Binomial Link Functions

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Binomial Link Functions

- Logit Link function: $\eta(p) = \ln\left(\frac{p}{1-p}\right)$

- Probit Link function: $\eta(p) = \Phi^{-1}(p)$

- Complentary Log Log function: $\eta(p) = \ln(-\ln(1-p))$

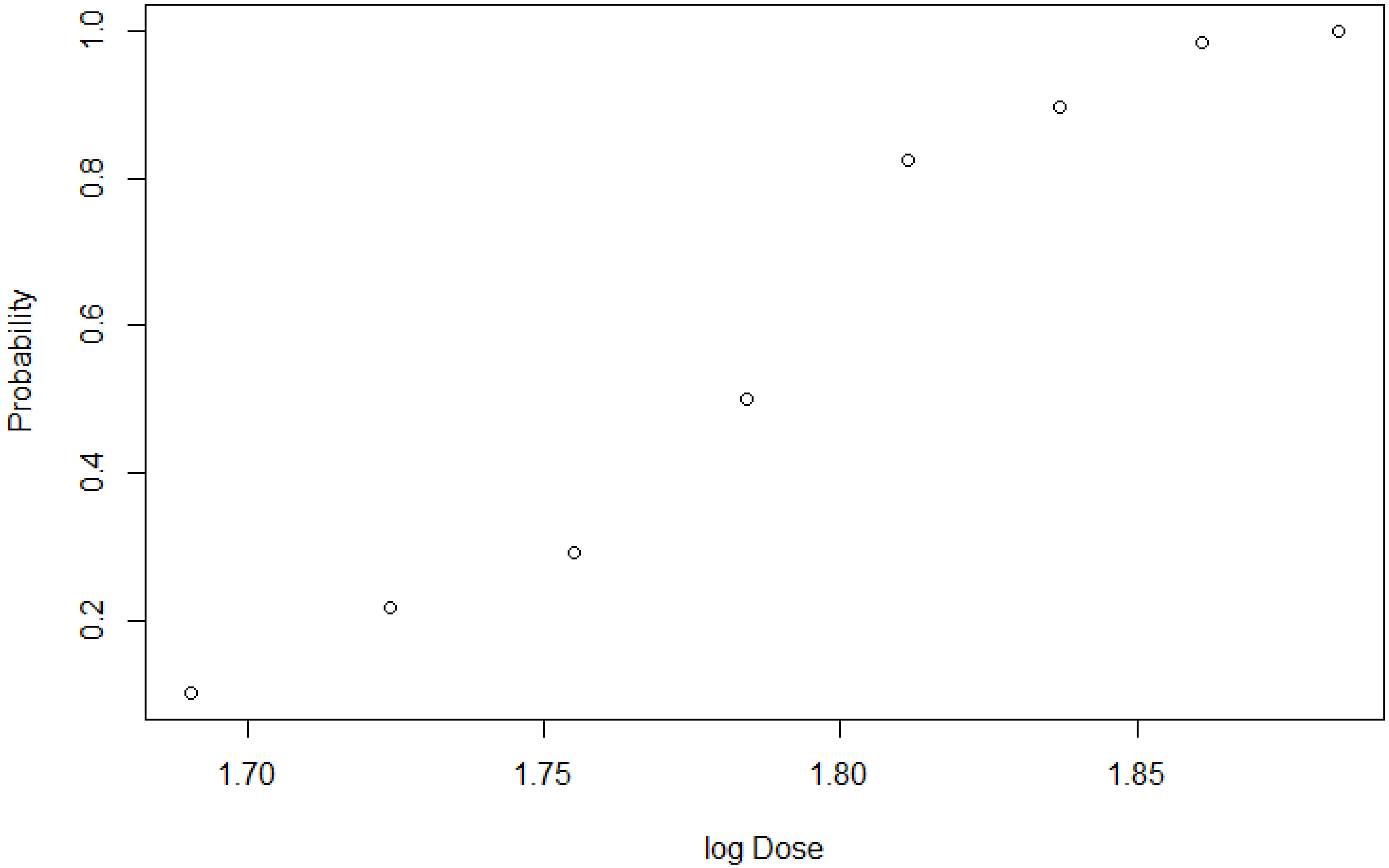
Motivating Example

- A researcher is examining beetle mortality after 5 hours of exposure to carbon disulphide, at various levels of concentration of the gas.
- Beetles were exposed to gaseous carbon disulphide at various concentrations (in mg/L) for five hours (Bliss, 1935) and the number of beetles killed were noted. The data are in the following table:

Example (continued)

```
> beetle<-read.table("BeetleData.txt",header=TRUE)
> head(beetle)
    Dose Num.Beetles Num.Killed
1 1.6907          59          6
2 1.7242          60         13
3 1.7552          62         18
4 1.7842          56         28
5 1.8113          63         52
6 1.8369          59         53

> logitmodel<-glm(cbind(Num.Killed,Num.Beetles-Num.Killed) ~ Dose, data = beetle,
        family = binomial) > summary(logitmodel)
> probitmodel<-glm(cbind(Num.Killed,Num.Beetles-Num.Killed) ~ Dose, data = beetle,
        family = binomial(link=probit))
> summary(probitmodel)
> logmodel<-glm(cbind(Num.Killed,Num.Beetles-Num.Killed) ~ Dose, data = beetle, family
        = binomial(link=cloglog))
> summary(logmodel)
```

Don’t forget to plot the data!



LOGIT MODEL:

```
Call:
glm(formula = cbind(Num.Killed, Num.Beetles - Num.Killed) ~ Dose,
    family = binomial, data = beetle)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5941  -0.3944   0.8329   1.2592   1.5940

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -60.717      5.181  -11.72   <2e-16 ***
Dose          34.270      2.912   11.77   <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: 284.202  on 7  degrees of freedom
Residual deviance:  11.232  on 6  degrees of freedom
AIC: 41.43

Number of Fisher Scoring iterations: 4
```

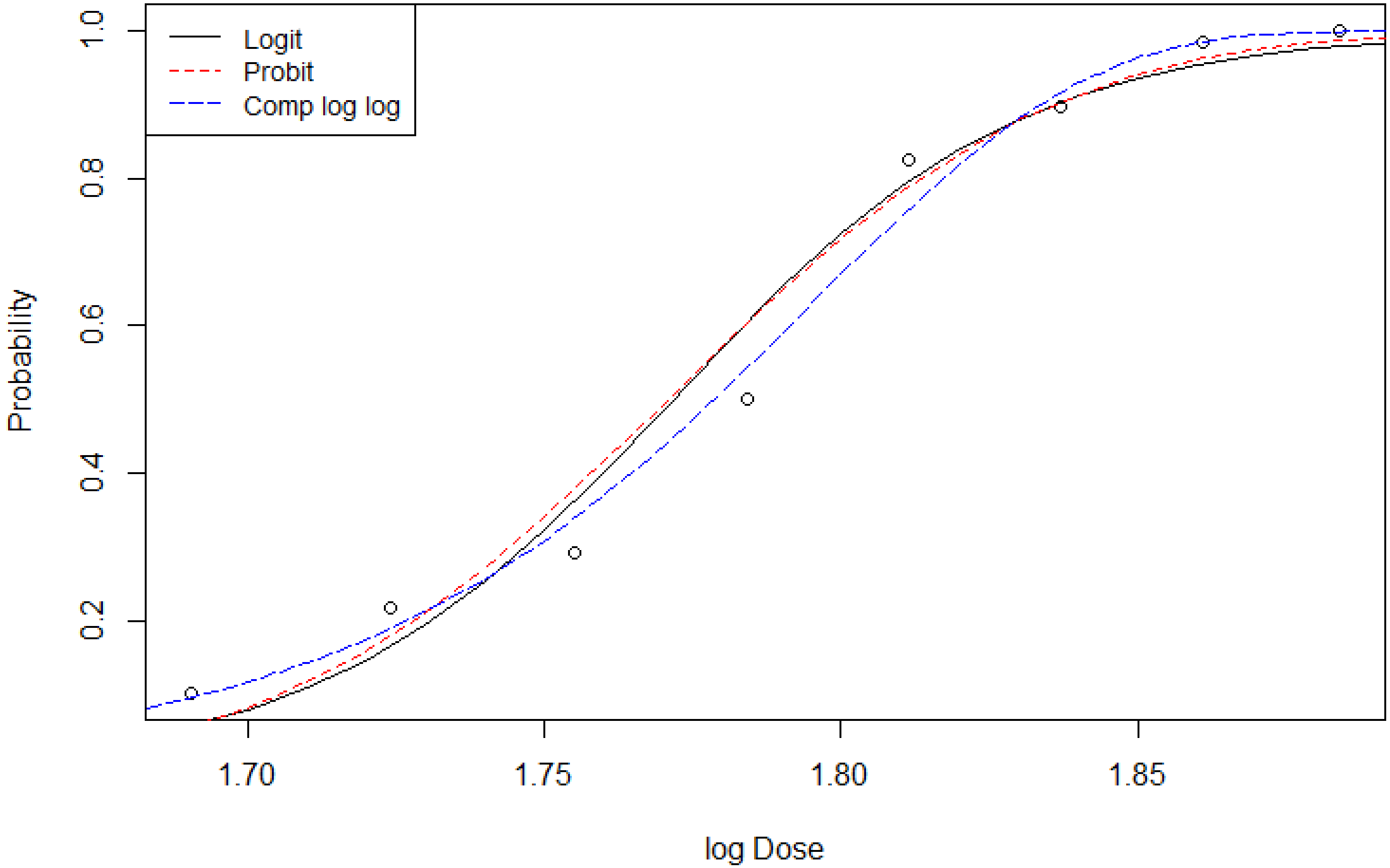
PROBIT MODEL:

```
Call:
glm(formula = cbind(Num.Killed, Num.Beetles - Num.Killed) ~ Dose,
    family = binomial(link = probit), data = beetle)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5714  -0.4703   0.7501   1.0632   1.3449

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -34.935      2.648  -13.19   <2e-16 ***
Dose          19.728      1.487   13.27   <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: 284.20  on 7  degrees of freedom
Residual deviance:  10.12  on 6  degrees of freedom
AIC: 40.318

Number of Fisher Scoring iterations: 4
```

COMPLEMENTARY LOG-LOG MODEL:

```
Call:
glm(formula = cbind(Num.Killed, Num.Beetles - Num.Killed) ~ Dose,
    family = binomial(link = cloglog), data = beetle)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.80329  -0.55135   0.03089   0.38315   1.28883

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -39.572      3.240  -12.21   <2e-16 ***
Dose          22.041      1.799   12.25   <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: 284.2024  on 7  degrees of freedom
Residual deviance:   3.4464  on 6  degrees of freedom
AIC: 33.644

Number of Fisher Scoring iterations: 4
```

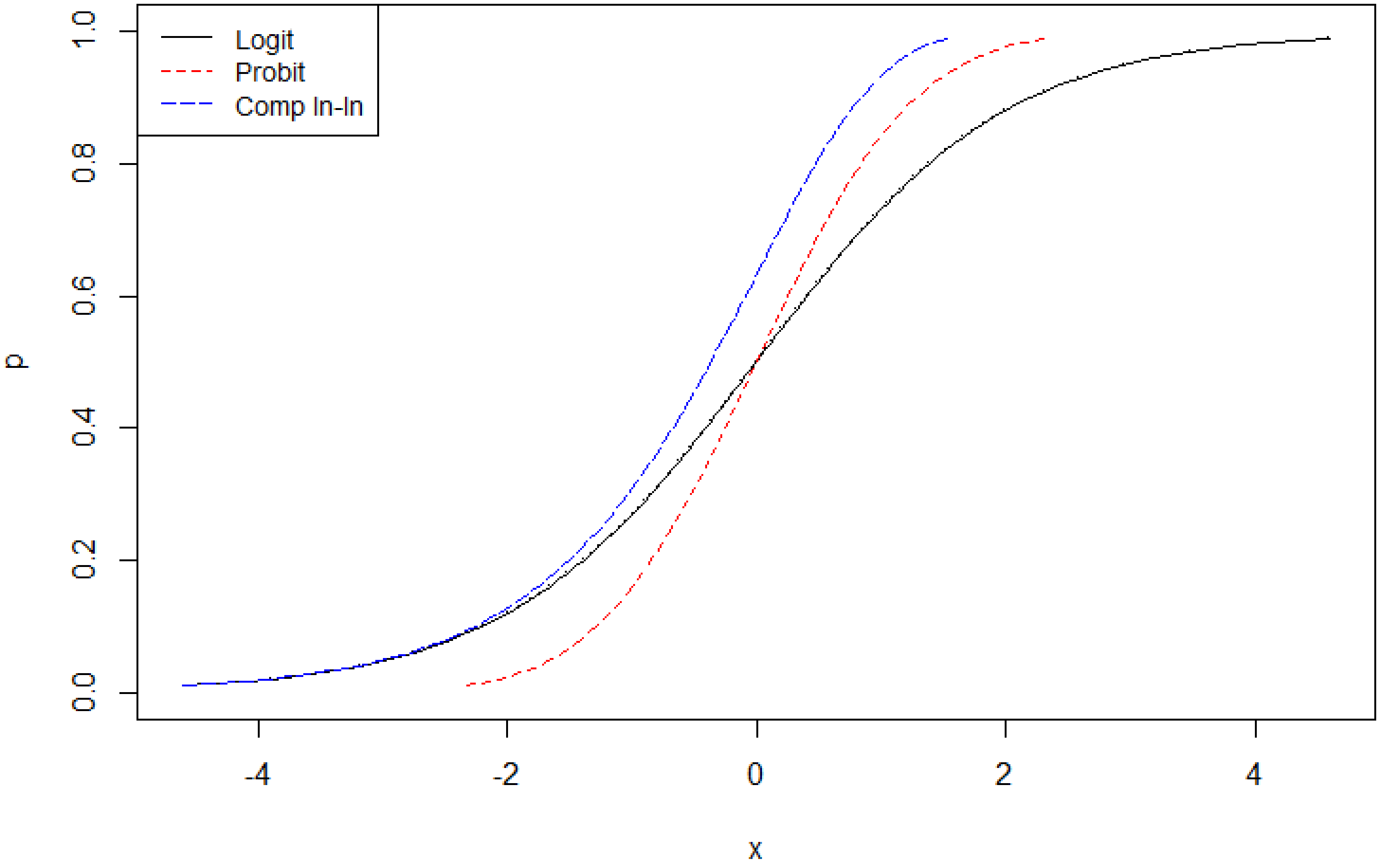
Example (continued)



Binomial Link Functions

- Differences in choice of link affect model and deviance.
- Why have 3 link functions and what about them cause these differences.
- “All models are wrong, but some are useful” – George Box

Differences in Link Functions



Differences in Link Functions

- Numerically, consider the specific value of each function corresponding to various levels of p:

p	Logit	Probit	C Log Log
0.005	-5.2933	-2.5758	-5.2958
0.5	0	0	-0.3665
0.99	4.5951	2.3263	1.5271

Deviances

$$D = 2\sum_{i=1}^{n}\left[y_i \ln\left({}^{y_i}\!\big/_{\hat{y}_i} \right) + (n_i - y_i)\ln\left({}^{n_i - y_i}\!\big/_{n_i - \hat{y}_i} \right) \right]; \hat{y}_i = n_i \hat{p}_i,$$

- Logit: $\hat{p}_i = \dfrac{e^{x_i^T \hat{\beta}}}{1 + e^{x_i^T \hat{\beta}}}$
- Probit: $\hat{p}_i = \Phi(x_i^T \hat{\beta})$
- C Log Log: $\hat{p}_i = 1 - \exp\{-\exp[x_i^T \hat{\beta}]\}$

Differences in Link Functions

```
probLowerlogit <- vector(length=1000)
probLowercloglog <-vector(length=1000)
logitDeviance <-vector(length=1000)
probitDeviance <-vector(length=1000)
cloglogDeviance <- vector(length=1000)
probLowerlogitclog <- vector(length=1000)
for(i in 1:1000){

  x <- rnorm(1000)
  y <- rbinom(n=1000, size=1, prob=pnorm(x))

  logitModel <- glm(y~x, family=binomial(link="logit"))
  probitModel <- glm(y~x, family=binomial(link="probit"))
  cloglogModel <- glm(y~x, family=binomial(link="cloglog"))

  logitDeviance[i] <- deviance(logitModel)
  probitDeviance[i] <- deviance(probitModel)
  cloglogDeviance[i] <- deviance(cloglogModel)

  probLowerlogit[i] <- probitDeviance[i] < logitDeviance[i]
  probLowercloglog[i] <- probitDeviance[i] < cloglogDeviance[i]
  probLowerlogitclog[i] <- logitDeviance[i] < cloglogDeviance[i]

}
```

Differences in Link Functions

```
>sum(probLowerlogit)/1000
[1] 0.695
> sum(probLowercloglog)/1000
[1] 0.906
>sum(probLowerlogitclog)/1000
[1] 0.877
```

Differences (last iteration):

```
> deviance(logitModel) - deviance(probitModel)
[1] 0.6076806
> deviance(cloglogModel) - deviance(probitModel)
[1] -1.152768
```

Consider the last iteration of the script:

Dev Probit	Dev Logit	Dev. cloglog
1025.759	1026.366	1024.606

Origins of the Binomial Link Functions

1. Complementary log log link (1922)

2. Probit link (1933)

3. Logit link (1944)

Complementary log-log link (1922)

- R. A. Fisher, English Statistician
- Dilution assay §12.3
- Describes an experiment where a series of dilutions were made of a soil or water sample to determine the presence or absence of some microbial contaminant.
- Used a cll transformation and applied maximum likelihood estimation.

Complementary log-log link (1922)

- Assume that dilutions are made in powers of 2, then after x dilutions the number of infective organisms, p_x, per unit volume is

$$p_x = p_0/2^x \qquad x = 0,1,\ldots$$

- where p_0 is the density of infective organisms in the original solution (we wish to estimate).
- The expected number of organisms on any plate is $p_x v$, and the actual number of organisms follows a Poisson distribution with this parameter.

Complementary log-log link (1922)

- The probability that a plate is infected is

$$\pi_x = 1 - \exp\{-p_x v\}$$

- At dilution x we have,

$$\begin{aligned}\log(-\log(1 - \pi_x)) &= \log v + \log p_x \\ &= \log v + \log p_o - x \log 2\end{aligned}$$

- If at dilution x we have *r* infected plates out of *m*, the observed proportion of infected plates is *y* = *r*/*m*, and E(Y| x) = π_x
- A complementary log-log transformation is

$$\log(-\log(1 - \pi_x)) = \alpha + \beta x$$

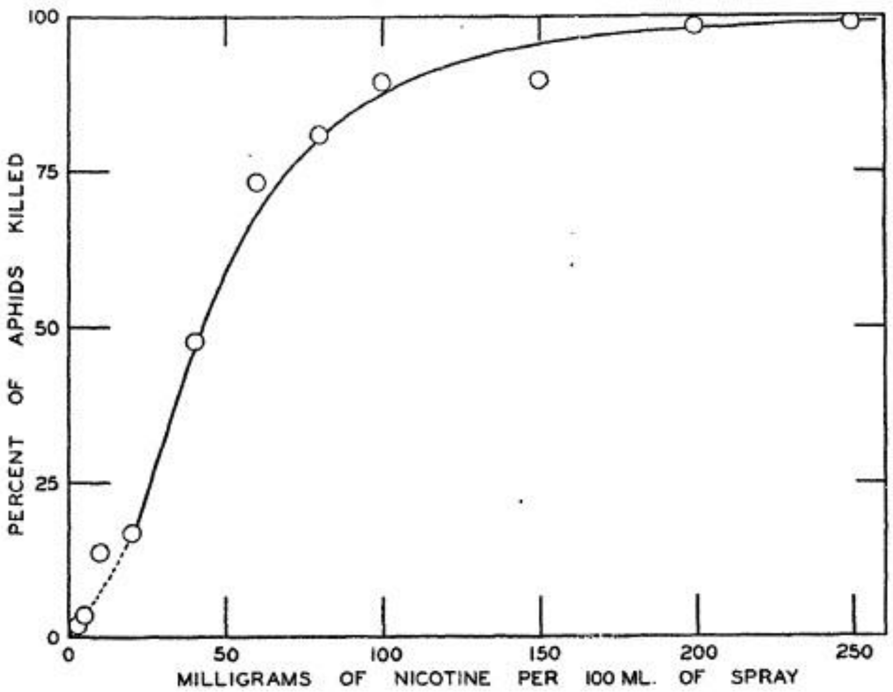
Probit link (1933/1934)

- John Gaddum was an English pharmacologist who wrote a comprehensive report on the statistical interpretation of bio-assay.

- Bliss was largely self taught, worked with Fisher, and eventually settled at Yale.
  - Published 2 brief notes in *Science* where he introduced the word ‘probit’ (probability unit).

Probit link (1933/1934)

- Bliss uses an example of the effectiveness of a pesticide to combat an insect pest.
  - Describes how a dosage-mortality curve has an asymmetrical S-shaped curve.



Probit link (1933/1934)

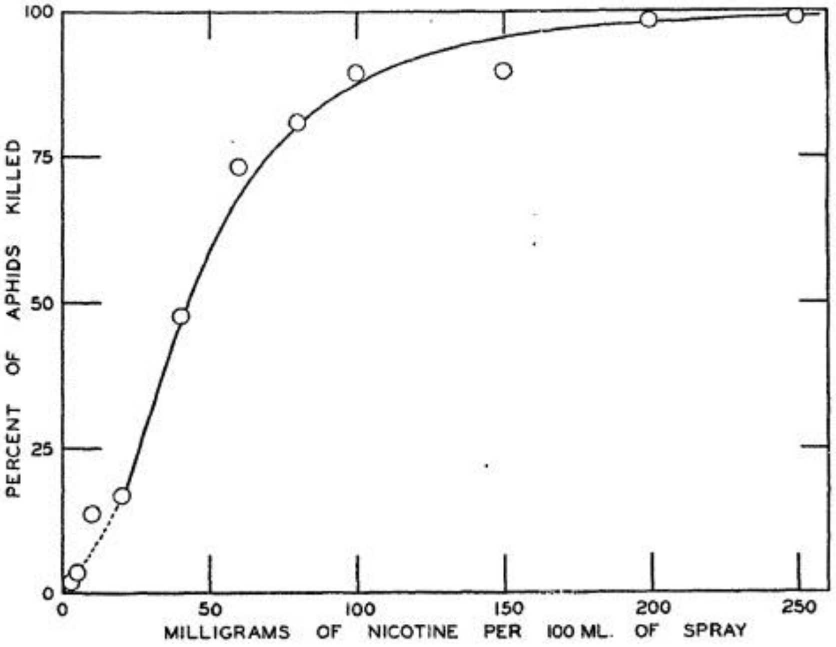
- Observation that in many physiological processes equal increments in response are produced when dose is increased by a constant proportion of the given dosage, rather than by a constant amount.

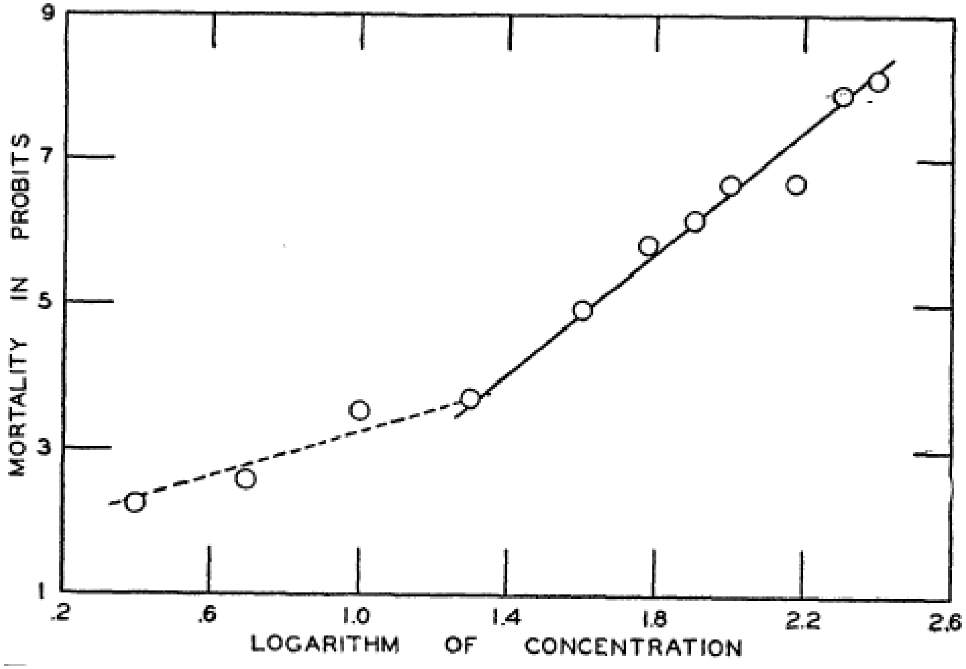
- Bliss proposed the same rule might hold for toxicological processes, in which case dosage would have to be plotted in logarithmic terms to show a uniform increase in mortality.

- Proposed to transform the percentage killed to a probit and then plot against the logarithm of the dose to achieve a straight line.

Probit link (1933/1934)

- Transformation by use of logarithms and probits.





Logit link (1944)

- Joseph Berkson was a medical doctor and chief statistician of the Mayo Clinic.
- Research was on statistical methodology of bio-assay.
- Proposed the use of the logistic instead of the normal probability function, coining the term ‘logit’ by analogy to the ‘probit’ of Bliss.

Logit link (1944)

- Berkson gives several reasons for using the logit
  - The logistic function is very close to the integrated normal curve.
  - Since it applies to a wide range of physiochemical phenomena, it may have a better theoretical basis than the integrated normal curve.
  - It is easier to handle statistically.

- Initially the logit was regarded as inferior and disreputable, since it cannot be related to an underlying normal distribution of tolerance levels.

Logit link (1944)

- By the 1960s, Berkson’s logit had gained acceptance.

- The power of the logistic’s analytical properties were starting to surface.

- By the 1970s, the logit takes the lead because it was now widely used among many disciplines.

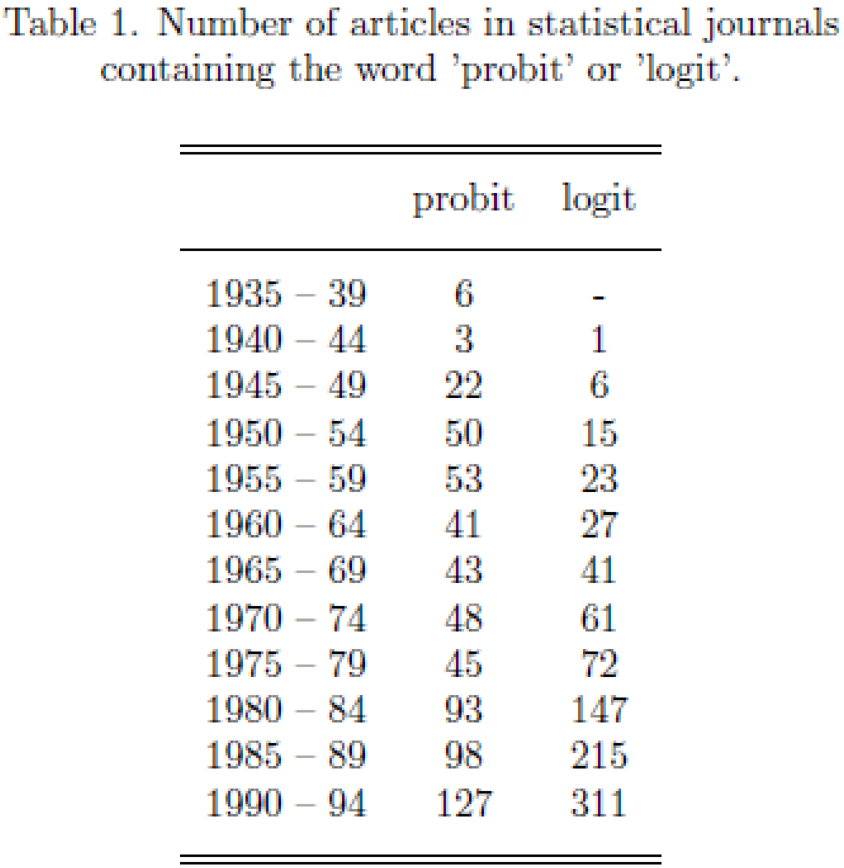


Table 1. Number of articles in statistical journals containing the word 'probit' or 'logit'.

	probit	logit
1935 – 39	6	-
1940 – 44	3	1
1945 – 49	22	6
1950 – 54	50	15
1955 – 59	53	23
1960 – 64	41	27
1965 – 69	43	41
1970 – 74	48	61
1975 – 79	45	72
1980 – 84	93	147
1985 – 89	98	215
1990 – 94	127	311

Logit is Considered the Default Link

- Advantages of Logit link function:
  - Leads to simpler mathematics due to complexity of the standard normal CDF
  - It is easier to interpret (Log odds)

Final Remarks

- If the logit link is considered the default link, why do we still use probit and Complementary log log?
  - Theoretical Considerations
  - Influences by disciplinary tradition
    - Economists favour probit models
    - Toxicologists favour logit models
  - Underlying characteristics of the data
    - Complementary log log works best with extremely skewed distributions

References

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Bliss, C. I. (1934). The Method of Probits. *Science* **79:** 38-39.

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Fitzmaurice, Laird and Ware. (2004). *Applied Longitudinal Analysis.* John Wiley & Sons: New Jersey.

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