Statistics of Signal Detection Models

usings GLMs in R

Guillermo Aguilar

Technische Universität Berlin

August 27th, 2017

Goal

Learn to analyze the most common experimental designs
in the framework of Signal Detection Theory using GLMs in R

Resources

Knoblauch & Maloney (2012). Modeling Psychophysical Data in R

Signal detection theory
- Wickens (2002). Elementary Signal Detection Theory.
- McNicol (2005). A premier of Signal Detection Theory
- Macmillian (2005). Detection Theory. A User's Guide
- Green & Swets (1966). Signal Detection Theory and Psychophysics.

R
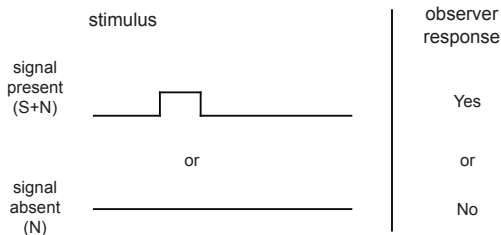- any statistical textbook that uses R

GLMs
- Wood ... (X)

Repository

All slides and code are available in the following *git* repository:

https://github.com/guillermoaguilar/sdt_tutorial.git

Yes/No detection experiment

On each trial, one stimulus is presented

Signal

		present	absent
Response	Yes	Hit	False Alarm
	No	Miss	Correct rejection
		N_s	N_n

- Hit rate
  $pH = \frac{\#H}{\#N_s}$
- False Alarm rate
  $pFA = \frac{\#FA}{\#N_n}$

Example

Signal

		present	absent
Response	Yes	180	50
	No	20	150
		200	200

- Hit rate
  $pH = \frac{\#H}{\#N_s} = \frac{180}{200} = 0.9$

- False Alarm rate
  $pFA = \frac{\#FA}{\#N_n} = \frac{50}{200} = 0.25$

Exercise 1: Analyze a detection experiment

Datafile: *data1.csv*
Description: columns are:
               Resp (response, 1: Yes, 0: No)
               Stim (type of stimulus, 'S': signal-present, 'A': signal-absent).

Steps:

1. Load *data1.csv* as a dataframe in R using

   ```
   read.csv()
   ```

2. Examine its contents with

   ```
   head()  summary()
   ```

3. Calculate Hit and False Alarm Rate (*pH* and *pFA*)

Hints: slicing the data in R can be done with square brackets ([ ]) and selecting a column is done with the dollar sign ($)

Exercise 1: Analyze a detection experiment

Datafile: *data1.csv*
Description: columns are:
                 Resp (response, 1: Yes, 0: No)
                 Stim (type of stimulus, 'S': signal-present, 'A': signal-absent).

Steps:

1. Load *data1.csv* as a dataframe in R using

   ```
   read.csv()
   ```

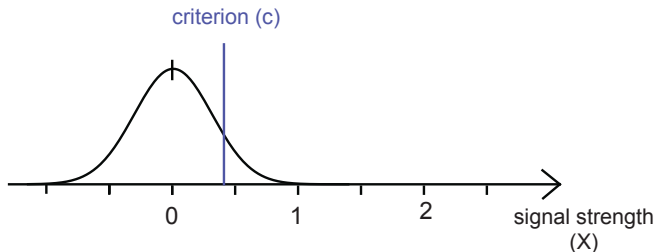2. Examine its contents with

   ```
   head()  summary()
   ```

3. Calculate Hit and False Alarm Rate (*pH* and *pFA*)

*Hints: slicing the data in R can be done with square brackets ([ ]) and
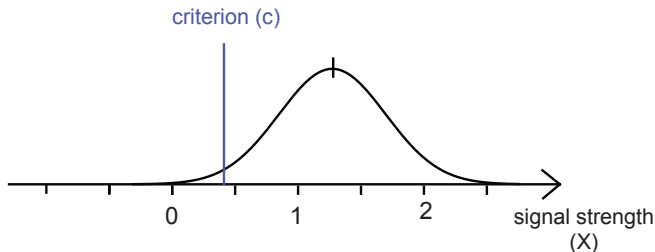selecting a column is done with the dollar sign ($)*

$$pH = 0.936$$
$$pFA = 0.288$$

Signal detection theory

Assumptions:

- Internal dimension representing some (sensory) evidence, X
- subjected to fluctuation (noise), X is a random var.
- simple decision rule: if $X > c$ then respond *YES*
  otherwise respond *NO*

Signal detection theory

Assumptions:

- Internal dimension representing some (sensory) evidence, *X*
- subjected to fluctuation (noise), *X* is a random var.
- simple decision rule: if $X > c$ then respond *YES*
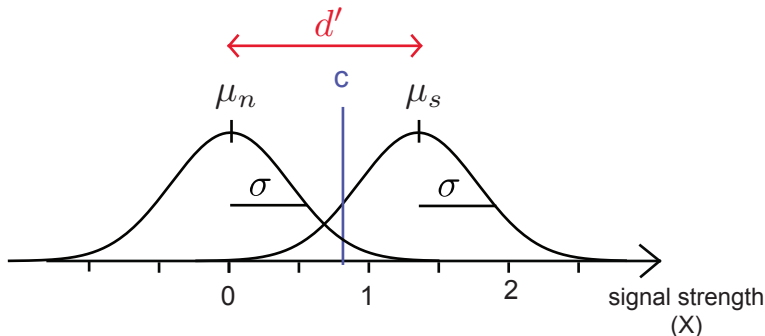 otherwise respond *NO*

SDT with some added assumptions

1. Assumption of Gaussian distribution

$X_n \sim \mathcal{N}(0, 1)$ and $X_s \sim \mathcal{N}(\mu_s, \sigma_s^2)$

2. Equal-variance assumption
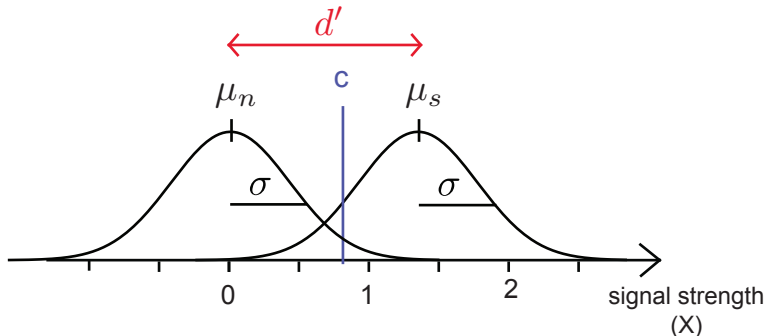
even further simplification $\sigma_s^2 = 1$

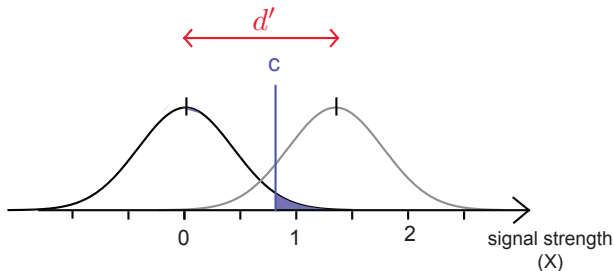# Equal-variance, Gaussian-distributed signal detection

It is then defined

d', a *measure of sensitivity* defined as the distance between the two distributions
c is the sensory criterion and a *measure of bias*.

Equal-variance, Gaussian-distributed signal detection

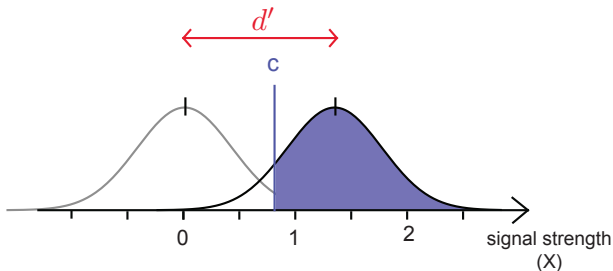Parameters d' and c can be calculated directly from pH and pFA.

$$pFA = 1 - \Phi(c)$$

Equal-variance, Gaussian-distributed signal detection

Parameters d' and c can be calculated directly from pH and pFA.

$$pH = 1 - \Phi(c - d')$$

Equal-variance, Gaussian-distributed signal detection

Parameters d' and c can be calculated directly from pH and pFA.
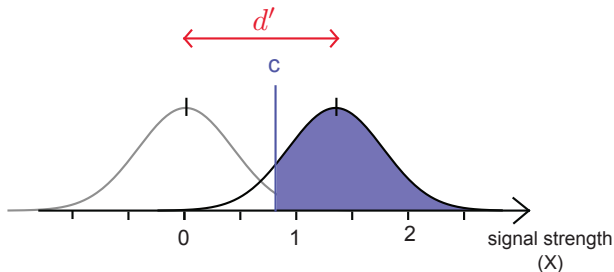
$$pFA = 1 - \Phi(c) \qquad pH = 1 - \Phi(c - d')$$

it can be solved for d' and c [full derivation in extra slides *1]

$$c = -\Phi^{-1}(pFA) \tag{1}$$

$$d' = \Phi^{-1}(pH) - \Phi^{-1}(pFA) \tag{2}$$

Exercise 2: explore the normal distribution

$\Phi()$ is the cumulative normal dist. function
and $\Phi^{-1}()$ its inverse, or *quantile* function
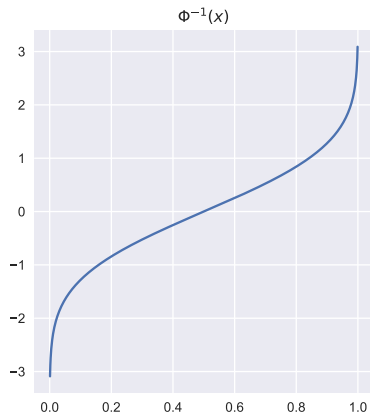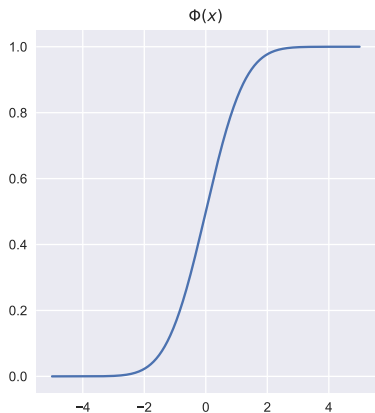
Exercise 3: Analyze a detection experiment

1. Use the Eqs. to calculate d' and c.

$$c = -\Phi^{-1}(pFA)$$
$$d' = \Phi^{-1}(pH) - \Phi^{-1}(pFA)$$

Exercise 3: Analyze a detection experiment

1. Use the Eqs. to calculate d' and c.

$$c = -\Phi^{-1}(pFA)$$
$$d' = \Phi^{-1}(pH) - \Phi^{-1}(pFA)$$

```
> dp_hat <- qnorm(pH) - qnorm(pFA)
2.081273
> c_hat <- -qnorm(pFA)
0.559237
```

$$\hat{d}' = 2.081273$$
$$\hat{c} = 0.559237$$

Exercise 3': Analyze a detection experiment

Some textbooks use the calculation of a modified criterion $c_{center} = C$ that is midway between the two distributions
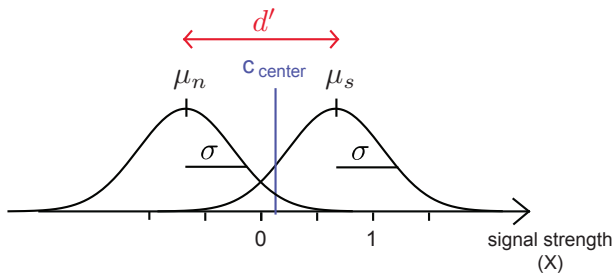
$$C = c_{center} = -\Phi^{-1}(pH) + d'/2 = -\Phi^{-1}(pFA) - d'/2$$
$$= -[\Phi^{-1}(pH) + \Phi^{-1}(pFA)]/2$$

Exercise 3': Analyze a detection experiment

Some textbooks use the calculation of a modified criterion $c_{center} = C$ that is midway between the two distributions
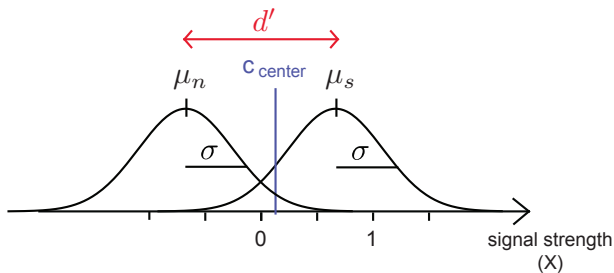
$$C = c_{center} = -\Phi^{-1}(pH) + d'/2 = -\Phi^{-1}(pFA) - d'/2$$
$$= -[\Phi^{-1}(pH) + \Phi^{-1}(pFA)]/2$$


```
> c_center <- -(qnorm(pH) + qnorm(pFA))/2.0
-0.4813996
```

Generalized Linear Models (GLMs)

Another approach to estimate $\hat{d}'$ and $\hat{c}$ is using GLMs.

A GLM is a linear model generalized for response variables that are not necessarily continuous.

Let's consider a linear model

$$y = \beta_1 \cdot x + \beta_0$$

GLMs made linear models **general** by having y replaced by a probability value (the expectation of Y, $E[Y]$), and adding a function $g()$ that 'links' the linear predictors (right-hand side) with the probability in the response variable.

$$g(E[y]) = \beta_1 \cdot x + \beta_0$$

There could be explanatory variables $(\beta_0, \beta_1, \beta_2 \dots)$, therefore GLMs are annotated in a vector form

$$g(E[\mathbf{Y}]) = \mathbf{X} \cdot \beta$$

Link function $g()$

For this case an appropriate choice of the link function is the quantile normal function $g() = \Phi^{-1}()$
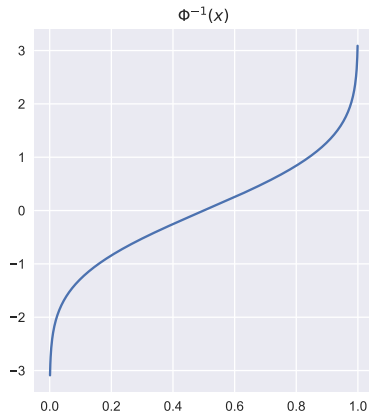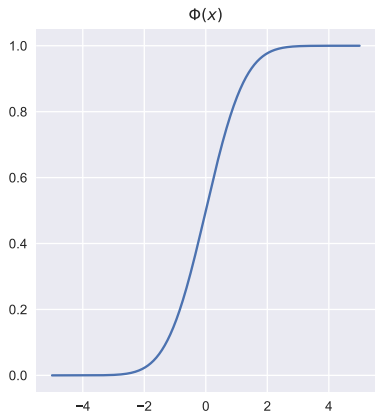
GLM and SDT

Note that the False Alarm and Hit Rates are probabilities

$$pFA = P[R = YES|S = absent] = P[Y = 1|X = 0]$$

$$pH = P[R = YES|S = present] = P[Y = 1|X = 1]$$

Thus, one could write

$$g(P[Y = 1]) = \beta_1 \cdot X + \beta_0$$

where
$X = 1$ for signal-present trials and
$X = 0$ for signal-absent trials.

GLM and SDT

Let's consider our detection experiment. The GLM for a detection experiment can be arranged

$$g(E[\mathbf{Y}]) = \mathbf{X} \cdot \beta$$

$$g(\begin{bmatrix} 0 \\ 1 \\ 0 \\ \vdots \\ 1 \\ 1 \\ 1 \end{bmatrix}) = \begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ \vdots & \\ 1 & 1 \\ 1 & 1 \\ 1 & 1 \end{bmatrix} \cdot \begin{bmatrix} \beta_0 \\ \beta_1 \end{bmatrix}$$

The first set of responses correspond to signal-absent trials, and the second set to signal-present trials.

This GLM can be then solved using maximum likelihood estimation (MLE).

The procedure returns estimates for β_0 and β_1.

Exercise 4: Analyze a detection experiment using a GLM

1. Use the *GLM method* to analyse the detection experiment data

Exercise 4: Analyze a detection experiment using a GLM

1. Use the *GLM method* to analyse the detection experiment data

```
> fit <- glm(Resp ˜ Stim, data=df,
                    family=binomial('probit'))
```

```
> summary(fit)
Call:
glm(formula = Resp ˜ Stim, family = binomial("probit"), data = df)
Deviance Residuals:
    Min        1Q     Median        3Q       Max
-2.3447   -0.8242    0.3637    0.3637    1.5778
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.55924    0.05935  -9.422   <2e-16 ***
StimS        2.08127    0.10563  19.704   <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: 1335.69  on 999  degrees of freedom
Residual deviance: 838.19  on 998  degrees of freedom
AIC: 842.19
Number of Fisher Scoring iterations: 5
```

Do these numbers look familiar?
$\beta_1 = 2.08127$ and $\beta_0 = -0.55924$

Explanation to the meaning of β_0 and β_1

Remember from before

$$d' = \Phi^{-1}(pH) - \Phi^{-1}(pFA)$$
$$c = -\Phi^{-1}(pFA)$$

For **signal-absent** trials, $X = 0$ and the expanded model is

$$g(P[Y = 1|X = 0]) = \beta_1 \cdot 0 + \beta_0$$
$$\Phi^{-1}(P[Y = 1|X = 0]) = \beta_0$$
$$\Phi^{-1}(pFA) = \beta_0$$
$$-c = \beta_0$$

Explanation to the meaning of β_0 and β_1

Remember from before

$$d' = \Phi^{-1}(pH) - \Phi^{-1}(pFA)$$
$$c = -\Phi^{-1}(pFA)$$

For **signal-present** trials, $X = 1$ and the expanded model is

$$g(P[Y = 1 | X = 1]) = \beta_1 \cdot 1 + \beta_0$$
$$\Phi^{-1}(P[Y = 1 | X = 1]) = \beta_1 \cdot 1 + \Phi^{-1}(pFA)$$
$$\Phi^{-1}(pH) = \beta_1 + \Phi^{-1}(pFA)$$
$$\Phi^{-1}(pH) - \Phi^{-1}(pFA) = \beta_1$$
$$d' = \beta_1$$

Therefore, the coefficients obtained from GLM have a direct correspondence to the parameters d' and c.

The power of GLMs

Confidence intervals

```
> confint(fit)
Waiting for profiling to be done...
                2.5 %      97.5 %
(Intercept) -0.6761901 -0.4434893
StimS        1.8773729  2.2917211
```

Exercise 5: Detection exp. in two conditions

To include different conditions in the GLM framework

Reading data from two exp. conditions

```
> df1 <- read.csv("data1.csv")
> df1$Cond <- "A"

> df2 <- read.csv("data2.csv")
> df2$Cond <- "B"

> df <- rbind(df1, df2)
```

Exercise 5: Detection exp. in two conditions

Fitting different models

(a) Unique model

```
> fit1 <- glm(Resp ~ Stim,
         family=binomial('probit'), data=df)
```

(b) Model with different criteria, same sensitivity (d′)

```
> fit2 <- glm(Resp ~ Stim + Cond,
         family=binomial('probit'), data=df)
```

(c) Model with different criteria and sensitivity (d′)

```
> fit3 <- glm(Resp ~ Stim + Cond + Stim:Cond,
         family=binomial('probit'), data=df)
```

Exercise 5: Detection exp. in two conditions

Model selection

```
> anova(fit1, fit2, fit3, test='Chisq')
Analysis of Deviance Table

Model 1: Resp ~ Stim
Model 2: Resp ~ Stim + Cond
Model 3: Resp ~ Stim + Cond + Stim:Cond
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1      1998     1735.5
2      1997     1701.8  1   33.698 6.435e-09 ***
3      1996     1701.7  1    0.140    0.7081
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

fit2 explains the data sig. better than fit1, but fit3 does not improve it further

Exercise 5: Detection experiment on two conditions

Parameter extraction

```
> coef(fit2)
(Intercept)        StimS         CondB
 -0.5500044    2.0521900    -0.3999372
```

How are these parameters encoded?

Exercise 5: Detection experiment on two conditions

Parameter extraction

```
> coef(fit2)
(Intercept)        StimS         CondB
 -0.5500044    2.0521900    -0.3999372
```

How are these parameters encoded?

Remember from earlier that $\beta_0 = -c$ and $\beta_1 = d'$

- The intercept applies for the first condition (*A*), thus $\beta_0 = -c_A$.
- $\beta_1 = d'$, assumed equal for both conditions A and B.
- The new parameter β_2 is the difference with respecto to β_0. Thus, $c_B = -(\beta_0 + \beta_2)$.

Thus,

```
> c_b <- -(coef(fit2)[[1]]+coef(fit2)[[3]])
0.9499416
```

Understanding the design matrix

For the unique model (a), the GLM looks like

$$g(E[\mathbf{Y}]) = \mathbf{X} \cdot \beta$$

$$g\left(\begin{bmatrix} 0 \\ 1 \\ \vdots \\ 1 \\ 1 \\ \vdots \\ 1 \\ 0 \\ \vdots \\ 1 \\ 1 \end{bmatrix}\right) = \begin{bmatrix} 1 & 0 \\ 1 & 0 \\ \vdots & \\ 1 & 1 \\ 1 & 1 \\ \vdots & \\ 1 & 0 \\ 1 & 0 \\ \vdots & \\ 1 & 1 \\ 1 & 1 \end{bmatrix} \cdot \begin{bmatrix} \beta_0 \\ \beta_1 \end{bmatrix}$$

Understanding the design matrix

For the model(b): different intercept (*fit2*), the GLM looks like

$$g(E[\mathbf{Y}]) = \mathbf{X} \cdot \beta$$

$$g(\begin{bmatrix} 0 \\ 1 \\ \vdots \\ 1 \\ 1 \\ \vdots \\ 1 \\ 0 \\ \vdots \\ 1 \\ 1 \end{bmatrix}) = \begin{bmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ \vdots & & \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ \vdots & & \\ 1 & 0 & 1 \\ 1 & 0 & 1 \\ \vdots & & \\ 1 & 1 & 1 \\ 1 & 1 & 1 \end{bmatrix} \cdot \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \end{bmatrix}$$

see [*2] for full derivation of parameters

Understanding the design matrix

For the model (c): different intercept and different d' (*fit*3), the GLM looks like

$$g(E[\mathbf{Y}]) = \mathbf{X} \cdot \beta$$

$$g\left(\begin{bmatrix} 0 \\ 1 \\ \vdots \\ 1 \\ 1 \\ \vdots \\ 1 \\ 0 \\ \vdots \\ 1 \\ 1 \end{bmatrix}\right) = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ \vdots & & & \\ 1 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 \\ \vdots & & & \\ 1 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 \\ \vdots & & & \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \end{bmatrix} \cdot \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \beta_3 \end{bmatrix}$$

see [*3] for full derivation of parameters

Design matrix

$$g(E[\mathbf{Y}]) = \mathbf{X} \cdot \beta$$

- The design matrix X is automatically generated by *R*.
- It can always be obtained using the function *model.matrix*()

Discrimination Experiment: 2-AFC
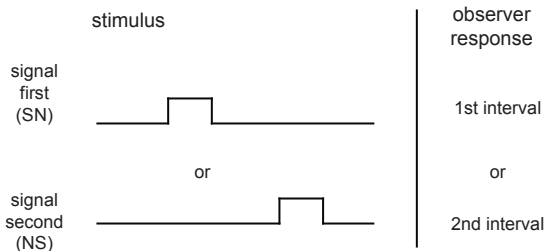
- Statistically similar as in a Yes/No detection experiment
- Signal-present or -absent can be relabeled to 'SN'/'NS' and responses as '1st interval'/'2nd interval', or '1st position'/'2nd position' depending on the exp. design
- Extra step of differencing

Discrimination Experiment: 2-AFC

On each trial, two stimuli are presented. Thus, two draws are taken, one from each distribution
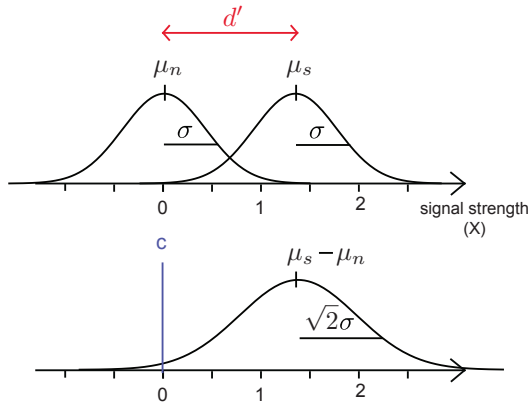
$$\Delta = X_s - X_n \qquad \Delta \sim \mathcal{N}(\mu_s - \mu_n, 2\sigma^2)$$

Discrimination Experiment: 2-AFC

$$\Delta = X_s - X_n \qquad \Delta \sim \mathcal{N}(\mu_s - \mu_n, 2\sigma^2)$$

As $\mu_n = 0$, $\mu_s = d'$, and $\sigma = 1$, we have

$$\Delta \sim \mathcal{N}(d', 2)$$

and the probability of correct when $\Delta > 0$,

$$Pc = 1 - \Phi\left(\frac{-d'}{\sqrt{2}}\right) = \Phi\left(\frac{d'}{\sqrt{2}}\right)$$

Thus, d' can be calculated from the percentage correct in a 2-AFC experiment

$$d' = \Phi^{-1}(Pc)\sqrt{2} \tag{3}$$

Discrimination Experiment: 2-AFC

Estimates of d' from 2AFC and Yes/No related to each other by

$$d'_{AFC} = d'_{YesNo}\sqrt{2}$$

(see derivation in Wickens 2002, or in McNicol 1972)

However, this relationship has been called into question recently (Yeshurun, Carrasco & Maloney, 2008)

Exercise 6: Discrimination experiment: 2-AFC

Analyze the data from a 2-AFC discrimination experiment using a GLM

Datafile: data2afc.csv

Description: columns are:

Resp (response, 1: 1st interval, 0: 2nd interval)

Stim (type of stimulus, 'SN': stimulus in 1st interval,

or 'NS': stimulus in 2nd interval).

Steps:

1. Load data
2. Calculate percentage correct *Pc* and from it *d'* using Eq. 3
3. Calculate *d'* and *c* using a GLM
4. Compare these two ways of obtaining *d'*

Exercise 6: Discrimination experiment: 2-AFC

Analyze the data from a 2-AFC discrimination experiment using a GLM

Datafile: data2afc.csv

Description: columns are:

Resp (response, 1: 1st interval, 0: 2nd interval)

Stim (type of stimulus, 'SN': stimulus in 1st interval,

or 'NS': stimulus in 2nd interval).

Steps:

1. Load data
2. Calculate percentage correct Pc and from it d' using Eq. 3
3. Calculate d' and c using a GLM
4. Compare these two ways of obtaining d'

Solution: $d' = 1.53$, $c = 0.77$, $c_{center} = 0.01$

MLDS

Application of GLMs to scaling methods: MLDS

Further Exercises

Thank you

*1: Derivation 1

Given $pFA = 1 - \Phi(c)$ and $pH = 1 - \Phi(c - d')$

$$\Phi(c) = 1 - pFA \qquad\qquad \Phi(c - d') = 1 - pH$$
$$c = \Phi^{-1}(1 - pFA) \qquad\qquad c - d' = \Phi^{-1}(1 - pH)$$
$$c = -\Phi^{-1}(pFA) \qquad\qquad d' = c - \Phi^{-1}(1 - pH)$$
$$d' = -\Phi^{-1}(pFA) - \Phi^{-1}(1 - pH)$$
$$d' = \Phi^{-1}(pH) - \Phi^{-1}(pFA)$$

Note the symmetry of the quantile function
$$\Phi^{-1}(1 - x) = -\Phi^{-1}(x)$$

*2: Derivation 2

For the model(b): different intercept (*fit2*), the GLM looks like

$$g(E[\mathbf{Y}]) = \mathbf{X} \cdot \beta$$

$$g\left(\begin{bmatrix} 0 \\ 1 \\ \vdots \\ 1 \\ 1 \\ \vdots \\ 1 \\ 0 \\ \vdots \\ 1 \\ 1 \end{bmatrix}\right) = \begin{bmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ \vdots & & \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ \vdots & & \\ 1 & 0 & 1 \\ 1 & 0 & 1 \\ \vdots & & \\ 1 & 1 & 1 \\ 1 & 1 & 1 \end{bmatrix} \cdot \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \end{bmatrix}$$

*2: Derivation 2

Writing each case we have

$$g(E[Y = 1|X = 0, C = A]) = 1 * \beta_0 + 0 * \beta_1 + 0 * \beta_2$$
$$g(E[Y = 1|X = 1, C = A]) = 1 * \beta_0 + 1 * \beta_1 + 0 * \beta_2$$
$$g(E[Y = 1|X = 0, C = B]) = 1 * \beta_0 + 0 * \beta_1 + 1 * \beta_2$$
$$g(E[Y = 1|X = 1, C = B]) = 1 * \beta_0 + 1 * \beta_1 + 1 * \beta_2$$

by replacing expectations for FA and Hit Rates, and by replacing the link function for the quantile function $g() = \Phi^{-1}()$, we have

$$\Phi^{-1}(pFA_A) = \beta_0 \tag{4}$$

$$\Phi^{-1}(pH_A) = \beta_0 + \beta_1 \tag{5}$$

$$\Phi^{-1}(pFA_B) = \beta_0 + \beta_2 \tag{6}$$

$$\Phi^{-1}(pH_B) = \beta_0 + \beta_1 + \beta_2 \tag{7}$$

*2: Derivation 2

Simplifying Eq. 4,

$$\beta_0 = \Phi^{-1}(pFA_A) = -c_A \qquad c_A = -\beta_0$$

inserting β_0 in Eq. 5...

$$\Phi^{-1}(pH_A) = \Phi^{-1}(pFA_A) + \beta_1$$
$$\Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A) = \beta_1$$
$$d' = \beta_1$$

Then, Eq. 6..

$$\Phi^{-1}(pFA_B) = \beta_0 + \beta_2$$
$$\Phi^{-1}(pFA_B) - \beta_0 = \beta_2$$
$$-c_B + c_A = \beta_2$$
$$-(c_B - c_A) = \beta_2$$

*2: Derivation 2

β_2 is the difference in intercept between conditions B and A

Finally inserting $\beta_0, \beta_1, \beta_2$ in Eq. 7 ..

$$
\begin{aligned}
\Phi^{-1}(pH_B) =& \beta_0 + \beta_1 + \beta_2 \\
\Phi^{-1}(pH_B) =& \Phi^{-1}(pFA_A) + \Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A) \\
& + \Phi^{-1}(pFA_B) - \Phi^{-1}(pFA_A) \\
\Phi^{-1}(pH_B) =& \Phi^{-1}(pH_A) + \Phi^{-1}(pFA_B) - \Phi^{-1}(pFA_A) \\
\Phi^{-1}(pH_B) - \Phi^{-1}(pFA_B) =& \Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A) \\
d'_B =& d'_A
\end{aligned}
$$

*3: Derivation 3

Writing each case we have

$$g(E[Y = 1|X = 0, C = A]) = 1 * \beta_0 + 0 * \beta_1 + 0 * \beta_2 + 0 * \beta_3$$
$$g(E[Y = 1|X = 1, C = A]) = 1 * \beta_0 + 1 * \beta_1 + 0 * \beta_2 + 0 * \beta_3$$
$$g(E[Y = 1|X = 0, C = B]) = 1 * \beta_0 + 0 * \beta_1 + 1 * \beta_2 + 0 * \beta_3$$
$$g(E[Y = 1|X = 1, C = B]) = 1 * \beta_0 + 1 * \beta_1 + 1 * \beta_2 + 1 * \beta_3$$

by replacing expectations for FA and Hit Rates, and by replacing the link function for the quantile function $g() = \Phi^{-1}()$, we have

$$\Phi^{-1}(pFA_A) = \beta_0 \tag{8}$$
$$\Phi^{-1}(pH_A) = \beta_0 + \beta_1 \tag{9}$$
$$\Phi^{-1}(pFA_B) = \beta_0 + \beta_2 \tag{10}$$
$$\Phi^{-1}(pH_B) = \beta_0 + \beta_1 + \beta_2 + \beta_3 \tag{11}$$

*3: Derivation 3

Simplifying Eq. 8,

$$\beta_0 = \Phi^{-1}(pFA_A) = -c_A$$

inserting β_0 in Eq. 9...

$$\Phi^{-1}(pH_A) = \Phi^{-1}(pFA_A) + \beta_1$$
$$\Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A) = \beta_1$$
$$d'_A = \beta_1$$

inserting β_0 in Eq. 10 ..

$$\Phi^{-1}(pFA_B) = \Phi^{-1}(pFA_A) + \beta_2$$
$$\Phi^{-1}(pFA_B) - \Phi^{-1}(pFA_A) = \beta_2$$
$$-(c_B - c_A) = \beta_2$$

β_2 is the difference in intercept between conditions B and A

*2: Derivation 2

Finally inserting $\beta_0, \beta_1, \beta_2$ in Eq. 11 ..

$$\Phi^{-1}(pH_B) = \beta_0 + \beta_1 + \beta_2 + \beta_3$$
$$\Phi^{-1}(pH_B) = \Phi^{-1}(pFA_A) + \Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A)$$
$$+ \Phi^{-1}(pFA_B) - \Phi^{-1}(pFA_A) + \beta_3$$
$$\Phi^{-1}(pH_B) = \Phi^{-1}(pH_A) + \Phi^{-1}(pFA_B) - \Phi^{-1}(pFA_A) + \beta_3$$
$$\Phi^{-1}(pH_B) - \Phi^{-1}(pFA_B) = \Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A) + \beta_3$$
$$d'_B = d'_A + + \beta_3$$
$$d'_B - d'_A = \beta_3$$

β_3 is the difference in d' between conditions B and A