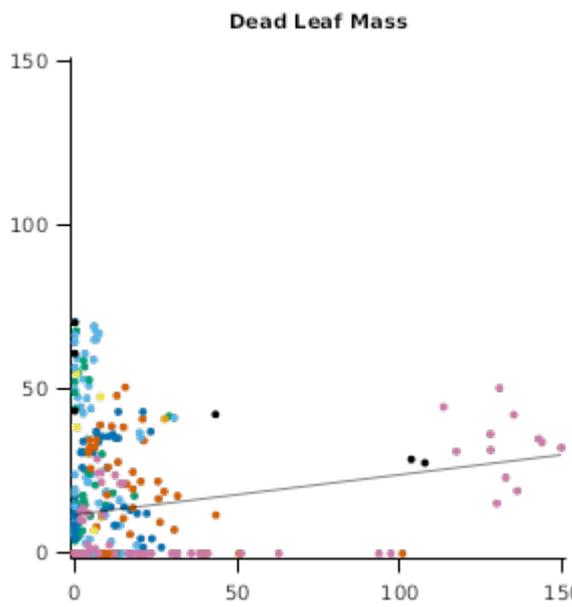
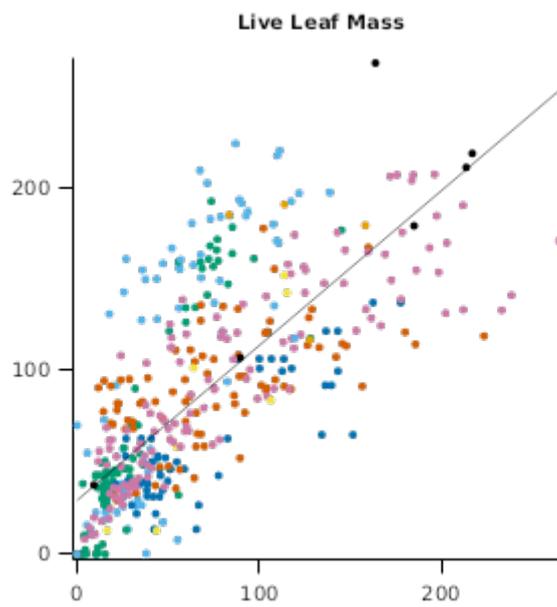
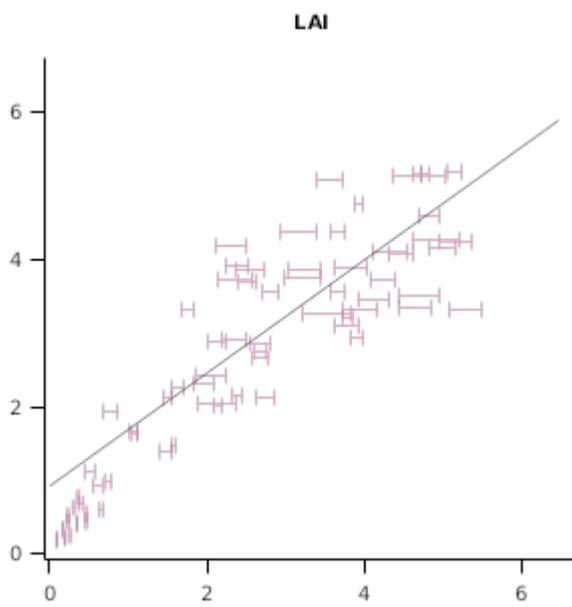
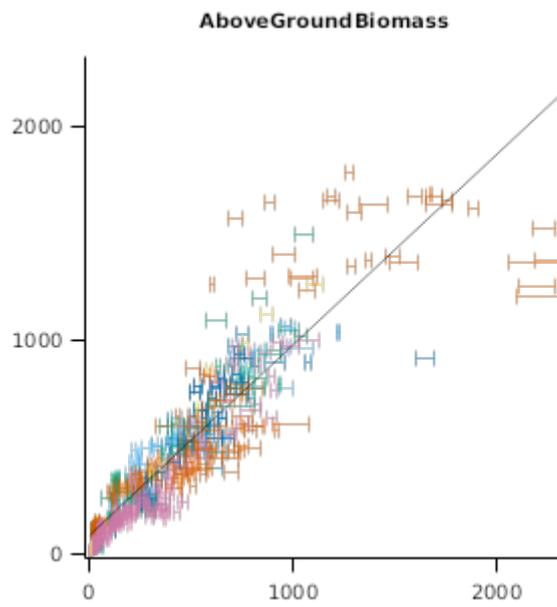
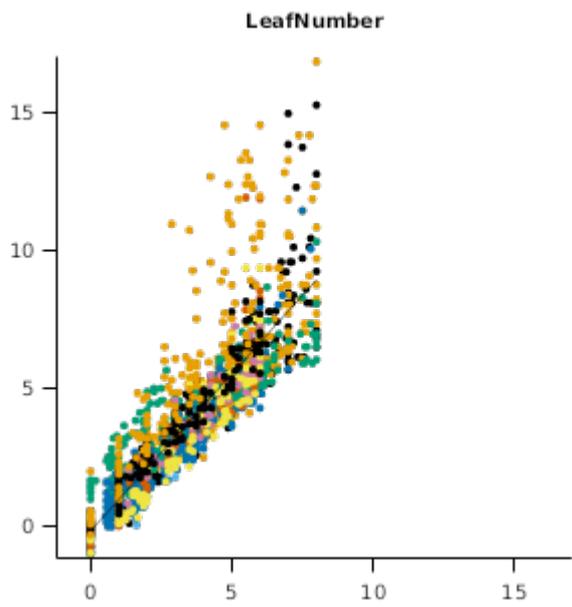
| Experiment Name | Design (Number of Treatments) |
|----------------------|-------------------------------|
| Greenethorpe2013_Ex1 | Cv (1) |
| Greenethorpe2013_Ex2 | Cv (1) |
| Greenethorpe2013_Ex3 | Cv (3) |
| Greenethorpe2014_Ex1 | Cv (1) |
| Greenethorpe2014_Ex2 | Cv (1) |
| Greenethorpe2014_Ex3 | Cv x TOS (24) |

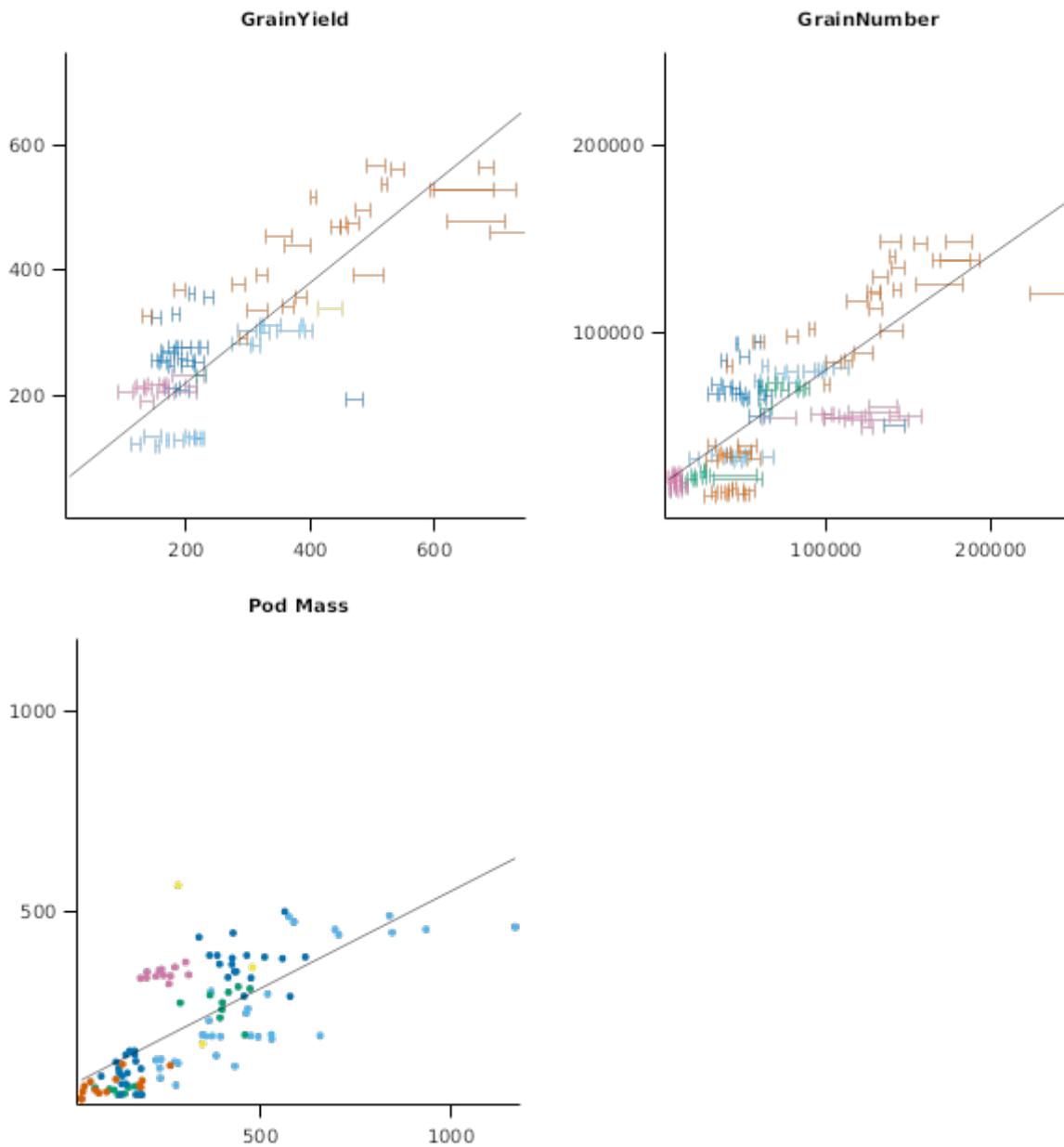
2.3.6 Merredin

2.3.6.1 List of experiments

| Experiment Name | Design (Number of Treatments) |
|-----------------|-------------------------------|
| Merredin2014 | Cv x Fert (20) |

2.4 Combined Results





3 Sensibility

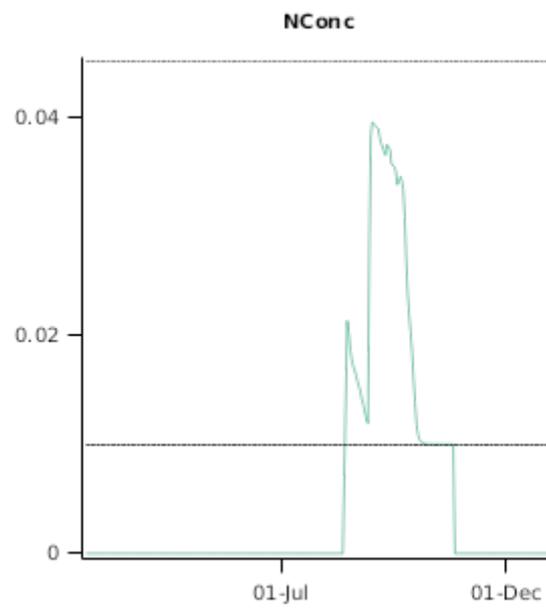
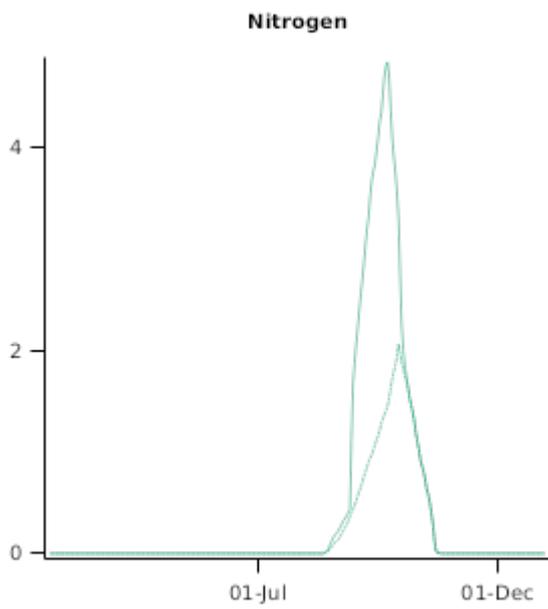
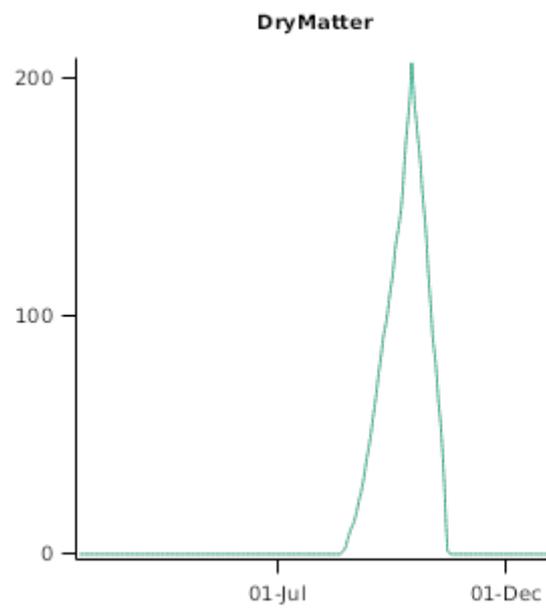
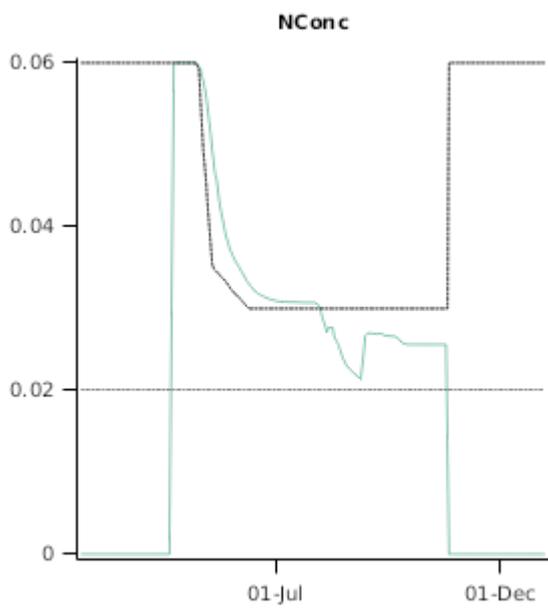
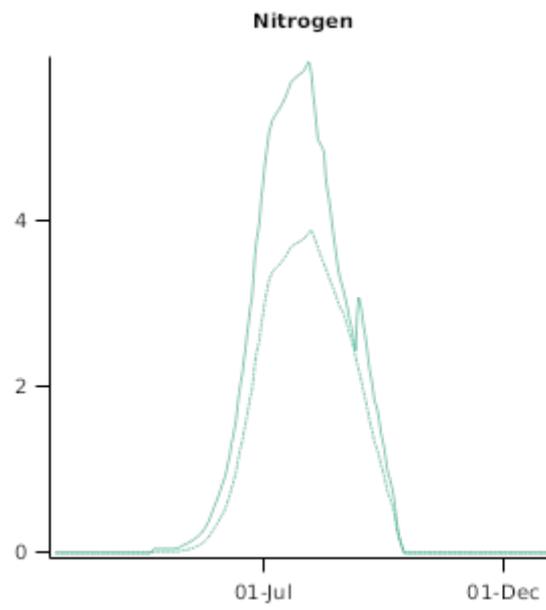
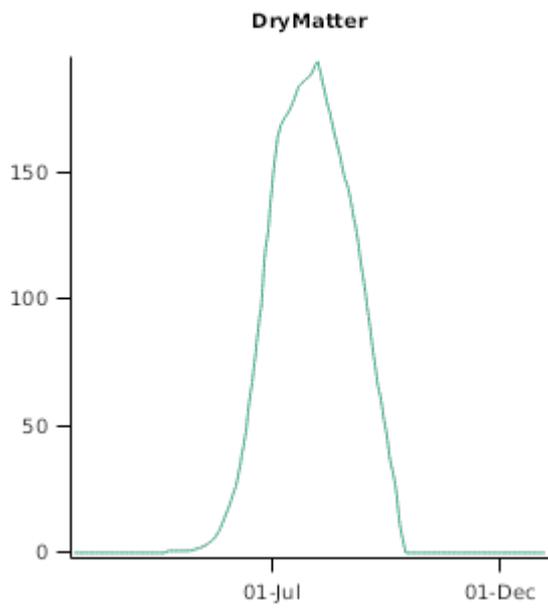
3.1 List of experiments

| Experiment Name | Design (Number of Treatments) |
|------------------|-------------------------------|
| DetailedDynamics | Cv (1) |
| CanolaGrazing | StockingRate (3) |
| Wagga | Cv x TOS (6) |

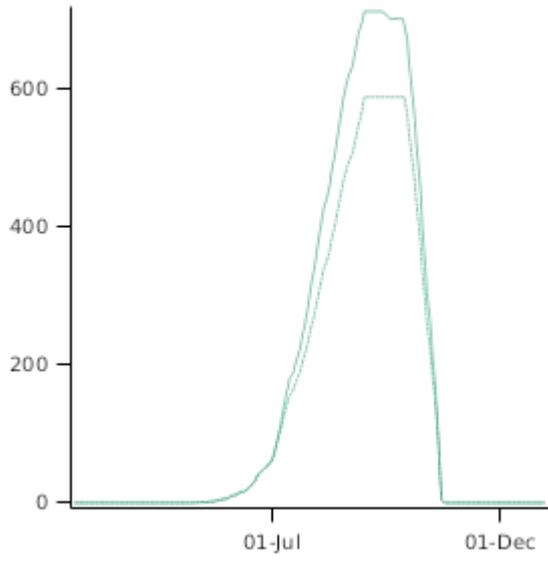
3.2 DetailedDynamics

This test demonstrates the detailed dynamics within a simple simulation of conola growth and resource use. This includes:

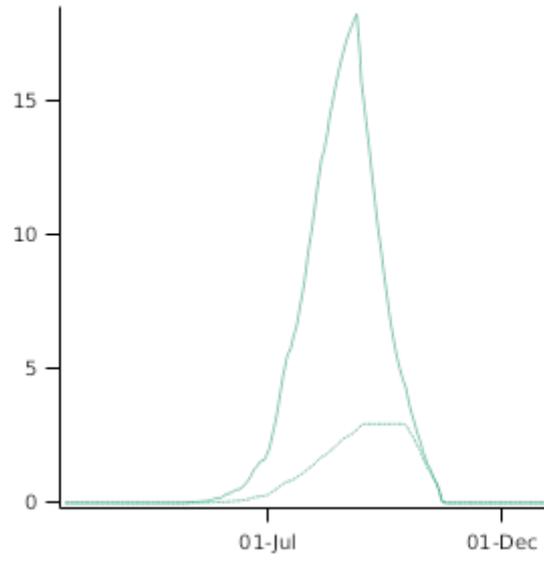
- * Dry matter and Nitrogen supply and demand for individual organs
- * Dry matter and Nitrogen content for live and dead components of each organ
- * Light interception for live and dead components for each organ



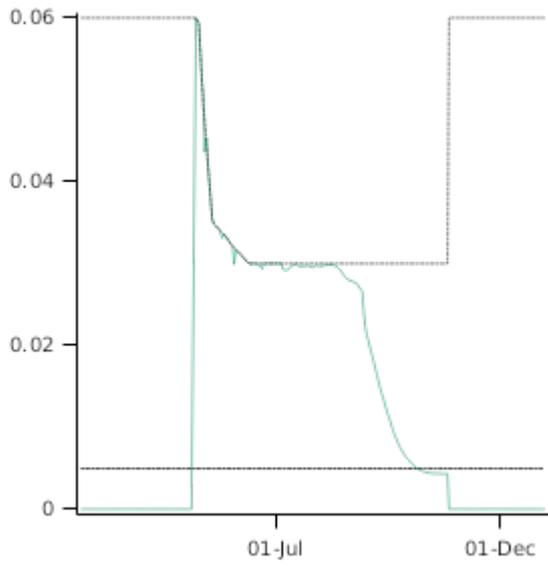
DryMatter



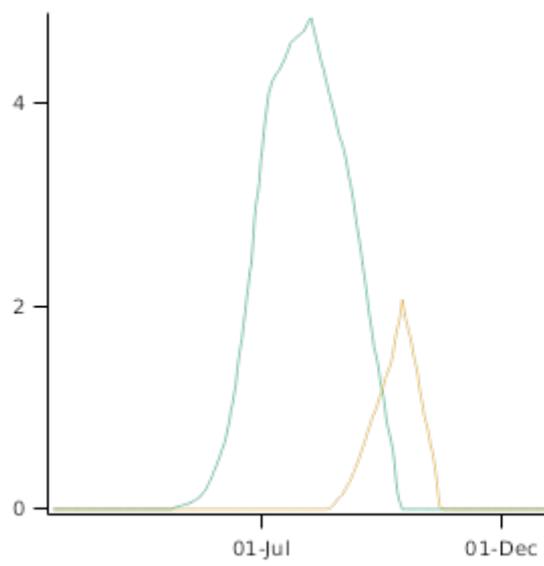
Nitrogen

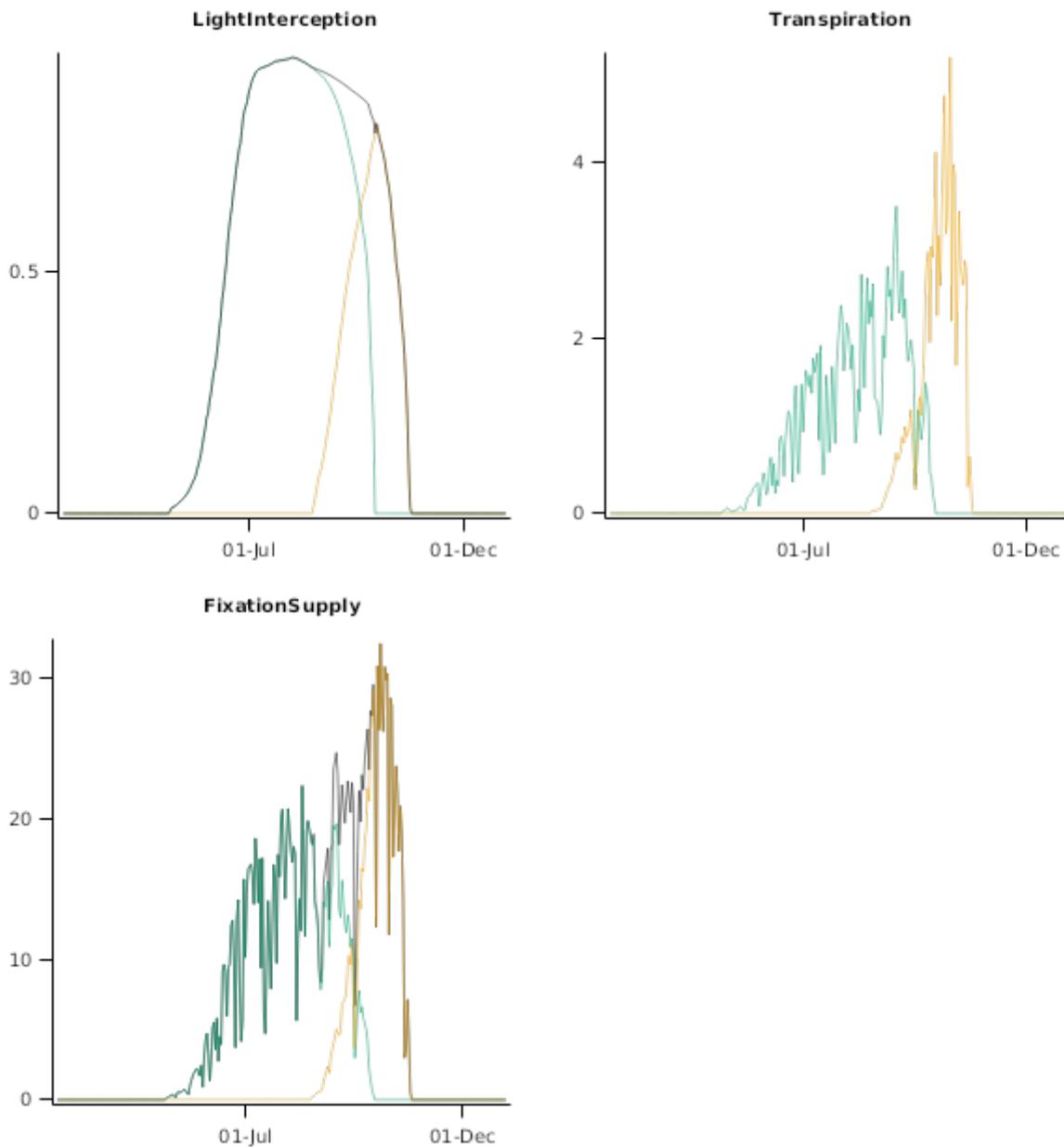


NConc



CanopyArea





3.3 CanolaGrazing

This sensibility test performs a livestock grazing simulation for canola planted in March, and grazed in late May as a dual-purpose crop.

3.4 Wagga

This test demonstrates the effect of time of sowing and cultivar (generic early, late or winter cultivars) on yield, biomass and time to harvest for long term simulations at Wagga Wagga, NSW.

4 References

[Brown, Hamish E., Huth, Neil I., Holzworth, Dean P., Teixeira, Edmar I., Zyskowski, Rob F., Hargreaves, John N. G., Moot, Derrick J., 2014. Plant Modelling Framework: Software for building and running crop models on the APSIM platform. Environmental Modelling and Software 62, 385-398.](#)

[Whish, JPM, Lilley, JM, Morrison, MJ, Cocks, B, Bullock, M, 2020. Vernalisation in Australian spring canola explains variable flowering responses. Field Crops Research 258, 107968.](#)