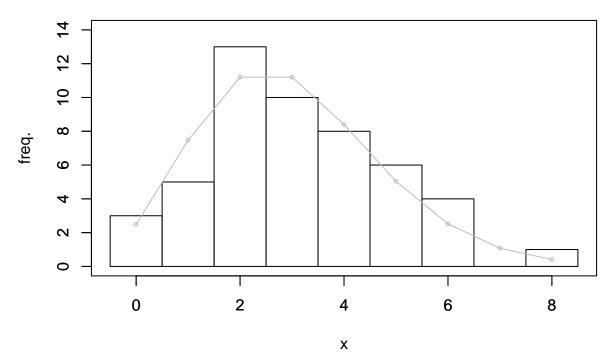
note12

Matts 966

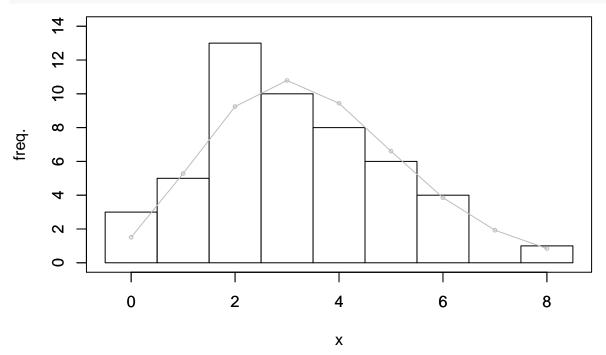
2018/01/30

```
set.seed(123)
# type=o はオーバーラップ
1 <- 3
d <- rpois(50, lambda=1)</pre>
hist(d, ylim=c(0, 14), breaks=c(-0.5:8.5), xlab="x", ylab="freq.", main="")
par(new=T)
x \leftarrow seq(0, 8, 1)
y \leftarrow 50*dpois(x, lambda=2)
plot(x, y, xlab="", ylab="", xlim=c(-0.5, 8.5), ylim=c(0, 14), type="o", col="grey", cex=0.5)
      12
      10
      \infty
      4
      \sim
      0
                 0
                                 2
                                                  4
                                                                  6
                                                                                  8
                                                  Χ
```

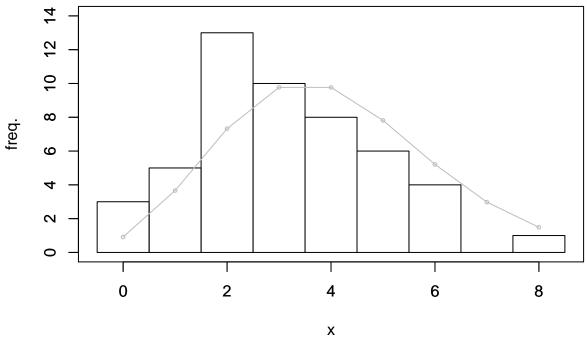
```
hist(d, ylim=c(0, 14), breaks=c(-0.5:8.5), xlab="x", ylab="freq.", main="")
par(new=T)
x <- seq(0, 8, 1)
y <- 50*dpois(x, lambda=3)
plot(x, y, xlab="", ylab="", xlim=c(-0.5, 8.5), ylim=c(0, 14), type="o", col="grey", cex=0.5)</pre>
```



```
hist(d, ylim=c(0, 14), breaks=c(-0.5:8.5), xlab="x", ylab="freq.", main="")
par(new=T)
x <- seq(0, 8, 1)
y <- 50*dpois(x, lambda=3.5)
plot(x, y, xlab="", ylab="", xlim=c(-0.5, 8.5), ylim=c(0, 14), type="o", col="grey", cex=0.5)
```



```
hist(d, ylim=c(0, 14), breaks=c(-0.5:8.5), xlab="x", ylab="freq.", main="")
par(new=T)
x <- seq(0, 8, 1)
y <- 50*dpois(x, lambda=4)
plot(x, y, xlab="", ylab="", xlim=c(-0.5,8.5), ylim=c(0, 14), type="o", col="grey", cex=0.5)</pre>
```



```
set.seed(123)
1 <- 3
d <- rpois(50, lambda=1)</pre>
logL <- sum(dpois(d, 2.0, log=T))</pre>
logL
## [1] -110.5617
logL <- sum(dpois(d, 3.0, log=T))</pre>
logL
## [1] -97.71459
logL <- sum(dpois(d, 3.5, log=T))</pre>
logL
## [1] -98.82124
logL <- sum(dpois(d, 4.0, log=T))</pre>
logL
## [1] -103.1239
# AICを計算して最小を提示
AIC = -2 * (-97.71459) + 2 * 2
AIC
## [1] 199.4292
# よって lambda3.0で AIC 最小
```

```
set.seed(123)
1 <- 3
d <- rpois(50, lambda=1)

logL <- function(m) sum(dpois(d, m, log=T))
lambda <- seq(2, 5, 0.1)
plot(lambda, sapply(lambda, logL), type="l", xlim=c(2, 5), xlab="lambda", ylab="logL")

00
1
00
1</pre>
```

2.0 2.5 3.0 3.5 4.0 4.5 5.0 lambda

setwd("/Users/masahiromatsui/Dropbox/R/Rで学ぶ統計学入門図版作成用(改訂版)/付録/")

```
setwd("/Users/masahiromatsui/Dropbox/R/Rで学ぶ統計学入門図版作成用(改訂版)/付録/")
d <- read.csv("table10-2.csv")
result <- glm(cbind(d$dead, 1-d$dead) ~ d$dose, family=binomial(logit))
logLik(result)
```

```
## 'log Lik.' -6.781799 (df=2)

AIC = -2 * (-6.781799) + 2 * 2

AIC
```

[1] 17.5636

```
setwd("/Users/masahiromatsui/Dropbox/R/R で学ぶ統計学入門図版作成用(改訂版)/付録/")
d <- read.csv("table10-3.csv")
result <- glm(d$flw ~ d$wt, family=poisson)
logLik(result)
```

'log Lik.' -82.84586 (df=2)

```
AIC = -2 * (-82.84586) + 2 * 2
AIC
## [1] 169.6917
library(lme4)
## Loading required package: Matrix
setwd("/Users/masahiromatsui/Dropbox/R/R で学ぶ統計学入門図版作成用(改訂版)/付録/")
d <- read.csv("table11-1.csv")</pre>
plot(d$y ~ d$x, pch=as.character(d$block))
                                   а
                     а
                               а
     10
                          а
                                                            b
     0
             а
                                                   b
                                                         b
                 а
      \infty
                                                                          С
                                                                                   С
                                         b
                                                                              С
                                                                   С
                            b
                                  b
     9
                                                     С
                     2
                                    4
                                                   6
                                                                   8
                                                                                 10
                                              d$x
res.1 <- glmer(d$y ~d$x + (1|d$block), family=gaussian(link = identity))</pre>
## Warning in glmer(d$y ~ d$x + (1 | d$block), family = gaussian(link =
## identity)): calling glmer() with family=gaussian (identity link) as a
## shortcut to lmer() is deprecated; please call lmer() directly
res.2 <- lmer(d\$y \sim d\$x + (1|d\$block))
summary(res.1)
## Linear mixed model fit by REML ['lmerMod']
## Formula: d$y \sim d$x + (1 \mid d$block)
##
## REML criterion at convergence: 45.9
##
## Scaled residuals:
##
       Min
                1Q Median
                                 ЗQ
                                        Max
```

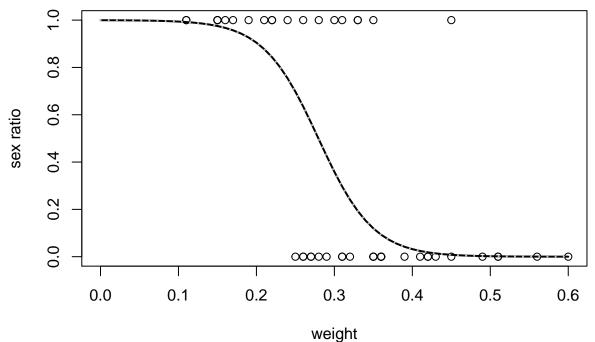
```
## -1.6493 -0.5949 0.1023 0.6671 1.5821
##
## Random effects:
## Groups
           Name
                        Variance Std.Dev.
## d$block (Intercept) 11.0023 3.3170
## Residual
                         0.3631 0.6026
## Number of obs: 18, groups: d$block, 3
##
## Fixed effects:
              Estimate Std. Error t value
## (Intercept)
               4.8738
                           2.0063 2.429
## d$x
                0.6470
                           0.1085 5.962
##
## Correlation of Fixed Effects:
       (Intr)
## d$x -0.290
summary(res.2)
## Linear mixed model fit by REML ['lmerMod']
## Formula: d$y \sim d$x + (1 \mid d$block)
## REML criterion at convergence: 45.9
##
## Scaled residuals:
      Min
               1Q Median
                               3Q
                                      Max
## -1.6493 -0.5949 0.1023 0.6671 1.5821
##
## Random effects:
## Groups Name
                       Variance Std.Dev.
## d$block (Intercept) 11.0023 3.3170
                         0.3631 0.6026
## Residual
## Number of obs: 18, groups: d$block, 3
## Fixed effects:
              Estimate Std. Error t value
## (Intercept) 4.8738
                           2.0063 2.429
## d$x
                0.6470
                           0.1085 5.962
##
## Correlation of Fixed Effects:
       (Intr)
## d$x -0.290
setwd("/Users/masahiromatsui/Dropbox/R/Rで学ぶ統計学入門図版作成用(改訂版)/付録/")
d <- read.csv("table11-3.csv")</pre>
```

```
matrix(c(d$y), nrow=4, ncol=12)
```

```
[,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
##
## [1,]
                                                        0
                             1
                                  0
                                        1
                                             1
                                                   0
## [2,]
            1
                 1
                                  1
                                                   0
## [3,]
            1
                                  0
                            0
                                             0
                                                   0
                                                               0
                                                                            0
## [4,]
                                        0
            0
                 0
                       1
                            0
                                  0
                                                   0
                                                        0
                                                               0
                                                                            0
                                             1
```

ここから

```
setwd("/Users/masahiromatsui/Dropbox/R/R で学ぶ統計学入門図版作成用(改訂版)/付録/")
library(lme4)
library(glmmML)
d <- read.csv("table11-3.csv")</pre>
mother <- as.factor(d$mother)</pre>
wt <- d$wt
y <- d$y
res.1 <-glmer(y ~ wt + (1 mother), family=binomial(logit))</pre>
res.1 <- summary(res.1)</pre>
res.2 <-glmmML(y ~ wt , cluster=mother)</pre>
plot(d$wt, d$y, xlab="weight", ylab="sex ratio", xlim=c(0, 0.6))
pred.wt \leftarrow seq(0, 0.6, 0.01)
pred.y1 <- 1/(1+exp(-(res.1$coefficient[1] + res.1$coefficient[2]*pred.wt)))</pre>
pred.y2 <- 1/(1+exp(-(res.2$coefficient[1] + res.2$coefficient[2]*pred.wt)))</pre>
lines(pred.wt, pred.y1, lwd=2, col="black")
lines(pred.wt, pred.y2, lwd=2, col="grey", lty=3)
```



```
# 演習 11-1
setwd("/Users/masahiromatsui/Dropbox/R/Rで学ぶ統計学入門図版作成用(改訂版)/付録/")
library(lme4)
library(glmmML)
d <- read.csv("enshu11-1.csv")</pre>
cond <- as.factor(d$cond)</pre>
x \leftarrow d$x
y <- as.factor(d$y)
res.1 <-glmer(y ~ x + (1|cond), family=binomial(logit))
res.1 <- summary(res.1)</pre>
res.2 <-glmmML(y \sim x , cluster=cond)
## Warning in model.response(mf, "numeric"): using type = "numeric" with a
## factor response will be ignored
res.1
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: y \sim x + (1 \mid cond)
##
##
        AIC
                 BIC
                       logLik deviance df.resid
       23.0
                26.5
                         -8.5
                                  17.0
                                             21
##
##
## Scaled residuals:
        Min
                  1Q Median
                                    3Q
                                            Max
## -2.44746 0.07865 0.17926 0.40859 1.40601
##
## Random effects:
## Groups Name
                       Variance Std.Dev.
           (Intercept) 0
## cond
## Number of obs: 24, groups: cond, 8
## Fixed effects:
               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.0546
                            1.4785 -1.390 0.1646
## x
                 0.9154
                                           0.0395 *
                            0.4446
                                     2.059
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
    (Intr)
## x -0.912
```

```
## [1] "-----
res.2
## Call: glmmML(formula = y ~ x, cluster = cond)
##
##
##
             coef se(coef) z Pr(>|z|)
## (Intercept) -2.0546 1.4785 -1.390 0.1650
            0.9154 0.4446 2.059
                              0.0395
## x
##
## Scale parameter in mixing distribution: 2.66e-07 gaussian
## Std. Error:
                                  0.6805
##
        LR p-value for H_0: sigma = 0: 0.5
##
## Residual deviance: 16.96 on 21 degrees of freedom AIC: 22.96
```

【考察】p-value 0.0395 で効果が検出された。