NTNU

Kunnskap for en bedre verden

Institutt for matematiske fag

Eksamensoppgave i
ST2304 Statistisk modellering for biologer og bioteknologer

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Hjelpemiddelkode/Tillatte hjelpemidler: Tabeller og formler i statistikk, Tapir Forlag, K. Rottmann: Matematisk formelsamling, Kalkulator Casio fx-82ES PLUS, CITIZEN SR-270X, CITIZEN SR-270X College eller HP30S, ett gult A4-ark med egne håndskrevne notater.

Annen informasjon:
Hjelpesider for noen R funksjoner som du kan få bruk for følger i vedlegget. Alle svar skal begrunnes og besvarelsen skal inneholde naturlig mellomregning.

Målform/språk: bokmål

Antall sider: 7

Antall sider vedlegg: 3

Kontrollert av:

Dato Sign

Oppgave 1 Anta at den stokastiske variabelen X er binomisk fordelt med parametere $n = 20$ og $p = 0.3$.

a) Skriv R-uttrykk som beregner følgende sannsynlighetene

$$P(X < 9), \qquad P(X \leq 9), \qquad P(X > 9), \qquad P(X \geq 9).$$

Skjevheten til en stokastisk variabel Y er definert som

$$\frac{E((Y-\mu)^3)}{(\sigma^2)^{3/2}}$$

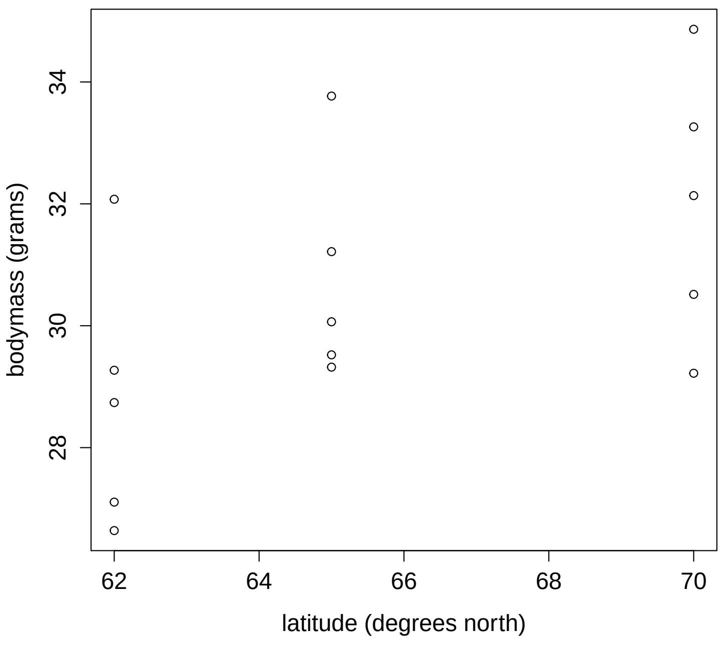
hvor μ og σ^2 er forventing og varians til Y.

b) Regn ut forventning og varians til X. Skriv et R-uttrykk som simulerer 1000 realisasjoner av X og tilordner dette til en vektor `x`. Skriv så et nytt uttrykk som basert på de simulerte verdiene estimerer skjevheten til X.

Oppgave 2 Bergmanns regel sier at gjennomsnittlig kroppstørrelse innen en art tenderer til å være større i subpopulasjoner med kaldt klima enn i subpopulasjoner med varmt klima. I en pilotstudie for å undersøke om dette gjelder for snømus (*Mustela nivalis*) samler en forsker inn tilsammen 15 individ fra subpopulasjoner lokalisert ved tre ulike breddegrader som vist i figur 1. Forskeren tilpasser så følgende modell i R.

```
> linear <- lm(bodymass~latitude)
> summary(linear)

Call:
lm(formula = bodymass ~ latitude)

Residuals:
    Min      1Q  Median      3Q     Max
-2.9749 -1.3083 -0.1913  1.0138  3.5128

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.0439    10.4535   0.483   0.6375
latitude      0.3879     0.1590   2.440   0.0298 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 2.032 on 13 degrees of freedom
Multiple R-squared:  0.3141,Adjusted R-squared:  0.2613
F-statistic: 5.952 on 1 and 13 DF,  p-value: 0.02979
```

a) Skriv opp modellen vi har tilpasset ovenfor i matematisk notasjon og gjør rede for modell-antakelsene. Hva er estimatene av de ukjente parameterene i modellen? Hva blir estimatet av forventet forskjell i kroppsstørrelse (antall gram) for to individ trukket fra henholdsvis 62. og 70. breddegrad?



Figur 1: Observerte kroppstørrelser (i gram) i subpopulasjoner ved tre ulike breddegrader.

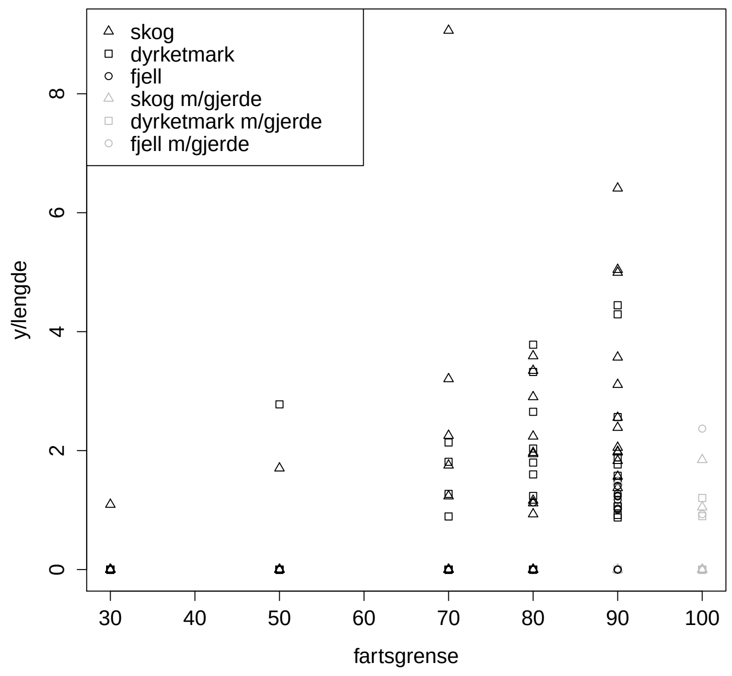
b) Er effekten av breddegrad på kroppstørrelse statistisk signifikant dersom vi bruker $\alpha = 0.05$ som signifikansnivå? Skriv et R-uttrykk som for samme hypotesetest beregner kritiske verdier dersom vi i stedet velger $\alpha = 0.01$ som signifikansnivå.

For å teste antakelsen om linearitet tilpasser forskeren en alternativ modell med breddegrad i stedet inkludert som en kategorisk forklaringsvariabel (faktor) som følger.

```
> latfactor <- factor(latitude)
> latfactor
 [1] 62 62 62 62 62 65 65 65 65 65 70 70 70 70 70
Levels: 62 65 70
> nonlinear <- lm(bodymass~latfactor)
> summary(nonlinear)

Call:
lm(formula = bodymass ~ latfactor)

Residuals:
    Min      1Q  Median      3Q     Max
-2.7790 -1.4715 -0.0266  0.8837  3.3096

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    28.7661     0.9272  31.024 7.91e-13 ***
latfactor65     2.0125     1.3113   1.535   0.1508
latfactor70     3.2336     1.3113   2.466   0.0297 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 2.073 on 12 degrees of freedom
Multiple R-squared:  0.3408,Adjusted R-squared:  0.2309
F-statistic: 3.101 on 2 and 12 DF,  p-value: 0.08209

> anova(linear,nonlinear)
Analysis of Variance Table

Model 1: bodymass ~ latitude
Model 2: bodymass ~ latfactor
  Res.Df    RSS Df Sum of Sq     F Pr(>F)
1     13 53.673
2     12 51.584  1    2.0891 0.486  0.499
```

c) Avgjør om modellene `linear` og `nonlinear` er nøstet. Er det grunnlag for å hevde at sammenhengen mellom kroppstørrelse og breddegrad er ikke-lineær om vi bruker $\alpha = 0.05$ som signifikansnivå? Hvilken av de modellene er å foretrekke?

d) Forskeren ønsker å publisere resultatet i en journal som opererer med $\alpha = 0.01$ som signifikansnivå (sannsynlighet for type I feil). Hun trenger derfor å beregne hvor mye mer data hun vil måtte regne med å måtte samle inn før effekten av breddegrad blir statistisk signifikant ved dette signifikansnivået. Anta at den lineære modellen er riktig og at de reelle parameterverdiene er som estimert over. Anta også at det nye større datasettet samles inn i form av kun to utvalg, begge av størrelse n, trukket fra populasjoner lokalisert ved 62. og 70. breddegrad. Skriv et R-utrykk som beregner nødvendig utvalgsstørrelse n under disse forutsetningene dersom vi krever at teststyrken skal være minst 0.9 (se vedlegg).



Figur 2: Antall påkjørsler dividert på vegsegmentlengde (km^{-1}) versus fartsgrense (km/time) for vegsegmenter innenfor ulike vegetasjonstyper og med eller uten viltgjerder (se symbolforklaring).

Oppgave 3 Vegmyndighetene ønsker å analysere hvordan antall elgpåkjørsler y langs ulike vegsegmenter registrert i løpet av en 10års-periode påvirkes av fartsgrensen for vegsegmentene (km/time), vegetasjonstypen langs vegsegmentene (skog, dyrket mark, fjell), lengden på de ulike vegsegmenter (målt i km), samt hvorvidt vegsegmentet er inngjærdet eller ikke (se figur 2). Dataene sammenstilles i følgende dataframe i R (de første 30 av totalt 300 observasjoner er vist) som vi så analyserer med en generalisert lineær modell.

```
   y vegetasjon fartsgrense gjerde lengde
1  0       skog          50    nei  0.699
2  0       skog          30    nei  0.948
3  0      fjell          90     ja  0.891
4  0 dyrketmark          70    nei  0.478
5  0      fjell          50    nei  0.384
6  0 dyrketmark          90     ja  1.089
7  0 dyrketmark          50    nei  0.411
8  0 dyrketmark          50    nei  0.382
9  1       skog          90     ja  0.680
10 0 dyrketmark          50    nei  1.043
11 0      fjell          50    nei  0.448
12 0 dyrketmark          80    nei  0.786
13 0 dyrketmark          50    nei  1.014
```

```
14 0       skog         30    nei  0.468
15 3       skog         80    nei  0.897
16 0 dyrketmark         30    nei  0.326
17 0      fjell         80    nei  0.752
18 0       skog         50    nei  0.644
19 0 dyrketmark        100     ja  1.134
20 0 dyrketmark        100     ja  0.522
21 0       skog         80    nei  0.846
22 0      fjell         80    nei  0.717
23 3       skog         90    nei  0.595
24 2       skog         50    nei  1.174
25 0       skog         50    nei  0.520
26 1       skog         70    nei  0.444
27 0      fjell        100     ja  0.805
28 0       skog        100     ja  1.126
29 0       skog         70    nei  0.574
30 0       skog         50    nei  0.880

Call:
glm(formula = y ~ log(fartsgrense) + vegetasjon + gjerde, family = poisson(link = "log"),
    offset = log(lengde))

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.81143  -0.54300  -0.30002  -0.08992   3.07849

Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept)          -21.1970     3.3543  -6.319 2.63e-10 ***
log(fartsgrense)       4.9203     0.7604   6.471 9.74e-11 ***
vegetasjondyrketmark  -0.4956     0.2257  -2.196   0.0281 *
vegetasjonfjell       -1.7222     0.3286  -5.241 1.59e-07 ***
gjerdeja              -2.8762     0.4191  -6.863 6.73e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 319.28  on 299  degrees of freedom
Residual deviance: 161.71  on 295  degrees of freedom
AIC: 325.02

Number of Fisher Scoring iterations: 6
```

a) Forklar hvorfor Poisson-antakelsen, log link-funksjon, og bruken av log til lengden av veg-segmentene som offset-variabel kan være rimelige antakelser.

b) Vi har inkludert log til fartsgrensen som numerisk forklaringsvariabel i modellen. Med hvor mange prosent reduseres forventet antall påkjørsler i følge den estimerte modellen dersom fartsgrensen reduseres fra 80 til 70 km/time gitt at andre forklaringsvariable holdes konstant? For hvilken vegetasjonstype gir en slik fartsgrensereduksjon størst forventet reduksjon i antall påkjørsler?

c) Er det grunnlag for å tro at det er overdispersjon i dataene? Diskuter konkrete mekanismer som kan generere overdispersjon i den konkrete situasjonen vi har modellert.

Oppgave 4 Anta at $x_1, x_2, \ldots, x_n$ er uavhengige observasjoner fra en såkalt Gamma-fordeling med sannsynlighetstetthetsfunksjon

$$f(x) = \frac{1}{\sigma^\alpha \Gamma(\alpha)} x^{\alpha-1} e^{-x/\sigma}, \text{for } x > 0.$$

Se eventuellt hjelpesider for beskrivelse av den matematiske funksjonen $\Gamma(\alpha)$.

a) Vi ønsker å estimere de ukjente parameterne α og σ. Skriv opp et matematisk uttrykk for likelihood- og log-likelihoodfunksjonen. Skriv også en R funksjon som beregner log likelihoodet for gitte parameterverdier og for et gitt tilfeldig utvalg $x_1, x_2, \ldots, x_n$ representert i R på passende måte. Forklar kort med ord hva vi mener med sannsynlighetsmaksimeringsestimatorene av de ukjente parameterne i modellen og hvordan disse kan beregnes numerisk i R.

power.t.test *Power calculations for one and two sample t tests*

Description

Compute the power of the one- or two- sample t test, or determine parameters to obtain a target power.

Usage

```
power.t.test(n = NULL, delta = NULL, sd = 1, sig.level = 0.05,
             power = NULL,
             type = c("two.sample", "one.sample", "paired"),
             alternative = c("two.sided", "one.sided"),
             strict = FALSE, tol = .Machine$double.eps^0.25)
```

Arguments

`n`	number of observations (per group)
`delta`	true difference in means
`sd`	standard deviation
`sig.level`	significance level (Type I error probability)
`power`	power of test (1 minus Type II error probability)
`type`	string specifying the type of t test. Can be abbreviated.
`alternative`	one- or two-sided test. Can be abbreviated.
`strict`	use strict interpretation in two-sided case
`tol`	numerical tolerance used in root finding, the default providing (at least) four significant digits.

Details

Exactly one of the parameters `n`, `delta`, `power`, `sd`, and `sig.level` must be passed as `NULL`, and that parameter is determined from the others. Notice that the last two have non-NULL defaults, so NULL must be explicitly passed if you want to compute them.

If `strict = TRUE` is used, the power will include the probability of rejection in the opposite direction of the true effect, in the two-sided case. Without this the power will be half the significance level if the true difference is zero.

Value

Object of class `"power.htest"`, a list of the arguments (including the computed one) augmented with `method` and `note` elements.

Note

`uniroot` is used to solve the power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given.

Author(s)

Peter Dalgaard. Based on previous work by Claus Ekstroem

See Also

`t.test`, `uniroot`

Examples

```
power.t.test(n = 20, delta = 1)
power.t.test(power = .90, delta = 1)
power.t.test(power = .90, delta = 1, alternative = "one.sided")
```

Binomial *The Binomial Distribution*

Description

Density, distribution function, quantile function and random generation for the binomial distribution with parameters `size` and `prob`.

This is conventionally interpreted as the number of 'successes' in `size` trials.

Usage

```
dbinom(x, size, prob, log = FALSE)
pbinom(q, size, prob, lower.tail = TRUE, log.p = FALSE)
qbinom(p, size, prob, lower.tail = TRUE, log.p = FALSE)
rbinom(n, size, prob)
```

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.
`size`	number of trials (zero or more).
`prob`	probability of success on each trial.
`log, log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \le x]$, otherwise, $P[X > x]$.

Details

The binomial distribution with `size` $= n$ and `prob` $= p$ has density

$$p(x) = \binom{n}{x} p^x (1-p)^{n-x}$$

for $x = 0, \ldots, n$. Note that binomial *coefficients* can be computed by `choose` in R.

If an element of `x` is not integer, the result of `dbinom` is zero, with a warning.

$p(x)$ is computed using Loader's algorithm, see the reference below.

The quantile is defined as the smallest value x such that $F(x) \ge p$, where F is the distribution function.

Value

`dbinom` gives the density, `pbinom` gives the distribution function, `qbinom` gives the quantile function and `rbinom` generates random deviates.

If `size` is not an integer, `NaN` is returned.

The length of the result is determined by `n` for `rbinom`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Source

For `dbinom` a saddle-point expansion is used: see

Catherine Loader (2000). *Fast and Accurate Computation of Binomial Probabilities*; available from `http://www.herine.net/stat/software/dbinom.html`.

`pbinom` uses `pbeta`.

`qbinom` uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.

`rbinom` (for `size < .Machine$integer.max`) is based on

Kachitvichyanukul, V. and Schmeiser, B. W. (1988) Binomial random variate generation. *Communications of the ACM*, **31**, 216–222.

For larger values it uses inversion.

See Also

Distributions for other standard distributions, including `dnbinom` for the negative binomial, and `dpois` for the Poisson distribution.

Examples

```
require(graphics)
# Compute P(45 < X < 55) for X Binomial(100,0.5)
sum(dbinom(46:54, 100, 0.5))

## Using "log = TRUE" for an extended range :
n <- 2000
k <- seq(0, n, by = 20)
plot (k, dbinom(k, n, pi/10, log = TRUE), type = "l", ylab = "log density",
      main = "dbinom(*, log=TRUE) is better than  log(dbinom(*))")
lines(k, log(dbinom(k, n, pi/10)), col = "red", lwd = 2)
## extreme points are omitted since dbinom gives 0.
mtext("dbinom(k, log=TRUE)", adj = 0)
mtext("extended range", adj = 0, line = -1, font = 4)
mtext("log(dbinom(k))", col = "red", adj = 1)
```

GammaDist *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 $P[X \le x]$, otherwise, $P[X > x]$.

Details

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

The Gamma distribution with parameters `shape` $= \alpha$ and `scale` $= \sigma$ has density

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

for $x \ge 0$, $\alpha > 0$ and $\sigma > 0$. (Here $\Gamma(\alpha)$ 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 $E(X) = \alpha\sigma$ and $Var(X) = \alpha\sigma^2$.

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` may 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.

The length of the result is determined by `n` for `rgamma`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

The S (Becker *et al* (1988) parametrization was via `shape` and `rate`: S had no `scale` parameter. In R 2.x.y `scale` took precedence over `rate`, but now it is an error to supply both.

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

$$P(a,x) = \frac{1}{\Gamma(a)} \int_0^x t^{a-1} e^{-t} dt$$

$P(a,x)$ is `pgamma(x, a)`. Other authors (for example Karl Pearson in his 1922 tables) omit the normalizing factor, defining the incomplete gamma function $\gamma(a,x)$ as $\gamma(a,x) = \int_0^x t^{a-1} e^{-t} dt$, i.e., `pgamma(x, a) * gamma(a)`. Yet other use the 'upper' incomplete gamma function,

$$\Gamma(a,x) = \int_x^\infty t^{a-1} e^{-t} dt,$$

which can be computed by `pgamma(x, a, lower = FALSE) * gamma(a)`.

Note however that `pgamma(x, a, ..)` currently requires $a > 0$, whereas the incomplete gamma function is also defined for negative a. In that case, you can use `gamma_inc(a,x)` (for $\Gamma(a,x)$) from package **gsl**.

See also `http://en.wikipedia.org/wiki/Incomplete_gamma_function`, or `http://dlmf.nist gov/8.2#i`.

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.

NIST Digital Library of Mathematical Functions. `http://dlmf.nist.gov/`, section 8.2.

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
```

Special *Special Functions of Mathematics*

Description

Special mathematical functions related to the beta and gamma functions.

Usage

```
beta(a, b)
lbeta(a, b)

gamma(x)
lgamma(x)
psigamma(x, deriv = 0)
digamma(x)
trigamma(x)

choose(n, k)
lchoose(n, k)
factorial(x)
lfactorial(x)
```

Arguments

`a, b`	non-negative numeric vectors.
`x, n`	numeric vectors.
`k, deriv`	integer vectors.

Details

The functions `beta` and `lbeta` return the beta function and the natural logarithm of the beta function,

$$B(a,b) = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)}.$$

The formal definition is

$$B(a,b) = \int_0^1 t^{a-1}(1-t)^{b-1} dt$$

(Abramowitz and Stegun section 6.2.1, page 258). Note that it is only defined in R for non-negative `a` and `b`, and is infinite if either is zero.

The functions `gamma` and `lgamma` return the gamma function $\Gamma(x)$ and the natural logarithm of *the absolute value of* the gamma function. The gamma function is defined by (Abramowitz and Stegun section 6.1.1, page 255)

$$\Gamma(x) = \int_0^\infty t^{x-1} e^{-t} dt$$

for all real `x` except zero and negative integers (when `NaN` is returned). There will be a warning on possible loss of precision for values which are too close (within about 10^{-8})) to a negative integer less than '`-10`'.

`factorial(x)` ($x!$ for non-negative integer `x`) is defined to be `gamma(x+1)` and `lfactorial` to be `lgamma(x+1)`.

The functions `digamma` and `trigamma` return the first and second derivatives of the logarithm of the gamma function. `psigamma(x, deriv)` (`deriv >= 0`) computes the `deriv`-th derivative of $\psi(x)$.

$$\texttt{digamma(x)} = \psi(x) = \frac{d}{dx} \ln \Gamma(x) = \frac{\Gamma'(x)}{\Gamma(x)}$$

ψ and its derivatives, the `psigamma()` functions, are often called the 'polygamma' functions, e.g. in Abramowitz and Stegun (section 6.4.1, page 260); and higher derivatives (`deriv = 2:4`) have occasionally been called 'tetragamma', 'pentagamma', and 'hexagamma'.

The functions `choose` and `lchoose` return binomial coefficients and the logarithms of their absolute values. Note that `choose(n, k)` is defined for all real numbers n and integer k. For $k \geq 1$ it is defined as $n(n-1)\cdots(n-k+1)/k!$, as 1 for $k = 0$ and as 0 for negative k. Non-integer values of `k` are rounded to an integer, with a warning.
`choose(*, k)` uses direct arithmetic (instead of `[l]gamma` calls) for small `k`, for speed and accuracy reasons. Note the function `combn` (package **utils**) for enumeration of all possible combinations.

The `gamma`, `lgamma`, `digamma` and `trigamma` functions are internal generic primitive functions: methods can be defined for them individually or via the `Math` group generic.

Source

`gamma`, `lgamma`, `beta` and `lbeta` are based on C translations of Fortran subroutines by W. Fullerton of Los Alamos Scientific Laboratory (now available as part of SLATEC).

`digamma`, `trigamma` and `psigamma` are based on

Amos, D. E. (1983). A portable Fortran subroutine for derivatives of the psi function, Algorithm 610, *ACM Transactions on Mathematical Software* **9(4)**, 494–502.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (For `gamma` and `lgamma`.)

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions*. New York: Dover. `http://en.wikipedia.org/wiki/Abramowitz_and_Stegun` provides links to the full text which is in public domain.
Chapter 6: Gamma and Related Functions.

See Also

`Arithmetic` for simple, `sqrt` for miscellaneous mathematical functions and `Bessel` for the real Bessel functions.

For the incomplete gamma function see `pgamma`.

Examples

```
require(graphics)

choose(5, 2)
for (n in 0:10) print(choose(n, k = 0:n))

factorial(100)
lfactorial(10000)


## gamma has 1st order poles at 0, -1, -2, ...
## this will generate loss of precision warnings, so turn off
op <- options("warn")
options(warn = -1)
x <- sort(c(seq(-3, 4, length.out = 201), outer(0:-3, (-1:1)*1e-6, "+")))
plot(x, gamma(x), ylim = c(-20,20), col = "red", type = "l", lwd = 2,
     main = expression(Gamma(x)))
abline(h = 0, v = -3:0, lty = 3, col = "midnightblue")
options(op)

x <- seq(0.1, 4, length.out = 201); dx <- diff(x)[1]
par(mfrow = c(2, 3))
for (ch in c("", "l","di","tri","tetra","penta")) {
  is.deriv <- nchar(ch) >= 2
  nm <- paste0(ch, "gamma")
  if (is.deriv) {
    dy <- diff(y) / dx # finite difference
    der <- which(ch == c("di","tri","tetra","penta")) - 1
    nm2 <- paste0("psigamma(*, deriv = ", der,")")
    nm  <- if(der >= 2) nm2 else paste(nm, nm2, sep = " ==\n")
    y <- psigamma(x, deriv = der)
  } else {
    y <- get(nm)(x)
  }
  plot(x, y, type = "l", main = nm, col = "red")
  abline(h = 0, col = "lightgray")
  if (is.deriv) lines(x[-1], dy, col = "blue", lty = 2)
}
par(mfrow = c(1, 1))

## "Extended" Pascal triangle:
fN <- function(n) formatC(n, width=2)
for (n in -4:10) {
    cat(fN(n),":", fN(choose(n, k = -2:max(3, n+2))))
    cat("\n")
}

## R code version of choose()  [simplistic; warning for k < 0]:
mychoose <- function(r, k)
    ifelse(k <= 0, (k == 0),
           sapply(k, function(k) prod(r:(r-k+1))) / factorial(k))
k <- -1:6
cbind(k = k, choose(1/2, k), mychoose(1/2, k))

## Binomial theorem for n = 1/2 ;
## sqrt(1+x) = (1+x)^(1/2) = sum_{k=0}^Inf  choose(1/2, k) * x^k :
k <- 0:10 # 10 is sufficient for ~ 9 digit precision:
sqrt(1.25)
sum(choose(1/2, k)* .25^k)
```