

A

```
%model ./model/BIOMD00000000144.xml
// -- Begin Antimony block converted from BIOMD00000000144.xml
model *Model_generated_by_BIOCHAM()
... // Antimony code elided
end
// -- End Antimony block

%tasks ./experiment/Calzone2007-simulation-figure-1B.xml --master=True
// -- Begin PhraSEDML block converted from Calzone2007-simulation-figure-
1B.xml
// Original Biomodel (Calzone Fig1B)
model1 = model "../model/BIOMD00000000144"
// Including String synthesis and degradation (Calzone Fig3)
model2 = model model1 with ksstg=0.02, kdstg = 0.015, StgPc=0

// Simulations
sim1 = simulate uniform(0, 250, 1000)
sim2 = simulate uniform(0, 180, 1000)

// Tasks
task1 = run sim1 on model1
task2 = run sim2 on model2

// First two plots: Calzone Fig1B
plot "Cytoplasmic compartment (after Calzone Fig1B)" task1.time vs
task1.Weelc, task1.MPFc, task1.StgPc, task1.CycBT

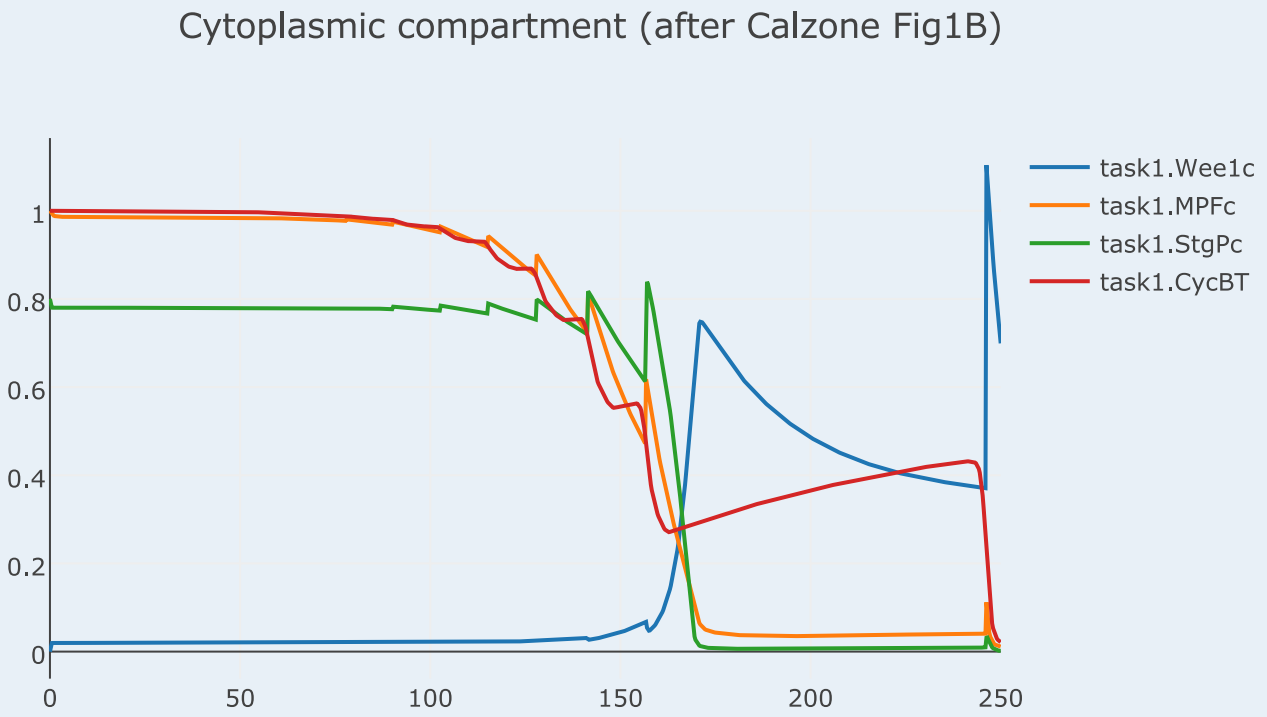
plot "Nuclear compartment (after Calzone Fig1B)" task1.time vs
task1.Weeln, task1.MPFn, task1.StgPn

// Remaining plots: Calzone Fig3

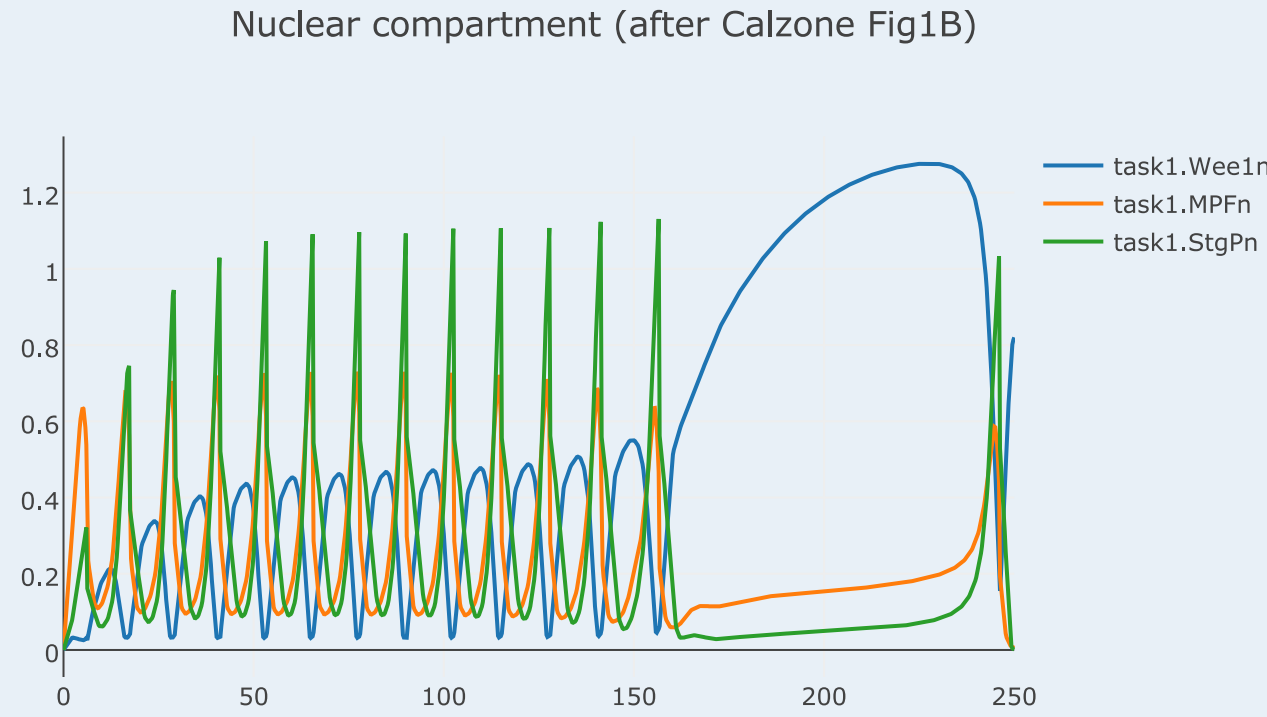
// Cytoplasmic compartment
plot "Cytoplasmic MPF, String, Wee1 and total CycBT (after Calzone Fig3A)"
task2.time vs task2.Weelc, task2.MPFc, task2.StgPc, task2.CycBT
// Nuclear compartment
plot "Same proteins as (A) but in the nucleus (after Calzone Fig3B)"
task2.time vs task2.Weeln, task2.MPFn, task2.StgPn
// String dynamics
plot "Total conc. of phospho-String vs both String phosphoforms (after
Calzone Fig3C)" task2.time vs task2.StringTotal, task2.StgPT
// String mRNA and factor X dynamics
plot "String mRNA and levels of String-degrading protein X (after Calzone
Fig3D)" task2.time vs task2.Stgm, task2.Xm, task2.Xp
// -- End PhraSEDML block
```

Reproduction of Fig 1 from Calzone et al.

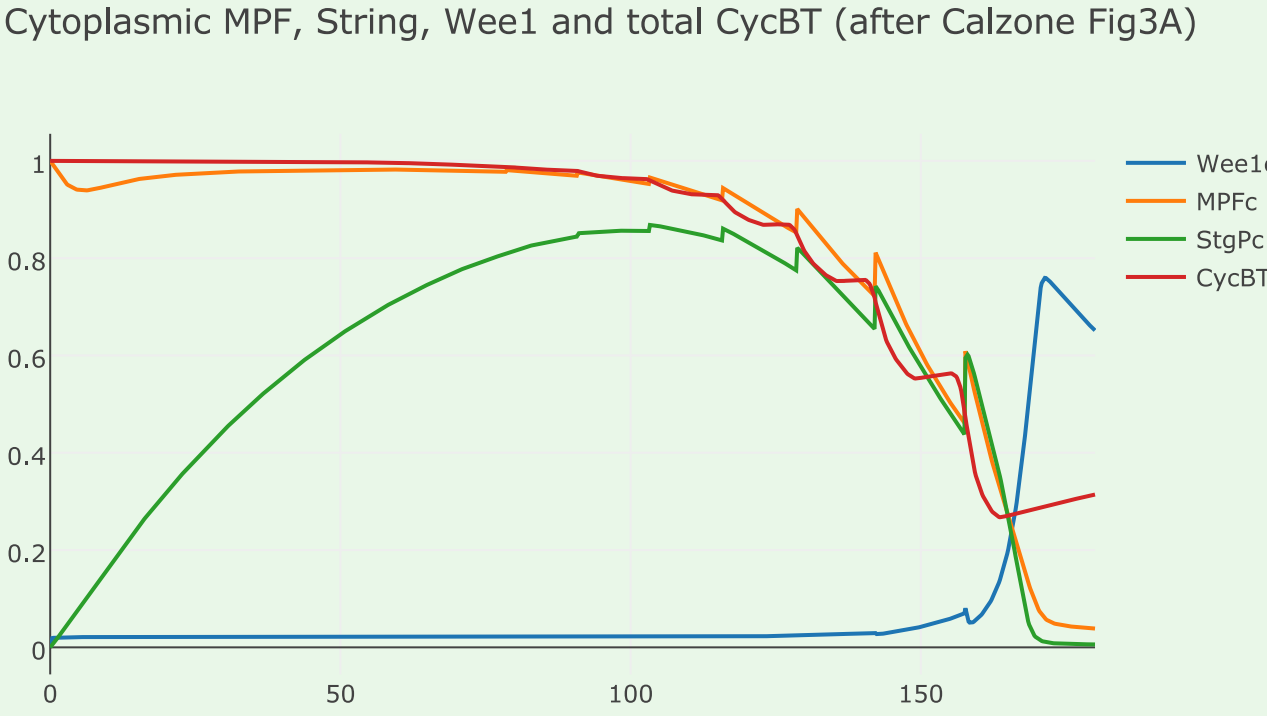
B



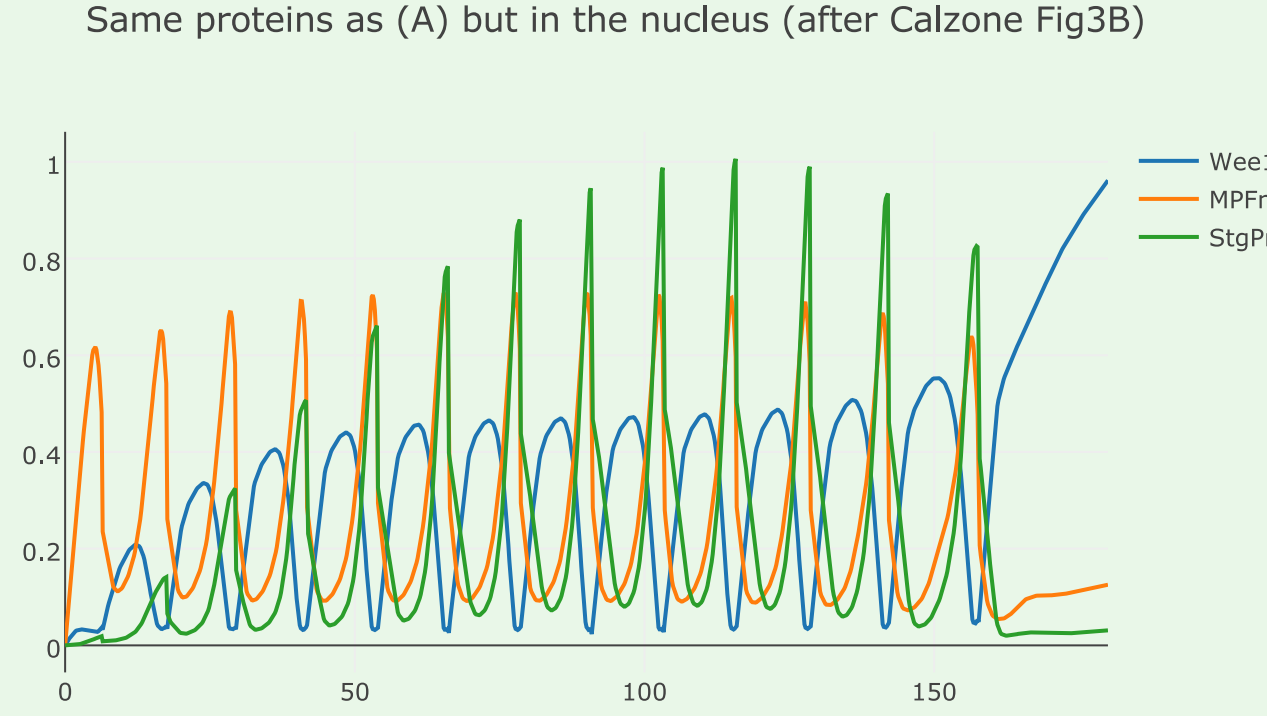
C



D

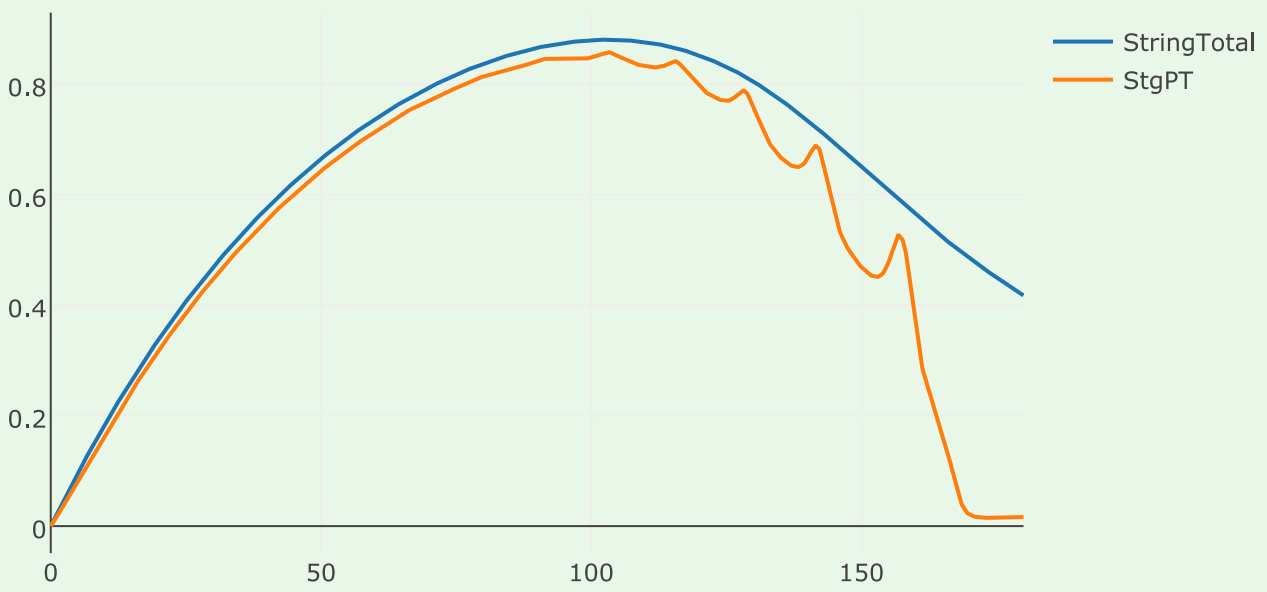


E



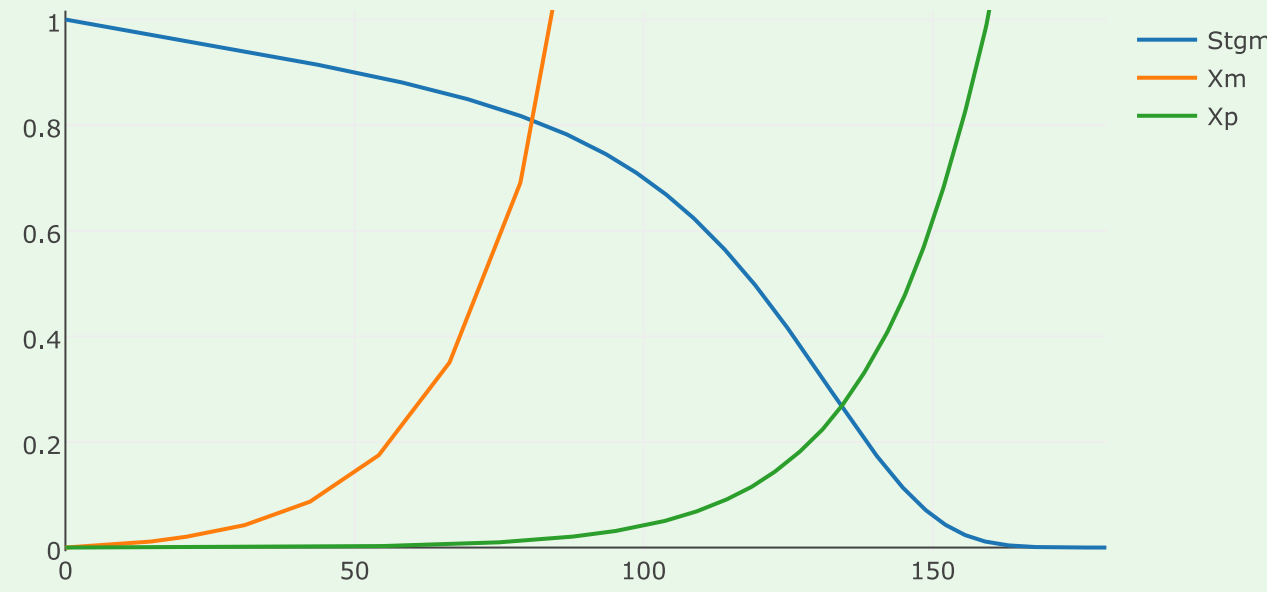
F

Total conc. of phospho-String vs both String phosphoforms (after Calzone Fig3C)



G

String mRNA and levels of String-degrading protein X (after Calzone Fig3D)



Reproduction of Fig 3 from Calzone et al.