Specifying Fixed Parameters

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Motivation

In finding optimal parameters in nonlinear optimization and nonlinear least squares problems, we frequently wish to fix one or more parameters while allowing the rest to be adjusted to explore or optimize an objective function.

This vignette discusses some ideas about specifying the fixed parameters. A lot of the material is drawn from Nash J C (2014) Nonlinear parameter optimization using R tools Chichester UK: Wiley, in particular chapters 11 and 12.

Background

Here are some of the ways fixed parameters may be specified in R packages.

From `nlxb()` in package `nlsr`. (This approach was previously in defunct package `nlmrt`.)

masked

Character vector of quoted parameter names. These parameters will NOT be altered by the algorithm. This approach has a simplicity that is attractive, but introduces an extra argument to calling sequences.

From `nlfb()` in `nlsr`.

maskidx

Vector of indices of the parameters to be masked. These parameters will NOT be altered by the algorithm. Note that the mechanism here is different from that in `nlxb` which uses the names of the parameters.

From `Rvmmin` and `Rcgmin`

bdmsk

An indicator vector, having 1 for each parameter that is “free” or unconstrained, and 0 for any parameter that is fixed or MASKED for the duration of the optimization.

Note that the function `bmchk()` in packages `optimx` and `optimz` contains a much more extensive examination of the bounds on parameters. In particular, it considers the issues of inadmissible bounds (lower > upper), when to convert a pair of bounds where upper[“parameter”] - lower[“parameter”] < tol to a fixed or masked parameter (`maskadded`) and whether parameters outside of bounds should be moved to the nearest bound (`parchanged`). It may be useful to use `inadmissible` to refer to situations where a lower bound is higher than an upper bound and `infeasible` where a parameter is outside the bounds.

From `optimx`

The function `optimr()` can call many different “optimizers” (actually function minimization methods that may include bounds and possibly masks). These may be specified by setting the lower and upper bounds equal for the parameters to be fixed. This seems a simple method for specifying masks, but does pose some
issues. For example, what happens when the upper bound is only very slightly greater than the lower bound. Also should we stop or declare an error if starting values are NOT on the fixed value.

Of these methods, my preference is now to use the last one – setting lower and upper bounds equal, and furthermore setting the starting value to this fixed value, and otherwise declaring an error. The approach does not add any special argument for masking, and is relatively obvious to novice users. However, such users may be tempted to put in narrow bounds rather than explicit equalities, and this could have deleterious consequences.

**Internal structures**

bdmsk is the internal structure used in Rcgmin and Rvmmin to handle bounds constraints as well as masks. There is one element of bdmsk for each parameter, and in Rcgmin and Rvmmin, this is used on input to specify parameter i as fixed or masked by setting bdmsk[i] <- 0. Free parameters have their bdmsk element 1, but during optimization in the presence of bounds, we can set other values. The full set is as follows

- 1 for a free or unconstrained parameter
- 0 for a masked or fixed parameter
- -0.5 for a parameter that is out of bounds high (> upper bound)
- -1 for a parameter at its upper bound
- -3 for a parameter at its lower bound
- -3.5 for a parameter that is out of bounds low (< lower bound)

Not all these possibilities will be used by all methods that use bdmsk.

The -1 and -3 are historical, and arose in the development of BASIC codes for Nash J C and Walker-Smith M (1987) *Nonlinear parameter estimation: and integrated system in BASIC* New York: Dekker. Now available for free download from archive.org. ([https://archive.org/details/NLPE87plus](https://archive.org/details/NLPE87plus)). In particular, adding 2 gives 1 for an upper bound and -1 for a lower bound, simplifying the expression to decide if an optimization trial step will move away from a bound.

**Proposed approaches**

Because masks (fixed parameters) reduce the dimensionality of the optimization problem, we can consider modifying the problem to the lower dimension space. This is Duncan Murdoch’s suggestion, using

- fn0(par0) to be the initial user function of the full dimension parameter vector par0
- fn1(par1) to be the reduced or internal function of the reduced dimension vector par1
- par1 <- forward(par0)
- par0 <- inverse(par1)

The major advantage of this approach is explicit dimension reduction. The main disadvantage is the effort of transformation at every step of an optimization.

An alternative is to use the bdmsk vector to mask the optimization search or adjustment vector, including gradients and (approximate) Hessian matrices. A 0 element of bdmsk “multiplies” any adjustment. The principal difficulty is to ensure we do not essentially divide by zero in applying any inverse Hessian. This approach avoids forward, inverse and fn1. However, it may hide the reduction in dimension, and caution is necessary in using the function and its derived gradient, Hessian and derived information.

**Examples of use**

More examples would be useful here.

```r
require(optimx)
```

```r
# Loading required package: optimx
```
sq<-function(x){
    nn<-length(x)
    yy<-1:nn
    f<-sum((yy-x)^2)
    # cat("Fv=",f," at ")
    # print(x)
    f
}

sq.g <- function(x){
    nn<-length(x)
    yy<-1:nn
    gg<- 2*(x - yy)
}

xx <- c(.3, 4)
uncans <- Rvmmin(xx, sq, sq.g)

## $par
## [1] 1 2
## $value
## [1] 0
## $counts
## function gradient
## 4 3
## $convergence
## [1] 2
## $message
## [1] "Rvmminu appears to have converged"

mybm <- c(0,1) # fix parameter 1

cans <- Rvmmin(xx, sq, sq.g, bdmsk=mybm)
cans

## $par
## [1] 0.3 2.0
## $value
## [1] 0.49
## $counts
## function gradient
## 6 4
## $convergence
## [1] 2
## $message
## [1] "Rvmminb appears to have converged"

## $bdmsk
## [1] 0 1
require(nlsr)

## Loading required package: nlsr


ii <- 1:12

data.frame(weed, ii)

weedux <- nlsb(weed ~ b1/(1 + b2 * exp(-b3*ii)), start=c(b1=200, b2=50, b3=0.3))

## nlsr object: x
## residual sumsquares = 2.5873 on 12 observations
## after 6 Jacobian and 7 function evaluations
## name  coeff    SE    tstat    pval   gradient   JSingval
## b1    196.186 11.31  17.35 3.167e-08  -1.334e-10  1011
## b2    49.0916 1.688 29.08 3.284e-10  -3.589e-09  0.4605
## b3    0.31357 0.006863 45.69 5.768e-12  4.09e-07  0.04714

weedcx <- nlsb(weed ~ b1/(1 + b2 * exp(-b3*ii)), start=c(b1=200, b2=50, b3=0.3), masked=c("b1"))

## nlsr object: x
## residual sumsquares = 2.6182 on 12 observations
## after 5 Jacobian and 6 function evaluations
## name  coeff    SE    tstat    pval   gradient   JSingval
## p_1   200 M    NA    NA    NA        0 1022
## p_2   49.5108 NA    NA    NA  -3.501e-10  0.4569
## p_3   0.311461 NA    NA    NA  -7.631e-08  0

rfn <- function(bvec, weed=weed, ii=ii)
{
  res <- rep(NA, length(ii))
  for (i in ii)
  {
  }
  res
}

weeduf <- nlfb(start=c(200, 50, 0.3), resfn=rfn, weed=weed, ii=ii)

## nlsr object: x
## residual sumsquares = 2.5873 on 12 observations
## after 6 Jacobian and 7 function evaluations
## name  coeff    SE    tstat    pval   gradient   JSingval
## p_1   196.186 11.31  17.35 3.167e-08   5.505e-10  1011
## p_2   49.0916 1.688 29.08 3.284e-10  1.314e-09  0.4605
## p_3   0.311461 0.006863 45.69 5.768e-12  5.034e-08  0.04714

weedcf <- nlfb(start=c(200, 50, 0.3), resfn=rfn, weed=weed, ii=ii, maskidx=c(1))

## nlsr object: x
## residual sumsquares = 2.6182 on 12 observations
## after 5 Jacobian and 6 function evaluations
## name  coeff    SE    tstat    pval   gradient   JSingval
## p_1   200 M    NA    NA    NA        0 1022
## p_2   49.5108 NA    NA    NA  -4.231e-13  0.4569
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