

```

model = sbiomodel('NikModel');
% The two bacteria:
compartment1 = addcompartment(model, 'cell1');
compartment2 = addcompartment(model, 'cell2');

% SPECIES
% in the first compartment:
s1 = addspecies(compartment1, 'Nikr');
s2 = addspecies(compartment1, 'Ni');
s3 = addspecies(compartment1, 'mRNArfp');
s4 = addspecies(compartment1, 'mRNAnikr');
s5 = addspecies(compartment1, 'DNAnikr');
s6 = addspecies(compartment1, 'DNArfp');
s7 = addspecies(compartment1, 'RFP');
s8 = addspecies(compartment1, 'LacI');
s9 = addspecies(compartment1, 'LacIDNA');
s10 = addspecies(compartment1, 'DNAgfp');
s11 = addspecies(compartment1, 'mRNAgfp');
s12 = addspecies(compartment1, 'GFP');
s13 = addspecies(compartment1, 'DNAluxi');
s14 = addspecies(compartment1, 'mRNAluxi');
s15 = addspecies(compartment1, 'LUXI');
s16 = addspecies(compartment1, 'SAM');
s17 = addspecies(compartment1, 'HSL');
s18 = addspecies(compartment1, 'Trans');
s19 = addspecies(compartment1, 'Cis');
s20 = addspecies(compartment1, 'DNAluxr');
s21 = addspecies(compartment1, 'mRNAluxr');
s22 = addspecies(compartment1, 'LUXR');
% in the second compartment:
s23 = addspecies(compartment2, 'DNAnikr');
s24 = addspecies(compartment2, 'mRNAnikr');
s25 = addspecies(compartment2, 'Nikr');
s26 = addspecies(compartment2, 'Trans');
s27 = addspecies(compartment2, 'Ni');
s28 = addspecies(compartment2, 'Cis');
s29 = addspecies(compartment2, 'LacI');
s30 = addspecies(compartment2, 'LacIDNA');
s31 = addspecies(compartment2, 'mRNAluxr');
s32 = addspecies(compartment2, 'LUXR');
s33 = addspecies(compartment2, 'HSL');
s34 = addspecies(compartment2, 'LUXRHSL');
s35 = addspecies(compartment2, 'DNAhpn');
s36 = addspecies(compartment2, 'mRNAhpn');
s37 = addspecies(compartment2, 'HPN');
s38 = addspecies(compartment2, 'DNAluxi');
s39 = addspecies(compartment2, 'mRNAluxi');
s40 = addspecies(compartment2, 'LUXI');
s41 = addspecies(compartment2, 'SAM');
s42 = addspecies(compartment2, 'HPNNi');

% PARAMETERS:
p1 = addparameter(model, 'k1', 0.2);
p2 = addparameter(model, 'k2', 20.0);
% parameter = addparameter(model, 'k3', '');
p3 = addparameter(model, 'k4', 1.5);
p4 = addparameter(model, 'k5', 1.0);
% parameter = addparameter(model, 'k6', '');
% parameter = addparameter(model, 'k7', '');
p5 = addparameter(model, 'k8', '1.5');
p6 = addparameter(model, 'k9', '1.0');
p7 = addparameter(model, 'k10', '1.5');
p8 = addparameter(model, 'k11', '1.0');
p9 = addparameter(model, 'k12', '1.0');
% parameter = addparameter(model, 'k13', '');
p10 = addparameter(model, 'k14', '1.0');
p11 = addparameter(model, 'k15', '1.5');
p12 = addparameter(model, 'k16', '1.0');
p13 = addparameter(model, 'k17', '1.0');
p14 = addparameter(model, 'k18', '1.0');
p15 = addparameter(model, 'k19', '1.0');
p16 = addparameter(model, 'k20', '1.5');
p17 = addparameter(model, 'k21', '1.0');
p18 = addparameter(model, 'k22', '1.0');
p19 = addparameter(model, 'k23', '1.0');
p20 = addparameter(model, 'k24', '1.0');
p21 = addparameter(model, 'k25', '1.0');
p22 = addparameter(model, 'k26', '1.0');
p23 = addparameter(model, 'k27', '1.0');
p24 = addparameter(model, 'k28', '1.0');
p25 = addparameter(model, 'k29', '1.0');
p26 = addparameter(model, 'k30', '1.0');
p27 = addparameter(model, 'k31', '1.0');
p28 = addparameter(model, 'k32', '1.0');
p29 = addparameter(model, 'k33', '1.0');
p30 = addparameter(model, 'k34', '1.5');
p31 = addparameter(model, 'k35', '1.0');
p32 = addparameter(model, 'k36', '1.0');
p33 = addparameter(model, 'k37', '1.0');
p34 = addparameter(model, 'k38b', '1.0');

```

```

% REACTIONS
% in the first compartement:
% reazione di repression da parte dell'IPTG? é la r1?
r1 = addreaction(model, 'cell1.LacI + cell1.DNAnikr -> cell1.LacIDNA', 'ReactionRate', 'k12'); % repression, mass
action
r2 = addreaction(model, 'cell1.DNAnikr -> cell1.DNAnikr + cell1.mRNAnikr', 'ReactionRate', 'k1'); % transcription
NIKR, mass action
% DOMANDA: la legge cinetica è PER DEFAULT MASS ACTION? oppure aggiungere
% per ogni reazione
% k#=addkineticlaw(r,'MassAction')
r3 = addreaction(model, 'cell1.mRNAnikr -> cell1.mRNAnikr + cell1.Nikr', 'ReactionRate', 'k2'); % translation
NIKR, mass action
% DOMANDA: anziché k3 si passa a k4 -- cambiare nomi a tutte?
r4 = addreaction(model, 'cell1.mRNAnikr -> null', 'ReactionRate', 'k4'); % mRNAikr degradation, mass action
% r4: NikR + Ni2 --> Nikr2Ni ? è diventato CIS?
%r = addreaction(model, 'cell1.[Nikr:2Ni] -> null', 'ReactionRate', 'k'); % Molecul Degradation
%r = addreaction(model, 'cell1.[Nikr:2Ni] -> cell1.Dimer', 'ReactionRate', 'k'); % Dimerization
%r = addreaction(model, 'cell1.Dimer -> null', 'ReactionRate', 'k'); % Dimer Degradation
r5 = addreaction(model, 'cell1.Nikr -> null', 'ReactionRate', 'k5'); % Nikr degradation, mass action
r6 = addreaction(model, 'cell1.Cis + cell1.DNArfp -> cell1.DNArfp + cell1.mRNArfp', 'ReactionRate', 'k9'); %
transcription RFP, mass action
r7 = addreaction(model, 'cell1.mRNArfp -> cell1.mRNArfp + cell1.RFP', 'ReactionRate', 'k9'); % translation RFP,
mass action
% RFP degradation ?
%r8= addreaction(model, 'cell1.mRNArfp -> null', 'ReactionRate', 'k15'); % mRNArfp degradation
%r9 = addreaction(model, 'cell1.RFP -> null', 'ReactionRate', 'k17'); % RFP degradation, mass action
r10 = addreaction(model, 'cell1.Nikr + cell1.DNAgfp -> cell1.DNAgfp + cell1.mRNAgfp', 'ReactionRate', 'k14'); %
transcription GFP, mass action
% non deve essere cell1.Cis nella r6 anzichè cell1.Nikr?
r11 = addreaction(model, 'cell1.mRNArfp -> null', 'ReactionRate', 'k10'); % mRNArfp degradation
r12 = addreaction(model, 'cell1.mRNAgfp -> cell1.mRNAgfp + cell1.GFP', 'k16') % GFP translation, mass action
r13 = addreaction(model, 'cell1.mRNAgfp -> null', 'ReactionRate', 'k15'); % mRNAgfp degradation
r14 = addreaction(model, 'cell1.GFP -> null', 'ReactionRate', 'k17'); % GFP degradation, mass action
r15 = addreaction(model, 'cell1.Cis + cell1.DNALuxi -> cell1.DNALuxi + cell1.mRNALuxi', 'k18') % LuxI
transcription, mass action
r16 = addreaction(model, 'cell1.mRNALuxi -> cell1.mRNALuxi + cell1.LUXI', 'k19') % LuxI translation, mass action
r17 = addreaction(model, 'cell1.mRNALuxi -> null', 'k21') % mRNALuxi degradation, mass action
r18 = addreaction(model, 'cell1.LUXI -> null', 'k21') % LuxI degradation, mass action
r19 = addreaction(model, '4 cell1.Nikr -> cell1.Trans', 'k22') %da rinominare
r20 = addreaction(model, 'cell1.Trans + 6 cell1.Ni -> cell1.Cis', 'k23') % da rinominare
r21 = addreaction(model, 'cell1.Cis -> null', 'k24') % cis degradation, mass action
rE1 = addreaction(model, 'cell1.SAM + cell1.LUXI -> cell1.HSL'); % HSL formation, enzymatic, Henri-Michaelis-
Menten: Vm*S/(Km+S)
kE1 = addkineticLaw(rE1, 'Henri-Michaelis-Menten')
% in the second compartement:
r22 = addreaction(model, 'cell2.LacI + cell2.DNAnikr -> cell2.LacIDNA', 'ReactionRate', 'k12'); % repression_1,
mass action
r23 = addreaction(model, 'cell2.DNAnikr -> cell2.DNAnikr + cell2.mRNAnikr', 'ReactionRate', 'k1'); % transcription
NIKR_1, mass action
r24 = addreaction(model, 'cell2.mRNAnikr -> cell2.mRNAnikr + cell2.Nikr', 'ReactionRate', 'k2'); % translation
NIKR_1, mass action
r25 = addreaction(model, 'cell2.mRNAnikr -> null', 'ReactionRate', 'k4'); % mRNAnikr degradation, mass action
r26 = addreaction(model, 'cell2.Nikr -> null', 'ReactionRate', 'k5'); % Nikr_1 degradation, mass action
r27 = addreaction(model, '4 cell2.Nikr -> cell1.Trans', 'k22') %
r28 = addreaction(model, 'cell2.Trans + 6 cell2.Ni -> cell2.Cis', 'k23') %
r29 = addreaction(model, 'cell2.Trans -> null', 'ReactionRate', 'k8'); % dimer_1 degradation, mass action
r30 = addreaction(model, 'cell2.Cis + cell1.DNALuxr -> cell1.DNALuxr + cell1.mRNALuxr', 'k25') % LuxR
transcription, mass action
r31 = addreaction(model, 'cell2.mRNALuxr -> cell2.mRNALuxr + cell1.LUXR', 'k26') % LuxR translation, mass action
r32 = addreaction(model, 'cell2.mRNALuxr -> null', 'k39') % mRNALuxr degradation, mass action
r33 = addreaction(model, 'cell2.Cis -> null', 'k24') % Cis degradation, mass action
r34 = addreaction(model, 'cell2.LUXR -> null', 'k27') % LuxR degradation, mass action
r35 = addreaction(model, 'cell2.HSL + cell2.LUXR -> cell2.LUXRHSL', 'k28') % ? LuxRHSL formation
r36 = addreaction(model, 'cell2.LUXRHSL + cell2.DNALuxi -> cell2.DNALuxi + cell2.mRNALuxi', 'ReactionRate',
'k32'); % LuxI_1 transcription, mass action
r37 = addreaction(model, 'cell2.mRNALuxi -> cell2.mRNALuxi + cell2.LUXI', 'ReactionRate', 'k33'); % LuxI_1
translation, mass action
r38 = addreaction(model, 'cell2.mRNALuxi -> null', 'ReactionRate', 'k34'); % mRNALuxi degradation, mass action
r39 = addreaction(model, 'cell2.LUXI -> null', 'ReactionRate', 'k35'); % LuxI_1 degradation, mass action
r40 = addreaction(model, 'cell2.mRNAhpn -> cell2.mRNAhpn + cell2.HPN', 'ReactionRate', 'k30'); % translation HPN,
mass action
r41 = addreaction(model, 'cell2.HPN -> null', 'k38b') % Hpn degradation, mass action
r42 = addreaction(model, 'cell2.LUXRHSL + cell2.DNAhpn -> cell2.DNAhpn + cell2.mRNAhpn', 'k29') %
% LuxI + Hpn?
r43 = addreaction(model, 'cell2.mRNAhpn -> null', 'ReactionRate', 'k31'); % mRNAhpn degradation, mass action
r44 = addreaction(model, 'cell2.HPN + 4 cell2.Ni -> cell2.HPNNi', 'k37') % Hpn protein formation (storage)
rE2 = addreaction(model, 'cell2.SAM + cell2.LUXI -> cell2.HSL') % HSL formation, enzymatic_1, Henri-Michaelis-
Menten: Vm*S/(Km+S)
kE2 = addkineticLaw(rE2, 'Henri-Michaelis-Menten')

% EVENTS:
e1 = addevent('time>=5','cell1.LacIDNA + cell1.IPTC -> cell1.DNAnikr') % binding
e2 = addevent('cell1.Cis>=50.0','mRNAgfp = 0') % activation - deactivation
e3 = addevent('time>=5','cell2.LacIDNA + cell2.IPTC -> cell2.DNAnikr') % binding_1

```