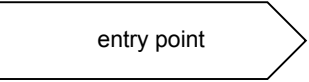| Functional Structure of Plant Model |
| --- |

KEY

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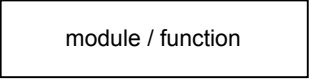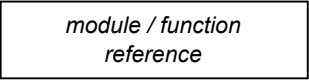
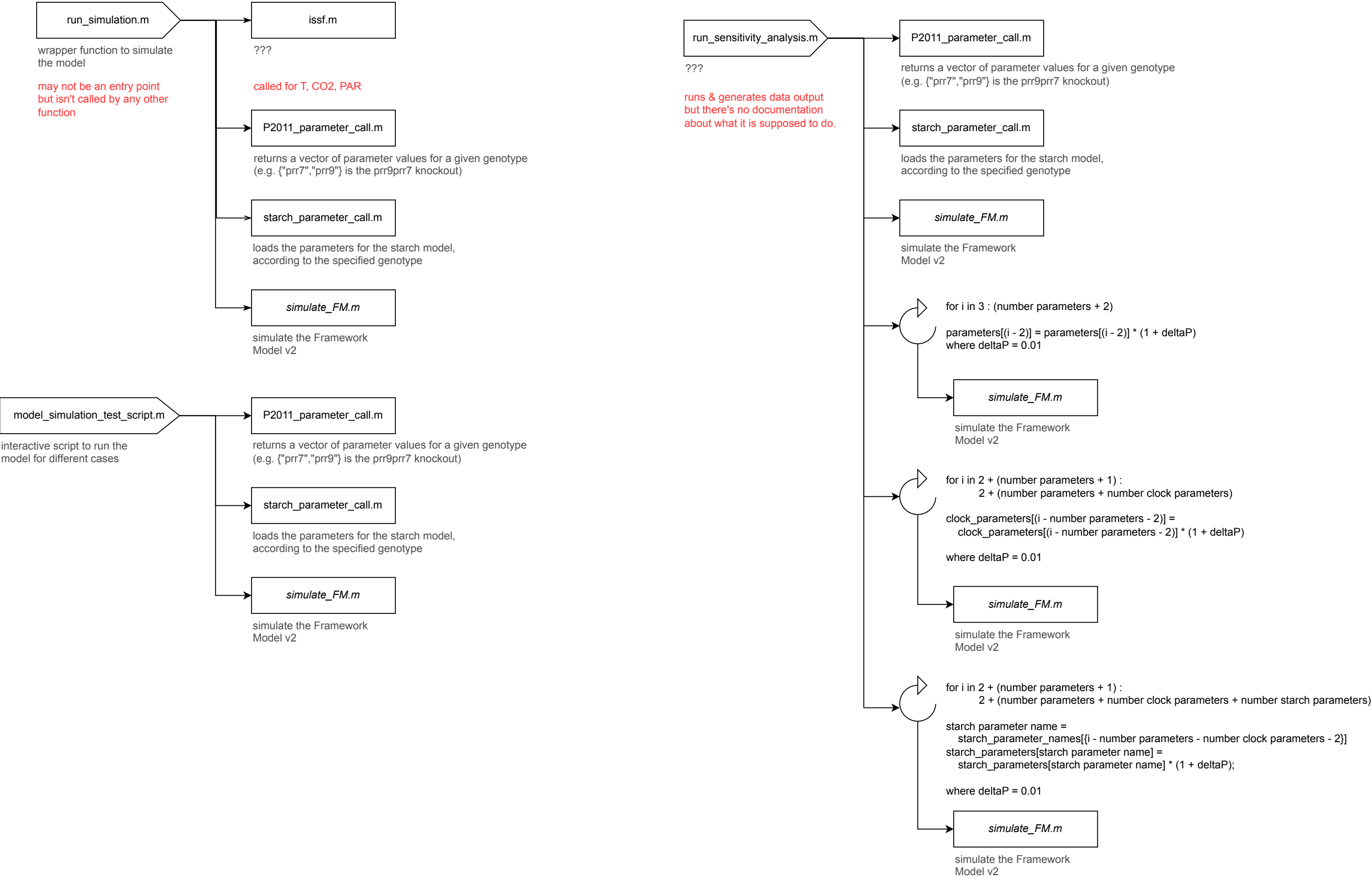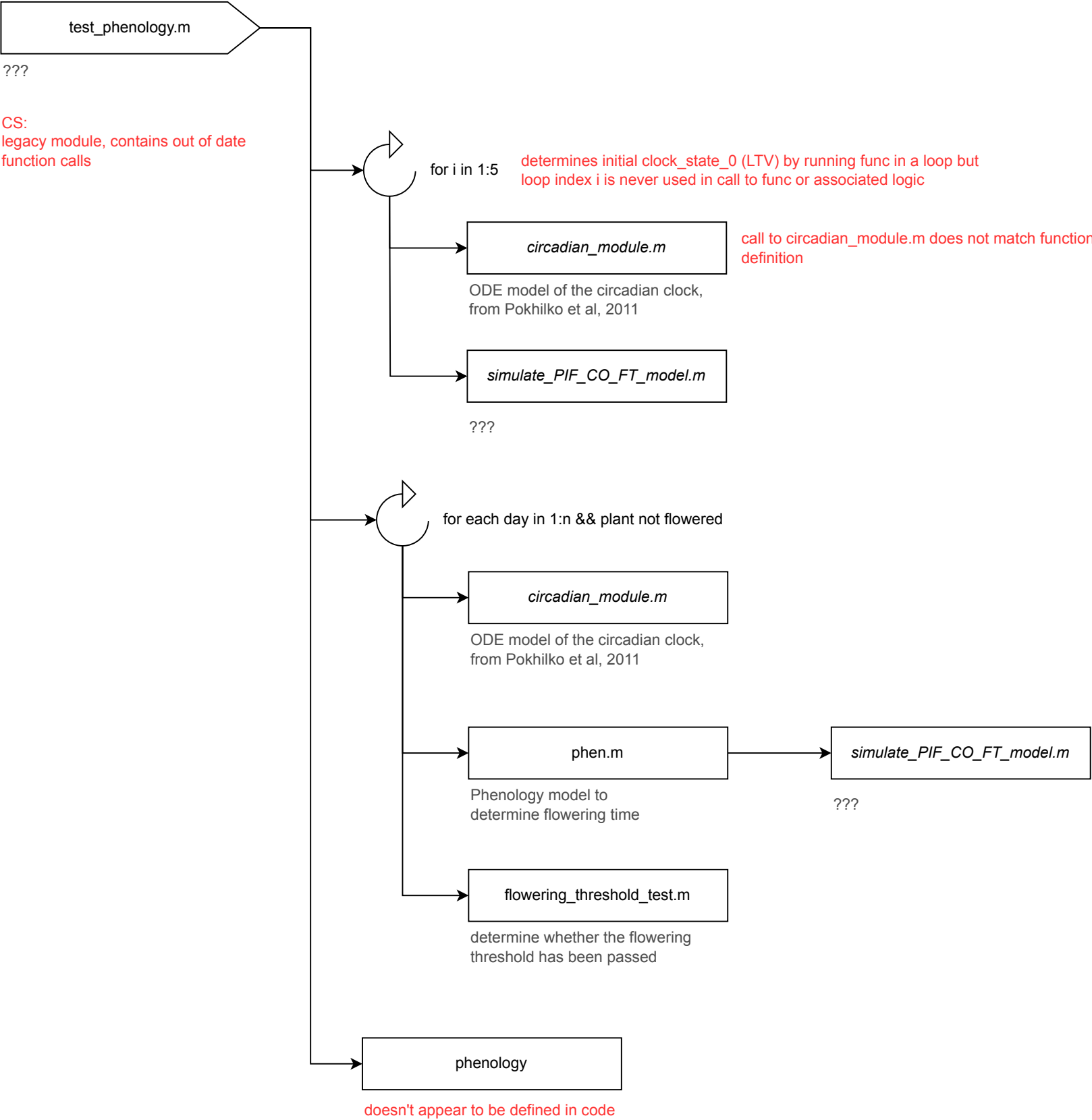| entry point | Entry point<br>— module / function that calls rest of functions |
| --- | --- |
| module / function | module / function<br>— functional component of model, may call other functions |
| *module / function reference* | reference<br>— placeholder / reference for module / function unpacked elsewhere in document |

run_simulation.m

wrapper function to simulate
the model

may not be an entry point
but isn't called by any other
function

issf.m

???

called for T, CO2, PAR

P2011_parameter_call.m

returns a vector of parameter values for a given genotype
(e.g. {"prr7","prr9"} is the prr9prr7 knockout)

starch_parameter_call.m

loads the parameters for the starch model,
according to the specified genotype

simulate_FM.m

simulate the Framework
Model v2

model_simulation_test_script.m

interactive script to run the
model for different cases

P2011_parameter_call.m

returns a vector of parameter values for a given genotype
(e.g. {"prr7","prr9"} is the prr9prr7 knockout)

starch_parameter_call.m

loads the parameters for the starch model,
according to the specified genotype

simulate_FM.m

simulate the Framework
Model v2

run_sensitivity_analysis.m

???

runs & generates data output
but there's no documentation
about what it is supposed to do.

P2011_parameter_call.m

returns a vector of parameter values for a given genotype
(e.g. {"prr7","prr9"} is the prr9prr7 knockout)

starch_parameter_call.m

loads the parameters for the starch model,
according to the specified genotype

simulate_FM.m

simulate the Framework
Model v2

for i in 3 : (number parameters + 2)

parameters[(i - 2)] = parameters[(i - 2)] * (1 + deltaP)
where deltaP = 0.01

simulate_FM.m

simulate the Framework
Model v2

for i in 2 + (number parameters + 1) :
        2 + (number parameters + number clock parameters)

clock_parameters[(i - number parameters - 2)] =
    clock_parameters[(i - number parameters - 2)] * (1 + deltaP)

where deltaP = 0.01

simulate_FM.m

simulate the Framework
Model v2

for i in 2 + (number parameters + 1) :
        2 + (number parameters + number clock parameters + number starch parameters)

starch parameter name =
    starch_parameter_names[{i - number parameters - number clock parameters - 2}]
starch_parameters[starch parameter name] =
    starch_parameters[starch parameter name] * (1 + deltaP);

where deltaP = 0.01

simulate_FM.m

simulate the Framework
Model v2

test_phenology.m

???

CS:
legacy module, contains out of date
function calls

for i in 1:5    determines initial clock_state_0 (LTV) by running func in a loop but
                loop index i is never used in call to func or associated logic

circadian_module.m    call to circadian_module.m does not match function
                       definition

ODE model of the circadian clock,
from Pokhilko et al, 2011

simulate_PIF_CO_FT_model.m

???

for each day in 1:n && plant not flowered

circadian_module.m

ODE model of the circadian clock,
from Pokhilko et al, 2011

phen.m    →    simulate_PIF_CO_FT_model.m

Phenology model to
determine flowering time          ???

flowering_threshold_test.m

determine whether the flowering
threshold has been passed

phenology

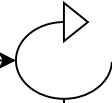doesn't appear to be defined in code

plot_comparison_to_experimental_data.m

???

produces 3 plots :
- starch profile (3 lines)
- malate + fumarate profile (3 lines)
- rosette fw (4 lines)

for i in 1:4

where: 1 = clock genotype @ default, starch genotype @ default, mf_use = 0.7, w = 0.91
2 = clock genotype @ default, starch genotype @ lsf1, mf_use = 0.7, w = 0.89
3 = clock genotype @ prr9 + prr7, starch genotype @ default, mf_use = 0.7, w= 0.89
4 = clock genotype @ prr9 + prr7, starch genotype @ default, mf_use = 0.25, w = 0.89
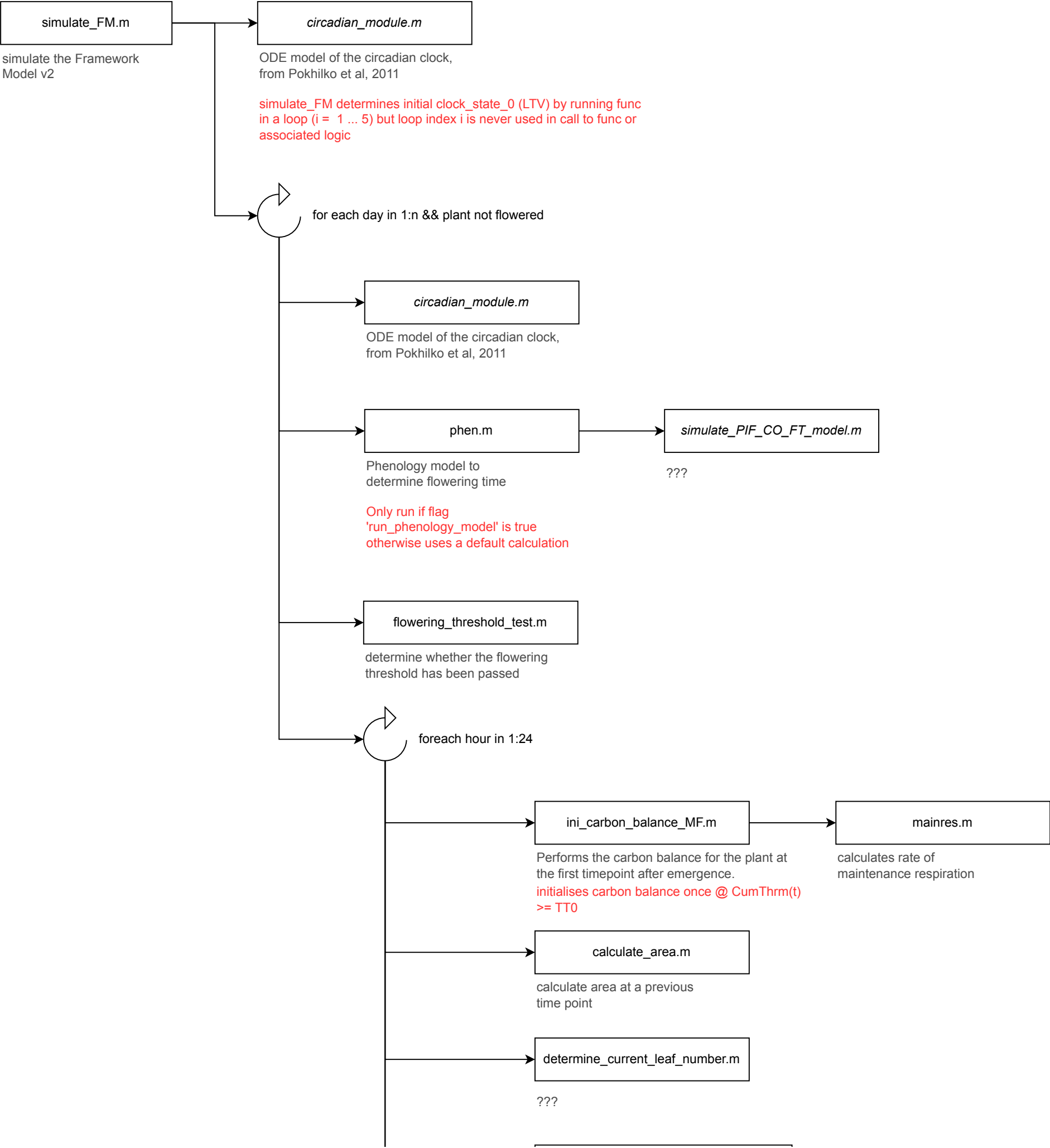
P2011_parameter_call.m

returns a vector of parameter values for a given genotype
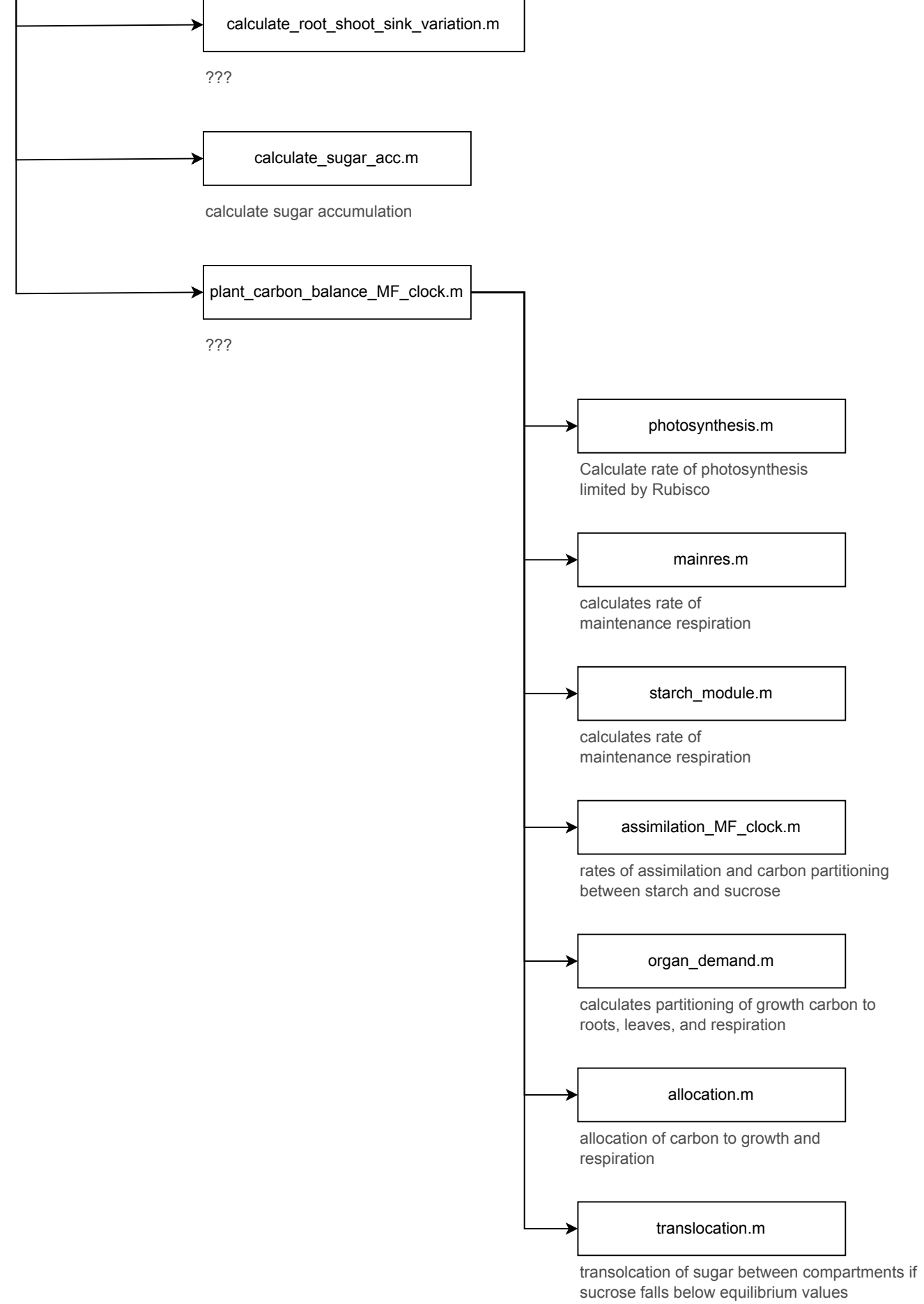(e.g. {"prr7","prr9"} is the prr9prr7 knockout)

starch_parameter_call.m

loads the parameters for the starch model,
according to the specified genotype

simulate_FM.m

simulate the Framework
Model v2

# Model Core

**simulate_FM.m**

simulate the Framework
Model v2

**circadian_module.m**

ODE model of the circadian clock,
from Pokhilko et al, 2011

simulate_FM determines initial clock_state_0 (LTV) by running func
in a loop (i = 1 ... 5) but loop index i is never used in call to func or
associated logic

for each day in 1:n && plant not flowered

**circadian_module.m**

ODE model of the circadian clock,
from Pokhilko et al, 2011

**phen.m**

Phenology model to
determine flowering time

Only run if flag
'run_phenology_model' is true
otherwise uses a default calculation

**simulate_PIF_CO_FT_model.m**

???

**flowering_threshold_test.m**

determine whether the flowering
threshold has been passed

foreach hour in 1:24

**ini_carbon_balance_MF.m**

Performs the carbon balance for the plant at
the first timepoint after emergence.
initialises carbon balance once @ CumThrm(t)
>= TT0

**mainres.m**

calculates rate of
maintenance respiration

**calculate_area.m**

calculate area at a previous
time point

**determine_current_leaf_number.m**

???

```
calculate_root_shoot_sink_variation.m
```

???

```
calculate_sugar_acc.m
```

calculate sugar accumulation

```
plant_carbon_balance_MF_clock.m
```

???

```
photosynthesis.m
```

Calculate rate of photosynthesis
limited by Rubisco

```
mainres.m
```

calculates rate of
maintenance respiration

```
starch_module.m
```

calculates rate of
maintenance respiration

```
assimilation_MF_clock.m
```

rates of assimilation and carbon partitioning
between starch and sucrose

```
organ_demand.m
```

calculates partitioning of growth carbon to
roots, leaves, and respiration

```
allocation.m
```

allocation of carbon to growth and
respiration

```
translocation.m
```

transolcation of sugar between compartments if
sucrose falls below equilibrium values

# Reused Functions

circadian_module.m → light_conditions.m

ODE model of the circadian clock,
from Pokhilko et al, 2011

simulate_PIF_CO_FT_model.m → wrap_P2011_model_dynamics.m

???

??? 

simulate_PIF_CO_FT_model.m → load_PIF_CO_FT_parameters.m

returns a vector of parameter values
for a given genotype

PIF_CO_FT_dynamics.m → light_conditions.m

???

???

check_plot.m

???