

Effect of Atomoxetine on Sodium-Channel Inactivation

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Load and Plot Data

Data is arranged in an Excel-Sheet observation-based. Each observation is represented by a row in the table with the following variables (columns):

- ID of observation (ID)
- Sweep/Run ID within experiment (Run)
- Atomoxetine concentration (Ato in $\mu\text{g/ml}$)
- Clamp potential (V_p in V)
- normalized current (I_n)
- Experiment identifier (Exp)

The Excel-Table has been imported into Matlab manually and saved in a *.mat-file.

The plot displays the experimental results. Blue control conditions, magenta if Atomoxetine (3 or 10 $\mu\text{g/ml}$) was present.

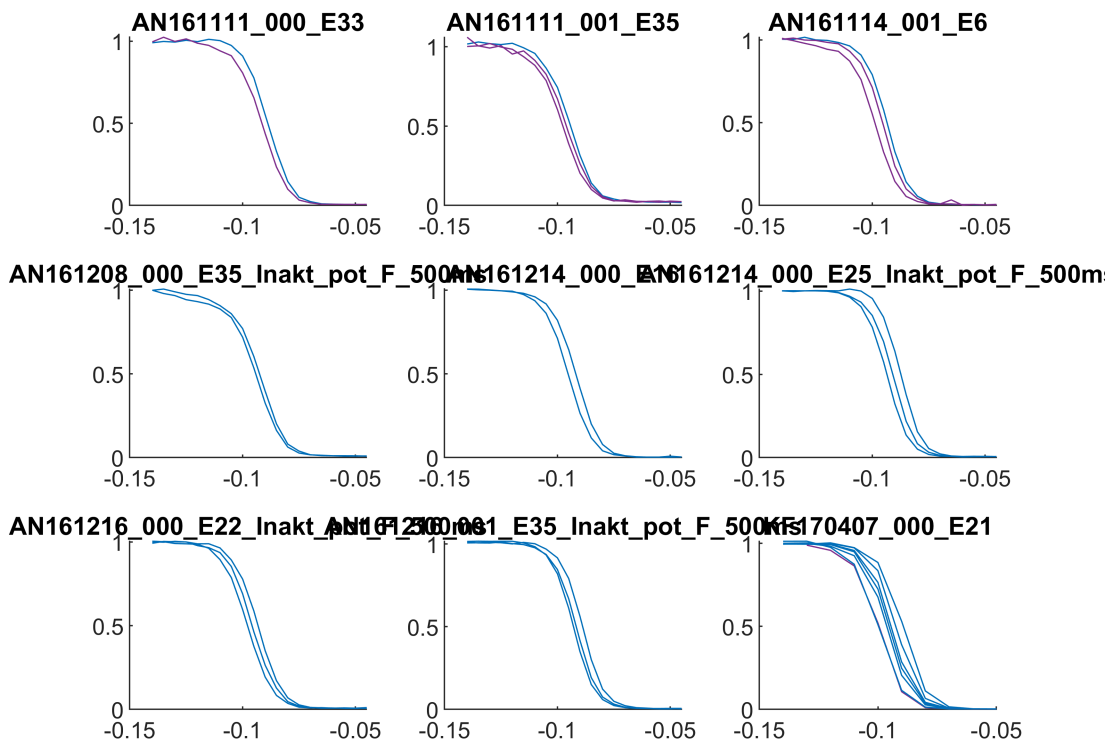
```
load 'inactivation_data_Ato_shift.mat';
exps = unique(Data.Exp);

figure;
cols = lines(11);
for k=1:numel(exps)
    idx_exp = Data.Exp==exps(k); %observations belonging to experiment exps(k)
    D = Data(idx_exp,:);
    runs = unique(D.Run); %sweeps
```

```

ato = unique(D.Ato); %Ato concentrations
subplot(3,3,k);
hold on;
for run=1: numel(ato)
    for r=1: numel(runs)
        idx_r = D.Run==r;
        Dr = D(idx_r,:); %Data of that run within experiment exp(k)
        plot(Dr.Vp,Dr.In,'-', 'Color', cols(Dr.Ato(1)+1,:));
    end
end
title(string(D.Exp(1)), 'Interpreter', 'none');
end

```



```
clearvars idx_exp D runs ato c r k idx_r Dr col;
```

There are 9 different experiments and a total of 28 runs.

```
disp(exps);
```

```

AN161111_000_E33
AN161111_001_E35
AN161114_001_E6
AN161208_000_E35_Inakt_pot_F_500ms
AN161214_000_E16
AN161214_000_E25_Inakt_pot_F_500ms
AN161216_000_E22_Inakt_pot_F_500ms
AN161216_001_E35_Inakt_pot_F_500ms
KF170407_000_E21

```

Fit Independent Inactivation Curves

The data has an hierarchical structure (top-down order):

1. experiment
2. various number of runs/sweeps in each experiment
3. single observations (data points) at different clamp potentials (V_p).

Each sweep is fitted independently. In the next section dependence of parameter values from experiment and/or sweep number is evaluated.

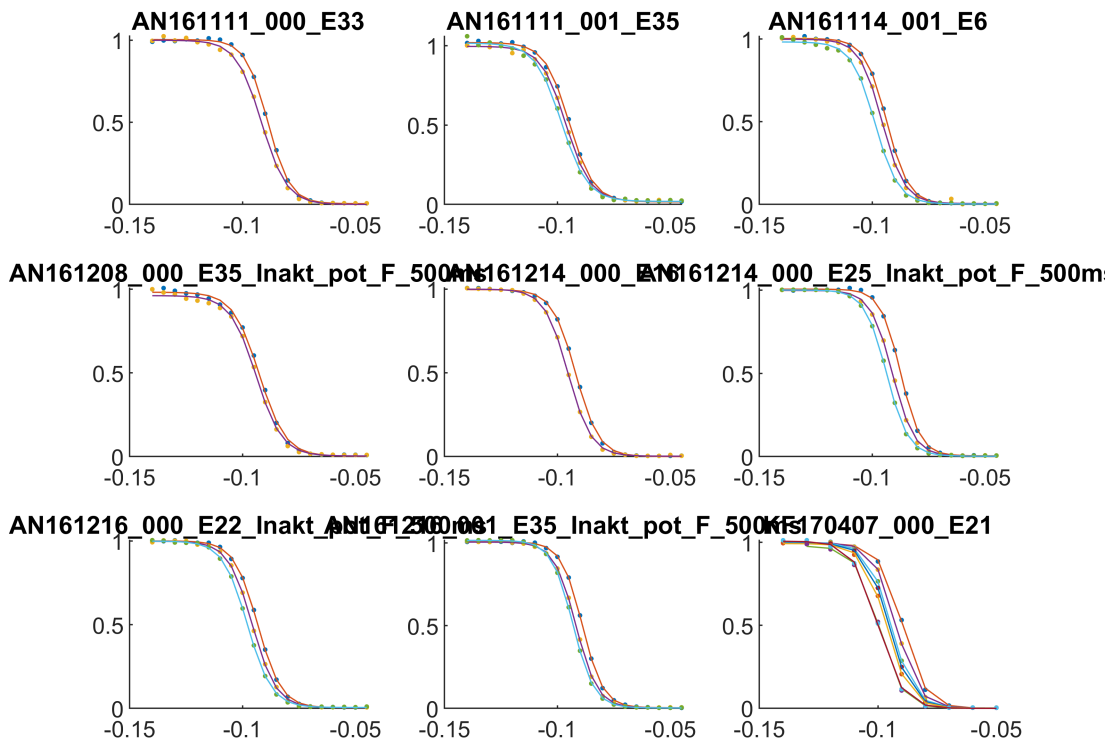
```
b0 = [ -.09, 1, 0, .01 ]; %initial values [ vh, a, i0, k ]
opts = statset( 'Display', 'final', ...
               'TolFun', 1e-8 ...
               );
j = 0;
figure;
for k=1:numel(exps)
    idx_exp = Data.Exp==exps(k); %selector for observations belonging to experiment exps(k)
    D = Data(idx_exp,:); %observations of experiment exps(k)
    yexp = D.In;%y_sim(idx_exp);%D.In;
    runs = unique(D.Run); %sweeps of that experiment
    CoeffNames = {'V_h','a','I_0','k'};
    subplot(3,3,k);
    hold on;
    for r=1:numel(runs)
        j = j + 1;
        fprintf('%i:\n', j);
        idx_r = D.Run==r; %selector for observations of sweep r
        Dr = D(idx_r,:);
        yr = yexp(idx_r);
        M{j,1} = exps(k); %experiment identifier
        M{j,2} = r; %sweep/run index
        M{j,3} = fitnlm( Dr.Vp, yr, ...
                        @inact_curve, ...
                        b0, ...
                        'CoefficientNames', CoeffNames, ...
                        'Options', opts ...
                        );
        Beta(j,:) = M{j,3}.Coefficients.Estimate;
        SE(j,:) = M{j,3}.Coefficients.SE;
        M{j,4} = Dr.Ato(1); %Ato concentration
        plot(Dr.Vp, yr, '.');
        plot(M{j,3}.Variables.X1,M{j,3}.Fitted,'-');
        fprintf('R^2=%g, p-value: %g\n',M{j,3}.Rsquared.Ordinary,coefTest(M{j,3}));
    end
    title(string(D.Exp(1)), 'Interpreter', 'none');
end
end
```

1:

Iterations terminated: relative change in SSE less than OPTIONS.TolFun

R²=0.99973, p-value: 1.02066e-36
2:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999392, p-value: 1.40254e-33
3:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999614, p-value: 1.82267e-35
4:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999472, p-value: 1.96144e-34
5:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.998887, p-value: 8.79282e-32
6:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999897, p-value: 2.24665e-40
7:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999583, p-value: 1.35655e-35
8:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999428, p-value: 1.36342e-34
9:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999002, p-value: 8.8849e-32
10:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.998863, p-value: 1.76539e-31
11:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999825, p-value: 3.0974e-38
12:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999918, p-value: 4.80363e-41
13:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999816, p-value: 2.37348e-38
14:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999812, p-value: 3.74692e-38
15:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999916, p-value: 3.94354e-41
16:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999899, p-value: 3.74065e-40
17:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999878, p-value: 1.33096e-39
18:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun

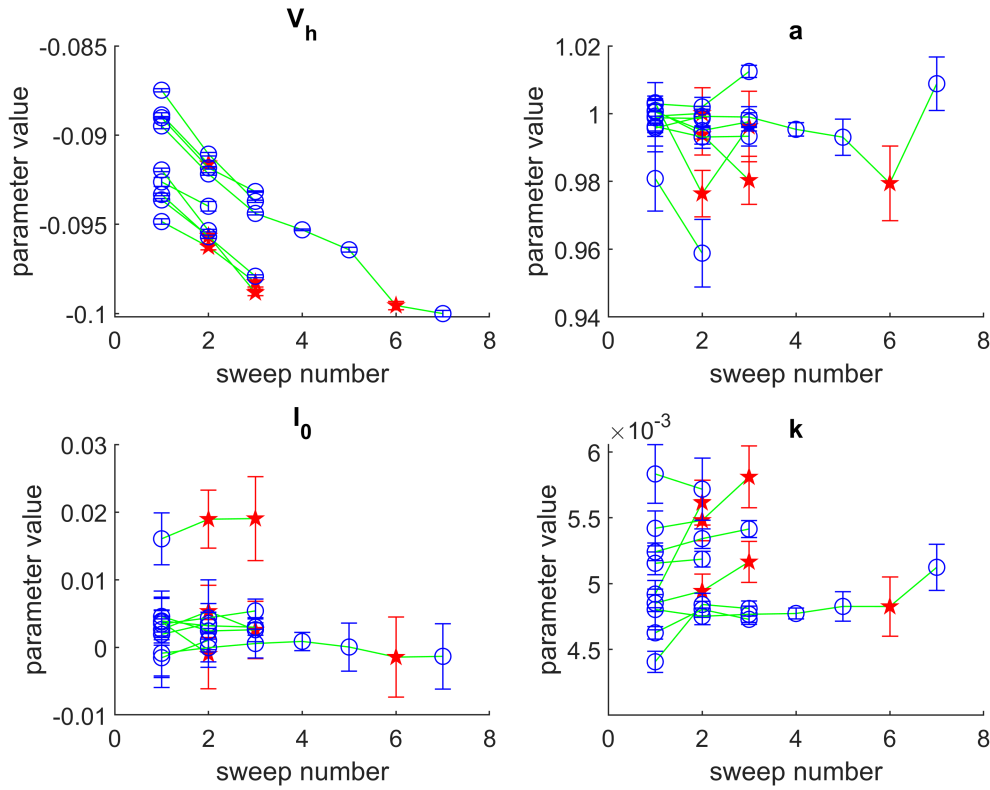
R²=0.999908, p-value: 1.07132e-40
19:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999938, p-value: 4.56499e-42
20:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999905, p-value: 1.33241e-40
21:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999962, p-value: 6.01504e-44
22:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999795, p-value: 1.87809e-14
23:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999961, p-value: 1.19339e-16
24:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999957, p-value: 1.69128e-16
25:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999982, p-value: 1.1497e-17
26:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999873, p-value: 3.79694e-15
27:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999608, p-value: 9.22427e-12
28:
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
R²=0.999752, p-value: 2.42761e-14



Dependence of Parameter Values from Experiment and Sweep Number

Large part of variance between sweeps (runs) depends on the experiment for all parameters. Only for parameter v_h variance is also determined by sweep number.

```
figure;
for p=1:4
    subplot(2,2,p);
    hold on;
    for k=1:numel(exps)
        idx_exp = [M{:,1}]==exps(k);
        runs = [M{idx_exp,2}]; %sweep number
        ato = [M{idx_exp,4}]; %Ato concentration
        b = Beta(idx_exp, p); %parameter with index p
        se = SE(idx_exp, p);
        plot(runs,b,'-g');
        errorbar(runs(ato==0),b(ato==0),se(ato==0),'ob');
        errorbar(runs(ato>0),b(ato>0),se(ato>0),'pr','MarkerFaceColor','r');
    end
    title(CoeffNames{p});
    xlabel('sweep number');
    ylabel('parameter value');
end
```



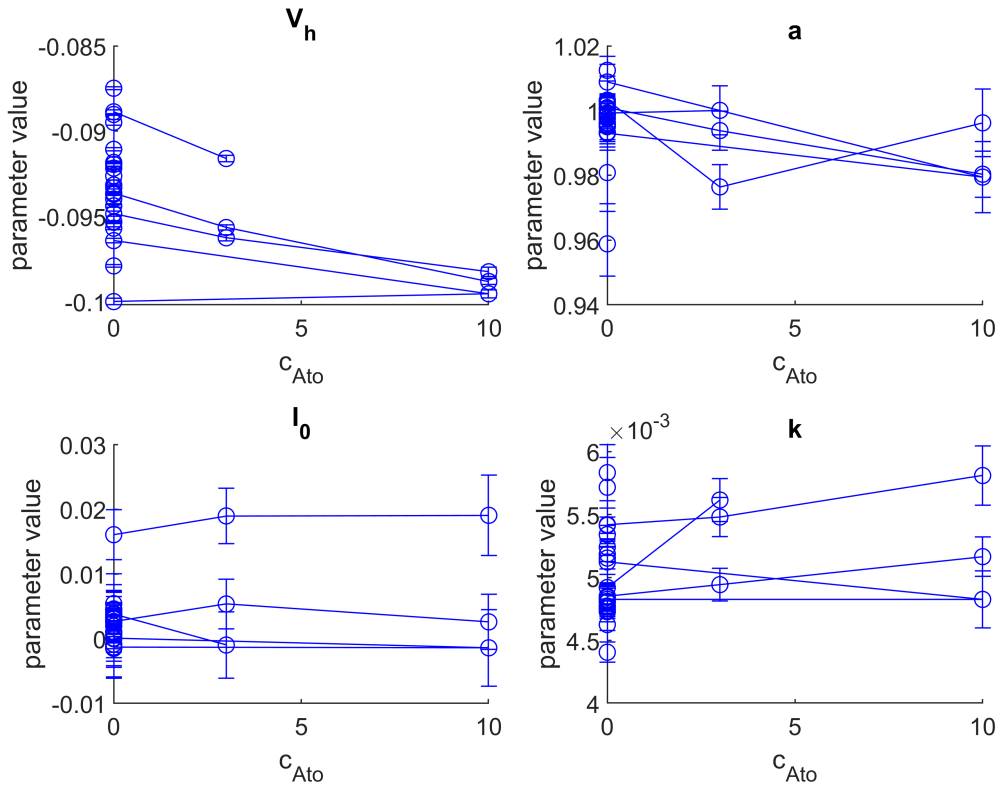
Thus a random effects (hierarchical) nonlinear modelling approach will be applied. V_h will be expressed as an apparent value by linear dependence from sweep number

$$V_h^* = \hat{V}_h + \delta \cdot s$$

where δ represents the change of V_h per run.

Dependence of Parameter Values from Atomoxetine Concentration

```
figure;
for p=1:4
    subplot(2,2,p);
    hold on;
    for k=1: numel(exps)
        idx_exp = [M{:,1}]==exps(k);
        c_ato = [M{idx_exp,4}]; %Ato concentration
        b = Beta(idx_exp,p);
        se = SE(idx_exp,p);
        errorbar(c_ato,b,se,'-ob');
    end
    title(CoeffNames{p});
    xlabel('c_{Ato}');
    ylabel('parameter value');
end
```



There might be a concentration dependence for V_h . There are only data at 2 concentrations available, not enough to fit a concentration-response curve. Therefore a constant shift parameter is introduced that takes effect only if $c_{Ato} > 0$, giving for V_h^*

$$V_h^* = \hat{V}_h + \delta_s \cdot s + \delta_{Ato} |_{c_{Ato} > 0}$$

Problem Definition

\hat{V}_h , a , I_0 , k get random components on the experiment level.

There are 3 predictors: The test potential V_p , the Atomoxetine concentration c_{Ato} and the sweep number s . V_p is observation-specific, c_{Ato} and s are sweep-specific while no predictor is group-specific on the experiment level. It is assumed that there is no random influence on the sweep level so that the observation- and sweep-levels merge to one lower level, while the experiment introduces an upper level at which random effects on \hat{V}_h , a , I_0 and k take effect.

The fixed-effects parameter vector takes the form $\beta = [\hat{V}_h, a, I_0, k, \delta_s, \delta_{Ato}]$.

Fit the Nonlinear Mixed-Effects Model

```
b0 = [-.095, ... %1 half max inact. Vh
      1, ... %2 amplitude
```



```

    0, ... %3 residual current I0
    .005, ... %4 slope k
    -.0015, ... %5 change of Vh/sweep
    -.003 ... %6 change of Vh by Ato
];
scale = [1e3 1 1e3 1e3 1e3 1e3];
b0 = b0.*scale;
X = Data(:, {'Run', 'Ato', 'Vp'}); %predictors
y = Data.In; %response
grp = Data.Exp; %grouping on experiment level
CoeffNames = { 'V_h', 'a', 'I_0', 'k', ...
                'd_s', 'd_Ato' ...
                };
opts = statset('Display','final', ...
              'TolFun', 1e-8 ...
              );
[beta,PSI,stats,RE] = nlmefit( X,y,grp,[], ...
                              @(phi,X)modelfun(phi,X,scale), ...
                              b0, ...
                              'FEParamsSelect', 1:6, ... %all parameters have fixed effects
                              'REParamsSelect', [1 4], ... %first 4 parameters have random effects
                              'ApproximationType', 'RELME', ...
                              'Options', opts ...
                              );

```

```

Beta_hat'   = [ -89.499102 0.994990 4.267955 5.177561 -1.980102 -0.454821 ]
theta_hat'  = [ -9.937587 -6.797320 ]
logLike     = 1287.486806
sigma2_hat  = 0.000248
Psi_hat     = [ 5.138225 0.000000
                0.000000 0.222337 ]
Delta_hat   = [ 0.006952 0.000000
                0.000000 0.033418 ]
Deg.Freedom = 9
AIC         = -2556.973612
BIC         = -2565.086101

```

8 iterations and 2043 model evaluations in 4.921875 seconds.

What follows is a NHST for the Null-Hypothesis that a parameter value is zero. The test statistic (Wald-statistic) is computed from the standard error returned by nlmefit in the stats structure.

```

alpha = 0.01;
n = numel(y);
n = size(M,1);
b = beta(:);
b_se = stats.sebeta(:);
mu = zeros(size(b));
W = (b - mu)./b_se;
df = n - numel(b) - numel(RE) - 1;
p_value = 2*tcdf(-abs(W), df);
h = p_value < (alpha/numel(b));
Beta_Stats = table(b,b_se,W,p_value,h)

```

Beta_Stats = 6x5 table

	b	b_se	W	p_value	h
1	-89.4991	0.7612	-117.5721	0.0000	1
2	0.9950	0.0019	520.0341	0.0000	1
3	4.2680	1.2621	3.3816	0.0430	0
4	5.1776	0.1629	31.7837	0.0001	1
5	-1.9801	0.0426	-46.4491	0.0000	1
6	-0.4548	0.1468	-3.0982	0.0534	0

Model Comparison to Deduce Significance of Atomoxetine Effect on Inactivation Shift

```
[beta0,PSI0,stats0,RE0] = nlmeFit( X,y,grp,[], ...
    @(phi,X)modelfun_no_dato(phi,X,scale(1:5)), ...
    b0(1:5), ...
    'FEPARAMSSelect', 1:5, ... %all parameters have fixed effects
    'REPARAMSSelect', 1:4, ... %first 4 parameters have random effect
    'Options', opts ...
);
```

```
Beta_hat' = [ -89.447292 0.994016 4.133197 5.153964 -2.040329 ]
theta_hat' = [ -9.977097 1.269347 -11.371545 -6.391624 ]
logLike = 1308.040515
sigma2_hat = 0.000226
Psi_hat = [ 4.860531 0.000000 0.000000 0.000000
            0.000000 0.000063 0.000000 0.000000
            0.000000 0.000000 19.601293 0.000000
            0.000000 0.000000 0.000000 0.134751 ]
Delta_hat = [ 0.006816 0.000000 0.000000 0.000000
              0.000000 1.886406 0.000000 0.000000
              0.000000 0.000000 0.003394 0.000000
              0.000000 0.000000 0.000000 0.040933 ]
Deg.Freedom = 10
AIC = -2596.081029
BIC = -2594.108783
```

8 iterations and 2178 model evaluations in 9.953125 seconds.

```
[beta1,PSI1,stats1,RE1] = nlmeFit( X,y,grp,[], ...
    @(phi,X)modelfun(phi,X,scale(1:6)), ...
    b0(1:6), ...
    'FEPARAMSSelect', 1:6, ... %all parameters have fixed effects
    'REPARAMSSelect', 1:4, ... %first 4 parameters have random effect
    'Options', opts ...
);
```

```
Beta_hat' = [ -89.473185 0.994047 4.128934 5.154811 -1.979292 -0.459311 ]
theta_hat' = [ -9.946315 1.240312 -11.407336 -6.419010 ]
logLike = 1313.490402
sigma2_hat = 0.000221
Psi_hat = [ 4.606062 0.000000 0.000000 0.000000
            0.000000 0.000064 0.000000 0.000000
            0.000000 0.000000 19.853759 0.000000
```

```

Delta_hat = [ 0.000000 0.000000 0.000000 0.135344 ]
              0.006921 0.000000 0.000000 0.000000
              0.000000 1.859218 0.000000 0.000000
              0.000000 0.000000 0.003334 0.000000
              0.000000 0.000000 0.000000 0.040377 ]
Deg.Freedom = 11
AIC          = -2604.980804
BIC          = -2602.811334

```

9 iterations and 2277 model evaluations in 9.625000 seconds.

```

% llog1 = stats.logl;
% llog0 = stats0.logl;
% D = 2*(llog1 - llog0); %test statistic for LR Test
% df = numel(beta)+numel(RE)-numel(beta0)-numel(RE0);
% p_value = 1 - chi2cdf(D, df);

```

1. Fit model without and with δ_{Ato} (*reduced model* vs. *full model*).
2. Simulate data from the *full* model by *parametric sampling*.
3. Fit *reduced* and *full* models to simulated data.
4. Compare models with respect to *AIC*, *BIC* and *log-likelihood*.

```

% Marginal normal distributions of random effects
% [mu,sigma] = normfit(RE0');
[mu,sigma] = normfit(RE1');
% Simulate data
n_sim = 1000;

aic0 = zeros(n_sim,1);
bic0 = zeros(n_sim,1);
logl0 = zeros(n_sim,1);
aic1 = zeros(n_sim,1);
bic1 = zeros(n_sim,1);
logl1 = zeros(n_sim,1);
d_ato = zeros(n_sim,1);
y_sim = zeros(size(y));
opts = statset('Display','off', ...
               'TolFun', 1e-6 ...
               );

timer1 = tic; %timer
Warnings = false(n_sim,2);
run = 1;
Beta_sim = [];
for j=1:n_sim
    for k=1:numel(exps)
        idx_exp = Data.Exp==exps(k); %selector for an experiment
        re_exp = sigma.*randn(1,numel(sigma)) + mu; %random effects for this experiment
        %     beta_exp = [ beta0(1:4)' + re_exp, ...
        %                 beta0(5) ...
        %                 ];
        beta_exp = [ beta1(1:4)' + re_exp, ...
                    beta1([5 6])' ...

```

```

];
X_exp = X(idx_exp,:); %predictors for experiment k
n_sweeps = X_exp(end,1); %number of sweeps/runs in experiment k
y = zeros(size(X_exp,1),1);
for s=1:n_sweeps
%     eps_sim = stats0.sebeta.*randn(1,numel(stats0.sebeta));
    eps_sim = stats1.sebeta.*randn(1,numel(stats1.sebeta));
    beta_sim = beta_exp + eps_sim;
    Beta_sim(run,:) = beta_sim;
    run = run + 1;
    idx_sweep = X_exp(:,1)==s;
    yt = modelfun_no_dato(beta_sim(1:5),X_exp(idx_sweep,:),scale(1:5));
    y(idx_sweep) = yt + stats1.errorparam*randn(sum(idx_sweep),1);
end
y_sim(idx_exp) = y;
end
lastwarn(''); % set lastwarn() to empty
[b_sim,~,stats_sim,~] = nlmefit( X,y_sim,grp,[], ...
    @(phi,X)modelfun_no_dato(phi,X,scale(1:5)), ...
    b0(1:5), ...
    'FEParamsSelect', 1:5, ... %all parameters have fixed effects
    'REParamsSelect', 1:4, ... %first 4 parameters have random effect
    'ApproximationType', 'RELME', ...
    'RefineBeta0', false, ...
    'Options', opts ...
);
Warnings(j,1) = ~isempty(lastwarn);
aic0(j) = stats_sim.aic;
bic0(j) = stats_sim.bic;
logl0(j) = stats_sim.logl;
lastwarn(''); % set lastwarn() to empty
[b_sim1,~,stats_sim1,~] = nlmefit( X,y_sim,grp,[], ...
    @(phi,X)modelfun(phi,X,scale(1:6)), ...
    b0, ...
    'FEParamsSelect', 1:6, ... %all parameters have fixed effects
    'REParamsSelect', 1:4, ... %first 4 parameters have random effect
    'ApproximationType', 'RELME', ...
    'RefineBeta0', false, ...
    'Options', opts ...
);
Warnings(j,2) = ~isempty(lastwarn);
aic1(j) = stats_sim1.aic;
bic1(j) = stats_sim1.bic;
logl1(j) = stats_sim1.logl;
d_ato(j) = b_sim1(6);
if any(Warnings(j,:))
    fprintf('%i: AIC0:%g|i AIC1:%g|i\n',j,aic0(j),Warnings(j,2),aic1(j),Warnings(j,2));
end
end
end

```

25: AIC0:-2406.93|0 AIC1:-2414.59|0

Warning: Unable to find a step that will decrease SSE in the Gauss-Newton algorithm while solving PNLS.
Returning results from last iteration.

```

32: AIC0:-2302.37|1 AIC1:-2299.11|1
107: AIC0:-2406.25|0 AIC1:-2405.15|0
158: AIC0:-2242.48|1 AIC1:-2239.22|1
183: AIC0:-2329.2|1 AIC1:-2327.17|1
200: AIC0:-2319.94|0 AIC1:-2327.11|0
223: AIC0:-2413.9|1 AIC1:-2419.57|1
305: AIC0:-2364.37|0 AIC1:-2362.41|0
453: AIC0:-2406.75|1 AIC1:-2402.65|1
482: AIC0:-2380.05|0 AIC1:-2378.4|0
Warning: Unable to find a step that will decrease SSE in the Gauss-Newton algorithm while solving PNLs.
Returning results from last iteration.
522: AIC0:-2399.78|1 AIC1:-2432.27|1
Warning: Unable to find a step that will decrease SSE in the Gauss-Newton algorithm while solving PNLs.
Returning results from last iteration.
562: AIC0:-2519.96|0 AIC1:-2516.11|0
637: AIC0:-2419.4|1 AIC1:-2415.74|1
773: AIC0:-2458.69|1 AIC1:-2459.09|1
Warning: Unable to find a step that will decrease SSE in the Gauss-Newton algorithm while solving PNLs.
Returning results from last iteration.
780: AIC0:-2375.93|1 AIC1:-2372.35|1
845: AIC0:-2301.75|0 AIC1:-2299.3|0
Warning: Unable to find a step that will decrease SSE in the Gauss-Newton algorithm while solving PNLs.
Returning results from last iteration.
874: AIC0:-2429.59|1 AIC1:-2426.26|1
909: AIC0:-2408.26|0 AIC1:-2415.39|0
929: AIC0:-2240.82|1 AIC1:-2254.29|1
Warning: Unable to find a step that will decrease SSE in the Gauss-Newton algorithm while solving PNLs.
Returning results from last iteration.
930: AIC0:-2384.58|1 AIC1:-2381.26|1

```

```
fprintf('total time taken: %g s\n',toc(timer1));
```

```
total time taken: 1181.3 s
```

```

dAIC = aic1 - aic0; %Change of Akaike's Information Criterion
dBIC = bic1 - bic0;
dlogl = logl1 - logl0;
fprintf('max|95%|50%|5%|min dAIC: %g|%g|%g|%g|%g\n',max(dAIC),prctile(dAIC,95),prctile(dAIC,50),prctile(dAIC,5),min(dAIC));

```

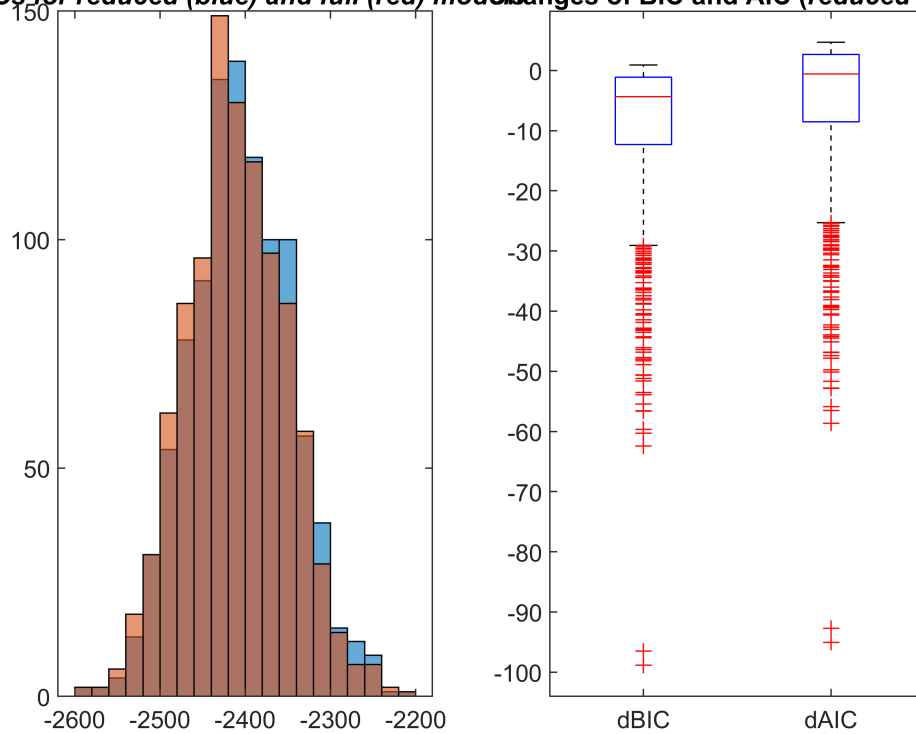
```
max|95%|50%|5%|min dAIC: 4.70004|3.64735|-0.568652|-29.6809|-95.09
```

```

figure;
subplot(1,2,1);
histogram(aic0);
hold on
histogram(aic1);
title('\it{AICs} for \it{reduced} (blue) and \it{full} (red) models')
subplot(1,2,2);
boxplot([dBIC dAIC], 'Labels', {'dBIC', 'dAIC'});
title('Changes of BIC and AIC (\it{reduced}\rightarrow\it{full})')

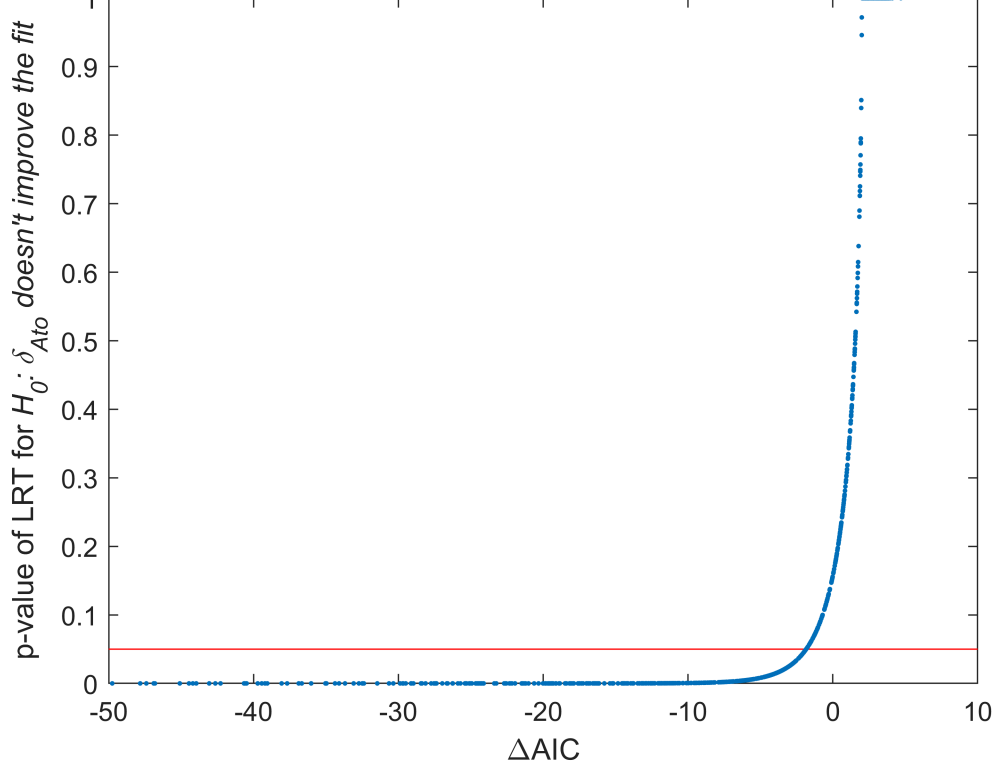
```

AICs for reduced (blue) and full (red) models **Changes of BIC and AIC (reduced → full)**



```
pval = 1 - chi2cdf(2*dlogl,1);
figure;
plot([min(dAIC) 50],[.05 .05],'r-');
hold on;
plot(dAIC,pval,'.');
xlabel('\DeltaAIC');
ylabel('p-value of LRT for \it{H}_0: \delta_{Ato} doesn't improve the fit');
xlim([-50 10]);
title('LRT results for Atomexitine effects on shift of inactivation for parametric samples')
```

LRT results for Atomoxetine effects on shift of inactivation for parametric sample



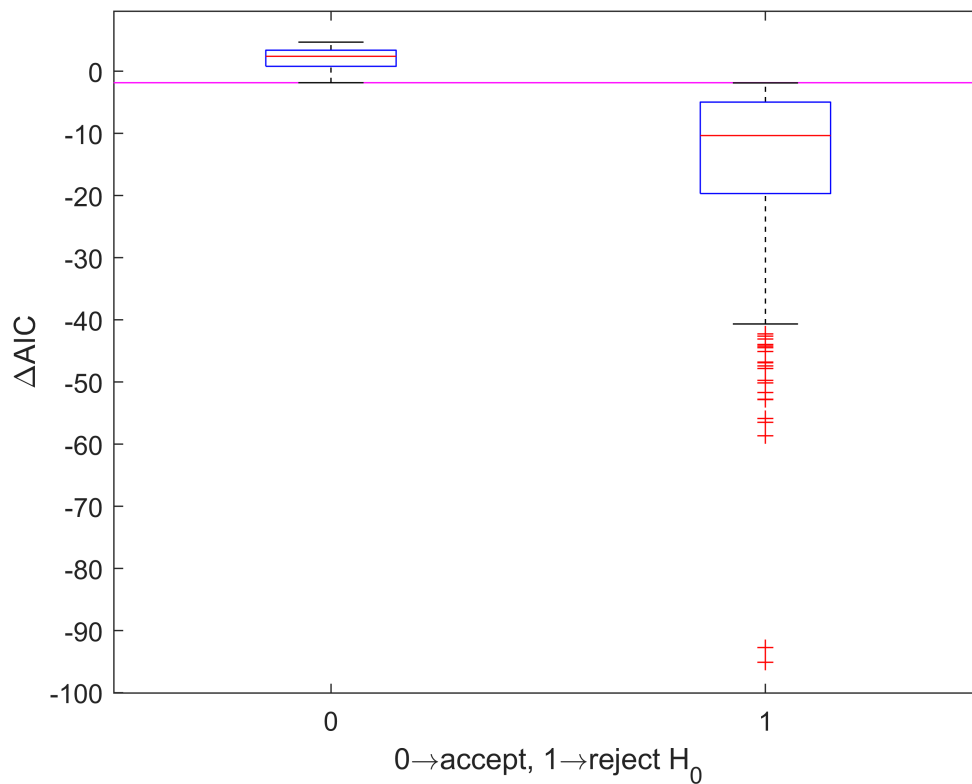
```
smallest_dAIC = min(dAIC(pval>=0.05));
fprintf('Rejection of H0 if dAIC<%.1f\n',smallest_dAIC);
```

Rejection of H0 if dAIC<-1.83395.

```
fprintf('Fraction of parametric samples resulting in a p-value>=0.05 in Likelihood-Ratio testing: %.3f\n',
```

Fraction of parametric samples resulting in a p-value>=0.05 in Likelihood-Ratio testing: 0.549.

```
figure;
plot([-0.5 3],[smallest_dAIC smallest_dAIC],'m-');
hold on;
boxplot(dAIC,pval<0.05);
ylabel('\Delta AIC');
xlabel('0\rightarrow accept, 1\rightarrow reject H_0');
```



Local Function Definitions

```
function y = inact_curve(b, vp)
    vh = b(1);
    a = b(2);
    i0 = b(3);
    k = b(4);
    dv = vp - vh;
    y = i0 + a./(1+exp(dv/k));
end
```

```
function y = modelfun(phi, X, scale)
% phi is the parameter vector
% phi(1): Vh
% phi(2): a
% phi(3): I0
% phi(4): k
% phi(5): ds
% phi(6): dato
% X is a n-by-3 matrix of predictors for each of n observations
% X(:,1) give the run/sweep number
% X(:,2) give the atomexitine concentration
phi = phi./scale;
sweeps = unique(X(:,1)); %sweeps
n_runs = numel(sweeps); %number of sweeps
n_steps = sum(X(:,1)==1);
```



```

Y = NaN(n_steps,n_runs);
for s=1:n_runs
    sel = X(:,1)==sweeps(s); %selector for sweep s
    c_ato = X(sel,2); %atomexitine concentrations during sweep (constant)
    vp = X(sel,3); %test potentials for each observation in sweep s
    vh_app = phi(1) + phi(5)*sweeps(s) + phi(6)*(c_ato(1)>0); %half max. inactivation
    dv = vp - vh_app;
    Y(1:numel(vp),s) = phi(3) + phi(2)./(1+exp(dv/phi(4)));
end
y = Y(:);
y = y(~isnan(y));
end

function y = modelfun_no_dato(phi,X,scale)
% phi is the parameter vector
%   phi(1): Vh
%   phi(2): a
%   phi(3): I0
%   phi(4): k
%   phi(5): ds
% X is a n-by-3 matrix of predictors for each of n observations
%   X(:,1) give the run/sweep number
%   X(:,2) give the atomexitine concentration
phi = phi./scale;
sweeps = unique(X(:,1)); %sweeps
n_runs = numel(sweeps); %number of sweeps
n_steps = sum(X(:,1)==1);
Y = NaN(n_steps,n_runs);
for s=1:n_runs
    sel = X(:,1)==sweeps(s); %selector for sweep s
    %   c_ato = X(sel,2); %atomexitine concentrations during sweep (constant)
    vp = X(sel,3); %test potentials for each observation in sweep s
    vh_app = phi(1) + phi(5)*sweeps(s); %half max. inactivation
    dv = vp - vh_app;
    Y(1:numel(vp),s) = phi(3) + phi(2)./(1+exp(dv/phi(4)));
end
y = Y(:);
y = y(~isnan(y));
end

```