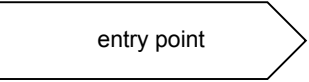
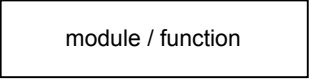


KEY



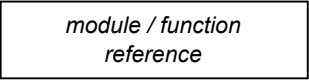
entry point

Entry point
— module / function that calls rest of functions



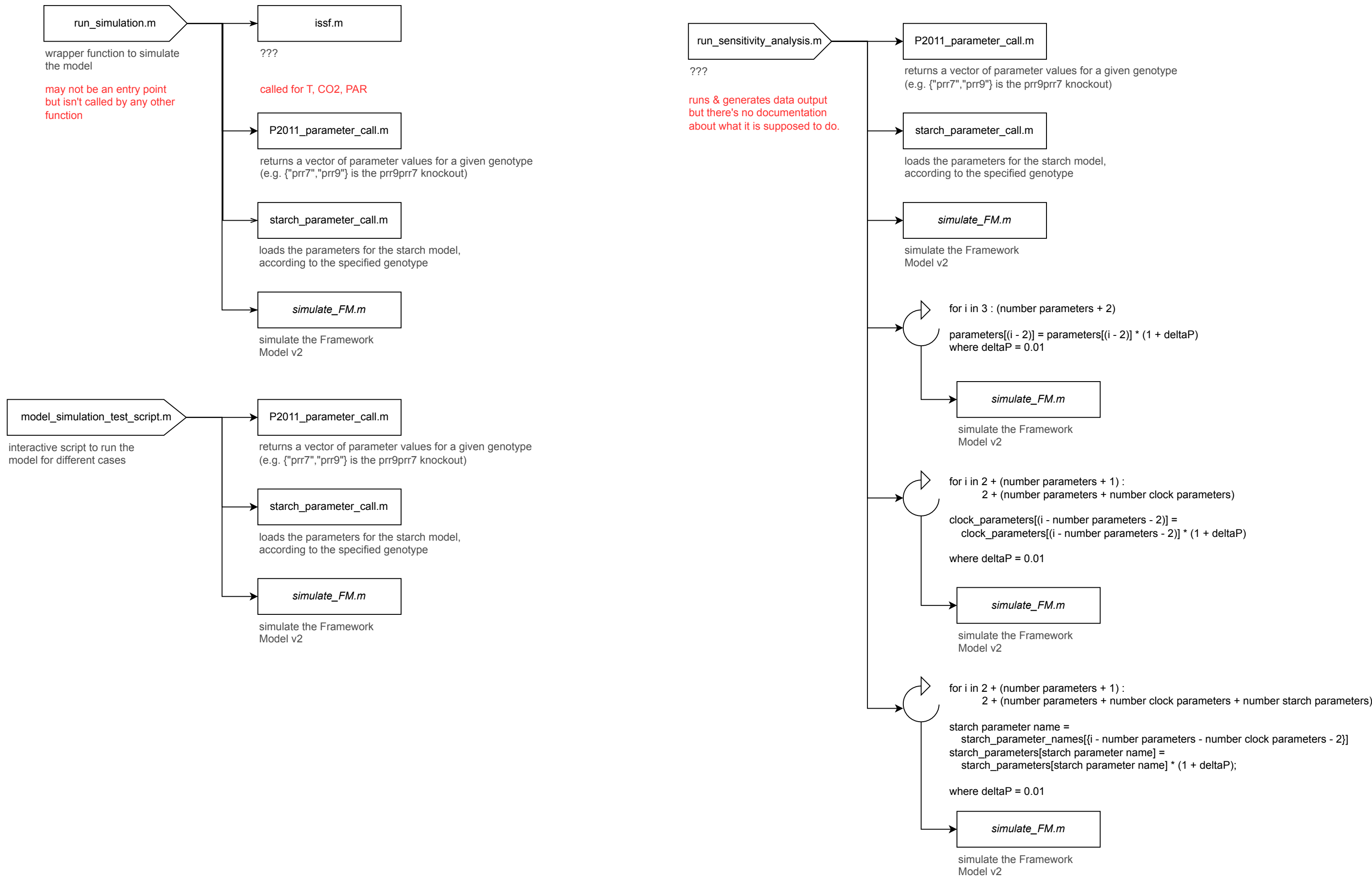
module / function

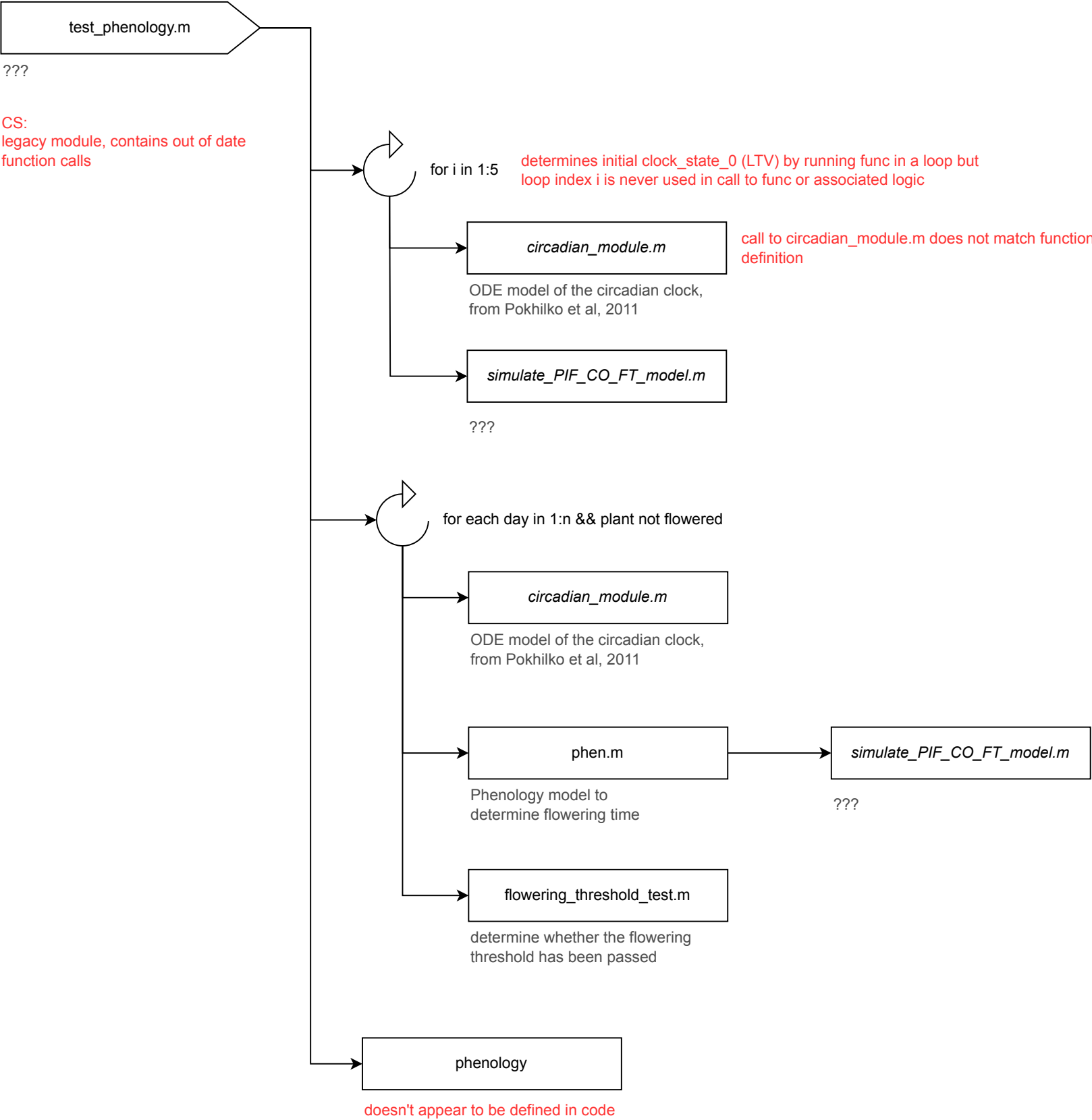
module / function
— functional component of model, may call other functions



*module / function
reference*

reference
— placeholder / reference for module / function unpacked elsewhere in document

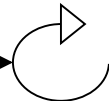




plot_comparison_to_experimental_data.m

???

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 @ Isf1, 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

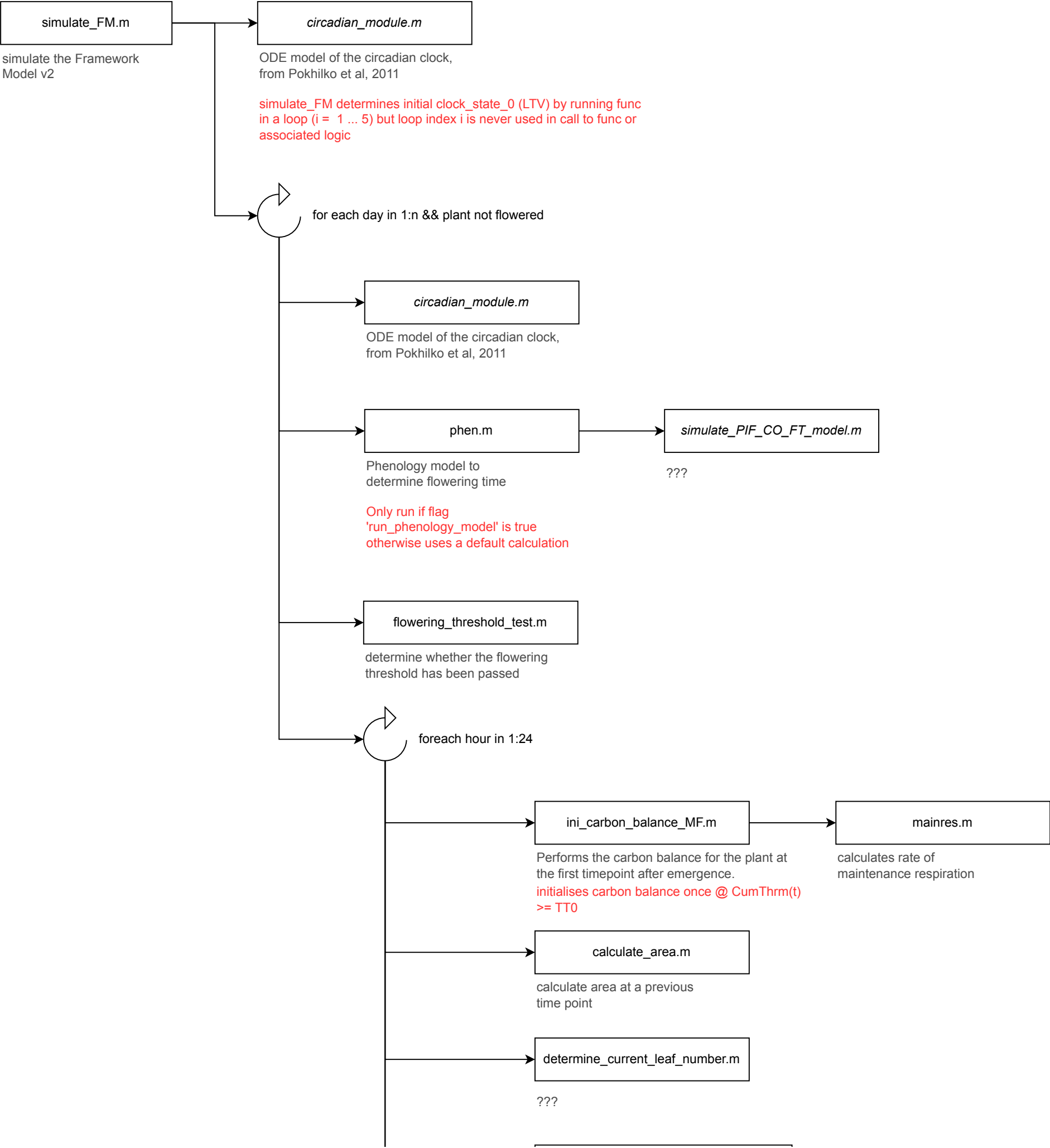
returns a vector of parameter values for a given genotype
(e.g. {"prr7","prr9"} is the prr9prr7 knockout)

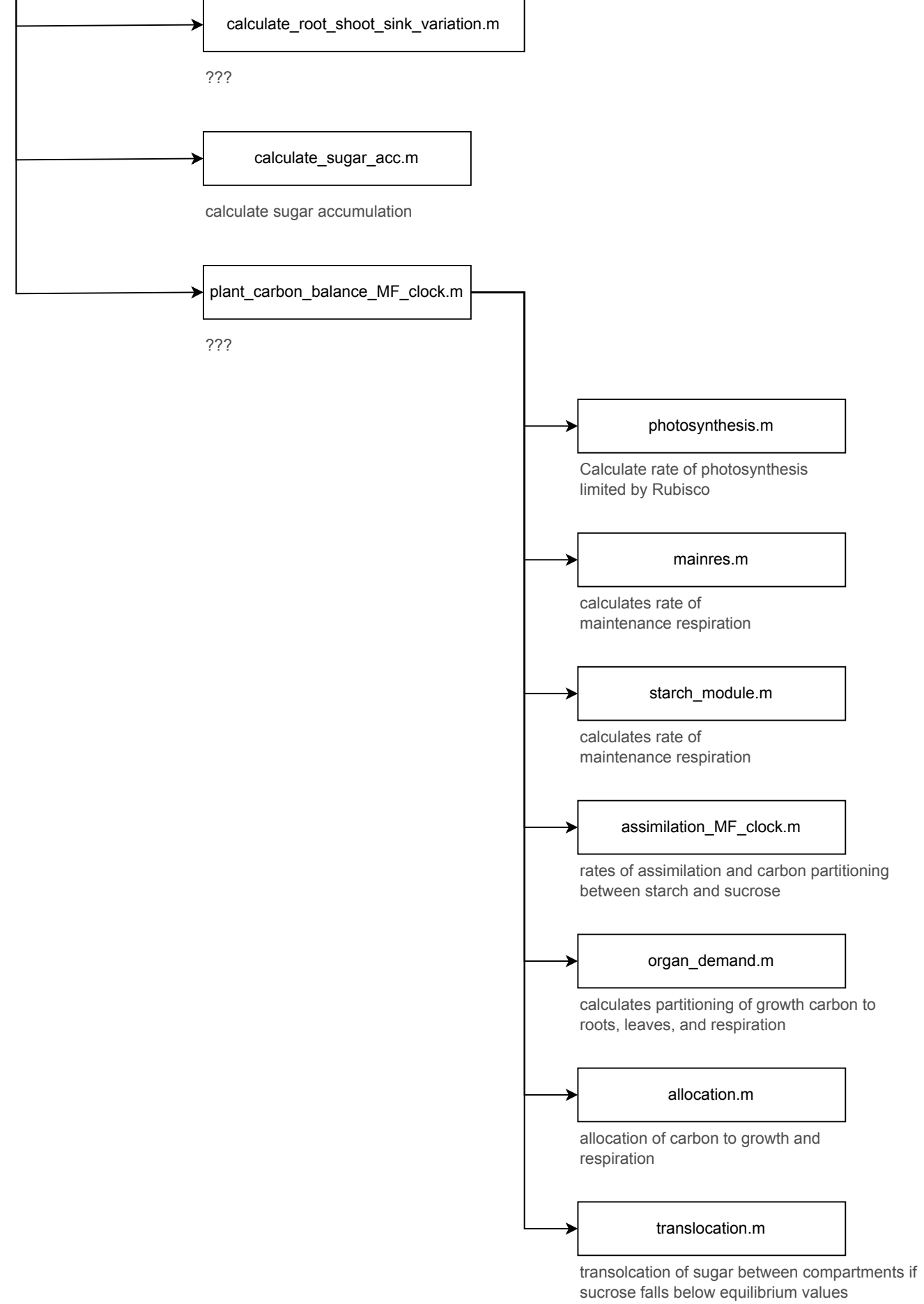
starch_parameter_call.m

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

simulate_FM.m

simulate the Framework
Model v2





Reused Functions

circadian_module.m

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

light_conditions.m

simulate_PIF_CO_FT_model.m

???

wrap_P2011_model_dynamics.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

???

