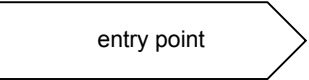
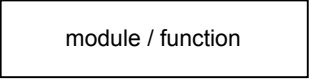


KEY



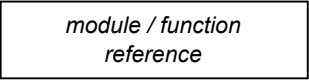
entry point

Entry point  
— module / function that calls rest of functions



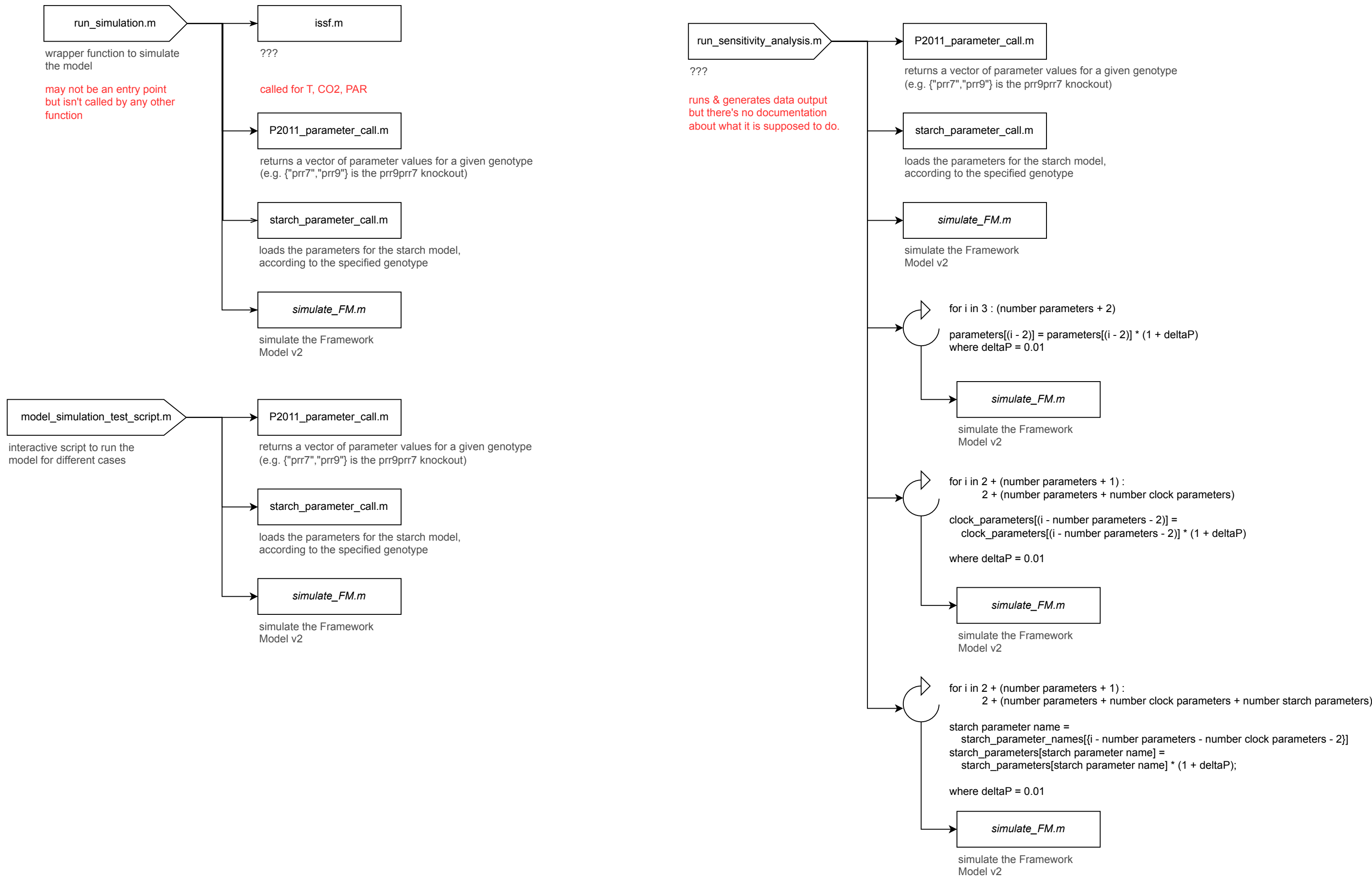
module / function

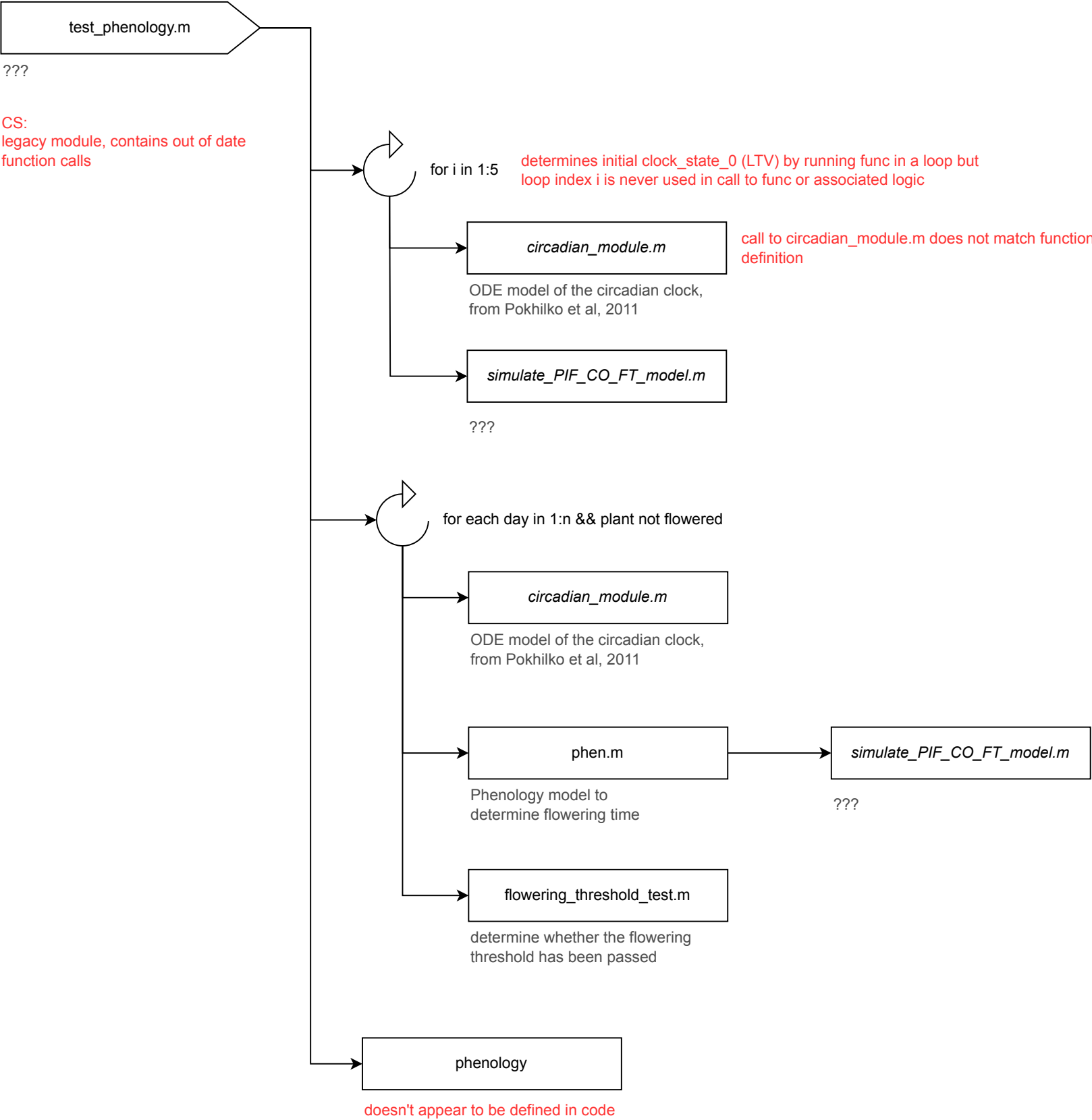
module / function  
— functional component of model, may call other functions



*module / function  
reference*

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

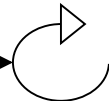




plot\_comparison\_to\_experimental\_data.m

???

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

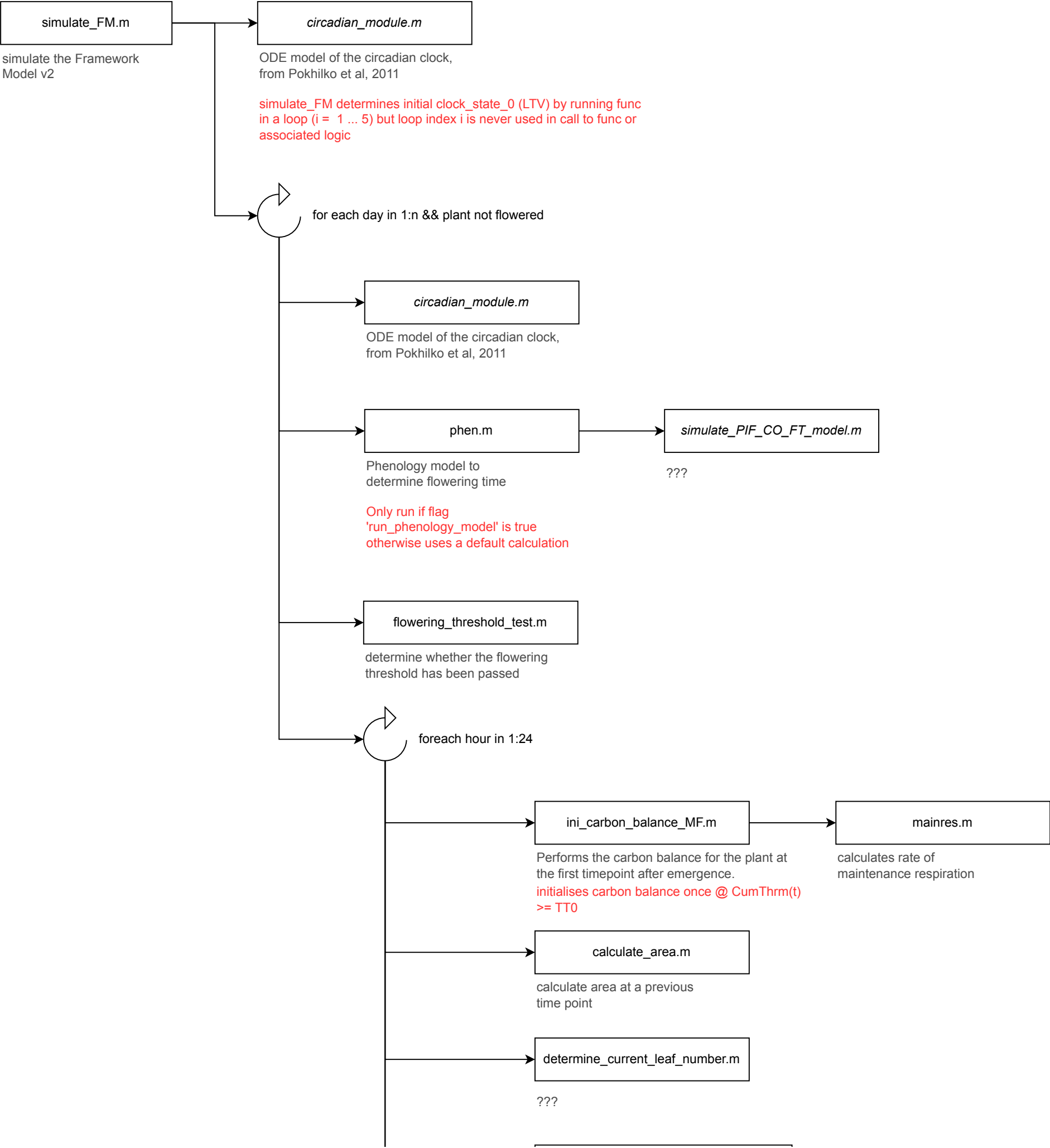
returns a vector of parameter values for a given genotype  
(e.g. {"prr7","prr9"} is the prr9prr7 knockout)

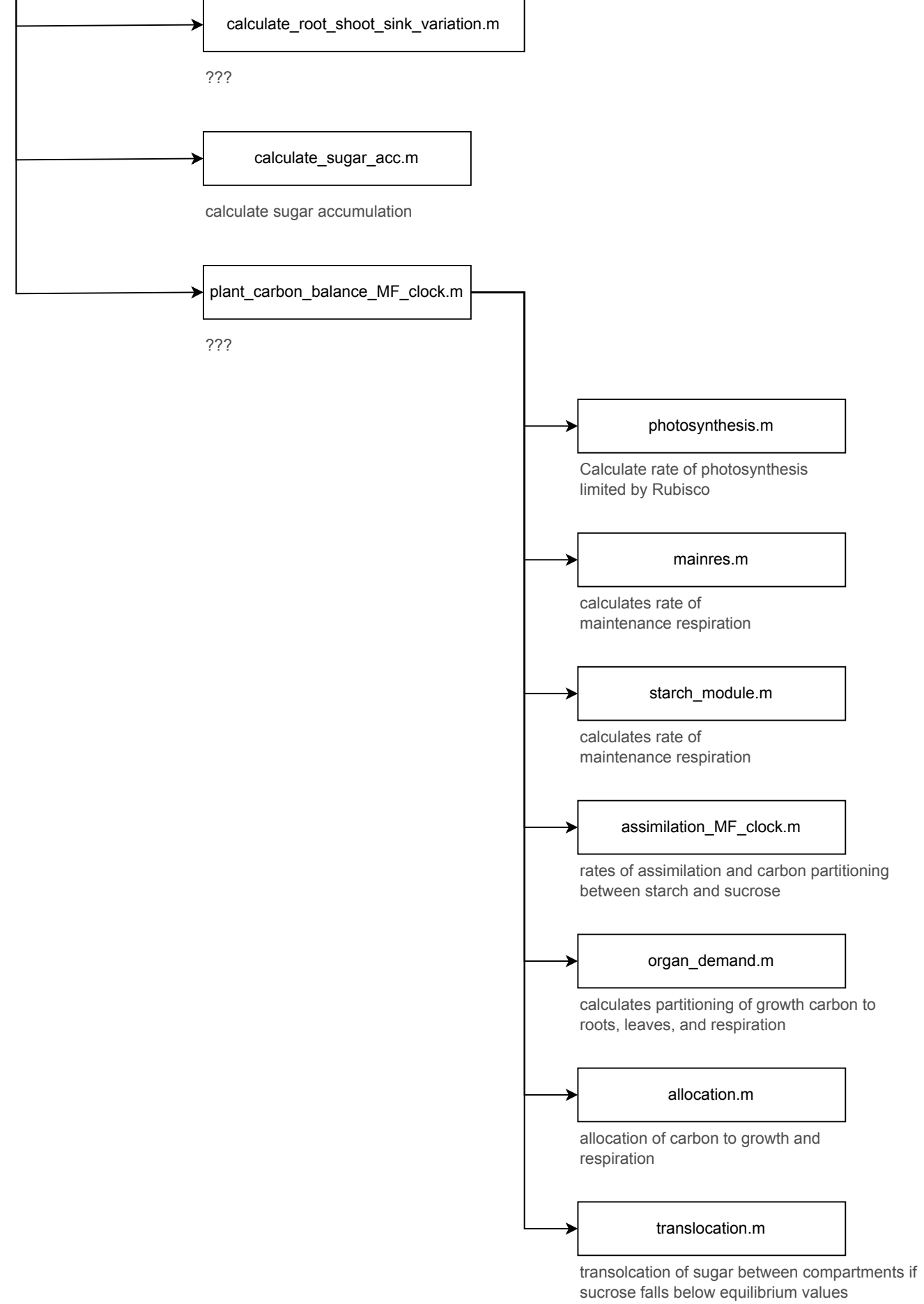
starch\_parameter\_call.m

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

???

Doesn't appear to be called from  
another module