

$$IKKKa \quad \partial y(1) = Ka \cdot B(KN - y(1)) \cdot ka20 / (ka20 + y(1)) - Ki \cdot y(1)$$

$$IKKKn \quad \partial y(2) = k4(KNN - y(2) - y(3) - y(4)) - K1 \cdot y(1)^2 \cdot y(2)$$

$$IKKa \quad \partial y(3) = K1 \cdot y(1)^2 \cdot y(2) - K3 \cdot y(3) \cdot (K2 + y(3)) / K2$$

$$IKKi \quad \partial y(4) = K3 \cdot y(3) \cdot (K2 + y(3)) / K2 - K4 \cdot y(4)$$

$$IKBp \quad \partial y(5) = a2 \cdot y(3) \cdot y(11) - tp \cdot y(5)$$

$$NFKB/IKBp \quad \partial y(6) = a3 \cdot y(3) \cdot y(14) - tp \cdot y(6)$$

$$NFKB \quad \partial y(7) = c6a \cdot y(14) - a1 \cdot y(7) \cdot y(11) + tp \cdot y(6) - i1 \cdot y(7)$$

$$NFKBn \quad \partial y(8) = a1 \cdot Kv \cdot y(12) \cdot y(8) + i1 \cdot y(7)$$

$$A20 \quad \partial y(9) = c4 \cdot y(10) - E5 \cdot y(9)$$

$$A20t \quad \partial y(10) = c1 \cdot GA20 - c3 \cdot y(10)$$

$$IKB \quad \partial y(11) = -a2 \cdot y(3) \cdot y(11) - a1 \cdot y(11) \cdot y(7) + c4 \cdot y(13) - c5a \cdot y(11) - c1a \cdot y(11) + eta \cdot y(12)$$

$$IKBn \quad \partial y(12) = -a1 \cdot Kv \cdot y(12) \cdot y(8) + c1a \cdot y(11) - c1a \cdot y(12)$$

$$IKBt \quad \partial y(13) = c1 \cdot GIKB - c3 \cdot y(13)$$

$$NFKB/IKB \quad \partial y(14) = a1 \cdot y(11) \cdot y(7) - c6a \cdot y(14) - a3 \cdot y(3) \cdot y(14) + c2a \cdot y(15)$$

$$NFKB/IKBn \quad \partial y(15) = a1 \cdot Kv \cdot y(12) \cdot y(8) - c2a \cdot y(15)$$

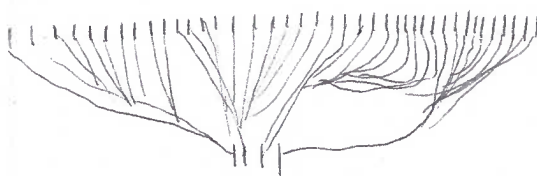
$$TNF_{ext} \quad \partial y(16) =$$

$$c1r - c3r \cdot y(17) + c1rR$$

1000 bottles

~~1000~~

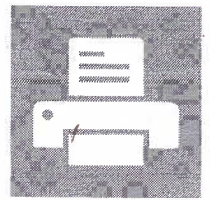
all but I need to drink each bottle



1 2 3 4 5 6 7 8 9 10
11 12 13 14 15 16 17 18 19 20
21 22 23 24 25 26 27 28 29 30

Transfection Protocol of each cell line of cytokines.
Find concentration. For STAT3-10...

Find times of reaction.

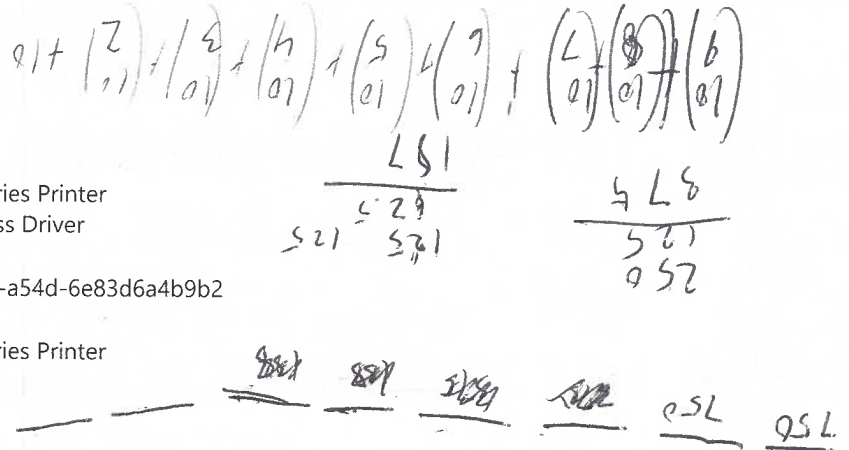


Windows Printer Test Page

You have correctly installed your Microsoft PWG Raster Class Driver on DESKTOP-3A4R1TE.

PRINTER PROPERTIES

Submitted Time: 12:59:25 PM
Date: 5/30/2019
User Name: UOFI\sarkar
Computer Name: DESKTOP-3A4R1TE
Printer Name: Brother DCP-L2550DW series Printer
Printer Model: Microsoft PWG Raster Class Driver
Color Support: No
Port Name(s): WSD-cd119b1f-c64f-4057-a54d-6e83d6a4b9b2
Data Format: RAW
Printer Share Name: Brother DCP-L2550DW series Printer
Print Processor: winprint
OS Environment: Windows NT x86

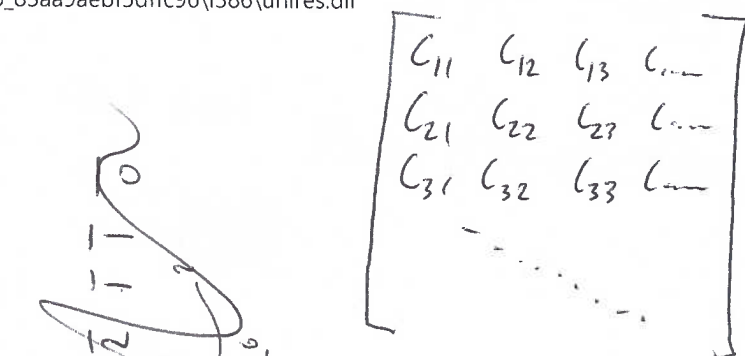
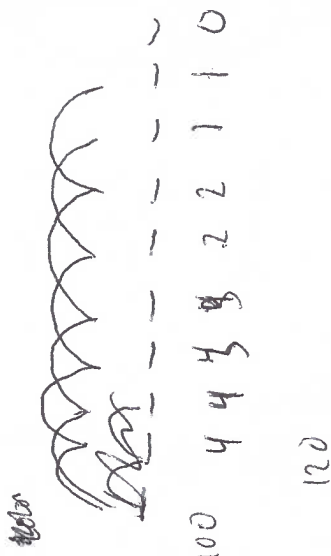


PRINT DRIVER PROPERTIES

Driver Name: Microsoft PWG Raster Class Driver
Driver Type: Type 4 - User Mode
Driver Version: 10.0.17763.1

ADDITIONAL PRINT DRIVER FILES

C:\WINDOWS\System32\DriverStore\FileRepository\prnms007.inf_x86_d694ba8720fe35d3\1386\MSPWGR-manifest.ini
C:\WINDOWS\System32\DriverStore\FileRepository\prnms007.inf_x86_d694ba8720fe35d3\1386\MSPWGR-pipelineconfig.xml
C:\WINDOWS\System32\DriverStore\FileRepository\ntprint4.inf_x86_34808b1c386b5dc1\1386\PWGRRenderFilter.dll
C:\WINDOWS\System32\DriverStore\FileRepository\ntprint.inf_x86_83aa9aebf5dff96\1386\StdNames.gpd
C:\WINDOWS\System32\DriverStore\FileRepository\ntprint.inf_x86_83aa9aebf5dff96\1386\unires.dll



2D → 3D Matrix
1. Random Knockout Cells
in matrix to open
up space.
2. Find clusters
number, DP
to determine cluster
size in matrix
+1, -1 for
cluster/no cluster.
3. Use 3DDM to build 3D
intensity plot. Simulate
model many times to
see if similar "looks"
occur.

```

1 ✓
2
3 Main Program for
4
5 STOCHASTIC SIMULATIONS OF NF-κB PATHWAY
6 S. Tay et al. 2010 Nature
7
8 Calls: Model, Parameters, AllCellPlotting and AvarageCellPlotting
9
10 After running MainFile you can run
11 AllCellPlotting and AvarageCellPlotting
12
13 Saves all data in 'last' - can be used to make plots latter on
14
15
16 ✓
17
18 clear; %reset all
19 clc; %clear comand window
20 starttime=clock; %current time
21 rand('twister', sum(1000*clock));
22
23
24 #####
25 ##### Simulation setup #####
26 #####
27
28 TNF=10; % TNF dose
29
30 ANa=2; AN=2; ANR=2; % ANa=2 - # IKBa alleles, AN=2 - # A20 alleles,
ANR=2 - # Reporter gene alleles
31
32 %Set AN=0 to study A20 knockout?
33
34 N=5; % number of cell to be simulated
35
36 #####
37 ##### Simulation time points #####
38 ##### Various time protocols can be studied within this frame #####
39 #####
40
41 t000=10*3600; %10h randomization of initial conditions
42 t00=10*3600; %10h equilibrium waiting time
43
44 t0=50*60; % 1 step, time when TNF is being introduced into the system
(in seconds)
45

```

Handwritten notes:
 XXX & YYY are outputs
 ↑ All cells. ↑ Average cells
 AB & AA on/off switches


```

46 tw1=5*60; % 2 step, length of TNF stimulation
47 te1=100*60; % 3 step length of first break (White breaks: 3600s,
6000s, 12000s, our break 170*60s)
48
49 tw2=5*60; % 4 step length of second TNF stimulation
50 te2=100*60; % 5 step length of second break
51
52 tw3=5*60; % 6 step length of third TNF stimulation
53 te3=100*60; % 7 step length of third break
54
55 % #####
56
57
58 tt=1000; % forward time for ODEs solving
59
60 YYY=0; %matrix of average, all variables y0(i)(t)
61 NFKB=0; %total nuclear NF-kB
62 GGa=0; GG=0; GGT=0; GGR=0; %status of Ikba, A20, TNF and reporter genes
63 Bb=0; %number of active receptors
64 MM=0; % TNF-R1 receptor
65 NFF=0; % NF-KB level
66
67 for i=1:N %beginning the mean loop
68
69 % #####
70 % ##### Initial conditions #####
71 % #####
72
73 i %cell number
74
75
76 [NF0,NF1,NF2,M0,M1,M2,k4,ka20,AB,kv,q1,q2,c1,c3,c4,c5,k1,k2,k3,a1,a2,a3,cla,
c5a,c6a,il,ila,ela,e2a,dt,tp,KN,KNN,ka,ki,kb,kf,Tdeg,q1r,q2r,q2rr,c1r,c1rr,c3r]
=Parameters;
77
78 %%% Randomizations of total TNF receptors and NF-kB levels %%%
79
80
81 NF=round(NF0*exp(NF2+randn*Nf1)) %NF-kB level
82 while NF > 10*Nf0
83 NF=round(NF0*exp(NF2+randn*Nf1))
84 end
85
86 %NF=Nf0; %uncomment to remove extrinsic noise
87
88 % Lognormal distribution with Median=Nf0, Mean=Nf0*Exp(Nf1^2/2),
89 % Variance = Nf0^2 * (Exp (Nf1^2 -1) * Exp(Nf1^2)
90
91

```

Time ODE Interval

Not used:

Loop through each cell.

Keep within order of magnitude.


```

92     M=round(M0*exp(M2+randn*M1)) % number of TNFR1 receptors
93     while M > 10*M0
94     M=round(M0*exp(M2+randn*M1))
95     end
96
97     M=M0; %uncomment to remove extrinsic noise
98
99     % Lognormal distribution with Median=M0, Mean=M0*Exp(M1^2/2), %
100    % Variance = M0^2 * (Exp (M1^2 -1) * Exp(M1^2)
101
102    %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
103
104
105
106    y0=zeros(1,19); %initial conditions set to zero and next:
107
108    y0(14)=NF; %NF-kB is given in cytoplasmic complex(IkBa|NFkB) (total
NF-kB kept constant), standard = 10^5
109    y0(2)=2*10^5; %initial IKK $\alpha$ , total IKK kept constant
110    y0(11)=0.14*y0(14); %free cytoplasmic IkBa protein
111    y0(12)=0.06*y0(14); %free nuclear IkBa protein
112    y0(13)=10; %IkBa mRNA
113    y0(10)=10; %10 A20 mRNA
114    y0(9)=10000; %10000 A20 protein
115
116
117    y0(10)=AB*y0(10);
118    y0(9)=AB*y0(9);
119
120    Ga=0; % initial status of IkBa promoter
121    G=0; % initial status of A20 promoter
122    GI=0; % initial status of TNF promoter
123    GR=0; % initial status of reporter gene promoter
124    B=0; % initial number of active receptors
125    yy0=y0; % initial conditions y0(i)
126
127    %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
128    %##### -1 step - randomization of initial condition #####
129    %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
130
131    realtime=0; %simulated time
132    phase=round(rand*(1000/dt)*dt); %random initial time (dt-simulation time
step -10s)
133    tspan=[0:dt:tt]; %time for which the solution is derived to
find the switching time, tt=1h
134
135    while (realtime<phase)
136        [T0,Y0]=ode23tb(@Model,tspan,yy0,[],Ga,G,GR,B);
137        Yact=Y0(:,8);

```

keep within order of magnitude

Logistic law of over

fraction of amount that are bound to NF-RB not

On/off switch

Knockout

IkBa

A20

Repk

(0,1) set time

1000

10 hr

10s

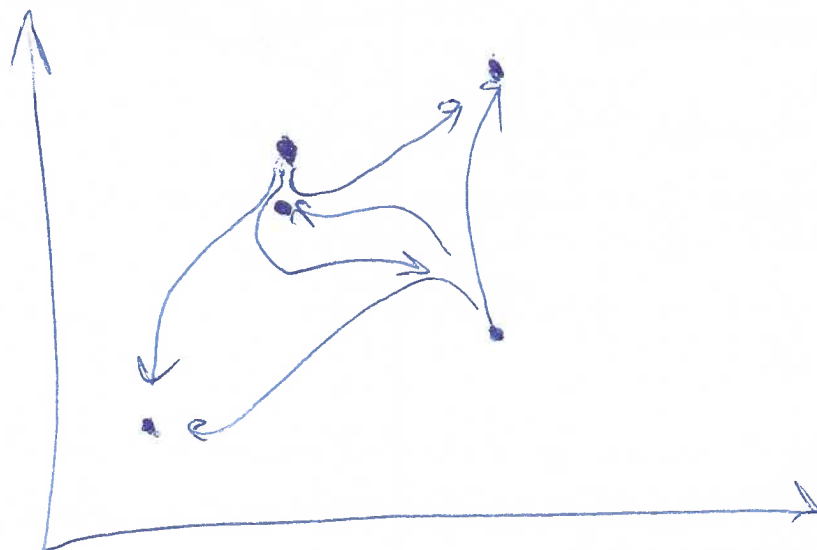
Factor of 10s

Risky

ODE 23tb argument

Options Open

Unknown from Pppl




```

138     Yin=Y0(:,12); %amount of IkBn
139     TR=Y0(:,16); %TNF level
140     Gax=Ga; Gx=G; GRx=GR; Bx=B;
141     [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TR,Gax,Gx,GRx,Bx,Yact,Yin,M); %
function determining the change of gene status, calls statuschange
142
143     tc=T0(mk); %time when the status changes
144     yy0=Y0(mk,:); %transfer of initial conditions to the next
iteration
145     realtime=realtime+tc;
146     end;
147
148     if (realtime>phase)
149         nn=(realtime-phase)/dt;
150         yy0=Y0(mk-nn,:);
151         Ga=Gax; G=Gx; GR=GRx; B=Bx;
152     end;
outside of the time interval
153
154     clear Yact Yin Y0 T0 nn mk phase tc;
155
156     %#####
157     %##### 0 step - waiting for "equilibrium" #####
158     %#####
159
160     realtime=0;
161
162     * while (realtime<t00)
163         [T0,Y0]=ode23tb(@Model,tspan,yy0,[],Ga,G,GR,B);
164         Yact=Y0(:,8); %amount of NF-kBn
165         Yin=Y0(:,12); %amount of IkBn
166         TR=Y0(:,16); %TNF level
167         Gax=Ga; Gx=G; GRx=GR; Bx=B;
168         [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TR,Gax,Gx,GRx,Bx,Yact,Yin,M); %
function determining the change of gene status, calls statuschange
169
170         tc=T0(mk); %time when the status changes
171         yy0=Y0(mk,:); %transfer of initial conditions to the next
iteration
172         realtime=realtime+tc;
173     end;
174
175     if (realtime>t00)
176         nn=(realtime-t00)/dt;
177         yy0=Y0(mk-nn,:);
178         Ga=Gax; G=Gx; GR=GRx; B=Bx;
179     end;
outside of the time interval
180

```

Vector

$[c_1, c_2, c_3, \dots]$

number of perturbations past phase.

No change from StatusChange if Δt is small - Not necessary rest of time

status before the last change it occurred

Log normal distributed

Can be time dependent

c_1	c_2	c_3	c_4	\dots
:	:	:	:	:


```

181 clear Yact Yin Y0 T0 nn mk tc;
182
183 #####
184 ##### 1 step- still no TNF #####
185 #####
186
187 realtime=0;
188 ga=[Ga];g=[G];gR=[GR]; % saves activity of IkBa A20 reporter
genes
189 bb=[B]; % saves number of active receptors
190 Y=yy0; % variables where single cell run is
stored
191 T=zeros(1,1); → [0] ←
192
193 while (realtime<t0)
194 [T0,Y0]=ode23tb(@Model,tspan,yy0,[],Ga,G,GR,B);
195 Yact=Y0(:,8); % amount of NF-κBn
196 Yin=Y0(:,12); % amount of IkBαn
197 TR=Y0(:,16); % TNF level
198 Gax=Ga;Gx=G;GRx=GR;Bx=B;
199 [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TR,Gax,Gx,GRx,Bx,Yact,Yin,M); %
function determining the change of gene status, call statuschange
200 tc=T0(mk); % time when the status changes
201 yy0=Y0(mk,:); % transfer of initial conditions to the next
iteration
202 Y=[Y;Y0(2:mk,:)]; % rows from 2 to mk, all columns
203 T=[T;T0(2:mk)+realtime];
204 ga=[ga;Gax*ones(mk-1,1)];
205 g=[g;Gx*ones(mk-1,1)];
206 gR=[gR;GRx*ones(mk-1,1)];
207 bb=[bb;Bx*ones(mk-1,1)];
208 realtime=realtime+tc;
209 end;
210
211
212 nn=(realtime-t0)/dt;
213 x=size(Y);
214 Y=Y(1:(x(1)-nn),:);
215 T=T(1:(x(1)-nn));
216
217 IC Y0(mk-nn,16)=TNF; % setting TNF ON for the next step
218
219 yy0=Y0(mk-nn,:); % consider TNF in last pos'n as IC.
220 x1=length(ga); % could be size(ga) x1(1) ← Rewrite Cumulative
221 ga=ga(1:x1-nn);g=g(1:x1-nn);gR=gR(1:x1-nn);bb=bb(1:x1-nn);
222 Ga=Gax;G=Gx;GR=GRx;B=Bx;
223
224
225 #####

```

Initialization

saves activity of IkBa A20 reporter
saves number of active receptors
variables where single cell run is

→ [0] ←

begs. Y is correctly to be the index. Therefore, only start of 2. plus runs into loop. Acumulate pattern.

[] Length is used. Cumulative Length

IC

consider TNF in last pos'n as IC.

could be size(ga) x1(1) ← Rewrite Cumulative

should be same as X.

states not being changed every 1 step.


```

226 ##### 2 step TNF on 1 time #####
227 #####
228
229
230 realtime=t0;
231
232 while (realtime<t0+tw1)
233     [T0,Y0]=ode23tb(@Model,tspan,yy0,[],Ga,G,GR,B);
234     Yact=Y0(:,8); %amount of NF-kBn
235     Yin=Y0(:,12); %amount of IkBn
236     TR=Y0(:,16); %TNF level
237     Gax=Ga;Gx=G;GTx=GT;GRx=GR;Bx=B;
238     [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TR,Gax,Gx,GRx,Bx,Yact,Yin,M); %
function determining the change of gene status, call statuschange
239     tc=T0(mk); %time when the status changes
240     yy0=Y0(mk,:); %transfer of initial conditions to the next
iteration
241     Y=[Y;Y0(2:mk,:)]; %rows from 2 do mk, all columns
242     T=[T;T0(2:mk)+realtime];
243     ga=[ga;Gax*ones(mk-1,1)];
244     g=[g;Gx*ones(mk-1,1)];
245     gR=[gR;GRx*ones(mk-1,1)];
246     bb=[bb;Bx*ones(mk-1,1)];
247     realtime=realtime+tc;
248 end;
249
250
251 nn=(realtime-t0-tw1)/dt;
252 x=size(Y);
253 Y=Y(1:(x(1)-nn),:);
254 T=T(1:(x(1)-nn));
255
256 Y0(mk-nn,16)=0; %setting TNF OFF for the next step
257
258 yy0=Y0(mk-nn,:);
259 x1=length(ga);
260 ga=ga(1:x1-nn);g=g(1:x1-nn);gR=gR(1:x1-nn);bb=bb(1:x1-nn);
261 Ga=Gax;G=Gx;GT=GTx;GR=GRx;B=Bx;
262
263
264 #####
265 ##### 3 step TNF washed out 1 time #####
266 #####
267
268
269 realtime=t0+tw1;
270
271 while (realtime<t0+tw1+tel)
272     [T0,Y0]=ode23tb(@Model,tspan,yy0,[],Ga,G,GR,B);

```



```

273      Yact=Y0(:,8);          %amount of NF-kBn
274      Yin=Y0(:,12);         %amount of IkBan
275      TR=Y0(:,16);          %TNF level
276      Gax=Ga;Gx=G;GRx=GR;Bx=B;
277      [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TR,Gax,Gx,GRx,Bx,Yact,Yin,M); %
function determining the change of gene status, call statuschange
278      tc=T0(mk);            %time when the status changes
279      yy0=Y0(mk,:);         %transfer of initial conditions to the next
iteration
280      Y=[Y;Y0(2:mk,:)];     %rows from 2 do mk, all columns
281      T=[T;T0(2:mk)+realtime];
282      ga=[ga;Gax*ones(mk-1,1)];
283      g=[g;Gx*ones(mk-1,1)];
284      gR=[gR;GRx*ones(mk-1,1)];
285      bb=[bb;Bx*ones(mk-1,1)];
286      realtime=realtime+tc;
287      end;
288
289
290      nn=(realtime-t0-tw1-tel)/dt;
291      x=size(Y);
292      Y=Y(1:(x(1)-nn),:);
293      T=T(1:(x(1)-nn));
294
295      Y0(mk-nn,16)=TNF;      %setting TNF ON for the next step
296
297      yy0=Y0(mk-nn,:);
298      x1=length(ga);
299      ga=ga(1:x1-nn);g=g(1:x1-nn);gR=gR(1:x1-nn);bb=bb(1:x1-nn);
300      Ga=Gax;G=Gx;GR=GRx;B=Bx;
301
302
303
304      #####
305      ##### 4 step TNF on for 2 time #####
306      #####
307
308
309      realtime=t0+tw1+tel;
310
311      while (realtime<t0+tw1+tel+tw2)
312          [T0,Y0]=ode23tb(@Model,tspan,yy0,[],Ga,G,GR,B);
313          Yact=Y0(:,8);      %amount of NF-kBn
314          Yin=Y0(:,12);      %amount of IkBan
315          TR=Y0(:,16);      %TNF level
316          Gax=Ga;Gx=G;GRx=GR;Bx=B;
317          [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TR,Gax,Gx,GRx,Bx,Yact,Yin,M); %
function determining the change of gene status, call statuschange
318          tc=T0(mk);        %time when the status changes

```



```

319      yy0=Y0(mk,:);          %transfer of initial conditions to the next
iteration
320      Y=[Y;Y0(2:mk,:)];      %rows from 2 do mk, all columns
321      T=[T;T0(2:mk)+realtime];
322      ga=[ga;Gax*ones(mk-1,1)];
323      g=[g;Gx*ones(mk-1,1)];
324      gR=[gR;GRx*ones(mk-1,1)];
325      bb=[bb;Bx*ones(mk-1,1)];
326      realtime=realtime+tc;
327  end;
328
329
330      nn=(realtime-t0-tw1-tel-tw2)/dt;
331      x=size(Y);
332      Y=Y(1:(x(1)-nn),:);
333      T=T(1:(x(1)-nn));
334
335      Y0(mk-nn,16)=0;          %setting TNF OFF for the next step
336
337      yy0=Y0(mk-nn,:);
338      x1=length(ga);
339      ga=ga(1:x1-nn);g=g(1:x1-nn);gR=gR(1:x1-nn);bb=bb(1:x1-nn);
340      Ga=Gax;G=Gx;GR=GRx;B=Bx;
341
342      #####
343      ##### 5 step TNF washed out 2 time #####
344      #####
345
346
347      realtime=t0+tw1+tel+tw2;
348
349      while (realtime<t0+tw1+tel+tw2+te2)
350          [T0,Y0]=ode23tb(@Model,tspan,yy0,[],Ga,G,GR,B);
351          Yact=Y0(:,8);          %amount of NF-kBn
352          Yin=Y0(:,12);          %amount of IkBan
353          TR=Y0(:,16);          %TNF level
354          Gax=Ga;Gx=G;GRx=GR;Bx=B;
355          [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TR,Gax,Gx,GRx,Bx,Yact,Yin,M); %
function determining the change of gene status, call statuschange
356          tc=T0(mk);          %time when the status changes
357          yy0=Y0(mk,:);          %transfer of initial conditions to the next
iteration
358          Y=[Y;Y0(2:mk,:)];      %rows from 2 do mk, all columns
359          T=[T;T0(2:mk)+realtime];
360          ga=[ga;Gax*ones(mk-1,1)];
361          g=[g;Gx*ones(mk-1,1)];
362          gR=[gR;GRx*ones(mk-1,1)];
363          bb=[bb;Bx*ones(mk-1,1)];
364          realtime=realtime+tc;

```



```

365     end;
366
367
368     nn=(realtime-t0-tw1-te1-tw2-te2)/dt;
369     x=size(Y);
370     Y=Y(1:(x(1)-nn),:);
371     T=T(1:(x(1)-nn));
372
373     Y0(mk-nn,16)=TNF;           %setting TNF ON for the next step
374
375     yy0=Y0(mk-nn,:);
376     x1=length(ga);
377     ga=ga(1:x1-nn);gR=g(1:x1-nn);gR=gR(1:x1-nn);bb=bb(1:x1-nn);
378     Ga=Gax;G=Gx;GR=GRx;B=Bx;
379
380
381     #####
382     ##### 6 step TNF on for the 3 time #####
383     #####
384
385
386     realtime=t0+tw1+te1+tw2+te2;
387
388     while (realtime<t0+tw1+te1+tw2+te2+tw3)
389         [T0,Y0]=ode23tb(@Model,tspan,yy0,[],Ga,G,GR,B);
390         Yact=Y0(:,8);           %amount of NF-kBn
391         Yin=Y0(:,12);          %amount of IkBan
392         TR=Y0(:,16);           %TNF level
393         Gax=Ga;Gx=G;GRx=GR;Bx=B;
394         [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TR,Gax,Gx,GRx,Bx,Yact,Yin,M); %
395         tc=T0(mk);             %time when the status changes
396         yy0=Y0(mk,:);          %transfer of initial conditions to the next
iteration
397         Y=[Y;Y0(2:mk,:)];      %rows from 2 do mk, all columns
398         T=[T;T0(2:mk)+realtime];
399         ga=[ga;Gax*ones(mk-1,1)];
400         g=[g;Gx*ones(mk-1,1)];
401         gR=[gR;GRx*ones(mk-1,1)];
402         bb=[bb;Bx*ones(mk-1,1)];
403         realtime=realtime+tc;
404     end;
405
406
407     nn=(realtime-t0-tw1-te1-tw2-te2-tw3)/dt;
408     x=size(Y);
409     Y=Y(1:(x(1)-nn),:);
410     T=T(1:(x(1)-nn));
411

```



```

412 Y0(mk-nn,16)=0; %setting TNF OFF for the next step
413
414 yy0=Y0(mk-nn,:);
415 x1=length(ga);
416 ga=ga(1:x1-nn);g=g(1:x1-nn);bb=bb(1:x1-nn);
417 Ga=Gax;G=Gx;GR=GRx;B=Bx;
418
419 #####
420 ##### 7 step TNF washed out 3 time #####
421 #####
422
423
424 realtime=t0+tw1+tel+tw2+te2+tw3;
425
426 while (realtime<t0+tw1+tel+tw2+te2+tw3+te3)
427 [T0,Y0]=ode23tb(@Model,tspan,yy0,[],Ga,G,GR,B);
428 Yact=Y0(:,8); %amount of NF-kBn
429 Yin=Y0(:,12); %amount of IkBn
430 TR=Y0(:,16); %TNF level
431 Gax=Ga;Gx=G;GRx=GR;Bx=B;
432 [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TR,Gax,Gx,GRx,Bx,Yact,Yin,M); %
function determining the change of gene status, call statuschange
433 tc=T0(mk); %time when the status changes
434 yy0=Y0(mk,:); %transfer of initial conditions to the next
iteration
435 Y=[Y;Y0(2:mk,:)]; %rows from 2 do mk, all columns
436 T=[T;T0(2:mk)+realtime];
437 ga=[ga;Gax*ones(mk-1,1)];
438 g=[g;Gx*ones(mk-1,1)];
439 gR=[gR;GRx*ones(mk-1,1)];
440 bb=[bb;Bx*ones(mk-1,1)];
441 realtime=realtime+tc;
442 end;
443
444
445 nn=(realtime-t0-tw1-tel-tw2-te2-tw3-te3)/dt;
446 x=size(Y);
447 Y=Y(1:(x(1)-nn),:);
448 T=T(1:(x(1)-nn));
449
450 Y0(mk-nn,16)=TNF; %setting TNF ON for the next step
451
452 yy0=Y0(mk-nn,:);
453 x1=length(ga);
454 ga=ga(1:x1-nn);g=g(1:x1-nn);gR=gR(1:x1-nn);bb=bb(1:x1-nn);
455 Ga=Gax;G=Gx;GR=GRx;B=Bx;
456
457 %%%%%%%%%%%
458

```



```

459
460   YYY=YYY+Y;
461   GGa=GGa+ga;
462   GG=GG+g;
463   GGR=GGR+gR;
464   Bb=Bb+bb;
465
466   MM(i)=M;
467   NFF(i)=NF;
468
469   %#####
470   %##### DATA FOR PLOTS #####
471   %#####
472
473
474   XXX(i, :, :) = Y( :, :, : );
475   XB(i, :) = bb( : );
476   XG(i, :) = g( : );
477   XGa(i, :) = ga( : );
478   XGR(i, :) = gR( : ); % data for all cells
479
480   end;
481
482   clear tspan tspanl g ga T0 Y0 Yact Yin Y y0 yy0 tindex;
483
484
485
486   YYY=YYY/N;
487   GGa=GGa/N;
488   GG=GG/N;
489   GGR=GGR/N;
490   Bb=Bb/N;
491   T=(T-t0)/60;
492
493
494   % % Data Processing : Counts Cells Responding to First and Second Pulse
495   % % designated for two pulses only
496   %
497   % RecetorsAverage=sum(MM)/N
498   % NFaverage=sum(NFF)/N
499   %
500   % NFKE=XXX(:, :, 8)+XXX(:, :, 15);
501   % both=0;
502   % onlyfirst=0;
503   % onlysecond=0;
504   %
505   % both2=0;
506   % onlyfirst2=0;
507   % onlysecond2=0;

```

} set to new variable
 Accomodate Pattern

Per Cell

Per Cell

Cell Loop

Time in min show first TAF start analyzing


```
508 %
509 % for i=1:N
510 %     s=0;
511 %     f=0;
512 %     s2=0;
513 %     f2=0;
514 %     aa=NFKB(i,:);
515 %     c1=size(aa);
516 %     c=round(c1(2)/2);
517 %     a1=aa(i:c);
518 %     a2=aa(c:2*c-1);
519 %
520 % if max(a1)>NF0/10
521 %     f=1;
522 % end
523 % if max(a1)>NF0/5
524 %     f2=1;
525 % end
526 % if max(a2)>NF0/10
527 %     s=1;
528 % end
529 % if max(a2)>NF0/5
530 %     s2=1;
531 % end
532 %     both=both+f*s;
533 %     onlyfirst=onlyfirst+f-f*s;
534 %     onlysecond=onlysecond+s-f*s;
535 %
536 %     both2=both2+f2*s2;
537 %     onlyfirst2=onlyfirst2+f2-f2*s2;
538 %     onlysecond2=onlysecond2+s2-f2*s2;
539 % end
540 %
541 % Threshold=0.1
542 %
543 % both
544 % onlyfirst
545 % onlysecond
546 % any=both+onlyfirst+onlysecond
547 %
548 % Threshold=0.2 % Used for this study
549 %
550 % both2
551 % onlyfirst2
552 % onlysecond2
553 % any2=both2+onlyfirst2+onlysecond2
554
555 %%% End of data processing %%%
556
```

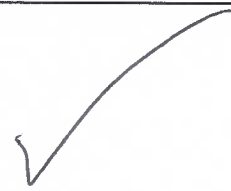

557

558 simulation_time=etime(clock,starttime) %simulation time seconds

559 save last

560 AllCellPlotting

561



Active Receptors

Activator
Inhibitor

```

1 #####
2 ##### Changes the values of the discrete variables #####
3 ##### First time to the next reaction is determined, then the reaction #####
4 #####
5
6 function [mk,Ga,G,GR,B]=StatusChange(AN,ANa,ANR,TRx,Gax,Gx,GRx,Bx,Yact,Yin,M)
7
8 Ga=Gax;G=Gx;GR=GRx;B=Bx;
9 %calls Parameters
10 [NF0,NF1,NF2,M0,M1,M2,k4,ka20,AB,kv,q1,q2,c1,c3,c4,c5,k1,k2,k3,a1,a2,a3,cla,c5a,
c6a,i1,ila,e1a,e2a,dt,tp,KN,KNN,ka,ki,kb,kf,Tdeg,q1r,q2r,q2rr,clr,clrr,c3r] =
=Parameters;
11
12 % Yact- amount of NFkBn -Y(:,8)
13 % Yin - amount of IKBa -Y(:,12)
14 % mk index (time) of gene status change
15
16 ro=(ANa-Gax)*q1*Yact+Gax*(q2*Yin)+(AN-Gx)*q1*Yact+Gx*(q2*Yin)+(ANR-GRx)*
q1r*Yact+GRx*(q2r*Yin+q2rr)+(M-Bx)*(kb*TRx)+Bx*kf; %total propensity function
17
18 roint=dt*cumtrapz(ro); % propensity function integrated
19 fd=1-exp(-roint); % Distribution of the switching time
20
21 r=rand; % r to last element in fd,
22 if (fd(length(fd))<r)
23
24     mk=length(fd);
25 end;
26
27 if (fd(length(fd))>=r)
28
29 a=abs(fd-r);
30 mk=find([a-min(a)]==0); % mk = index (time) of next reaction
31 clear a fd ro roint; % r not cleared.
32
33 #####
34 ##### Determining which reaction takes place #####
35 #####
36
37 pla=(ANa-Gax)*q1*Yact(mk); % risk of NF-kB association to IKBa site at time mk
38 p2a=Gax*(q2*Yin(mk)); % risk of NF-kB dissociation from IKBa at time mk
39
40 p1=(AN-Gx)*q1*Yact(mk); % risk of NF-kB association to A20 site
41 p2=Gx*(q2*Yin(mk)); % risk of NF-kB dissociation from A20 site
42
43 p1r=(ANR-GRx)*q1r*Yact(mk); % risk of NF-kB association to reporter gene
44 p2r=GRx*(q2r*Yin(mk)+q2rr); % risk of NF-kB dissociation from reporter gene
45
46 p3=(M-Bx)*kb*TRx(mk); % risk of TNFR1-TNF binding

```

Gene copy

TNF α level

Gene On/Off Status

Nuclear NFkB

Nuclear TRAF6

to sum

$$\begin{bmatrix} t_0 \\ b_0 \\ \vdots \end{bmatrix} \rightarrow \begin{bmatrix} t_0 \\ b_0, b_1 \\ b_2, b_3 \\ \vdots \end{bmatrix}$$

Binding Probability Distribution
Method Area?
Lognormal?

Compare r to last element in fd ,
 $mk \Leftarrow$ last position

$\Delta \equiv$ error from r

$mk \equiv$ Index of reaction error from r .

from previous


```

47 p4=Bx*kf;          % list of TNFR1 inactivation
48
49 ss=(p1a+p2a+p1+p2+plr+p2r+p3+p4);
50 p1a=p1a/ss;p2a=p2a/ss;
51 p1=p1/ss;p2=p2/ss;
52 plr=plr/ss;p2r=p2r/ss;
53 p3=p3/ss;p4=p4/ss;
54
55 rnumber=rand;
56 if (rnumber<p1a)          Ga=Ga+1; end;    %IKBa
activates
57 if (rnumber>=p1a)&(rnumber<p1a+p2a)      Ga=Ga-1; end;    %IKBa
inactivates
58
59 if (rnumber>=p1a+p2a)&(rnumber<p1a+p2a+p1)  G=G+1; end;    %A20
activates
60 if (rnumber>=p1a+p2a+p1)&(rnumber<p1a+p2a+p1+p2)  G=G-1; end;    %A20
inactivates
61
62 if (rnumber>=p1a+p2a+p1+p2)&(rnumber<p1a+p2a+p1+p2+plr)  GR=GR+1;
end;    %reporter gene activates
63 if (rnumber>=p1a+p2a+p1+p2+plr)&(rnumber<p1a+p2a+p1+p2+plr+p2r)  GR=GR-1;
end;    %reporter gene inactivates
64
65 if (rnumber>=p1a+p2a+p1+p2+plr+p2r)&(rnumber<p1a+p2a+p1+p2+plr+p2r+p3)
B=B+1;end;    %receptor activation
66 if (rnumber>=p1a+p2a+p1+p2+plr+p2r+p3)&(rnumber<p1a+p2a+p1+p2+plr+p2r+p3+p4)
B=B-1;end    %receptor deactivation
67
68 end;

```

Misty
function



For random number

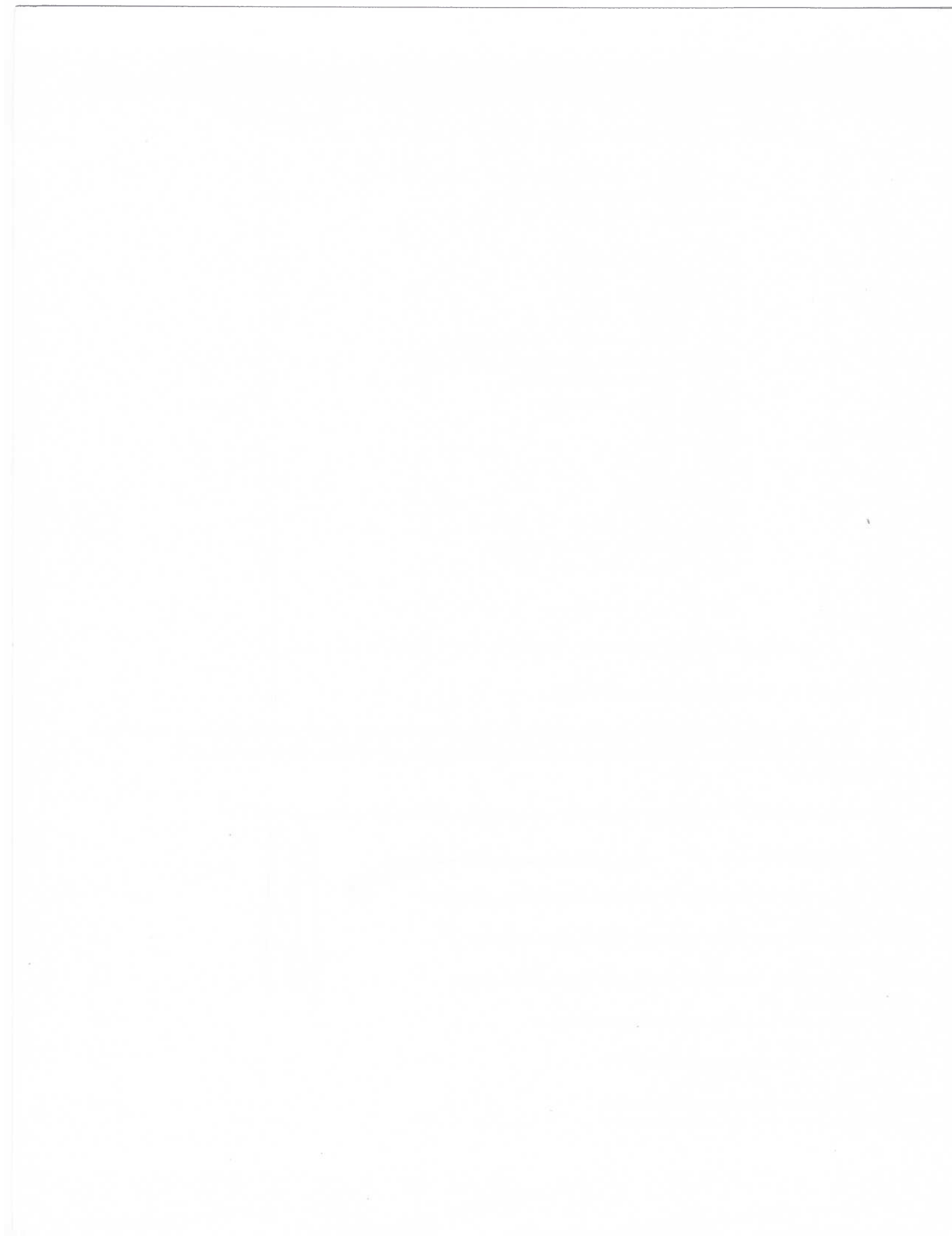
Probability / Proportion could $\neq 0$. Then results cannot be.
 The values are thus 0, 1, 2 for each of the
 three activation quantities.


```

1  %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
2  %
3  %      Function includes system of ODEs describing
4  %      NF-kB regulatory pathway.
5  %      Substrates are coded as follows:
6  %
7  %      y(1)    IKK $\alpha$  active
8  %      y(2)    IKK $\beta$  neutral
9  %      y(3)    IKK $\alpha$  active
10 %      y(4)    IKK $\beta$  inactive
11 %      y(5)    phospho-IkBa cytoplasmic
12 %      y(6)    phospho-IkBa|NFkB cytoplasmic
13 %      y(7)    NFkB cytoplasmic
14 %      y(8)    NFkB $\beta$  nuclear
15 %      y(9)    A20
16 %      y(10)   A20t
17 %      y(11)   IkBa
18 %      y(12)   IkB $\alpha$ 
19 %      y(13)   IkB $\beta$ 
20 %      y(14)   (IkBa|NFkB) cytoplasmic
21 %      y(15)   (IkB $\alpha$ |NFkB $\beta$ ) nuclear
22 %      y(16)   extracellular TNF
23 %
24 %      y(17)   mRNA reporter
25 %
26  %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
27
28 function dy=Model(t,y,Ga,G,GR,B)
29
30 [NF0,NF1,NF2,M0,M1,M2,k4,ka20,AB,kv,q1,q2,c1,c3,c4,c5,k1,k2,k3,a1,a2,a3,c1a,c5a,
31 c6a,i1,ila,ela,e2a,dt,tp,KN,KNN,ka,ki,kb,kf,Tdeg,q1r,q2r,q2rr,c1r,c1rr,c3r]
32 =Parameters;
33
34 %#####
35
36 dy=zeros(19,1);
37
38 dy(1)=ka*B*(KN-y(1))* ka20/(ka20+y(9))-ki*y(1);
39 % active IKK kinase
40
41 dy(2)=-y(1)^2*k1*y(2)+k4*(KNN-y(2)-y(3)-y(4));
42 % neutral IKK
43
44 dy(3)=y(1)^2*k1*y(2)-k3*y(3)*(k2+y(9))/k2;
45 % free active IKK
46
47 dy(4)=k3*y(3)*(k2+y(9))/k2-k4*y(4);
48 % inactive IKK
49
50 dy(5)=a2*y(3)*y(11)-tp*y(5);
51 % Phospho-IkBa cytoplasmic
52
53 dy(6)=a3*y(3)*y(14)-tp*y(6);
54 % cytoplasmic (phospho-IkBa|NF-kB)

```

1
2
3
:
18
19



```
✓42 dy(7)=c6a*y(14)-a1*y(7)*y(11)+tp*y(6)-i1*y(7);
✓free cytoplasmic NFkB
43 dy(8)=i1*y(7)-a1*kv*y(12)*y(8);
✓free nuclear NFkB
44 dy(9)=c4*y(10)-c5*y(9);
✓cytoplasmic A20
45 dy(10)=c1*G-c3*y(10);
A20 transcript
✓46 dy(11)=-a2*y(3)*y(11)-a1*y(11)*y(7)+c4*y(13)-c5a*y(11)-i1a*y(11)+e1a*y(12);
free cytoplasmic IkBa
✓47 dy(12)=-a1*kv*y(12)*y(8)+i1a*y(11)-e1a*y(12);
free nuclear IkBa
48 dy(13)=c1a*Ga-c3*y(13);
IkBa transcript
✓49 dy(14)=a1*y(11)*y(7)-c6a*y(14)-a3*y(3)*y(14)+e2a*y(15);
cytoplasmic (IkBa|NFkB) complex
✓50 dy(15)=a1*kv*y(12)*y(8)-e2a*y(15);
nuclear (IkBa|NFkB) complex
51 dy(16)=-Tdeg*y(16);
extracellular TNF
✓52 dy(17)=c1rr+c1r*GR-c3r*y(17);
Reporter transcript
53
54
55
```



```

1 % #####
2 % ##### PARAMETERS corresponding to S. Tay et al. 2010, Nature ##
3 % ##### Some frequently changed parameters are defined in MainFile ##
4 % #####
5
6
7 function [NF0,NF1,NF2,M0,M1,M2,k4,ka20,AB,kv,q1,q2,c1,c3,c4,c5,k1,k2,k3,a1,a2,a3,
cla,c5a,c6a,i1,ila,e1a,e2a,dt,tp,KN,KNN,ka,ki,kb,kf,Tdeg,q1r,q2r,q2rr,clr,clrr,c3r]
=Parameters
8
9 % #####
10 dt=10; %simulation step s
11 % #####
12
13 kv=5; %kv=5, Volume Ratio
14
15 %##### Randomization of Receptors and NF-kB levels #####
16
17 M0=5000; % 2000 mean number of TNF $\alpha$  receptors assumed for 3T3 cells (our
experiment) Receptor count per cell
18 % Assumed M0=10000 for MEFs, M0=5000 for SK-N-AS, 500 for HeLa to
account
19 % for different cell sensitivities
20 M1=sqrt(2);  $\sigma$ 
21 M2=-1;  $\mu$ 
22
23 % Lognormal distribution with Median=M0*Exp(M2), Mean=M0*Exp(M2+M1^2/2)=M0
24 % Variance = M0^2 * (Exp (M1^2 -1) * Exp(2*M2+M1^2)
25
26
27 NF0=10^5; % mean NF-kB
28 NF1=1/sqrt(2);  $\sigma$ 
29 NF2=-1/4;  $\mu$ 
30
31 % Lognormal distribution with Median=NF0*Exp(NF2), Mean=NF0*Exp(NF2+NF1^2/2)=NF0
32 % Variance = NF0^2 * (Exp (NF1^2 -1) * Exp(2*NF2+NF1^2)
33
34
35 #####
36 ##### Parametrization for the genes and receptor part #####
37 #####
38
39 ##### Receptors activation #####
40
41 kb=1.2*10^-5; %default 1.2*10^-5 = receptor activation rate
42 kf=1.2*10^-3; %default 1.2*10^-3 = receptor inactivation rate
43
44 ##### A20 IkBa Promoters binding #####
45

```



```

✓46 q1=4*10^-7;      %default 4*10^-7 - NF-kB attaching at A20 and IkBa site
✓47 q2=10^-6;       %default 10^-6 - IkBa inducible detaching from A20 and IkBa site
48
49
50 #####
51 ##### Parametrization for the deterministic part #####
52 #####
53
54
✓55 Tdeg=7.7*10^-4; % TNF loss
56 % 2*10^-4 for 10ng (t1/2=60min)
57 % 7*10^-4 for 1ng,
58 % 7.7*10^-4 for 0.1ng
59 % 8.3*10^-4 for 0.01ng
60
61 % use 2*10^-4 for experiments in other than microfluidics
62
63 ##### Transduction pathway #####
64
✓65 KN=10^5;         %default 10^5 - total number of IKKK kinase molecules, ✓
Assumption
✓66 KNN=2*10^5;      %default 2*10^5 - total number of IKK kinase molecules, ✓
Assumption
✓67 ka=2*10^-5;      %default 2*10^-5 - IKKK kinase activation rate (at most 1/s), ✓
Assumption
✓68 ki=0.01;         %default 0.01 - IKKK kinase inactivation rate, Assumption
69
70 ##### A20 and IKK #####
71
→ 72 AB=1;           %A20 on (or off)
73
✓74 c0=0.1;          %default 0.1 - inducible A20 and IkBa mRNA synthesis, Assumption
✓75 c1=AB*c0;        %inducible A20 mRNA synthesis
✓76 c3=0.00075;      %default 0.00075 - A20 and IkBa mRNA degradation rate
✓77 c4=0.5;          %default 0.5 - A20 and IkBa translation rate, FIT
✓78 c5=0.0005;       %default 0.0005 - A20 degradation rate, FIT
✓79 ka20=10^5;        %default 10^5 - A20 TNFR1 block, FIT
✓80 k2=10000;         %default 10000 - IKKa inactivation caused by A20, FIT
✓81 k1=6*10^-10;     %default 6*10^-10; IKKn activation caused by active IKKK, ✓
Assumption
✓82 k3=0.002;        %default 0.002 - IKKa inactivation, FIT
✓83 k4=0.001;        %default 0.001 - IKKii transformation, FIT
84
85 ##### IkB alpha #####
86
→ 87 AA=1;           %IkBa on (or off)
✓88 cla=AA*c0;       %inducible IkBa mRNA synthesis
✓89 a1=5*10^-7;       %default 5*10^-7 - IkBa*NFkB association, Assumption
✓90 a2=10^-7;        %default 10^-7 - IkBa phosphorylation due to action of IKKa, FIT

```

cdeg/kdeg in paper.


```
✓ 91 a3=5*10^-7;      %default 5*10^-7 - (IkBa|NFkB) phosphorylation due to action of
IkKa, FIT
✓ 92 tp=0.01;        %default 0.01 - degradation of phospho-IkBa and phospho-IkBa
complexed to NF-kB, FIT
✓ 93 c5a=0.0001;     %default 0.0001 - IkBa degradation rate
✓ 94 c6a=0.00002;    %default 0.00002 - spontaneous (IkBa|NFkB) degradation of IkBa
complexed to NF-kB
95
96
97 ##### Reporter gene #####
98
✓ 99 q1r=1*10^-7;     %default 1*10^-7 NF-kB attaching at reporter gene site
✓ 100 q2r=1*10^-7;   %default 1*10^-7 inducible NF-kB detaching from reporter gene
site
✓ 101 q2rr=1*10^-3;  %default 1*10^-3 spontaneous NF-kB detaching from reporter gene
site
102
103
✓ 104 c1r=0.05;      %default 0.05 Reporter gene mRNA inducible synthesis
✓ 105 c1rr=0.001;    %default 0.001 Reporter gene mRNA constitutive synthesis
✓ 106 c3r=0.001;     %various considered, Reporter mRNA degradation rate
107
108
109 ##### Transport #####
110
✓ 111 i1=0.01;       %default 0.01 - NFkB nuclear import, FIT
✓ 112 e2a=0.05;      %default 0.05 - (IkBa|NFkB) nuclear export, FIT
✓ 113 i1a=0.002;     %default 0.002 - IkBa nuclear import, FIT
✓ 114 e1a=0.005;     %default 0.005 - IkBa nuclear export, FIT
115
```

