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% This script is to perform Monte Carlo simulations for 1CellPK
% This script includes the following situations (for figure 4):
% Case# 1: AP->BL transport, pHa = 6.5, 0.4um-membrane, 5min
% Case# 2: AP->BL transport, pHa = 6.5, 3um-membrane, 5min
% Case# 3: AP->BL transport, pHa = 7.4, 0.4um-membrane, 5min
% Case# 4: AP->BL transport, pHa = 7.4, 3um-membrane, 5min

% Case# 5: BL->AP transport, pHb = 6.5, 0.4um-membrane, 5min
% Case# 6: BL->AP transport, pHb = 6.5, 3um-membrane, 5min
% Case# 7: BL->AP transport, pHb = 7.4, 0.4um-membrane, 5min
% Case# 8: BL->AP transport, pHb = 7.4, 3um-membrane, 5min

% =====Case#1: AP->BL transport, pHa = 6.5, 0.4um-
membrane,5min=====

clear ; % Clear the memory
z1 = 1 ; % ionization group 1 of CQ
z2 = 2 ; % ionization group 2 of CQ
i1 = sign(z1) ;
i2 = sign(z2) ;

T = 310.15 ; % temperature
R = 8.314 ; % universal gas constant
F = 96484.56 ; % faraday constant
C_a = 1 ; % initial drug concentration (mM)

sim = 10000; % number of simulations
paraNo = 25;
outputNo = 7; % number of output parameters
Para = zeros(sim,paraNo);
Results = zeros(sim,outputNo);

dMdt_exp = 2.2E-6; % +/- 7.18E-7, pmol/sec/cell, measured after
4hrs
Ppore_exp = 2.18E+02; % +/- 34.4, 10^-6 cm/sec, measured after 4hrs
Peff_exp = 1.35; % +/- 0.442, 10^-6 cm/sec, measured after 4hrs
IntraMass_exp = 0.00373; % +/- 0.00014 pmol/cell , measured after 5min

for i = 1:sim

% Drug information -- ChemAxon calculation including logPn, pKa1, and pKa2
logPn = 3.93-0.5+rand(); % unif [3.43, 4.43] ;
pKa1 = 9.96-0.5+rand(); % unif [9.46, 10.46] ;
pKa2 = 7.47-0.5+rand(); % unif [6.97, 7.97] ;
logPd1 = 0.43-0.5+rand(); % unif [-0.07, 0.93] ;
logPd2 = -0.91-0.5+rand(); % unif [-1.41, 0.41] ;
Pn = 10^(logPn-6.7);
Pd1 = 10^(logPd1-6.7);
Pd2 = 10^(logPd2-6.7);

CellNo = 2*10^5*(1+rand()); % cell
number/insert: unif [2*10^5, 4*10^5]
PoreDens = 4*10^6*0.4*(2+rand()); % pore
number/cm^2: unif [3.2*10^6, 4.8*10^6]
A_insert = 1.12*10^(-4) ; % insert area:
1.12 cm^2

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    PoreNo_insert = PoreDens*A_insert*10^(4);           % pore
number/insert
    PoreNo_cell = PoreNo_insert/CellNo ;               % average pore
number/cell
    A_pore_insert = 3.14*((0.4/2)*10^(-6))^2*PoreNo_insert ; % pore area /
insert (m^2)
    A_pore_cell = 3.14*((0.4/2)*10^(-6))^2*PoreNo_cell ; % average pore
area / cell (m^2)

    A_a = 10^(-10)*(1+9*rand());                       % apical
membrane surface area: unif [10^(-10),10*(10)^(-10)] (m^2)
    A_aa = A_pore_cell;                                % pore area/cell
(m^2)
    A_b = A_aa+(10^(-10)-A_aa)*rand();                 % basolateral
membrane surface area: unif [A_aa, 10^(-10)] (m^2)
    A_l = 100*3.14*10^(-12);                           % lysosomal
membrane surface area (m^2)
    A_m = 100*3.14*10^(-12);                           % mitochondrial
membrane surface area (m^2)
    V_c = 0.5*10^(-15)*(1+5*rand());                   % cytosolic
volume: unif [0.5*10^(-15), 3*10^(-15)] (m^3)
    V_l = 10^(-18)*(9.24+(23.8-9.24)*rand());          % lysosomal
volume: unif [9.24*10^(-18), 23.8*10^(-18)] (m^3)
    V_m = 100*5.24*10^(-19)/5*(1+24*rand());          % mitochondrial
volume: unif [10.48*10^(-18), 262*10^(-18)](m^3)
    V_b = 1.5*10^(-6);                                 % basolateral
volume: 1.5 mL

    % Membrane potential (unit in 'Voltage')
    E_a = -0.0093-0.005+0.01*rand();                   % apical
membrane potential: unif [-0.0143, -0.0043]
    E_l = 0.01-0.005+0.01*rand();                     % lysosomal
membrane potential: unif [0.005, 0.015]
    E_m = -0.16 ;                                     % mitochondrial
membrane potential
    E_b = 0.0119-0.005+0.01*rand();                   % basolateral
membrane potential: unif [0.0069, 0.0169]

    % pH values
    pH_a = 6.4+0.2*rand();                             % pH in apical
compartment: unif [6.4, 6.6]
    pH_c = 7.0+0.4*rand();                             % pH in cytosol:
unif [7.0, 7.4]
    pH_l = 4.8+0.4*rand();                             % pH in
lysosomes: unif [4.8, 5.2]
    pH_m = 7.8+0.4*rand();                             % pH in
mitochondria: unif[7.8, 8.2]
    pH_b = 7.4;                                       % pH in
basolateral compartment

    % Apical Compartment
fn_a = 1 / (1 + 10^(i1*(pKa1-pH_a)) + 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a))) ;
fd2_a = fn_a * 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a)) ;
fd1_a = fn_a * 10^(i1*(pKa1-pH_a)) ;
Nd2_a = z2*E_a*F/(R*T) ;
Nd1_a = z1*E_a*F/(R*T) ;

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% Cytoplasm
L_c = 0.05+0.1*rand(); % lipid
fraction in cytosol: unif [0.05, 0.15]
W_c = 1-L_c; % water
fraction in cytosol
Is_c = 0.3; % ion
strength in cytosol (mol)
gamman_c = 10^(0.3*Is_c); %
activity coefficient of neutral molecules in cytosol
gammad1_c = 10^(-0.5*z1*z1*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of monovalent base in cytosol
gammad2_c = 10^(-0.5*z2*z2*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of bivalent base in cytosol
Kn_c = L_c*1.22*10^(logPn);
Kd1_c = L_c*1.22*10^(logPd1);
Kd2_c = L_c*1.22*10^(logPd2);
an_c = 1 / (1 + 10^(i1*(pKa1-pH_c)) + 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c)));
ad2_c = an_c * 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c));
ad1_c = an_c * 10^(i1*(pKa1-pH_c));
Dd2_c = ad2_c / an_c;
Dd1_c = ad1_c / an_c;
fn_c = 1 / (W_c/gamman_c + Kn_c/gamman_c + Dd2_c*W_c/gammad2_c +
Dd2_c*Kd2_c/gammad2_c ...
+ Dd1_c*W_c/gammad1_c + Dd1_c*Kd1_c/gammad1_c );
fd2_c = fn_c * Dd2_c;
fd1_c = fn_c * Dd1_c;

% Mitochondria
L_m = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_m = 1-L_m; % water
fraction in mitochondria
Is_m = 0.3; % ion
strength in mitochondria (mol)
Nd2_m = z2*E_m*F/(R*T);
Nd1_m = z1*E_m*F/(R*T);
gamman_m = 10^(0.3*Is_m); %
activity coefficient of neutral molecules in mitochondria
gammad1_m = 10^(-0.5*z1*z1*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of monovalent base in mitochondria
gammad2_m = 10^(-0.5*z2*z2*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of bivalent base in mitochondria
Kn_m = L_m*1.22*10^(logPn);
Kd1_m = L_m*1.22*10^(logPd1);
Kd2_m = L_m*1.22*10^(logPd2);
an_m = 1 / (1 + 10^(i1*(pKa1-pH_m)) + 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m)));
ad2_m = an_m * 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m));
ad1_m = an_m * 10^(i1*(pKa1-pH_m));
Dd2_m = ad2_m / an_m;
Dd1_m = ad1_m / an_m;
fn_m = 1 / (W_m/gamman_m + Kn_m/gamman_m + Dd2_m*W_m/gammad2_m +
Dd2_m*Kd2_m/gammad2_m ...
+ Dd1_m*W_m/gammad1_m + Dd1_m*Kd1_m/gammad1_m );
fd2_m = fn_m * Dd2_m;
fd1_m = fn_m * Dd1_m;

% Lysosomes

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L_1 = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_1 = 1-L_1 ; % water
fraction in lysosomes
Is_1 = 0.3 ; % ion
strength in lysosomes (mol)
Nd2_1 = z2*E_1*F/(R*T) ;
Nd1_1 = z1*E_1*F/(R*T) ;
gamman_1 = 10^(0.3*Is_1) ; %
activity coefficient of neutral molecules in lysosomes
gammad1_1 = 10^(-0.5*z1*z1*(sqrt(Is_1)/(1+sqrt(Is_1))-0.3*Is_1)); %
activity coefficient of monovalent base in lysosomes
gammad2_1 = 10^(-0.5*z2*z2*(sqrt(Is_1)/(1+sqrt(Is_1))-0.3*Is_1)); %
activity coefficient of bivalent base in lysosomes
Kn_1 = L_1*1.22*10^(logPn) ;
Kd1_1 = L_1*1.22*10^(logPd1) ;
Kd2_1 = L_1*1.22*10^(logPd2) ;
an_1 = 1 / (1 + 10^(i1*(pKa1-pH_1)) + 10^(i1*(pKa1-pH_1)+i2*(pKa2-pH_1))) ;
ad2_1 = an_1 * 10^(i1*(pKa1-pH_1)+i2*(pKa2-pH_1)) ;
ad1_1 = an_1 * 10^(i1*(pKa1-pH_1)) ;
Dd2_1 = ad2_1 / an_1 ;
Dd1_1 = ad1_1 / an_1 ;
fn_1 = 1 / (W_1/gamman_1 + Kn_1/gamman_1 + Dd2_1*W_1/gammad2_1 +
Dd2_1*Kd2_1/gammad2_1 ...
+ Dd1_1*W_1/gammad1_1 + Dd1_1*Kd1_1/gammad1_1 ) ;
fd2_1 = fn_1 * Dd2_1 ;
fd1_1 = fn_1 * Dd1_1 ;

% Basolateral Compartment
fn_b = 1 / (1 + 10^(i1*(pKa1-pH_b)) + 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b))) ;
fd2_b = fn_b * 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b)) ;
fd1_b = fn_b * 10^(i1*(pKa1-pH_b)) ;
Nd2_b = z2*(-E_b)*F/(R*T) ;
Nd1_b = z1*(-E_b)*F/(R*T) ;

% Solve the differential equation system:
% Given a system of linear ODE's expressed in matrix form:
% Y' = AY+G with initial conditions Y(0) = RR,
k11 = -(A_a/V_c)*Pn*fn_c-
(A_a/V_c)*Pd1*Nd1_a*fd1_c*exp(Nd1_a)/(exp(Nd1_a)-1)...
-(A_a/V_c)*Pd2*Nd2_a*fd2_c*exp(Nd2_a)/(exp(Nd2_a)-1)...
-(A_m/V_c)*Pn*fn_c-(A_m/V_c)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)...
-(A_m/V_c)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1)...
-(A_l/V_c)*Pn*fn_c-(A_l/V_c)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)...
-(A_l/V_c)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1)...
-(A_b/V_c)*Pn*fn_c-(A_b/V_c)*Pd1*Nd1_b*fd1_c/(exp(Nd1_b)-1)...
-(A_b/V_c)*Pd2*Nd2_b*fd2_c/(exp(Nd2_b)-1) ;

k12 =
(A_m/V_c)*Pn*fn_m+(A_m/V_c)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-1)...
+(A_m/V_c)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;

k13 =
(A_l/V_c)*Pn*fn_l+(A_l/V_c)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-1)...
+(A_l/V_c)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;

k14 =
(A_b/V_c)*Pn*fn_b+(A_b/V_c)*Pd1*Nd1_b*fd1_b*exp(Nd1_b)/(exp(Nd1_b)-1)...
+(A_b/V_c)*Pd2*Nd2_b*fd2_b*exp(Nd2_b)/(exp(Nd2_b)-1) ;
S1 = (A_a/V_c)*C_a*(Pn*fn_a+Pd1*Nd1_a*fd1_a/(exp(Nd1_a)-1)...

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+Pd2*Nd2_a*fd2_a/(exp(Nd2_a)-1) ) ;

k21 = (A_m/V_m)*Pn*fn_c+(A_m/V_m)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)...
      +(A_m/V_m)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1) ;
k22 = -(A_m/V_m)*Pn*fn_m-
(A_m/V_m)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-1)...
      -(A_m/V_m)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k23 = 0;
k24 = 0 ;
S2 = 0;

k31 = (A_l/V_l)*Pn*fn_c+(A_l/V_l)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)...
      +(A_l/V_l)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1) ;
k32 = 0;
k33 = -(A_l/V_l)*Pn*fn_l-
(A_l/V_l)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-1)...
      -(A_l/V_l)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;

k34 = 0 ;
S3 = 0;

k41 = (A_b/V_b)*Pn*fn_c+(A_b/V_b)*Pd1*Nd1_b*fd1_c/(exp(Nd1_b)-1)...
      +(A_b/V_b)*Pd2*Nd2_b*fd2_c/(exp(Nd2_b)-1) ;
k42 = 0;
k43 = 0;
k44 = -(A_b/V_b)*Pn*fn_b-
(A_b/V_b)*Pd1*Nd1_b*fd1_b*exp(Nd1_b)/(exp(Nd1_b)-1)...
      -(A_b/V_b)*Pd2*Nd2_b*fd2_b*exp(Nd2_b)/(exp(Nd2_b)-1);
S4 = 0;

A = [k11, k12, k13, k14; k21, k22, k23, k24; k31, k32, k33, k34; k41,
k42, k43, k44];
G = [S1, S2, S3, S4]';
RR = [0,0,0,0]';
t = 300 ; % time in sec (5min)

[V,E] = eig(A);
E = diag(E);
H = inv(V)*G;
B = V \ RR;
C = B + H./E;
Z = -(H./E) + exp(t * E).*C ;
Y = real(V * Z);
Y = Y' ;

Ppore = Y(4)*V_b / (t*A_aa*C_a)*10^(2)*10^6 ; %
Pcell, 10^(-6)cm/sec
Peff = Y(4)*V_b*CellNo/(t*A_insert*C_a)*10^(2)*10^6; %
Peff, 10^(-6)cm/sec, normalized by insert area, which is 1.12 cm^2
Mass_cell = (Y(1)*V_c + Y(2)*V_m + Y(3)*V_l)*10^12 ; %
cellular mass, pmol/cell
dMdt = Y(4)*V_b/t*10^12; %
transport rate: pmol/sec/cell

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    Para(i,:) = [A_a*10^12,PoreNo_cell,
A_l*10^12,A_m*10^12,A_b*10^12,V_c*10^18,V_l*10^18,V_m*10^18,V_b*10^6,E_a*1000,E_
l*1000,E_m*1000,E_b*1000,...
                pH_a,pH_c,pH_l,pH_m,pH_b,CellNo,PoreDens,
pKa1,pKa2,logPn,logPd1, logPd2];
    Results(i,:)= [Y(1),Y(2),Y(3),Ppore, Peff, dMdt, Mass_cell];

end

comb = [Results(:,1:7),Para];
fid5 = fopen('AtoB_pH65_04um_5min.dat','w');
fprintf(fid5,'%12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.2e %12.0f %1
2.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4f %12.4f %12.4f %12.4f %12.
2f %12.2f %12.2f %12.2f %12.2f %12.0f %12.0f %12.2f %12.2f %12.2f %12.2f %12.2f
\n', comb) ;
fclose(fid5);

figure(1) ; clf ; hold on ;
grid on;
hist (log10(comb(:,4)),1000);
line([log10(Ppore_exp), log10(Ppore_exp)],[0,50],'Color','r','LineWidth',3);
xlabel('log_{10} (P_{cell}, 10^{-6}
cm/sec)','FontSize',30,'FontWeight','Bold','FontName','Times');
xlim([0, 6]);
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','Fo
ntName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;
title ('histogram of cell
permeability','FontSize',30,'FontWeight','Bold','FontName','Times') ;

figure(2) ; clf ; hold on ;
grid on;
hist (log10(comb(:,5)),1000);
xlim([-3, 3]);
line([log10(Peff_exp), log10(Peff_exp)],[0,50],'Color','r','LineWidth',3);
xlabel('log_{10} (P_{app}, 10^{-6}
cm/sec)','FontSize',30,'FontWeight','Bold','FontName','Times');
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','Fo
ntName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;
title ('histogram of apparent
permeability','FontSize',30,'FontWeight','Bold','FontName','Times') ;

figure(3) ; clf ; hold on ;
grid on;
hist (log10(comb(:,6)),1000);
xlim([-8,-2]);
line([log10(dMdt_exp), log10(dMdt_exp)],[0,50],'Color','r','LineWidth',3);
xlabel('log_{10} (dM/dt,
pmol/sec/cell)','FontSize',30,'FontWeight','Bold','FontName','Times');
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','Fo
ntName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;

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title ('histogram of transport
rate','FontSize',30,'FontWeight','Bold','FontName','Times') ;

figure(4) ; clf ; hold on ;
grid on;
hist (log10(comb(:,7)),1000);
xlim([-5,-0]);
line([log10(IntraMass_exp),
log10(IntraMass_exp)], [0,50], 'Color','r','LineWidth',3);
xlabel('log_{10} (intracellular mass, pmol/cell)
','FontSize',30,'FontWeight','Bold','FontName','Times');
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','Fo
ntName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;
title ('histogram of intracellular
mass','FontSize',30,'FontWeight','Bold','FontName','Times') ;

% =====Case# 2: AP->BL transport, pHa = 6.5, 3um-membrane,
5min=====

clear ; % Clear the memory
z1 = 1 ; % ionization group 1 of CQ
z2 = 2 ; % ionization group 2 of CQ
i1 = sign(z1) ;
i2 = sign(z2) ;

T = 310.15 ; % temperature
R = 8.314 ; % universal gas constant
F = 96484.56 ; % faraday constant
C_a = 1 ; % initial drug concentration (mM)

sim = 10000; % number of simulations
paraNo = 25;
outputNo = 7; % number of output parameters
Para = zeros(sim,paraNo);
Results = zeros(sim,outputNo);

dMdt_exp = 5.19e-6; % +/- 1.01e-6, pmol/sec/cell, measured after 4hrs
Ppore_exp = 1.40E+01; % +/- 3.33, 10^(-6) cm/sec, measured after 4hrs
Peff_exp = 1.98E+00; % +/- 0.471, 10^(-6) cm/sec, measured after 4hrs
IntraMass_exp = 0.00188; % +/- 0.00054, pmol/cell, measured after 5min

for i = 1:sim

% Drug information -- ChemAxon calculation including logPn, pKa1, and pKa2
logPn = 3.93-0.5+rand(); % unif [3.43, 4.43] ;
pKa1 = 9.96-0.5+rand(); % unif [9.46, 10.46] ;
pKa2 = 7.47-0.5+rand(); % unif [6.97, 7.97] ;
logPd1 = 0.43-0.5+rand(); % unif [-0.07, 0.93] ;
logPd2 = -0.91-0.5+rand(); % unif [-1.41, 0.41] ;
Pn = 10^(logPn-6.7);
Pd1 = 10^(logPd1-6.7);
Pd2 = 10^(logPd2-6.7);

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    CellNo = 2*10^5*(1+rand()); % cell
number/insert: unif [2*10^5, 4*10^5]
    PoreDens = 2*10^6*0.4*(2+rand()); % pore
number/cm^2: unif [1.6*10^6, 2.4*10^6]
    A_insert = 1.12*10^(-4) ; % insert area:
1.12 cm^2
    PoreNo_insert = PoreDens*A_insert*10^(4); % pore
number/insert
    PoreNo_cell = PoreNo_insert/CellNo ; % average pore
number/cell
    A_pore_insert = 3.14*((3/2)*10^(-6))^2*PoreNo_insert ; % pore area /
insert (m^2)
    A_pore_cell = 3.14*((3/2)*10^(-6))^2*PoreNo_cell ; % average pore
area / cell (m^2)

    A_a = 10^(-10)*(1+9*rand()); % apical
membrane surface area: unif [10^(-10),10*(10)^(-10)] (m^2)
    A_aa = A_pore_cell; % pore area/cell
(m^2)
    A_b = A_aa+(10^(-10)-A_aa)*rand(); % basolateral
membrane surface area: unif [A_aa, 10^(-10)] (m^2)
    A_l = 100*3.14*10^(-12); % lysosomal
membrane surface area (m^2)
    A_m = 100*3.14*10^(-12); % mitochondrial
membrane surface area (m^2)
    V_c = 0.5*10^(-15)*(1+5*rand()); % cytosolic
volume: unif [0.5*10^(-15), 3*10^(-15)] (m^3)
    V_l = 10^(-18)*(9.24+(23.8-9.24)*rand()); % lysosomal
volume: unif [9.24*10^(-18), 23.8*10^(-18)] (m^3)
    V_m = 100*5.24*10^(-19)/5*(1+24*rand()); % mitochondrial
volume: unif [10.48*10^(-18), 262*10^(-18)](m^3)
    V_b = 1.5*10^(-6); % basolateral
volume: 1.5 mL

    % Membrane potential (unit in 'Voltage')
    E_a = -0.0093-0.005+0.01*rand(); % apical
membrane potential: unif [-0.0143, -0.0043]
    E_l = 0.01-0.005+0.01*rand(); % lysosomal
membrane potential: unif [0.005, 0.015]
    E_m = -0.16 ; % mitochondrial
membrane potential
    E_b = 0.0119-0.005+0.01*rand(); % basolateral
membrane potential: unif [0.0069, 0.0169]

    % pH values
    pH_a = 6.4+0.2*rand(); % pH in apical
compartment: unif [6.4, 6.6]
    pH_c = 7.0+0.4*rand(); % pH in cytosol:
unif [7.0, 7.4]
    pH_l = 4.8+0.4*rand(); % pH in
lysosomes: unif [4.8, 5.2]
    pH_m = 7.8+0.4*rand(); % pH in
mitochondria: unif[7.8, 8.2]
    pH_b = 7.4; % pH in
basolateral compartment

```



```

% Apical Compartment
fn_a = 1 / (1 + 10^(i1*(pKa1-pH_a)) + 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a))) ;
fd2_a = fn_a * 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a)) ;
fd1_a = fn_a * 10^(i1*(pKa1-pH_a)) ;
Nd2_a = z2*E_a*F/(R*T) ;
Nd1_a = z1*E_a*F/(R*T) ;

% Cytoplasm
L_c = 0.05+0.1*rand(); % lipid
fraction in cytosol: unif [0.05, 0.15]
W_c = 1-L_c ; % water
fraction in cytosol
Is_c = 0.3 ; % ion
strength in cytosol (mol)
gamman_c = 10^(0.3*Is_c) ; %
activity coefficient of neutral molecules in cytosol
gammad1_c = 10^(-0.5*z1*z1*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of monovalent base in cytosol
gammad2_c = 10^(-0.5*z2*z2*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of bivalent base in cytosol
Kn_c = L_c*1.22*10^(logPn) ;
Kd1_c = L_c*1.22*10^(logPd1) ;
Kd2_c = L_c*1.22*10^(logPd2) ;
an_c = 1 / (1 + 10^(i1*(pKa1-pH_c)) + 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c))) ;
ad2_c = an_c * 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c)) ;
ad1_c = an_c * 10^(i1*(pKa1-pH_c)) ;
Dd2_c = ad2_c / an_c ;
Dd1_c = ad1_c / an_c ;
fn_c = 1 / (W_c/gamman_c + Kn_c/gamman_c + Dd2_c*W_c/gammad2_c +
Dd2_c*Kd2_c/gammad2_c ...
+ Dd1_c*W_c/gammad1_c + Dd1_c*Kd1_c/gammad1_c ) ;
fd2_c = fn_c * Dd2_c ;
fd1_c = fn_c * Dd1_c ;

% Mitochondria
L_m = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_m = 1-L_m ; % water
fraction in mitochondria
Is_m = 0.3 ; % ion
strength in mitochondria (mol)
Nd2_m = z2*E_m*F/(R*T) ;
Nd1_m = z1*E_m*F/(R*T) ;
gamman_m = 10^(0.3*Is_m) ; %
activity coefficient of neutral molecules in mitochondria
gammad1_m = 10^(-0.5*z1*z1*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of monovalent base in mitochondria
gammad2_m = 10^(-0.5*z2*z2*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of bivalent base in mitochondria
Kn_m = L_m*1.22*10^(logPn) ;
Kd1_m = L_m*1.22*10^(logPd1) ;
Kd2_m = L_m*1.22*10^(logPd2) ;
an_m = 1 / (1 + 10^(i1*(pKa1-pH_m)) + 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m))) ;
ad2_m = an_m * 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m)) ;
ad1_m = an_m * 10^(i1*(pKa1-pH_m)) ;
Dd2_m = ad2_m / an_m ;
Dd1_m = ad1_m / an_m ;

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fn_m = 1 / (W_m/gamman_m + Kn_m/gamman_m + Dd2_m*W_m/gammad2_m +
Dd2_m*Kd2_m/gammad2_m ...
+ Dd1_m*W_m/gammad1_m + Dd1_m*Kd1_m/gammad1_m ) ;
fd2_m = fn_m * Dd2_m ;
fd1_m = fn_m * Dd1_m ;

% Lysosomes
L_l = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_l = 1-L_l ; % water
fraction in lysosomes
Is_l = 0.3 ; % ion
strength in lysosomes (mol)
Nd2_l = z2*E_l*F/(R*T) ;
Nd1_l = z1*E_l*F/(R*T) ;
gamman_l = 10^(0.3*Is_l) ; %
activity coefficient of neutral molecules in lysosomes
gammad1_l = 10^(-0.5*z1*z1*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of monovalent base in lysosomes
gammad2_l = 10^(-0.5*z2*z2*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of bivalent base in lysosomes
Kn_l = L_l*1.22*10^(logPn) ;
Kd1_l = L_l*1.22*10^(logPd1) ;
Kd2_l = L_l*1.22*10^(logPd2) ;
an_l = 1 / (1 + 10^(i1*(pKa1-pH_l)) + 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l))) ;
ad2_l = an_l * 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l)) ;
ad1_l = an_l * 10^(i1*(pKa1-pH_l)) ;
Dd2_l = ad2_l / an_l ;
Dd1_l = ad1_l / an_l ;
fn_l = 1 / (W_l/gamman_l + Kn_l/gamman_l + Dd2_l*W_l/gammad2_l +
Dd2_l*Kd2_l/gammad2_l ...
+ Dd1_l*W_l/gammad1_l + Dd1_l*Kd1_l/gammad1_l ) ;
fd2_l = fn_l * Dd2_l ;
fd1_l = fn_l * Dd1_l ;

% Basolateral Compartment
fn_b = 1 / (1 + 10^(i1*(pKa1-pH_b)) + 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b))) ;
fd2_b = fn_b * 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b)) ;
fd1_b = fn_b * 10^(i1*(pKa1-pH_b)) ;
Nd2_b = z2*(-E_b)*F/(R*T) ;
Nd1_b = z1*(-E_b)*F/(R*T) ;

% Solve the differential equation system:
% Given a system of linear ODE's expressed in matrix form:
% Y' = AY+G with initial conditions Y(0) = RR,
k11 = -(A_a/V_c)*Pn*fn_c-
(A_a/V_c)*Pd1*Nd1_a*fd1_c*exp(Nd1_a)/(exp(Nd1_a)-1)...
-(A_a/V_c)*Pd2*Nd2_a*fd2_c*exp(Nd2_a)/(exp(Nd2_a)-1)...
-(A_m/V_c)*Pn*fn_c-(A_m/V_c)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)...
-(A_m/V_c)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1)...
-(A_l/V_c)*Pn*fn_c-(A_l/V_c)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)...
-(A_l/V_c)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1)...
-(A_b/V_c)*Pn*fn_c-(A_b/V_c)*Pd1*Nd1_b*fd1_c/(exp(Nd1_b)-1)...
-(A_b/V_c)*Pd2*Nd2_b*fd2_c/(exp(Nd2_b)-1) ;

k12 =
(A_m/V_c)*Pn*fn_m+(A_m/V_c)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-1)...
+(A_m/V_c)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;

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k13 =
(A_l/V_c)*Pn*fn_l+(A_l/V_c)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-1)...
+ (A_l/V_c)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1);
k14 =
(A_b/V_c)*Pn*fn_b+(A_b/V_c)*Pd1*Nd1_b*fd1_b*exp(Nd1_b)/(exp(Nd1_b)-1)...
+ (A_b/V_c)*Pd2*Nd2_b*fd2_b*exp(Nd2_b)/(exp(Nd2_b)-1);
S1 = (A_a/V_c)*C_a*(Pn*fn_a+Pd1*Nd1_a*fd1_a/(exp(Nd1_a)-1)...
+Pd2*Nd2_a*fd2_a/(exp(Nd2_a)-1)) ;

k21 = (A_m/V_m)*Pn*fn_c+(A_m/V_m)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)...
+ (A_m/V_m)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1) ;
k22 = -(A_m/V_m)*Pn*fn_m-
(A_m/V_m)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-1)...
- (A_m/V_m)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k23 = 0;
k24 = 0 ;
S2 = 0;

k31 = (A_l/V_l)*Pn*fn_c+(A_l/V_l)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)...
+ (A_l/V_l)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1) ;
k32 = 0;
k33 = -(A_l/V_l)*Pn*fn_l-
(A_l/V_l)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-1)...
- (A_l/V_l)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;

k34 = 0 ;
S3 = 0;

k41 = (A_b/V_b)*Pn*fn_c+(A_b/V_b)*Pd1*Nd1_b*fd1_c/(exp(Nd1_b)-1)...
+ (A_b/V_b)*Pd2*Nd2_b*fd2_c/(exp(Nd2_b)-1) ;
k42 = 0;
k43 = 0;
k44 = -(A_b/V_b)*Pn*fn_b-
(A_b/V_b)*Pd1*Nd1_b*fd1_b*exp(Nd1_b)/(exp(Nd1_b)-1)...
- (A_b/V_b)*Pd2*Nd2_b*fd2_b*exp(Nd2_b)/(exp(Nd2_b)-1);
S4 = 0;

A = [k11, k12, k13, k14; k21, k22, k23, k24; k31, k32, k33, k34; k41,
k42, k43, k44];
G = [S1, S2, S3, S4]';
RR = [0,0,0,0]';
t = 300 ; % time in sec (5min)

[V,E] = eig(A);
E = diag(E);
H = inv(V)*G;
B = V \ RR;
C = B + H./E;
Z = -(H./E) + exp(t * E).*C ;
Y = real(V * Z);
Y = Y' ;

Ppore = Y(4)*V_b / (t*A_aa*C_a)*10^(2)*10^6 ; %
Pcell, 10^(-6)cm/sec
Peff = Y(4)*V_b*CellNo/(t*A_insert*C_a)*10^(2)*10^6; %
Peff, 10^(-6)cm/sec, normalized by insert area, which is 1.12 cm^2

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```

        Mass_cell = (Y(1)*V_c + Y(2)*V_m + Y(3)*V_l)*10^12 ;           %
cellular mass, pmol/cell
        dMdt = Y(4)*V_b/t*10^12;                                       %
transport rate: pmol/sec/cell

        Para(i,:) = [A_a*10^12,PoreNo_cell,
A_l*10^12,A_m*10^12,A_b*10^12,V_c*10^18,V_l*10^18,V_m*10^18,V_b*10^6,E_a*1000,E_
l*1000,E_m*1000,E_b*1000,...
                pH_a,pH_c,pH_l,pH_m,pH_b,CellNo,PoreDens,
pKa1,pKa2,logPn,logPd1, logPd2];
        Results(i,:)= [Y(1),Y(2),Y(3),Ppore, Peff, dMdt, Mass_cell];

end

comb = [Results(:,1:7),Para];
fid5 = fopen('AtoB_pH65_3um_5min.dat','w');
fprintf(fid5,'%12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.2e %12.0f %1
2.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4f %12.4f %12.4f %12.4f %12.
2f %12.2f %12.2f %12.2f %12.2f %12.0f %12.0f %12.2f %12.2f %12.2f %12.2f %12.2f
\n', comb) ;
fclose(fid5);

figure(5) ; clf ; hold on ;
grid on;
hist (log10(comb(:,4)),1000);
line([log10(Ppore_exp), log10(Ppore_exp)], [0,50], 'Color','r', 'LineWidth',3);
xlabel('log_{10} (P_{cell}, 10^{-6}
cm/sec)', 'FontSize',30, 'FontWeight', 'Bold', 'FontName', 'Times');
xlim([0, 6]);
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize',30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth',2.0, 'FontSize',30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of cell
permeability', 'FontSize',30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(6) ; clf ; hold on ;
grid on;
hist (log10(comb(:,5)),1000);
xlim([-3, 3]);
line([log10(Peff_exp), log10(Peff_exp)], [0,50], 'Color','r', 'LineWidth',3);
xlabel('log_{10} (P_{app}, 10^{-6}
cm/sec)', 'FontSize',30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize',30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth',2.0, 'FontSize',30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of apparent
permeability', 'FontSize',30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(7) ; clf ; hold on ;
grid on;
hist (log10(comb(:,6)),1000);
xlim([-8,-2]);
line([log10(dMdt_exp), log10(dMdt_exp)], [0,50], 'Color','r', 'LineWidth',3);
xlabel('log_{10} (dM/dt,
pmol/sec/cell)', 'FontSize',30, 'FontWeight', 'Bold', 'FontName', 'Times');

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ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','FontName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;
title ('histogram of transport
rate','FontSize',30,'FontWeight','Bold','FontName','Times') ;

figure(8) ; clf ; hold on ;
grid on;
hist (log10(comb(:,7)),1000);
xlim([-5,-0]);
line([log10(IntraMass_exp),
log10(IntraMass_exp)], [0,50], 'Color','r','LineWidth',3);
xlabel('log_{10} (intracellular mass, pmol/cell)
','FontSize',30,'FontWeight','Bold','FontName','Times');
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','FontName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;
title ('histogram of intracellular
mass','FontSize',30,'FontWeight','Bold','FontName','Times') ;

% =====Case# 3: AP->BL transport, pHa = 7.4, 0.4um-membrane,
5min=====
clear ; % Clear the memory
z1 = 1 ; % ionization group 1 of CQ
z2 = 2 ; % ionization group 2 of CQ
i1 = sign(z1) ;
i2 = sign(z2) ;

T = 310.15 ; % temperature
R = 8.314 ; % universal gas constant
F = 96484.56 ; % faraday constant
C_a = 1 ; % initial drug concentration (mM)

sim = 10000; % number of simulations
paraNo = 25;
outputNo = 7; % number of output parameters
Para = zeros(sim,paraNo);
Results = zeros(sim,outputNo);

dMdt_exp = 2.28e-5; % +/- 7.41e-7, pmol/sec/cell, measured after
4hrs
Ppore_exp = 1.56E+03; % +/- 161, 10^-6 cm/sec, measured after 4hrs
Peff_exp = 7.85; % +/- 0.81, 10^-6 cm/sec, measured after 4hrs
IntraMass_exp = 0.00872; % +/- 0.00094 pmol/cell, measured after 5min

for i = 1:sim

% Drug information -- ChemAxon calculation including logPn, pKa1, and pKa2
logPn = 3.93-0.5+rand(); % unif [3.43, 4.43] ;
pKa1 = 9.96-0.5+rand(); % unif [9.46, 10.46] ;
pKa2 = 7.47-0.5+rand(); % unif [6.97, 7.97] ;
logPd1 = 0.43-0.5+rand(); % unif [-0.07, 0.93] ;
logPd2 = -0.91-0.5+rand(); % unif [-1.41, 0.41] ;

```

```

Pn = 10^(logPn-6.7);
Pd1 = 10^(logPd1-6.7);
Pd2 = 10^(logPd2-6.7);

CellNo = 2*10^5*(1+rand()); % cell
number/insert: unif [2*10^5, 4*10^5]
PoreDens = 4*10^6*0.4*(2+rand()); % pore
number/cm^2: unif [3.2*10^6, 4.8*10^6]
A_insert = 1.12*10^(-4) ; % insert area:
1.12 cm^2
PoreNo_insert = PoreDens*A_insert*10^(4); % pore
number/insert
PoreNo_cell = PoreNo_insert/CellNo ; % average pore
number/cell
A_pore_insert = 3.14*((0.4/2)*10^(-6))^2*PoreNo_insert ; % pore area /
insert (m^2)
A_pore_cell = 3.14*((0.4/2)*10^(-6))^2*PoreNo_cell ; % average pore
area / cell (m^2)

A_a = 10^(-10)*(1+9*rand()); % apical
membrane surface area: unif [10^(-10),10*(10)^(-10)] (m^2)
A_aa = A_pore_cell; % pore area/cell
(m^2)
A_b = A_aa+(10^(-10)-A_aa)*rand(); % basolateral
membrane surface area: unif [A_aa, 10^(-10)] (m^2)
A_l = 100*3.14*10^(-12); % lysosomal
membrane surface area (m^2)
A_m = 100*3.14*10^(-12); % mitochondrial
membrane surface area (m^2)
V_c = 0.5*10^(-15)*(1+5*rand()); % cytosolic
volume: unif [0.5*10^(-15), 3*10^(-15)] (m^3)
V_l = 10^(-18)*(9.24+(23.8-9.24)*rand()); % lysosomal
volume: unif [9.24*10^(-18), 23.8*10^(-18)] (m^3)
V_m = 100*5.24*10^(-19)/5*(1+24*rand()); % mitochondrial
volume: unif [10.48*10^(-18), 262*10^(-18)](m^3)
V_b = 1.5*10^(-6); % basolateral
volume: 1.5 mL

% Membrane potential (unit in 'Voltage')
E_a = -0.0093-0.005+0.01*rand(); % apical
membrane potential: unif [-0.0143, -0.0043]
E_l = 0.01-0.005+0.01*rand(); % lysosomal
membrane potential: unif [0.005, 0.015]
E_m = -0.16 ; % mitochondrial
membrane potential
E_b = 0.0119-0.005+0.01*rand(); % basolateral
membrane potential: unif [0.0069, 0.0169]

% pH values
pH_a = 7.0+0.4*rand(); % pH in apical
compartment: unif [7.0, 7.4]
pH_c = 7.0+0.4*rand(); % pH in cytosol:
unif [7.0, 7.4]
pH_l = 4.8+0.4*rand(); % pH in
lysosomes: unif [4.8, 5.2]

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```

    pH_m = 7.8+0.4*rand(); % pH in
mitochondria: unif[7.8, 8.2]
    pH_b = 7.4; % pH in
basolateral compartment

% Apical Compartment
fn_a = 1 / (1 + 10^(i1*(pKa1-pH_a)) + 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a))) ;
fd2_a = fn_a * 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a)) ;
fd1_a = fn_a * 10^(i1*(pKa1-pH_a)) ;
Nd2_a = z2*E_a*F/(R*T) ;
Nd1_a = z1*E_a*F/(R*T) ;

% Cytoplasm
L_c = 0.05+0.1*rand(); % lipid
fraction in cytosol: unif [0.05, 0.15]
W_c = 1-L_c ; % water
fraction in cytosol
Is_c = 0.3 ; % ion
strength in cytosol (mol)
gamman_c = 10^(0.3*Is_c) ; %
activity coefficient of neutral molecules in cytosol
gammad1_c = 10^(-0.5*z1*z1*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of monovalent base in cytosol
gammad2_c = 10^(-0.5*z2*z2*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of bivalent base in cytosol
Kn_c = L_c*1.22*10^(logPn) ;
Kd1_c = L_c*1.22*10^(logPd1) ;
Kd2_c = L_c*1.22*10^(logPd2) ;
an_c = 1 / (1 + 10^(i1*(pKa1-pH_c)) + 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c))) ;
ad2_c = an_c * 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c)) ;
ad1_c = an_c * 10^(i1*(pKa1-pH_c)) ;
Dd2_c = ad2_c / an_c ;
Dd1_c = ad1_c / an_c ;
fn_c = 1 / (W_c/gamman_c + Kn_c/gamman_c + Dd2_c*W_c/gammad2_c +
Dd2_c*Kd2_c/gammad2_c ...
+ Dd1_c*W_c/gammad1_c + Dd1_c*Kd1_c/gammad1_c ) ;
fd2_c = fn_c * Dd2_c ;
fd1_c = fn_c * Dd1_c ;

% Mitochondria
L_m = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_m = 1-L_m ; % water
fraction in mitochondria
Is_m = 0.3 ; % ion
strength in mitochondria (mol)
Nd2_m = z2*E_m*F/(R*T) ;
Nd1_m = z1*E_m*F/(R*T) ;
gamman_m = 10^(0.3*Is_m) ; %
activity coefficient of neutral molecules in mitochondria
gammad1_m = 10^(-0.5*z1*z1*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of monovalent base in mitochondria
gammad2_m = 10^(-0.5*z2*z2*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of bivalent base in mitochondria
Kn_m = L_m*1.22*10^(logPn) ;
Kd1_m = L_m*1.22*10^(logPd1) ;
Kd2_m = L_m*1.22*10^(logPd2) ;

```

```

an_m = 1 / (1 + 10^(i1*(pKa1-pH_m)) + 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m))) ;
ad2_m = an_m * 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m)) ;
ad1_m = an_m * 10^(i1*(pKa1-pH_m)) ;
Dd2_m = ad2_m / an_m ;
Dd1_m = ad1_m / an_m ;
fn_m = 1 / (W_m/gamman_m + Kn_m/gamman_m + Dd2_m*W_m/gammad2_m +
Dd2_m*Kd2_m/gammad2_m ...
+ Dd1_m*W_m/gammad1_m + Dd1_m*Kd1_m/gammad1_m ) ;
fd2_m = fn_m * Dd2_m ;
fd1_m = fn_m * Dd1_m ;

% Lysosomes
L_l = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_l = 1-L_l ; % water
fraction in lysosomes
Is_l = 0.3 ; % ion
strength in lysosomes (mol)
Nd2_l = z2*E_l*F/(R*T) ;
Nd1_l = z1*E_l*F/(R*T) ;
gamman_l = 10^(0.3*Is_l) ; %
activity coefficient of neutral molecules in lysosomes
gammad1_l = 10^(-0.5*z1*z1*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of monovalent base in lysosomes
gammad2_l = 10^(-0.5*z2*z2*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of bivalent base in lysosomes
Kn_l = L_l*1.22*10^(logPn) ;
Kd1_l = L_l*1.22*10^(logPd1) ;
Kd2_l = L_l*1.22*10^(logPd2) ;
an_l = 1 / (1 + 10^(i1*(pKa1-pH_l)) + 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l))) ;
ad2_l = an_l * 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l)) ;
ad1_l = an_l * 10^(i1*(pKa1-pH_l)) ;
Dd2_l = ad2_l / an_l ;
Dd1_l = ad1_l / an_l ;
fn_l = 1 / (W_l/gamman_l + Kn_l/gamman_l + Dd2_l*W_l/gammad2_l +
Dd2_l*Kd2_l/gammad2_l ...
+ Dd1_l*W_l/gammad1_l + Dd1_l*Kd1_l/gammad1_l ) ;
fd2_l = fn_l * Dd2_l ;
fd1_l = fn_l * Dd1_l ;

% Basolateral Compartment
fn_b = 1 / (1 + 10^(i1*(pKa1-pH_b)) + 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b))) ;
fd2_b = fn_b * 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b)) ;
fd1_b = fn_b * 10^(i1*(pKa1-pH_b)) ;
Nd2_b = z2*(-E_b)*F/(R*T) ;
Nd1_b = z1*(-E_b)*F/(R*T) ;

% Solve the differential equation system:
% Given a system of linear ODE's expressed in matrix form:
% Y' = AY+G with initial conditions Y(0) = RR,
k11 = -(A_a/V_c)*Pn*fn_c-
(A_a/V_c)*Pd1*Nd1_a*fd1_c*exp(Nd1_a)/(exp(Nd1_a)-1)...
-(A_a/V_c)*Pd2*Nd2_a*fd2_c*exp(Nd2_a)/(exp(Nd2_a)-1)...
-(A_m/V_c)*Pn*fn_c-(A_m/V_c)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)...
-(A_m/V_c)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1)...
-(A_l/V_c)*Pn*fn_c-(A_l/V_c)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)...
-(A_l/V_c)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1)...

```



```

- (A_b/V_c) * Pn * fn_c - (A_b/V_c) * Pd1 * Nd1_b * fd1_c / (exp(Nd1_b) - 1) ...
- (A_b/V_c) * Pd2 * Nd2_b * fd2_c / (exp(Nd2_b) - 1) ;
k12 =
(A_m/V_c) * Pn * fn_m + (A_m/V_c) * Pd1 * Nd1_m * fd1_m * exp(Nd1_m) / (exp(Nd1_m) - 1) ...
+ (A_m/V_c) * Pd2 * Nd2_m * fd2_m * exp(Nd2_m) / (exp(Nd2_m) - 1) ;
k13 =
(A_l/V_c) * Pn * fn_l + (A_l/V_c) * Pd1 * Nd1_l * fd1_l * exp(Nd1_l) / (exp(Nd1_l) - 1) ...
+ (A_l/V_c) * Pd2 * Nd2_l * fd2_l * exp(Nd2_l) / (exp(Nd2_l) - 1) ;
k14 =
(A_b/V_c) * Pn * fn_b + (A_b/V_c) * Pd1 * Nd1_b * fd1_b * exp(Nd1_b) / (exp(Nd1_b) - 1) ...
+ (A_b/V_c) * Pd2 * Nd2_b * fd2_b * exp(Nd2_b) / (exp(Nd2_b) - 1) ;
S1 = (A_a/V_c) * C_a * (Pn * fn_a + Pd1 * Nd1_a * fd1_a / (exp(Nd1_a) - 1) ...
+ Pd2 * Nd2_a * fd2_a / (exp(Nd2_a) - 1)) ;

k21 = (A_m/V_m) * Pn * fn_c + (A_m/V_m) * Pd1 * Nd1_m * fd1_c / (exp(Nd1_m) - 1) ...
+ (A_m/V_m) * Pd2 * Nd2_m * fd2_c / (exp(Nd2_m) - 1) ;
k22 = - (A_m/V_m) * Pn * fn_m -
(A_m/V_m) * Pd1 * Nd1_m * fd1_m * exp(Nd1_m) / (exp(Nd1_m) - 1) ...
- (A_m/V_m) * Pd2 * Nd2_m * fd2_m * exp(Nd2_m) / (exp(Nd2_m) - 1) ;
k23 = 0 ;
k24 = 0 ;
S2 = 0 ;

k31 = (A_l/V_l) * Pn * fn_c + (A_l/V_l) * Pd1 * Nd1_l * fd1_c / (exp(Nd1_l) - 1) ...
+ (A_l/V_l) * Pd2 * Nd2_l * fd2_c / (exp(Nd2_l) - 1) ;
k32 = 0 ;
k33 = - (A_l/V_l) * Pn * fn_l -
(A_l/V_l) * Pd1 * Nd1_l * fd1_l * exp(Nd1_l) / (exp(Nd1_l) - 1) ...
- (A_l/V_l) * Pd2 * Nd2_l * fd2_l * exp(Nd2_l) / (exp(Nd2_l) - 1) ;
k34 = 0 ;
S3 = 0 ;

k41 = (A_b/V_b) * Pn * fn_c + (A_b/V_b) * Pd1 * Nd1_b * fd1_c / (exp(Nd1_b) - 1) ...
+ (A_b/V_b) * Pd2 * Nd2_b * fd2_c / (exp(Nd2_b) - 1) ;
k42 = 0 ;
k43 = 0 ;
k44 = - (A_b/V_b) * Pn * fn_b -
(A_b/V_b) * Pd1 * Nd1_b * fd1_b * exp(Nd1_b) / (exp(Nd1_b) - 1) ...
- (A_b/V_b) * Pd2 * Nd2_b * fd2_b * exp(Nd2_b) / (exp(Nd2_b) - 1) ;
S4 = 0 ;

A = [k11, k12, k13, k14; k21, k22, k23, k24; k31, k32, k33, k34; k41,
k42, k43, k44];
G = [S1, S2, S3, S4]';
RR = [0, 0, 0, 0]';
t = 300 ; % time in sec (5min)

[V, E] = eig(A);
E = diag(E);
H = inv(V) * G;
B = V \ RR;
C = B + H ./ E;
Z = -(H ./ E) + exp(t * E) .* C ;
Y = real(V * Z);
Y = Y' ;

```

```

        Ppore = Y(4)*V_b / (t*A_aa*C_a)*10^(2)*10^6 ; %
Pcell, 10^(-6)cm/sec
        Peff = Y(4)*V_b*CellNo/(t*A_insert*C_a)*10^(2)*10^6; %
Peff, 10^(-6)cm/sec, normalized by insert area, which is 1.12 cm^2
        Mass_cell = (Y(1)*V_c + Y(2)*V_m + Y(3)*V_l)*10^12 ; %
cellular mass, pmol/cell
        dMdt = Y(4)*V_b/t*10^12; %
transport rate: pmol/sec/cell

        Para(i,:) = [A_a*10^12,PoreNo_cell,
A_l*10^12,A_m*10^12,A_b*10^12,V_c*10^18,V_l*10^18,V_m*10^18,V_b*10^6,E_a*1000,E_
l*1000,E_m*1000,E_b*1000,...
        pH_a,pH_c,pH_l,pH_m,pH_b,CellNo,PoreDens,
pKa1,pKa2,logPn,logPd1, logPd2];
        Results(i,:)= [Y(1),Y(2),Y(3),Ppore, Peff, dMdt, Mass_cell];

end

comb = [Results(:,1:7),Para];
fid5 = fopen('AtoB_pH74_04um_5min.dat','w');
fprintf(fid5,'%12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.2e %12.0f %1
2.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4f %12.4f %12.4f %12.4f %12.
2f %12.2f %12.2f %12.2f %12.2f %12.0f %12.0f %12.2f %12.2f %12.2f %12.2f %12.2f
\n', comb) ;
fclose(fid5);

figure(9) ; clf ; hold on ;
grid on;
hist (log10(comb(:,4)),1000);
line([log10(Ppore_exp), log10(Ppore_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (P_{cell}, 10^{-6}
cm/sec)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
xlim([0, 6]);
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of cell
permeability', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(10) ; clf ; hold on ;
grid on;
hist (log10(comb(:,5)),1000);
xlim([-3, 3]);
line([log10(Peff_exp), log10(Peff_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (P_{app}, 10^{-6}
cm/sec)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of apparent
permeability', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(11) ; clf ; hold on ;
grid on;

```

```

hist (log10(comb(:,6)),1000);
xlim([-8,-2]);
line([log10(dMdt_exp), log10(dMdt_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (dM/dt,
pmol/sec/cell)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of transport
rate', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(12) ; clf ; hold on ;
grid on;
hist (log10(comb(:,7)),1000);
xlim([-5,-0]);
line([log10(IntraMass_exp),
log10(IntraMass_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (intracellular mass, pmol/cell)
', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of intracellular
mass', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

% =====Case# 4: AP->BL transport, pHa = 7.4, 3um-membrane,
5min=====

clear ; % Clear the memory
z1 = 1 ; % ionization group 1 of CQ
z2 = 2 ; % ionization group 2 of CQ
i1 = sign(z1) ;
i2 = sign(z2) ;

T = 310.15 ; % temperature
R = 8.314 ; % universal gas constant
F = 96484.56 ; % faraday constant
C_a = 1 ; % initial drug concentration (mM)

sim = 10000; % number of simulations
paraNo = 25;
outputNo = 7; % number of output parameters
Para = zeros(sim,paraNo);
Results = zeros(sim,outputNo);

dMdt_exp = 4.66e-5; % +/- 6.28e-6, pmol/sec/cell, measured after 4hrs
Ppore_exp = 8.59E+01; % +/- 15.6, 10^(-6) cm/sec, measured after 4hrs
Peff_exp = 1.21E+01; % +/- 2.21, 10^(-6) cm/sec, measured after 4hrs
IntraMass_exp = 0.00890; % +/- 0.00026, pmol/cell, measured after 5min

for i = 1:sim

% Drug information -- ChemAxon calculation including logPn, pKa1, and pKa2

```

```

logPn = 3.93-0.5+rand();      % unif [3.43, 4.43] ;
pKa1 = 9.96-0.5+rand();      % unif [9.46, 10.46] ;
pKa2 = 7.47-0.5+rand();      % unif [6.97, 7.97] ;
logPd1 = 0.43-0.5+rand();    % unif [-0.07, 0.93] ;
logPd2 = -0.91-0.5+rand();   % unif [-1.41, 0.41] ;
Pn = 10^(logPn-6.7);
Pd1 = 10^(logPd1-6.7);
Pd2 = 10^(logPd2-6.7);

CellNo = 2*10^5*(1+rand());   % cell
number/insert: unif [2*10^5, 4*10^5]
PoreDens = 2*10^6*0.4*(2+rand()); % pore
number/cm^2: unif [1.6*10^6, 2.4*10^6]
A_insert = 1.12*10^(-4) ;     % insert area:
1.12 cm^2
PoreNo_insert = PoreDens*A_insert*10^(4); % pore
number/insert
PoreNo_cell = PoreNo_insert/CellNo ; % average pore
number/cell
A_pore_insert = 3.14*((3/2)*10^(-6))^2*PoreNo_insert ; % pore area /
insert (m^2)
A_pore_cell = 3.14*((3/2)*10^(-6))^2*PoreNo_cell ; % average pore
area / cell (m^2)

A_a = 10^(-10)*(1+9*rand()); % apical
membrane surface area: unif [10^(-10),10*(10)^(-10)] (m^2)
A_aa = A_pore_cell;          % pore area/cell
(m^2)
A_b = A_aa+(10^(-10)-A_aa)*rand(); % basolateral
membrane surface area: unif [A_aa, 10^(-10)] (m^2)
A_l = 100*3.14*10^(-12);    % lysosomal
membrane surface area (m^2)
A_m = 100*3.14*10^(-12);    % mitochondrial
membrane surface area (m^2)
V_c = 0.5*10^(-15)*(1+5*rand()); % cytosolic
volume: unif [0.5*10^(-15), 3*10^(-15)] (m^3)
V_l = 10^(-18)*(9.24+(23.8-9.24)*rand()); % lysosomal
volume: unif [9.24*10^(-18), 23.8*10^(-18)] (m^3)
V_m = 100*5.24*10^(-19)/5*(1+24*rand()); % mitochondrial
volume: unif [10.48*10^(-18), 262*10^(-18)](m^3)
V_b = 1.5*10^(-6);         % basolateral
volume: 1.5 mL

% Membrane potential (unit in 'Voltage')
E_a = -0.0093-0.005+0.01*rand(); % apical
membrane potential: unif [-0.0143, -0.0043]
E_l = 0.01-0.005+0.01*rand(); % lysosomal
membrane potential: unif [0.005, 0.015]
E_m = -0.16 ;              % mitochondrial
membrane potential
E_b = 0.0119-0.005+0.01*rand(); % basolateral
membrane potential: unif [0.0069, 0.0169]

% pH values
pH_a = 7.0+0.4*rand();     % pH in apical
compartment: unif [7.0, 7.4]

```

```

    pH_c = 7.0+0.4*rand(); % pH in cytosol:
unif [7.0, 7.4]
    pH_l = 4.8+0.4*rand(); % pH in
lysosomes: unif [4.8, 5.2]
    pH_m = 7.8+0.4*rand(); % pH in
mitochondria: unif[7.8, 8.2]
    pH_b = 7.4; % pH in
basolateral compartment

% Apical Compartment
fn_a = 1 / (1 + 10^(i1*(pKa1-pH_a)) + 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a))) ;
fd2_a = fn_a * 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a)) ;
fd1_a = fn_a * 10^(i1*(pKa1-pH_a)) ;
Nd2_a = z2*E_a*F/(R*T) ;
Nd1_a = z1*E_a*F/(R*T) ;

% Cytoplasm
L_c = 0.05+0.1*rand(); % lipid
fraction in cytosol: unif [0.05, 0.15]
W_c = 1-L_c ; % water
fraction in cytosol
Is_c = 0.3 ; % ion
strength in cytosol (mol)
gamman_c = 10^(0.3*Is_c) ; %
activity coefficient of neutral molecules in cytosol
gammad1_c = 10^(-0.5*z1*z1*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of monovalent base in cytosol
gammad2_c = 10^(-0.5*z2*z2*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of bivalent base in cytosol
Kn_c = L_c*1.22*10^(logPn) ;
Kd1_c = L_c*1.22*10^(logPd1) ;
Kd2_c = L_c*1.22*10^(logPd2) ;
an_c = 1 / (1 + 10^(i1*(pKa1-pH_c)) + 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c))) ;
ad2_c = an_c * 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c)) ;
ad1_c = an_c * 10^(i1*(pKa1-pH_c)) ;
Dd2_c = ad2_c / an_c ;
Dd1_c = ad1_c / an_c ;
fn_c = 1 / (W_c/gamman_c + Kn_c/gamman_c + Dd2_c*W_c/gammad2_c +
Dd2_c*Kd2_c/gammad2_c ...
+ Dd1_c*W_c/gammad1_c + Dd1_c*Kd1_c/gammad1_c ) ;
fd2_c = fn_c * Dd2_c ;
fd1_c = fn_c * Dd1_c ;

% Mitochondria
L_m = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_m = 1-L_m ; % water
fraction in mitochondria
Is_m = 0.3 ; % ion
strength in mitochondria (mol)
Nd2_m = z2*E_m*F/(R*T) ;
Nd1_m = z1*E_m*F/(R*T) ;
gamman_m = 10^(0.3*Is_m) ; %
activity coefficient of neutral molecules in mitochondria
gammad1_m = 10^(-0.5*z1*z1*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of monovalent base in mitochondria

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```

    gammad2_m = 10^(-0.5*z2*z2*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of bivalent base in mitochondria
    Kn_m = L_m*1.22*10^(logPn) ;
    Kd1_m = L_m*1.22*10^(logPd1) ;
    Kd2_m = L_m*1.22*10^(logPd2) ;
    an_m = 1 / (1 + 10^(i1*(pKa1-pH_m)) + 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m))) ;
    ad2_m = an_m * 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m)) ;
    ad1_m = an_m * 10^(i1*(pKa1-pH_m)) ;
    Dd2_m = ad2_m / an_m ;
    Dd1_m = ad1_m / an_m ;
    fn_m = 1 / (W_m/gamman_m + Kn_m/gamman_m + Dd2_m*W_m/gammad2_m +
Dd2_m*Kd2_m/gammad2_m ...
    + Dd1_m*W_m/gammad1_m + Dd1_m*Kd1_m/gammad1_m ) ;
    fd2_m = fn_m * Dd2_m ;
    fd1_m = fn_m * Dd1_m ;

% Lysosomes
    L_l = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
    W_l = 1-L_l ; % water
fraction in lysosomes
    Is_l = 0.3 ; % ion
strength in lysosomes (mol)
    Nd2_l = z2*E_l*F/(R*T) ;
    Nd1_l = z1*E_l*F/(R*T) ;
    gamman_l = 10^(0.3*Is_l) ; %
activity coefficient of neutral molecules in lysosomes
    gammad1_l = 10^(-0.5*z1*z1*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of monovalent base in lysosomes
    gammad2_l = 10^(-0.5*z2*z2*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of bivalent base in lysosomes
    Kn_l = L_l*1.22*10^(logPn) ;
    Kd1_l = L_l*1.22*10^(logPd1) ;
    Kd2_l = L_l*1.22*10^(logPd2) ;
    an_l = 1 / (1 + 10^(i1*(pKa1-pH_l)) + 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l))) ;
    ad2_l = an_l * 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l)) ;
    ad1_l = an_l * 10^(i1*(pKa1-pH_l)) ;
    Dd2_l = ad2_l / an_l ;
    Dd1_l = ad1_l / an_l ;
    fn_l = 1 / (W_l/gamman_l + Kn_l/gamman_l + Dd2_l*W_l/gammad2_l +
Dd2_l*Kd2_l/gammad2_l ...
    + Dd1_l*W_l/gammad1_l + Dd1_l*Kd1_l/gammad1_l ) ;
    fd2_l = fn_l * Dd2_l ;
    fd1_l = fn_l * Dd1_l ;

% Basolateral Compartment
    fn_b = 1 / (1 + 10^(i1*(pKa1-pH_b)) + 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b))) ;
    fd2_b = fn_b * 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b)) ;
    fd1_b = fn_b * 10^(i1*(pKa1-pH_b)) ;
    Nd2_b = z2*(-E_b)*F/(R*T) ;
    Nd1_b = z1*(-E_b)*F/(R*T) ;

% Solve the differential equation system:
% Given a system of linear ODE's expressed in matrix form:
% Y' = AY+G with initial conditions Y(0) = RR,
    k11 = -(A_a/V_c)*Pn*fn_c-
(A_a/V_c)*Pd1*Nd1_a*fd1_c*exp(Nd1_a)/(exp(Nd1_a)-1)...

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- (A_a/V_c) * Pd2 * Nd2_a * fd2_c * exp(Nd2_a) / (exp(Nd2_a) - 1) ...
- (A_m/V_c) * Pn * fn_c - (A_m/V_c) * Pd1 * Nd1_m * fd1_c / (exp(Nd1_m) - 1) ...
- (A_m/V_c) * Pd2 * Nd2_m * fd2_c / (exp(Nd2_m) - 1) ...
- (A_l/V_c) * Pn * fn_c - (A_l/V_c) * Pd1 * Nd1_l * fd1_c / (exp(Nd1_l) - 1) ...
- (A_l/V_c) * Pd2 * Nd2_l * fd2_c / (exp(Nd2_l) - 1) ...
- (A_b/V_c) * Pn * fn_c - (A_b/V_c) * Pd1 * Nd1_b * fd1_c / (exp(Nd1_b) - 1) ...
- (A_b/V_c) * Pd2 * Nd2_b * fd2_c / (exp(Nd2_b) - 1) ;

k12 =
(A_m/V_c) * Pn * fn_m + (A_m/V_c) * Pd1 * Nd1_m * fd1_m * exp(Nd1_m) / (exp(Nd1_m) - 1) ...
+ (A_m/V_c) * Pd2 * Nd2_m * fd2_m * exp(Nd2_m) / (exp(Nd2_m) - 1) ;

k13 =
(A_l/V_c) * Pn * fn_l + (A_l/V_c) * Pd1 * Nd1_l * fd1_l * exp(Nd1_l) / (exp(Nd1_l) - 1) ...
+ (A_l/V_c) * Pd2 * Nd2_l * fd2_l * exp(Nd2_l) / (exp(Nd2_l) - 1) ;

k14 =
(A_b/V_c) * Pn * fn_b + (A_b/V_c) * Pd1 * Nd1_b * fd1_b * exp(Nd1_b) / (exp(Nd1_b) - 1) ...
+ (A_b/V_c) * Pd2 * Nd2_b * fd2_b * exp(Nd2_b) / (exp(Nd2_b) - 1) ;

S1 = (A_a/V_c) * C_a * (Pn * fn_a + Pd1 * Nd1_a * fd1_a / (exp(Nd1_a) - 1) ...
+ Pd2 * Nd2_a * fd2_a / (exp(Nd2_a) - 1)) ;

k21 = (A_m/V_m) * Pn * fn_c + (A_m/V_m) * Pd1 * Nd1_m * fd1_c / (exp(Nd1_m) - 1) ...
+ (A_m/V_m) * Pd2 * Nd2_m * fd2_c / (exp(Nd2_m) - 1) ;

k22 = - (A_m/V_m) * Pn * fn_m -
(A_m/V_m) * Pd1 * Nd1_m * fd1_m * exp(Nd1_m) / (exp(Nd1_m) - 1) ...
- (A_m/V_m) * Pd2 * Nd2_m * fd2_m * exp(Nd2_m) / (exp(Nd2_m) - 1) ;

k23 = 0 ;
k24 = 0 ;
S2 = 0 ;

k31 = (A_l/V_l) * Pn * fn_c + (A_l/V_l) * Pd1 * Nd1_l * fd1_c / (exp(Nd1_l) - 1) ...
+ (A_l/V_l) * Pd2 * Nd2_l * fd2_c / (exp(Nd2_l) - 1) ;

k32 = 0 ;
k33 = - (A_l/V_l) * Pn * fn_l -
(A_l/V_l) * Pd1 * Nd1_l * fd1_l * exp(Nd1_l) / (exp(Nd1_l) - 1) ...
- (A_l/V_l) * Pd2 * Nd2_l * fd2_l * exp(Nd2_l) / (exp(Nd2_l) - 1) ;

k34 = 0 ;
S3 = 0 ;

k41 = (A_b/V_b) * Pn * fn_c + (A_b/V_b) * Pd1 * Nd1_b * fd1_c / (exp(Nd1_b) - 1) ...
+ (A_b/V_b) * Pd2 * Nd2_b * fd2_c / (exp(Nd2_b) - 1) ;

k42 = 0 ;
k43 = 0 ;
k44 = - (A_b/V_b) * Pn * fn_b -
(A_b/V_b) * Pd1 * Nd1_b * fd1_b * exp(Nd1_b) / (exp(Nd1_b) - 1) ...
- (A_b/V_b) * Pd2 * Nd2_b * fd2_b * exp(Nd2_b) / (exp(Nd2_b) - 1) ;

S4 = 0 ;

A = [k11, k12, k13, k14; k21, k22, k23, k24; k31, k32, k33, k34; k41,
k42, k43, k44];
G = [S1, S2, S3, S4]';
RR = [0, 0, 0, 0]';
t = 300 ; % time in sec (5min)

[V, E] = eig(A);
E = diag(E);
H = inv(V) * G;

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B = V \ RR;
C = B + H./E;
Z = -(H./E) + exp(t * E).*C ;
Y = real(V * Z);
Y = Y' ;

Ppore = Y(4)*V_b / (t*A_aa*C_a)*10^(2)*10^6 ; %
Pcell, 10^(-6)cm/sec
Peff = Y(4)*V_b*CellNo/(t*A_insert*C_a)*10^(2)*10^6; %
Peff, 10^(-6)cm/sec, normalized by insert area, which is 1.12 cm^2
Mass_cell = (Y(1)*V_c + Y(2)*V_m + Y(3)*V_l)*10^12 ; %
cellular mass, pmol/cell
dMdt = Y(4)*V_b/t*10^12; %
transport rate: pmol/sec/cell

Para(i,:) = [A_a*10^12,PoreNo_cell,
A_l*10^12,A_m*10^12,A_b*10^12,V_c*10^18,V_l*10^18,V_m*10^18,V_b*10^6,E_a*1000,E_
l*1000,E_m*1000,E_b*1000,...
pH_a,pH_c,pH_l,pH_m,pH_b,CellNo,PoreDens,
pKa1,pKa2,logPn,logPd1, logPd2];
Results(i,:)= [Y(1),Y(2),Y(3),Ppore, Peff, dMdt, Mass_cell];

end

comb = [Results(:,1:7),Para];
fid5 = fopen('AtoB_pH74_3um_5min.dat','w');
fprintf(fid5,'%12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.2e %12.0f %1
2.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4f %12.4f %12.4f %12.4f %12.
2f %12.2f %12.2f %12.2f %12.2f %12.0f %12.0f %12.2f %12.2f %12.2f %12.2f %12.2f
\n', comb) ;
fclose(fid5);

figure(13) ; clf ; hold on ;
grid on;
hist (log10(comb(:,4)),1000);
line([log10(Ppore_exp), log10(Ppore_exp)],[0,50],'Color','r','LineWidth',3);
xlabel('log_{10} (P_{cell}, 10^{-6}
cm/sec)','FontSize',30,'FontWeight','Bold','FontName','Times');
xlim([0, 6]);
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','Fo
ntName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;
title ('histogram of cell
permeability','FontSize',30,'FontWeight','Bold','FontName','Times') ;

figure(14) ; clf ; hold on ;
grid on;
hist (log10(comb(:,5)),1000);
xlim([-3, 3]);
line([log10(Peff_exp), log10(Peff_exp)],[0,50],'Color','r','LineWidth',3);
xlabel('log_{10} (P_{app}, 10^{-6}
cm/sec)','FontSize',30,'FontWeight','Bold','FontName','Times');
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','Fo
ntName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;

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title ('histogram of apparent
permeability','FontSize',30,'FontWeight','Bold','FontName','Times') ;

figure(15) ; clf ; hold on ;
grid on;
hist (log10(comb(:,6)),1000);
xlim([-8,-2]);
line([log10(dMdt_exp), log10(dMdt_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (dM/dt,
pmol/sec/cell)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of transport
rate', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(16) ; clf ; hold on ;
grid on;
hist (log10(comb(:,7)),1000);
xlim([-5,-0]);
line([log10(IntraMass_exp),
log10(IntraMass_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (intracellular mass, pmol/cell)
', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of intracellular
mass', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

% =====Case# 5: BL->AP transport, pHb = 6.5, 0.4um-membrane,
5min=====

clear ; % Clear the memory
z1 = 1 ; % ionization group 1 of CQ
z2 = 2 ; % ionization group 2 of CQ
i1 = sign(z1) ;
i2 = sign(z2) ;

T = 310.15 ; % temperature
R = 8.314 ; % universal gas constant
F = 96484.56 ; % faraday constant
C_b = 1 ; % initial drug concentration (mM)

sim = 10000; % number of simulations
paraNo = 25;
outputNo = 7; % number of output parameters
Para = zeros(sim, paraNo);
Results = zeros(sim, outputNo);

dMdt_exp = 5.25e-6; % +/- 1.24e-6, pmol/sec/cell, measured after
4hrs
Ppore_exp = 3.82E+02; % +/- 81.7, 10^-6 cm/sec, measured after 4hrs
Peff_exp = 1.92; % +/- 0.411, 10^-6 cm/sec, measured after 4hrs

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IntraMass_exp = 0.00352;          % +/- 0.00093 pmol/cell, measured after 5min

for i = 1:sim

    % Drug information -- ChemAxon calculation including logPn, pKa1, and pKa2
    logPn = 3.93-0.5+rand();      % unif [3.43, 4.43] ;
    pKa1 = 9.96-0.5+rand();      % unif [9.46, 10.46] ;
    pKa2 = 7.47-0.5+rand();      % unif [6.97, 7.97] ;
    logPd1 = 0.43-0.5+rand();    % unif [-0.07, 0.93] ;
    logPd2 = -0.91-0.5+rand();   % unif [-1.41, 0.41] ;
    Pn = 10^(logPn-6.7);
    Pd1 = 10^(logPd1-6.7);
    Pd2 = 10^(logPd2-6.7);

    CellNo = 2*10^5*(1+rand());   % cell
number/insert: unif [2*10^5, 4*10^5]
    PoreDens = 4*10^6*0.4*(2+rand()); % pore
number/cm^2: unif [3.2*10^6, 4.8*10^6]
    A_insert = 1.12*10^(-4) ;     % insert area:
1.12 cm^2
    PoreNo_insert = PoreDens*A_insert*10^(4); % pore
number/insert
    PoreNo_cell = PoreNo_insert/CellNo ; % average pore
number/cell
    A_pore_insert = 3.14*((0.4/2)*10^(-6))^2*PoreNo_insert ; % pore area /
insert (m^2)
    A_pore_cell = 3.14*((0.4/2)*10^(-6))^2*PoreNo_cell ; % average pore
area / cell (m^2)

    A_a = 10^(-10)*(1+9*rand()); % apical
membrane surface area: unif [10^(-10),10*(10)^(-10))] (m^2)
    A_aa = A_pore_cell;          % pore area/cell
(m^2)
    A_b = A_aa+(10^(-10)-A_aa)*rand(); % basolateral
membrane surface area: unif [A_aa, 10^(-10))] (m^2)
    A_l = 100*3.14*10^(-12);     % lysosomal
membrane surface area (m^2)
    A_m = 100*3.14*10^(-12);     % mitochondrial
membrane surface area (m^2)
    V_c = 0.5*10^(-15)*(1+5*rand()); % cytosolic
volume: unif [0.5*10^(-15), 3*10^(-15)] (m^3)
    V_l = 10^(-18)*(9.24+(23.8-9.24)*rand()); % lysosomal
volume: unif [9.24*10^(-18), 23.8*10^(-18)] (m^3)
    V_m = 100*5.24*10^(-19)/5*(1+24*rand()); % mitochondrial
volume: unif [10.48*10^(-18), 262*10^(-18)](m^3)
    V_a = 0.5*10^(-6);          % apical volume:
0.5 mL

    % Membrane potential (unit in 'Voltage')
    E_a = 0.0093-0.005+0.01*rand(); % apical
membrane potential: unif [0.0043, 0.0143]
    E_l = 0.01-0.005+0.01*rand(); % lysosomal
membrane potential: unif [0.005, 0.015]
    E_m = -0.16 ;               % mitochondrial
membrane potential

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E_b = -0.0119-0.005+0.01*rand(); % basolateral
membrane potential: unif [-0.0169, -0.0069]

% pH values
pH_a = 7.4; % pH in apical
compartment
pH_c = 7.0+0.4*rand(); % pH in cytosol:
unif [7.0, 7.4]
pH_l = 4.8+0.4*rand(); % pH in
lysosomes: unif [4.8, 5.2]
pH_m = 7.8+0.4*rand(); % pH in
mitochondria: unif[7.8, 8.2]
pH_b = 6.4+0.2*rand(); % pH in
basolateral compartment: unif [6.4, 6.6]

% BL Compartment (donor)
fn_b = 1 / (1 + 10^(i1*(pKa1-pH_b)) + 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b))) ;
fd2_b = fn_b * 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b)) ;
fd1_b = fn_b * 10^(i1*(pKa1-pH_b)) ;
Nd2_b = z2*E_b*F/(R*T) ;
Nd1_b = z1*E_b*F/(R*T) ;

% Cytoplasm
L_c = 0.05+0.1*rand(); % lipid
fraction in cytosol: unif [0.05, 0.15]
W_c = 1-L_c ; % water
fraction in cytosol
Is_c = 0.3 ; % ion
strength in cytosol (mol)
gamman_c = 10^(0.3*Is_c) ; %
activity coefficient of neutral molecules in cytosol
gammad1_c = 10^(-0.5*z1*z1*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of monovalent base in cytosol
gammad2_c = 10^(-0.5*z2*z2*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of bivalent base in cytosol
Kn_c = L_c*1.22*10^(logPn) ;
Kd1_c = L_c*1.22*10^(logPd1) ;
Kd2_c = L_c*1.22*10^(logPd2) ;
an_c = 1 / (1 + 10^(i1*(pKa1-pH_c)) + 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c))) ;
ad2_c = an_c * 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c)) ;
ad1_c = an_c * 10^(i1*(pKa1-pH_c)) ;
Dd2_c = ad2_c / an_c ;
Dd1_c = ad1_c / an_c ;
fn_c = 1 / (W_c/gamman_c + Kn_c/gamman_c + Dd2_c*W_c/gammad2_c +
Dd2_c*Kd2_c/gammad2_c ...
+ Dd1_c*W_c/gammad1_c + Dd1_c*Kd1_c/gammad1_c ) ;
fd2_c = fn_c * Dd2_c ;
fd1_c = fn_c * Dd1_c ;

% Mitochondria
L_m = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_m = 1-L_m ; % water
fraction in mitochondria
Is_m = 0.3 ; % ion
strength in mitochondria (mol)
Nd2_m = z2*E_m*F/(R*T) ;

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Nd1_m = z1*E_m*F/(R*T) ;
gamman_m = 10^(0.3*Is_m) ; %
activity coefficient of neutral molecules in mitochondria
gammad1_m = 10^(-0.5*z1*z1*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of monovalent base in mitochondria
gammad2_m = 10^(-0.5*z2*z2*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of bivalent base in mitochondria
Kn_m = L_m*1.22*10^(logPn) ;
Kd1_m = L_m*1.22*10^(logPd1) ;
Kd2_m = L_m*1.22*10^(logPd2) ;
an_m = 1 / (1 + 10^(i1*(pKa1-pH_m)) + 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m))) ;
ad2_m = an_m * 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m)) ;
ad1_m = an_m * 10^(i1*(pKa1-pH_m)) ;
Dd2_m = ad2_m / an_m ;
Dd1_m = ad1_m / an_m ;
fn_m = 1 / (W_m/gamman_m + Kn_m/gamman_m + Dd2_m*W_m/gammad2_m +
Dd2_m*Kd2_m/gammad2_m ...
+ Dd1_m*W_m/gammad1_m + Dd1_m*Kd1_m/gammad1_m ) ;
fd2_m = fn_m * Dd2_m ;
fd1_m = fn_m * Dd1_m ;

% Lysosomes
L_l = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_l = 1-L_l ; % water
fraction in lysosomes
Is_l = 0.3 ; % ion
strength in lysosomes (mol)
Nd2_l = z2*E_l*F/(R*T) ;
Nd1_l = z1*E_l*F/(R*T) ;
gamman_l = 10^(0.3*Is_l) ; %
activity coefficient of neutral molecules in lysosomes
gammad1_l = 10^(-0.5*z1*z1*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of monovalent base in lysosomes
gammad2_l = 10^(-0.5*z2*z2*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of bivalent base in lysosomes
Kn_l = L_l*1.22*10^(logPn) ;
Kd1_l = L_l*1.22*10^(logPd1) ;
Kd2_l = L_l*1.22*10^(logPd2) ;
an_l = 1 / (1 + 10^(i1*(pKa1-pH_l)) + 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l))) ;
ad2_l = an_l * 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l)) ;
ad1_l = an_l * 10^(i1*(pKa1-pH_l)) ;
Dd2_l = ad2_l / an_l ;
Dd1_l = ad1_l / an_l ;
fn_l = 1 / (W_l/gamman_l + Kn_l/gamman_l + Dd2_l*W_l/gammad2_l +
Dd2_l*Kd2_l/gammad2_l ...
+ Dd1_l*W_l/gammad1_l + Dd1_l*Kd1_l/gammad1_l ) ;
fd2_l = fn_l * Dd2_l ;
fd1_l = fn_l * Dd1_l ;

% AP Compartment (receiver compartment)
fn_a = 1 / (1 + 10^(i1*(pKa1-pH_a)) + 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a))) ;
fd2_a = fn_a * 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a)) ;
fd1_a = fn_a * 10^(i1*(pKa1-pH_a)) ;
Nd2_a = z2*(-E_a)*F/(R*T) ;
Nd1_a = z1*(-E_a)*F/(R*T) ;

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% Solve the differential equation system for each drug:
% Given a system of linear ODE's expressed in matrix form:
% Y' = AY+G with initial conditions Y(0) = RR,
% Ccyto = Y(1)
k11 = -(A_b/V_c)*Pn*fn_c-
(A_b/V_c)*Pd1*Nd1_b*fd1_c*exp(Nd1_b)/(exp(Nd1_b)-1)-
(A_b/V_c)*Pd2*Nd2_b*fd2_c*exp(Nd2_b)/(exp(Nd2_b)-1)...
-(A_m/V_c)*Pn*fn_c-(A_m/V_c)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)-
(A_m/V_c)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1)...
-(A_l/V_c)*Pn*fn_c-(A_l/V_c)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)-
(A_l/V_c)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1)...
-(A_a/V_c)*Pn*fn_c-(A_a/V_c)*Pd1*Nd1_a*fd1_c/(exp(Nd1_a)-1)-
(A_a/V_c)*Pd2*Nd2_a*fd2_c/(exp(Nd2_a)-1) ;
k12 =
(A_m/V_c)*Pn*fn_m+(A_m/V_c)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-
1)+(A_m/V_c)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k13 =
(A_l/V_c)*Pn*fn_l+(A_l/V_c)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-
1)+(A_l/V_c)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;
k14 =
(A_a/V_c)*Pn*fn_a+(A_a/V_c)*Pd1*Nd1_a*fd1_a*exp(Nd1_a)/(exp(Nd1_a)-
1)+(A_a/V_c)*Pd2*Nd2_a*fd2_a*exp(Nd2_a)/(exp(Nd2_a)-1) ;
S1 = (A_b/V_c)*C_b*(Pn*fn_b+Pd1*Nd1_b*fd1_b/(exp(Nd1_b)-
1)+Pd2*Nd2_b*fd2_b/(exp(Nd2_b)-1)) ;

% Cmito = Y(2)
k21 = (A_m/V_m)*Pn*fn_c+(A_m/V_m)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)...
+(A_m/V_m)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1) ;
k22 = -(A_m/V_m)*Pn*fn_m-
(A_m/V_m)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-1)...
-(A_m/V_m)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k23 = 0;
k24 = 0 ;
S2 = 0;

% Clyso = Y(3)
k31 = (A_l/V_l)*Pn*fn_c+(A_l/V_l)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)...
+(A_l/V_l)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1) ;
k32 = 0;
k33 = -(A_l/V_l)*Pn*fn_l-
(A_l/V_l)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-1)...
-(A_l/V_l)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;

k34 = 0 ;
S3 = 0;

% Cap = Y(4)
k41 = (A_a/V_a)*Pn*fn_c+(A_a/V_a)*Pd1*Nd1_a*fd1_c/(exp(Nd1_a)-1)...
+(A_a/V_a)*Pd2*Nd2_a*fd2_c/(exp(Nd2_a)-1) ;
k42 = 0;
k43 = 0;
k44 = -(A_a/V_a)*Pn*fn_a-
(A_a/V_a)*Pd1*Nd1_a*fd1_a*exp(Nd1_a)/(exp(Nd1_a)-1)...
-(A_a/V_a)*Pd2*Nd2_a*fd2_a*exp(Nd2_a)/(exp(Nd2_a)-1) ;
S4 = 0;

```

```

A = [k11, k12, k13, k14; k21, k22, k23, k24; k31, k32, k33, k34; k41,
k42, k43, k44];
G = [S1, S2, S3, S4]';
RR = [0,0,0,0]';
t = 300;

[V,E] = eig(A);
E = diag(E);
H = inv(V)*G;
B = V \ RR;
C = B + H./E;
Z = -(H./E) + exp(t * E).*C ;
Y = real(V * Z);
Y = Y' ;

Ppore = Y(4)*V_a / (t*A_aa*C_b)*10^(2)*10^6 ; %
Pcell, 10^(-6)cm/sec
Peff = Y(4)*V_a*CellNo/(t*A_insert*C_b)*10^(2)*10^6; %
Peff, 10^(-6)cm/sec, normalized by insert area, which is 1.12 cm^2
Mass_cell = (Y(1)*V_c + Y(2)*V_m + Y(3)*V_l)*10^12 ; %
cellular mass, pmol/cell
dMdt = Y(4)*V_a/t*10^12; %
transport rate: pmol/sec/cell

Para(i,:) = [A_a*10^12,PoreNo_cell,
A_l*10^12,A_m*10^12,A_b*10^12,V_c*10^18,V_l*10^18,V_m*10^18,V_a*10^6,E_a*1000,E_
l*1000,E_m*1000,E_b*1000,...
pH_a,pH_c,pH_l,pH_m,pH_b,CellNo,PoreDens,
pKa1,pKa2,logPn,logPd1, logPd2];
Results(i,:)= [Y(1),Y(2),Y(3),Ppore, Peff, dMdt, Mass_cell];

end

comb = [Results(:,1:7),Para];
fid5 = fopen('BtoA_pH65_04um_5min.dat','w');
fprintf(fid5,'%12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.2e %12.0f %1
2.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4f %12.4f %12.4f %12.4f %12.
2f %12.2f %12.2f %12.2f %12.2f %12.0f %12.0f %12.2f %12.2f %12.2f %12.2f %12.2f
\n', comb) ;
fclose(fid5);

figure(17) ; clf ; hold on ;
grid on;
hist (log10(comb(:,4)),1000);
line([log10(Ppore_exp), log10(Ppore_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (P_{cell}, 10^{-6}
cm/sec)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
xlim([0, 6]);
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of cell
permeability', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(18) ; clf ; hold on ;
grid on;

```

```

hist (log10(comb(:,5)),1000);
xlim([-3, 3]);
line([log10(Peff_exp), log10(Peff_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (P_{app}, 10^{-6}
cm/sec)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of apparent
permeability', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(19) ; clf ; hold on ;
grid on;
hist (log10(comb(:,6)),1000);
xlim([-8,-2]);
line([log10(dMdt_exp), log10(dMdt_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (dM/dt,
pmol/sec/cell)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of transport
rate', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(20) ; clf ; hold on ;
grid on;
hist (log10(comb(:,7)),1000);
xlim([-5,-0]);
line([log10(IntraMass_exp),
log10(IntraMass_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (intracellular mass, pmol/cell)
', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of intracellular
mass', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

% =====Case# 6: BL->AP transport, pHb = 6.5, 3um-membrane,
5min=====

clear ; % Clear the memory
z1 = 1 ; % ionization group 1 of CQ
z2 = 2 ; % ionization group 2 of CQ
i1 = sign(z1) ;
i2 = sign(z2) ;

T = 310.15 ; % temperature
R = 8.314 ; % universal gas constant
F = 96484.56 ; % faraday constant
C_b = 1 ; % initial drug concentration (mM)

```

```

sim = 10000; % number of simulations
paraNo = 25;
outputNo = 7; % number of output parameters
Para = zeros(sim,paraNo);
Results = zeros(sim,outputNo);

dMdt_exp = 7.12e-6; % +/- 4.73e-7, pmol/sec/cell, measured after 4hrs
Ppore_exp = 1.58E+01; % +/- 2.45, 10^(-6) cm/sec, measured after 4hrs
Peff_exp = 2.24; % +/- 0.346, 10^(-6) cm/sec, measured after 4hrs
IntraMass_exp = 0.00494; % +/- 0.00106, pmol/cell, measured after 5min

for i = 1:sim

    % Drug information -- ChemAxon calculation including logPn, pKa1, and pKa2
    logPn = 3.93-0.5+rand(); % unif [3.43, 4.43] ;
    pKa1 = 9.96-0.5+rand(); % unif [9.46, 10.46] ;
    pKa2 = 7.47-0.5+rand(); % unif [6.97, 7.97] ;
    logPd1 = 0.43-0.5+rand(); % unif [-0.07, 0.93] ;
    logPd2 = -0.91-0.5+rand(); % unif [-1.41, 0.41] ;
    Pn = 10^(logPn-6.7);
    Pd1 = 10^(logPd1-6.7);
    Pd2 = 10^(logPd2-6.7);

    CellNo = 2*10^5*(1+rand()); % cell
    number/insert: unif [2*10^5, 4*10^5]
    PoreDens = 2*10^6*0.4*(2+rand()); % pore
    number/cm^2: unif [1.6*10^6, 2.4*10^6]
    A_insert = 1.12*10^(-4) ; % insert area:
    1.12 cm^2
    PoreNo_insert = PoreDens*A_insert*10^(4); % pore
    number/insert
    PoreNo_cell = PoreNo_insert/CellNo ; % average pore
    number/cell
    A_pore_insert = 3.14*((3/2)*10^(-6))^2*PoreNo_insert ; % pore area /
    insert (m^2)
    A_pore_cell = 3.14*((3/2)*10^(-6))^2*PoreNo_cell ; % average pore
    area / cell (m^2)

    A_a = 10^(-10)*(1+9*rand()); % apical
    membrane surface area: unif [10^(-10),10*(10)^(-10)] (m^2)
    A_aa = A_pore_cell; % pore area/cell
    (m^2)
    A_b = A_aa+(10^(-10)-A_aa)*rand(); % basolateral
    membrane surface area: unif [A_aa, 10^(-10)] (m^2)
    A_l = 100*3.14*10^(-12); % lysosomal
    membrane surface area (m^2)
    A_m = 100*3.14*10^(-12); % mitochondrial
    membrane surface area (m^2)
    V_c = 0.5*10^(-15)*(1+5*rand()); % cytosolic
    volume: unif [0.5*10^(-15), 3*10^(-15)] (m^3)
    V_l = 10^(-18)*(9.24+(23.8-9.24)*rand()); % lysosomal
    volume: unif [9.24*10^(-18), 23.8*10^(-18)] (m^3)
    V_m = 100*5.24*10^(-19)/5*(1+24*rand()); % mitochondrial
    volume: unif [10.48*10^(-18), 262*10^(-18)](m^3)
    V_a = 0.5*10^(-6); % apical volume:
    0.5 mL

```



```

    % Membrane potential (unit in 'Voltage')
    E_a = 0.0093-0.005+0.01*rand(); % apical
membrane potential: unif [0.0043, 0.0143]
    E_l = 0.01-0.005+0.01*rand(); % lysosomal
membrane potential: unif [0.005, 0.015]
    E_m = -0.16 ; % mitochondrial
membrane potential
    E_b = -0.0119-0.005+0.01*rand(); % basolateral
membrane potential: unif [-0.0169, -0.0069]

    % pH values
    pH_a = 7.4; % pH in apical
compartment
    pH_c = 7.0+0.4*rand(); % pH in cytosol:
unif [7.0, 7.4]
    pH_l = 4.8+0.4*rand(); % pH in
lysosomes: unif [4.8, 5.2]
    pH_m = 7.8+0.4*rand(); % pH in
mitochondria: unif[7.8, 8.2]
    pH_b = 6.4+0.2*rand(); % pH in
basolateral compartment: unif [6.4, 6.6]

    % BL Compartment (donor)
    fn_b = 1 / (1 + 10^(i1*(pKa1-pH_b)) + 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b))) ;
    fd2_b = fn_b * 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b)) ;
    fd1_b = fn_b * 10^(i1*(pKa1-pH_b)) ;
    Nd2_b = z2*E_b*F/(R*T) ;
    Nd1_b = z1*E_b*F/(R*T) ;

    % Cytoplasm
    L_c = 0.05+0.1*rand(); % lipid
fraction in cytosol: unif [0.05, 0.15]
    W_c = 1-L_c ; % water
fraction in cytosol
    Is_c = 0.3 ; % ion
strength in cytosol (mol)
    gamman_c = 10^(0.3*Is_c) ; %
activity coefficient of neutral molecules in cytosol
    gammad1_c = 10^(-0.5*z1*z1*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of monovalent base in cytosol
    gammad2_c = 10^(-0.5*z2*z2*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of bivalent base in cytosol
    Kn_c = L_c*1.22*10^(logPn) ;
    Kd1_c = L_c*1.22*10^(logPd1) ;
    Kd2_c = L_c*1.22*10^(logPd2) ;
    an_c = 1 / (1 + 10^(i1*(pKa1-pH_c)) + 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c))) ;
    ad2_c = an_c * 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c)) ;
    ad1_c = an_c * 10^(i1*(pKa1-pH_c)) ;
    Dd2_c = ad2_c / an_c ;
    Dd1_c = ad1_c / an_c ;
    fn_c = 1 / (W_c/gamman_c + Kn_c/gamman_c + Dd2_c*W_c/gammad2_c +
Dd2_c*Kd2_c/gammad2_c ...
    + Dd1_c*W_c/gammad1_c + Dd1_c*Kd1_c/gammad1_c ) ;
    fd2_c = fn_c * Dd2_c ;
    fd1_c = fn_c * Dd1_c ;

```

```

% Mitochondria
L_m = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_m = 1-L_m; % water
fraction in mitochondria
Is_m = 0.3; % ion
strength in mitochondria (mol)
Nd2_m = z2*E_m*F/(R*T);
Nd1_m = z1*E_m*F/(R*T);
gamman_m = 10^(0.3*Is_m); %
activity coefficient of neutral molecules in mitochondria
gammad1_m = 10^(-0.5*z1*z1*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of monovalent base in mitochondria
gammad2_m = 10^(-0.5*z2*z2*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of bivalent base in mitochondria
Kn_m = L_m*1.22*10^(logPn);
Kd1_m = L_m*1.22*10^(logPd1);
Kd2_m = L_m*1.22*10^(logPd2);
an_m = 1 / (1 + 10^(i1*(pKa1-pH_m)) + 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m)));
ad2_m = an_m * 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m));
ad1_m = an_m * 10^(i1*(pKa1-pH_m));
Dd2_m = ad2_m / an_m;
Dd1_m = ad1_m / an_m;
fn_m = 1 / (W_m/gamman_m + Kn_m/gamman_m + Dd2_m*W_m/gammad2_m +
Dd2_m*Kd2_m/gammad2_m ...
+ Dd1_m*W_m/gammad1_m + Dd1_m*Kd1_m/gammad1_m);
fd2_m = fn_m * Dd2_m;
fd1_m = fn_m * Dd1_m;

% Lysosomes
L_l = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_l = 1-L_l; % water
fraction in lysosomes
Is_l = 0.3; % ion
strength in lysosomes (mol)
Nd2_l = z2*E_l*F/(R*T);
Nd1_l = z1*E_l*F/(R*T);
gamman_l = 10^(0.3*Is_l); %
activity coefficient of neutral molecules in lysosomes
gammad1_l = 10^(-0.5*z1*z1*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of monovalent base in lysosomes
gammad2_l = 10^(-0.5*z2*z2*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of bivalent base in lysosomes
Kn_l = L_l*1.22*10^(logPn);
Kd1_l = L_l*1.22*10^(logPd1);
Kd2_l = L_l*1.22*10^(logPd2);
an_l = 1 / (1 + 10^(i1*(pKa1-pH_l)) + 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l)));
ad2_l = an_l * 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l));
ad1_l = an_l * 10^(i1*(pKa1-pH_l));
Dd2_l = ad2_l / an_l;
Dd1_l = ad1_l / an_l;
fn_l = 1 / (W_l/gamman_l + Kn_l/gamman_l + Dd2_l*W_l/gammad2_l +
Dd2_l*Kd2_l/gammad2_l ...
+ Dd1_l*W_l/gammad1_l + Dd1_l*Kd1_l/gammad1_l);
fd2_l = fn_l * Dd2_l;
fd1_l = fn_l * Dd1_l;

```

```

% AP Compartment (receiver compartment)
fn_a = 1 / (1 + 10^(i1*(pKa1-pH_a)) + 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a))) ;
fd2_a = fn_a * 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a)) ;
fd1_a = fn_a * 10^(i1*(pKa1-pH_a)) ;
Nd2_a = z2*(-E_a)*F/(R*T) ;
Nd1_a = z1*(-E_a)*F/(R*T) ;

% Solve the differential equation system for each drug:
% Given a system of linear ODE's expressed in matrix form:
% Y' = AY+G with initial conditions Y(0) = RR,
% Ccyto = Y(1)
k11 = -(A_b/V_c)*Pn*fn_c-
(A_b/V_c)*Pd1*Nd1_b*fd1_c*exp(Nd1_b)/(exp(Nd1_b)-1)-
(A_b/V_c)*Pd2*Nd2_b*fd2_c*exp(Nd2_b)/(exp(Nd2_b)-1)...
-(A_m/V_c)*Pn*fn_c-(A_m/V_c)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)-
(A_m/V_c)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1)...
-(A_l/V_c)*Pn*fn_c-(A_l/V_c)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)-
(A_l/V_c)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1)...
-(A_a/V_c)*Pn*fn_c-(A_a/V_c)*Pd1*Nd1_a*fd1_c/(exp(Nd1_a)-1)-
(A_a/V_c)*Pd2*Nd2_a*fd2_c/(exp(Nd2_a)-1) ;
k12 =
(A_m/V_c)*Pn*fn_m+(A_m/V_c)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-
1)+(A_m/V_c)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k13 =
(A_l/V_c)*Pn*fn_l+(A_l/V_c)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-
1)+(A_l/V_c)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;
k14 =
(A_a/V_c)*Pn*fn_a+(A_a/V_c)*Pd1*Nd1_a*fd1_a*exp(Nd1_a)/(exp(Nd1_a)-
1)+(A_a/V_c)*Pd2*Nd2_a*fd2_a*exp(Nd2_a)/(exp(Nd2_a)-1) ;
S1 = (A_b/V_c)*C_b*(Pn*fn_b+Pd1*Nd1_b*fd1_b/(exp(Nd1_b)-
1)+Pd2*Nd2_b*fd2_b/(exp(Nd2_b)-1)) ;

% Cmito = Y(2)
k21 = (A_m/V_m)*Pn*fn_c+(A_m/V_m)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)...
+(A_m/V_m)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1) ;
k22 = -(A_m/V_m)*Pn*fn_m-
(A_m/V_m)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-1)...
-(A_m/V_m)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k23 = 0 ;
k24 = 0 ;
S2 = 0 ;

% Clyso = Y(3)
k31 = (A_l/V_l)*Pn*fn_c+(A_l/V_l)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)...
+(A_l/V_l)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1) ;
k32 = 0 ;
k33 = -(A_l/V_l)*Pn*fn_l-
(A_l/V_l)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-1)...
-(A_l/V_l)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;
k34 = 0 ;
S3 = 0 ;

% Cap = Y(4)
k41 = (A_a/V_a)*Pn*fn_c+(A_a/V_a)*Pd1*Nd1_a*fd1_c/(exp(Nd1_a)-1)...
+(A_a/V_a)*Pd2*Nd2_a*fd2_c/(exp(Nd2_a)-1) ;

```

```

k42 = 0;
k43 = 0;
k44 = -(A_a/V_a)*Pn*fn_a-
(A_a/V_a)*Pd1*Nd1_a*fd1_a*exp(Nd1_a)/(exp(Nd1_a)-1)...
      -(A_a/V_a)*Pd2*Nd2_a*fd2_a*exp(Nd2_a)/(exp(Nd2_a)-1);
S4 = 0;

A = [k11, k12, k13, k14; k21, k22, k23, k24; k31, k32, k33, k34; k41,
k42, k43, k44];
G = [S1, S2, S3, S4]';
RR = [0,0,0,0]';
t = 300;

[V,E] = eig(A);
E = diag(E);
H = inv(V)*G;
B = V \ RR;
C = B + H./E;
Z = -(H./E) + exp(t * E).*C ;
Y = real(V * Z);
Y = Y' ;

Ppore = Y(4)*V_a / (t*A_aa*C_b)*10^(2)*10^6 ; %
Pcell, 10^(-6)cm/sec
Peff = Y(4)*V_a*CellNo/(t*A_insert*C_b)*10^(2)*10^6; %
Peff, 10^(-6)cm/sec, normalized by insert area, which is 1.12 cm^2
Mass_cell = (Y(1)*V_c + Y(2)*V_m + Y(3)*V_l)*10^12 ; %
cellular mass, pmol/cell
dMdt = Y(4)*V_a/t*10^12; %
transport rate: pmol/sec/cell

Para(i,:) = [A_a*10^12,PoreNo_cell,
A_l*10^12,A_m*10^12,A_b*10^12,V_c*10^18,V_l*10^18,V_m*10^18,V_a*10^6,E_a*1000,E_
l*1000,E_m*1000,E_b*1000,...
pH_a,pH_c,pH_l,pH_m,pH_b,CellNo,PoreDens,
pKa1,pKa2,logPn,logPd1, logPd2];
Results(i,:)=[Y(1),Y(2),Y(3),Ppore, Peff, dMdt, Mass_cell];

end

comb = [Results(:,1:7),Para];
fid5 = fopen('BtoA_pH65_3um_5min.dat','w');
fprintf(fid5,'%12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.2e %12.0f %1
2.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4f %12.4f %12.4f %12.4f %12.
2f %12.2f %12.2f %12.2f %12.2f %12.2f %12.0f %12.0f %12.2f %12.2f %12.2f %12.2f %12.2f
\n', comb) ;
fclose(fid5);

figure(21) ; clf ; hold on ;
grid on;
hist (log10(comb(:,4)),1000);
line([log10(Ppore_exp), log10(Ppore_exp)],[0,50], 'Color','r', 'LineWidth',3);
xlabel('log_{10} (P_{cell}, 10^{-6}
cm/sec)', 'FontSize',30, 'FontWeight', 'Bold', 'FontName', 'Times');
xlim([0, 6]);
ax1 = gca;

```

```

set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of cell permeability', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(22) ; clf ; hold on ;
grid on;
hist (log10(comb(:,5)),1000);
xlim([-3, 3]);
line([log10(Peff_exp), log10(Peff_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (P_{app}, 10^{-6} cm/sec)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of apparent permeability', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(23) ; clf ; hold on ;
grid on;
hist (log10(comb(:,6)),1000);
xlim([-8,-2]);
line([log10(dMdt_exp), log10(dMdt_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (dM/dt, pmol/sec/cell)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of transport rate', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(24) ; clf ; hold on ;
grid on;
hist (log10(comb(:,7)),1000);
xlim([-5,-0]);
line([log10(IntraMass_exp), log10(IntraMass_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (intracellular mass, pmol/cell)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of intracellular mass', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

% =====Case# 7: BL->AP transport, pHb = 7.4, 0.4um-membrane, 5min=====
clear ; % Clear the memory
z1 = 1 ; % ionization group 1 of CQ
z2 = 2 ; % ionization group 2 of CQ
i1 = sign(z1) ;

```

```

i2 = sign(z2) ;

T = 310.15 ;           % temperature
R = 8.314 ;           % universal gas constant
F = 96484.56 ;       % faraday constant
C_b = 1 ;             % initial drug concentration (mM)

sim = 10000;          % number of simulations
paraNo = 25;
outputNo = 7;        % number of output parameters
Para = zeros(sim,paraNo);
Results = zeros(sim,outputNo);

dMdt_exp = 2.94e-5;   % +/- 1.54e-6, pmol/sec/cell, measured after
4hrs
Ppore_exp = 2.00E+03; % +/- 353, 10^-6 cm/sec, measured after 4hrs
Peff_exp = 1.00E+01; % +/- 1.77, 10^-6 cm/sec, measured after
4hrs
IntraMass_exp = 0.00828; % +/- 0.00075 pmol/cell , measured after
5min

for i = 1:sim

    % Drug information -- ChemAxon calculation including logPn, pKa1, and pKa2
    logPn = 3.93-0.5+rand(); % unif [3.43, 4.43] ;
    pKa1 = 9.96-0.5+rand(); % unif [9.46, 10.46] ;
    pKa2 = 7.47-0.5+rand(); % unif [6.97, 7.97] ;
    logPd1 = 0.43-0.5+rand(); % unif [-0.07, 0.93] ;
    logPd2 = -0.91-0.5+rand(); % unif [-1.41, 0.41] ;
    Pn = 10^(logPn-6.7);
    Pd1 = 10^(logPd1-6.7);
    Pd2 = 10^(logPd2-6.7);

    CellNo = 2*10^5*(1+rand()); % cell
number/insert: unif [2*10^5, 4*10^5]
    PoreDens = 4*10^6*0.4*(2+rand()); % pore
number/cm^2: unif [3.2*10^6, 4.8*10^6]
    A_insert = 1.12*10^(-4) ; % insert area:
1.12 cm^2
    PoreNo_insert = PoreDens*A_insert*10^(4); % pore
number/insert
    PoreNo_cell = PoreNo_insert/CellNo ; % average pore
number/cell
    A_pore_insert = 3.14*((0.4/2)*10^(-6))^2*PoreNo_insert ; % pore area /
insert (m^2)
    A_pore_cell = 3.14*((0.4/2)*10^(-6))^2*PoreNo_cell ; % average pore
area / cell (m^2)

    A_a = 10^(-10)*(1+9*rand()); % apical
membrane surface area: unif [10^(-10),10*(10)^(-10)] (m^2)
    A_aa = A_pore_cell; % pore area/cell
(m^2)
    A_b = A_aa+(10^(-10)-A_aa)*rand(); % basolateral
membrane surface area: unif [A_aa, 10^(-10)] (m^2)
    A_l = 100*3.14*10^(-12); % lysosomal
membrane surface area (m^2)

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```

    A_m = 100*3.14*10^(-12); % mitochondrial
membrane surface area (m^2)
    V_c = 0.5*10^(-15)*(1+5*rand()); % cytosolic
volume: unif [0.5*10^(-15), 3*10^(-15)] (m^3)
    V_l = 10^(-18)*(9.24+(23.8-9.24)*rand()); % lysosomal
volume: unif [9.24*10^(-18), 23.8*10^(-18)] (m^3)
    V_m = 100*5.24*10^(-19)/5*(1+24*rand()); % mitochondrial
volume: unif [10.48*10^(-18), 262*10^(-18)](m^3)
    V_a = 0.5*10^(-6); % apical volume:
0.5 mL

    % Membrane potential (unit in 'Voltage')
    E_a = 0.0093-0.005+0.01*rand(); % apical
membrane potential: unif [0.0043, 0.0143]
    E_l = 0.01-0.005+0.01*rand(); % lysosomal
membrane potential: unif [0.005, 0.015]
    E_m = -0.16 ; % mitochondrial
membrane potential
    E_b = -0.0119-0.005+0.01*rand(); % basolateral
membrane potential: unif [-0.0169, -0.0069]

    % pH values
    pH_a = 7.4; % pH in apical
compartment
    pH_c = 7.0+0.4*rand(); % pH in cytosol:
unif [7.0, 7.4]
    pH_l = 4.8+0.4*rand(); % pH in
lysosomes: unif [4.8, 5.2]
    pH_m = 7.8+0.4*rand(); % pH in
mitochondria: unif[7.8, 8.2]
    pH_b = 7.0+0.4*rand(); % pH in
basolateral compartment: unif [7.0, 7.4]

    % BL Compartment (donor)
    fn_b = 1 / (1 + 10^(i1*(pKa1-pH_b)) + 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b))) ;
    fd2_b = fn_b * 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b)) ;
    fd1_b = fn_b * 10^(i1*(pKa1-pH_b)) ;
    Nd2_b = z2*E_b*F/(R*T) ;
    Nd1_b = z1*E_b*F/(R*T) ;

    % Cytoplasm
    L_c = 0.05+0.1*rand(); % lipid
fraction in cytosol: unif [0.05, 0.15]
    W_c = 1-L_c ; % water
fraction in cytosol
    Is_c = 0.3 ; % ion
strength in cytosol (mol)
    gamman_c = 10^(0.3*Is_c) ; %
activity coefficient of neutral molecules in cytosol
    gammad1_c = 10^(-0.5*z1*z1*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of monovalent base in cytosol
    gammad2_c = 10^(-0.5*z2*z2*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of bivalent base in cytosol
    Kn_c = L_c*1.22*10^(logPn) ;
    Kd1_c = L_c*1.22*10^(logPd1) ;
    Kd2_c = L_c*1.22*10^(logPd2) ;
    an_c = 1 / (1 + 10^(i1*(pKa1-pH_c)) + 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c))) ;

```

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ad2_c = an_c * 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c)) ;
ad1_c = an_c * 10^(i1*(pKa1-pH_c)) ;
Dd2_c = ad2_c / an_c ;
Dd1_c = ad1_c / an_c ;
fn_c = 1 / (W_c/gamman_c + Kn_c/gamman_c + Dd2_c*W_c/gammad2_c +
Dd2_c*Kd2_c/gammad2_c ...
+ Dd1_c*W_c/gammad1_c + Dd1_c*Kd1_c/gammad1_c ) ;
fd2_c = fn_c * Dd2_c ;
fd1_c = fn_c * Dd1_c ;

% Mitochondria
L_m = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_m = 1-L_m ; % water
fraction in mitochondria
Is_m = 0.3 ; % ion
strength in mitochondria (mol)
Nd2_m = z2*E_m*F/(R*T) ;
Nd1_m = z1*E_m*F/(R*T) ;
gamman_m = 10^(0.3*Is_m) ; %
activity coefficient of neutral molecules in mitochondria
gammad1_m = 10^(-0.5*z1*z1*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of monovalent base in mitochondria
gammad2_m = 10^(-0.5*z2*z2*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of bivalent base in mitochondria
Kn_m = L_m*1.22*10^(logPn) ;
Kd1_m = L_m*1.22*10^(logPd1) ;
Kd2_m = L_m*1.22*10^(logPd2) ;
an_m = 1 / (1 + 10^(i1*(pKa1-pH_m)) + 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m))) ;
ad2_m = an_m * 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m)) ;
ad1_m = an_m * 10^(i1*(pKa1-pH_m)) ;
Dd2_m = ad2_m / an_m ;
Dd1_m = ad1_m / an_m ;
fn_m = 1 / (W_m/gamman_m + Kn_m/gamman_m + Dd2_m*W_m/gammad2_m +
Dd2_m*Kd2_m/gammad2_m ...
+ Dd1_m*W_m/gammad1_m + Dd1_m*Kd1_m/gammad1_m ) ;
fd2_m = fn_m * Dd2_m ;
fd1_m = fn_m * Dd1_m ;

% Lysosomes
L_l = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
W_l = 1-L_l ; % water
fraction in lysosomes
Is_l = 0.3 ; % ion
strength in lysosomes (mol)
Nd2_l = z2*E_l*F/(R*T) ;
Nd1_l = z1*E_l*F/(R*T) ;
gamman_l = 10^(0.3*Is_l) ; %
activity coefficient of neutral molecules in lysosomes
gammad1_l = 10^(-0.5*z1*z1*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of monovalent base in lysosomes
gammad2_l = 10^(-0.5*z2*z2*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of bivalent base in lysosomes
Kn_l = L_l*1.22*10^(logPn) ;
Kd1_l = L_l*1.22*10^(logPd1) ;
Kd2_l = L_l*1.22*10^(logPd2) ;

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an_1 = 1 / (1 + 10^(i1*(pKa1-pH_1)) + 10^(i1*(pKa1-pH_1)+i2*(pKa2-pH_1))) ;
ad2_1 = an_1 * 10^(i1*(pKa1-pH_1)+i2*(pKa2-pH_1)) ;
ad1_1 = an_1 * 10^(i1*(pKa1-pH_1)) ;
Dd2_1 = ad2_1 / an_1 ;
Dd1_1 = ad1_1 / an_1 ;
fn_1 = 1 / (W_1/gamman_1 + Kn_1/gamman_1 + Dd2_1*W_1/gammad2_1 +
Dd2_1*Kd2_1/gammad2_1 ...
+ Dd1_1*W_1/gammad1_1 + Dd1_1*Kd1_1/gammad1_1 ) ;
fd2_1 = fn_1 * Dd2_1 ;
fd1_1 = fn_1 * Dd1_1 ;

% AP Compartment (receiver compartment)
fn_a = 1 / (1 + 10^(i1*(pKa1-pH_a)) + 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a))) ;
fd2_a = fn_a * 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a)) ;
fd1_a = fn_a * 10^(i1*(pKa1-pH_a)) ;
Nd2_a = z2*(-E_a)*F/(R*T) ;
Nd1_a = z1*(-E_a)*F/(R*T) ;

% Solve the differential equation system for each drug:
% Given a system of linear ODE's expressed in matrix form:
% Y' = AY+G with initial conditions Y(0) = RR,
% Ccyto = Y(1)
k11 = -(A_b/V_c)*Pn*fn_c-
(A_b/V_c)*Pd1*Nd1_b*fd1_c*exp(Nd1_b)/(exp(Nd1_b)-1)-
(A_b/V_c)*Pd2*Nd2_b*fd2_c*exp(Nd2_b)/(exp(Nd2_b)-1)...
- (A_m/V_c)*Pn*fn_c- (A_m/V_c)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)-
(A_m/V_c)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1)...
- (A_l/V_c)*Pn*fn_c- (A_l/V_c)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)-
(A_l/V_c)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1)...
- (A_a/V_c)*Pn*fn_c- (A_a/V_c)*Pd1*Nd1_a*fd1_c/(exp(Nd1_a)-1)-
(A_a/V_c)*Pd2*Nd2_a*fd2_c/(exp(Nd2_a)-1) ;
k12 =
(A_m/V_c)*Pn*fn_m+ (A_m/V_c)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-
1)+(A_m/V_c)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k13 =
(A_l/V_c)*Pn*fn_l+ (A_l/V_c)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-
1)+(A_l/V_c)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;
k14 =
(A_a/V_c)*Pn*fn_a+ (A_a/V_c)*Pd1*Nd1_a*fd1_a*exp(Nd1_a)/(exp(Nd1_a)-
1)+(A_a/V_c)*Pd2*Nd2_a*fd2_a*exp(Nd2_a)/(exp(Nd2_a)-1) ;
S1 = (A_b/V_c)*C_b*(Pn*fn_b+Pd1*Nd1_b*fd1_b/(exp(Nd1_b)-
1)+Pd2*Nd2_b*fd2_b/(exp(Nd2_b)-1)) ;

% Cmito = Y(2)
k21 = (A_m/V_m)*Pn*fn_c+ (A_m/V_m)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)...
+ (A_m/V_m)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1) ;
k22 = -(A_m/V_m)*Pn*fn_m-
(A_m/V_m)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-1)...
- (A_m/V_m)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k23 = 0 ;
k24 = 0 ;
S2 = 0 ;

% Clyso = Y(3)
k31 = (A_l/V_l)*Pn*fn_c+ (A_l/V_l)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)...
+ (A_l/V_l)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1) ;
k32 = 0 ;

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k33 = -(A_l/V_l)*Pn*fn_l-
(A_l/V_l)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-1)...
      -(A_l/V_l)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;
k34 = 0 ;
S3 = 0;

% Cap = Y(4)
k41 = (A_a/V_a)*Pn*fn_c+(A_a/V_a)*Pd1*Nd1_a*fd1_c/(exp(Nd1_a)-1)...
      +(A_a/V_a)*Pd2*Nd2_a*fd2_c/(exp(Nd2_a)-1) ;
k42 = 0;
k43 = 0;
k44 = -(A_a/V_a)*Pn*fn_a-
(A_a/V_a)*Pd1*Nd1_a*fd1_a*exp(Nd1_a)/(exp(Nd1_a)-1)...
      -(A_a/V_a)*Pd2*Nd2_a*fd2_a*exp(Nd2_a)/(exp(Nd2_a)-1);
S4 = 0;

A = [k11, k12, k13, k14; k21, k22, k23, k24; k31, k32, k33, k34; k41,
k42, k43, k44];
G = [S1, S2, S3, S4]';
RR = [0,0,0,0]';
t = 300;

[V,E] = eig(A);
E = diag(E);
H = inv(V)*G;
B = V \ RR;
C = B + H./E;
Z = -(H./E) + exp(t * E).*C ;
Y = real(V * Z);
Y = Y' ;

Ppore = Y(4)*V_a /(t*A_aa*C_b)*10^(2)*10^6 ; %
Pcell, 10^(-6)cm/sec
Peff = Y(4)*V_a*CellNo/(t*A_insert*C_b)*10^(2)*10^6; %
Peff, 10^(-6)cm/sec, normalized by insert area, which is 1.12 cm^2
Mass_cell = (Y(1)*V_c + Y(2)*V_m + Y(3)*V_l)*10^12 ; %
cellular mass, pmol/cell
dMdt = Y(4)*V_a/t*10^12; %
transport rate: pmol/sec/cell

Para(i,:) = [A_a*10^12,PoreNo_cell,
A_l*10^12,A_m*10^12,A_b*10^12,V_c*10^18,V_l*10^18,V_m*10^18,V_a*10^6,E_a*1000,E_
l*1000,E_m*1000,E_b*1000,...
pH_a,pH_c,pH_l,pH_m,pH_b,CellNo,PoreDens,
pKa1,pKa2,logPn,logPd1, logPd2];
Results(i,:)= [Y(1),Y(2),Y(3),Ppore, Peff, dMdt, Mass_cell];

end

comb = [Results(:,1:7),Para];
fid5 = fopen('BtoA_pH74_04um_5min.dat','w');
fprintf(fid5,'%12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.2e %12.0f %1
2.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4f %12.4f %12.4f %12.4f %12.
2f %12.2f %12.2f %12.2f %12.2f %12.0f %12.0f %12.2f %12.2f %12.2f %12.2f %12.2f
\n', comb) ;

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```

fclose(fid5);

figure(25) ; clf ; hold on ;
grid on;
hist (log10(comb(:,4)),1000);
line([log10(Ppore_exp), log10(Ppore_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (P_{cell}, 10^{-6}
cm/sec)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
xlim([0, 6]);
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of cell
permeability', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(26) ; clf ; hold on ;
grid on;
hist (log10(comb(:,5)),1000);
xlim([-3, 3]);
line([log10(Peff_exp), log10(Peff_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (P_{app}, 10^{-6}
cm/sec)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of apparent
permeability', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(27) ; clf ; hold on ;
grid on;
hist (log10(comb(:,6)),1000);
xlim([-8, -2]);
line([log10(dMdt_exp), log10(dMdt_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (dM/dt,
pmol/sec/cell)', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
title ('histogram of transport
rate', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

figure(28) ; clf ; hold on ;
grid on;
hist (log10(comb(:,7)),1000);
xlim([-5, -0]);
line([log10(IntraMass_exp),
log10(IntraMass_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);
xlabel('log_{10} (intracellular mass, pmol/cell)
', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');
ax1 = gca;
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo
ntName', 'Times') ;
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;

```

```

title ('histogram of intracellular
mass','FontSize',30,'FontWeight','Bold','FontName','Times') ;

% =====Case# 8: BL->AP transport, pHb = 7.4, 3um-membrane,
5min=====

clear ; % Clear the memory
z1 = 1 ; % ionization group 1 of CQ
z2 = 2 ; % ionization group 2 of CQ
i1 = sign(z1) ;
i2 = sign(z2) ;

T = 310.15 ; % temperature
R = 8.314 ; % universal gas constant
F = 96484.56 ; % faraday constant
C_b = 1 ; % initial drug concentration (mM)

sim = 10000; % number of simulations
paraNo = 25;
outputNo = 7; % number of output parameters
Para = zeros(sim,paraNo);
Results = zeros(sim,outputNo);

dMdt_exp = 6.38e-5; % +/- 1.59e-5, pmol/sec/cell, measured after 4hrs
Ppore_exp = 1.14E+02; % +/- 19, 10^(-6) cm/sec, measured after 4hrs
Peff_exp = 1.62E+01; % +/- 2.69, 10^(-6) cm/sec, measured after 4hrs
IntraMass_exp = 0.01177; % +/- 0.00190, pmol/cell, measured after 5min

for i = 1:sim

    % Drug information -- ChemAxon calculation including logPn, pKa1, and pKa2
    logPn = 3.93-0.5+rand(); % unif [3.43, 4.43] ;
    pKa1 = 9.96-0.5+rand(); % unif [9.46, 10.46] ;
    pKa2 = 7.47-0.5+rand(); % unif [6.97, 7.97] ;
    logPd1 = 0.43-0.5+rand(); % unif [-0.07, 0.93] ;
    logPd2 = -0.91-0.5+rand(); % unif [-1.41, 0.41] ;
    Pn = 10^(logPn-6.7);
    Pd1 = 10^(logPd1-6.7);
    Pd2 = 10^(logPd2-6.7);

    CellNo = 2*10^5*(1+rand()); % cell
    number/insert: unif [2*10^5, 4*10^5]
    PoreDens = 2*10^6*0.4*(2+rand()); % pore
    number/cm^2: unif [1.6*10^6, 2.4*10^6]
    A_insert = 1.12*10^(-4) ; % insert area:
    1.12 cm^2
    PoreNo_insert = PoreDens*A_insert*10^(4); % pore
    number/insert
    PoreNo_cell = PoreNo_insert/CellNo ; % average pore
    number/cell
    A_pore_insert = 3.14*((3/2)*10^(-6))^2*PoreNo_insert ; % pore area /
    insert (m^2)
    A_pore_cell = 3.14*((3/2)*10^(-6))^2*PoreNo_cell ; % average pore
    area / cell (m^2)

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    A_a = 10^(-10)*(1+9*rand()); % apical
membrane surface area: unif [10^(-10),10*(10)^(-10)] (m^2)
    A_aa = A_pore_cell; % pore area/cell
(m^2)
    A_b = A_aa+(10^(-10)-A_aa)*rand(); % basolateral
membrane surface area: unif [A_aa, 10^(-10)] (m^2)
    A_l = 100*3.14*10^(-12); % lysosomal
membrane surface area (m^2)
    A_m = 100*3.14*10^(-12); % mitochondrial
membrane surface area (m^2)
    V_c = 0.5*10^(-15)*(1+5*rand()); % cytosolic
volume: unif [0.5*10^(-15), 3*10^(-15)] (m^3)
    V_l = 10^(-18)*(9.24+(23.8-9.24)*rand()); % lysosomal
volume: unif [9.24*10^(-18), 23.8*10^(-18)] (m^3)
    V_m = 100*5.24*10^(-19)/5*(1+24*rand()); % mitochondrial
volume: unif [10.48*10^(-18), 262*10^(-18)](m^3)
    V_a = 0.5*10^(-6); % apical volume:
0.5 mL

    % Membrane potential (unit in 'Voltage')
    E_a = 0.0093-0.005+0.01*rand(); % apical
membrane potential: unif [0.0043, 0.0143]
    E_l = 0.01-0.005+0.01*rand(); % lysosomal
membrane potential: unif [0.005, 0.015]
    E_m = -0.16 ; % mitochondrial
membrane potential
    E_b = -0.0119-0.005+0.01*rand(); % basolateral
membrane potential: unif [-0.0169, -0.0069]

    % pH values
    pH_a = 7.4; % pH in apical
compartment
    pH_c = 7.0+0.4*rand(); % pH in cytosol:
unif [7.0, 7.4]
    pH_l = 4.8+0.4*rand(); % pH in
lysosomes: unif [4.8, 5.2]
    pH_m = 7.8+0.4*rand(); % pH in
mitochondria: unif[7.8, 8.2]
    pH_b = 7.0+0.4*rand(); % pH in
basolateral compartment: unif [7.0, 7.4]

    % BL Compartment (donor)
fn_b = 1 / (1 + 10^(i1*(pKa1-pH_b)) + 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b))) ;
fd2_b = fn_b * 10^(i1*(pKa1-pH_b)+i2*(pKa2-pH_b)) ;
fd1_b = fn_b * 10^(i1*(pKa1-pH_b)) ;
Nd2_b = z2*E_b*F/(R*T) ;
Nd1_b = z1*E_b*F/(R*T) ;

    % Cytoplasm
    L_c = 0.05+0.1*rand(); % lipid
fraction in cytosol: unif [0.05, 0.15]
    W_c = 1-L_c ; % water
fraction in cytosol
    Is_c = 0.3 ; % ion
strength in cytosol (mol)

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    gamman_c = 10^(0.3*Is_c) ; %
activity coefficient of neutral molecules in cytosol
    gammad1_c = 10^(-0.5*z1*z1*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of monovalent base in cytosol
    gammad2_c = 10^(-0.5*z2*z2*(sqrt(Is_c)/(1+sqrt(Is_c))-0.3*Is_c)); %
activity coefficient of bivalent base in cytosol
    Kn_c = L_c*1.22*10^(logPn) ;
    Kd1_c = L_c*1.22*10^(logPd1) ;
    Kd2_c = L_c*1.22*10^(logPd2) ;
    an_c = 1 / (1 + 10^(i1*(pKa1-pH_c)) + 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c))) ;
    ad2_c = an_c * 10^(i1*(pKa1-pH_c)+i2*(pKa2-pH_c)) ;
    ad1_c = an_c * 10^(i1*(pKa1-pH_c)) ;
    Dd2_c = ad2_c / an_c ;
    Dd1_c = ad1_c / an_c ;
    fn_c = 1 / (W_c/gamman_c + Kn_c/gamman_c + Dd2_c*W_c/gammad2_c +
Dd2_c*Kd2_c/gammad2_c ...
    + Dd1_c*W_c/gammad1_c + Dd1_c*Kd1_c/gammad1_c ) ;
    fd2_c = fn_c * Dd2_c ;
    fd1_c = fn_c * Dd1_c ;

% Mitochondria
    L_m = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
    W_m = 1-L_m ; % water
fraction in mitochondria
    Is_m = 0.3 ; % ion
strength in mitochondria (mol)
    Nd2_m = z2*E_m*F/(R*T) ;
    Nd1_m = z1*E_m*F/(R*T) ;
    gamman_m = 10^(0.3*Is_m) ; %
activity coefficient of neutral molecules in mitochondria
    gammad1_m = 10^(-0.5*z1*z1*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of monovalent base in mitochondria
    gammad2_m = 10^(-0.5*z2*z2*(sqrt(Is_m)/(1+sqrt(Is_m))-0.3*Is_m)); %
activity coefficient of bivalent base in mitochondria
    Kn_m = L_m*1.22*10^(logPn) ;
    Kd1_m = L_m*1.22*10^(logPd1) ;
    Kd2_m = L_m*1.22*10^(logPd2) ;
    an_m = 1 / (1 + 10^(i1*(pKa1-pH_m)) + 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m))) ;
    ad2_m = an_m * 10^(i1*(pKa1-pH_m)+i2*(pKa2-pH_m)) ;
    ad1_m = an_m * 10^(i1*(pKa1-pH_m)) ;
    Dd2_m = ad2_m / an_m ;
    Dd1_m = ad1_m / an_m ;
    fn_m = 1 / (W_m/gamman_m + Kn_m/gamman_m + Dd2_m*W_m/gammad2_m +
Dd2_m*Kd2_m/gammad2_m ...
    + Dd1_m*W_m/gammad1_m + Dd1_m*Kd1_m/gammad1_m ) ;
    fd2_m = fn_m * Dd2_m ;
    fd1_m = fn_m * Dd1_m ;

% Lysosomes
    L_l = 0.05+0.1*rand(); % lipid
fraction in mitochondria: unif [0.05, 0.15]
    W_l = 1-L_l ; % water
fraction in lysosomes
    Is_l = 0.3 ; % ion
strength in lysosomes (mol)
    Nd2_l = z2*E_l*F/(R*T) ;

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Nd1_l = z1*E_l*F/(R*T) ;
gamman_l = 10^(0.3*Is_l) ; %
activity coefficient of neutral molecules in lysosomes
gammad1_l = 10^(-0.5*z1*z1*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of monovalent base in lysosomes
gammad2_l = 10^(-0.5*z2*z2*(sqrt(Is_l)/(1+sqrt(Is_l))-0.3*Is_l)); %
activity coefficient of bivalent base in lysosomes
Kn_l = L_l*1.22*10^(logPn) ;
Kd1_l = L_l*1.22*10^(logPd1) ;
Kd2_l = L_l*1.22*10^(logPd2) ;
an_l = 1 / (1 + 10^(i1*(pKa1-pH_l)) + 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l))) ;
ad2_l = an_l * 10^(i1*(pKa1-pH_l)+i2*(pKa2-pH_l)) ;
ad1_l = an_l * 10^(i1*(pKa1-pH_l)) ;
Dd2_l = ad2_l / an_l ;
Dd1_l = ad1_l / an_l ;
fn_l = 1 / (W_l/gamman_l + Kn_l/gamman_l + Dd2_l*W_l/gammad2_l +
Dd2_l*Kd2_l/gammad2_l ...
+ Dd1_l*W_l/gammad1_l + Dd1_l*Kd1_l/gammad1_l ) ;
fd2_l = fn_l * Dd2_l ;
fd1_l = fn_l * Dd1_l ;

% AP Compartment (receiver compartment)
fn_a = 1 / (1 + 10^(i1*(pKa1-pH_a)) + 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a))) ;
fd2_a = fn_a * 10^(i1*(pKa1-pH_a)+i2*(pKa2-pH_a)) ;
fd1_a = fn_a * 10^(i1*(pKa1-pH_a)) ;
Nd2_a = z2*(-E_a)*F/(R*T) ;
Nd1_a = z1*(-E_a)*F/(R*T) ;

% Solve the differential equation system for each drug:
% Given a system of linear ODE's expressed in matrix form:
% Y' = AY+G with initial conditions Y(0) = RR,
% Ccyto = Y(1)
k11 = -(A_b/V_c)*Pn*fn_c-
(A_b/V_c)*Pd1*Nd1_b*fd1_c*exp(Nd1_b)/(exp(Nd1_b)-1)-
(A_b/V_c)*Pd2*Nd2_b*fd2_c*exp(Nd2_b)/(exp(Nd2_b)-1)...
-(A_m/V_c)*Pn*fn_c-(A_m/V_c)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)-
(A_m/V_c)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1)...
-(A_l/V_c)*Pn*fn_c-(A_l/V_c)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)-
(A_l/V_c)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1)...
-(A_a/V_c)*Pn*fn_c-(A_a/V_c)*Pd1*Nd1_a*fd1_c/(exp(Nd1_a)-1)-
(A_a/V_c)*Pd2*Nd2_a*fd2_c/(exp(Nd2_a)-1) ;
k12 =
(A_m/V_c)*Pn*fn_m+(A_m/V_c)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-
1)+(A_m/V_c)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k13 =
(A_l/V_c)*Pn*fn_l+(A_l/V_c)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-
1)+(A_l/V_c)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;
k14 =
(A_a/V_c)*Pn*fn_a+(A_a/V_c)*Pd1*Nd1_a*fd1_a*exp(Nd1_a)/(exp(Nd1_a)-
1)+(A_a/V_c)*Pd2*Nd2_a*fd2_a*exp(Nd2_a)/(exp(Nd2_a)-1) ;
S1 = (A_b/V_c)*C_b*(Pn*fn_b+Pd1*Nd1_b*fd1_b/(exp(Nd1_b)-
1)+Pd2*Nd2_b*fd2_b/(exp(Nd2_b)-1)) ;

% Cmito = Y(2)
k21 = (A_m/V_m)*Pn*fn_c+(A_m/V_m)*Pd1*Nd1_m*fd1_c/(exp(Nd1_m)-1)...
+(A_m/V_m)*Pd2*Nd2_m*fd2_c/(exp(Nd2_m)-1) ;

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k22 = -(A_m/V_m)*Pn*fn_m-
(A_m/V_m)*Pd1*Nd1_m*fd1_m*exp(Nd1_m)/(exp(Nd1_m)-1)...
      -(A_m/V_m)*Pd2*Nd2_m*fd2_m*exp(Nd2_m)/(exp(Nd2_m)-1) ;
k23 = 0;
k24 = 0 ;
S2 = 0;

% Clyso = Y(3)
k31 = (A_l/V_l)*Pn*fn_c+(A_l/V_l)*Pd1*Nd1_l*fd1_c/(exp(Nd1_l)-1)...
      +(A_l/V_l)*Pd2*Nd2_l*fd2_c/(exp(Nd2_l)-1) ;
k32 = 0;
k33 = -(A_l/V_l)*Pn*fn_l-
(A_l/V_l)*Pd1*Nd1_l*fd1_l*exp(Nd1_l)/(exp(Nd1_l)-1)...
      -(A_l/V_l)*Pd2*Nd2_l*fd2_l*exp(Nd2_l)/(exp(Nd2_l)-1) ;
k34 = 0 ;
S3 = 0;

% Cap = Y(4)
k41 = (A_a/V_a)*Pn*fn_c+(A_a/V_a)*Pd1*Nd1_a*fd1_c/(exp(Nd1_a)-1)...
      +(A_a/V_a)*Pd2*Nd2_a*fd2_c/(exp(Nd2_a)-1) ;
k42 = 0;
k43 = 0;
k44 = -(A_a/V_a)*Pn*fn_a-
(A_a/V_a)*Pd1*Nd1_a*fd1_a*exp(Nd1_a)/(exp(Nd1_a)-1)...
      -(A_a/V_a)*Pd2*Nd2_a*fd2_a*exp(Nd2_a)/(exp(Nd2_a)-1);
S4 = 0;

A = [k11, k12, k13, k14; k21, k22, k23, k24; k31, k32, k33, k34; k41,
k42, k43, k44];
G = [S1, S2, S3, S4]';
RR = [0,0,0,0]';
t = 300;

[V,E] = eig(A);
E = diag(E);
H = inv(V)*G;
B = V \ RR;
C = B + H./E;
Z = -(H./E) + exp(t * E).*C ;
Y = real(V * Z);
Y = Y' ;

Ppore = Y(4)*V_a / (t*A_aa*C_b)*10^(2)*10^6 ; %
Pcell, 10^(-6)cm/sec
Peff = Y(4)*V_a*CellNo/(t*A_insert*C_b)*10^(2)*10^6; %
Peff, 10^(-6)cm/sec, normalized by insert area, which is 1.12 cm^2
Mass_cell = (Y(1)*V_c + Y(2)*V_m + Y(3)*V_l)*10^12 ; %
cellular mass, pmol/cell
dMdt = Y(4)*V_a/t*10^12; %
transport rate: pmol/sec/cell

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    Para(i,:) = [A_a*10^12,PoreNo_cell,
A_l*10^12,A_m*10^12,A_b*10^12,V_c*10^18,V_l*10^18,V_m*10^18,V_a*10^6,E_a*1000,E_
l*1000,E_m*1000,E_b*1000,...
                pH_a,pH_c,pH_l,pH_m,pH_b,CellNo,PoreDens,
pKa1,pKa2,logPn,logPd1, logPd2];
    Results(i,:)= [Y(1),Y(2),Y(3),Ppore, Peff, dMdt, Mass_cell];

end

comb = [Results(:,1:7),Para];
fid5 = fopen('BtoA_pH74_3um_5min.dat','w');
fprintf(fid5,'%12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.2e %12.0f %1
2.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4e %12.4f %12.4f %12.4f %12.4f %12.
2f %12.2f %12.2f %12.2f %12.2f %12.0f %12.0f %12.2f %12.2f %12.2f %12.2f %12.2f
\n', comb) ;
fclose(fid5);

figure(29) ; clf ; hold on ;
grid on;
hist (log10(comb(:,4)),1000);
line([log10(Ppore_exp), log10(Ppore_exp)],[0,50],'Color','r','LineWidth',3);
xlabel('log_{10} (P_{cell}, 10^{-6}
cm/sec)','FontSize',30,'FontWeight','Bold','FontName','Times');
xlim([0, 6]);
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','Fo
ntName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;
title ('histogram of cell
permeability','FontSize',30,'FontWeight','Bold','FontName','Times') ;

figure(30) ; clf ; hold on ;
grid on;
hist (log10(comb(:,5)),1000);
xlim([-3, 3]);
line([log10(Peff_exp), log10(Peff_exp)],[0,50],'Color','r','LineWidth',3);
xlabel('log_{10} (P_{app}, 10^{-6}
cm/sec)','FontSize',30,'FontWeight','Bold','FontName','Times');
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','Fo
ntName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;
title ('histogram of apparent
permeability','FontSize',30,'FontWeight','Bold','FontName','Times') ;

figure(31) ; clf ; hold on ;
grid on;
hist (log10(comb(:,6)),1000);
xlim([-8,-2]);
line([log10(dMdt_exp), log10(dMdt_exp)],[0,50],'Color','r','LineWidth',3);
xlabel('log_{10} (dM/dt,
pmol/sec/cell)','FontSize',30,'FontWeight','Bold','FontName','Times');
ax1 = gca;
set(get(ax1,'Ylabel'),'String','Frequency','FontSize',30,'FontWeight','Bold','Fo
ntName','Times') ;
set(ax1,'LineWidth',2.0,'FontSize',30,'FontWeight','Bold','FontName','Times') ;

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```
title ('histogram of transport  
rate', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;  
  
figure(32) ; clf ; hold on ;  
grid on;  
hist (log10(comb(:,7)),1000);  
xlim([-5,-0]);  
line([log10(IntraMass_exp),  
log10(IntraMass_exp)], [0,50], 'Color', 'r', 'LineWidth', 3);  
xlabel('log_{10} (intracellular mass, pmol/cell)  
, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times');  
ax1 = gca;  
set(get(ax1, 'Ylabel'), 'String', 'Frequency', 'FontSize', 30, 'FontWeight', 'Bold', 'Fo  
ntName', 'Times') ;  
set(ax1, 'LineWidth', 2.0, 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;  
title ('histogram of intracellular  
mass', 'FontSize', 30, 'FontWeight', 'Bold', 'FontName', 'Times') ;
```