salData=read.csv('Expt1\_ChoiceData.csv',header=TRUE);

salData$sal=factor(salData$sal, levels=c("hs","ls", "dist"))

aggregate(salData$prop,list(Saliency=salData$sal),mean)

Saliency x

1 hs 0.57773636

2 ls 0.36535536

3 dist 0.05690828

aggregate(salData$prop,list(Saliency=salData$sal),sd)

Saliency x

1 hs 0.13404281

2 ls 0.10864591

3 dist 0.08208966

**CHOICE PROPORTION ANALYSIS**

**No random factor (BEST MODEL)**

m=glm(cbind(numbers, (total-numbers))~sal, data=salData, family=binomial(link="logit"))

summary(m)

Call:

glm(formula = cbind(numbers, (total - numbers)) ~ sal, family = binomial(link = "logit"),

data = salData)

Deviance Residuals:

Min 1Q Median 3Q Max

-2.3571 -1.0179 -0.1396 0.7127 3.6648

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 0.31168 0.09949 3.133 0.00173 \*\*

salls -0.83541 0.14226 -5.872 4.3e-09 \*\*\*

saldist -3.24096 0.24508 -13.224 < 2e-16 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 395.823 on 59 degrees of freedom

Residual deviance: 91.328 on 57 degrees of freedom

AIC: 256.91

Number of Fisher Scoring iterations: 5

**SEQUENCE INDEX ANALYSIS**

salSwitch=read.csv('Expt1\_TransitionData.csv')

mean(salSwitch$seqInd)

[1] 0.5052503

sd(salSwitch$seqInd)

[1] 0.1673788

wilcox.test(salSwitch$seqInd,salSwitch$randRef)

Wilcoxon rank sum test with continuity correction

data: salSwitch$seqInd and salSwitch$randRef

W = 200, p-value = 1

alternative hypothesis: true location shift is not equal to 0