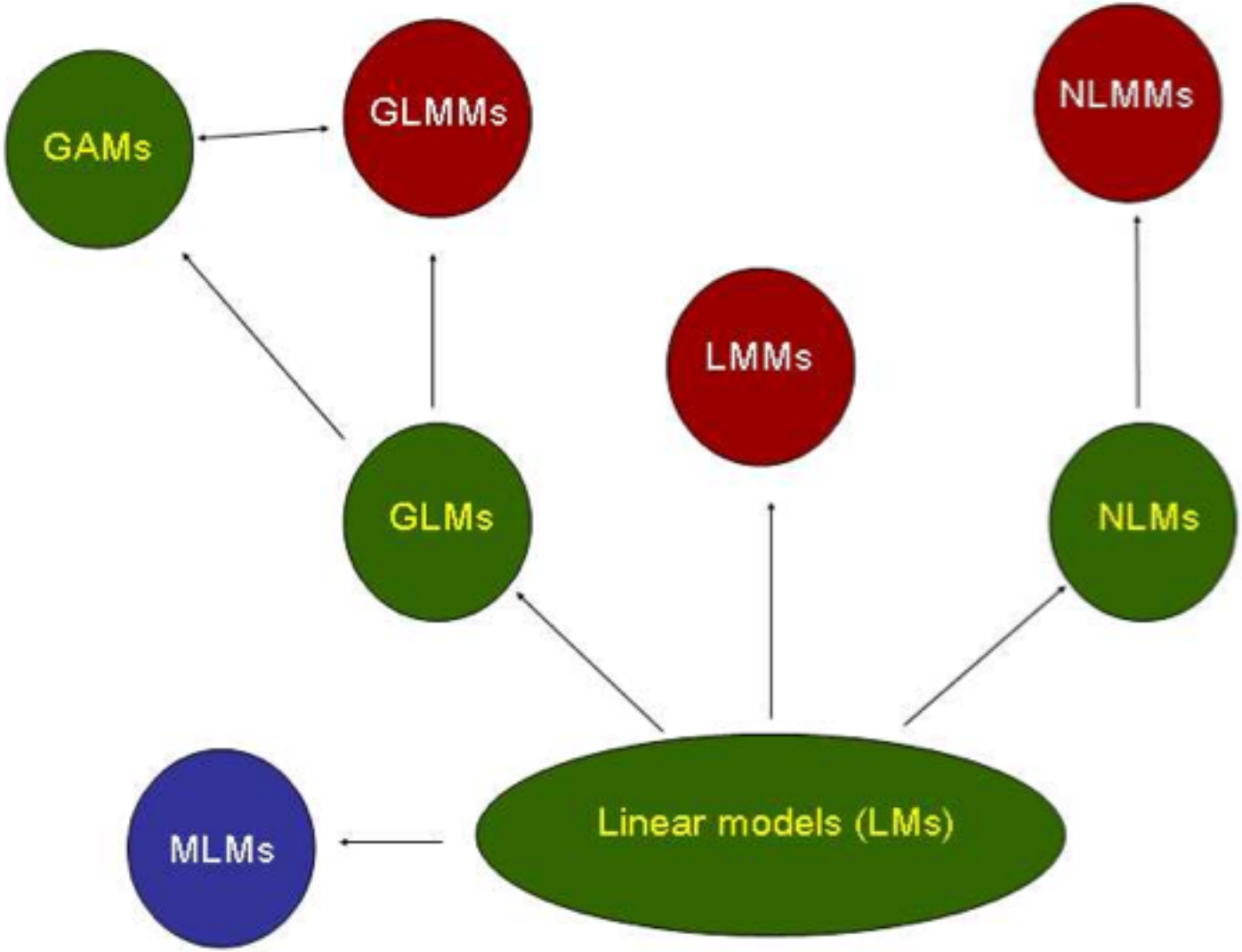
Generalized Linear Models

based on Zuur et al.

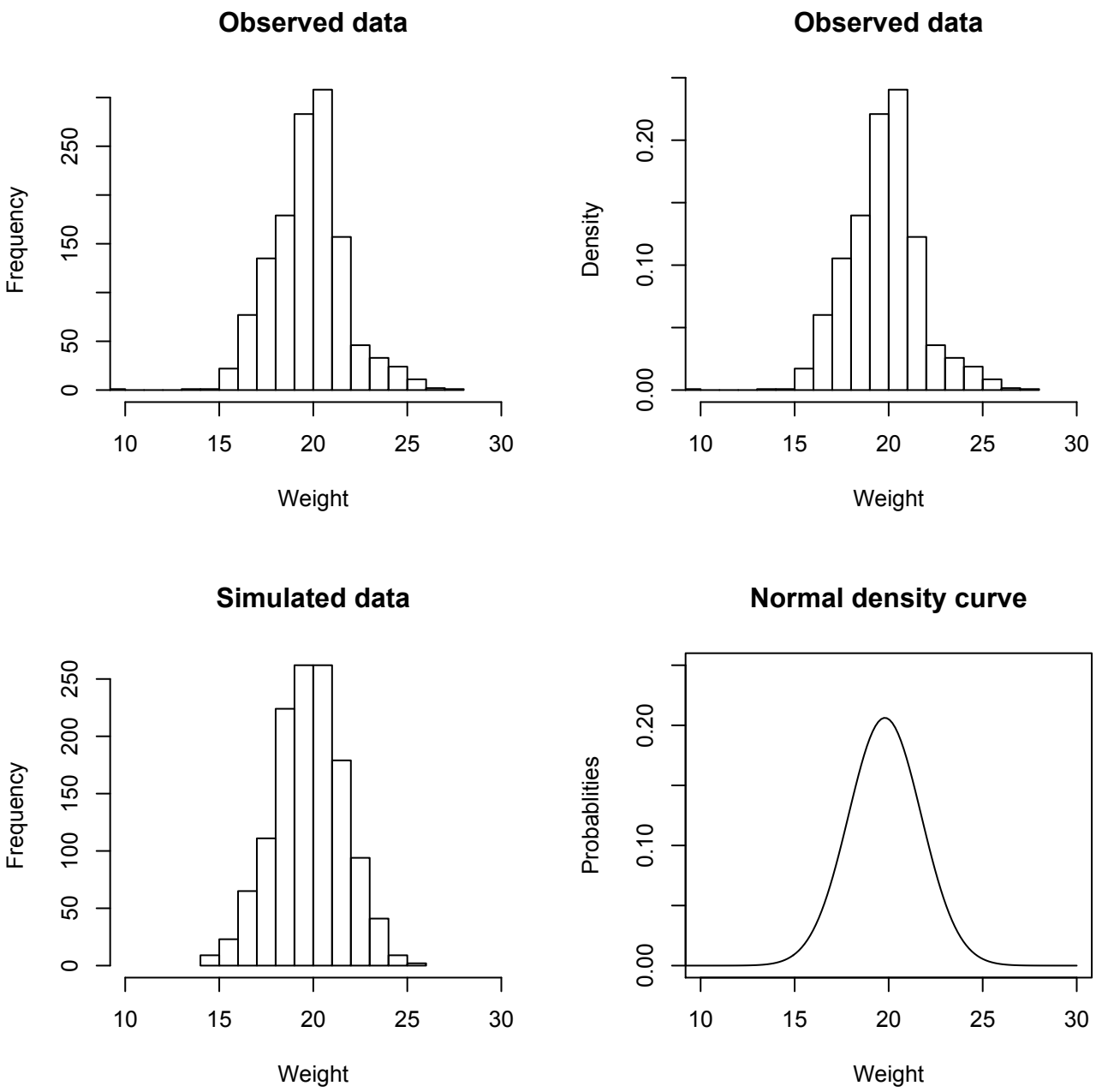


Kuhnert and Venables

Normal Distribution example: weights of 1280 sparrows

```
Sparrows<-read.table("/Users/dbm/Documents/W2025/ZuurDataMixedModelling/
Sparrows.txt",header=TRUE)
par(mfrow = c(2, 2))
hist(Sparrows$wt, nclass = 15, xlab = "Weight", main = "Observed data",xlim=c(10,30))
hist(Sparrows$wt, nclass = 15, xlab = "Weight", main = "Observed data", freq =
FALSE,xlim=c(10,30))
Y <- rnorm(1281, mean = mean(Sparrows$wt), sd = sd(Sparrows$wt))
hist(Y, nclass = 15, main = "Simulated data",xlab = "Weight",xlim=c(10,30))

X <-seq(from = 0,to = 30,length = 200)
Y <- dnorm(X, mean = mean(Sparrows$wt), sd = sd(Sparrows$wt))
plot(X, Y, type = "l", xlab = "Weight", ylab = "Probablities", ylim = c(0, 0.25), xlim = c(10, 30),
main = "Normal density curve")
par(mfrow = c(1, 1))
```


Observed data
Frequency
0
50
150
250
10
15
20
25
30
Weight
Observed data
Density
0.00
0.10
0.20
10
15
20
25
30
Weight
Simulated data
Frequency
0
50
100
150
200
250
10
15
20
25
30
Weight
Normal density curve
Probablities
0.00
0.10
0.20
10
15
20
25
30
Weight

$$f(y_i;\mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{(y_i-\mu)^2}{2\sigma^2}}$$

$$E(Y) = \mu \qquad \text{and} \qquad \text{var}(Y) = \sigma^2$$

Poisson Distribution

$$f(y;\mu) = \frac{\mu^y \times e^{-\mu}}{y!} \qquad y \geq 0,\ y \text{ intger}$$

$$E(Y) = \mu \qquad \text{and} \qquad \text{var}(Y) = \mu$$

In practice the variance is often bigger than the mean -> overdispersion

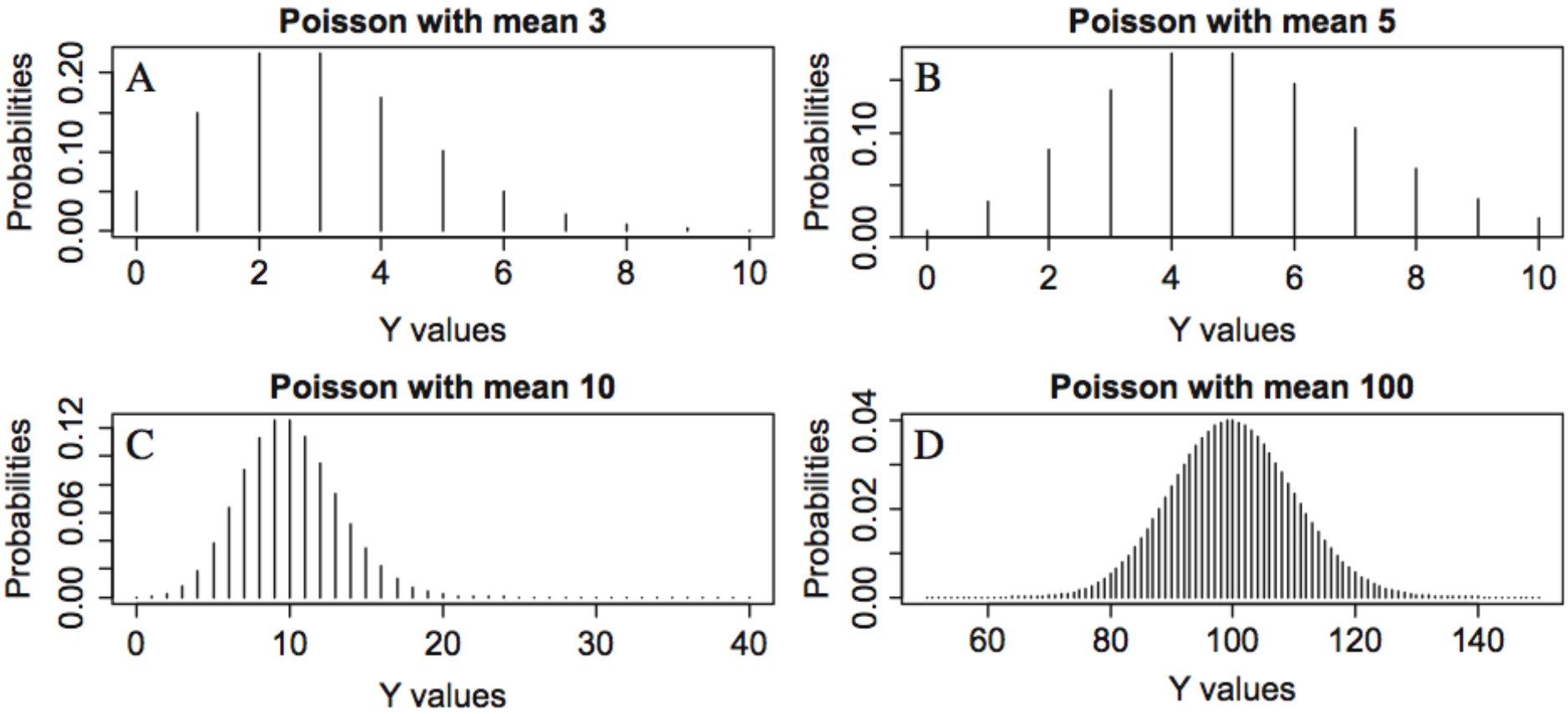


Fig. 8.2 Poisson probabilities for $\mu = 3$ (**A**), $\mu = 5$ (**B**), $\mu = 10$ (**C**), and $\mu = 100$ (**D**). Equation (8.3) is used to calculate the probabilities for certain values. Because the outcome variable y is a count, vertical lines are used instead of a line connecting all the points

Gamma Distribution

$$f(y;\mu,\nu) = \frac{1}{\Gamma(\nu)} \times \left(\frac{\nu}{\mu}\right)^{\nu} \times y^{\nu-1} \times e^{\frac{y\times\nu}{\mu}} \qquad y > 0$$

$$E(Y) = \mu \qquad \text{and} \qquad \text{var}(Y) = \frac{\mu^2}{\nu}$$

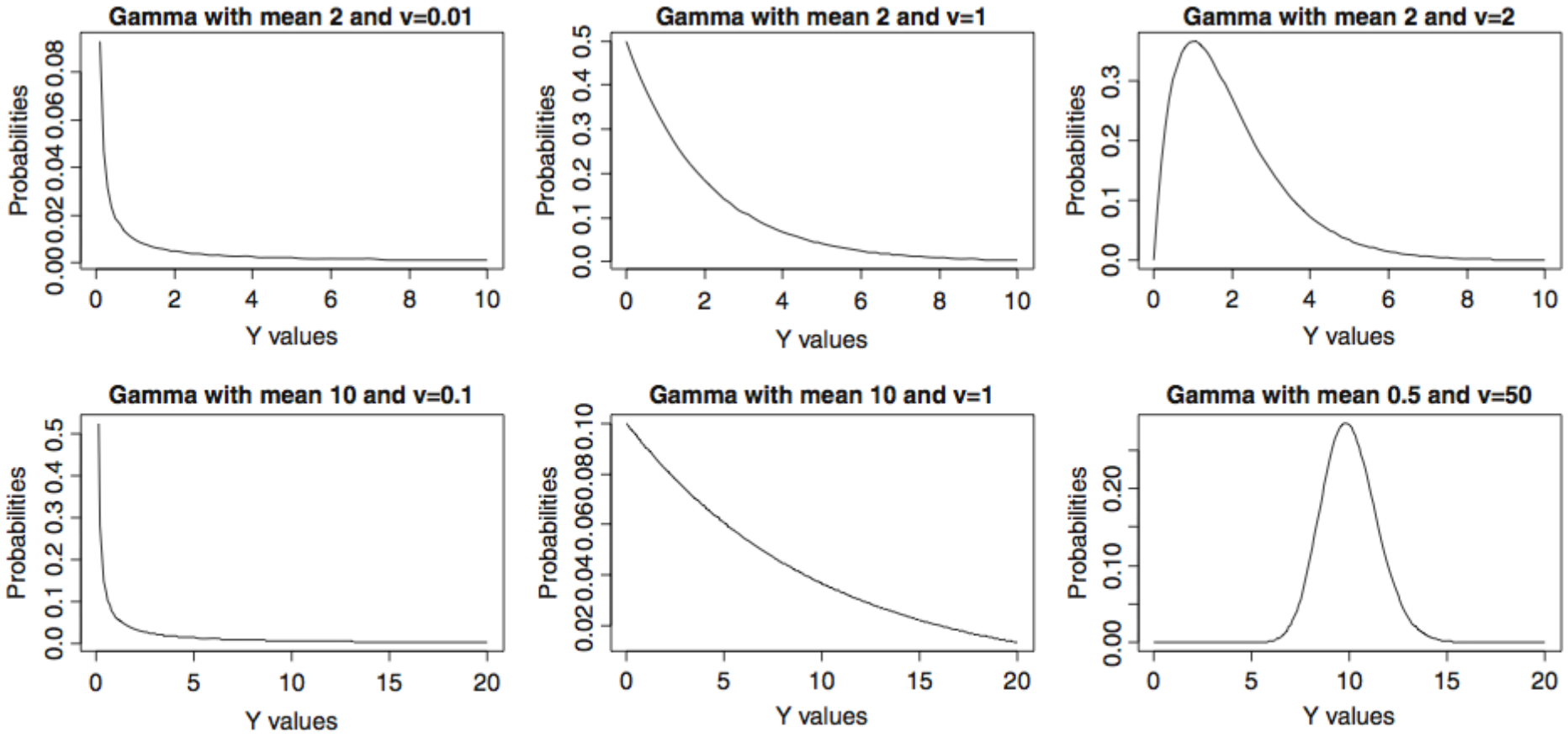


Fig. 8.4 Gamma distributions for different values of μ and v. The R function `dgamma` was applied, which uses a slightly different parameterisation: $\mathrm{E}(Y) = a \times s$ and $\mathrm{var}(Y) = a \times s^2$, where a is called the shape and s the scale. In our parameterisation, $v = a$ and $\mu = a \times s$

Binomial Distribution

$$f(y;\pi) = \binom{N}{y} \times \pi^{y} \times (1-\pi)^{N-y}$$

$$E(Y) = N \times \pi \qquad \text{var}(Y) = N \times \pi \times (1-\pi)$$

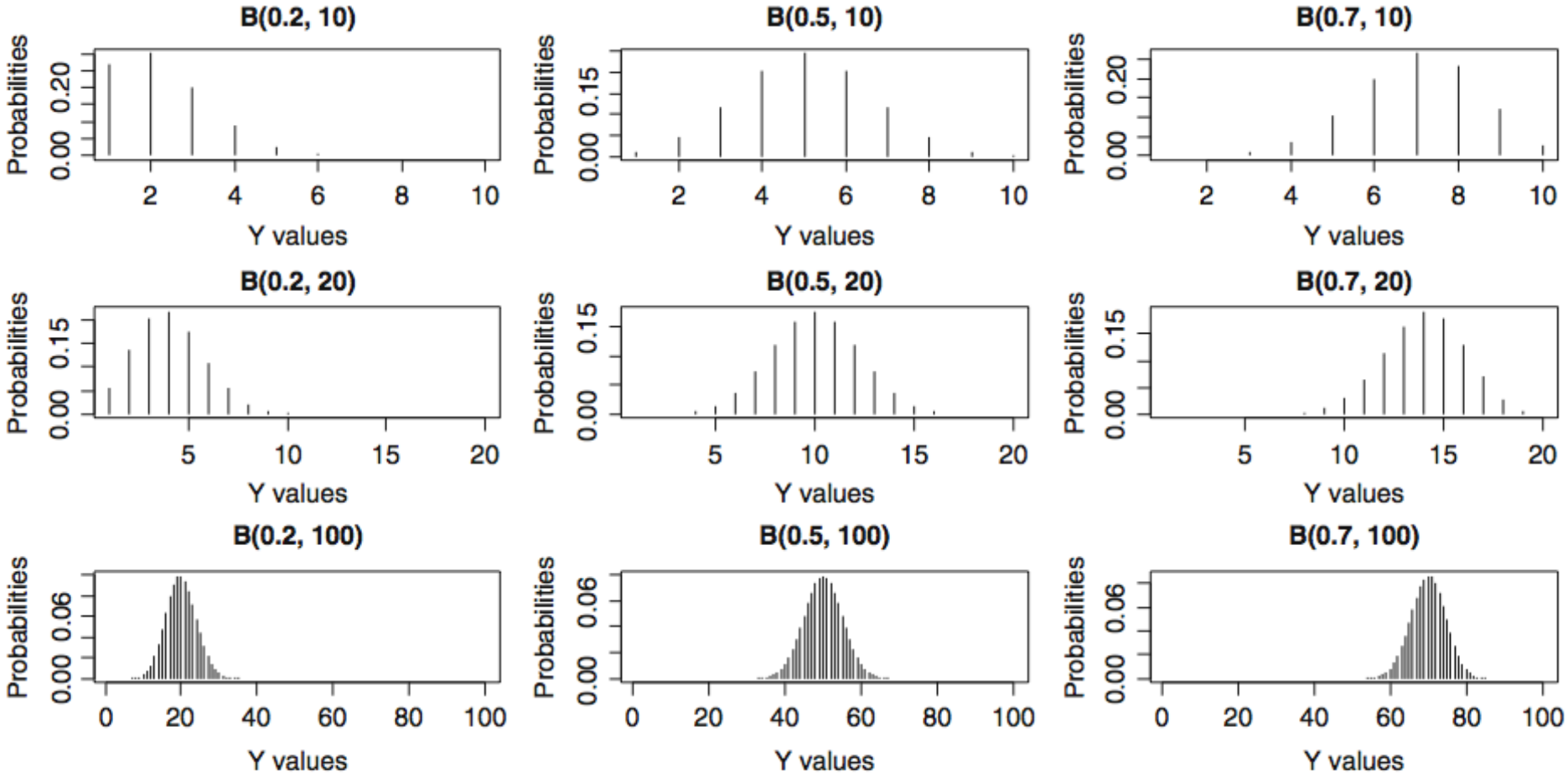


Fig. 8.5 Binomial density curves B(π, N) for various values of π (namely 0.2, 0.5, and 0.7) and N (namely 10, 20, and 100). R code to create this graph is on the book website

Natural Exponential Family

$$f(y;\theta,\phi) = e^{\frac{y\times\theta - b(\theta)}{a(\phi)} + c(y,\theta)}$$

$$E(Y) = b'(\theta)$$
$$\text{var}(Y) = b''(\theta) \times a(\phi)$$

to get, e.g., Poisson:

$$\theta = \log(\mu),\ \phi = 1,\ a(\phi) = 1,\ b(\theta) = \exp(\theta),\ c(y,\phi) = -\log(y!)$$

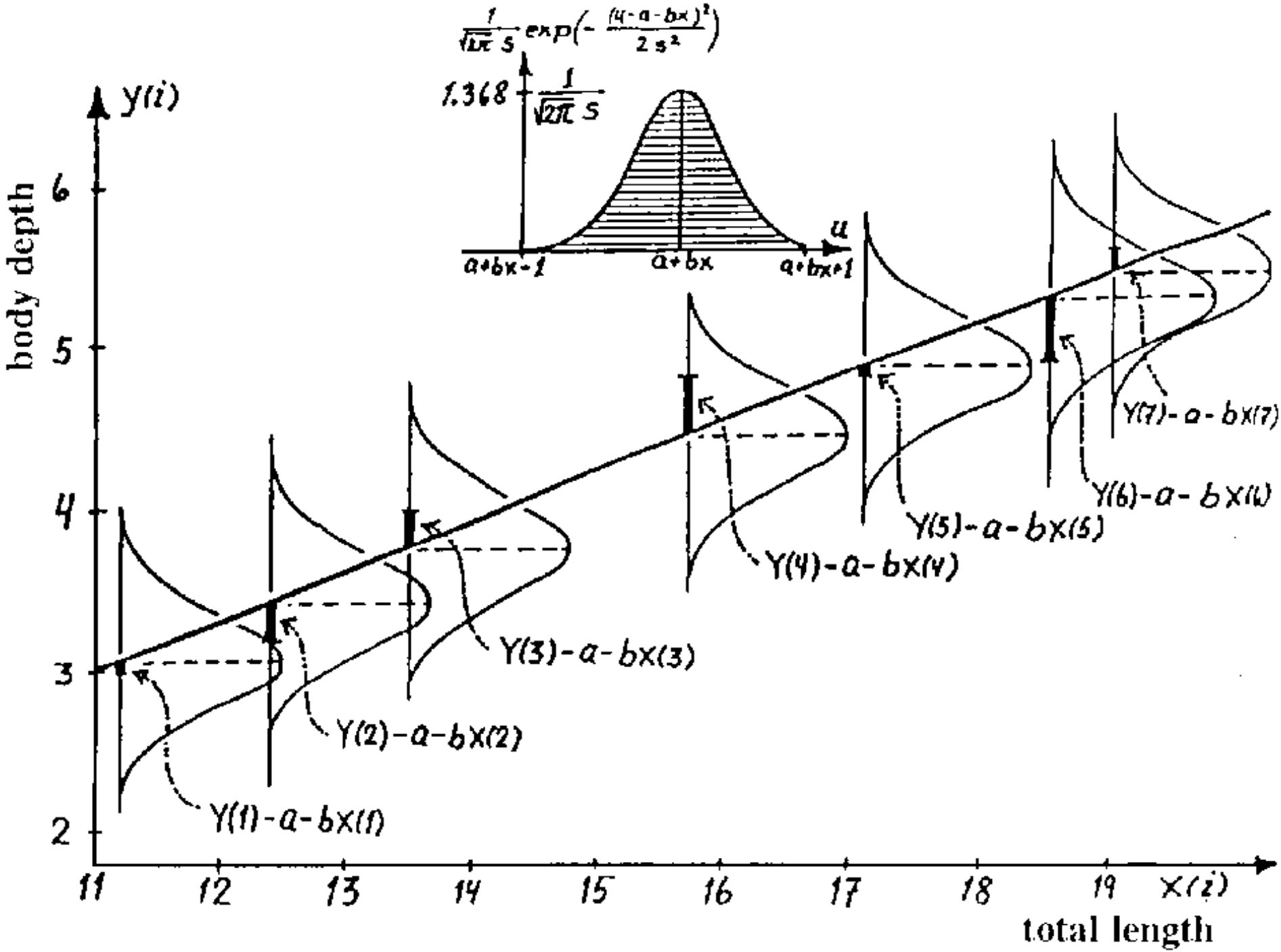
Table 8.1 List of distributions for the response variable. Density means numbers per Area (or volume, range, etc), and in this case the offset option is needed in the Poisson or NB GLM

Distribution	Type of data	Mean – variance relationship
Normal	Continuous	Equation (8.2)
Poisson	Counts (integers) and density	Equation (8.4)
Negative binomial	Overdispersed counts and density	Equation (8.7)
Geometric	Overdispersed counts and density	Equation (8.8)
Gamma	Continuous	Equation (8.10)
Binomial	Proportional data	Equation (8.12)
Bernoulli	Presence absence data	Equation (8.12) with $N = 1$

Generalized Linear Models

A GLM consists of three steps:

1. An assumption on the distribution of the response variable Y_i. This also defines the mean and variance of Y_i.
2. Specification of the systematic part. This is a function of the explanatory variables.
3. The relationship between the mean value of Y_i and the systematic part. This is also called the link between the mean and the systematic part.


$\frac{1}{\sqrt{2\pi}\,s}\exp\left(-\frac{(u-a-bx)^2}{2s^2}\right)$
1.368 $\frac{1}{\sqrt{2\pi}\,s}$
u
a+bx-1
a+bx
a+bx+1
Y(i)
body depth
6
5
4
3
2
11
12
13
14
15
16
17
18
19
X(i)
total length
Y(1)-a-bX(1)
Y(2)-a-bX(2)
Y(3)-a-bX(3)
Y(4)-a-bX(4)
Y(5)-a-bX(5)
Y(6)-a-bX(6)
Y(7)-a-bX(7)

Step 1: In a Gaussian linear regression, we assume that the response variable Y_i is normally distributed with mean μ_i and variance σ^2. The index i refers to a case or observation.

Step 2: In the second step, we specify the systematic part of the model. This means that we need to select the explanatory variables. Define the predictor function $\eta(X_{i1}, \ldots, X_{iq})$ by:

$$\eta(X_{i1}, \ldots, X_{iq}) = \alpha + \beta_1 \times X_{i1} + \cdots + \beta_q \times X_{iq} \tag{9.1}$$

The systematic part is given by the predictor function $\eta(X_{i1}, \ldots, X_{iq})$.

Step 3: In the third step, we need to specify the link between the expected value of Y_i (which is μ_i) and the predictor function $\eta(X_{i1}, \ldots, X_{iq})$. We use the identity link, which means that $\mu_i = \eta(X_{i1}, \ldots, X_{iq})$.

These three steps give the following GLM:

$$\begin{aligned} Y_i &\sim N(\mu_i, \sigma^2) \\ E(Y_i) &= \mu_i \quad \text{and} \quad \text{var}(Y_i) = \sigma^2 \\ \mu_i &= \eta(X_{i1}, \cdots, X_{iq}) \end{aligned} \tag{9.2}$$

Generalized Linear Models: Poisson regression

1. Y_i is Poisson distributed with mean μ_i. By definition of this distribution, the variance of Y_i is also equal to μ_i.
2. The systematic part is given by $\eta(X_{i1}, \ldots, X_{iq}) = \alpha + \beta_1 \times X_{i1} + \cdots + \beta_q \times X_{iq}$.
3. There is a logarithmic link between the mean of Y_i and the predictor function $\eta(X_{i1}, \ldots, X_{iq})$. The logarithmic link (also called a log link) ensures that the fitted values are always non-negative.

$$Y_i \sim P(\mu_i)$$

$$E(Y_i) = \mu_i \quad \text{and} \quad \text{var}(Y_i) = \mu_i$$

$$\log(\mu_i) = \eta(X_{i1}, \cdots, X_{iq}) \quad \text{or} \quad \mu_i = e^{\eta(X_{i1} \cdots, X_{iq})}$$

```
x <- 0:100
y <- rpois(101,exp(0.01+0.03*x))
MyData <- data.frame(x,y)
MyModel <- glm(y~x,data=MyData,family=poisson)
summary(MyModel)
coefs <- coef(MyModel)
plot(y~x,MyData,ylim=c(0,26))
par(new=TRUE)
plot(x,exp(0.01+0.03*x),ylim=c(0,26),type="l")
par(new=TRUE)
plot(x,exp(coefs[1]+coefs[2]*x),ylim=c(0,26),type="l",col="red")
```

Estimates parameters by maximizing the likelihood:

$$L = \prod_i \frac{\mu_i \times e^{-\mu_i}}{y_i!}, \qquad \mu_i = \exp(\beta_0 + \beta_1 x_1 + \ldots + \beta_d x_d)$$

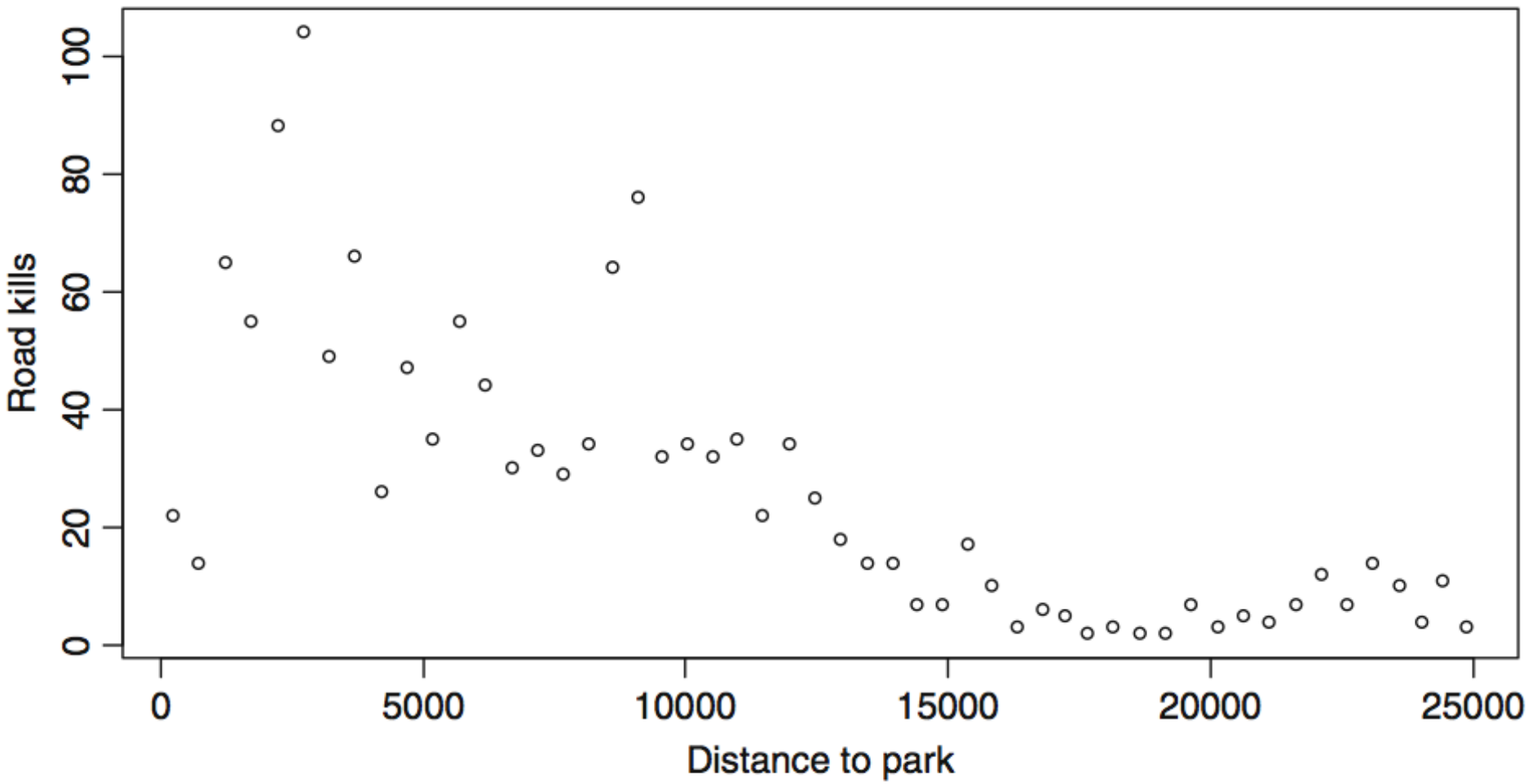


Fig. 9.3 Scatterplot of amphibian road kills versus distance (in metres) to a nearby Natural Park

1. Y_i, the number of killed animals at site i, is Poisson distributed with mean μ_i.
2. The systematic part is given by $\eta(D.PARK_i) = \alpha + \beta \times D.PARK_i$.
3. There is a logarithm link between the mean of Y_i and the predictor function $\eta(D.PARK_i)$.

As a result of these three steps, we have

$$
\begin{aligned}
&Y_i \sim p(\mu_i) \\
&E(Y_i) = \mu_i \quad \text{and} \quad \text{var}(Y_i) = \mu_i \\
&\log(\mu_i) = \alpha + \beta \times D.PARK_i \quad \text{or} \quad \mu_i = e^{\alpha+\beta\times D.PARK_i}
\end{aligned}
\tag{9.6}
$$

```
RoadKills <- read.table("/Users/dbm/Documents/W2025/
ZuurDataMixedModelling/RoadKills.txt",header=TRUE)
RK <- RoadKills #Saves some space in the code
plot(RK$D.PARK, RK$TOT.N, xlab = "Distance to park", ylab = "Road kills")
M1 <- glm(TOT.N ~ D.PARK, family=poisson, data=RK)
summary(M1)



M2 <- glm(TOT.N ~ D.PARK, family=gaussian, data=RK)
summary(M2)
```

```
Call:
glm(formula = TOT.N ~ D.PARK, family = poisson, data = RK)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-8.1100  -1.6950  -0.4708   1.4206   7.3337

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  4.316e+00  4.322e-02   99.87   <2e-16 ***
D.PARK      -1.059e-04  4.387e-06  -24.13   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1071.4  on 51  degrees of freedom
Residual deviance:  390.9  on 50  degrees of freedom
AIC: 634.29

Number of Fisher Scoring iterations: 4
```

Residual Deviance:

Difference in G^2 = -2 *log* L between a maximal model where every observation has Poisson parameter equal to the observed value and your model

Null Deviance:

Difference in G^2 = -2 *log* L between a maximal model where every observation has Poisson parameter equal to the observed value and the model with just an intercept

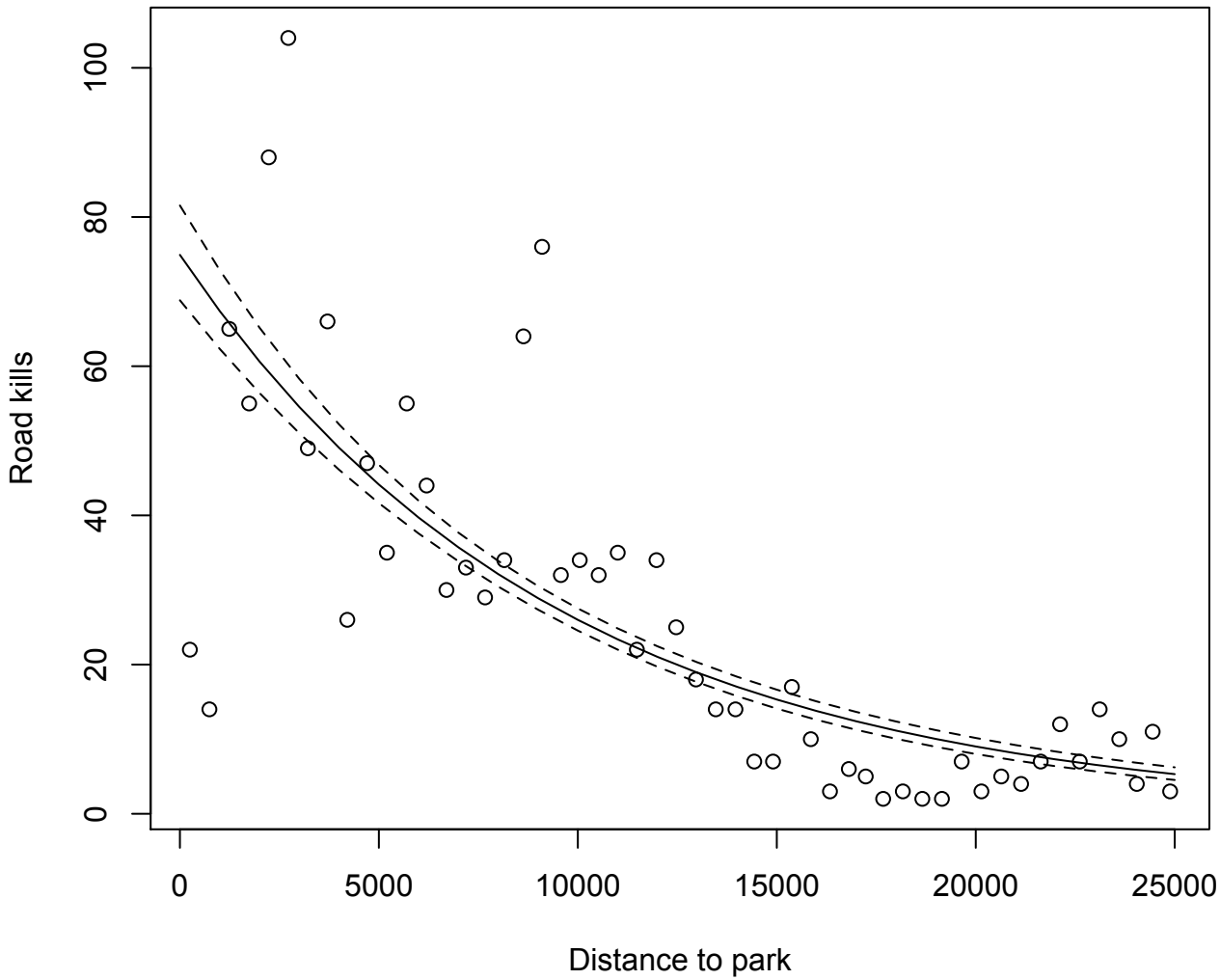
Sometimes useful to compare residual deviances for two models. Differences are chi-square distributed with degrees of freedom equal to the change in the number of parameters

We do not have an R^2 in GLM models, but the closest we can get is the explained deviance, which is calculated as

$$100 \times \frac{\text{null deviance} - \text{residual deviance}}{\text{null deviance}} = 100 \times \frac{1071.4 - 390.9}{1071.4} = 63.51\%$$

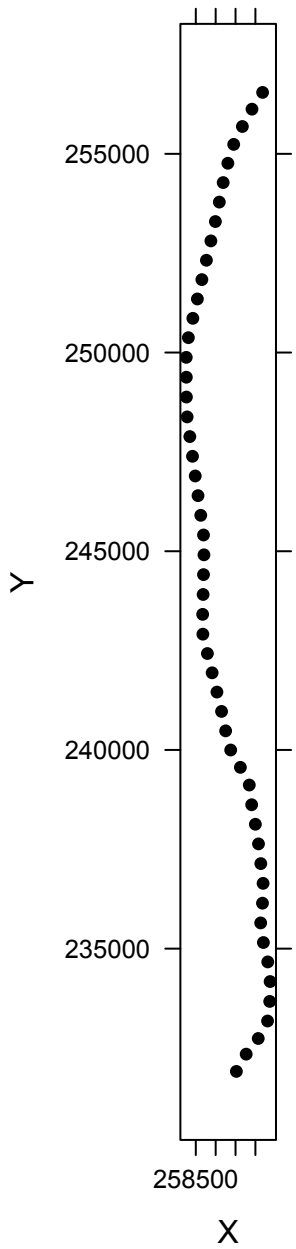
So the explanatory variable distance to the park explains 63.51% of the variation in road kills. Dobson (2002) called this proportional increase in explained deviance the pseudo R^2.

```
MyData <- data.frame(D.PARK = seq(from = 0, to = 25000, by = 1000))
G <- predict(M1, newdata = MyData, type = "link", se = TRUE)
F <- exp(G$fit)
FSEUP <- exp(G$fit + 1.96 * G$se.fit)
FSELOW <- exp(G$fit - 1.96 * G$se.fit)
lines(MyData$D.PARK, F, lty = 1)
lines(MyData$D.PARK, FSEUP, lty = 2)
lines(MyData$D.PARK, FSELOW, lty = 2)
```

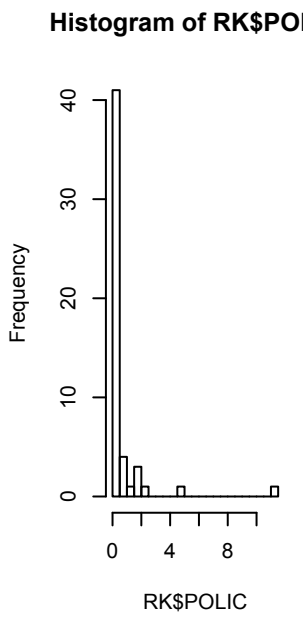

Road kills
0
20
40
60
80
100
0
5000
10000
15000
20000
25000
Distance to park

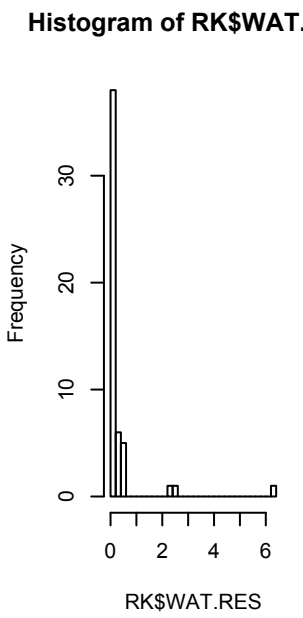
Model Selection in Generalized Linear Models

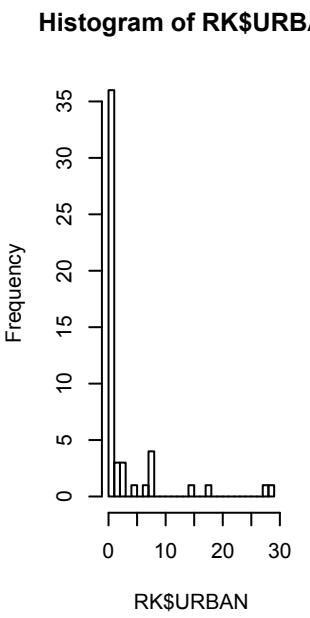
Variable	Abbreviation
Open lands (ha)	OPEN.L
Olive grooves (ha)	OLIVE
Montado with shrubs (ha)	MONT.S
Montado without shrubs (ha)	MONT
Policulture (ha)	POLIC
Shrubs (ha)	SHRUB
Urban (ha)	URBAN
Water reservoirs (ha)	WAT.RES
Length of water courses (km)	L.WAT.C
Dirty road length (m)	L.D.ROAD
Paved road length (km)	L.P.ROAD
Distance to water reservoirs	D.WAT.RES
Distance to water courses	D.WAT.COUR
Distance to Natural Park (m)	D.PARK
Number of habitat Patches	N.PATCH
Edges perimeter	P.EDGE
Landscape Shannon diversity index	L.SDI

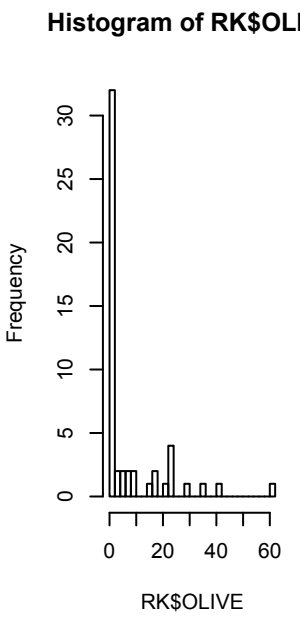


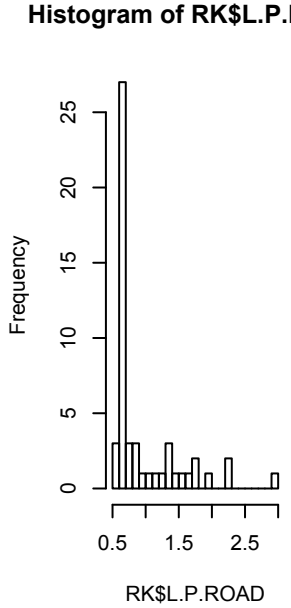

```
library(AED)
library(lattice)
xyplot(Y ~ X, aspect = "iso", col = 1, pch = 16, data = RoadKills)
```

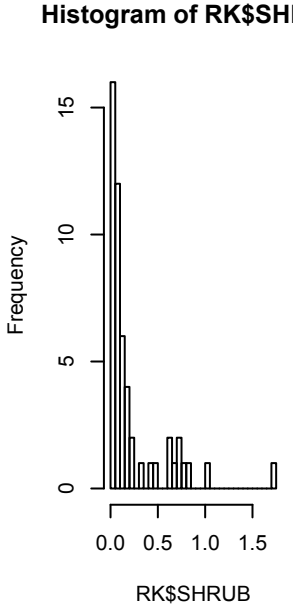

Histogram of RK$POLIC
Frequency
0
10
20
30
40
0
4
8
RK$POLIC

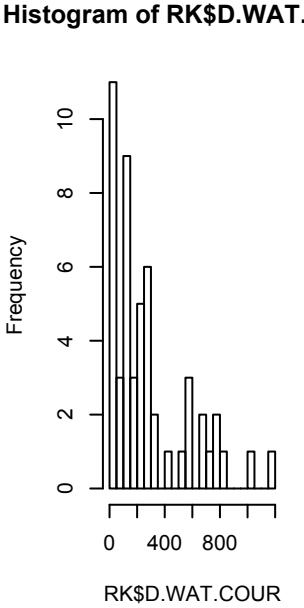

Histogram of RK$WAT.RE
Frequency
0
10
20
30
0
2
4
6
RK$WAT.RES


Histogram of RK$URBAN
Frequency
0
5
10
15
20
25
30
35
0
10
20
30
RK$URBAN


Histogram of RK$OLIVE
Frequency
0
5
10
15
20
25
30
0
20
40
60
RK$OLIVE


Histogram of RK$L.P.ROA
Frequency
0
5
10
15
20
25
0.5
1.5
2.5
RK$L.P.ROAD


Histogram of RK$SHRUB
Frequency
0
5
10
15
0.0
0.5
1.0
1.5
RK$SHRUB


Histogram of RK$D.WAT.CO
Frequency
0
2
4
6
8
10
0
400
800
RK$D.WAT.COUR

```
> RK$SQ.POLIC    <- sqrt(RK$POLIC)
> RK$SQ.WATRES   <- sqrt(RK$WAT.RES)
> RK$SQ.URBAN    <- sqrt(RK$URBAN)
> RK$SQ.OLIVE    <- sqrt(RK$OLIVE)
> RK$SQ.LPROAD   <- sqrt(RK$L.P.ROAD)
> RK$SQ.SHRUB    <- sqrt(RK$SHRUB)
> RK$SQ.DWATCOUR <- sqrt(RK$D.WAT.COUR)
> M2 <- glm(TOT.N ~ OPEN.L + MONT.S + SQ.POLIC +
            D.PARK + SQ.SHRUB + SQ.WATRES + L.WAT.C +
            SQ.LPROAD + SQ.DWATCOUR, family = poisson,
            data = RK)
> summary(M2)
```

```
> summary(M2)

Call:
glm(formula = TOT.N ~ OPEN.L + MONT.S + SQ.POLIC + D.PARK + SQ.SHRUB +
    SQ.WATRES + L.WAT.C + SQ.LPROAD + SQ.DWATCOUR, family = poisson,
    data = RK)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-6.8398  -1.3965  -0.1409   1.4641   4.3749

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.749e+00  1.567e-01  23.935  < 2e-16 ***
OPEN.L      -3.025e-03  1.580e-03  -1.915 0.055531 .
MONT.S       8.697e-02  1.359e-02   6.398 1.57e-10 ***
SQ.POLIC    -1.787e-01  4.676e-02  -3.822 0.000133 ***
D.PARK      -1.301e-04  5.936e-06 -21.923  < 2e-16 ***
SQ.SHRUB    -6.112e-01  1.176e-01  -5.197 2.02e-07 ***
SQ.WATRES    2.243e-01  7.050e-02   3.181 0.001468 **
L.WAT.C      3.355e-01  4.127e-02   8.128 4.36e-16 ***
SQ.LPROAD    4.517e-01  1.348e-01   3.351 0.000804 ***
SQ.DWATCOUR  7.355e-03  4.879e-03   1.508 0.131629
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1071.44  on 51  degrees of freedom
Residual deviance:  270.23  on 42  degrees of freedom
AIC: 529.62

Number of Fisher Scoring iterations: 5
```

How to select variables for inclusion in the model

- Hypothesis testing
  - Use the z-statistic produced by summary
  - drop1(M2,test="Chi")
  - anova(M2,M3,test="Chi")

- AIC, BIC, etc. - use step(M2) etc.

```
> drop1(M2,test="Chi")
Single term deletions

Model:
TOT.N ~ OPEN.L + MONT.S + SQ.POLIC + D.PARK + SQ.SHRUB + SQ.WATRES +
    L.WAT.C + SQ.LPROAD + SQ.DWATCOUR
            Df Deviance     AIC    LRT   Pr(Chi)
<none>           270.23  529.62
OPEN.L       1   273.93  531.32   3.69 0.0546474 .
MONT.S       1   306.89  564.28  36.66 1.410e-09 ***
SQ.POLIC     1   285.53  542.92  15.30 9.181e-05 ***
D.PARK       1   838.09 1095.48 567.85 < 2.2e-16 ***
SQ.SHRUB     1   298.31  555.70  28.08 1.167e-07 ***
SQ.WATRES    1   280.02  537.41   9.79 0.0017539 **
L.WAT.C      1   335.47  592.86  65.23 6.648e-16 ***
SQ.LPROAD    1   281.25  538.64  11.02 0.0009009 ***
SQ.DWATCOUR  1   272.50  529.89   2.27 0.1319862
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> step(M2)
Start:  AIC=529.62
TOT.N ~ OPEN.L + MONT.S + SQ.POLIC + D.PARK + SQ.SHRUB + SQ.WATRES +
    L.WAT.C + SQ.LPROAD + SQ.DWATCOUR

              Df Deviance     AIC
<none>             270.23  529.62
- SQ.DWATCOUR  1   272.50  529.89
- OPEN.L       1   273.93  531.32
- SQ.WATRES    1   280.02  537.41
- SQ.LPROAD    1   281.25  538.64
- SQ.POLIC     1   285.53  542.92
- SQ.SHRUB     1   298.31  555.70
- MONT.S       1   306.89  564.28
- L.WAT.C      1   335.47  592.86
- D.PARK       1   838.09 1095.48

Call:  glm(formula = TOT.N ~ OPEN.L + MONT.S + SQ.POLIC + D.PARK + SQ.SHRUB +
    SQ.WATRES + L.WAT.C + SQ.LPROAD + SQ.DWATCOUR, family = poisson,
    data = RK)

Coefficients:
(Intercept)       OPEN.L       MONT.S     SQ.POLIC       D.PARK     SQ.SHRUB    SQ.WATRES      L.WAT.C    SQ.LPROAD  SQ.DWATCOUR
  3.7493885   -0.0030250    0.0869656   -0.1787178   -0.0001301   -0.6111864    0.2242561    0.3354676    0.4517172    0.0073554

Degrees of Freedom: 51 Total (i.e. Null);  42 Residual
Null Deviance:      1071
Residual Deviance: 270.2    AIC: 529.6
```

```
> step(M2,k=log(n))
Start:  AIC=555.67
TOT.N ~ OPEN.L + MONT.S + SQ.POLIC + D.PARK + SQ.SHRUB + SQ.WATRES +
    L.WAT.C + SQ.LPROAD + SQ.DWATCOUR

              Df Deviance     AIC
- SQ.DWATCOUR  1   272.50  553.34
- OPEN.L       1   273.93  554.76
<none>             270.23  555.67
- SQ.WATRES    1   280.02  560.86
- SQ.LPROAD    1   281.25  562.09
- SQ.POLIC     1   285.53  566.37
- SQ.SHRUB     1   298.31  579.14
- MONT.S       1   306.89  587.72
- L.WAT.C      1   335.47  616.30
- D.PARK       1   838.09 1118.92

Step:  AIC=553.34
TOT.N ~ OPEN.L + MONT.S + SQ.POLIC + D.PARK + SQ.SHRUB + SQ.WATRES +
    L.WAT.C + SQ.LPROAD

            Df Deviance     AIC
<none>           272.50  553.34
- OPEN.L     1   277.60  553.83
- SQ.WATRES  1   281.22  557.46
- SQ.POLIC   1   285.62  561.86
- SQ.LPROAD  1   286.31  562.54
- SQ.SHRUB   1   300.59  576.82
- MONT.S     1   311.91  588.14
- L.WAT.C    1   339.08  615.31
- D.PARK     1   843.43 1119.66

Call:  glm(formula = TOT.N ~ OPEN.L + MONT.S + SQ.POLIC + D.PARK + SQ.SHRUB +
    SQ.WATRES + L.WAT.C + SQ.LPROAD, family = poisson, data = RK)

Coefficients:
(Intercept)       OPEN.L       MONT.S     SQ.POLIC       D.PARK     SQ.SHRUB    SQ.WATRES      L.WAT.C    SQ.LPROAD
  3.8516067   -0.0034641    0.0892662   -0.1583426   -0.0001286   -0.6159894    0.2079514    0.3112948    0.4935665

Degrees of Freedom: 51 Total (i.e. Null);  43 Residual
Null Deviance:      1071
Residual Deviance: 272.5    AIC: 529.9
```

Overdispersion

Recall that in the Poisson model we assume the mean = variance

With no overdispersion, residual mean deviance should be close to 1:

270.23 / 42 = 6.43…not close to 1

Or, consider mean squared residuals:

sum(resid(M2, type="pearson")^2) / 42 = 5.93

(suggests standard errors should be increased by sqrt(5.93) = 2.44)

Quasi-Poisson model accounts for overdispersion:

```
M4 <- glm(TOT.N ~ OPEN.L + MONT.S + SQ.POLIC +
          SQ.SHRUB + SQ.WATRES + L.WAT.C + SQ.LPROAD +
          SQ.DWATCOUR + D.PARK,
          family = quasipoisson, data = RK)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	3.749e+00	3.814e-01	9.830	1.86e-12
OPEN.L	-3.025e-03	3.847e-03	-0.786	0.43604
MONT.S	8.697e-02	3.309e-02	2.628	0.01194
SQ.POLIC	-1.787e-01	1.139e-01	-1.570	0.12400
SQ.SHRUB	-6.112e-01	2.863e-01	-2.135	0.03867
SQ.WATRES	2.243e-01	1.717e-01	1.306	0.19851
L.WAT.C	3.355e-01	1.005e-01	3.338	0.00177
SQ.LPROAD	4.517e-01	3.282e-01	1.376	0.17597
SQ.DWATCOUR	7.355e-03	1.188e-02	0.619	0.53910
D.PARK	-1.301e-04	1.445e-05	-9.004	2.33e-11

Dispersion parameter for quasipoisson family taken to be 5.928003

Null deviance: 1071.44 on 51 degrees of freedom

Residual deviance: 270.23 on 42 degrees of freedom

AIC: NA

Overdispersion

AIC not defined for quasi-Poisson model

Use drop1(M4, test="F") is approximately correct
or, better, do cross-validation

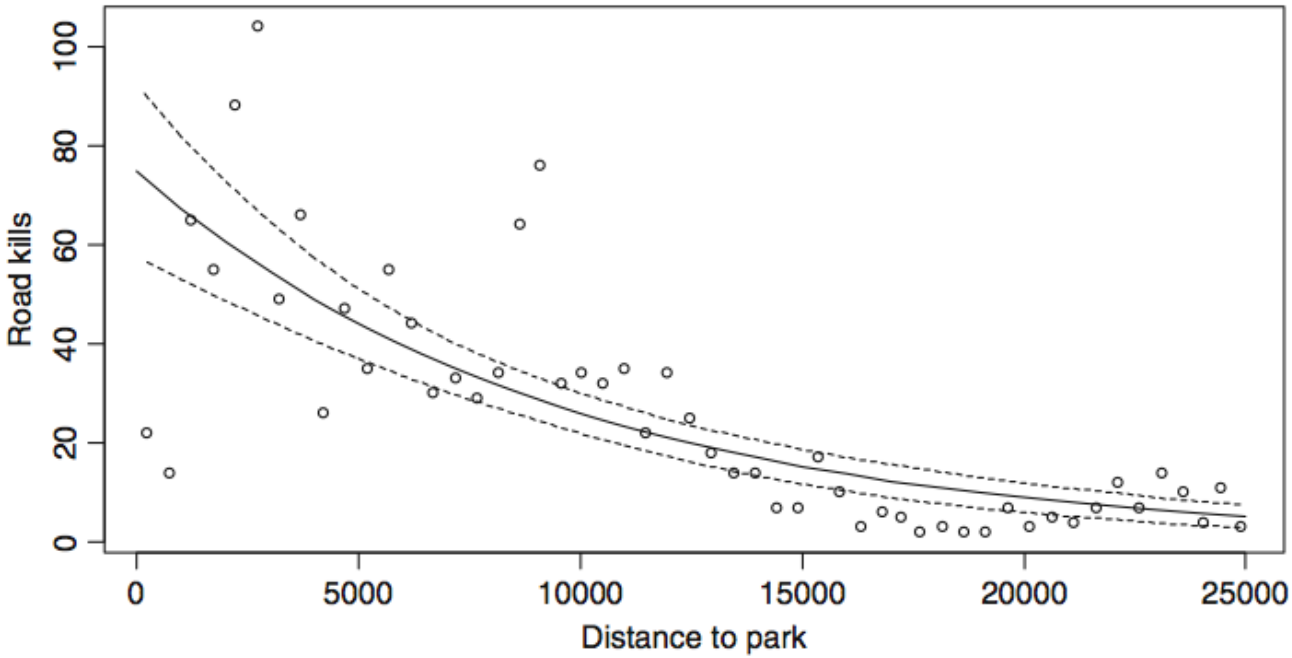


Fig. 9.5 Fitted line of the optimal quasi-Poisson model using only `D.PARK` as the explanatory variables. R code to make this graph is given on the book's website

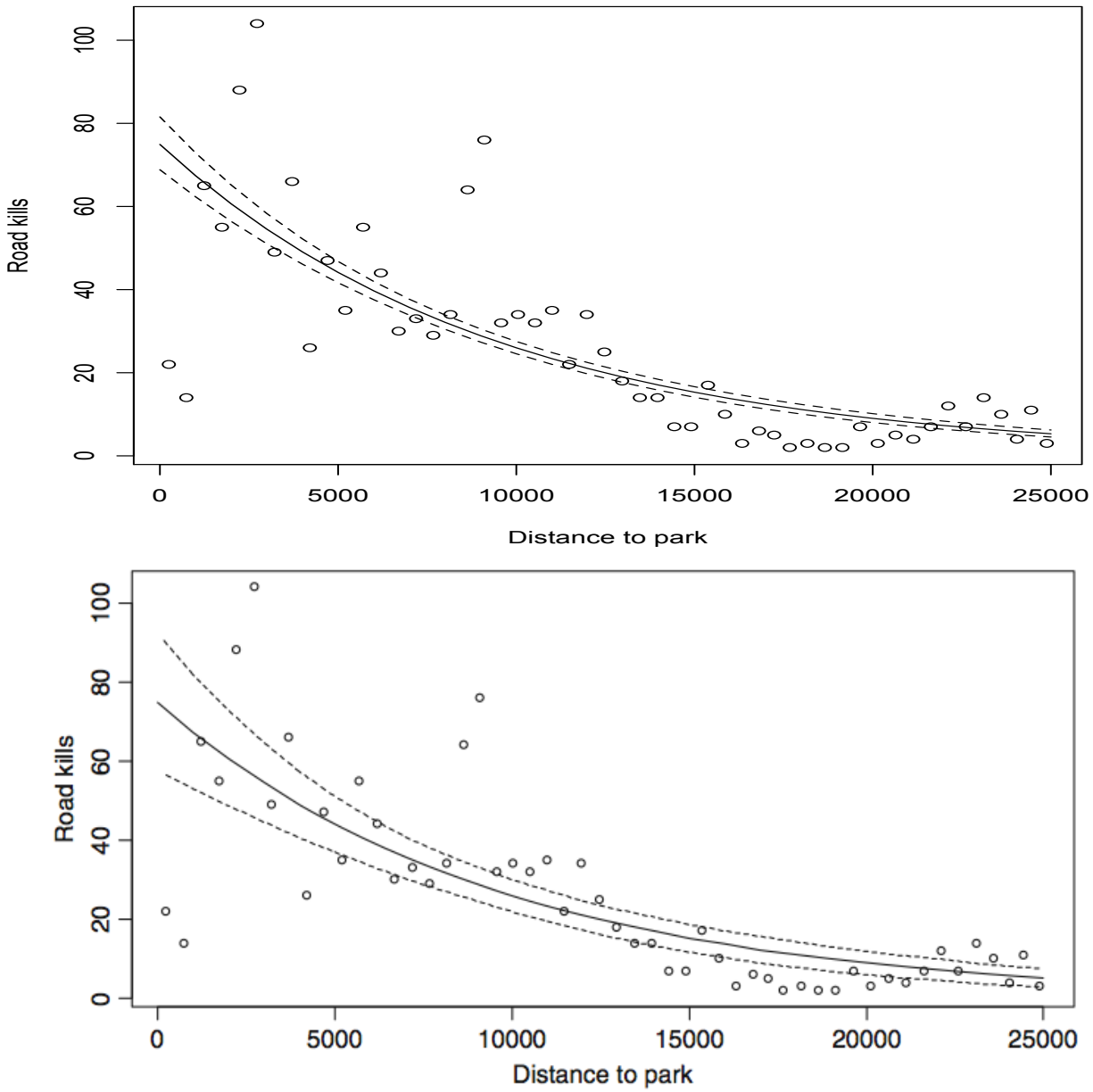


Fig. 9.5 Fitted line of the optimal quasi-Poisson model using only `D.PARK` as the explanatory variables. R code to make this graph is given on the book's website

Residuals for Poisson Model

Because variance increases with the mean, standard residual doesn't make much sense. Can use "Pearson residuals"

$$\hat{\varepsilon}_i^P = \frac{y_i - \hat{\mu}_i}{\sqrt{\text{var}(Y_i)}} = \frac{y_i - \hat{\mu}_i}{\sqrt{\hat{\mu}_i}}$$

For quasi-Poisson should also divide by the square root of the overdispersion parameter

Negative Binomial GLM

1. Y_i is negative binomial distributed with mean μ_i and parameter k (see also Chapter 8). By definition, the variance of Y_i is also equal to μ_i and its variance is $\mu_i + \mu_i^2 / k$.
2. The systematic part is given by $\eta(X_{i1}, \ldots, X_{iq}) = \alpha + \beta_1 \times X_{i1} + \ldots + \beta_q \times X_{iq}$.
3. There is a logarithm link between the mean of Y_i and the predictor function $\eta(X_{i1}, \ldots, X_{iq})$. The logarithmic link (also called log link) ensures that the fitted values are always non-negative.

$$Y_i \sim NB(\mu_i, k)$$

$$E(Y_i) = \mu_i \quad \text{and} \quad \text{var}(Y_i) = \mu_i + \frac{\mu_i^2}{k}$$

$$\log(\mu_i) = \eta(X_{i1}, \cdots, X_{iq}) \quad \text{or} \quad \mu_i = e^{\eta(X_{i1}, \cdots, X_{iq})}$$

```
> library(MASS)
> M6 <- glm.nb(TOT.N ~ OPEN.L + MONT.S + SQ.POLIC +
          SQ.SHRUB + SQ.WATRES + L.WAT.C + SQ.LPROAD +
          SQ.DWATCOUR + D.PARK, link = "log", data = RK)
```

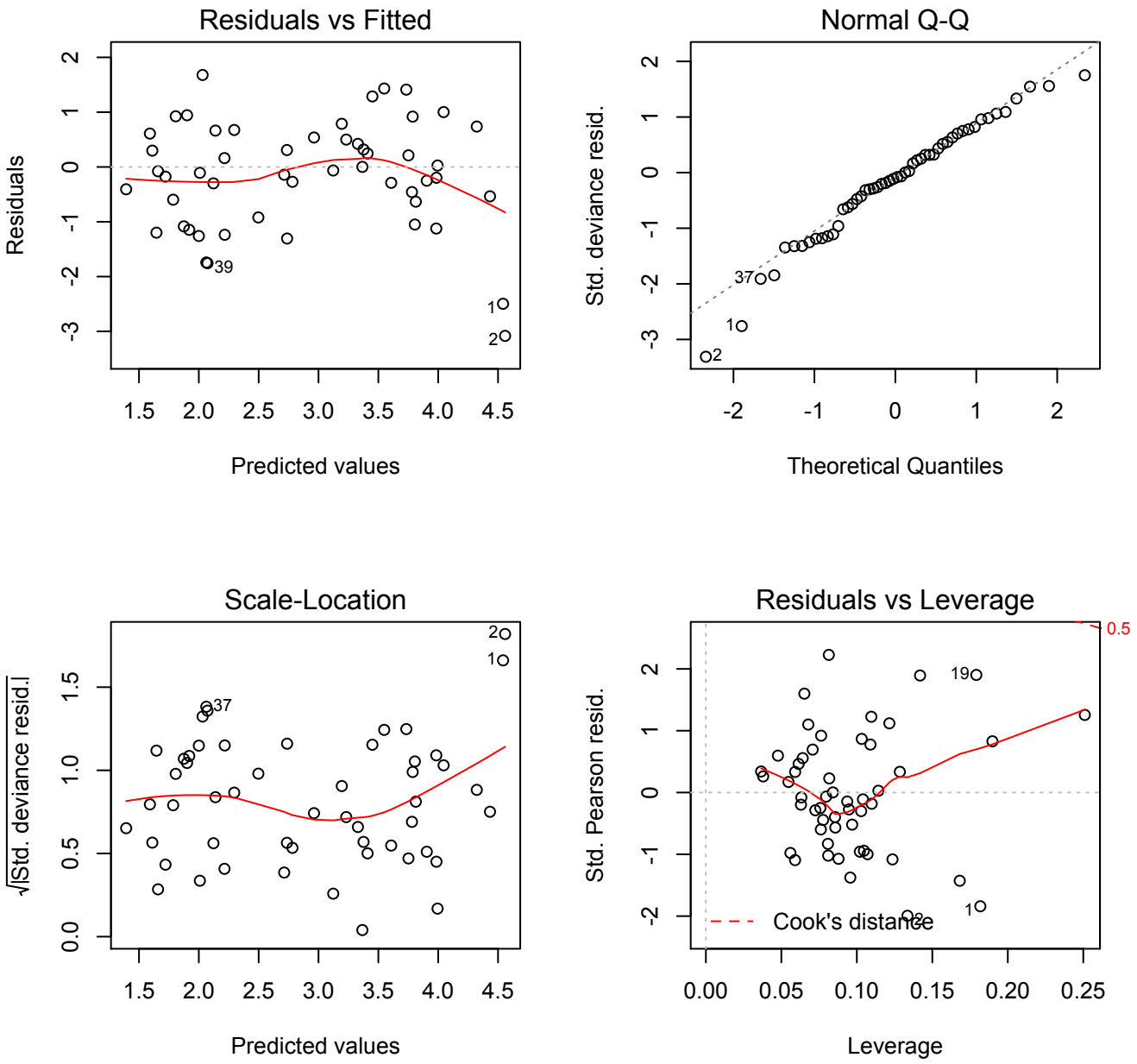
	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	3.951e+00	4.145e-01	9.532	<2e-16
OPEN.L	-9.419e-03	3.245e-03	-2.903	0.0037
MONT.S	5.846e-02	3.481e-02	1.679	0.0931
SQ.POLIC	-4.618e-02	1.298e-01	-0.356	0.7221
SQ.SHRUB	-3.881e-01	2.883e-01	-1.346	0.1784
SQ.WATRES	1.631e-01	1.675e-01	0.974	0.3301
L.WAT.C	2.076e-01	9.636e-02	2.154	0.0312
SQ.LPROAD	5.944e-01	3.214e-01	1.850	0.0644
SQ.DWATCOUR	-1.489e-05	1.139e-02	-0.001	0.9990
D.PARK	-1.235e-04	1.292e-05	-9.557	<2e-16

Dispersion parameter for Negative Binomial(5.5178) family taken to be 1

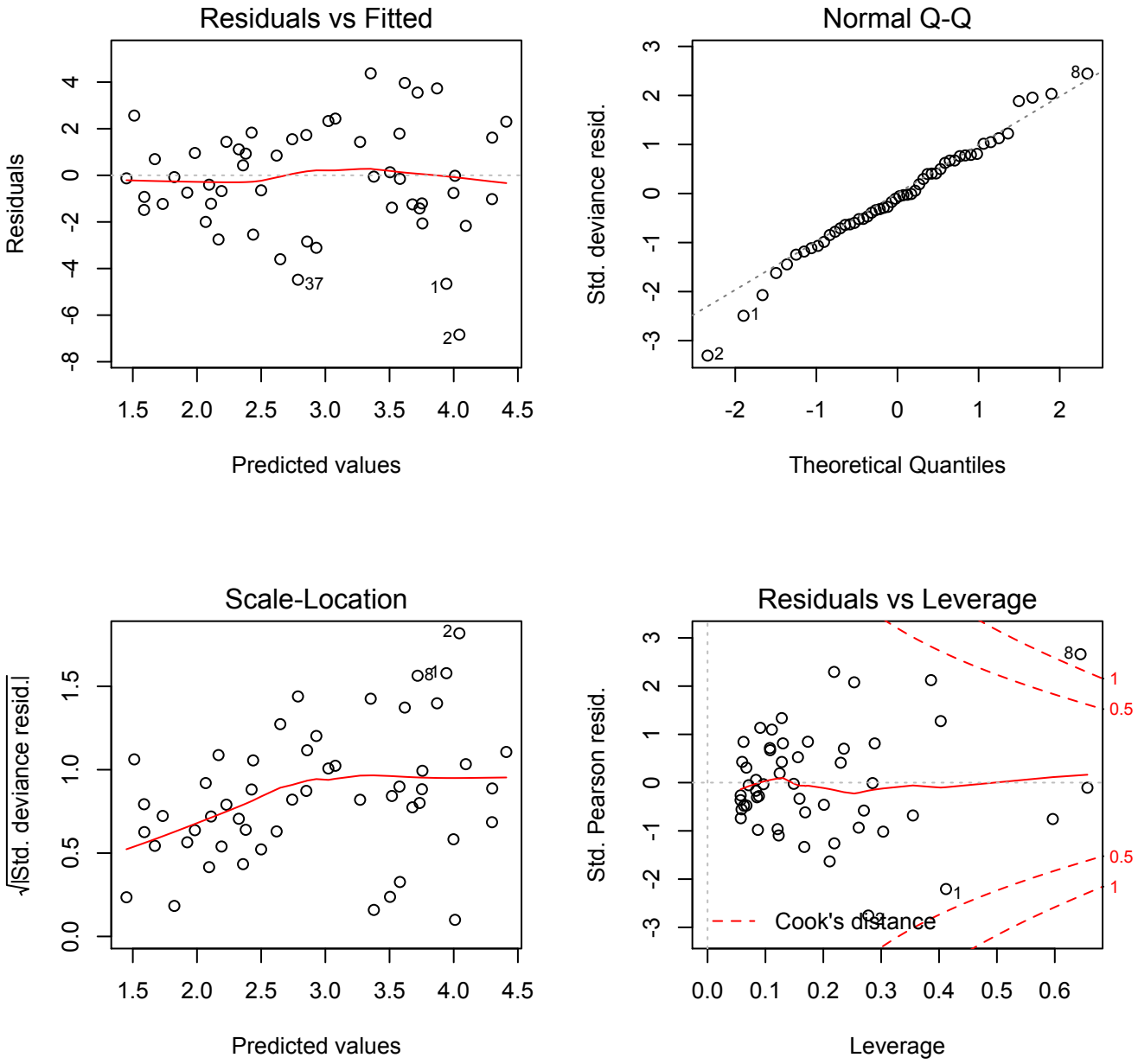
Null deviance: 213.674 on 51 degrees of freedom
Residual deviance: 51.803 on 42 degrees of freedom
AIC: 390.11
Theta: 5.52
Std. Err.: 1.41
2 x log-likelihood: -368.107

```
M7 <- glm.nb(formula = TOT.N ~ OPEN.L + L.WAT.C + SQ.LPROAD + D.PARK,  data = RK)

plot(M7)
```


Residuals vs Fitted
Residuals
Predicted values
39
1
2
Normal Q-Q
Std. deviance resid.
Theoretical Quantiles
37
1
2
Scale-Location
√|Std. deviance resid.|
Predicted values
2
1
37
Residuals vs Leverage
Std. Pearson resid.
Leverage
Cook's distance
0.5
19
1
2

Contrast with quasi-Poisson model M4



What if zero is impossible?

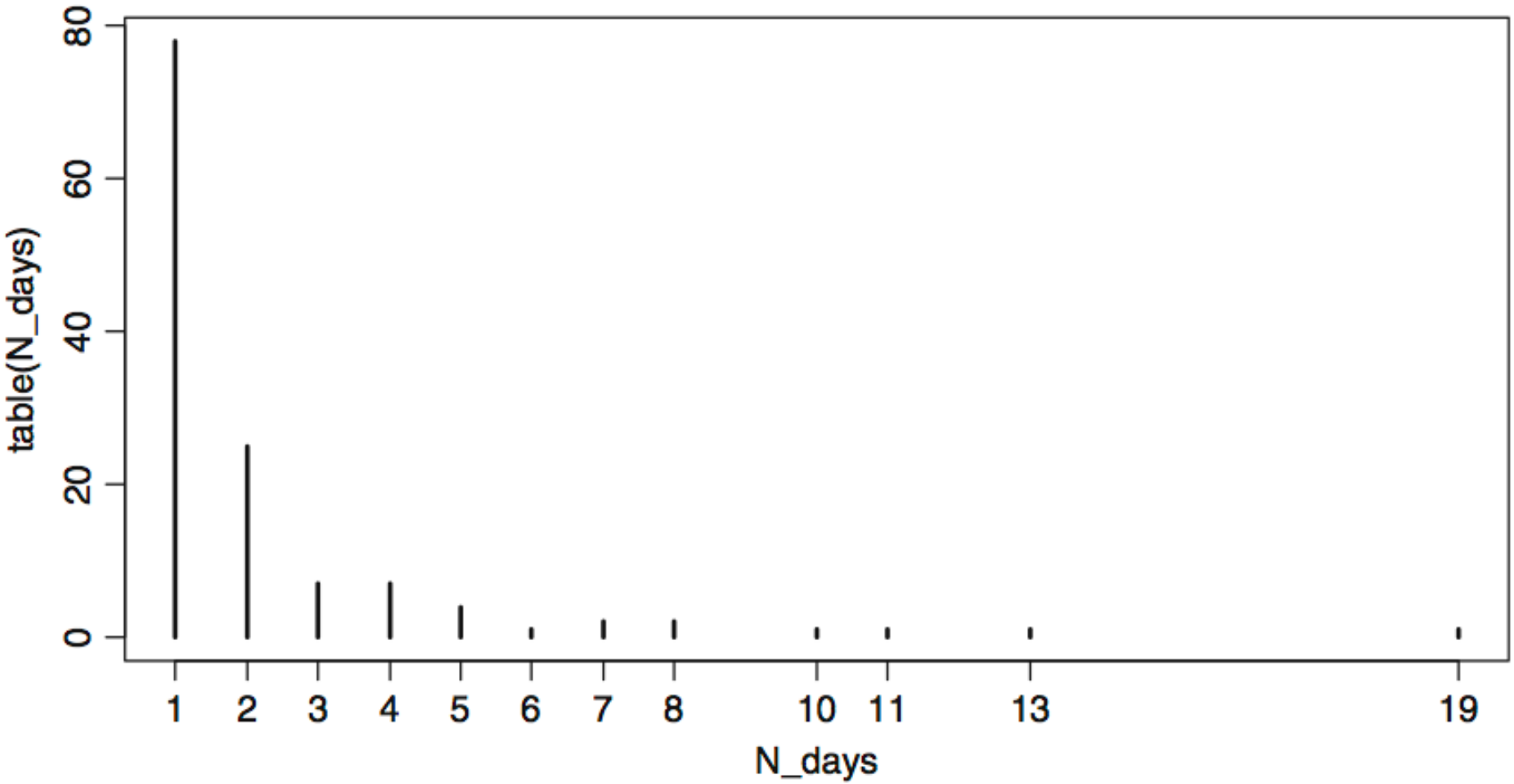


Fig. 11.2 Frequency plot of the response variable `N_days`, the number of days snake carcasses remain on the road. Note that a value of 0 cannot occur

$$f(y_i;\mu_i|y_i \geq 0) = \frac{\mu^{y_i} \times e^{-\mu_i}}{y_i!}$$

$$f(0;\mu_i) = \frac{\mu^0 \times e^{-\mu_i}}{0!} = e^{-\mu_i}$$

$$f(y_i;\mu_i|y_i > 0) = \frac{\mu^{y_i} \times e^{-\mu_i}}{(1 - e^{-\mu_i}) \times y_i!}$$

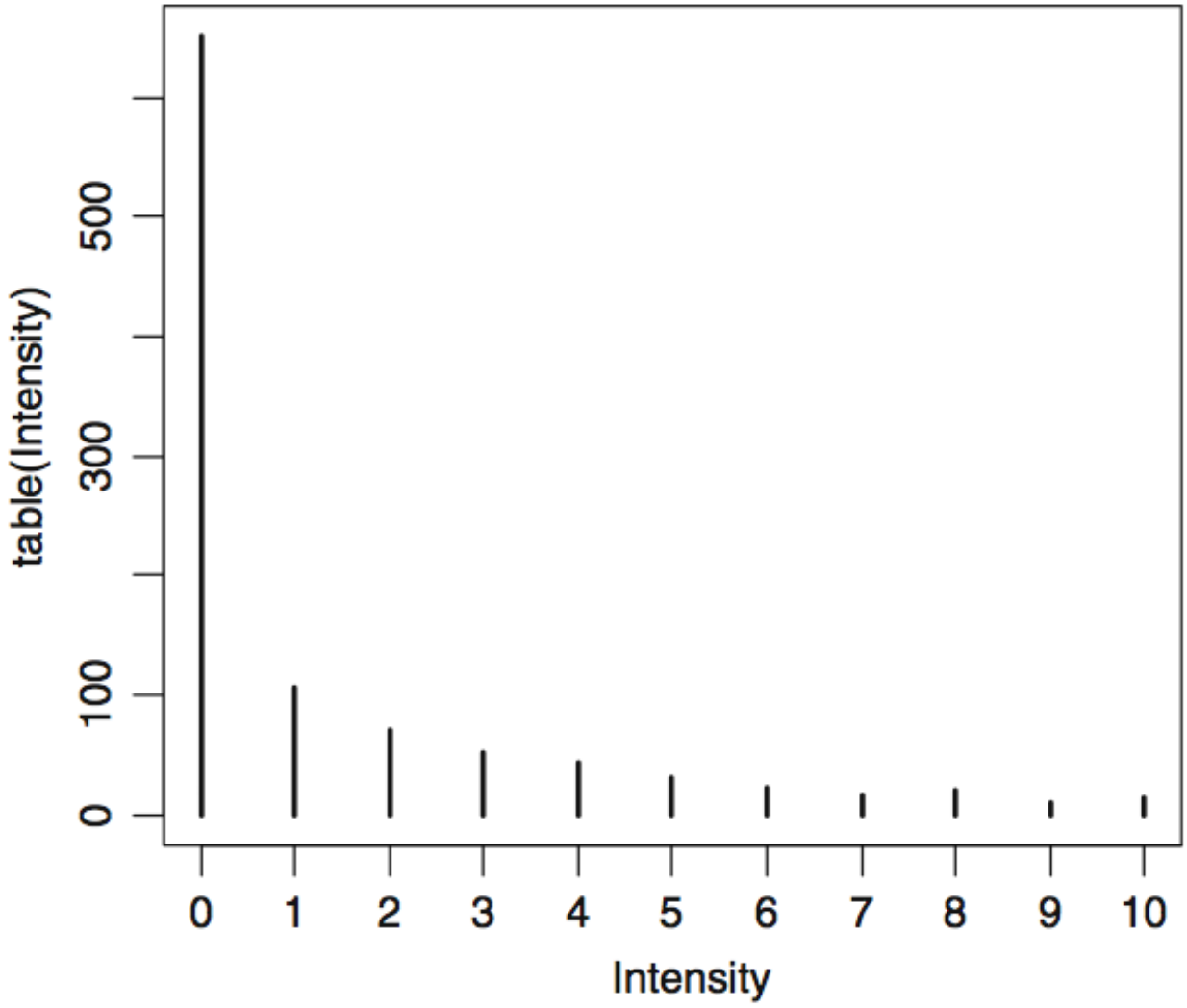
$$L = \prod_i f(y_i;\mu_i|y_i > 0) = \prod_i \frac{\mu^{y_i} \times e^{-\mu_i}}{(1 - e^{-\mu_i}) \times y_i!}$$

```
Library(VGAM)
data(Snakes)
M3A <- vglm(N_days~PDayRain + Tot_Rain + Road_Loc +
PDayRain:Tot_Rain, family = posnegbinomial, data = Snakes)


M4A <- vglm(N_days~PDayRain + Tot_Rain + Road_Loc +
PDayRain:Tot_Rain, family = pospoisson, data = Snakes)
```

Too many zeroes much more common

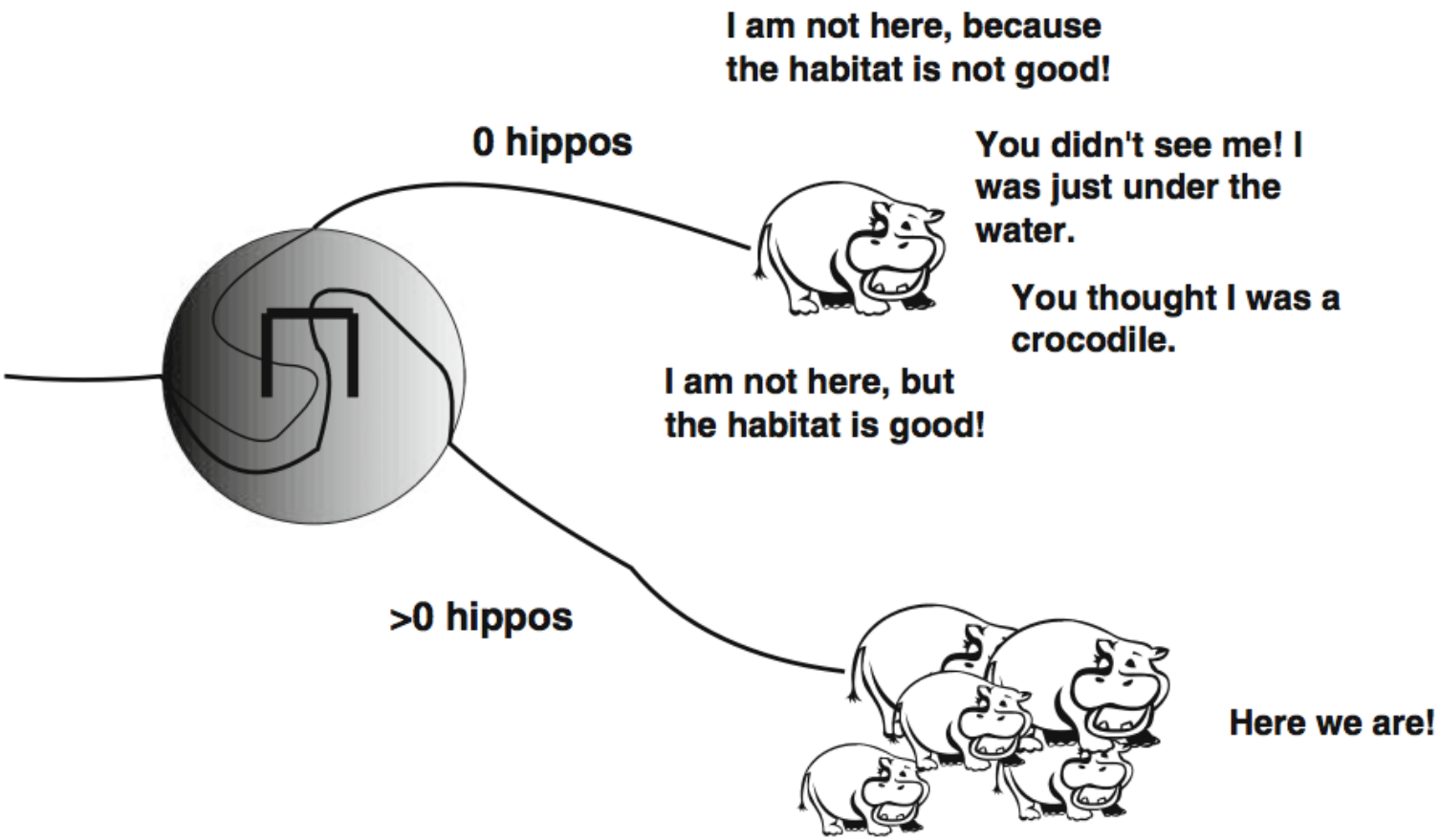
Fig. 11.3 Intensity of parasites in cod. This is the same graph as Fig. 11.1, except that only frequencies between 0 and 10 are shown



try plot(table(rpois(10000,lambda)))

Model	Full name	Type of model
ZIP	Zero-inflated Poisson	Mixture
ZINB	Zero-inflated negative binomial	Mixture
ZAP	Zero-altered Poisson	Two-part
ZANB	Zero-altered negative binomial	Two-part

Zero-altered Models



Zero-altered Models

$$f_{\text{ZAP}}(y;\beta,\gamma) = \begin{cases} f_{\text{binomial}}(y=0;\gamma) & y=0 \\ (1-f_{\text{binomial}}(y=0;\gamma)) \times \dfrac{f_{\text{Poisson}}(y;\beta)}{1-f_{\text{Poisson}}(y=0;\beta)} & y>0 \end{cases}$$

Get the estimates of γ and β via maximum likelihood estimation

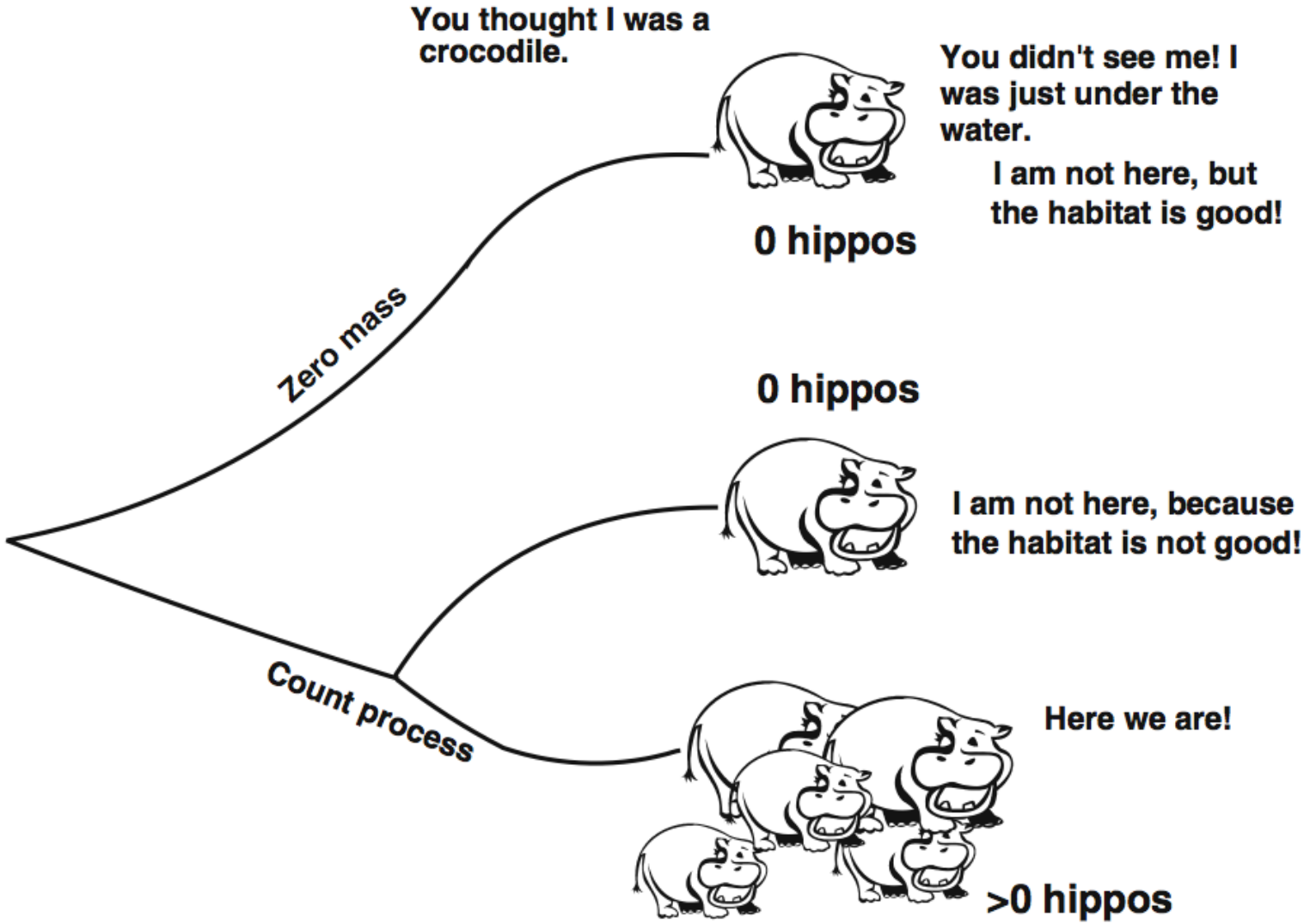
count part

logistic part

```
library(pscl)
f1 <- formula(Intensity~fArea*fYear + Length | fArea * fYear + Length)
H1A <- hurdle(f1, dist = "poisson", link = "logit", data = ParasiteCod2)
H1B <- hurdle(f1, dist = "negbin", link = "logit", data = ParasiteCod2)
AIC(H1A,H1B)
```

Can still have overdispersion in ZIP/ZAP models so check ZINB/ZANB

Zero-inflated Models



$$f(y_i = 0) \quad = \pi_i + (1 - \pi_i) \times e^{-\mu_i}$$

$$f(y_i | y_i > 0) = (1 - \pi_i) \times \frac{\mu^{y_i} \times e^{-\mu_i}}{y_i!}$$

$$\mu_i = e^{\alpha + \beta_1 \times X_{i1} + \cdots + \beta_q \times X_{iq}}$$

$$\pi_i = \frac{e^{\nu + \gamma_1 \times Z_{i1} + \cdots \gamma_q \times Z_{iq}}}{1 + e^{\nu + \gamma_1 \times Z_{i1} + \cdots \gamma_q \times Z_{iq}}}$$

$$E(Y_i) = \mu_i \times (1 - \pi_i)$$

$$\text{var}(Y_i) = (1 - \pi_i) \times (\mu_i + \pi_i \times \mu_i^2)$$

```
> library(pscl)
> f1 <- formula(Intensity ~ fArea*fYear +
                Length | fArea * fYear + Length)
> Zip1 <- zeroinfl(f1, dist = "poisson",
                link = "logit", data = ParasiteCod2)
```