

Statistics of Signal Detection Models

usings GLMs in R

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August 27th, 2017

Goal

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

- 1 Introduction
 - Signal detection theory
 - Yes/No detection experiment
 - Equal-variance, Gaussian SDT
- 2 Generalized Linear Models
 - GLMs and SDT
 - Conditions and model comparison with GLMs
- 3 Discrimination Experiment: 2-AFC
- 4 MLDS

Resources

R

- Knoblauch & Maloney (2012). Modeling Psychophysical Data in R
- any statistical textbook that uses R

Signal detection theory

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

GLMs

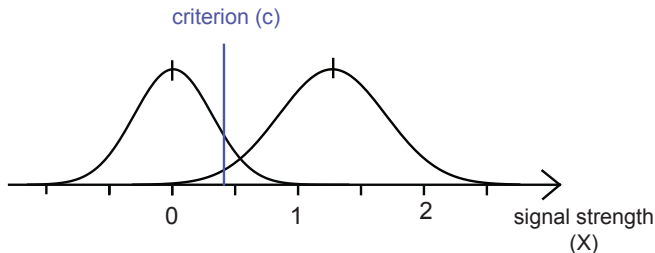
- Wood ... (X)

Repository

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

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

Signal detection theory

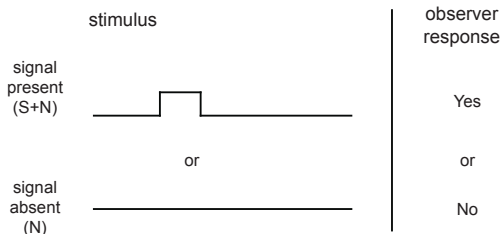


Assumptions:

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

Yes/No detection experiment

On each trial, one stimulus are presented. Thus, one draw is taken, either from one or the other distribution



		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 1a: 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 (p_H and p_{FA})

Exercise 1a: Analyze a detection experiment

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- 3 Calculate Hit and False Alarm Rate (pH and pFA)

$$pH = 0.936$$

$$pFA = 0.288$$

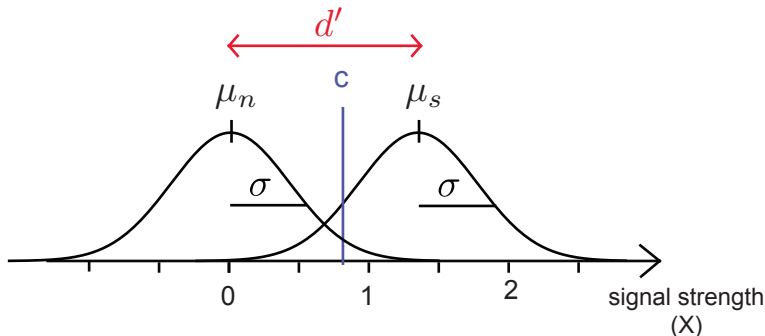
SDT with some added assumptions

1. Assumption of Gaussian distribution

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

2. Equal-variance assumption

even further simplification $\sigma_s^2 = 1$

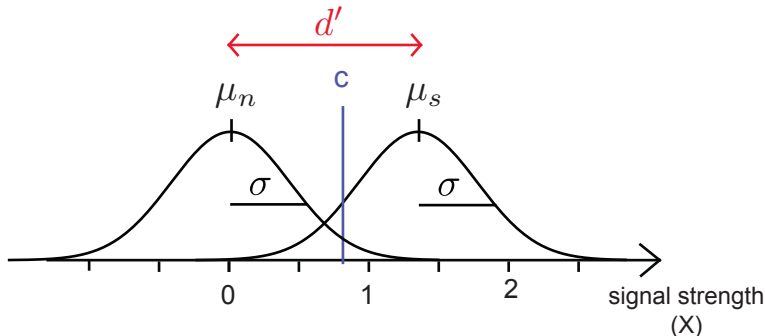


Equal-variance, Gaussian-distributed signal detection

It is then defined

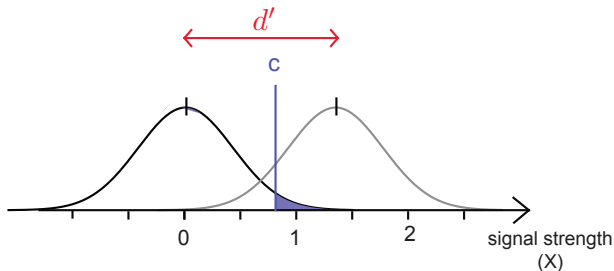
d' , a *measure of sensitivity* defined as the distance between the two distributions

c is the sensory criterion and a *measure of bias*.



Equal-variance, Gaussian-distributed signal detection

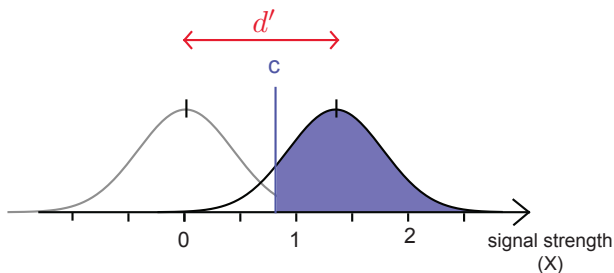
Parameters d' and c can be calculated directly from pH and pFA .



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

Equal-variance, Gaussian-distributed signal detection

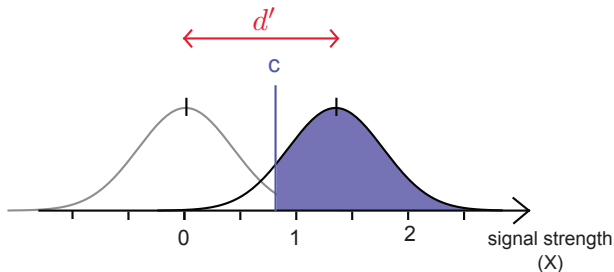
Parameters d' and c can be calculated directly from pH and pFA .



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

Equal-variance, Gaussian-distributed signal detection

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



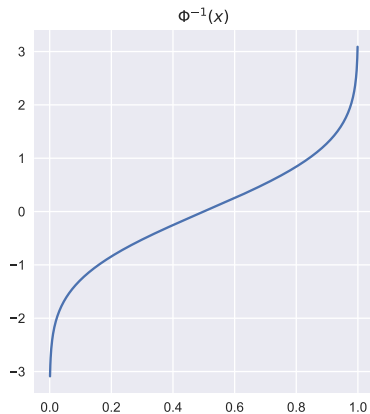
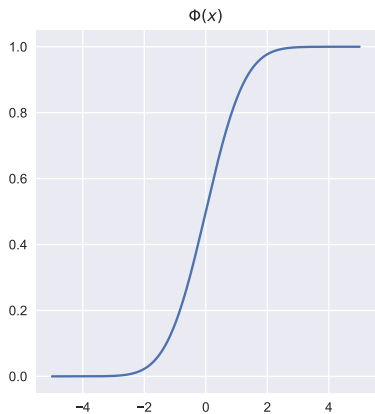
$$pFA = 1 - \Phi(c) \quad pH = 1 - \Phi(c - d')$$

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

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

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

$\Phi()$ is the cumulative normal dist. function
and $\Phi^{-1}()$ its inverse, or *quantile* function



Exercise 1b: Analyze a detection experiment

- 1 Use Eqs. (1) and (2) to calculate d' and c .
Hint: check functions $qnorm()$ and $pnorm()$

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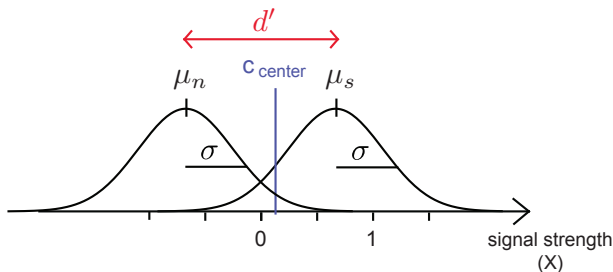
```
> dp_hat <- qnorm(pH) - qnorm(pFA)
2.081273
> c_hat <- -qnorm(pFA)
0.559237
```

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

Exercise 1b: Analyze a detection experiment

Some textbooks use the calculation of a modified criterion $c_{center} = C$ that is midway between the two distributions

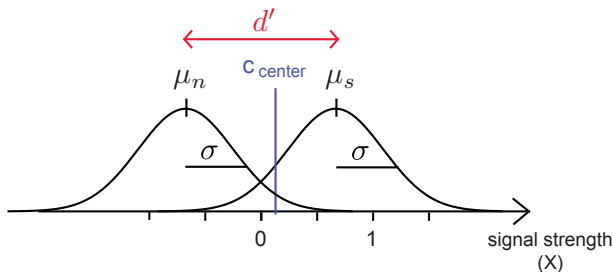
$$\begin{aligned} C = c_{center} &= -\Phi^{-1}(pH) + d'/2 = -\Phi^{-1}(pFA) - d'/2 \\ &= -[\Phi^{-1}(pH) + \Phi^{-1}(pFA)]/2 \end{aligned}$$



Exercise 1b: Analyze a detection experiment

Some textbooks use the calculation of a modified criterion $c_{center} = C$ that is midway between the two distributions

$$\begin{aligned} C = c_{center} &= -\Phi^{-1}(pH) + d'/2 = -\Phi^{-1}(pFA) - d'/2 \\ &= -[\Phi^{-1}(pH) + \Phi^{-1}(pFA)]/2 \end{aligned}$$



```
> 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 the variable y replaced by a probability value (the expectation of Y , $E[Y]$).

Because $E[Y]$ ranges from 0 to 1, it needs a function $g()$ that 'links' the linear predictors (right-hand side) with the response variable.

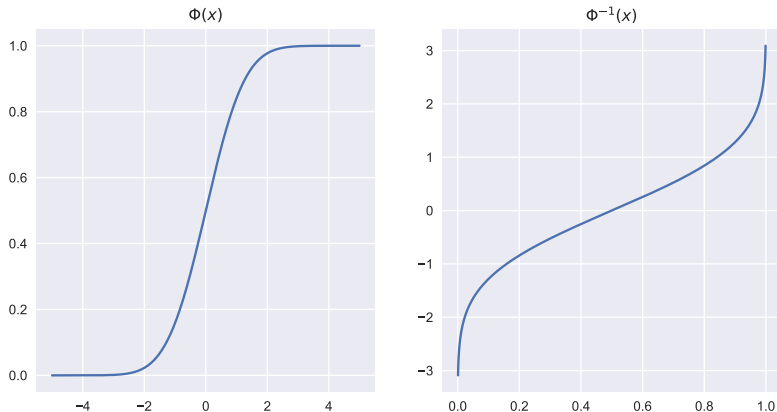
$$g(E[y]) = \beta_1 \cdot x + \beta_0$$

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

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

Link function $g()$

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



GLM and SDT

Let's consider our detection experiment:

$$\mathbf{Y} = \begin{bmatrix} 0 \\ 1 \\ 0 \\ \vdots \\ 1 \\ 1 \\ 1 \end{bmatrix}$$

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

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

Then the GLM for a detection experiment can be arranged

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

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

This GLM can be then solved using maximum likelihood estimation (MLE). The procedure returns estimates for β_0 and β_1 .

Exercise 1c: Analyze a detection experiment using a GLM

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

Exercise 1c: Analyze a detection experiment using a GLM

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

```
> fit <- glm(Resp ~ Stim, data=df, link=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?

$$\beta_1 = 2.08127 \text{ and } \beta_0 = -0.55924$$

Explanation to the meaning of β_0 and β_1

Remember from before

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

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

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

Explanation to the meaning of β_0 and β_1

Remember from before

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

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

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

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 2: Detection exp. in two conditions

To include different conditions is straightforward in the GLM framework

Reading data of two conditions

```
> df1 <- read.csv("data1.csv")  
> df1$Cond <- "A"  
  
> df2 <- read.csv("data2.csv")  
> df2$Cond <- "B"  
  
> df <- rbind(df1, df2)
```


Exercise 2: 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 2: 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 2: Detection experiment on two conditions

Parameter extraction

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

How are these parameters encoded?

Exercise 2: 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 respect 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

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

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

Understanding the design matrix

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

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

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

see [*2] for full derivation of parameters

Understanding the design matrix

For the model (c): different intercept and different d' (*fit3*), the GLM looks like

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

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

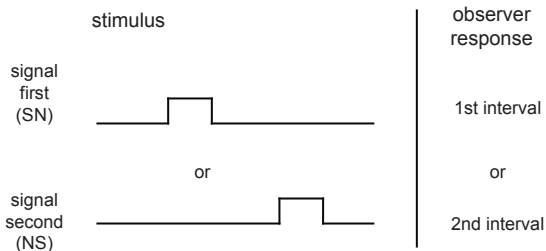
see [*3] for full derivation of parameters

Design matrix

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

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

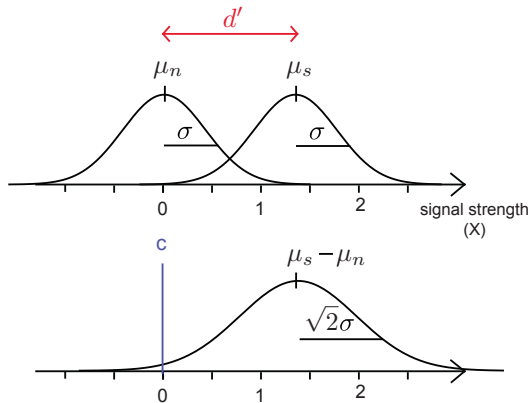
Discrimination Experiment: 2-AFC



- 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



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

Discrimination Experiment: 2-AFC

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

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 3: 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 P_c and from it d' using Eq. 3
- 3 Calculate d' and c using a GLM
- 4 Compare these two ways of obtaining d'

Exercise 3: Discrimination experiment: 2-AFC

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

Datafile: data2afc.csv

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

Steps:

- 1 Load data
- 2 Calculate percentage correct P_c 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

Thank you

*1: Derivation 1

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

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

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

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

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

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

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

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

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

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

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

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

*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,

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

inserting β_0 in Eq. 5...

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

Then, Eq. 6..

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

*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 ..

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

$$\begin{aligned}\Phi^{-1}(pH_B) &= \Phi^{-1}(pFA_A) + \Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A) \\ &\quad + \Phi^{-1}(pFA_B) - \Phi^{-1}(pFA_A)\end{aligned}$$

$$\Phi^{-1}(pH_B) = \Phi^{-1}(pH_A) + \Phi^{-1}(pFA_B) - \Phi^{-1}(pFA_A)$$

$$\Phi^{-1}(pH_B) - \Phi^{-1}(pFA_B) = \Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A)$$

$$d'_B = d'_A$$

*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...

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

inserting β_0 in Eq. 10 ..

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

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 ..

$$\Phi^{-1}(pH_B) = \beta_0 + \beta_1 + \beta_2 + \beta_3$$

$$\begin{aligned} \Phi^{-1}(pH_B) = & \Phi^{-1}(pFA_A) + \Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A) \\ & + \Phi^{-1}(pFA_B) - \Phi^{-1}(pFA_A) + \beta_3 \end{aligned}$$

$$\Phi^{-1}(pH_B) = \Phi^{-1}(pH_A) + \Phi^{-1}(pFA_B) - \Phi^{-1}(pFA_A) + \beta_3$$

$$\Phi^{-1}(pH_B) - \Phi^{-1}(pFA_B) = \Phi^{-1}(pH_A) - \Phi^{-1}(pFA_A) + \beta_3$$

$$d'_B = d'_A + \beta_3$$

$$d'_B - d'_A = \beta_3$$

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