

Contents

1

Since the lillietest did not indicate that y2 is normally distributed, a ranksum test seemed more appropriate. The hypothesis that the two conditions are different cannot be rejected since $p > 0.05$. 61% of the variability is accounted for.

```
load ps4_problem1.mat

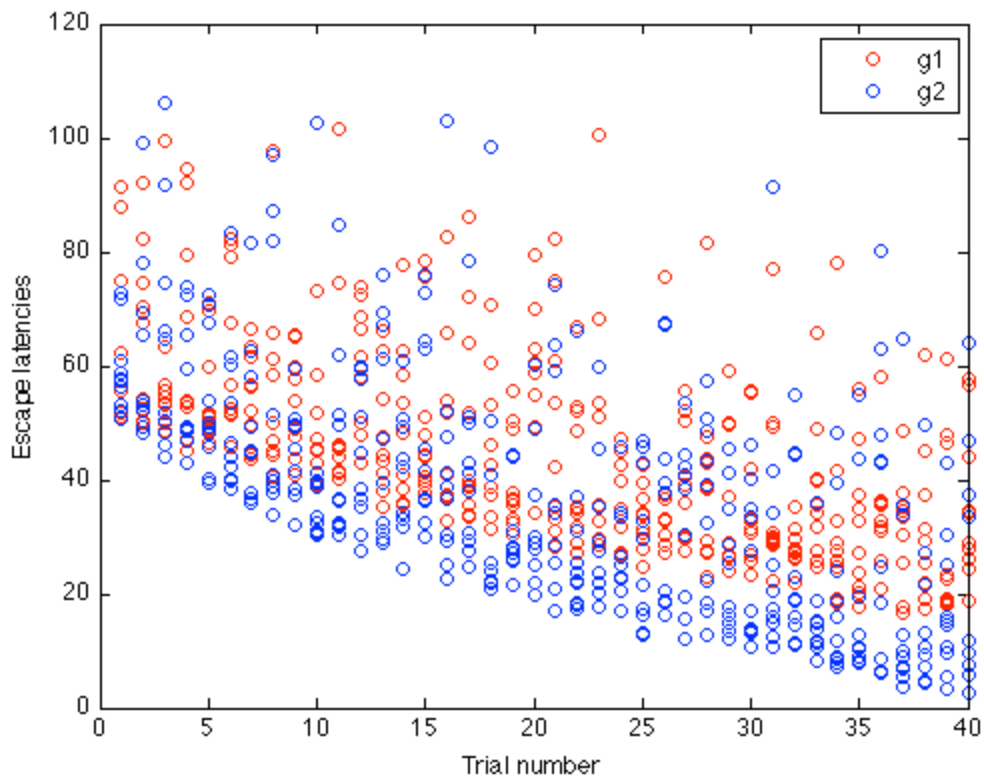
if ~lillietest(y1) | ~lillietest(y2)
    p = ranksum(y1,y2)
end

x = [ones(91,1) x'];
[b,bint,r,rint,stats] = regress(y1',x);
stats(1)
```

```
p =
    0.1322
ans =
    0.6179
```

2

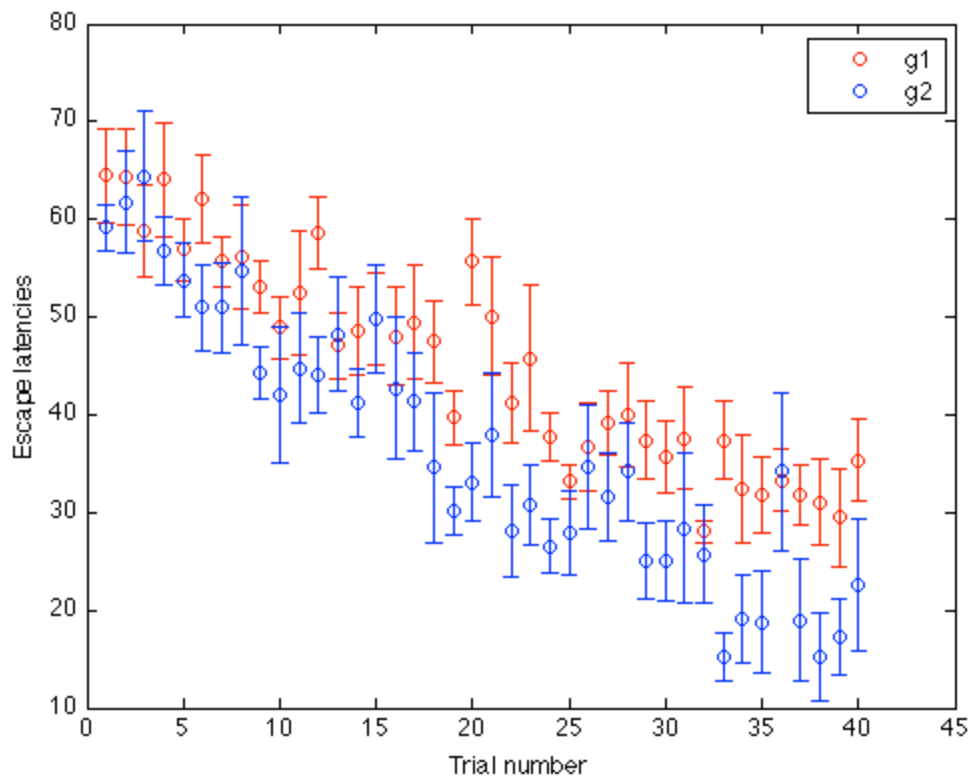
```
close all
clear
load ps4_problem2.mat
x = repmat([1:40],10, 1)';
g1 = g1';
g2 = g2';
figure(1);
plot(x(:), g1(:), 'ro', x(:), g2(:), 'bo');
legend('g1', 'g2')
xlabel('Trial number')
ylabel('Escape latencies')
```



2b

The groups show differences in the later trials (30+)

```
load ps4_problem2.mat
mg1 = mean(g1,1);
mg2 = mean(g2,1);
err1 = std(g1)/sqrt(10);
err2 = std(g2)/sqrt(10);
figure;
errorbar(1:40, mg1, err1, 'ro'); hold on
errorbar(1:40, mg2, err2, 'bo');
legend('g1', 'g2')
xlabel('Trial number')
ylabel('Escape latencies')
```



2c

the ANOVA shows significant differences between trials and groups

```
load ps4_problem2.mat
y = [g1; g2];
group = [ones(size(g1)); 2*ones(size(g2))];
time = repmat(1:40, 2*size(g1,1),1);
y = reshape(y,[],1);
group = reshape(group,[],1);
time = reshape(time,[],1);

[p atab stats] = anovan(y, {group time}, 3, 3, strvcats('group', 'time'));
comp = multcompare(stats);
```

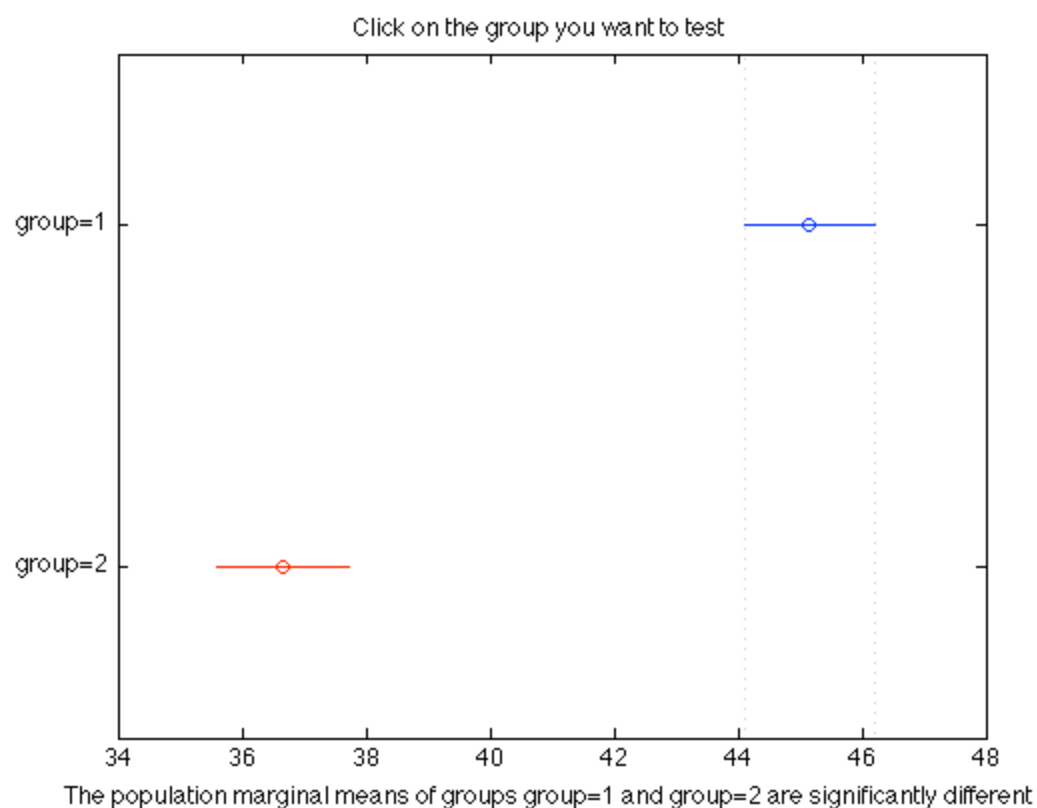


Figure 4: N-Way ANOVA

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Analysis of Variance

| Source | Sum Sq. | d.f. | Mean Sq. | F | Prob>F |
|------------|----------|------|----------|-------|--------|
| group | 14465.9 | 1 | 14465.9 | 62.18 | 0 |
| time | 111191.4 | 39 | 2851.1 | 12.26 | 0 |
| group*time | 7036.4 | 39 | 180.4 | 0.78 | 0.8368 |
| Error | 167497 | 720 | 232.6 | | |
| Total | 300190.7 | 799 | | | |

Constrained (Type III) sums of squares.

2d

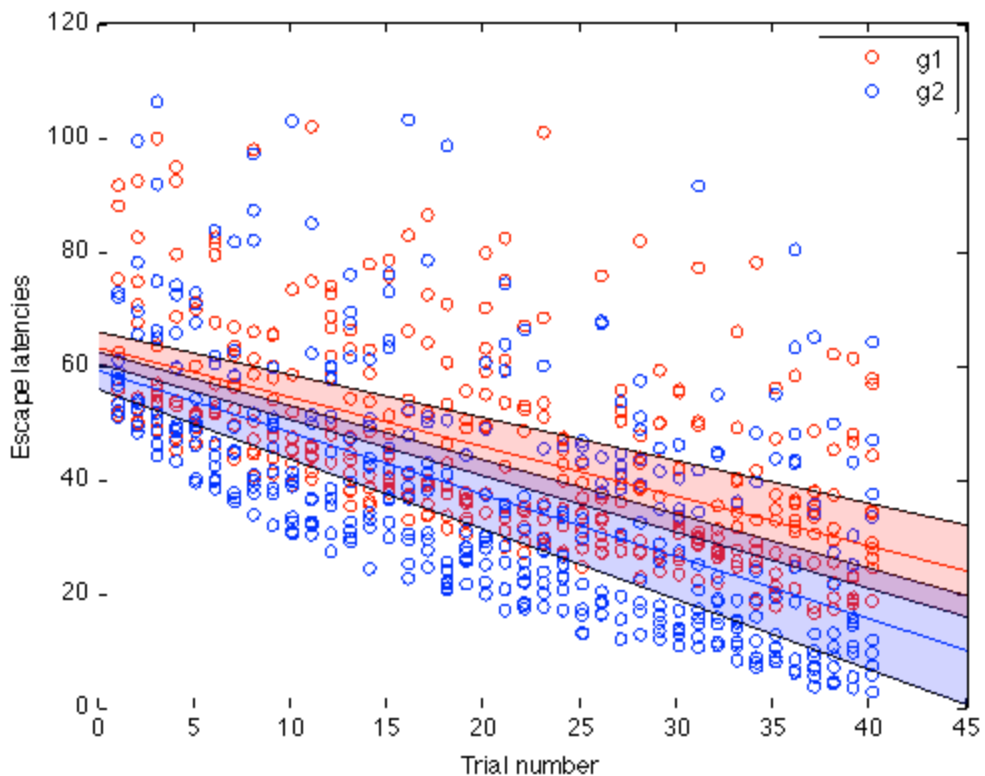
The intervals overlap, so this does not indicate that the groups are different.

```
load ps4_problem2.mat
x = repmat([1:40], [10,1]);
x = reshape(x,[],1);
x = [ones(size(x)) x];
g1= reshape(g1,[],1);
g2 = reshape(g2,[],1);

[b1,bint1,r1,rint1,stats1] = regress(g1,x);
[b2,bint2,r2,rint2,stats2] = regress(g2,x);
y1 = b1(1) + b1(2)*[0:45];
y1_ci1 = bint1(1,1) + bint1(2,1)*[0:45];
y1_ci2 = bint1(1,2) + bint1(2,2)*[0:45];

y2 = b2(1) + b2(2)*[0:45];
y2_ci1 = bint2(1,1) + bint2(2,1)*[0:45];
y2_ci2 = bint2(1,2) + bint2(2,2)*[0:45];

figure(1); hold on
plot([0:45], y1, 'r');
fill( [0:45 45:-1:0], [y1_ci1 fliplr(y1_ci2)], 'r'); alpha(.2)
plot([0:45], y2, 'b');
fill( [0:45 45:-1:0], [y2_ci1 fliplr(y2_ci2)], 'b'); alpha(.2)
```



2e

```

close all
load ps4_problem2.mat
figure;
errorbar(1:40, mg1, err1, 'ro'); hold on
errorbar(1:40, mg2, err2, 'bo');
legend('g1', 'g2')
xlabel('Trial number')
ylabel('Escape latencies')

load ps4_problem2.mat
x = repmat([1:40], [10,1]);
x = reshape(x,[],1);
g1= reshape(g1,[],1);
g2 = reshape(g2,[],1);

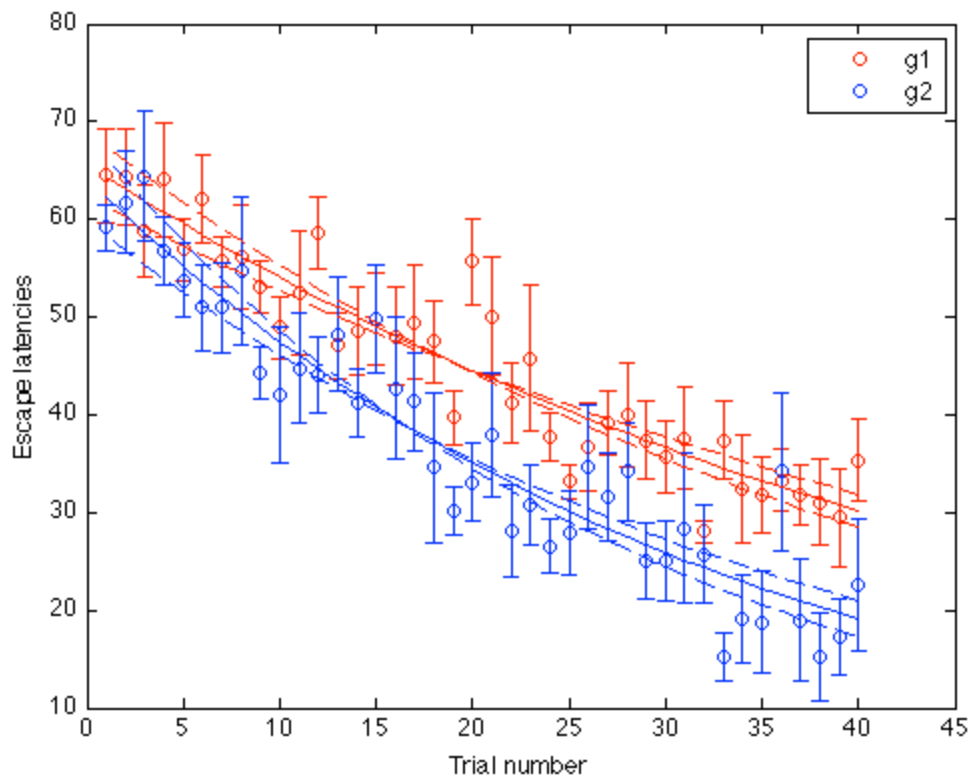
[b1,rnl1,j1,covb1,mse1] = nlinfit(x,g1,@expfun,[50 1/50]);
ci1 = nlparci(b1,rnl1,'jacobian',j1);
y1_ci1 = expfun(ci1(:,1), x);
y1_ci2 = expfun(ci1(:,2), x);

[b2,rnl2,j2,covb2,mse2] = nlinfit(x,g2,@expfun,[50 1/50]);
ci2 = nlparci(b2,rnl2,'jacobian',j2);
y2_ci1 = expfun(ci2(:,1), x);
y2_ci2 = expfun(ci2(:,2), x);

hold on
plot(1:40, expfun(b1,1:40), 'r')
plot(x,y1_ci1, 'r--')
plot(x,y1_ci2, 'r--')
% fill( [x fliplr(x)], [y1_ci1 fliplr(y1_ci2)], 'r'); alpha(.2)

plot(1:40, expfun(b2,1:40), 'b')
plot(x,y2_ci1, 'b--')
plot(x,y2_ci2, 'b--')
% fill( [x fliplr(x)], [y2_ci1 fliplr(y2_ci2)], 'b'); alpha(.2)

```



2f

Looking at the sum square error, the nonlinear fit is better

```
sum(rn11.^2)
sum(rn12.^2)
sum(r1.^2)
sum(r2.^2)
```

```
ans =
    7.4994e+04
ans =
    1.0551e+05
ans =
    7.5406e+04
ans =
    1.0683e+05
```

3a

It does not seem like there is a difference between the two

```
clear
load ps4_problem3.mat

edges = [0:0.01:0.300];
spk1 = [];
```

```

spk2 = [];
for iTrial = 1:size(spiketimes1,1)
    n = histc(spiketimes1{iTrial,1},edges);
    spk1 = [spk1; n];

    n = histc(spiketimes2{iTrial,1},edges);
    spk2 = [spk2; n];
end

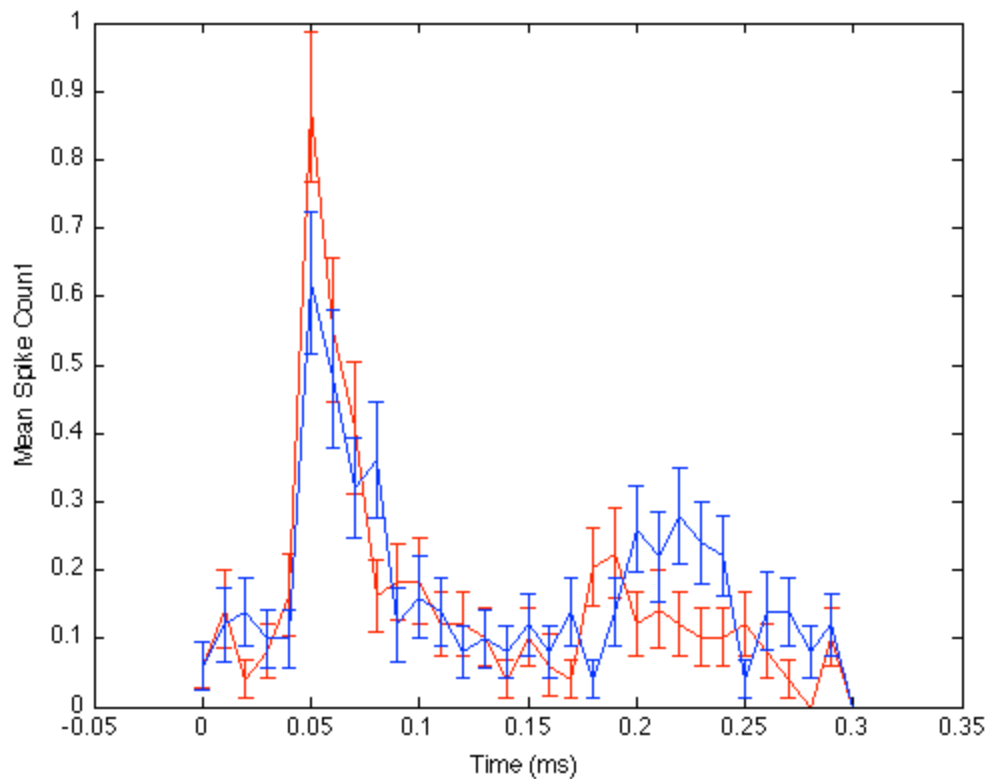
mspk1 = mean(spk1);
sepk1 = std(spk1)/sqrt(50);

mspk2 = mean(spk2);
sepk2 = std(spk2)/sqrt(50);

figure
errorbar(edges,mspk1,sepk1,'Color','r')
hold on
errorbar(edges,mspk2,sepk2,'Color','b')
xlabel('Time (ms)')
ylabel('Mean Spike Count')

```

Warning: Concatenation involves an empty array with an incorrect number of columns. This may not be allowed in a future release.



3b

The p-values are not significant


```
spk1rate = sum(spkl,2)/0.300;  
spk2rate = sum(spkl,2)/0.300;  
totalSpks = [spk1rate; spk1rate];  
  
y = [zeros(49,1); ones(49,1)];  
y = [y ones(98,1)];  
[b, dev, stats] = glmfit(totalSpks, y, 'binomial');  
stats(1).p
```

```
ans =  
    1.0000  
    1.0000
```

3c

```
spk1rate = sum(spkl,1);  
spk2rate = sum(spkl,1);
```

3d