

1 Generalized Deming regression

Deming regression solves the dual minimization

$$\min_{ab} \sum (y_i - \hat{y}_i)^2 + \sum (x - \hat{x})^2$$

The underlying model is that we have true values u and v with

$$\begin{aligned} u &= \alpha + \beta v \\ x_i &= u_i + \epsilon \\ y_i &= v_i + \delta \end{aligned}$$

where ϵ and δ are mean 0 errors. The usual Deming method assumes that the variances of ϵ and δ are equal. For general Deming regression let them vary such that

$$\begin{aligned} \text{std}(\epsilon) &= \sigma * (c + du) \equiv \sqrt{\kappa_i} \\ \text{std}(\delta) &= \sigma * (e + fv) \equiv \sqrt{\lambda_i} \end{aligned}$$

Standard Deming regression corresponds to $d = f = 0$ and $c = e$, the constant coefficient model of Linnet to $d = f$ and $c = e = 0$.

Ripley and Thompsen (Analyst 1987, 377-383) work out the following equation with a full page of work. If the fitted line is $\alpha + \beta x$, and β is known then the optimal solution for α is

$$\begin{aligned} w_i &= 1/(\lambda_i + \beta^2 \kappa_i) \\ \alpha &= \frac{\sum w_i (y_i - \beta x_i)}{\sum w_i} \end{aligned}$$

Prior case weights simply add a multiplicative factor to w . This allows the use of the optimize routine, which is a very fast for one dimensional maximization. As starting estimates, we know that the slope lies between the two least-squares regressions of x on y and of y on x . The code below allows for model without an intercept.

```
<demingfit-afun>=
# The estimate of alpha-hat, given beta
afun <-function(beta, x, y, wt, xv, yv) {
  w <- wt/(yv + beta^2*xv)
  sum(w * (y - beta*x))/ sum(w)
}

minfun <- function(beta, x, y, wt, xv, yv) {
  w <- wt/(yv + beta^2*xv)
  alphahat <- sum(w * (y - beta*x))/ sum(w)
  sum(w*(y-(alphahat + beta*x))^2)
```

```

}
minfun0 <- function(beta, x, y, wt, xv, yv) {
  w <- wt/(yv + beta^2*xv)
  alphahat <- 0 #constrain to zero
  sum(w* (y-(alphahat + beta*x))^2)
}

<deming.fit1>=
# Fit for fixed std values
deming.fit1 <- function(x, y, wt, xstd, ystd, intercept) {
  <demingfit-afun>
  if (intercept) {
    fit1 <- lm.wfit(cbind(1,x), y, wt/ystd)
    fit2 <- lm.wfit(cbind(1,y), x, wt/xstd)
    init <- sort(c(fit1$coef[2], 1/fit2$coef[2]))

    fit <- optimize(minfun, init, x=x, y=y, wt=wt,
                    xv=xstd^2, yv=ystd^2)
  }
  browser()
  list(coefficients=c(afun(fit$minimum, x,y, wt=wt, xstd^2, ystd^2),
                      fit$minimum))
}
else {
  fit1 <- lm.wfit(x, y, wt/ystd)
  fit2 <- lm.wfit(y, x, wt/xstd)
  init <- sort(c(fit1$coef, 1/fit2$coef))

  fit <- optimize(minfun0, init, x=x, y=y, wt=wt,
                  xv=xstd^2, yv=ystd^2)
  list(coefficients=fit$minimum)
}
}

```

When called with a pattern argument the code is just a bit more complex, since the weights are updated as well. As starting estimates for the weights we use the data itself. the weights are not allowed to be negative. Given a tentative line $y = a + bx$ what is the closest point on the line to any given data point (x_i, y_i) ? We want to find that point x such that $f(x)$ is minimal. Referring again to Ripley, the solution is

$$\hat{x}_i = w_i[\lambda x_i + \kappa\beta(y - \alpha)]$$

```

<deming.fit2>=
# Fit when there is a pattern argument
deming.fit2 <- function(x, y, wt, stdpat, intercept,
                        tol=.Machine$double.eps^0.25) {
  <demingfit-afun>

```

```

xstd <- stdpat[1] + stdpat[2]*pmax(x,0)
ystd <- stdpat[3] + stdpat[4]*pmax(y,0)
if (sum(xstd>0) <2 || sum(ystd>0) <2)
  stop("initial weight estimates must be positive for at least 2 points")

ifit <- deming.fit1(x, y, wt, xstd, ystd, intercept)
if (intercept) {
  alpha <- ifit$coefficients[1]
  beta <- ifit$coefficients[2]
}
else {
  alpha <- 0
  beta <- ifit$coefficients
}

# 20 to stop any runaway failures. usually 1-2 suffice.
for(i in 1:20) {
  w <- 1/(ystd^2 + beta^2*xstd^2)
  newx <- w*(ystd^2*x + xstd^2* beta*(y- alpha))
  newy <- alpha + beta*newx
  xstd <- stdpat[1] + stdpat[2]*pmax(0, newx)
  ystd <- stdpat[3] + stdpat[4]*pmax(0, newy)

  if (intercept)
    fit <- optimize(minfun, c(.2, 5)*beta, x=x, y=y, wt=wt,
                    xv=xstd^2, yv=ystd^2)
  else fit <- optimize(minfun0, c(.2, 5)*beta, x=x, y=y, wt=wt,
                      xv=xstd^2, yv=ystd^2)

  if (abs(fit$minimum - beta)/(abs(beta)+tol) <= tol) break
  beta <- fit$minimum
  if (intercept) alpha <- afun(beta, x, y, wt=wt, xstd^2, ystd^2)
}

if (intercept)
  list(coefficients=c(afun(fit$minimum, x,y, wt=wt, xstd^2, ystd^2),
                      fit$minimum))
else list(coefficients=c(0, fit$minimum))
}

```

The main deming routine starts with the standard material for creating a data frame.

```

<deming>=
deming <- function(formula, data, subset, weights, na.action,
                   ccv=FALSE, xstd, ystd, stdpat,

```

```

        conf= .95, nboot=0, dfbeta=FALSE,
        x=FALSE, y=FALSE, model=TRUE) {
  Call <- match.call()
  # create a call to model.frame() that contains the formula (required)
  # and any other of the relevant optional arguments
  # then evaluate it in the proper frame
  indx <- match(c("formula", "data", "weights", "subset", "na.action",
                  "xstd", "ystd"),
                names(Call), nomatch=0)
  if (indx[1] ==0) stop("A formula argument is required")
  temp <- Call[c(1,indx)] # only keep the arguments we wanted
  temp[[1]] <- as.name('model.frame') # change the function called
  mf <- eval(temp, parent.frame())
  Terms <- terms(mf)
  n <- nrow(mf)

  <deming-check>
  <deming-compute>
  <deming-se>
  <deming-finish>
}

<deming.fit1>

<deming.fit2>

<deming.print>

```

Check all of the options for legality. Tedious but simple

```

<deming-check>=
if (n < 3) stop("less than 3 non-missing observations in the data set")

xstd <- model.extract(mf, "xstd")
ystd <- model.extract(mf, "ystd")
Y <- model.response(mf, type="numeric")
if (is.null(Y))
  stop ("a response variable is required")
wt <- model.weights(mf)
if (length(wt)==0) wt <- rep(1.0, n)

usepattern <- FALSE
if (is.null(xstd)) {
  if (!is.null(ystd))
    stop("both of xstd and ystd must be given, or neither")
  if (missing(stdpat)) {
    if (ccv) stdpat <- c(0,1,0,1)
  }
}

```

```

      else      stdpat <- c(1,0,1,0)
    }
    else {
      if (any(stdpat <0) || all(stdpat[1:2] ==0) || all(stdpat[3:4]==0))
        stop("invalid stdpat argument")
    }
    if (stdpat[2] >0 || stdpat[4] >0) usepattern <- TRUE
    else {xstd <- rep(stdpat[1], n); ystd <- rep(stdpat[3], n)}
  } else {
    if (is.null(ystd))
      stop("both of xstd and ystd must be given, or neither")
    if (!is.numeric(xstd)) stop("xstd must be numeric")
    if (!is.numeric(ystd)) stop("ystd must be numeric")
    if (any(xstd <=0)) stop("xstd must be positive")
    if (any(ystd <=0)) stop("ystd must be positive")
  }
  if (conf <0 || conf>=1) stop("invalid confidence level")
  if (!is.logical(dfbeta)) stop("dfbeta must be TRUE or FALSE")

```

Now do the computation. If the std is self referencing, i.e., either the ccv argument is used or the stdpat argument with nozero term for elements 2 and 4, then we need to use the iterative routine deming.fit2; otherwise we can use the simpler one.

```

<deming-compute>=
X <- model.matrix(Terms, mf)
if (ncol(X) != (1 + attr(Terms, "intercept")))
  stop("Deming regression requires a single predictor variable")
xx <- X[,ncol(X)] #actual regressor

if (!usepattern)
  fit <- deming.fit1(xx, Y, wt, xstd, ystd,
                    intercept= attr(Terms, "intercept"))
else
  fit <- deming.fit2(xx, Y, wt, stdpat,
                    intercept= attr(Terms, "intercept"))
names(fit$coefficients) <- dimnames(X)[[2]]
yhat <- fit$coefficients[1] + fit$coefficients[2]*xx
fit$residuals <- Y-yhat

```

Jackknife or bootstrap estimates of error

```

<deming-se>=
if (nboot > 0) {
  # Compute a bootstrap estimate of variance
  stop("bootstrap not yet done")
}
else if (conf>0) {

```

```

# jackknife it
delta <- matrix(0., nrow=n, ncol=2)
for (i in 1:n) {
  if (usepattern)
    tfit <-deming.fit2(xx[-i], Y[-i], wt[-i], stdpat,
                      intercept= attr(Terms, "intercept"))
  else
    tfit <-deming.fit1(xx[-i], Y[-i], wt[-i], xstd[-i], ystd[-i],
                      intercept= attr(Terms, "intercept"))

  delta[i,] <- fit$coefficients - tfit$coefficients
  fit$variance <- t(delta) %*% delta
  if (dfbeta) fit$dfbeta <- delta
}
z <- -qnorm((1- conf)/2)
se <- sqrt(diag(fit$variance))
ci <- cbind(fit$coefficients - z*se,
            fit$coefficients + z*se)
dimnames(ci) <- list(names(fit$coefficients),
                    paste(c("lower", "upper"), format(conf)))
fit$ci <- ci
}

```

And last, all the little bits for cleaning up

```

<deming-finish>=
if (x) fit$x <- X
if (y) fit$y <- Y
if (model) fit$model <- mf

na.action <- attr(mf, "na.action")
if (length(na.action)) fit$na.action <- na.action
fit$n <- length(Y)
fit$terms <- Terms
class(fit) <- "deming"
fit$call <- Call
fit

<deming.print>=
print.deming <- function(x, ...) {
  cat("\nCall:\n", deparse(x$call), "\n\n", sep = "")
  cat("n=", x$n)
  if (length(x$na.action))
    cat(" (", naprint(x$na.action), ")\n", sep='')
  else cat("\n")

  if (!is.null(x$ci)) {

```

```

table <- matrix(0., nrow=2, ncol=4)
table[,1] <- x$coefficients
if (is.null(x$variance)) table[,2] <- x$std
else table[,2] <- sqrt(diag(x$variance))
table[,3:4] <- x$ci

dimnames(table) <- list(c("Intercept", "Slope"),
                        c("Coef", "se(coef)", dimnames(x$ci)[[2]]))
}
else {
table <- matrix(0., nrow=2, ncol=2)
table[,1] <- x$coefficients
if (is.null(x$variance)) table[,2] <- x$std
else table[,2] <- sqrt(diag(x$variance))

dimnames(table) <- list(c("Intercept", "Slope"),
                        c("Coef", "se(coef)"))
}
print(table, ...)
cat("\n Scale=", format(x$scale), "\n")
invisible(x)
}

```