

Table S1. Deterministic model variables

Variable	Description
V	Cell size
$[Cln3]$	Concentration of G1 cyclin Cln3
$[Bck2]$	Concentration of Bck2, an activator for START transition
$[WHI5dep]$	Concentration of dephosphorylated (active) Whi5
$[SBFdep]$	Concentration of dephosphorylated SBF
$[Cln2]$	Total concentration of G1 cyclins Cln1,2
$[CKI_T]$	Total concentration of Sic1+Cdc6 (stoichiometric inhibitors of Clb5,6 and Clb1,2)
$[CKI_P]$	Concentration of phosphorylated form of Sic1+Cdc6
$[Clb5_T]$	Total concentration of free B cyclins Clb5,6
$[Clb2_T]$	Total concentration of free B cyclins Clb1,2
$[BUD]$	Variable for bud emergence progression
$[ORI]$	Variable for DNA synthesis progression
$[SPN]$	Variable for spindle assembly progression
$[Swi5_T]$	Total concentration (number of molecules) of Swi5, transcription factor for CKI synthesis
$[CDC20_T]$	Total concentration of Cdc20, a protein involved in Clb5,6, Clb1,2 and Pds1 degradation
$[Mad2_A]$	Concentration of active Mad2, a spindle checkpoint protein that sequesters (inactivates) Cdc20
$[APCP]$	Concentration of phosphorylated (active) APC, activates Cdc20 by complex formation
$[Cdh1_A]$	Concentration of active Cdh1 degrading Clb1,2 and Polo kinase
$[Net1dep]$	Concentration of dephosphorylated (active) Net1, a stoichiometric inhibitor of Cdc14
$[PPX]$	Concentration of phosphatase that dephosphorylates Net1
$[Pds1_T]$	Concentration of securin, Esp1's stoichiometric inhibitor
$[Cdc15]$	Concentration of a kinase, when complexed with Tem1, phosphorylates Net1
$[Tem1]$	Concentration of a protein, when complexed with Cdc15, phosphorylates Net1
$[Polo_T]$	Total concentration of Polo kinase that activates Tem1
$[Polo_A]$	Concentration of phosphorylated (active) Polo kinase that activates Tem1
$[UDNA]$	Set to 1 when $[ORI]=1$, and set back to 0 when cell divides.
$[SPNALIGN]$	Set to 1 when $[SPN]=1$, and set back to 0 when cell divides.
$[ORIFLAG]$	Set to 0 when $[ORI]=1$, and set back to 1 when $[ORI]=0$.

Each variable corresponds to a single ODE. Deterministic model variables, which represent the concentration values, are converted to stochastic model variables that represent the numbers of molecules. The conversion process is described in [8,11].