Computer Algebra Systems in R with

caracas

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Abstract The capability of R to do symbolic mathematics is enhanced by the **caracas** package. This package uses the Python computer algebra library SymPy as a back-end but **caracas** is tightly integrated in the R environment, thereby enabling the R user with symbolic mathematics within R. Key components of the **caracas** package are illustrated in this paper. Examples are taken from statistics and mathematics. The **caracas** package integrates well with e.g. **Rmarkdown**, and as such creation of scientific reports and teaching is supported.

Keywords

Differentiation, Factor analysis, Hessian matrix, Integration, Lagrange multiplier, Limit, Linear algebra, Principal component analysis, Score function, Symbolic mathematics, Taylor expansion, Teaching.

Introduction

The capability of R (R Core Team, 2021) to handle symbolic mathematics is greatly enhanced by two packages: The caracas package, which is the main topic of this paper, and the Ryacas package described in Andersen and Højsgaard (2019). The caracas package is based on interfacing the Python library SymPy (Meurer et al., 2017), using the reticulate package, (Ushey et al., 2020). Similarly, Ryacas is based on interfacing the computer algebra system (CAS) yacas (Pinkus et al., 2016; Pinkus and Winitzki, 2002). The caracas package is open-source and the source code is available at https://github.com/r-cas/caracas. Several vignettes illustrating caracas are provided and these are also available online, see https://r-cas.github.io/caracas/.

One particular instance where we have found the packages useful is in connection with teaching where symbolic mathematics is helpful strongly aided by the packages ability to enter in a reproducible framework (provided e.g. by **Rmarkdown**). In this paper we provide a few examples of this, and we address the issue more generally towards the end of the paper.

The caracas package versus other computer algebra systems Neither caracas nor Ryacas are as powerful as some of the large commercial computer algebra systems. The virtue of the caracas and Ryacas packages lie elsewhere:

- 1. Tools like solving equations, summation, limits, symbolic linear algebra, outputting in tex format etc. are directly available from within R.
- 2. The packages enable working with the same language and in the same environment as the user does for statistical analyses.
- 3. Symbolic mathematics can easily be combined with data which is helpful in e.g. numerical optimization.
- 4. Lastly, the packages are part of the R project (since the packages are on CRAN). As such the packages are freely available, and therefore support e.g. education also of people with limited economical means and thus contributing to United Nations sustainable development goals, cfr. United Nations General Assembly (2015).

With respect to freely available resources in a CAS context, we would like to draw attention to WolframAlpha, see https://www.wolframalpha.com/, which is an online for answering (mathematical) queries.

Introductory examples

There are no other system requirements than Python for using caracas. This paper is based on the following version of caracas:

```
R> library(caracas)
R> packageVersion("caracas")
#> [1] '1.1.0'
```

The interplay between R and SymPy

As mentioned above, **caracas** provides an interface from R to the Python package SymPy. This means that SymPy is "running under the hood" of R via the **reticulate** package. In **caracas** we have symbols, which is an R list with a pyobj slot and the class caracas_symbol. The pyobj refers to an object in Python (often a SymPy object). As such, a symbol (in R) provides a handle to a Python object. In the design of **caracas** we have tried to make this distinction something the user should not be concerned with, but it is worthwhile being aware of the distinction. There are several ways of creating symbols; one is with def_sym() that both declares the symbol in R and in Python:

```
R> ## Define symbols and assign in global environment
 R> def_sym(s1, s2); s1 # Declares 's1'/'s2' in both R and Python
  #> [caracas]: s1
 R> str(s1)
  #> List of 1
  #> $ pyobj:s1
  #> - attr(*, "class")= chr "caracas_symbol"
 R> ## Create new symbol from existing ones
 R> s3 <- s1 * s2; s3 # 's3' is a symbol in R; no corresponding object in Python
  #> [caracas]: s1*s2
 R> str(s3)
  #> List of 1
  #> $ pyobj:s1*s2
  #> - attr(*, "class")= chr "caracas_symbol"
Note that above def_sym(s1, s2) is a short-hand for the following:
 R> s1 <- symbol("s1")
 R> s2 <- symbol("s2")
```

We can further exemplify that objects in R and Python are not necessarily identical. We look into a symbol, and to make the distinction clear we use different names. Symbols can be created with the symbol() function.

```
R> ## Create a symbol 'b1' corresponding to an entity called 'a' in SymPy:
R> b1 <- symbol("a"); str(b1)

#> List of 1

#> $ pyobj:a

#> - attr(*, "class")= chr "caracas_symbol"

R> ## A new symbol can be created as:
R> b2 <- b1 + 1; str(b2)

#> List of 1

#> $ pyobj:a + 1

#> - attr(*, "class")= chr "caracas_symbol"

R> ## The Python entity 'a' in the symbol can be modified with:
R> b3 <- subs(b2, "a", "k"); str(b3)

#> List of 1

#> $ pyobj:k + 1

#> - attr(*, "class")= chr "caracas_symbol"
```

Going back to the first example, we can substitute one symbol with another and simplify the result as (where we use the pipe operator %>% from magrittr by Bache and Wickham (2020)):

It is also possible to convert to and from symbols and standard R expressions:

```
R> ## Coerce from symbol to expression:
R> e5 <- as_expr(s5); e5
#> expression(u^2 - v^2)
R> ## Coerce from expression to symbol:
R> as_sym(e5) # identical to s5
```

Finding a limit - the Euler constant

Define symbols n and f:

```
R> def_sym(n)
R> f <- (1 + 1/n)^n
```

We can calculate the limit of f for $n \to \infty$:

```
R> lim_f <- lim(f, n, Inf)
R> lim_f
#> [caracas]: exp(1)
R> as_expr(lim_f)
#> [1] 2.72
```

We can also tell **caracas** not to evaluate the limit (with the doit = FALSE argument) but only set up the symbol for later evaluation and/or for additional algebraic manipulations:

By default caracas uses UTF-8 printing, but in this paper we have used pretty ASCII printing which can be set globally by options(caracas.print.prettyascii = TRUE).

The unevaluated symbol can be evaluated as follows:

```
R> lim_f <- doit(lim_f_sym)
R> lim_f
#> [caracas]: exp(1)
```

Hence, three caracas symbols have been created above: f, lim_f_sym and lim_f. Objects can be printed in TeX form using tex(), e.g.

```
R> tex(lim_f_sym)
#> [1] "\\lim_{n \\to \\infty} \\left(1 + \\frac{1}{n}\\right)^{n}"
```

This can be used in a TEX environment as e.g.

```
\[
`r tex(f)`, \quad `r tex(lim_f_sym)`, \quad `r tex(lim_f)`.
\]
giving
```

$$\left(1+\frac{1}{n}\right)^n$$
, $\lim_{n\to\infty}\left(1+\frac{1}{n}\right)^n$, e .

Differentiation and integration

Consider this function (taken from a vignette for the **mosaicCalc** package (Kaplan et al., 2020)). Using the **Deriv** package, the derivative can be found as follows:

```
R> f <- function(x){
+   a * x + b * x^2 + c * sin(x^2)
+ }
R> Deriv::Deriv(f, "x")
#> function (x)
#> a + x * (2 * (c * cos(x^2)) + 2 * b)
```

The anti-derivative, however, is not easily obtained in R. Using caracas we get derivative and anti-derivative as:

```
R> f_c <- as_sym("a * x + b * x^2 + c * sin(x^2)")
R> def_sym(x) # To get handle on x in R
R> D_f <- der(f_c, x) # Or: der(f_c, "x")
R> aD_f <- int(f_c, x) %>% simplify()
```

$$D_f = a + 2bx + 2cx\cos\left(x^2\right), \quad aD_f = \frac{ax^2}{2} + \frac{bx^3}{3} + \frac{\sqrt{2}\sqrt{\pi}cS\left(\frac{\sqrt{2}x}{\sqrt{\pi}}\right)}{2}$$

Above, S() is the Fresnel integral $S(z) = \int_0^z \sin\left(\frac{\pi}{2}t^2\right) dt$. Evaluation in R requires a definition of fresnels():

```
R> as_expr(aD_f) # Evaluation requires user-defined fresnels()
#> expression(a * x^2/2 + b * x^3/3 + sqrt(2) * sqrt(pi) * c * fresnels(sqrt(2) *
#> x/sqrt(pi))/2)
```

Exact and numerical evaluations

We can make exact as well as numerical evaluations as follows:

```
R> def_sym(x)
R> f <- exp(x^2)
R> subs(f, x, "1/3")
#> [caracas]: exp(1/9)
R> subs(f, x, 1/3)
#> [caracas]: 1.11751906874186
```

In the first case, 1/3 is regarded as a fraction. In the second case, 1/3 is evaluated numerically in R before caracas gets the value. As a consequence we have:

```
R> subs(f, x, "1/3 + 1/4")

#> [caracas]: / 49\

#> exp|---|

#> \144/

R> subs(f, x, 1/3 + 1/4)

#> [caracas]: 1.40533790799144
```

An exact evaluation can be evaluated numerically afterwards:

We can also convert the caracas symbol to an R expression that is subsequently evaluated:

```
R> f %>% as_expr()
#> expression(exp(x^2))
R> f %>% as_expr() %>% eval(list(x = 1/3 + 1/4))
#> [1] 1.41
```

Taylor expansion

We perform a fourth order Taylor expansion of $f(x) = \cos(x)$ around x = 0:

The order term can be removed:

```
\#> expression(x^4/24 - x^2/2 + 1)
```

Matrix algebra

We briefly demonstrate the use matrices in caracas (see also https://r-cas.github.io/caracas/):

Note that rbind() and cbind() also works on caracas (vector) symbols:

Some routines are demonstrated below:

$$\mathrm{detA} = ad - bc, \quad \mathrm{Ai} = \begin{bmatrix} \frac{d}{ad - bc} & -\frac{c}{ad - bc} \\ -\frac{b}{ad - bc} & \frac{a}{ad - bc} \end{bmatrix}, \quad \mathrm{AD} = \begin{bmatrix} ae_1 & ce_2 \\ be_1 & de_2 \end{bmatrix}$$

R> evec <- eigenvec(A)

R> evec1 <-evec[[1]]\$eigvec %>% simplify()

R> eval <- eigenval(A)</pre>

R> eval1 <- eval[[1]]\$eigval %>% simplify()

$$\text{evec1} = \begin{bmatrix} -\frac{2c}{a - d + \sqrt{a^2 - 2ad + 4bc + d^2}} \\ 1 \end{bmatrix} \text{,} \quad \text{eval1} = \frac{a}{2} + \frac{d}{2} - \frac{\sqrt{a^2 - 2ad + 4bc + d^2}}{2}.$$

R> B <- matrix_(c("b", "0", "0", "1"), nrow = 2, ncol = 2)

R> qr_res <- QRdecomposition(B)</pre>

 $R> Q <- qr_res$Q$

 $R> R <- qr_res$R$

$$\mathbf{Q} = \begin{bmatrix} \frac{b}{|b|} & 0 \\ 0 & 1 \end{bmatrix}, \quad \mathbf{R} = \begin{bmatrix} |b| & 0 \\ 0 & 1 \end{bmatrix}.$$

Lagrange multiplier and maximizing a likelihood

Here we illustrate how to maximize a multinomial likelihood using Lagrange multiplier. Consider a multinomial model with three categories with probabilities p_1 , p_2 and p_3 such that $p_1 + p_2 + p_3 = 1$. We then observe counts y_1 , y_2 and y_3 of each category. The multinomial log-likelihood for this model is

$$l(p) = y_1 \log(p_1) + y_2 \log(p_2) + y_3 \log(p_3). \tag{1}$$

We wish to maximize l(p) under the constraint that $p_1 + p_2 + p_3 = 1$. This can be achieved using Lagrange multiplier where we instead solve the unconstrained optimization problem $\max_p L(p)$ where

$$L(p) = -l(p) + \lambda g(p)$$
 under the constraint that (2)

$$g(p) = p_1 + p_2 + p_3 - 1 = 0. (3)$$

The function L can be expressed in caracas as follows where we create character vectors in R and convert them to a caracas symbol using as_sym():

$$R> p \leftarrow as_sym(paste0("p", 1:3))$$

```
R> y <- as_sym(paste0("y", 1:3))
R> def_sym(a)
R> l <- sum(y * log(p))
R> L <- -l + a * (sum(p) - 1); L
#> [caracas]: a*(p1 + p2 + p3 - 1) - y1*log(p1) - y2*log(p2) - y3*log(p3)
```

To solve the unconstrained optimization problem we find the critical points and afterwards check the eigenvalues of the Hessian (at the critical points). The critical points are found as follows by first finding the gradient with der() (for derivative) and then equating the gradient to zero:

Hence, caracas computes the gradient to be

$$\nabla L(p_1, p_2, p_3, a) = \begin{bmatrix} a - \frac{y_1}{p_1} & a - \frac{y_2}{p_2} & a - \frac{y_3}{p_3} & p_1 + p_2 + p_3 - 1 \end{bmatrix}.$$

Next we solve $\nabla L(p_1, p_2, p_3, a) = 0$:

 $R\!>$ sols <- solve_sys(gL, list(p, a)) # takes an RHS argument which defaults to zero $R\!>$ sols

One critical point is found. (Notice that in general it is difficult to know how many critical points a function has. We will not go into details about this aspect of the problem.) Next we verify that we have found a minimum: We find the Hessian as a symbol and evaluate it in the critical point:

```
R> H <- der2(l, p) # der2(...) is shorthand for calling der() twice R> H_sol <- subs_lst(H, sols[[1]]) # Substitute solution into H
```

$$H = \begin{bmatrix} -\frac{y_1}{p_1^2} & 0 & 0\\ 0 & -\frac{y_2}{p_2^2} & 0\\ 0 & 0 & -\frac{y_3}{p_3^2} \end{bmatrix}, \quad H_{\text{sol}} = \begin{bmatrix} -\frac{(y_1 + y_2 + y_3)^2}{y_1} & 0 & 0\\ 0 & -\frac{(y_1 + y_2 + y_3)^2}{y_2} & 0\\ 0 & 0 & -\frac{(y_1 + y_2 + y_3)^2}{y_2} \end{bmatrix}$$

We verify that the solution is indeed a minimum: As $H_{\rm sol}$ is a diagonal matrix, its eigenvalues are the diagonal entries. (In general, eigenvalues/eigenvectors can be found using eigenval()/eigenvec().) Provided that all $y_i > 0$, all eigenvalues are negative and the likelihood reached a maximum.

Extending caracas - calling SymPy functions directly

The **caracas** can be extended as it is possible to call SymPy functions directly with the sympy_func() function. Please refer to the SymPy documentation at https://docs.sympy.org/latest/index.html for documentation of SymPy functions.

At the time of writing, the SymPy functions collect() and factor() are not implemented in caracas, but they can be invoked as shown in the following. For example, we can collect terms in a polynomial expression:

We can also expand and factor a polynomium:

```
R> def_sym(x)
R> p <- (x - 1)^7
R> q <- p %>% expand(); q # or p %>% sympy_func("expand")
```

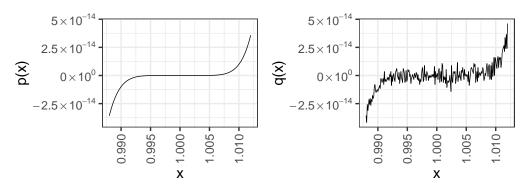


Figure 1: Difference between symbolic and numerical mathematics. Left: Plot of polynonial $p(x) = (x-1)^7$. Right: Plot of explansion of same polynomium.

In passing we illustrate a difference between symbolic and numerical mathematics: Floating point arithmetic can lead to catastrophic cancelations when nearly identical quantities are subtracted. This can be demonstrated as follows. Evaluate p and q on a range of x-values near 1, and plot the results in Fig. 1.

Statistics examples

In a linear model setting where $\mathbf{E}(y) = X\beta$, the least squares estimate of β can be written as $\hat{\beta} = (X^{\top}X)^{-1}X^{\top}y$. It is illustrative to use symbolic mathematics for illustrating what is computed in the matrix algebra.

One-way analysis of variance (one-way ANOVA)

First consider one-way analysis of variance (ANOVA).

```
R> ngrp <- 3 # Number of groups
R> spg <- 2 # Number of subjects per group
R> g <- seq_len(ngrp)
R> f <- factor(rep(g, each = spg))
R> y <- as_sym(paste0("y", seq_along(f)))
R> X <- as_sym(model.matrix(~ f))</pre>
```

We compute the usual quantities needed for finding the least squares estimate for the regression coefficients.

$$X = \begin{bmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \end{bmatrix}, \quad X^{\top}X = \begin{bmatrix} 6 & 2 & 2 \\ 2 & 2 & 0 \\ 2 & 0 & 2 \end{bmatrix}, \quad (X^{\top}X)^{-1} = \begin{bmatrix} \frac{1}{2} & -\frac{1}{2} & -\frac{1}{2} \\ -\frac{1}{2} & 1 & \frac{1}{2} \\ -\frac{1}{2} & \frac{1}{2} & 1 \end{bmatrix}$$

Likewise.

$$X^{\top}y = \begin{bmatrix} y_1 + y_2 + y_3 + y_4 + y_5 + y_6 \\ y_3 + y_4 \\ y_5 + y_6 \end{bmatrix}, \quad \hat{\beta} = \frac{1}{2} \begin{bmatrix} y_1 + y_2 \\ -y_1 - y_2 + y_3 + y_4 \\ -y_1 - y_2 + y_5 + y_6 \end{bmatrix}, \quad \hat{y} = \frac{1}{2} \begin{bmatrix} y_1 + y_2 \\ y_1 + y_2 \\ y_3 + y_4 \\ y_5 + y_6 \\ y_5 + y_6 \end{bmatrix}$$

Hence X^Ty consists of the sum of all observations, the sum of observations in group 2 and the sum of observations in group 3. Similarly, $\hat{\beta}$ consists of the average in group 1, the average in group 2 minus the average in group 1 and the average in group 3 minus the average in group 1. Fitted values are simply group averages.

Next consider a linear model setting, i.e. $y \sim N(X\beta, \sigma^2 I)$. The score function and Hessian matrix can be derived in closed form as follows: Define residuals $r = y - X\hat{\beta}$ and residual-sum-of-squares as $RSS = \sum_i r_i^2$. The log-likelihood based on n observations is

$$l = -\frac{n}{2}\sigma^2 - \frac{1}{2\sigma^2}RSS.$$

Here we can find critical points of l for RSS and σ^2 independently, so we ignore σ^2 and proceed focusing on RSS as follows:

```
R> beta <- as_sym(paste0("beta", 1:3))
R> res <- y - X %*% beta
R> RSS <- sum(res^2)
R> logL <- - RSS / 2</pre>
```

We find the score function and Hessian matrix by differentiation.

R> Score <- der(logL, beta) %>% matrify() # Convert Python list to vector
R> Hessian <- der2(logL, beta) %>% matrify() # Convert Python list to matrix

$$\mathsf{Score} = \begin{bmatrix} -6\beta_1 - 2\beta_2 - 2\beta_3 + y_1 + y_2 + y_3 + y_4 + y_5 + y_6 \\ -2\beta_1 - 2\beta_2 + y_3 + y_4 \\ -2\beta_1 - 2\beta_3 + y_5 + y_6 \end{bmatrix}, \quad \mathsf{Hessian} = \begin{bmatrix} -6 & -2 & -2 \\ -2 & -2 & 0 \\ -2 & 0 & -2 \end{bmatrix}$$

Notice the following: The output from der and der2 are lists in Python, and to be able to work with these quantities as we normally do a coercion to matrices is needed. The matrify() function does this. We conclude this example by solving the likelihood equations which, fortunately, leads to the same quantity as $\hat{\beta}$ derived above:

Similar considerations can be done for other linear models, e.g. a (balanced) two-way analysis of variance (two-way ANOVA).

Probabilistic principal component analysis

A probabilistic principal component analysis (PCA) model arises as follows, see e.g. Bishop (2006), pp. 570: There is a latent vector z and it is assumed that $z \sim N(0, I)$. There is a vector x of observables and it is assumed that $x \mid z \sim N(Wz + \mu, v^2I)$. It is not a restriction to assume that $\mu = 0$ because we center each variable around its average. We can write the model as

$$z = e_z$$
 and $x = Wz + e_x$, (4)

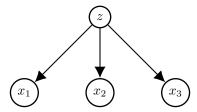


Figure 2: A directed acyclic graph (DAG) illustrating probabilistic PCA: The observables $x = (x_1, x_2, x_3)$ are conditionally independent given z.

where $e_z \sim N(0, I)$ and $e_x \sim N(0, v^2 I)$ are error terms that are assumed independent. The W matrix is the model matrix of weights that reflects model assumptions about how z impacts x.

In a statistical inference setting, the unknown parameters (v^2 and the components of W) must be estimated. To do this the covariance matrix and concentration matrix are needed. The first step is to identify the structural form of the covariance matrix $V = \mathbf{Var}(z, x)$ and concentration matrix $K = V^{-1}$, and caracas can do this for us. The next step is to use these structural forms in the likelihood function which can then be maximized.

Define

$$V = \mathbf{Var}(z, x) = \left(\begin{array}{cc} V_{zz} & V_{zx} \\ V_{xz} & V_{xx} \end{array} \right), \quad K = V^{-1} = \left(\begin{array}{cc} K_{zz} & K_{zx} \\ K_{xz} & K_{xx} \end{array} \right), \quad V_e = \mathbf{Var}(e) = \left(\begin{array}{cc} I & 0 \\ 0 & v^2 I \end{array} \right).$$

Also define

$$L = \begin{pmatrix} I & 0 \\ -W & I \end{pmatrix} \text{ and note that } L^{-1} = \begin{pmatrix} I & 0 \\ W & I \end{pmatrix}.$$
 (5)

Isolating error terms in (4) gives

$$e = \begin{pmatrix} e_z \\ e_x \end{pmatrix} = \begin{pmatrix} I & 0 \\ -W & I \end{pmatrix} \begin{pmatrix} z \\ x \end{pmatrix} = L \begin{pmatrix} z \\ x \end{pmatrix}.$$

Hence $Var(e) = LVar(z, x)L^{\top}$ and therefore

$$V = \mathbf{Var}(z, x) = L^{-1}\mathbf{Var}(e)(L^{-1})^{\top} \text{ and } K = V^{-1} = L^{\top}\mathbf{Var}(e)^{-1}L.$$
 (6)

Since the error terms are independent, a direct calculation gives

$$V = \begin{pmatrix} I & W^{\top} \\ W & WW^{\top} + v^{2}I \end{pmatrix} \text{ and } K = \begin{pmatrix} I + v^{-2}W^{\top}W & -v^{-2}W^{\top} \\ v^{-2}W & v^{-2}I \end{pmatrix}$$
 (7)

The following observations can be made:

- 1. First recall a general result on the multivariate normal distribution. Suppose $U = (U_1, \dots, U_d) \sim N(\mu, V)$, and let $K = V^{-1}$. Then $K_{ij} = 0$ if and only if U_i and U_j are conditionally independent given all other components of U. Next return to the specific setting. The lower right corner, K_{xx} , of K is $v^{-2}I$ and the fact that this matrix is diagonal reflects that all pairs of observables x_u and x_v are conditionally independent given the latent variables z.
- 2. The lower right corner, V_{xx} , of V is $WW^{\top} + v^2I$ and this matrix is the covariance matrix of observables x. The inverse of $WW^{\top} + v^2I$ is the concentration matrix of x (in the marginal distribution of x) and this concentration matrix does not in general contain zeros. There are no conditional independencies among the observables alone; conditional independencies arise from conditioning on the latent variables.
- 3. To estimate the parameters W and v^2 we can maximize the log-likelihood for the observables with covariance matrix $V_{obs} = WW^\top + v^2I$. This can often be done directly using optim(). (Notice that we can just center data to eliminate the parameter μ).

A simple example A particularly simple example is the following where z is one–dimensional and x is three–dimensional and W is a 3×1 matrix with a in all entries:

$$x_i = az + e_i$$
, $i = 1, ..., 3$, $z = u$

All e_1, \ldots, e_3 are $N(0, v^2)$ distributed, $u \sim N(0, 1)$ and all error terms are independent. See an illustration of this model in Fig. 2. Let $e = (e, \ldots, e_3)$ and $x = (x_1, \ldots, x_3)$. Hence $e \sim N(0, v^2I)$ and $\mathbf{Var}(u, e)$ is a diagonal matrix, $V_{ue} = \mathbf{diag}(1, v^2, \ldots, v^2)$. Isolating error terms gives

$$(u,e) = \begin{bmatrix} u \\ e_1 \\ e_2 \\ e_3 \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ -a & 1 & 0 & 0 \\ -a & 0 & 1 & 0 \\ -a & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} z \\ x_1 \\ x_2 \\ x_3 \end{bmatrix} = L(z,x), \text{ say.}$$

R> N <- 3

R> L <- diag_("1", N + 1)

R> L[cbind(1 + (1:N), 1)] <- "-a"

R> Vue <- matrix_("0", nrow = N + 1, ncol = N + 1)

R> diag(Vue) <- c("1", rep("v2", N))</pre>

Following (6) we find V and K as:

R> V <- inv(L) %*% Vue %*% t(inv(L))

R> K <- t(L) %*% inv(Vue) %*% L

$$V = \begin{bmatrix} 1 & a & a & a \\ a & a^2 + v_2 & a^2 & a^2 \\ a & a^2 & a^2 + v_2 & a^2 \\ a & a^2 & a^2 & a^2 + v_2 \end{bmatrix}, \quad K = \begin{bmatrix} \frac{3a^2}{v_2} + 1 & -\frac{a}{v_2} & -\frac{a}{v_2} & -\frac{a}{v_2} \\ -\frac{a}{v_2} & \frac{1}{v_2} & 0 & 0 \\ -\frac{a}{v_2} & 0 & \frac{1}{v_2} & 0 \\ -\frac{a}{v_2} & 0 & 0 & \frac{1}{v_2} \end{bmatrix}$$

Introducing data Let *S* is the empirical covariance matrix for the observed variables based on *n* observations. The observed-data log–likelihood is

$$l = \frac{n}{2}(\log \det(V_{xx}^{-1}) - \operatorname{tr}(V_{xx}^{-1}S)) = \frac{n}{2}(\log \det(K_{xx}) - \operatorname{tr}(K_{xx}S)).$$

Now $K_{xx} = V_{xx}^{-1}$ can be extracted and used in the likelihood function:

Alternatively, K_{xx} can be found as

$$K_{xx} = \frac{1}{v_2 (3a^2 + v_2)} \begin{bmatrix} 2a^2 + v_2 & -a^2 & -a^2 \\ -a^2 & 2a^2 + v_2 & -a^2 \\ -a^2 & -a^2 & 2a^2 + v_2 \end{bmatrix}$$

It remains to be investigated in practice whether it is computationally more efficient to construct V_{xx} numerically first and then invert V_{xx} to obtain K_{xx} numerically instead of finding K_{xx} symbolically and subsequently evaluating this numerically.

With a view towards teaching

We have found ANOVA examples (and variants hereof) useful in connection with teaching: Students are often exposed to estimating the vector of regression coefficients as

$$\hat{\beta} = (X^{\top} X)^{-1} X^{\top} y.$$

However, in the computer area, students are not always exposed to what is really computed in simple cases: Various group sums and differences of these. It is often illustrative for students to study, for example, the effect of: (1) including/excluding the intercept term in a model, (2) working with different contrasts in the models, and (3) making a design imbalanced.

For the probabilistic PCA example it is illustrative for students (1) to take the step from the symbolic model formulation to estimation (using e.g. optim()). (2) It can also be illustrative to realize the interpretation implied by forcing certain elements of W to be identical (as the case was above). (3) Likewise, it is straight forward to change the conditional variance of x given z from $\sigma^2 I$ to a diagonal matrix Ψ (which is the case in standard factor analysis). Elaborting further, it is illustrative for students to see for example and autoregression and a dynamic linear model formulated in similar way.

Discussion

We have presented the **caracas** package and argued that the package extends the functionality of R significantly with respect to symbolic mathematics. One practical virtue of **caracas** is that the package integrates nicely with **Rmarkdown**, Allaire et al. (2021), (e.g. with the tex() functionality) and thus supports creating of scientific documents and teaching material. As for the usability in practice we await feedback from users.

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Appendix: Technicalities

To avoid confusion we elaborate on the construction of symbols in the following:

- as_sym() converts an R object (or string) to symbol.
- symbol() declares a symbol by string, and allows for assumptions.
- def_sym() declares a symbol (either by string or non-standard evaluation) and assigns to an R variable with same name.

The behaviour of def_sym() can be obtained by both symbol() and as_sym(), but the two latter require an explicit assignment. Thus the following three statements are equivalent:

```
R> a <- as_sym("a")
R> a <- symbol("a")
R> def_sym(a)
```

To elaborate, consider a vector in R: Using symbol - the following fails because a is an a object and not a string:

```
R> a <- c(-1, 1); a
#> [1] -1  1
R> a <- symbol(a)
#> Error in verify_variable_name(x): The name must have length 1
```

On the other hand, as_sym works as expected. Using def_sym also works, but not as the user expects: A new variable a is created and the old a (the vector) is no longer bound to a variable:

```
R> a2 <- as_sym(a); t(a2)
#> [caracas]: [-1 1]
R> a ## a is unchanged
#> [1] -1 1
R> def_sym(a); a
#> [caracas]: a
```

Appendix: Assumptions

It is sometimes required to impose assumptions on variables. There is currently (limited) support for this in caracas:

```
R> x <- symbol("x")
 R > sol <- solve_sys(x^2 + 1, x); sol
  #> Solution 1:
  \#> x = -I
  #> Solution 2:
  \#> x = I
Requiring x to be real:
 R> x <- symbol("x", real = TRUE)</pre>
 R> ask(x, 'real')
  #> [1] TRUE
 R > sol <- solve_sys(x^2 + 1, x); sol
  #> No solutions
Requiring x to be positive:
 R> x <- symbol("x", positive = TRUE)
 R> ask(x, 'positive')
  #> [1] TRUE
 R> sol <- solve_sys(x^2 - 1, x); sol
  #> Solution 1:
  \#> x = 1
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