[1]
```
import tellurium as te
te.newTiledFigure(rows=2, cols=1)
```

```
<tellurium.plotting.engine_plotly.PlotlyTiledFigure at 0x7f28fc4125f0>
```

[2]
```
// Created by libAntimony v2.9.3
model *novak()

  // Compartments and Species:
  compartment cytoplasm;
  species cyclin in cytoplasm, dimer in cytoplasm, dimer_p in cytoplasm, p_dimer in
cytoplasm;
  species p_dimer_p in cytoplasm, cdc25_p in cytoplasm, wee1_p in cytoplasm;
  species IE_p in cytoplasm, UbE_star in cytoplasm, Scdc2 in cytoplasm, Scdc25 in cytoplasm;
  species $wee1 in cytoplasm, $IE in cytoplasm, $UbE in cytoplasm;

  // Assignment Rules:
  cdc2 := total_cdc2 - (dimer + p_dimer + p_dimer_p + dimer_p);
  cdc25 := total_cdc25 - cdc25_p;
  wee1 := total_wee1 - wee1_p;
  IE := total_IE - IE_p;
  UbE := total_UbE - UbE_star;
  k25 := V25_prime*(total_cdc25 - cdc25_p) + V25_double_prime*cdc25_p;
  kwee := Vwee_prime*wee1_p + Vwee_double_prime*(total_wee1 - wee1_p);
  k2 := V2_prime*(total_UbE - UbE_star) + V2_double_prime*UbE_star;
  total_cyclin := cyclin + dimer + dimer_p + p_dimer + p_dimer_p;
  Y15P := p_dimer + p_dimer_p;

  // Reactions:
  R1:  => cyclin; k1AA;
  R2: cyclin => ; k2*cyclin;
  R3: cyclin + $cdc2 => dimer; k3*cyclin*cdc2;
  R4: dimer_p => dimer; kinh*dimer_p;
  R5: dimer => p_dimer; kwee*dimer;
  R6: dimer => dimer_p; kcak*dimer;
  R7: dimer => ; k2*dimer;
  R8: p_dimer => dimer; k25*p_dimer;
  R9: p_dimer => p_dimer_p; kcak*p_dimer;
  R10: p_dimer => ; k2*p_dimer;
  R11: p_dimer_p => p_dimer; kinh*p_dimer_p;
  R12: dimer_p => p_dimer_p; kwee*dimer_p;
  R13: p_dimer_p => dimer_p; k25*p_dimer_p;
  R14: p_dimer_p => ; k2*p_dimer_p;
  R15: dimer_p => ; k2*dimer_p;
  R17: $cdc25 => cdc25_p; ka*dimer_p*(total_cdc25 - cdc25_p)/(K_a + total_cdc25 - cdc25_p);
  R18: cdc25_p => $cdc25; kbPPase*cdc25_p/(K_b + cdc25_p);
  R19: $wee1 => wee1_p; ka*dimer_p*(total_wee1 - wee1_p)/(K_a + total_wee1 - wee1_p);
  R20: wee1_p => $wee1; kfPPase*wee1_p/(K_f + wee1_p);
  R21: $IE => IE_p; kp*dimer_p*(total_IE - IE_p)/(K_g + total_IE - IE_p);
  R22: IE_p => $IE; khPPase*IE_p/(K_h + IE_p);
  R23: $UbE => UbE_star; kc*IE_p*(total_UbE - UbE_star)/(K_c + total_UbE - UbE_star);
  R24: UbE_star => $UbE; kd_anti_IE*UbE_star/(K_d + UbE_star);

  // Species initializations:
  cyclin = 100;
  dimer = 0;
  dimer_p = 0;
  p_dimer = 0;
  p_dimer_p = 0;
  cdc25_p = 0;
  wee1_p = 0;
  IE_p = 0;
  UbE_star = 0;

  // Compartment initializations:
  cytoplasm = 1;

  // Variable initializations:
  total_cdc2 = 100;
  total_cdc25 = 1;
  total_wee1 = 1;
  total_IE = 1;
  total_UbE = 1;
  V25_prime = 0.1;
  V25_double_prime = 2;
  Vwee_prime = 0.1;
  Vwee_double_prime = 1;
  V2_prime = 0.015;
  V2_double_prime = 1;
  k1AA = 1;
  k3 = 0.01;
  kinh = 0.025;
  kcak = 0.25;
  ka = 0.01;
  K_a = 0.1;
  kbPPase = 0.125;
  K_b = 0.1;
  kw = 0.0133;
  K_e = 0.3;
  kfPPase = 0.1;
  K_f = 0.3;
  kg = 0.0065;
  K_g = 0.01;
  khPPase = 0.087;
  K_h = 0.01;
  kc = 0.1;
  K_c = 0.01;
  kd_anti_IE = 0.095;
  K_d = 0.01;

  // Other declarations:
  var k25, kwee, k2, total_cyclin, Y15P;
  const cytoplasm, total_cdc2, total_cdc25, total_wee1, total_IE, total_UbE;
  const V25_prime, V25_double_prime, Vwee_prime, Vwee_double_prime, V2_prime;
  const V2_double_prime, k1AA, k3, kinh, kcak, ka, K_a, kbPPase, K_b, kw;
  const K_e, kfPPase, K_f, kg, K_g, khPPase, K_h, kc, K_c, kd_anti_IE, K_d;

  // Unit definitions:
  unit substance = 1e-9 mole;
  unit time_unit = 60 second;

  // Display Names:
  substance is "nanomole";
  time_unit is "minutes";
  dimer is "cyclin-cdc2 dimer";
  dimer_p is "Thr161 phosphorylated dimer(active MPF)";
  p_dimer is "Tyr15 phosphorylated dimer";
  p_dimer_p is "Thr161-Tyr15 phosphorylated dimer";
  cdc25_p is "phosphorylated cdc25";
  wee1_p is "phosphorylated wee1";
  IE_p is "phosphorylated intermediary enzyme";
  UbE_star is "ubiquitin conjugating enzyme";
  IE is "intermediary enzyme";
  UbE is "ubiquitin conjugating enzyme";
  R1 is "cyclin synthesis";
  R2 is "cyclin degradation";
  R3 is "cyclin-cdc2 dimer formation";
  R4 is "Thr161 dephosphorylation";
  R5 is "Tyr15 phosphorylation";
  R6 is "Thr161 phosphorylation";
  R7 is "cyclin degradation";
  R8 is "Tyr15 dephosphorylation";
  R9 is "Thr161 phosphorylation";
  R10 is "cyclin degradation";
  R11 is "Thr161 dephosphorylation";
  R12 is "Tyr15 phosphorylation";
  R13 is "Tyr15 dephosphorylation";
  R14 is "cyclin degradation";
  R15 is "cyclin degradation";
  R17 is "cdc25 activation";
  R18 is "cdc25 deactivation";
  R19 is "wee1 deactivation";
  R20 is "wee1 activation";
  R21 is "intermediary enzyme activation";
  R22 is "intermediary enzyme deactivation";
  R23 is "ubiquitin conjugating enzyme activation";
  R24 is "ubiquitin conjugating enzyme deactivation";
end


model_extract = model "novak"
model_intact = model "novak" with k1AA = 1.8, V2_prime = 0.03, ka = 0.05, kc = 0.4, ke =
0.0067, kg = 0.02, kbPPase = 0.0375, kd_anti_IE = 0.25, kfPPase = 0.05, khPPase = 0.27

sim1 = simulate uniform(0, 200, 1000)

extract = run sim1 on model_extract
intact = run sim1 on model_intact

plot "M-phase Control, Extract (Novak, 1993)" extract.time vs extract.total_cyclin,
extract.p_dimer_p, extract.dimer_p
plot "M-phase Control, Intact Embryo (Novak, 1993)" intact.time vs intact.total_cyclin,
intact.p_dimer_p, intact.dimer_p
```