affyContam: structured corruption of CEL-level data

VJ Carey stvjc at channing.harvard.edu

October 13, 2015

1 Introduction

Microarray quality assessment is a major concern of microarray analysts. This package provides some simple approaches to *in silico* creation of quality problems in CEL-level data to help evaluate performance of quality metrics.

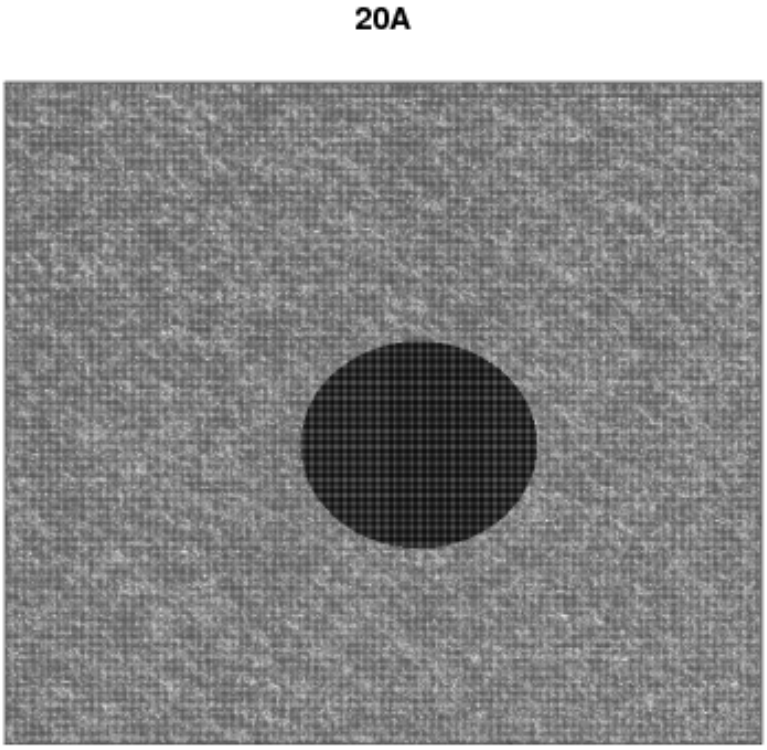
2 A small dataset

The *affydata* package includes a dataset called Dilution.

```
> library(affydata)

     Package    LibPath                                      Item
[1,] "affydata" "/home/biocbuild/bbs-3.2-bioc/R/library" "Dilution"
     Title
[1,] "AffyBatch instance Dilution"

> data(Dilution)
> image(Dilution[,1])
```

We can introduce a circular defect as follows:

```
> library(affyContam)
> dilc = setCircRegion(Dilution, chip=1)

> image(dilc[,1])
```



Note that the extents of the region (which may be rectangular, see `setRectRegion`) can be varied using arguments to the set*Region functions. The distribution of intensity values used to reset the raw data can also be specified using the `valgen` parameter.

3 Systematic demonstration

The following code shows how one might explore several procedures for sensitivity to artifacts. It runs very slowly so all evaluation has been turned off, but eval=FALSE can be reset by interested users.

```
> library(affyMvout)
> library(affy)
> library(SpikeIn)
> data(SpikeIn133)
> library(mdqc)
> library(affyContam)
> library(limma)
```

```
> s12 = SpikeIn133[,1:12]
> s12rma = rma(s12)
> mads = apply(exprs(s12rma),1,mad)
> kp = which(mads > quantile(mads,.95))
> kppn = featureNames(s12rma)[kp]
> # these are the 18 genes found to be mostly monotone over 12 chips
> mostmr = c("203508_at", "204563_at", "204513_s_at", "204205_at", "204959_at",
+ "207655_s_at", "204836_at", "205291_at", "209795_at", "207777_s_at",
+ "204912_at", "205569_at", "207160_at", "205692_s_at", "212827_at",
+ "AFFX-LysX-3_at", "AFFX-PheX-3_at", "AFFX-ThrX-3_at")
>
> fullrun = function( abatch, arma, contFun, filtpn, targpn, chips=1, ... ) {
+ # assess detectability in original data
+  dvec = (1:ncol(exprs(abatch)))
+  des = model.matrix(~dvec)
+  af1 = lmFit( arma[filtpn,], des, method="robust", maxit=300 )
+  eaf1 = eBayes(af1)
+  orig.tt = eaf1$t[targpn,2]
+ # contaminate
+  cbat = contFun(abatch, chip=chips[1], ...)
+  if (length(chips)>1) {
+    for (i in 2:(length(chips)))
+      cbat = contFun(cbat, chip=chips[i], ...)
+    }
+ # assess detectability in contaminated data
+  crma = rma(cbat)[filtpn,]
+  dvec = (1:ncol(exprs(abatch)))
+  des = model.matrix(~dvec)
+  cf1 = lmFit( crma, des, method="robust", maxit=300 )
+  ecf1 = eBayes(cf1)
+  contam.tt = ecf1$t[targpn,2]
+ # now test for outliers
+  caos = ArrayOutliers(cbat)
+  if (nrow(caos[[1]]) < 1) {
+     warning("no outliers by affyMvout")
+     return(list(aos=caos, md=mdqc(caos[[3]][,2:10])))
+     }
+  todrop = as.numeric(rownames(caos[[1]]))
+  cbatf = cbat[,-todrop]
+ # assess detectability in repaired data
+  frma = rma(cbatf)[filtpn,]
+  dvec = (1:ncol(exprs(abatch)))[-todrop]
```

```
+  des = model.matrix(~dvec)
+  f1 = lmFit( frma, des, method="robust", maxit=300 )
+  ef1 = eBayes(f1)
+  repair.tt = ef1$t[targpn,2]
+ # compute the mdqc result
+  md = mdqc(caos[[3]][,2:10], robust="MCD")
+  list(orig=orig.tt, contam=contam.tt, repair=repair.tt, md=md, todrop=todrop)
+ }
>

> ff = fullrun( s12, s12rma, setCircRegion, kppn, mostmr, chips=1:2 )
```

Here are some contaminator procedures.
First, a modest sized circle with constant low intensity (40)

```
> scr.40 = function (x, chip = 1, center = c(150, 150), rad = 75, vals = 30,
+     valgen = NULL)
+ {
+     cdfname = paste(annotation(x), "cdf", sep = "")
+     require(cdfname, character.only = TRUE, quietly = TRUE)
+     xext = seq(center[1] - rad, center[1] + rad)
+     yext = seq(center[2] - rad, center[2] + rad)
+     badco = expand.grid(xext, yext)
+     badco = badco[(badco[, 1] - center[1])^2 + (badco[, 2] -
+         center[2])^2 < rad^2, ]
+     indsbad = apply(badco, 1, function(x) xy2indices(x[1], x[2],
+         cdf = cdfname))
+     if (is.null(valgen))
+         exprs(x)[indsbad, chip] = vals
+     else exprs(x)[indsbad, chip] = valgen(length(indsbad))
+     x
+ }
```

A similar contamination procedure with constant high intensity (20000):

```
> scr.20k = function (x, chip = 1, center = c(500, 500), rad = 75, vals = 30000,
+     valgen = NULL)
+ {
+     cdfname = paste(annotation(x), "cdf", sep = "")
+     require(cdfname, character.only = TRUE, quietly = TRUE)
+     xext = seq(center[1] - rad, center[1] + rad)
+     yext = seq(center[2] - rad, center[2] + rad)
+     badco = expand.grid(xext, yext)
+     badco = badco[(badco[, 1] - center[1])^2 + (badco[, 2] -
```

```
+         center[2])^2 < rad^2, ]
+     indsbad = apply(badco, 1, function(x) xy2indices(x[1], x[2],
+         cdf = cdfname))
+     if (is.null(valgen))
+         exprs(x)[indsbad, chip] = vals
+     else exprs(x)[indsbad, chip] = valgen(length(indsbad))
+     x
+ }
```

Second, a somewhat larger circle with rescaled variance:

```
> incvarCircRegion = function(x, chip=1, center=c(150,500), rad=100, fac=3) {
+  tmp = fac*getCircRegion(x, chip, center, rad)
+  setCircRegion(x, chip, center, rad, vals=tmp)
+ }
```

Third, a large rectangular region with rescaled variance:

```
> incvarRectRegion = function(x, chip=1, xinds=350:700, yinds=1:700, fac=3) {
+  tmp = fac*getRectRegion(x, chip, xinds, yinds)
+  setRectRegion(x, chip, xinds, yinds, vals=tmp)
+ }

> tryout = scr.40(s12)
> tryout = scr.20k(tryout)
> tryout = incvarCircRegion(tryout)
> fin = incvarRectRegion(tryout)
> png(file="lkcomp.png")
> image(fin[,1], main="composite contamination")
> dev.off()

> d1b = fullrun( s12, s12rma, scr.40, kppn, mostmr, chips=1 )
> save(d1b, file="d1b.rda")
> d2b = fullrun( s12, s12rma, scr.40, kppn, mostmr, chips=1:2 )
> save(d2b, file="d2b.rda")
> d3b = fullrun( s12, s12rma, scr.40, kppn, mostmr, chips=c(1:2,11) )
> save(d3b, file="d3b.rda")
> H1b = fullrun( s12, s12rma, scr.20k, kppn, mostmr, chips=1 )
> save(H1b, file="H1b.rda")
> H2b = fullrun( s12, s12rma, scr.20k, kppn, mostmr, chips=1:2 )
> save(H2b, file="H2b.rda")
> H3b = fullrun( s12, s12rma, scr.20k, kppn, mostmr, chips=c(1:2,11) )
> save(H3b, file="H3b.rda")
> I1b = fullrun( s12, s12rma, incvarCircRegion, kppn, mostmr, chips=1 )
```

```
> save(I1b, file="I1b.rda")
> I2b = fullrun( s12, s12rma, incvarCircRegion, kppn, mostmr, chips=1:2 )
> save(I2b, file="I2b.rda")
> I3b = fullrun( s12, s12rma, incvarCircRegion, kppn, mostmr, chips=c(1:2,11) )
> save(I3b, file="I3b.rda")
> R1b = fullrun( s12, s12rma, incvarRectRegion, kppn, mostmr, chips=1 )
> save(R1b, file="R1b.rda")
> R2b = fullrun( s12, s12rma, incvarRectRegion, kppn, mostmr, chips=1:2 )
> save(R2b, file="R2b.rda")
> R3b = fullrun( s12, s12rma, incvarRectRegion, kppn, mostmr, chips=c(1:2,11) )
> save(R3b, file="R3b.rda")
```