

Package ‘Rmpfr’

November 15, 2016

Title R MPFR - Multiple Precision Floating-Point Reliable

Version 0.6-1

Date 2016-11-15

DateNote Previous CRAN version 0.6-0 on 2015-12-04

Type Package

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SystemRequirements gmp (>= 4.2.3), mpfr (>= 3.0.0)

SystemRequirementsNote MPFR (MP Floating-Point Reliable Library, <http://mpfr.org/>) and GMP (GNU Multiple Precision library, <http://gmplib.org/>), see >> README.md

Depends gmp (>= 0.5-8), R (>= 3.0.1)

Imports stats, utils, methods

Suggests MASS, polynom, sfsmisc (>= 1.0-20), Matrix

SuggestsNote MASS, polynom, sfsmisc: only for vignette; Matrix:
test-tools

URL <http://rmpfr.r-forge.r-project.org/>

Description Arithmetic (via S4 classes and methods) for arbitrary precision floating point numbers, including transcendental (“special”) functions. To this end, Rmpfr interfaces to the LGPL’ed MPFR (Multiple Precision Floating-Point Reliable) Library which itself is based on the GMP (GNU Multiple Precision) Library.

License GPL (>= 2)

NeedsCompilation yes

Repository CRAN

Date/Publication 2016-11-15 19:38:16

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Rmpfr-package

R MPFR - Multiple Precision Floating-Point Reliable

Description

Rmpfr provides S4 classes and methods for arithmetic including transcendental ("special") functions for arbitrary precision floating point numbers, here often called "mpfr - numbers". To this end, it interfaces to the LGPL'ed MPFR (Multiple Precision Floating-Point Reliable) Library which itself is based on the GMP (GNU Multiple Precision) Library.

Details

Package: Rmpfr
 SystemRequirements: gmp ($\geq 4.2.3$), mpfr ($\geq 3.0.0$)
 (C (not R!) libraries; must be installed)
 Depends: methods, gmp ($\geq 0.5-8$), R ($\geq 2.12.0$)
 Imports: gmp, stats, utils
 Suggests: MASS, polynom, sfsmisc ($\geq 1.0-20$), Matrix
 SuggestNotes: MASS, polynom, sfsmisc are only needed for vignette; Matrix only because of its test-tools
 URL: <http://rmpfr.r-forge.r-project.org/>
 License: GPL (≥ 2)

The following (help pages) index does not really mention that we provide *many* methods for mathematical functions, including [gamma](#), [digamma](#), etc, namely, all of R's (S4) Math group (with the only exception of [trigamma](#)), see the list in the examples. Additionally also [pnorm](#), the "error function", and more, see the list in [zeta](#), and further note the first vignette (below).

Partial index:

mpfr	Create "mpfr" Numbers (Objects)
mpfrArray	Construct "mpfrArray" almost as by array()
mpfr-class	Class "mpfr" of Multiple Precision Floating Point Numbers
mpfrMatrix-class	Classes "mpfrMatrix" and "mpfrArray"
Bernoulli	Bernoulli Numbers in Arbitrary Precision
Bessel_mpfr	Bessel functions of Integer Order in multiple precisions
c.mpfr	MPFR Number Utilities
cbind	"mpfr" . . . - Methods for Functions cbind() , rbind()
chooseMpfr	Binomial Coefficients and Pochhammer Symbol aka Rising Factorial
factorialMpfr	Factorial 'n!' in Arbitrary Precision
formatMpfr	Formatting MPFR (multiprecision) Numbers
getPrec	Rmpfr - Utilities for Precision Setting, Printing, etc
roundMpfr	Rounding to Binary bits, "mpfr-internally"
seqMpfr	"mpfr" Sequence Generation
sumBinomMpfr	(Alternating) Binomial Sums via Rmpfr
zeta	Special Mathematical Functions (MPFR)
integrateR	One-Dimensional Numerical Integration - in pure R
unirootR	One Dimensional Root (Zero) Finding - in pure R
optimizeR	High Precision One-Dimensional Optimization
hjkMpfr	Hooke-Jeeves Derivative-Free Minimization R (working for MPFR)

Further information is available in the following vignettes:

Rmpfr-pkg	Rmpfr (source, pdf)
log1mexp-note	Accurately Computing $\log(1 - \exp(\cdot))$ – Assessed by Rmpfr (source, pdf)

Author(s)

Martin Maechler

References

MPFR (MP Floating-Point Reliable Library), <http://mpfr.org/>

GMP (GNU Multiple Precision library), <http://gmplib.org/>

and see the vignettes mentioned above.

See Also

The R package `gmp` for big integer and rational numbers ([bigrational](#)) on which **Rmpfr** now depends.

Examples

```
## Using "mpfr" numbers instead of regular numbers...
n1.25 <- mpfr(5, precBits = 256)/4
n1.25

## and then "everything" just works with the desired chosen precision:hig
n1.25 ^ c(1:7, 20, 30) ## fully precise; compare with
print(1.25 ^ 30, digits=19)

exp(n1.25)

## Show all math functions which work with "MPFR" numbers (1 exception: trigamma)
getGroupMembers("Math")

## We provide *many* arithmetic, special function, and other methods:
showMethods(classes = "mpfr")
showMethods(classes = "mpfrArray")
```

array_or_vector-class *Auxiliary Class "array\or_vector"*

Description

"array_or_vector" is the class union of `c("array", "matrix", "vector")` and exists for its use in signatures of method definitions.

Details

Using "array_or_vector" instead of just "vector" in a signature makes an important difference: E.g., if we had `setMethod(crossprod, c(x="mpfr", y="vector"), function(x,y) CPR(x,y))`, a call `crossprod(x, matrix(1:6, 2,3))` would extend into a call of `CPR(x, as(y, "vector"))` such that `CPR()`'s second argument would simply be a vector instead of the desired 2×3 matrix.

Objects from the Class

A virtual Class: No objects may be created from it.

Examples

```
showClass("array_or_vector")
```

```
asNumeric-methods      Methods for asNumeric(<mpfr>)
```

Description

Methods for function `asNumeric` (in package `gmp`).

Usage

```
## S4 method for signature 'mpfrArray'
asNumeric(x)
```

Arguments

`x` a “number-like” object, here, a `mpfr` or typically `mpfrArray`one.

Value

an R object of type (`typeof`) `"numeric"`, a `matrix` or `array` if `x` had non-NULL dimension `dim()`.

Methods

`signature(x = "mpfrArray")` this method also dispatches for `mpfrMatrix` and returns a numeric array.

`signature(x = "mpfr")` for non-array/matrix, `asNumeric(x)` is basically the same as `as.numeric(x)`.

Author(s)

Martin Maechler

See Also

our lower level (non-generic) `toNum()`. Further, `asNumeric` (package `gmp`), standard R's `as.numeric()`.

Examples

```
x <- (0:7)/8 # (exact)
X <- mpfr(x, 99)
stopifnot(identical(asNumeric(x), x),
  identical(asNumeric(X), x))

m <- matrix(1:6, 3,2)
(M <- mpfr(m, 99) / 5) ##-> "mpfrMatrix"
asNumeric(M) # numeric matrix
stopifnot(all.equal(asNumeric(M), m/5),
  identical(asNumeric(m), m))# remains matrix
```

atomicVector-class *Virtual Class "atomicVector" of Atomic Vectors*

Description

The `class` "atomicVector" is a *virtual* class containing all atomic vector classes of base `R`, as also implicitly defined via `is.atomic`.

Objects from the Class

A virtual Class: No objects may be created from it.

Methods

In the `Matrix` package, the "atomicVector" is used in signatures where typically "old-style" "matrix" objects can be used and can be substituted by simple vectors.

Extends

The atomic classes "logical", "integer", "double", "numeric", "complex", "raw" and "character" are extended directly. Note that "numeric" already contains "integer" and "double", but we want all of them to be direct subclasses of "atomicVector".

Author(s)

Martin Maechler

See Also

`is.atomic`, `integer`, `numeric`, `complex`, etc.

Examples

```
showClass("atomicVector")
```

Description

Computes the Bernoulli numbers in the desired (binary) precision. The computation happens via the [zeta](#) function and the formula

$$B_k = -k\zeta(1 - k),$$

and hence the only non-zero odd Bernoulli number is $B_1 = +1/2$. (Another tradition defines it, equally sensibly, as $-1/2$.)

Usage

```
Bernoulli(k, precBits = 128)
```

Arguments

k	non-negative integer vector
precBits	the precision in <i>bits</i> desired.

Value

an [mpfr](#) class vector of the same length as k, with i-th component the k[i]-th Bernoulli number.

Author(s)

Martin Maechler

References

http://en.wikipedia.org/wiki/Bernoulli_number

See Also

[zeta](#) is used to compute them.

Examples

```
Bernoulli(0:10)
plot(as.numeric(Bernoulli(0:15)), type = "h")

curve(-x*zeta(1-x), -.2, 15.03, n=300,
      main = expression(-x %% zeta(1-x)))
legend("top", paste(c("even", "odd "), "Bernoulli numbers"),
      pch=c(1,3), col=2, pt.cex=2, inset=1/64)
abline(h=0,v=0, lty=3, col="gray")
k <- 0:15; k[1] <- 1e-4
```

```

points(k, -k*zeta(1-k), col=2, cex=2, pch=1+2*(k%2))

## They pretty much explode for larger k :
k2 <- 2*(1:120)
plot(k2, abs(as.numeric(Bernoulli(k2))), log = "y")
title("Bernoulli numbers exponential growth")

Bernoulli(10000)# - 9.0494239636 * 10^27677

```

Bessel_mpfr

Bessel functions of Integer Order in multiple precisions

Description

Bessel functions of integer orders, provided via arbitrary precision algorithms from the MPFR library.

Note that the computation can be very slow when n and x are large (and of similar magnitude).

Usage

```

Ai(x)
j0(x)
j1(x)
jn(n, x, rnd.mode = c("N", "D", "U", "Z", "A"))
y0(x)
y1(x)
yn(n, x, rnd.mode = c("N", "D", "U", "Z", "A"))

```

Arguments

<code>x</code>	a numeric or mpfr vector.
<code>n</code>	non-negative integer (vector).
<code>rnd.mode</code>	a 1-letter string specifying how <i>rounding</i> should happen at C-level conversion to MPFR, see mpfr .

Value

Computes multiple precision versions of the Bessel functions of *integer* order, $J_n(x)$ and $Y_n(x)$, and—when using MPFR library 3.0.0 or newer—also of the Airy function $Ai(x)$.

See Also

[besselJ](#), and [besselY](#) compute the same bessel functions but for arbitrary *real* order and only precision of a bit more than ten digits.

Examples

```
x <- (0:100)/8 # (have exact binary representation)
stopifnot( all.equal(besselY(x, 0), bY0 <- y0(x))
           , all.equal(besselJ(x, 1), bJ1 <- j1(x))
           , all.equal(yn(0,x), bY0)
           , all.equal(jn(1,x), bJ1)
           )
```

bind-methods *"mpfr" '...' - Methods for Functions cbind(), rbind()*

Description

`cbind` and `rbind` methods for signature `...` (see [dotsMethods](#) are provided for class `Mnumber`, i.e., for binding numeric vectors and class `"mpfr"` vectors and matrices (`"mpfrMatrix"`) together.

Usage

```
cbind(..., deparse.level = 1)
rbind(..., deparse.level = 1)
```

Arguments

`...` matrix-/vector-like R objects to be bound together, see the **base** documentation, [cbind](#).

`deparse.level` integer determining under which circumstances column and row names are built from the actual arguments' 'expression', see [cbind](#).

Value

typically a 'matrix-like' object, here typically of class `"mpfrMatrix"`.

Methods

`...` = **"Mnumber"** is used to (c|r)bind multiprecision "numbers" (inheriting from class `"mpfr"`) together, maybe combined with simple numeric vectors.

`...` = **"ANY"** reverts to `cbind` and `rbind` from package **base**.

Author(s)

Martin Maechler

See Also

[cbind2](#), [cbind](#), Documentation in base R's **methods** package

Examples

```
cbind(1, mpfr(6:3, 70)/7, 3:0)
```

chooseMpfr

*Binomial Coefficients and Pochhammer Symbol aka Rising Factorial***Description**

Compute binomial coefficients, `chooseMpfr(a, n)` being mathematically the same as `choose(a, n)`, but using high precision (MPFR) arithmetic.

`chooseMpfr.all(n)` means the vector `choose(n, 1:n)`, using enough bits for exact computation via MPFR. However, `chooseMpfr.all()` is now **deprecated** in favor of `chooseZ` from package **gmp**, as that is now vectorized.

`pochMpfr()` computes the Pochhammer symbol or “rising factorial”, also called the “Pochhammer function”, “Pochhammer polynomial”, “ascending factorial”, “rising sequential product” or “upper factorial”,

$$x^{(n)} = x(x+1)(x+2)\cdots(x+n-1) = \frac{(x+n-1)!}{(x-1)!} = \frac{\Gamma(x+n)}{\Gamma(x)}.$$

Usage

```
chooseMpfr(a, n, rnd.mode = c("N", "D", "U", "Z", "A"))
chooseMpfr.all(n, precBits=NULL, k0=1, alternating=FALSE)
pochMpfr(a, n, rnd.mode = c("N", "D", "U", "Z", "A"))
```

Arguments

<code>a</code>	a numeric or <code>mpfr</code> vector.
<code>n</code>	an integer vector; if not of length one, <code>n</code> and <code>a</code> are recycled to the same length.
<code>rnd.mode</code>	a 1-letter string specifying how <i>rounding</i> should happen at C-level conversion to MPFR, see <code>mpfr</code> .
<code>precBits</code>	integer or NULL for increasing the default precision of the result.
<code>k0</code>	integer scalar
<code>alternating</code>	logical, for <code>chooseMpfr.all()</code> , indicating if <i>alternating sign</i> coefficients should be returned, see below.

Value

For

`chooseMpfr()`, `pochMpfr()`: an `mpfr` vector of length $\max(\text{length}(a), \text{length}(n))$;

`chooseMpfr.all(n, k0)`: a `mpfr` vector of length $n-k0+1$, of binomial coefficients $C_{n,m}$ or, if `alternating` is true, $(-1)^m \cdot C_{n,m}$ for $m \in k0:n$.

Note

If you need high precision `choose(a, n)` (or `Pochhammer(a,n)`) for large `n`, maybe better work with the corresponding `factorial(mpfr(...))`, or `gamma(mpfr(...))` terms.

See Also

`choose(n,m)` (**base R**) computes the binomial coefficient $C_{n,m}$ which can also be expressed via Pochhammer symbol as $C_{n,m} = (n - m + 1)^{(m)}/m!$.

`chooseZ` from package **gmp**; for now, `factorialMpfr`.

For (alternating) binomial sums, directly use `sumBinomMpfr`, as that is potentially more efficient.

Examples

```
pochMpfr(100, 4) == 100*101*102*103 # TRUE
a <- 100:110
pochMpfr(a, 10) # exact (but too high precision)
x <- mpfr(a, 70)# should be enough
(px <- pochMpfr(x, 10)) # the same as above (needing only 70 bits)
stopifnot(pochMpfr(a, 10) == px,
          px[1] ==prod(mpfr(100:109, 100)))# used to fail

(c1 <- chooseMpfr(1000:997, 60)) # -> automatic "correct" precision
stopifnot(all.equal(c1, choose(1000:997, 60), tolerance=1e-12))

## --- Experimenting & Checking
n.set <- c(1:10, 20, 50:55, 100:105, 200:203, 300:303, 500:503,
          699:702, 999:1001)
if(!Rmpfr:::doExtras()) { ## speed up: smaller set
  n. <- n.set[-(1:10)]
  n.set <- c(1:10, n.[ c(TRUE, diff(n.) > 1)])
}
C1 <- C2 <- numeric(length(n.set))
for(i.n in seq_along(n.set)) {
  cat(n <- n.set[i.n],":")
  C1[i.n] <- system.time(c.c <- chooseMpfr.all(n) )[1]
  C2[i.n] <- system.time(c.2 <- chooseMpfr(n, 1:n))[1]
  stopifnot(is.whole(c.c), c.c == c.2,
            if(n > 60) TRUE else all.equal(c.c, choose(n, 1:n), tolerance = 1e-15))
  cat(" [0k]\n")
}
matplot(n.set, cbind(C1,C2), type="b", log="xy",
        xlab = "n", ylab = "system.time(.) [s]")
legend("topleft", c("chooseMpfr.all(n)", "chooseMpfr(n, 1:n)"),
      pch=as.character(1:2), col=1:2, lty=1:2, bty="n")

## Currently, chooseMpfr.all() is faster only for large n (>= 300)
## That would change if we used C-code for the *.all() version
```


formatHex

*Flexibly Format Numbers in Binary, Hex and Decimal Format***Description**

Show numbers in binary, hex and decimal format. The resulting character-like objects can be back-transformed to "mpfr" numbers via `mpfr()`.

Usage

```
formatHex(x, precBits = min(getPrec(x)), style = "+")
```

```
formatBin(x, precBits = min(getPrec(x)), scientific = TRUE,
          left.pad = "_", right.pad = left.pad, style = "+")
```

```
formatDec(x, precBits = min(getPrec(x)), digits = decdigits,
          nsmall = NULL, scientific = FALSE, style = "+", ...)
```

Arguments

<code>x</code>	a numeric or <code>mpfr</code> R object.
<code>precBits</code>	integer, the number of bits of precision, typically derived from <code>x</code> , see <code>getPrec</code> . Numeric, i.e., double precision numbers have 53 bits. For more detail, see <code>mpfr</code> .
<code>style</code>	a single character, to be used in <code>sprintf</code> 's format (<code>fmt</code>), immediately after the <code>"</code> sets a sign in the output, i.e., <code>"+"</code> or <code>"-"</code> , where as <code>style = " "</code> may seem more standard.
<code>scientific</code>	logical indicating that <code>formatBin</code> should display the binary representation in scientific notation (<code>mpfr(3, 5)</code> is displayed as <code>+0b1.1000p+1</code>). When <code>FALSE</code> , <code>formatBin</code> will display the binary representation in regular format shifted to align binary points (<code>mpfr(3, 5)</code> is displayed <code>+0b11.000</code>).
<code>...</code>	additional optional arguments. <code>formatHex, formatBin</code> : <code>precBits</code> is the only <code>...</code> argument acted on. Other <code>...</code> arguments are ignored. <code>formatDec</code> : <code>precBits</code> is acted on. Any argument accepted by <code>format</code> (except <code>nsmall</code>) is acted on. Other <code>...</code> arguments are ignored.
<code>left.pad, right.pad</code>	characters (one-character strings) that will be used for left- and right-padding of the formatted string when <code>scientific=FALSE</code> . <i>Do not change these unless for display-only purpose !!</i>
<code>nsmall</code>	only used when <code>scientific</code> is false, then passed to <code>format()</code> . If <code>NULL</code> , the default is computed from the range of the non-zero values of <code>x</code> .

`digits` integer; the number of decimal digits displayed is the larger of this argument and the internally generated value that is a function of `precBits`. This is related to but different than `digits` in `format`.

Details

For the hexadecimal representation, when the precision is not larger than double precision, `sprintf()` is used directly, otherwise `formatMpfr()` is used and post processed. For the binary representation, the hexadecimal value is calculated and then edited by substitution of the binary representation of the hex characters coded in the `HextoBin` vector. For binary with `scientific=FALSE`, the result of the `scientific=TRUE` version is edited to align binary points. For the decimal representation, the hexadecimal value is calculated with the specified precision and then sent to the `format` function for `scientific=FALSE` or to the `sprintf` function for `scientific=TRUE`.

Value

a character vector (or matrix) like `x`, say `r`, containing the formatted representation of `x`, with a `class` (unless `left.pad` or `right.pad` were not `"_"`). In that case, `formatHex()` returns class `"Hcharacter"` and `formatBin()` gives class `"Bcharacter"`; for these, `mpfr(.)` has methods and will basically return `x`, i.e., work as *inverse* function.

Author(s)

Richard M. Heiberger <rmh@temple.edu>, with minor tweaking by Martin M.

References

R FAQ 7.31: Why doesn't R think these numbers are equal? `system.file("../..doc/FAQ")`

See Also

`mpfr`, `sprintf`

Examples

```
FourBits <- mpfr(matrix(0:31, 8, 4, dimnames = list(0:7, c(0,8,16,24))),
                 precBits=4) ## 4 significant bits
FourBits

formatHex(FourBits)
formatBin(FourBits, style = " ")
formatBin(FourBits, scientific=FALSE)
formatDec(FourBits)

FBB <- formatBin(FourBits)
(nFBB <- mpfr(FBB))
stopifnot(all.equal(nFBB, FourBits, tol=0))

FBH <- formatHex(FourBits)
(nFBH <- mpfr(FBH))
stopifnot(all.equal(nFBH, FourBits, tol=0))
```

```
TenFrac <- matrix((1:10)/10, dimnames=list(1:10, expression(1/x)))
TenFrac9 <- mpfr(TenFrac, precBits=9) ## 9 significant bits
TenFrac9
formatHex(TenFrac9)
formatBin(TenFrac9)
formatBin(TenFrac9, scientific=FALSE)
formatDec(TenFrac9)
formatDec(TenFrac9, precBits=10)
```

formatMpfr

Formatting MPFR (multiprecision) Numbers

Description

Flexible formatting of “multiprecision numbers”, i.e., objects of class `mpfr`. `formatMpfr()` is also the `mpfr` method of the generic `format` function.

The `formatN()` methods for `mpfr` numbers renders them differently than their double precision equivalents, by appending “_M”.

Usage

```
formatMpfr(x, digits = NULL, trim = FALSE, scientific = NA,
  base = 10, showNeg0 = TRUE,
  big.mark = "", big.interval = 3L,
  small.mark = "", small.interval = 5L,
  decimal.mark = ".",
  exponent.char = if(base <= 14) "e" else if(base <= 36) "E" else "|e",
  zero.print = NULL, drop0trailing = FALSE, ...)
## S3 method for class 'mpfr'
formatN(x, drop0trailing = TRUE, ...)
```

Arguments

<code>x</code>	an MPFR number (vector or array).
<code>digits</code>	how many significant digits (in the base chosen!) are to be used in the result. The default, <code>NULL</code> , uses enough digits to represent the full precision, often one or two digits more than “you” would expect.
<code>trim</code>	logical; if <code>FALSE</code> , numbers are right-justified to a common width: if <code>TRUE</code> the leading blanks for justification are suppressed.
<code>scientific</code>	either a logical specifying whether MPFR numbers should be encoded in scientific format, or an integer penalty (see <code>options("scipen")</code>). Missing values correspond to the current default penalty.
<code>base</code>	an integer in 2, 3, ..., 62; the base (“basis”) in which the numbers should be represented. Apart from the default base 10, binary (<code>base = 2</code>) or hexadecimal (<code>base = 16</code>) are particularly interesting.

showNeg0 logical indicating if “**negative**” zeros should be shown with a “-”. The default, TRUE is intentionally different from `format(<numeric>)`.

exponent.char the “exponent” character to be used in scientific notation. The default takes into account that for base $B \geq 15$, “e” is part of the (mantissa) digits and the same is true for “E” when $B \geq 37$.

big.mark, big.interval, small.mark, small.interval, decimal.mark, zero.print, drop0trailing used for prettying decimal sequences, these are passed to `prettyNum` and that help page explains the details.

... further arguments passed to or from other methods.

Value

a character vector or array, say `cx`, of the same length as `x`. Since Rmpfr version 0.5-3 (2013-09), if `x` is an `mpfrArray`, then `cx` is a character `array` with the same `dim` and `dimnames` as `x`.

Note that in scientific notation, the integer exponent is always in *decimal*, i.e., base 10 (even when base is not 10), but of course meaning base powers, e.g., in base 32, “u.giE3” is the same as “ugi0” which is 32^3 times “u.gi”. This is in contrast, e.g., with `sprintf("%a", x)` where the powers after “p” are powers of 2.

Author(s)

Martin Maechler

References

The MPFR manual’s description of ‘`mpfr_get_str()`’ which is the C-internal workhorse for the (internal) R function `.mpfr2str()` on which `formatMpfr` builds.

See Also

`mpfr` for creation and the `mpfr` class description with its many methods. The `format` generic, and the `prettyNum` utility on which `formatMpfr` is based as well. The S3 generic function `formatN` from package `gmp`.

Examples

```
## Printing of MPFR numbers uses formatMpfr() internally.
## Note how each components uses the "necessary" number of digits:
( x3 <- c(Const("pi", 168), mpfr(pi, 140), 3.14) )
format(x3[3], 15)
format(x3[3], 15, drop0 = TRUE)# "3.14" .. dropping the trailing zeros
x3[4] <- 2^30
x3[4] # automatically drops trailing zeros
format(x3[1], dig = 41, small.mark = "'') # (41 - 1 = ) 40 digits after "."

rbind(formatN(          x3, digits = 15),
       formatN(as.numeric(x3), digits = 15))

(Zero <- mpfr(c(0,1/-Inf), 20)) # 0 and "-0"
xx <- c(Zero, 1:2, Const("pi", 120), -100*pi, -.00987)
```

```

format(xx, digits = 2)
format(xx, digits = 1, showNeg0 = FALSE)# "-0" no longer shown

## Output in other bases :
formatMpfr(mpfr(10^6, 40), base=32, drop0trailing=TRUE)
## "ugi0"
mpfr("ugi0", base=32) #-> 1'000'000

i32 <- mpfr(1:32, precBits = 64)
format(i32, base= 2, drop0trailing=TRUE)
format(i32, base= 16, drop0trailing=TRUE)
format(1/i32, base= 2, drop0trailing=TRUE)# using scientific notation for [17..32]
format(1/i32, base= 32)
format(1/i32, base= 62, drop0trailing=TRUE)
format(mpfr(2, 64)^(1:16), base=16, drop0trailing=TRUE)

```

gmp-conversions

Conversion Utilities gmp <-> Rmpfr

Description

Coerce from and to big integers ([bigz](#)) and [mpfr](#) numbers.

Further, coerce from big rationals ([bigq](#)) to [mpfr](#) numbers.

Usage

```

.bigz2mpfr(x, precB = NULL, rnd.mode = c('N','D','U','Z','A'))
.bigq2mpfr(x, precB = NULL, rnd.mode = c('N','D','U','Z','A'))
.mpfr2bigz(x, mod = NA)

```

Arguments

x	an R object of class <code>bigz</code> , <code>bigq</code> or <code>mpfr</code> respectively.
precB	precision in bits for the result. The default, <code>NULL</code> , means to use the <i>minimal</i> precision necessary for correct representation.
rnd.mode	a 1-letter string specifying how <i>rounding</i> should happen at C-level conversion to MPFR, see details of mpfr .
mod	a possible modulus, see as.bigz in package <code>gmp</code> .

Details

Note that we also provide the natural (S4) coercions, `as(x, "mpfr")` for `x` inheriting from class `"bigz"` or `"bigq"`.

Value

a numeric vector of the same length as `x`, of the desired class.

See Also

`mpfr()`, `as.bigz` and `as.bigq` in package `gmp`.

Examples

```
S <- gmp::Stirling2(50,10)
show(S)
SS <- S * as.bigz(1:3)^128
stopifnot(all.equal(log2(SS[2]) - log2(S), 128, tolerance=1e-15),
          identical(SS, .mpfr2bigz(.bigz2mpfr(SS))))

.bigz2mpfr(S)          # 148 bit precision
.bigz2mpfr(S, precB=256) # 256 bit

## rational --> mpfr:
sq <- SS / as.bigz(2)^100
MP <- as(sq, "mpfr")
stopifnot(identical(MP, .bigq2mpfr(sq)),
          SS == MP * as(2, "mpfr")^100)
```

hjkMpfr

Hooke-Jeeves Derivative-Free Minimization R (working for MPFR)

Description

An implementation of the Hooke-Jeeves algorithm for derivative-free optimization.

This is a slight adaption `hjk()` from package `dfoptim`

Usage

```
hjkMpfr(par, fn, control = list(), ...)
```

Arguments

<code>par</code>	Starting vector of parameter values. The initial vector may lie on the boundary. If <code>lower[i]=upper[i]</code> for some <code>i</code> , the <code>i</code> -th component of the solution vector will simply be kept fixed.
<code>fn</code>	Nonlinear objective function that is to be optimized. A scalar function that takes a real vector as argument and returns a scalar that is the value of the function at that point.
<code>control</code>	<code>list</code> of control parameters. See Details for more information.
<code>...</code>	Additional arguments passed to <code>fn</code> .

Details

Argument `control` is a list specifying changes to default values of algorithm control parameters. Note that parameter names may be abbreviated as long as they are unique.

The list items are as follows:

`tol` Convergence tolerance. Iteration is terminated when the step length of the main loop becomes smaller than `tol`. This does *not* imply that the optimum is found with the same accuracy. Default is `1.e-06`.

`maxfeval` Maximum number of objective function evaluations allowed. Default is `Inf`, that is no restriction at all.

`maximize` A logical indicating whether the objective function is to be maximized (`TRUE`) or minimized (`FALSE`). Default is `FALSE`.

`target` A real number restricting the absolute function value. The procedure stops if this value is exceeded. Default is `Inf`, that is no restriction.

`info` A logical variable indicating whether the step number, number of function calls, best function value, and the first component of the solution vector will be printed to the console. Default is `FALSE`.

If the minimization process threatens to go into an infinite loop, set either `maxfeval` or `target`.

Value

A `list` with the following components:

<code>par</code>	Best estimate of the parameter vector found by the algorithm.
<code>value</code>	value of the objective function at termination.
<code>convergence</code>	indicates convergence (<code>TRUE</code>) or not (<code>FALSE</code>).
<code>feval</code>	number of times the objective fn was evaluated.
<code>niter</code>	number of iterations (“steps”) in the main loop.

Note

This algorithm is based on the Matlab code of Prof. C. T. Kelley, given in his book “Iterative methods for optimization”. It has been implemented for package **dfoptim** with the permission of Prof. Kelley.

This version does not (yet) implement a cache for storing function values that have already been computed as searching the cache makes it slower.

Author(s)

Hans W Borchers <hwborchers@googlemail.com>; for **Rmpfr**: John Nash, June 2012. Modifications by Martin Maechler.

References

- C.T. Kelley (1999), Iterative Methods for Optimization, SIAM.
 Quarteroni, Sacco, and Saleri (2007), Numerical Mathematics, Springer.

See Also

Standard R's `optim`; `optimizer` provides *one*-dimensional minimization methods that work with `mpfr`-class numbers.

Examples

```
## simple smooth example:
ff <- function(x) sum((x - c(2:4))^2)
str(rr <- hjkMpfr(rep(mpfr(0,128), 3), ff, control=list(info=TRUE)))

## Hooke-Jeeves solves high-dim. Rosenbrock function {but slowly!}
rosenbrock <- function(x) {
  n <- length(x)
  sum (100*((x1 <- x[1:(n-1)])^2 - x[2:n])^2 + (x1 - 1)^2)
}

par0 <- rep(0, 10)
str(rb.db <- hjkMpfr(rep(0, 10), rosenbrock, control=list(info=TRUE)))

## rosenbrock() is quite slow with mpfr-numbers:
str(rb.M. <- hjkMpfr(mpfr(numeric(10), prec=128), rosenbrock,
  control = list(tol = 1e-8, info=TRUE)))

## Hooke-Jeeves does not work well on non-smooth functions
nsf <- function(x) {
  f1 <- x[1]^2 + x[2]^2
  f2 <- x[1]^2 + x[2]^2 + 10 * (-4*x[1] - x[2] + 4)
  f3 <- x[1]^2 + x[2]^2 + 10 * (-x[1] - 2*x[2] + 6)
  max(f1, f2, f3)
}
par0 <- c(1, 1) # true min 7.2 at (1.2, 2.4)
h.d <- hjkMpfr(par0, nsf) # fmin=8 at xmin=(2,2)

## and this is not at all better (but slower!)
h.M <- hjkMpfr(mpfr(c(1,1), 128), nsf, control = list(tol = 1e-15))

## --> demo(hjkMpfr) # -> Fletcher's chebyquad function m = n -- residuals
```

Description

Numerical integration of one-dimensional functions in pure R, with care so it also works for "mpfr"-numbers.

Currently, only classical Romberg integration of order `ord` is available.

Usage

```
integrateR(f, lower, upper, ..., ord = NULL,
           rel.tol = .Machine$double.eps^0.25, abs.tol = rel.tol,
           max.ord = 19, verbose = FALSE)
```

Arguments

<code>f</code>	an R function taking a numeric or "mpfr" first argument and returning a numeric (or "mpfr") vector of the same length. Returning a non-finite element will generate an error.
<code>lower, upper</code>	the limits of integration. Currently <i>must</i> be finite. Do use "mpfr"-numbers to get higher than double precision, see the examples.
<code>...</code>	additional arguments to be passed to <code>f</code> .
<code>ord</code>	integer, the order of Romberg integration to be used. If this is <code>NULL</code> , as per default, and either <code>rel.tol</code> or <code>abs.tol</code> are specified, the order is increased until convergence.
<code>rel.tol</code>	relative accuracy requested. The default is $1.2e-4$, about 4 digits only, see the Note.
<code>abs.tol</code>	absolute accuracy requested.
<code>max.ord</code>	only used, when neither <code>ord</code> or one of <code>rel.tol</code> , <code>abs.tol</code> are specified: Stop Romberg iterations after the order reaches <code>max.ord</code> ; may prevent infinite loops or memory explosion.
<code>verbose</code>	logical or integer, indicating if and how much information should be printed during computation.

Details

Note that arguments after `...` must be matched exactly.

For convergence, *both* relative and absolute changes must be smaller than `rel.tol` and `abs.tol`, respectively.

`rel.tol` cannot be less than $\max(50 \cdot \text{Machine\$double.eps}, 0.5e-28)$ if `abs.tol` ≤ 0 .

Value

A list of class "integrateR" (as from standard R's `integrate()`) with a `print` method and components

<code>value</code>	the final estimate of the integral.
<code>abs.error</code>	estimate of the modulus of the absolute error.
<code>subdivisions</code>	for Romberg, the number of function evaluations.

message "OK" or a character string giving the error message.
 call the matched call.

Note

f must accept a vector of inputs and produce a vector of function evaluations at those points. The [Vectorize](#) function may be helpful to convert f to this form.

If you want to use higher accuracy, you *must* set lower or upper to "mpfr" numbers (and typically lower the relative tolerance, rel.tol), see also the examples.

Note that the default tolerances (rel.tol, abs.tol) are not very accurate, but the same as for [integrate](#), which however often returns considerably more accurate results than requested. This is typically *not* the case for integrateR().

Note

We use practically the same print S3 method as [print.integrate](#), provided by R, with a difference when the message component is not "Ok".

Author(s)

Martin Maechler

References

Bauer, F.L. (1961) Algorithm 60 – Romberg Integration, *Communications of the ACM* **4**(6), p.255.

See Also

R's standard, [integrate](#), is much more adaptive, also allowing infinite integration boundaries, and typically considerably faster for a given accuracy.

Examples

```
## See more from ?integrate
## this is in the region where integrate() can get problems:
integrateR(dnorm,0,2000)
integrateR(dnorm,0,2000, rel.tol=1e-15)
(Id <- integrateR(dnorm,0,2000, rel.tol=1e-15, verbose=TRUE))
Id$value == 0.5 # exactly

## Demonstrating that 'subdivisions' is correct:
Exp <- function(x) { .N <- .N+ length(x); exp(x) }
.N <- 0; str(integrateR(Exp, 0,1, rel.tol=1e-10, digits=15); .N

### Using high-precision functions -----

## Polynomials are very nice:
integrateR(function(x) (x-2)^4 - 3*(x-3)^2, 0, 5, verbose=TRUE)
# n= 1, 2^n=      2 | I =      46.04, abs.err =      98.9583
```

```

# n= 2, 2^n=      4 | I =                20, abs.err =      26.0417
# n= 3, 2^n=      8 | I =                20, abs.err =  7.10543e-15
## 20 with absolute error < 7.1e-15
## Now, using higher accuracy:
I <- integrateR(function(x) (x-2)^4 - 3*(x-3)^2, 0, mpfr(5,128),
                rel.tol = 1e-20, verbose=TRUE)
I ; I$value ## all fine

## with floats:
integrateR(exp,      0      , 1, rel.tol=1e-15, verbose=TRUE)
## with "mpfr":
(I <- integrateR(exp, mpfr(0,200), 1, rel.tol=1e-25, verbose=TRUE))
(I.true <- exp(mpfr(1, 200)) - 1)
## true absolute error:
stopifnot(print(as.numeric(I.true - I$value)) < 4e-25)

## Want absolute tolerance check only (=> set 'rel.tol' very high, e.g. 1):
(Ia <- integrateR(exp, mpfr(0,200), 1, abs.tol = 1e-6, rel.tol=1, verbose=TRUE))

## Set 'ord' (but no '*.tol') --> Using 'ord'; no convergence checking
(I <- integrateR(exp, mpfr(0,200), 1, ord = 13, verbose=TRUE))

```

is.whole

Whole ("Integer") Numbers

Description

Check which elements of `x[]` are integer valued aka “whole” numbers, including MPFR numbers (class `mpfr`).

Usage

```
## S3 method for class 'mpfr'
is.whole(x)
```

Arguments

`x` any R vector, here of class `mpfr`.

Value

logical vector of the same length as `x`, indicating where `x[.]` is integer valued.

Author(s)

Martin Maechler

See Also

`is.integer(x)` (**base** package) checks for the *internal* mode or class, not if `x[i]` are integer valued.
The `is.whole()` methods in package **gmp**.

Examples

```
is.integer(3) # FALSE, it's internally a double
is.whole(3)   # TRUE
x <- c(as(2,"mpfr") ^ 100, 3, 3.2, 1000000, 2^40)
is.whole(x)  # one FALSE, only
```

Mnumber-class	<i>Class "Mnumber" and "mNumber" of "mpfr" and regular numbers and arrays from them</i>
---------------	---

Description

Classes "Mnumber" "mNumber" are class unions of "mpfr" and regular numbers and arrays from them.

Its purpose is for method dispatch, notably defining a `cbind(...)` method where `...` contains objects of one of the member classes of "Mnumber".

Classes "mNumber" is considerably smaller as it does *not* contain "matrix" and "array" since these also extend "character" which is not really desirable for generalized numbers. It extends the simple "numericVector" class by `mpfr*` classes.

Methods

`%*%` signature(x = "mpfrMatrix", y = "Mnumber"): ...

crossprod signature(x = "mpfr", y = "Mnumber"): ...

tcrossprod signature(x = "Mnumber", y = "mpfr"): ...

etc. These are documented with the classes `mpfr` and or `mpfrMatrix`.

See Also

the `array_or_vector` sub class; `cbind-methods`.

Examples

```
## "Mnumber" encompasses (i.e., "extends") quite a few
## "vector / array - like" classes:
showClass("Mnumber")
stopifnot(extends("mpfrMatrix", "Mnumber"),
          extends("array", "Mnumber"))

Mnsub <- names(getClass("Mnumber")@subclasses)
```

```
(mNsub <- names(getClass("mNumber")@subclasses))
## mNumber has *one* subclass which is not in Mnumber:
setdiff(mNsub, Msub)# namely "numericVector"
## The following are only subclasses of "Mnumber", but not of "mNumber":
setdiff(Msub, mNsub)
```

mpfr Create "mpfr" Numbers (Objects)

Description

Create multiple (i.e. typically *high*) precision numbers, to be used in arithmetic and mathematical computations with R.

Usage

```
mpfr(x, precBits, ...)
## Default S3 method:
mpfr(x, precBits, base = 10,
     rnd.mode = c("N", "D", "U", "Z", "A"), scientific = NA, ...)

Const(name = c("pi", "gamma", "catalan", "log2"), prec = 120L,
     rnd.mode = c("N", "D", "U", "Z", "A"))
```

Arguments

<code>x</code>	a numeric , mpfr , bigz , bigq , or character vector or array .
<code>precBits</code> , <code>prec</code>	a number, the maximal precision to be used, in <i>bits</i> ; i.e. 53 corresponds to double precision. Must be at least 2. If missing , getPrec(x) determines a default precision.
<code>base</code>	(only when <code>x</code> is character) the base with respect to which <code>x[i]</code> represent numbers; base b must fulfill $2 \leq b \leq 62$.
<code>rnd.mode</code>	a 1-letter string specifying how <i>rounding</i> should happen at C-level conversion to MPFR, see details.
<code>scientific</code>	(used only when <code>x</code> is the result of formatBin() , i.e., of class "Bcharacter") logical indicating that the binary representation of <code>x</code> is in scientific notation. When TRUE, <code>mpfr()</code> will substitute 0 for <code>_</code> ; when NA, <code>mpfr()</code> will guess, and use TRUE when finding a "p" in <code>x</code> ; see also formatBin .
<code>name</code>	a string specifying the mpfrlib - internal constant computation. "gamma" is Euler's gamma (γ), and "catalan" Catalan's constant.
<code>...</code>	potentially further arguments passed to and from methods.

Details

The "mpfr" method of `mpfr()` is a simple wrapper around `roundMpfr()`.

MPFR supports the following rounding modes,

GMP_RNDN: round to nearest (roundTiesToEven in IEEE 754-2008).

GMP_RNDZ: round toward zero (roundTowardZero in IEEE 754-2008).

GMP_RNDU: round toward plus infinity ("Up", roundTowardPositive in IEEE 754-2008).

GMP_RNDD: round toward minus infinity ("Down", roundTowardNegative in IEEE 754-2008).

GMP_RNDA: round away from zero (new since MPFR 3.0.0).

The 'round to nearest' ("N") mode, the default here, works as in the IEEE 754 standard: in case the number to be rounded lies exactly in the middle of two representable numbers, it is rounded to the one with the least significant bit set to zero. For example, the number $5/2$, which is represented by (10.1) in binary, is rounded to (10.0)=2 with a precision of two bits, and not to (11.0)=3. This rule avoids the "drift" phenomenon mentioned by Knuth in volume 2 of *The Art of Computer Programming* (Section 4.2.2).

When `x` is `character`, `mpfr()` will detect the precision of the input object.

Value

an object of (S4) class `mpfr`, or for `mpfr(x)` when `x` is an array, `mpfrMatrix`, or `mpfrArray` which the user should just as a normal numeric vector or array.

Author(s)

Martin Maechler

References

The MPFR team. (201x). *GNU MPFR – The Multiple Precision Floating-Point Reliable Library*; see <http://www.mpfr.org/mpfr-current/#doc> or directly <http://www.mpfr.org/mpfr-current/mpfr.pdf>.

See Also

The class documentation `mpfr` contains more details. Use `asNumeric` to transform back to double precision ("numeric").

Examples

```
mpfr(pi, 120) ## the double-precision pi "translated" to 120-bit precision

pi. <- Const("pi", prec = 260) # pi "computed" to correct 260-bit precision
pi. # nicely prints 80 digits [260 * log10(2) ~ 78.3 ~ 80]

Const("gamma", 128L) # 0.5772...
Const("catalan", 128L) # 0.9159...
```

```

x <- mpfr(0:7, 100)/7 # a more precise version of k/7, k=0,...,7
x
1 / x

## character input :
mpfr("2.718281828459045235360287471352662497757") - exp(mpfr(1, 150))
## ~= -4 * 10^-40
## Also works for NA, NaN, ... :
cx <- c("1234567890123456", 345, "NA", "NaN", "Inf", "-Inf")
mpfr(cx)

## with some 'base' choices :
print(mpfr("111.1111", base=2)) * 2^4

mpfr("af21.01020300a0b0c", base=16)
## 68 bit prec. 44833.00393694653820642

mpfr("ugi0", base = 32) == 10^6 ## TRUE

## --- Large integers from package 'gmp':
Z <- as.bigz(7)^(1:200)
head(Z, 40)
## mpfr(Z) by default chooses the correct *maximal* default precision:
mZ. <- mpfr(Z)
## more efficiently chooses precision individually
m.Z <- mpfr(Z, precBits = frexpZ(Z)$exp)
## the precBits chosen are large enough to keep full precision:
stopifnot(identical(cZ <- as.character(Z),
                    as(mZ., "character")),
          identical(cZ, as(m.Z, "character")))

## compare mpfr-arithmetic with exact rational one:
stopifnot(all.equal(mpfr(as.bigq(355,113), 99),
                    mpfr(355, 99) / 113, tol = 2^-98))

## look at different "rounding modes":
sapply(c("N", "D", "U", "Z", "A"), function(RND)
  mpfr(c(-1,1)/5, 20, rnd.mode = RND), simplify=FALSE)

symnum(sapply(c("N", "D", "U", "Z", "A"),
              function(RND) mpfr(0.2, prec = 5:15, rnd.mode = RND) < 0.2 ))

```

mpfr-class

Class "mpfr" of Multiple Precision Floating Point Numbers

Description

"mpfr" is the class of **M**ultiple **P**recision **F**loatingpoint numbers with **R**eliable arithmetic.

For the high-level user, "mpfr" objects should behave as standard R's `numeric` vectors. They would just print differently and use the prespecified (typically high) precision instead of the double precision of 'traditional' R numbers (with `class(.) == "numeric"` and `typeof(.) == "double"`).

`hypot(x,y)` computes the hypotenuse length z in a rectangular triangle with “leg” side lengths x and y , i.e.,

$$z = \text{hypot}(x, y) = \sqrt{x^2 + y^2},$$

in a numerically stable way.

Usage

```
hypot(x,y, rnd.mode = c("N", "D", "U", "Z", "A"))
```

Arguments

<code>x,y</code>	an object of class <code>mpfr</code> .
<code>rnd.mode</code>	a 1-letter string specifying how <i>rounding</i> should happen at C-level conversion to MPFR, see <code>mpfr</code> .

Objects from the Class

Objects are typically created by `mpfr(<number>, precBits)`.

Slots

Internally, “mpfr” objects just contain standard **R lists** where each list element is of class “mpfr1”, representing *one* MPFR number, in a structure with four slots, very much parallelizing the C `struc` in the `mpfr` C library to which the **Rmpfr** package interfaces.

An object of class “mpfr1” has slots

`prec`: “integer” specifying the maximal precision in **bits**.

`exp`: “integer” specifying the base-2 exponent of the number.

`sign`: “integer”, typically -1 or 1, specifying the sign (i.e. `sign(.)`) of the number.

`d`: an “integer” vector (of 32-bit “limbs”) which corresponds to the full mantissa of the number.

Methods

abs signature(`x = "mpfr"`): ...

atan2 signature(`y = "mpfr"`, `x = "ANY"`), and

atan2 signature(`x = "ANY"`, `y = "mpfr"`): compute the arc-tangent of two arguments: `atan2(y, x)` returns the angle between the x-axis and the vector from the origin to (x, y) , i.e., for positive arguments `atan2(y, x) == atan(y/x)`.

lbeta signature(`a = "ANY"`, `b = "mpfrArray"`), is $\log(|B(a, b)|)$ where $B(a, b)$ is the Beta function, `beta(a, b)`.

beta signature(`a = "mpfr"`, `b = "ANY"`),

beta signature(`a = "mpfr"`, `b = "mpfr"`), ..., etc: Compute the beta function $B(a, b)$, using high precision, building on internal `gamma` or `lgamma`. See the help for R’s base function `beta` for more. Currently, there, $a, b \geq 0$ is required. Here, we provide (non-NaN) for all numeric `a, b`.

When either a , b , or $a + b$ is a negative *integer*, $\Gamma(\cdot)$ has a pole there and is undefined (NaN). However the Beta function can be defined there as “limit”, in some cases. Following other software such as SAGE, Maple or Mathematica, we provide finite values in these cases. However, note that these are not proper limits (two-dimensional in (a, b)), but useful for some applications. E.g., $B(a, b)$ is defined as zero when $a + b$ is a negative integer, but neither a nor b is. Further, if $a > b > 0$ are integers, $B(-a, b) = B(b, -a)$ can be seen as $(-1)^b * B(a - b + 1, b)$.

dim<- signature(x = "mpfr"): Setting a dimension **dim** on an "mpfr" object makes it into an object of class "**mpfrArray**" or (more specifically) "**mpfrMatrix**" for a length-2 dimension, see their help page; note that **t(x)** (below) is a special case of this.

Ops signature(e1 = "mpfr", e2 = "ANY"): ...

Ops signature(e1 = "ANY", e2 = "mpfr"): ...

Arith signature(e1 = "mpfr", e2 = "missing"): ...

Arith signature(e1 = "mpfr", e2 = "mpfr"): ...

Arith signature(e1 = "mpfr", e2 = "integer"): ...

Arith signature(e1 = "mpfr", e2 = "numeric"): ...

Arith signature(e1 = "integer", e2 = "mpfr"): ...

Arith signature(e1 = "numeric", e2 = "mpfr"): ...

Compare signature(e1 = "mpfr", e2 = "mpfr"): ...

Compare signature(e1 = "mpfr", e2 = "integer"): ...

Compare signature(e1 = "mpfr", e2 = "numeric"): ...

Compare signature(e1 = "integer", e2 = "mpfr"): ...

Compare signature(e1 = "numeric", e2 = "mpfr"): ...

Logic signature(e1 = "mpfr", e2 = "mpfr"): ...

Summary signature(x = "mpfr"): The S4 **Summary** group functions, **max**, **min**, **range**, **prod**, **sum**, **any**, and **all** are all defined for MPFR numbers. **mean**(x, trim) for non-0 trim works analogously to **mean.default**.

median signature(x = "mpfr"): works via

quantile signature(x = "mpfr"): a simple wrapper of the **quantile.default** method from **stats**.

Math signature(x = "mpfr"): All the S4 **Math** group functions are defined, using multiple precision (MPFR) arithmetic, from **getGroupMembers("Math")**, these are (in alphabetical order):

abs, **sign**, **sqrt**, **ceiling**, **floor**, **trunc**, **cummax**, **cummin**, **cumprod**, **cumsum**, **exp**, **expm1**, **log**, **log10**, **log2**, **log1p**, **cos**, **cosh**, **sin**, **sinh**, **tan**, **tanh**, **acos**, **acosh**, **asin**, **asinh**, **atan**, **atanh**, **gamma**, **lgamma**, **digamma**, and **trigamma**.

Currently, **trigamma** is not provided by the MPFR library and hence not yet implemented.

Further, the **cum*()** methods are *not yet* implemented.

factorial signature(x = "mpfr"): this will **round** the result when x is integer valued. Note however that **factorialMpfr**(n) for integer n is slightly more efficient, using the MPFR function 'mpfr_fac_ui'.

Math2 signature(x = "mpfr"): **round**(x,digits) and **signif**(x, digits) methods. Note that these do not change the formal precision ('prec' slot), and you may often want to apply **roundMpfr()** in addition or preference.

as.numeric signature(x = "mpfr"): ...

as.vector signature(x = "mpfrArray"): as for standard [arrays](#), this “drops” the dim (and dimnames), i.e., transforms x into an ‘MPFR’ number vector, i.e., class [mpfr](#).

[signature(x = "mpfr", i = "ANY"), and

[signature(x = "mpfr", i = "ANY", j = "missing", drop = "missing"): subsetting aka “indexing” happens as for numeric vectors.

format signature(x = "mpfr"), further arguments digits = NULL, scientific = NA, etc: returns [character](#) vector of same length as x; when digits is NULL, with *enough* digits to recreate x accurately. For details, see [formatMpfr](#).

is.finite signature(x = "mpfr"): ...

is.infinite signature(x = "mpfr"): ...

is.na signature(x = "mpfr"): ...

is.nan signature(x = "mpfr"): ...

log signature(x = "mpfr"): ...

show signature(object = "mpfr"): ...

sign signature(x = "mpfr"): ...

Re, Im signature(z = "mpfr"): simply return z or 0 (as “mpfr” numbers of correct precision), as mpfr numbers are ‘real’ numbers.

Arg, Mod, Conj signature(z = "mpfr"): these are trivial for our ‘real’ mpfr numbers, but defined to work correctly when used in R code that also allows complex number input.

all.equal signature(target = "mpfr", current = "mpfr"),

all.equal signature(target = "mpfr", current = "ANY"), and

all.equal signature(target = "ANY", current = "mpfr"): methods for numerical (approximate) equality, [all.equal](#) of multiple precision numbers. Note that the default tolerance (argument) is taken to correspond to the (smaller of the two) precisions when both main arguments are of class “mpfr”, and hence can be considerably less than double precision machine epsilon `.Machine$double.eps`.

coerce signature(from = "numeric", to = "mpfr"): [as](#)(., “mpfr”) coercion methods are available for [character](#) strings, [numeric](#), [integer](#), [logical](#), and even [raw](#). Note however, that [mpfr](#)(., precBits, base) is more flexible.

coerce signature(from = "mpfr", to = "bigz"): coerces to biginteger, see [bigz](#) in package [gmp](#).

coerce signature(from = "mpfr", to = "numeric"): ...

coerce signature(from = "mpfr", to = "character"): ...

unique signature(x = "mpfr"): and

duplicated signature(x = "mpfr"): just work as with numbers.

t signature(x = "mpfr"): makes x into an $n \times 1$ [mpfrMatrix](#).

which.min signature(x = "mpfr"): gives the index of the first minimum, see [which.min](#).

which.max signature(x = "mpfr"): gives the index of the first maximum, see [which.max](#).

Note

Many more methods (“functions”) automagically work for “mpfr” number vectors (and matrices, see the `mpfrMatrix` class doc), notably `sort`, `order`, `quantile`, `rank`.

Author(s)

Martin Maechler

See Also

The “`mpfrMatrix`” class, which extends the “mpfr” one.

`roundMpfr` to *change* precision of an “mpfr” object which is typically desirable *instead* of or in addition to `signif()` or `round()`; `is.whole()` etc.

Special mathematical functions such as some Bessel ones, e.g., `jn`; further, `zeta(.)` ($= \zeta(.)$), `Ei()` etc. `Bernoulli` numbers and the Pochhammer function `pochMpfr`.

Examples

```
## 30 digit precision
str(x <- mpfr(c(2:3, pi), prec = 30 * log2(10)))
x^2
x[1] / x[2] # 0.66666... ~ 30 digits

## indexing - as with numeric vectors
stopifnot(identical(x[2], x[[2]]),
  ## indexing "outside" gives NA (well: "mpfr-NaN" for now):
  is.na(x[5]),
  ## whereas "[" cannot index outside:
  is(try(x[[5]]), "try-error"),
  ## and only select *one* element:
  is(try(x[[2:3]]), "try-error"))

## factorial() & lfactorial would work automagically via [1]gamma(),
## but factorial() additionally has an "mpfr" method which rounds
f200 <- factorial(mpfr(200, prec = 1500)) # need high prec.!
f200
as.numeric(log2(f200))# 1245.38 -- need precBits >~ 1246 for full precision

##--> see factorialMpfr() for more such computations.

##--- "Underflow" **much** later -- exponents have 30(+1) bits themselves:

mpfr.min.exp2 <- - (2^30 + 1)
two <- mpfr(2, 55)
stopifnot(two ^ mpfr.min.exp2 == 0)
## whereas
two ^ (mpfr.min.exp2 * (1 - 1e-15))
## 2.38256490488795107e-323228497 ["typically"]

##--- "Assert" that {sort}, {order}, {quantile}, {rank}, all work :
```

```

p <- mpfr(rpois(32, lambda=500), precBits=128)^10
np <- as.numeric(log(p))
stopifnot(all(diff(sort(p)) >= 0),
  identical(order(p), order(np)),
  identical(rank (p), rank (np)),
  all.equal(sapply(1:9, function(Typ) quantile(np, type=Typ, names=FALSE)),
    sapply(lapply(1:9, function(Typ) quantile( p, type=Typ, names=FALSE)),
      function(x) as.numeric(log(x))),
    tol = 1e-3),# quantiles: interpolated in orig. <--> log scale
  TRUE)

m0 <- mpfr(numeric(), 99)
xy <- expand.grid(x = -2:2, y = -2:2) ; x <- xy[,"x"] ; y <- xy[,"y"]
a2. <- atan2(y,x)

stopifnot(identical(which.min(m0), integer(0)),
  identical(which.max(m0), integer(0)),
  all.equal(a2., atan2(as(y,"mpfr"), x)),
  max(m0) == mpfr(-Inf, 53), # (53 is not a feature, but ok)
  min(m0) == mpfr(+Inf, 53),
  sum(m0) == 0, prod(m0) == 1)

```

mpfr-distr-etc

Distribution Functions etc (MPFR)

Description

For some R standard (probability) density, distribution or quantile functions, we provide MPFR versions.

Usage

```

dpois (x, lambda, log = FALSE)
dbinom(x, size, prob, log = FALSE)
dnorm (x, mean = 0, sd = 1, log = FALSE)

pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)

```

Arguments

x, q, lambda, size, prob, mean, sd
 numeric or mpfr vectors. All of these are “recycled” to the length of the longest one.

log, log.p, lower.tail
 logical, see [pnorm](#), [dpois](#), etc.

Details

pnorm() is based on [erf\(\)](#) and [erfc\(\)](#) which have direct MPFR counter parts and are both reparametrizations of pnorm , $\text{erf}(x) = 2 * \text{pnorm}(\sqrt{2} * x)$ and $\text{erfc}(x) = 2 * \text{pnorm}(\sqrt{2} * x, \text{lower}=\text{FALSE})$.

Value

A vector of the same length as the longest of x , q , \dots , of class `mpfr` with the high accuracy results of the corresponding standard R function.

See Also

`pnorm`, `dbinom`, `dpois` in standard package `stats`.

`pbetaI(x, a, b)` is a `mpfr` version of `pbeta` only for *integer* a and b .

Examples

```
x <- 1400+ 0:10
print(dpois(x, 1000), digits =18) ## standard R's double precision
dpois(mpfr(x, 120), 1000)## more accuracy for the same
```

mpfr-special-functions

Special Mathematical Functions (MPFR)

Description

Special Mathematical Functions, supported by the MPFR Library.

Usage

```
zeta(x)
Ei(x)
Li2(x)
```

```
erf(x)
erfc(x)
```

Arguments

x a `numeric` or `mpfr` vector.

Details

`zeta(x)` computes Riemann's Zeta function $\zeta(x)$ important in analytical number theory and related fields. The traditional definition is

$$\zeta(x) = \sum_{n=1}^{\infty} \frac{1}{n^x}.$$

`Ei(x)` computes the exponential integral,

$$\int_{-\infty}^x \frac{e^t}{t} dt.$$

`Li2(x)` computes the dilogarithm,

$$\int_0^x \frac{-\log(1-t)}{t} dt.$$

`erf(x)` and `erfc(x)` are the error, respectively complementary error function which are both reparametrizations of `pnorm`, `erf(x) = 2*pnorm(sqrt(2)*x)` and `erfc(x) = 2* pnorm(sqrt(2)*x, lower=FALSE)`, and hence **Rmpfr** provides its own version of `pnorm`.

Value

A vector of the same length as `x`, of class `mpfr`.

See Also

`pnorm` in standard package **stats**; the class description `mpfr` mentioning the generic arithmetic and mathematical functions (`sin`, `log`, ...) for which "mpfr" methods are available.

Examples

```
curve(Ei, 0, 5, n=2001)

if(mpfrVersion() >= "2.4.0") { ## Li2() is not available in older MPFR versions
curve(Li2, 0, 5, n=2001)

curve(Li2, -2, 13, n=2000); abline(h=0,v=0, lty=3)
curve(Li2, -200,400, n=2000); abline(h=0,v=0, lty=3)
}

curve(erf, -3,3, col = "red", ylim = c(-1,2))
curve(erfc, add = TRUE, col = "blue")
abline(h=0, v=0, lty=3)
legend(-3,1, c("erf(x)", "erfc(x)"), col = c("red","blue"), lty=1)
```

Description

This page documents utilities from package **Rmpfr** which are typically not called by the user, but may come handy in some situations.

Usage

```
getPrec(x, base = 10, doNumeric = TRUE, is.mpfr = NA, bigq. = 128L)
getD(x)
mpfr_default_prec(prec)
## S3 method for class 'mpfrArray'
print(x, digits = NULL, drop0trailing = FALSE,
```

```

    right = TRUE, ...)
## S3 method for class 'mpfr'
print(x, digits = NULL, drop0trailing = TRUE,
      right = TRUE, ...)
toNum(from, rnd.mode = c('N','D','U','Z','A'))
mpfr2array(x, dim, dimnames = NULL, check = FALSE)

mpfrXport(x)
mpfrImport(mxp)

```

Arguments

<code>x</code> , <code>from</code>	typically, an R object of class <code>"mpfr"</code> , or <code>"mpfrArray"</code> , respectively. For <code>getPrec()</code> , any number-like R object, or <code>NULL</code> .
<code>base</code>	(only when <code>x</code> is <code>character</code>) the base with respect to which <code>x[i]</code> represent numbers; base b must fulfill $2 \leq b \leq 62$.
<code>doNumeric</code>	logical indicating <code>integer</code> or <code>double</code> typed <code>x</code> should be accepted and a default precision be returned. Should typically be kept at default <code>TRUE</code> .
<code>is.mpfr</code>	logical indicating if <code>class(x)</code> is already known to be <code>"mpfr"</code> ; typically should be kept at default, <code>NA</code> .
<code>bigq.</code>	for <code>getPrec()</code> , the precision to use for a big rational (class <code>"bigq"</code>); if not specified gives warning when used.
<code>prec</code>	a positive integer, or missing.
<code>drop0trailing</code>	logical indicating if trailing <code>"0"</code> s should be omitted.
<code>right</code>	logical indicating <code>print()</code> ing should right justify the strings; see <code>print.default()</code> to which it is passed.
<code>digits</code> , ...	further arguments to print methods.
<code>rnd.mode</code>	a 1-letter string specifying how <i>rounding</i> should happen at C-level conversion to MPFR, see details of <code>mpfr</code> .
<code>dim</code> , <code>dimnames</code>	for <code>"mpfrArray"</code> construction.
<code>check</code>	logical indicating if the <code>mpfrArray</code> construction should happen with internal safety check. Previously, the implicit default used to be <code>true</code> .
<code>mxp</code>	an <code>"mpfrXport"</code> object, as resulting from <code>mpfrXport()</code> .

Details

The `print` method is currently built on the `format` method for class `mpfr`. This, currently does *not* format columns jointly which leads to suboptimally looking output. There are plans to change this.

Value

`getPrec(x)` returns a `integer` vector of the same length as `x` when that is positive, whereas `getPrec(NULL)` returns `mpfr_default_prec()`, see below.

If you need to *change* the precision of `x`, i.e., need something like “setPrec”, use `roundMpfr()`.

getD(x) is intended to be a fast version of x@.Data, and should not be used outside of lower level functions.

mpfr_default_prec() returns the current MPFR default precision, an `integer`. This is currently not made use of, in all of package **Rmpfr**, where functions have their own default precision where needed.

mpfr_default_prec(prec) *sets* the current MPFR default precision and returns the previous one; see above.

toNum(m) returns a numeric `array` or `matrix`, when m is of class `"mpfrArray"` or `"mpfrMatrix"`, respectively. It should be equivalent to `as(m, "array")` or `... "matrix"`. Note that the slightly more general `asNumeric()` is preferred now.

mpfr2array() a slightly more flexible alternative to `dim(.) <- dd`.

Note

mpfrXport() and mpfrImport() are **experimental** and used to explore reported platform incompatibilities of `save()`d and `load()`ed "mpfr" objects between Windows and non-Windows platforms.

In other words, the format of the result of mpfrXport() and hence the `mxp` argument to mpfrImport() are considered internal, not part of the API and subject to change.

See Also

Start using `mpfr(. .)`, and compute with these numbers.

`mpfrArray(x)` is for numeric ("non-mpfr") x, whereas `mpfr2array(x)` is for "mpfr" classed x, only.

Examples

```
getPrec(as(c(1,pi), "mpfr")) # 128 for both

(opr <- mpfr_default_prec()) ## typically 53, the MPFR system default
stopifnot(opr == (oprec <- mpfr_default_prec(70)),
          70 == mpfr_default_prec())
## and reset it:
mpfr_default_prec(opr)

## Explore behavior of rounding modes 'rnd.mode':
x <- mpfr(10,99)^512 # too large for regular (double prec. / numeric):
sapply(c("N", "D", "U", "Z", "A"), function(RM)
  sapply(list(-x,x), function(.) toNum(., RM)))
##   N          D          U          Z          A
## -Inf          -Inf -1.797693e+308 -1.797693e+308 -Inf
##  Inf 1.797693e+308          Inf 1.797693e+308  Inf

## Printing of "MPFR" matrices is less nice than R's usual matrix printing:
m <- outer(c(1, 3.14, -1024.5678), c(1, 1e-3, 10,100))
m[3,3] <- round(m[3,3])
m
mpfr(m, 50)
```

```

B6 <- mpfr2array(Bernoulli(1:6, 60), c(2,3),
                dimnames = list(LETTERS[1:2], letters[1:3]))
B6

## Looking at internal representation [for power users only!]:

i8 <- mpfr(-2:5, 32)
x4 <- mpfr(c(NA, NaN, -Inf, Inf), 32)
## The output of the following depends on the GMP "numb" size
## (32 bit vs. 64 bit), and may be even more platform specifics:
str( .mpfr2list(i8) )
str( .mpfr2list(x4) )

str(xp4 <- mpfrXport(x4))
stopifnot(identical(x4, mpfrImport(mpfrXport(x4))),
          identical(i8, mpfrImport(mpfrXport(i8))))
if(FALSE) ## FIXME: not yet working:
  stopifnot(identical(B6, mpfrImport(mpfrXport(B6))))

```

mpfr.utils

MPFR Number Utilities

Description

`mpfrVersion()` returns the version of the MPFR library which **Rmpfr** is currently linked to.

`c(x,y,...)` can be used to combine MPFR numbers in the same way as regular numbers **IFF** the first argument `x` is of class `mpfr`.

`mpfrIs0(.)` uses the MPFR library in the documented way to check if (a vector of) MPFR numbers are zero. It was called `mpfr.is.0` which is strongly deprecated now.

`.mpfr.is.whole(x)` uses the MPFR library in the documented way to check if (a vector of) MPFR numbers is integer *valued*. This is equivalent to `x == round(x)`, but *not* at all to `is.integer(as(x, "numeric"))`. You should typically rather use (the "mpfr" method of the generic function) `is.whole(x)` instead. The former name `mpfr.is.integer` is deprecated now.

Usage

```

mpfrVersion()
mpfrIs0(x)

## S3 method for class 'mpfr'
c(...)
## S3 method for class 'mpfr'
diff(x, lag = 1L, differences = 1L, ...)

```

Arguments

`x` an object of class `mpfr`.

`...` for `diff`, further `mpfr` class objects or simple numbers (`numeric` vectors) which are coerced to `mpfr` with default precision of 128 bits.

`lag, differences` for `diff()`: exact same meaning as in `diff()`'s default method, `diff.default`.

Value

`mpfrIs0` returns a logical vector of length `length(x)` with values `TRUE` iff the corresponding `x[i]` is an MPFR representation of zero (`0`).

Similarly, `.mpfr.is.whole` and `is.whole` return a logical vector of length `length(x)`.

`mpfrVersion` returns an object of S3 class `"numeric_version"`, so it can be used in comparisons.

The other functions return MPFR number (vectors), i.e., extending class `mpfr`.

See Also

`str.mpfr` for the `str` method. `erf` for special mathematical functions on MPFR.

The class description `mpfr` page mentions many generic arithmetic and mathematical functions for which `"mpfr"` methods are available.

Examples

```
mpfrVersion()

(x <- c(Const("pi", 64), mpfr(-2:2, 64)))
mpfrIs0(x) # one of them is
x[mpfrIs0(x)] # but it may not have been obvious..
str(x)

x <- rep(-2:2, 5)
stopifnot(is.whole(mpfr(2, 500) ^ (1:200)),
          all.equal(diff(x), diff(as.numeric(x))))
```

`mpfrArray`

Construct "mpfrArray" almost as by 'array()'

Description

Utility to construct an R object of class `mpfrArray`, very analogously to the numeric `array` function.

Usage

```
mpfrArray(x, precBits, dim = length(x), dimnames = NULL,
          rnd.mode = c("N", "D", "U", "Z", "A"))
```

Arguments

x	numeric(like) vector, typically of length <code>prod(dim)</code> or shorter in which case it is recycled.
precBits	a number, the maximal precision to be used, in <i>bits</i> ; i.e., 53 corresponds to double precision. Must be at least 2.
dim	the dimension of the array to be created, that is a vector of length one or more giving the maximal indices in each dimension.
dimnames	either NULL or the names for the dimensions. This is a list with one component for each dimension, either NULL or a character vector of the length given by <code>dim</code> for that dimension.
rnd.mode	a 1-letter string specifying how <i>rounding</i> should happen at C-level conversion to MPFR, see details of <code>mpfr</code> .

Value

an object of class "`mpfrArray`", specifically "`mpfrMatrix`" when `length(dim) == 2`.

See Also

`mpfr`, `array`; `asNumeric()` as “inverse” of `mpfrArray()`, to get back a numeric array.

`mpfr2array(x)` is for “mpfr” classed x, only, whereas `mpfrArray(x)` is for numeric (“non-mpfr”) x.

Examples

```
## preallocating is possible here too
ma <- mpfrArray(NA, prec = 80, dim = 2:4)
validObject(A2 <- mpfrArray(1:24, prec = 64, dim = 2:4))

## recycles, gives an "mpfrMatrix" and dimnames :
mat <- mpfrArray(1:5, 64, dim = c(5,3), dimnames=list(NULL, letters[1:3]))
mat
asNumeric(mat)
stopifnot(identical(asNumeric(mat),
                    matrix(1:5 +0, 5,3, dimnames=dimnames(mat))))

## Testing the apply() method :
apply(mat, 2, range)
apply(A2, 1:2, range)
apply(A2, 2:3, max)
apply(A2, 2, fivenum)
stopifnot(as(apply(A2, 2, range), "matrix") ==
          apply(as(A2,"array"), 2, range))
```

mpfrMatrix

Classes "mpfrMatrix" and "mpfrArray"

Description

The classes "mpfrMatrix" and "mpfrArray" are, analogously to the **base** `matrix` and `array` functions and classes simply "numbers" of class `mpfr` with an additional `Dim` and `Dimnames` slot.

Objects from the Class

Objects should typically be created by `mpfrArray()`, but can also be created by `new("mpfrMatrix", ...)` or `new("mpfrArray", ...)`, or also by `t(x), dim(x) <- dd`, or `mpfr2array(x, dim=dd)` where `x` is a an `mpfr` "number vector".

A (slightly more flexible) alternative to `dim(x) <- dd` is `mpfr2array(x, dd, dimnames)`.

Slots

`.Data`: as for the `mpfr` class, a "list" of `mpfr1` numbers.

`Dim`: of class "integer", specifying the array dimension.

`Dimnames`: of class "list" and the same length as `Dim`, each list component either `NULL` or a `character` vector of length `Dim[j]`.

Extends

Class "mpfrMatrix" extends "mpfrArray", directly.

Class "mpfrArray" extends class "`mpfr`", by class "mpfrArray", distance 2; class "`list`", by class "mpfrArray", distance 3; class "`vector`", by class "mpfrArray", distance 4.

Methods

Arith signature(e1 = "mpfr", e2 = "mpfrArray"): ...

Arith signature(e1 = "numeric", e2 = "mpfrArray"): ...

Arith signature(e1 = "mpfrArray", e2 = "mpfrArray"): ...

Arith signature(e1 = "mpfrArray", e2 = "mpfr"): ...

Arith signature(e1 = "mpfrArray", e2 = "numeric"): ...

as.vector signature(x = "mpfrArray", mode = "missing"): drops the dimension 'attribute', i.e., transforms `x` into a simple `mpfr` vector. This is an inverse of `t(.)` or `dim(.) <- * on such a vector.`

atan2 signature(y = "ANY", x = "mpfrArray"): ...

atan2 signature(y = "mpfrArray", x = "mpfrArray"): ...

atan2 signature(y = "mpfrArray", x = "ANY"): ...

[<- signature(x = "mpfrArray", i = "ANY", j = "ANY", value = "ANY"): ...

[signature(x = "mpfrArray", i = "ANY", j = "ANY", drop = "ANY"): ...

[signature(x = "mpfrArray", i = "ANY", j = "missing", drop = "missing"): "mpfrArray"s can be subset ("indexed") as regular **R arrays**.

%% signature(x = "mpfr", y = "mpfrMatrix"): Compute the matrix/vector product xy when the dimensions (**dim**) of x and y match. If x is not a matrix, it is treated as a 1-row or 1-column matrix (aka "row vector" or "column vector") depending on which one makes sense, see the documentation of the **base** function **%*%**.

%% signature(x = "mpfr", y = "Mnumber"): method definition for cases with one **mpfr** and any "number-like" argument are to use MPFR arithmetic as well.

%% signature(x = "mpfrMatrix", y = "mpfrMatrix"),
 %% signature(x = "mpfrMatrix", y = "mpfr"), etc. Further method definitions with identical semantic.

crossprod signature(x = "mpfr", y = "missing"): Computes $x'x$, i.e., $t(x) \%*\% x$, typically more efficiently.

crossprod signature(x = "mpfr", y = "mpfrMatrix"): Computes $x'y$, i.e., $t(x) \%*\% y$, typically more efficiently.

crossprod signature(x = "mpfrMatrix", y = "mpfrMatrix"): ...

crossprod signature(x = "mpfrMatrix", y = "mpfr"): ...

tcrossprod signature(x = "mpfr", y = "missing"): Computes xx' , i.e., $x \%*\% t(x)$, typically more efficiently.

tcrossprod signature(x = "mpfrMatrix", y = "mpfrMatrix"): Computes xy' , i.e., $x \%*\% t(y)$, typically more efficiently.

tcrossprod signature(x = "mpfrMatrix", y = "mpfr"): ...

tcrossprod signature(x = "mpfr", y = "mpfrMatrix"): ...

coerce signature(from = "mpfrArray", to = "array"): coerces from to a *numeric* array of the same dimension.

coerce signature(from = "mpfrArray", to = "vector"): as for standard **arrays**, this "drops" the dim (and dimnames), i.e., returns an **mpfr** vector.

Compare signature(e1 = "mpfr", e2 = "mpfrArray"): ...

Compare signature(e1 = "numeric", e2 = "mpfrArray"): ...

Compare signature(e1 = "mpfrArray", e2 = "mpfr"): ...

Compare signature(e1 = "mpfrArray", e2 = "numeric"): ...

dim signature(x = "mpfrArray"): ...

dimnames<- signature(x = "mpfrArray"): ...

dimnames signature(x = "mpfrArray"): ...

show signature(object = "mpfrArray"): ...

sign signature(x = "mpfrArray"): ...

norm signature(x = "mpfrMatrix", type = "character"): computes the matrix norm of x, see **norm** or the one in package **Matrix**.

t signature(x = "mpfrMatrix"): tranpose the **mpfrMatrix**.

aperm signature(a = "mpfrArray"): **aperm(a,perm)** is a generalization of **t(.)** to *permute* the dimensions of an **mpfrArray**; it has the same semantics as the standard **aperm()** method for simple **R arrays**.

Author(s)

Martin Maechler

See Also[mpfrArray](#), also for more examples.**Examples**

```

showClass("mpfrMatrix")

validObject(mm <- new("mpfrMatrix"))
validObject(aa <- new("mpfrArray"))

v6 <- mpfr(1:6, 128)
m6 <- new("mpfrMatrix", v6, Dim = c(2L, 3L))
validObject(m6)
m6
which(m6 == 3, arr.ind = TRUE) # |--> (1, 2)
## Coercion back to "vector": Both of these work:
stopifnot(identical(as(m6, "mpfr"), v6),
  identical(as.vector(m6), v6)) # < but this is a "coincidence"

S2 <- m6[,-3] # 2 x 2
S3 <- rbind(m6, c(1:2,10)) ; s3 <- asNumeric(S3)
det(S2)
str(determinant(S2))
det(S3)
stopifnot(all.equal(det(S2), det(asNumeric(S2)), tol=1e-15),
  all.equal(det(S3), det(s3), tol=1e-15))

## 2-column matrix indexing and replacement:
(sS <- S3[i2 <- cbind(1:2, 2:3)])
stopifnot(identical(asNumeric(sS), s3[i2]))
C3 <- S3; c3 <- s3
C3[i2] <- 10:11
c3[i2] <- 10:11
stopifnot(identical(asNumeric(C3), c3))

AA <- new("mpfrArray", as.vector(cbind(S3, -S3)), Dim=c(3L,3:2))
stopifnot(identical(AA[,1] , S3), identical(AA[,2] , -S3))
aa <- asNumeric(AA)

i3 <- cbind(3:1, 1:3, c(2L, 1:2))
ii3 <- Rmpfr:::mat2ind(i3, dim(AA), dimnames(AA))
stopifnot(aa[i3] == new("mpfr", getD(AA)[ii3]))
stopifnot(identical(aa[i3], asNumeric(AA[i3])))
CA <- AA; ca <- aa
ca[i3] <- ca[i3] ^ 3
CA[i3] <- CA[i3] ^ 3

## scale():

```

```

S2. <- scale(S2)
stopifnot(all.equal(abs(as.vector(S2.)), rep(sqrt(1/mpfr(2, 128)), 4),
  tol = 1e-30))

## norm() :
norm(S2)
stopifnot(identical(norm(S2), norm(S2, "1")),
  norm(S2, "I") == 6,
  norm(S2, "M") == 4,
  abs(norm(S2, "F") - 5.477225575051661) < 1e-15)

```

mpfrMatrix-utils *Functions for mpfrMatrix Objects*

Description

`determinant(x, ...)` computes the determinant of the mpfr square matrix `x`. May work via coercion to "numeric", i.e., compute `determinant(asNumeric(x), logarithm)`, if `asNumeric` is true, by default, if the dimension is larger than three. Otherwise, use precision `precBits` for the "accumulator" of the result, and use the recursive mathematical definition of the determinant (with computational complexity $n!$, where n is the matrix dimension, i.e., **very** inefficient for all but small matrices!)

Usage

```

## S3 method for class 'mpfrMatrix'
determinant(x, logarithm = TRUE,
  asNumeric = (d[1] > 3), precBits = max(.getPrec(x)), ...)

```

Arguments

<code>x</code>	an <code>mpfrMatrix</code> object of <i>square</i> dimension.
<code>logarithm</code>	logical indicating if the <code>log</code> of the absolute determinant should be returned.
<code>asNumeric</code>	logical ... if rather <code>determinant(asNumeric(x), ...)</code> should be computed.
<code>precBits</code>	the number of binary digits for the result (and the intermediate accumulations).
<code>...</code>	unused (potentially further arguments passed to methods).

Value

as `determinant()`, an object of S3 class "det", a `list` with components

<code>modulus</code>	the (logarithm of) the absolute value (<code>abs</code>) of the determinant of <code>x</code> .
<code>sign</code>	the sign of the determinant.

Author(s)

Martin Maechler

See Also

[determinant](#) in base R, which relies on a fast LU decomposition. [mpfrMatrix](#)

Examples

```
m6 <- mpfrArray(1:6, prec=128, dim = c(2L, 3L))
m6
S2 <- m6[,-3] # 2 x 2
S3 <- rbind(m6, c(1:2,10))
det(S2)
str(determinant(S2))
det(S3)
stopifnot(all.equal(det(S2), det(asNumeric(S2)), tolerance=1e-15),
  all.equal(det(S3), det(asNumeric(S3)), tolerance=1e-15))
```

 optimizeR

High Precision One-Dimensional Optimization

Description

optimizeR searches the interval from lower to upper for a minimum of the function f with respect to its first argument.

Usage

```
optimizeR(f, lower, upper, ..., tol = 1e-20,
  method = c("Brent", "GoldenRatio"),
  maximum = FALSE,
  precFactor = 2.0, precBits = -log2(tol) * precFactor,
  maxiter = 1000, trace = FALSE)
```

Arguments

f	the function to be optimized. $f(x)$ must work “in Rmpfr arithmetic” for optimizer() to make sense. The function is either minimized or maximized over its first argument depending on the value of maximum.
...	additional named or unnamed arguments to be passed to f.
lower	the lower end point of the interval to be searched.
upper	the upper end point of the interval to be searched.
tol	the desired accuracy, typically higher than double precision, i.e., $tol < 2e-16$.
method	character string specifying the optimization method.
maximum	logical indicating if $f()$ should be maximized or minimized (the default).
precFactor	only for default precBits construction: a factor to multiply with the number of bits directly needed for tol.
precBits	number of bits to be used for mpfr numbers used internally.

maxiter	maximal number of iterations to be used.
trace	integer or logical indicating if and how iterations should be monitored; if an integer k , print every k -th iteration.

Details

"Brent": Brent(1973)'s simple and robust algorithm is a hybrid, using a combination of the golden ratio and local quadratic ("parabolic") interpolation. This is the same algorithm as standard R's `optimize()`, adapted to high precision numbers.

In smooth cases, the convergence is considerably faster than the golden section or Fibonacci ratio algorithms.

"GoldenRatio": The golden ratio method works as follows: from a given interval containing the solution, it constructs the next point in the golden ratio between the interval boundaries.

Value

A `list` with components `minimum` (or `maximum`) and `objective` which give the location of the minimum (or maximum) and the value of the function at that point; `iter` specifying the number of iterations, the logical `convergence` indicating if the iterations converged and `estim.prec` which is an estimate or an upper bound of the final precision (in x). `method` the string of the method used.

Author(s)

"GoldenRatio" is based on Hans W Borchert's `golden_ratio`; modifications and "Brent" by Martin Maechler.

See Also

R's standard `optimize`; **Rmpfr**'s `unirootR`.

Examples

```
iG5 <- function(x) -exp(-(x-5)^2/2)
curve(iG5, 0, 10, 200)
o.dp <- optimize(iG5, c(0, 10)) #-> 5 of course
oM.gs <- optimizeR(iG5, 0, 10, method="Golden")
oM.Br <- optimizeR(iG5, 0, 10, method="Brent", trace=TRUE)
oM.gs$min ; oM.gs$iter
oM.Br$min ; oM.Br$iter
(doExtras <- Rmpfr::doExtras())
if(doExtras) {## more accuracy {takes a few seconds}
  oM.gs <- optimizeR(iG5, 0, 10, method="Golden", tol = 1e-70)
  oM.Br <- optimizeR(iG5, 0, 10,
                    tol = 1e-70)
}
rbind(Golden = c(err = as.numeric(oM.gs$min -5), iter = oM.gs$iter),
      Brent = c(err = as.numeric(oM.Br$min -5), iter = oM.Br$iter))

## ==> Brent is orders of magnitude more efficient !

## Testing on the sine curve with 40 correct digits:
```

```

sol <- optimizeR(sin, 2, 6, tol = 1e-40)
str(sol)
sol <- optimizeR(sin, 2, 6, tol = 1e-50,
                 precFactor = 3.0, trace = TRUE)
pi.. <- 2*sol$min/3
print(pi.., digits=51)
stopifnot(all.equal(pi.., Const("pi", 256), tolerance = 10*1e-50))

if(doExtras) { # considerably more expensive

## a harder one:
f.sq <- function(x) sin(x-2)^4 + sqrt(pmax(0, (x-1)*(x-4)))*(x-2)^2
curve(f.sq, 0, 4.5, n=1000)
msq <- optimizeR(f.sq, 0, 5, tol = 1e-50, trace=5)
str(msq) # ok
stopifnot(abs(msq$minimum - 2) < 1e-49)

## find the other local minimum: -- non-smooth ==> Golden-section is used
msq2 <- optimizeR(f.sq, 3.5, 5, tol = 1e-50, trace=10)
stopifnot(abs(msq2$minimum - 4) < 1e-49)

## and a local maximum:
msq3 <- optimizeR(f.sq, 3, 4, maximum=TRUE, trace=2)
stopifnot(abs(msq3$maximum - 3.57) < 1e-2)

}#end {doExtras}

##----- "impossible" one to get precisely -----

ff <- function(x) exp(-1/(x-8)^2)
curve(exp(-1/(x-8)^2), -3, 13, n=1001)
(opt. <- optimizeR(function(x) exp(-1/(x-8)^2), -3, 13, trace = 5))
## -> close to 8 {but not very close!}
ff(opt.$minimum) # gives 0
if(doExtras) {
  ## try harder ... in vain ..
  str(opt1 <- optimizeR(ff, -3,13, tol = 1e-60, precFactor = 4))
  print(opt1$minimum, digits=20)
  ## still just 7.99998038 or 8.000036655 {depending on method}
}

```

Description

For integers a, b , $I_x(a, b)$ aka $\text{pbeta}(x, a, b)$ is a polynomial in x with rational coefficients, and hence arbitrarily accurately computable.

Usage

```
pbetaI(q, shape1, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE,
       precBits = NULL, rnd.mode = c("N", "D", "U", "Z", "A"))
```

Arguments

`q` called x , above; vector of quantiles, in $[0, 1]$.

`shape1`, `shape2` the positive Beta “shape” parameters, called a, b , above. **Must** be integer valued for this function.

`ncp` unused, only for compatibility with `pbeta`, must be kept at its default, 0.

`lower.tail` logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

`log.p` logical; if TRUE, probabilities p are given as $\log(p)$.

`precBits` the precision (in number of bits) to be used in `sumBinomMpfr()`.

`rnd.mode` a 1-letter string specifying how *rounding* should happen at C-level conversion to MPFR, see `mpfr`.

Value

an “`mpfr`” vector of the same length as `q`.

Note

For upper tail probabilities, i.e., when `lower.tail=FALSE`, we may need large `precBits`, because the implicit or explicit $1 - P$ computation suffers from severe cancellation.

Author(s)

Martin Maechler

See Also

`pbeta`, `sumBinomMpfr` `chooseZ`.

Examples

```
x <- (0:12)/16 # not all the way up ..
a <- 7; b <- 788

p. <- pbetaI(x, a, b) ## still slow: %% T00 slow -- FIXME
pp <- pbetaI(x, a, b, precBits = 2048)
## Currently, the lower.tail=FALSE are computed "badly":
lp <- log(pp)    ## = pbetaI(x, a, b, log.p=TRUE)
lIp <- log1p(-pp) ## = pbetaI(x, a, b, lower.tail=FALSE, log.p=TRUE)
Ip <- 1 - pp     ## = pbetaI(x, a, b, lower.tail=FALSE)

if(Rmpfr:::doExtras()) { ## somewhat slow
  stopifnot(
    all.equal(lp, pbetaI(x, a, b, precBits = 2048, log.p=TRUE)),
    all.equal(lIp, pbetaI(x, a, b, precBits = 2048, lower.tail=FALSE, log.p=TRUE)),
```

```

        tol = 1e-230),
    all.equal( Ip, pbetaI(x, a, b, precBits = 2048, lower.tail=FALSE))
  )
}

rErr <- function(approx, true, eps = 1e-200) {
  true <- as.numeric(true) # for "mpfr"
  ifelse(Mod(true) >= eps,
        ## relative error, catching '-Inf' etc :
    ifelse(true == approx, 0, 1 - approx / true),
        ## else: absolute error (e.g. when true=0)
    true - approx)
}

rErr(pbeta(x, a, b), pp)
rErr(pbeta(x, a, b, lower=FALSE), Ip)
rErr(pbeta(x, a, b, log = TRUE), lp)
rErr(pbeta(x, a, b, lower=FALSE, log = TRUE), lIp)

a.EQ <- function(..., tol=1e-15) all.equal(..., tolerance=tol)
stopifnot(
  a.EQ(pp, pbeta(x, a, b)),
  a.EQ(lp, pbeta(x, a, b, log.p=TRUE)),
  a.EQ(lIp, pbeta(x, a, b, lower.tail=FALSE, log.p=TRUE)),
  a.EQ( Ip, pbeta(x, a, b, lower.tail=FALSE))
)

```

pmax

Parallel Maxima and Minima

Description

Returns the parallel maxima and minima of the input values.

The functions `pmin` and `pmax` have been made S4 generics, and this page documents the “... method for class `"mNumber"`”, i.e., for arguments that are numeric or from `class "mpfr"`.

Usage

```

pmax(..., na.rm = FALSE)
pmin(..., na.rm = FALSE)

```

Arguments

... numeric or arbitrary precision numbers (class `mpfr`).

na.rm a logical indicating whether missing values should be removed.

Details

See `pmax`, the documentation of the base functions, i.e., default methods.

Value

vector-like, of length the longest of the input vectors; typically of class `mpfr`, for the methods here.

Methods

`... = "ANY"` the default method, really just `base::pmin` or `base::pmax`, respectively.

`... = "mNumber"` the method for `mpfr` arguments, mixed with numbers; designed to follow the same semantic as the default method.

See Also

The documentation of the **base** functions, `pmin` and `pmax`; also `min` and `max`; further, `range` (both `min` and `max`).

Examples

```
(pm <- pmin(1.35, mpfr(0:10, 77)))
stopifnot(pm == pmin(1.35, 0:10))
```

roundMpfr

Rounding to Binary bits, "mpfr-internally"

Description

Rounding to binary bits, not decimal digits. Closer to the number representation, this also allows to *increase* or decrease a number's `precBits`. In other words, it acts as `setPrec()`, see `getPrec()`.

Usage

```
roundMpfr(x, precBits, rnd.mode = c("N", "D", "U", "Z", "A"))
```

Arguments

<code>x</code>	an <code>mpfr</code> number (vector)
<code>precBits</code>	integer specifying the desired precision in bits.
<code>rnd.mode</code>	a 1-letter string specifying how <i>rounding</i> should happen at C-level conversion to MPFR, see <code>mpfr</code> .

Value

an `mpfr` number as `x` but with the new 'precBits' precision

See Also

The `mpfr` class group method `Math2` implements a method for `round(x, digits)` which rounds to *decimal* digits.

Examples

```
(p1 <- Const("pi", 100)) # 100 bit prec
roundMpfr(p1, 120) # 20 bits more, but "random noise"
Const("pi", 120) # same "precision", but really precise
```

seqMpfr

*"mpfr" Sequence Generation***Description**

Generate ‘regular’, i.e., arithmetic sequences. This is in lieu of methods for [seq](#) (dispatching on all three of from, to, and by).

Usage

```
seqMpfr(from = 1, to = 1, by = ((to - from)/(length.out - 1)),
        length.out = NULL, along.with = NULL, ...)
```

Arguments

from, to	the starting and (maximal) end value (numeric or <i>"mpfr"</i>) of the sequence.
by	number (numeric or <i>"mpfr"</i>): increment of the sequence.
length.out	desired length of the sequence. A non-negative number, which will be rounded up if fractional.
along.with	take the length from the length of this argument.
...	arguments passed to or from methods.

Details

see [seq](#) (default method in package **base**), whose semantic we want to replicate (almost).

Value

a ‘vector’ of class *"mpfr"*, when one of the first three arguments was.

Author(s)

Martin Maechler

See Also

The documentation of the **base** function [seq](#); [mpfr](#)

Examples

```
seqMpfr(0, 1, by = mpfr(0.25, prec=88))
```

```
seqMpfr(7, 3) # -> default prec.
```

```
str.mpfr
```

Compactly Show STRucture of Rmpfr Number Object

Description

The `str` method for objects of class `mpfr` produces a bit more useful output than the default method `str.default`.

Usage

```
## S3 method for class 'mpfr'
str(object, nest.lev, give.head=TRUE,
     digits.d = 12, vec.len = NULL, drop0trailing=TRUE,
     width = getOption("width"), ...)
```

Arguments

<code>object</code>	an object of class <code>mpfr</code> .
<code>nest.lev</code>	for <code>str()</code> , typically only used when called by a higher level <code>str()</code> .
<code>give.head</code>	logical indicating if the “header” should be printed.
<code>digits.d</code>	the number of digits to be used, will be passed <code>formatMpfr()</code> and hence <code>NULL</code> will use “as many as needed”, i.e. often too many. If this is a number, as per default, less digits will be used in case the precision (<code>getPrec(object)</code>) is smaller.
<code>vec.len</code>	the number of <i>elements</i> that will be shown. The default depends on the precision of object and width (since Rmpfr 0.6-0, it was 3 previously).
<code>drop0trailing</code>	logical, passed to <code>formatMpfr()</code> (with a different default here).
<code>width</code>	the (approximately) desired width of output, see <code>options(width = .)</code> .
<code>...</code>	further arguments, passed to <code>formatMpfr()</code> .

See Also

`mpfrIs0` for many more utilities.

Examples

```
(x <- c(Const("pi", 64), mpfr(-2:2, 64)))
str(x)
str(list(pi = pi, x.mpfr = x))
str(x ^ 1000)
str(x ^ -1e4, digits=NULL) # full precision

uu <- Const("pi", 16)# unaccurate
str(uu) # not using default of 12 digits
```

sumBinomMpfr

(Alternating) Binomial Sums via Rmpfr

Description

Compute (alternating) binomial sums via high-precision arithmetic. If $sBn(f, n) := \text{sumBinomMpfr}(n, f)$, (default alternating is true, and $n_0 = 0$),

$$sBn(f, n) = \sum_{k=n_0}^n (-1)^{(n-k)} \binom{n}{k} \cdot f(k) = \Delta^n f,$$

see Details for the n -th forward difference operator $\Delta^n f$. If `alternating` is false, the $(-1)^{(n-k)}$ factor is dropped (or replaced by 1) above.

Such sums appear in different contexts and are typically challenging, i.e., currently impossible, to evaluate reliably as soon as n is larger than around 50 – 70.

Usage

```
sumBinomMpfr(n, f, n0 = 0, alternating = TRUE, precBits = 256,
             f.k = f(mpfr(k, precBits=precBits)))
```

Arguments

<code>n</code>	upper summation index (integer).
<code>f</code>	function to be evaluated at k for k in $n_0:n$ (and which must return <i>one</i> value per k).
<code>n0</code>	lower summation index, typically 0 (= default) or 1.
<code>alternating</code>	logical indicating if the sum is alternating, see below.
<code>precBits</code>	the number of bits for MPFR precision, see mpfr .
<code>f.k</code>	can be specified instead of <code>f</code> and <code>precBits</code> , and must contain the equivalent of its default, <code>f(mpfr(k, precBits=precBits))</code> .

Details

The alternating binomial sum $sB(f, n) := \text{sumBinom}(n, f, n0 = 0)$ is equal to the n -th forward difference operator $\Delta^n f$,

$$sB(f, n) = \Delta^n f,$$

where

$$\Delta^n f = \sum_{k=0}^n (-1)^{n-k} \binom{n}{k} \cdot f(k),$$

is the n -fold iterated forward difference $\Delta f(x) = f(x+1) - f(x)$ (for $x = 0$).

The current implementation might be improved in the future, notably for the case where $sB(f, n) = \text{sumBinomMpfr}(n, f, *)$ is to be computed for a whole sequence $n = 1, \dots, N$.

Value

an `mpfr` number of precision `precBits`. s . If `alternating` is true (as per default),

$$s = \sum_{k=n0}^n (-1)^k \binom{n}{k} \cdot f(k),$$

if `alternating` is false, the $(-1)^k$ factor is dropped (or replaced by 1) above.

Author(s)

Martin Maechler, after conversations with Christophe Dutang.

References

Wikipedia (2012) The N"orlund-Rice integral, http://en.wikipedia.org/wiki/Rice_integral
 Flajolet, P. and Sedgewick, R. (1995) Mellin Transforms and Asymptotics: Finite Differences and Rice's Integrals, *Theoretical Computer Science* **144**, 101–124.

See Also

[chooseMpfr](#), [chooseZ](#) from package `gmp`.

Examples

```
## "naive" R implementation:
sumBinom <- function(n, f, n0=0, ...) {
  k <- n0:n
  sum( choose(n, k) * (-1)^(n-k) * f(k, ...) )
}

## compute sumBinomMpfr(.) for a whole set of 'n' values:
sumBin.all <- function(n, f, n0=0, precBits = 256, ...)
{
  N <- length(n)
  precBits <- rep(precBits, length = N)
  ll <- lapply(seq_len(N), function(i)
```

```

        sumBinomMpfr(n[i], f, n0=n0, precBits=precBits[i], ...)
    sapply(1l, as, "double")
}
sumBin.all.R <- function(n, f, n0=0, ...)
  sapply(n, sumBinom, f=f, n0=n0, ...)

n.set <- 5:80
system.time(res.R <- sumBin.all.R(n.set, f = sqrt)) ## instantaneous..
system.time(resMpfr <- sumBin.all (n.set, f = sqrt)) ## ~ 0.6 seconds

matplot(n.set, cbind(res.R, resMpfr), type = "l", lty=1,
        ylim = extendrange(resMpfr, f = 0.25), xlab = "n",
        main = "sumBinomMpfr(n, f = sqrt) vs. R double precision")
legend("topleft", leg=c("double prec.", "mpfr"), lty=1, col=1:2, bty = "n")

```

unirootR

One Dimensional Root (Zero) Finding – in pure R

Description

The function `unirootR` searches the interval from lower to upper for a root (i.e., zero) of the function `f` with respect to its first argument.

`unirootR()` is “clone” of `uniroot()`, written entirely in R, in a way that it works with `mpfr`-numbers as well.

Usage

```

unirootR(f, interval, ...,
        lower = min(interval), upper = max(interval),
        f.lower = f(lower, ...), f.upper = f(upper, ...),
        verbose = FALSE,
        tol = .Machine$double.eps^0.25, maxiter = 1000,
        epsC = NULL)

```

Arguments

<code>f</code>	the function for which the root is sought.
<code>interval</code>	a vector containing the end-points of the interval to be searched for the root.
<code>...</code>	additional named or unnamed arguments to be passed to <code>f</code>
<code>lower, upper</code>	the lower and upper end points of the interval to be searched.
<code>f.lower, f.upper</code>	the same as <code>f(upper)</code> and <code>f(lower)</code> , respectively. Passing these values from the caller where they are often known is more economical as soon as <code>f()</code> contains non-trivial computations.
<code>verbose</code>	logical (or integer) indicating if (and how much) verbose output should be produced during the iterations.

<code>tol</code>	the desired accuracy (convergence tolerance).
<code>maxiter</code>	the maximum number of iterations.
<code>epsC</code>	positive number or NULL in which case a smart default is sought. This should specify the “achievable machine precision” <i>for</i> the given numbers and their arithmetic. The default will set this to <code>.Machine\$double.eps</code> for double precision numbers, and will basically use $2^{-\min(\text{getPrec}(f.\text{lower}), \text{getPrec}(f.\text{upper}))}$ when that works (as, e.g., for <code>mpfr</code> -numbers) otherwise. This is factually a lower bound for the achievable lower bound, and hence, setting <code>tol</code> smaller than <code>epsC</code> is typically non-sensical sense and produces a warning.

Details

Note that arguments after `...` must be matched exactly.

Either `interval` or both `lower` and `upper` must be specified: the upper endpoint must be strictly larger than the lower endpoint. The function values at the endpoints must be of opposite signs (or zero).

The function only uses R code with basic arithmetic, such that it should also work with “generalized” numbers (such as `mpfr`-numbers) as long the necessary `Ops` methods are defined for those.

The underlying algorithm assumes a continuous function (which then is known to have at least one root in the interval).

Convergence is declared either if $f(x) = 0$ or the change in `x` for one step of the algorithm is less than `tol` (plus an allowance for representation error in `x`).

If the algorithm does not converge in `maxiter` steps, a warning is printed and the current approximation is returned.

`f` will be called as `f(x, ...)` for a (generalized) numeric value of `x`.

Value

A list with four components: `root` and `f.root` give the location of the root and the value of the function evaluated at that point. `iter` and `estim.prec` give the number of iterations used and an approximate estimated precision for `root`. (If the root occurs at one of the endpoints, the estimated precision is `NA`.)

Source

Based on `zeroIn()` (in package **rootoned**) by John Nash who manually translated the C code in R’s `zeroIn.c` and on `uniroot()` in R’s sources.

References

Brent, R. (1973), see `uniroot`.

See Also

`polyroot` for all complex roots of a polynomial; `optimize`, `nlm`.

Examples

```

require(utils) # for str

## some platforms hit zero exactly on the first step:
## if so the estimated precision is 2/3.
f <- function(x,a) x - a
str(xmin <- unirootR(f, c(0, 1), tol = 0.0001, a = 1/3))

## handheld calculator example: fixpoint of cos(.):
rc <- unirootR(function(x) cos(x) - x, lower=-pi, upper=pi, tol = 1e-9)
rc$root

## the same with much higher precision:
rcM <- unirootR(function(x) cos(x) - x,
                interval= mpfr(c(-3,3), 300), tol = 1e-40)
rcM
x0 <- rcM$root
stopifnot(all.equal(cos(x0), x0,
                    tol = 1e-40))## 40 digits accurate!

str(unirootR(function(x) x*(x^2-1) + .5, lower = -2, upper = 2,
            tol = 0.0001), digits.d = 10)
str(unirootR(function(x) x*(x^2-1) + .5, lower = -2, upper = 2,
            tol = 1e-10 ), digits.d = 10)

## A sign change of f(.), but not a zero but rather a "pole":
tan. <- function(x) tan(x * (Const("pi",200)/180))# == tan( <angle> )
(rtan <- unirootR(tan., interval = mpfr(c(80,100), 200), tol = 1e-40))
## finds 90 {"ok"}, and now gives a warning

## Find the smallest value x for which exp(x) > 0 (numerically):
r <- unirootR(function(x) 1e80*exp(x)-1e-300, c(-1000,0), tol = 1e-15)
str(r, digits.d = 15) ##> around -745, depending on the platform.

exp(r$root)      # = 0, but not for r$root * 0.999...
minexp <- r$root * (1 - 10*.Machine$double.eps)
exp(minexp)      # typically denormalized

## --- using mpfr-numbers :

## Find the smallest value x for which exp(x) > 0 ("numerically");
## Note that mpfr-numbers underflow *MUCH* later than doubles:
## one of the smallest mpfr-numbers {see also ?mpfr-class } :
(ep.M <- mpfr(2, 55) ^ - ((2^30 + 1) * (1 - 1e-15)))
r <- unirootR(function(x) 1e99* exp(x) - ep.M, mpfr(c(-1e20, 0), 200))
r # 97 iterations; f.root is very similar to ep.M

```

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