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function singlecell_noise
% this file is based on the mathematica notebook provided in the
% supplemental data section of the paper 'the zebrafish somitogenesis
% oscillator'.

% -----
% ----- CONSTANTS -----
% -----
% Molecules (RR):           Attenuation (MM):
% 1: her1                   1: normal
% 2: her7                   2: 1/10th of normal
%                           3: 1/20th of normal

bPrintOnFile = 0;           % 0 = false, 1 = true
RR = 2;                     % which molecule?
MM = 1;                     % which a value do we check?
koff = 1;                   % 1/mean life time of bound state

aa = [4.5, 0.45, 0.225];    % ammount of attunation
b = 0.23;
c = 0.23;

herr = {'her1','her7'};
a=aa(MM);
att={'normal','one 10th','one 20th'};
strFilePath = ['C:\\SYSBIO\\fig3N_',herr{RR},'_normal_',att{MM}];

tfinal = 1000;
eps = 0.1;                  % timestep (dt)
tpher7 = 1.7;               % Tp for HER7
tmher7 = 7.1;               % 5.9<Tm<20.1 for HER7
tpher1 = 2.8;               % Tp for HER1
tmher1 = 12;                % 10.2<Tm<31.5 for HER1
pcrit = 40;
k = 33;
k1=k/2;

if RR==1
    TM = tmher1;
    TP = tpher1;
else
    TM = tmher7;
    TP = tpher7;
end

ndelaym = floor(TM/eps);    % ADJUST FOR HER1/7
ndelayp = floor(TP/eps);    % ADJUST FOR HER1/7
nfinal = floor(tfinal/eps);

p = zeros(1,nfinal); % nfinal
m = p;
xx = ones(1,nfinal);

% numerize the differential equations
for i=2:nfinal
    if i>ndelayp
        p(i) = p(i-1)+eps*(a*m(i-ndelayp)-b*p(i-1));
    else

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        p(i) = p(i-1)+eps*(0-b*p(i-1));
    end
    if i>ndelaym
        m(i) = m(i-1)+eps*(k1*xx(i-ndelaym)-c*m(i-1));
    else
        m(i) = m(i-1)+eps*(1-c*m(i-1));
    end
    v = g(p(i-1),koff,pcrit)+koff;
    u = koff/v;
    expveps = exp(-v*eps);
    p00 = 1-u*(1-expveps);
    p10 = u*(1-expveps);
    p01 = (1-u)*(1-expveps);
    p11 = u*(1-expveps)+expveps;
    pp00 = p00*p00;
    pp10 = 2*p10*p00;
    pp20 = p10*p10;
    pp01 = p01*p00;
    pp11 = p11*p00+p01*p10;
    pp21 = p10*p11;
    pp02 = p01*p01;
    pp12 = 2*p01*p11;
    pp22 = p11*p11;

    temp = rand(1);
    if xx(i-1) == 0
        if temp < pp00
            xx(i) = 0;
        elseif temp>=pp00 && temp <= pp00+pp10
            xx(i) = 1;
        else
            xx(i) = 2;
        end
    elseif xx(i-1) == 1
        if temp<pp01
            xx(i)=0;
        elseif temp >=pp01 && temp <= pp01+pp11
            xx(i)=1;
        else
            xx(i)=2;
        end
    elseif xx(i-1) == 2
        if temp < pp02
            xx(i)=0;
        elseif temp >=pp02 && temp <=pp02+pp12
            xx(i)=1;
        else
            xx(i)=2;
        end
    end
end
end

pt = ones(1,nfinal);
for i =1:nfinal
    pt(i)=i*eps;
end
mt = pt;

if (bPrintOnFile)
    figure('Visible','off')
else
    figure
end
end

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[AX,H1,H2] = plotyy(pt,p,mt,m,'plot');
title([herr{RR},' ', with ',att{MM},' rate protein synthesis'])
set(get(AX(1),'Ylabel'),'String','Protein')
set(get(AX(2),'Ylabel'),'String','mRNA')
set(AX(1),'ylim',[0 1200],'YTick',0:400:1200)
set(AX(2),'ylim',[0 120],'YTick',0:40:120)
set(AX,'XTick',0:200:1000,'XTickLabel',{'0','200','400','600','800','time (min)'})
set(gcf,'Units','centimeters');
aFigurePosition = [5 5 20 6];
set(gcf,'Position',aFigurePosition);
set(gcf,'PaperPositionMode','auto');
set(gca,'Units','normalized','Position',[0.15 0.2 0.75 0.7]);

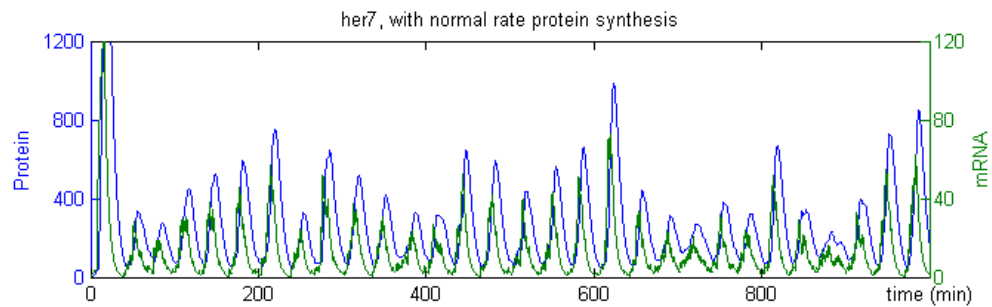
if (bPrintOnFile)
    print('-dpng','-loose', sprintf('-r%d', 300),strcat(strFilePath, '.png'));
end

% -----
function kon = g(x,koff,pcrit)
kon = koff*x^2/pcrit^2;

% -----
function y = f(x,k,pcrit)
y = k/(1+x^2/pcrit^2);

% -----

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