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Bokmål

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Statistisk modellering for biologer og bioteknologer, ST2304

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Tillatte hjelpemidler: Et håndskrevet gult A4 ark, kalkulator, "Tabeller og formler i statistikk" (Tapir forlag), K. Rottmann: Matematisk formelsamling.

Hjelpesider for noen R funksjoner det kan hende du får bruk for følger på side 7.

Oppgave 1 Anta at antall individ av en gitt art i ruter av størrelse A er Poissonfordelt med forventning λA hvor $\lambda = 0.5$ per kvadratmeter.

a) Skriv et uttrykk i R som beregner sannsynligheten for at det er eksakt 5 individ i en rute på 10 kvadratmeter.

Vi betrakter 5 ruter og lager en vektor `A` i R som representerer arealet (i kvadratmeter) til disse på følgende måte.

```
A <- c(10,15,20,25,30)
```

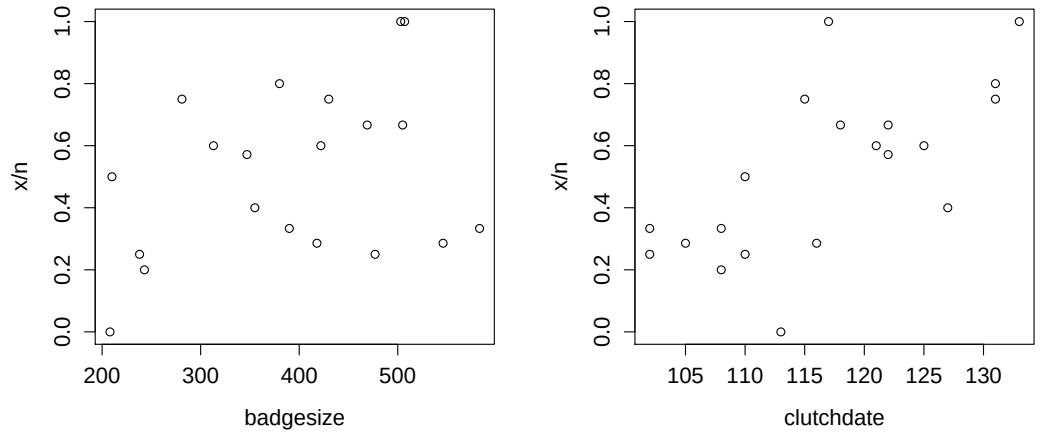
b) Skriv et uttrykk i R som, for hver av de 5 rutene, beregner sannsynligheten for at det er mer enn 5 individ i ruten.

c) Skriv et uttrykk i R som simulerer antallet individ i hver av de 5 rutene.

Oppgave 2 Vi studerer overlevelse i 20 ulike gråspurvkull og observerer antall overlevende unger `x` etter 12 dager, totalt antall egg `n` i hvert reir, brystflekkstørrelse til faren (variabelen `badgesize`, mm^2), og klekketidspunkt (variabelen `clutchdate`, antall dager siden 1. januar).

```
> sparrows
   x n badgesize clutchdate
1  1 3       583        108
2  1 4       477        102
3  3 3       507        133
4  1 3       390        102
5  3 5       313        121
6  2 7       546        116
7  3 5       422        125
8  2 3       505        122
9  2 4       210        110
10 4 5       380        131
11 2 5       355        127
12 2 3       469        118
13 3 4       281        115
14 1 5       243        108
15 3 4       430        131
16 4 7       347        122
17 4 4       503        117
18 1 4       238        110
19 0 3       208        113
20 2 7       418        105
```

Plot av andelen overlevende versus brystflekkstørrelse og klekketidspunkt følger under.



a) Vi tilpasser først en lineær regresjonsmodell hvor vi bruker andelen overlevende som

responsvariabel og klekketidspunkt som eneste forklaringsvariabel etter å ha tatt brystflekkstørrelse ut av modellen.

```
> prop <- x/n
> summary(lm(prop ~ clutchdate))

Call:
lm(formula = prop ~ clutchdate)

Residuals:
     Min       1Q   Median       3Q      Max
-0.43890 -0.08541  0.00396  0.10957  0.48400

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.73908    0.57646  -3.017  0.00741 **
clutchdate   0.01927    0.00492   3.918  0.00101 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.206 on 18 degrees of freedom
Multiple R-squared: 0.4603,Adjusted R-squared: 0.4303
F-statistic: 15.35 on 1 and 18 DF,  p-value: 0.001009
```

Basert på denne modellen, hva er predikert andel overlevende i et kull med klekketidspunkt lik 150? Gir denne prediksjonen mening? Er det andre antakelser i modellen som ikke er oppfyllt? Ville du stolt på konklusjonen at klekketidspunkt har en signifikant effekt på overlevelse basert på denne modellen?

Anta at vi i stedet tilpasser en generalisert lineær modell på følgende måte.

```
> summary(glm(prop ~ clutchdate+badgesize,weight=n,family=binomial(link=logit)))

Call:
glm(formula = prop ~ clutchdate + badgesize, family = binomial,
    weights = n)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.62259  -0.28653  -0.04847   0.37706   2.19469
```

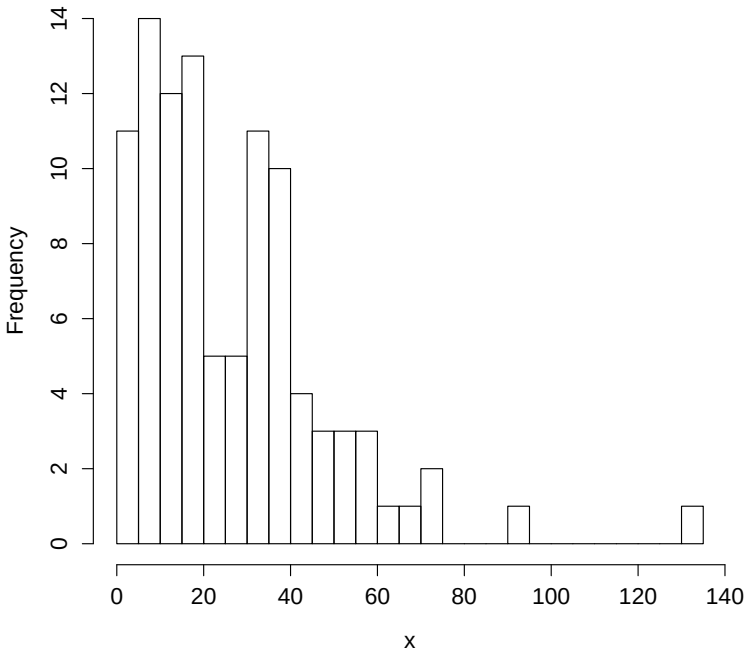
```
Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -9.730598   3.116205  -3.123  0.00179 **
clutchdate   0.077864   0.026339   2.956  0.00311 **
badgesize    0.001614   0.002110   0.765  0.44426
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 26.667  on 19  degrees of freedom
Residual deviance: 15.571  on 17  degrees of freedom
AIC: 53.893

Number of Fisher Scoring iterations: 4
```

b) Skriv ned antakelsene for denne modellen og en ligning som representerer modellen i matematisk notasjon.

c) Hva er predikert overlevelse i et kull med klekketidspunkt lik 150 og hvor faren har en brystflekkstørrelse på 400 mm^2.

d) Er det tegn på over- eller under-dispersjon i dataene? Diskuter kort mulige mekanismer som kan generere over- og under-dispersjon i dette tilfelle.

Oppgave 3 Anta at vi observerer levetidene X (i år) til 100 furutrær. Et histogram av de observerte levetidene (inneholdt i vektoren `x`) er vist under.



Vi antar at disse levetidene følger en gamma fordeling med tetthetsfunksjon

$$f(x) = \frac{1}{\beta^{\alpha}\Gamma(\alpha)} x^{\alpha-1} e^{-x/\beta} \tag{1}$$

a) Skriv en funskjon `lnL` som tar to argument; en vektor som inneholder parameterne α og β og en andre vektor som inneholder observasjonene. Funskjonen skal returnere det negative log likelihoodet som funksjonsverdi.

Vi minimaliserer så det negative log likelihood på følgende måte i R.

```
> fit <- optim(c(1,1),lnL,x=x,hessian=TRUE)
> fit
$par
[1]  1.270927 20.400906

$value
[1] 423.9039

$counts
```

```
function gradient
      73       NA

$convergence
[1] 0

$message
NULL

$hessian
           [,1]      [,2]
[1,] 117.014163 4.9017432
[2,]   4.901743 0.3055501

> solve(fit$hessian)
            [,1]       [,2]
[1,]  0.02605615 -0.4180021
[2,] -0.41800208  9.9785242
```

b) Hvilke parameter verdier maksimaliser likelihoodfunksjonen? Hva er det maksimale log likelihoodet? Finn tilnærmede standardfeil til estimatene.

Anta at vi også tilpasser en enklere eksponentiell modell til dataene og at dette gir et observert maksimalt log likelihood lik -425.56.

c) Forklar hvorfor den ekponentielle modellen er nøstet i gamma modellen. Om vi bruker en asymptotisk tilnærming, kan vi forkaste den eksponentielle modellen i favør av gamma modellen?

```
Poisson                 package:stats                 R Documentation

The Poisson Distribution

Description:

     Density, distribution function, quantile function and random
     generation for the Poisson distribution with parameter 'lambda'.

Usage:

     dpois(x, lambda, log = FALSE)
     ppois(q, lambda, lower.tail = TRUE, log.p = FALSE)
     qpois(p, lambda, lower.tail = TRUE, log.p = FALSE)
     rpois(n, lambda)

Arguments:

       x: vector of (non-negative integer) quantiles.

       q: vector of quantiles.

       p: vector of probabilities.

       n: number of random values to return.

  lambda: vector of (non-negative) means.

log, log.p: logical; if TRUE, probabilities p are given as log(p).

lower.tail: logical; if TRUE (default), probabilities are P[X <= x],
         otherwise, P[X > x].

Details:

     The Poisson distribution has density

                       p(x) = lambda^x exp(-lambda)/x!

     for x = 0, 1, 2, ... .  The mean and variance are E(X) = Var(X) =
     lambda.

     If an element of 'x' is not integer, the result of 'dpois' is
     zero, with a warning.  p(x) is computed using Loader's algorithm,
     see the reference in 'dbinom'.

     The quantile is right continuous: 'qpois(p, lambda)' is the
     smallest integer x such that P(X <= x) >= p.

     Setting 'lower.tail = FALSE' allows to get much more precise
     results when the default, 'lower.tail = TRUE' would return 1, see
     the example below.

Value:

     'dpois' gives the (log) density, 'ppois' gives the (log)
     distribution function, 'qpois' gives the quantile function, and
     'rpois' generates random deviates.

     Invalid 'lambda' will result in return value 'NaN', with a
     warning.

Source:

     'dpois' uses C code contributed by Catherine Loader (see
     'dbinom').

     'ppois' uses 'pgamma'.

     'qpois' uses the Cornish-Fisher Expansion to include a skewness
     correction to a normal approximation, followed by a search.

     'rpois' uses

     Ahrens, J. H. and Dieter, U. (1982).  Computer generation of
     Poisson deviates from modified normal distributions.  _ACM
     Transactions on Mathematical Software_, *8*, 163-179.

See Also:

     Distributions for other standard distributions, including 'dbinom'
     for the binomial and 'dnbinom' for the negative binomial
     distribution.

     'poisson.test'.

Examples:

     require(graphics)

     -log(dpois(0:7, lambda=1) * gamma(1+ 0:7)) # == 1
     Ni <- rpois(50, lambda = 4); table(factor(Ni, 0:max(Ni)))

     1 - ppois(10*(15:25), lambda=100)  # becomes 0 (cancellation)
         ppois(10*(15:25), lambda=100, lower.tail=FALSE)  # no cancellation

     par(mfrow = c(2, 1))
     x <- seq(-0.01, 5, 0.01)
     plot(x, ppois(x, 1), type="s", ylab="F(x)", main="Poisson(1) CDF")
     plot(x, pbinom(x, 100, 0.01),type="s", ylab="F(x)",
          main="Binomial(100, 0.01) CDF")
--------------------------------------------------------------------------------
GammaDist               package:stats                 R Documentation

The Gamma Distribution

Description:

     Density, distribution function, quantile function and random
     generation for the Gamma distribution with parameters 'shape' and
     'scale'.

Usage:

     dgamma(x, shape, rate = 1, scale = 1/rate, log = FALSE)
     pgamma(q, shape, rate = 1, scale = 1/rate, lower.tail = TRUE,
            log.p = FALSE)
     qgamma(p, shape, rate = 1, scale = 1/rate, lower.tail = TRUE,
            log.p = FALSE)
     rgamma(n, shape, rate = 1, scale = 1/rate)

Arguments:

    x, q: vector of quantiles.

       p: vector of probabilities.

       n: number of observations. If 'length(n) > 1', the length is
          taken to be the number required.

    rate: an alternative way to specify the scale.

shape, scale: shape and scale parameters.  Must be positive, 'scale'
          strictly.

log, log.p: logical; if 'TRUE', probabilities/densities p are returned
          as log(p).

lower.tail: logical; if TRUE (default), probabilities are P[X <= x],
          otherwise, P[X > x].

Details:

     If 'scale' is omitted, it assumes the default value of '1'.

     The Gamma distribution with parameters 'shape' = a and 'scale' = s
     has density

                  f(x)= 1/(s^a Gamma(a)) x^(a-1) e^-(x/s)

     for x >= 0, a > 0 and s > 0.  (Here Gamma(a) is the function
     implemented by R's 'gamma()' and defined in its help.  Note that
     a=0 corresponds to the trivial distribution with all mass at point
     0.)

     The mean and variance are E(X) = a*s and Var(X) = a*s^2.

     The cumulative hazard H(t) = - log(1 - F(t)) is '-pgamma(t, ...,
     lower = FALSE, log = TRUE)'.

     Note that for smallish values of 'shape' (and moderate 'scale') a
     large parts of the mass of the Gamma distribution is on values of
     x so near zero that they will be represented as zero in computer
     arithmetic.  So 'rgamma' can well return values which will be
     represented as zero.  (This will also happen for very large values
     of 'scale' since the actual generation is done for 'scale=1'.)
```

```
Value:

     'dgamma' gives the density, 'pgamma' gives the distribution
     function, 'qgamma' gives the quantile function, and 'rgamma'
     generates random deviates.

     Invalid arguments will result in return value 'NaN', with a
     warning.

Note:

     The S parametrization is via 'shape' and 'rate': S has no 'scale'
     parameter.

     'pgamma' is closely related to the incomplete gamma function.  As
     defined by Abramowitz and Stegun 6.5.1 (and by 'Numerical
     Recipes') this is

          P(a,x) =      1/Gamma(a) integral_0^x t^(a-1) exp(-t) dt

     P(a, x) is 'pgamma(x, a)'.  Other authors (for example Karl
     Pearson in his 1922 tables) omit the normalizing factor, defining
     the incomplete gamma function as 'pgamma(x, a) * gamma(a)'.  A few
     use the 'upper' incomplete gamma function, the integral from x to
     infinity which can be computed by 'pgamma(x, a, lower=FALSE) *
     gamma(a)', or its normalized version. See also <URL:
     http://en.wikipedia.org/wiki/Incomplete_gamma_function>.

Source:

     'dgamma' is computed via the Poisson density, using code
     contributed by Catherine Loader (see 'dbinom').

     'pgamma' uses an unpublished (and not otherwise documented)
     algorithm 'mainly by Morten Welinder'.

     'qgamma' is based on a C translation of

     Best, D. J. and D. E. Roberts (1975).  Algorithm AS91. Percentage
     points of the chi-squared distribution.  _Applied Statistics_,
     *24*, 385-388.

     plus a final Newton step to improve the approximation.

     'rgamma' for 'shape >= 1' uses

     Ahrens, J. H. and Dieter, U. (1982).  Generating gamma variates by
     a modified rejection technique.  _Communications of the ACM_,
     *25*, 47-54,

     and for '0 < shape < 1' uses

     Ahrens, J. H. and Dieter, U. (1974).  Computer methods for
     sampling from gamma, beta, Poisson and binomial distributions.
     _Computing_, *12*, 223-246.

References:

     Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) _The New S
     Language_.  Wadsworth & Brooks/Cole.

     Shea, B. L. (1988) Algorithm AS 239, Chi-squared and incomplete
     Gamma integral, _Applied Statistics (JRSS C)_ *37*, 466-473.

     Abramowitz, M. and Stegun, I. A. (1972) _Handbook of Mathematical
     Functions._ New York: Dover.  Chapter 6: Gamma and Related
     Functions.

See Also:

     'gamma' for the gamma function.

     Distributions for other standard distributions, including 'dbeta'
     for the Beta distribution and 'dchisq' for the chi-squared
     distribution which is a special case of the Gamma distribution.

Examples:

     -log(dgamma(1:4, shape=1))
     p <- (1:9)/10
     pgamma(qgamma(p,shape=2), shape=2)
     1 - 1/exp(qgamma(p, shape=1))

     # even for shape = 0.001 about half the mass is on numbers
     # that cannot be represented accurately (and most of those as zero)
     pgamma(.Machine$double.xmin, 0.001)
     pgamma(5e-324, 0.001)  # on most machines 5e-324 is the smallest
                            # representable non-zero number
     table(rgamma(1e4, 0.001) == 0)/1e4
```