

Affy array outlier detection via dimension reduction

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1 Introduction

Clinical trials groups now routinely produce hundreds of microarrays to generate measures of clinical conditions and treatment responses at the level of mRNA abundance. Objective, quantitative measures of array quality are important to support these projects. Numerous packages in Bioconductor address quality assessment procedures. *ArrayQualityMetrics* is a particularly attractive set of tools. We provide *arrayMvout* as a module that performs parametric outlier detection after data reduction to support formal decisionmaking about array acceptability. Ultimately the measures and procedures provided by *arrayMvout* may be useful as components of other packages for quality assessment. Another closely related package is *mdqc*, which employs a variety of robustifications of Mahalanobis distance to help identify outlying arrays.

Suppose there are N affymetrix arrays to which N independent samples have been hybridized. The *arrayMvout* package computes Q quality measures which constitute

array-specific features. These features are then analyzed in two steps. First, principal components analysis is applied to the $N \times Q$ feature matrix. Second, parametric multivariate outlier detection with calibration for multiple testing is applied to a subset of the resulting principal components. Arrays identified as outliers by this procedure are then subject to additional inspection and/or exclusion as warranted.

In this vignette we illustrate application of the procedure for a ‘negative control’ (raw MAQC data) and several constructed quality defect situations.

2 Illustration with MAQC data

We have serialized sufficient information on the MAQC subset to allow a simple demonstration of a negative control set. The MAQC data should be free of outliers.

We will manually search for outliers in this data resource. We compute principal components and take the first three.

```
> library(arrayMvout)
> data(maqcQA)
> mm = ArrayOutliers(maqcQA[, 3:11], alpha=.01)
> mm
```

ArrayOutliers result.

The call was:

```
.local(data = data, alpha = alpha, alphaSeq = alphaSeq)
```

No outliers. First row of QC features

| | avgBG | SF Present | HSAC07 | GAPDH | NUSE | RLE | RLE_IQR |
|---|----------|------------|---------|----------|----------|----------|------------|
| 1 | 60.05505 | 1.17657 | 52.4225 | 1.245477 | 1.015217 | 1.057659 | 0.04185417 |
| | RNAslope | | | | | | |
| 1 | 3.141527 | | | | | | |

There are no outliers found at a false labeling rate of 0.01.

3 Illustration with arrays from a clinical trial network

Another data resource with some problematic arrays is also included.

```
> data(itnQA)
> ii = ArrayOutliers(itnQA, alpha=.01)
> ii
```

ArrayOutliers result.

The call was:

```
.local(data = data, alpha = alpha, alphaSeq = alphaSeq)
```

There were 507 samples with 18 outliers detected.

Coordinate-wise means of inlying arrays:

| avgBG | SF | Present | HSAC07 | GAPDH | NUSE |
|--------------|--------------|--------------|--------------|--------------|--------------|
| 4.498102e+01 | 1.731430e+00 | 4.162066e+01 | 2.187432e+00 | 1.770430e+00 | 1.000867e+00 |
| RLE | RLE_IQR | RNAslope | | | |
| 6.050559e-05 | 2.976345e-01 | 3.427889e+00 | | | |

Features of outlying arrays:

| | avgBG | SF | Present | HSAC07 | GAPDH | NUSE | RLE |
|-----|-----------|-------------|----------|-----------|------------|-----------|--------------|
| 403 | 77.07796 | 0.4374264 | 47.55007 | 1.433827 | 1.307327 | 0.9991413 | 0.005285121 |
| 16 | 41.00919 | 1.9288207 | 39.60311 | 12.647909 | 4.707294 | 1.0097374 | 0.021545990 |
| 449 | 37.26800 | 6.2588701 | 24.39140 | 4.131615 | 2.047267 | 1.0284928 | 0.127501020 |
| 189 | 40.61447 | 1.9891220 | 39.39095 | 10.360385 | 6.718598 | 1.0103497 | 0.036462661 |
| 445 | 36.28049 | 9.1599338 | 25.08642 | 5.930873 | 2.189993 | 1.1064651 | 0.036035969 |
| 473 | 54.36467 | 3.6423721 | 26.03567 | 2.497312 | 1.893548 | 1.0438432 | 0.108838227 |
| 235 | 40.36647 | 2.3888050 | 39.61957 | 8.852826 | 7.201938 | 1.0302444 | 0.051526272 |
| 323 | 31.73768 | 5.6643255 | 32.43347 | 16.760480 | 11.955661 | 1.0507761 | 0.052612806 |
| 268 | 50.32263 | 2.6636200 | 34.85871 | 23.990430 | 7.101770 | 1.0542473 | 0.092065904 |
| 274 | 39.08553 | 2.9476038 | 36.66575 | 22.884391 | 12.036149 | 1.0457600 | 0.087581891 |
| 132 | 85.82265 | 1.8183446 | 34.61363 | 1.432298 | 1.510193 | 1.0822086 | 0.009663181 |
| 499 | 30.14740 | 29.3554869 | 17.02423 | 2.629898 | 1.718535 | 1.0874808 | 0.132794452 |
| 41 | 33.71813 | 15.6434771 | 17.80887 | 1.073282 | 2.643669 | 1.1669600 | 0.321298991 |
| 400 | 95.45017 | 1.2115402 | 36.64563 | 3.508757 | 2.479803 | 1.1128690 | -0.000687765 |
| 485 | 129.10624 | 1.5643922 | 23.87197 | 3.057225 | 1.810761 | 1.1098076 | 0.073777325 |
| 188 | 142.44325 | 1.4429218 | 30.23137 | 2.907469 | 2.101054 | 1.1475918 | -0.018917415 |
| 313 | 25.37851 | 16.8069277 | 25.72474 | 56.917203 | 11.840316 | 1.1360326 | 0.073802881 |
| 305 | 38.11554 | 19.0772560 | 11.60677 | 67.021339 | 120.011952 | 1.1987268 | 0.349949413 |
| | RLE_IQR | RNAslope | | | | | |
| 403 | 0.2197193 | 3.66807105 | | | | | |
| 16 | 0.3299879 | 5.42259351 | | | | | |
| 449 | 0.5672631 | 1.89557125 | | | | | |
| 189 | 0.3305528 | 5.80774028 | | | | | |
| 445 | 0.5465581 | 2.54468591 | | | | | |
| 473 | 0.6448400 | 1.32173147 | | | | | |
| 235 | 0.3657481 | 6.54325480 | | | | | |
| 323 | 0.4407913 | 5.88500524 | | | | | |
| 268 | 0.5755214 | 5.74973052 | | | | | |
| 274 | 0.4367455 | 7.09471717 | | | | | |
| 132 | 0.6664186 | 1.19952480 | | | | | |
| 499 | 0.6250615 | 1.87786720 | | | | | |
| 41 | 1.0754575 | 1.11521819 | | | | | |
| 400 | 0.6759216 | 2.46627267 | | | | | |
| 485 | 0.9486388 | -0.04085089 | | | | | |

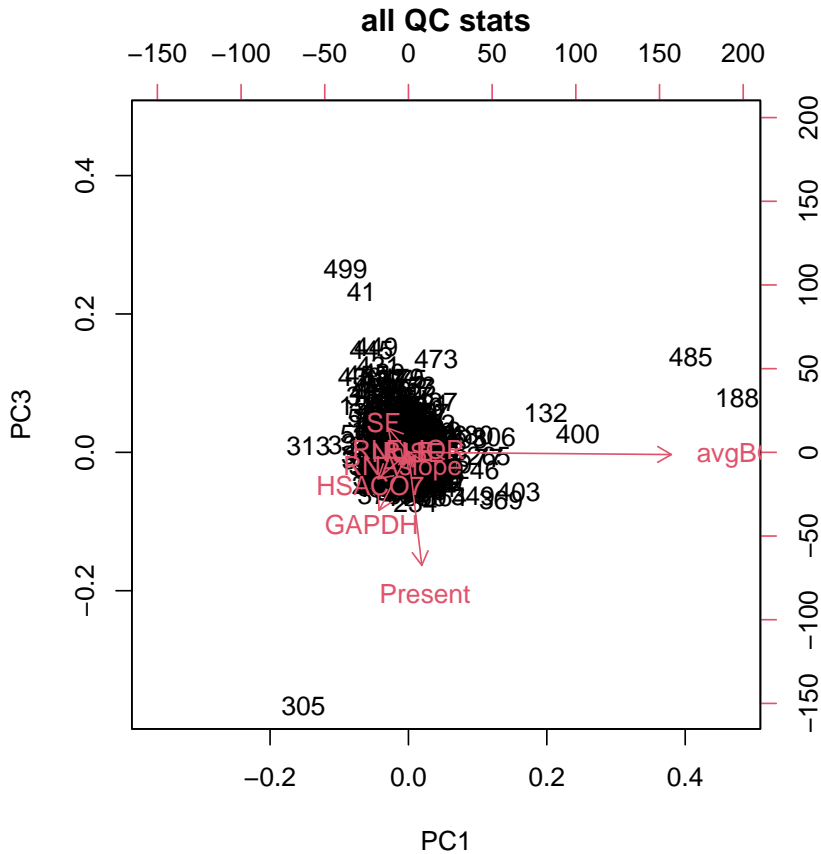
```

188 0.8908112 1.76393357
313 0.6503561 6.13572050
305 1.3208768 6.96678147

```

We have a simple visualization.

```
> plot(ii, choices=c(1,3))
```



4 Manual work with the MAQC subset

The remaining text of this vignette is computed statically. The source code with `eval=FALSE` is given as an appendix.

We consider an `AffyBatch` supplied with the Bioconductor `MAQCsubset` package. Marginal boxplots of raw intensity data are provided in the next figure. Sample labels are decoded `AFX _ [lab] _ [type] [replicate] .CEL` where `[lab] ∈ {1, 2, 3}`, `[type]` denotes mixture type (A = 100% USRNA, B = 100% Ambion brain, C = 75% USRNA, 25% brain, D = 25% USRNA, 75% brain), and `[replicate] ∈ {1, 2}`.

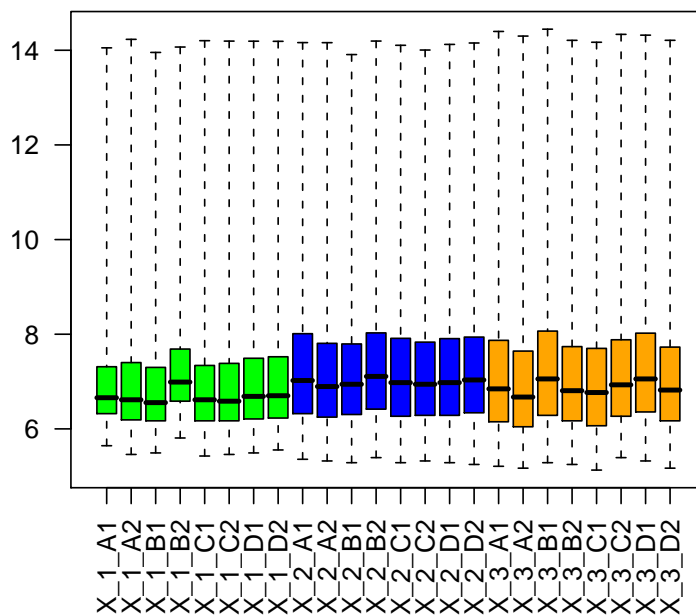
```

> library(arrayMvout)
> library(MAQCsubset)
> if (!exists("afxsub")) data(afxsub)
> sn = sampleNames(afxsub)
> if (nchar(sn)[1] > 6) {
+   sn = substr(sn, 3, 8)
+   sampleNames(afxsub) = sn
+ }

> opar = par(no.readonly = TRUE)
> par(mar = c(10, 5, 5, 5), las = 2)
> boxplot(afxsub, main = "MAQC subset", col = rep(c("green", "blue",
+   "orange"), c(8, 8, 8)))
> par(opar)

```

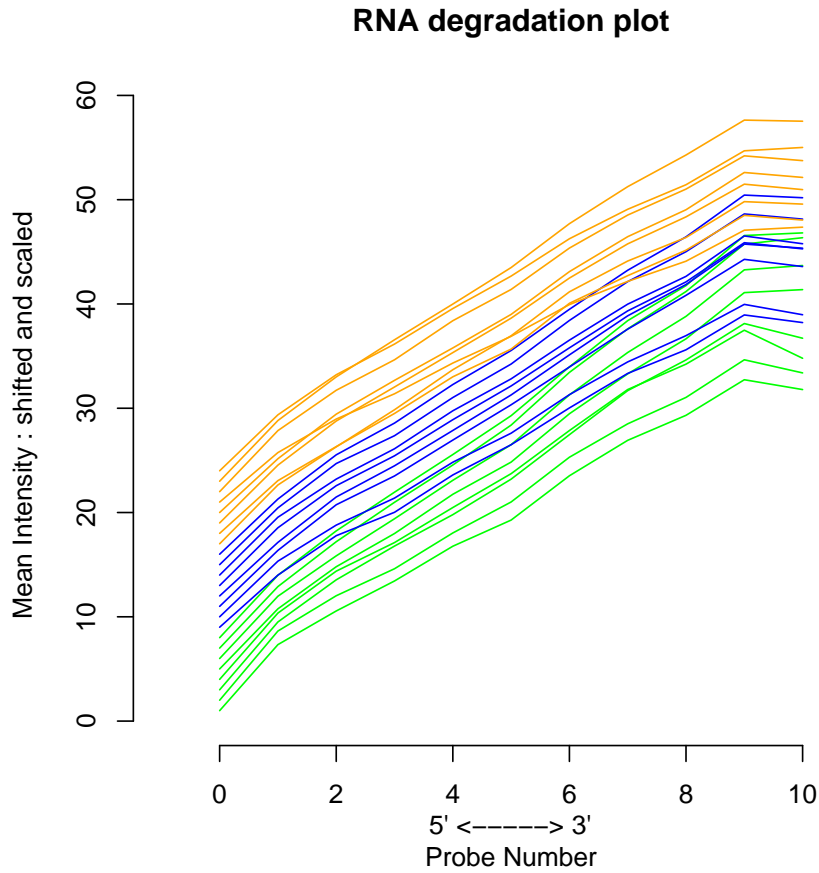
MAQC subset



4.1 QA diagnostics

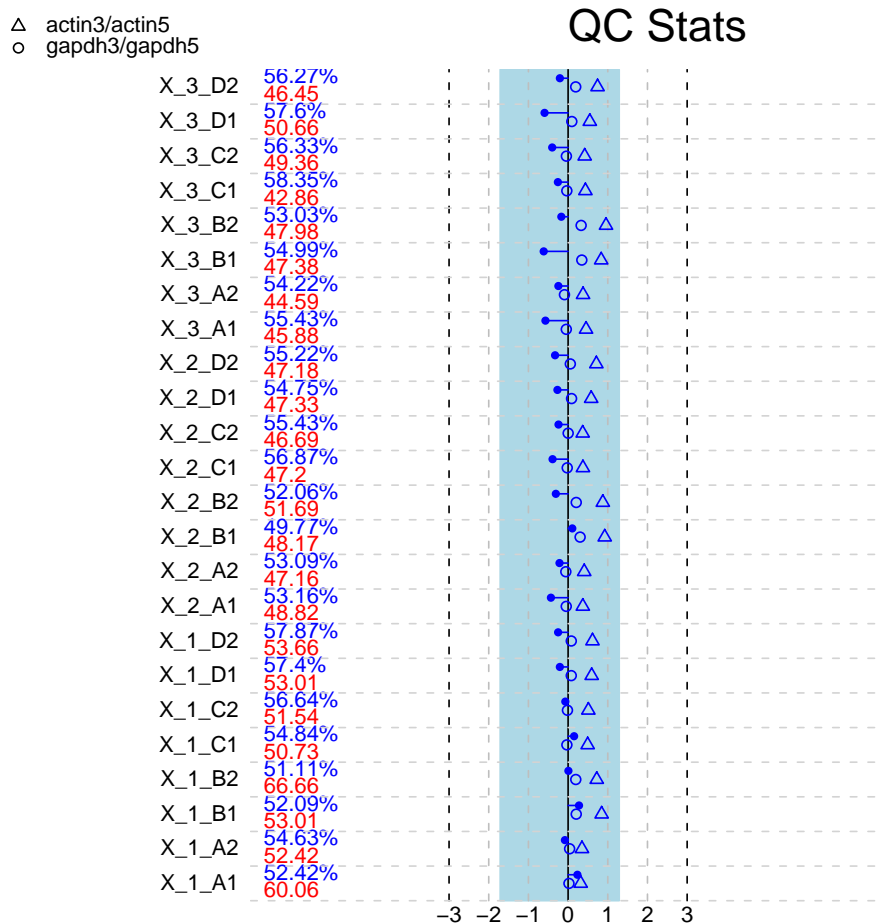
Of interest are measures of RNA degradation:

```
> library(arrayMvout)
> data(afxsubDEG)
> plotAffyRNAdeg(afxsubDEG, col = rep(c("green", "blue", "orange"),
+   c(8, 8, 8)))
```



and the general 'simpleaffy' QC display:

```
> data(afxsubQC)
> plot(afxsubQC)
```

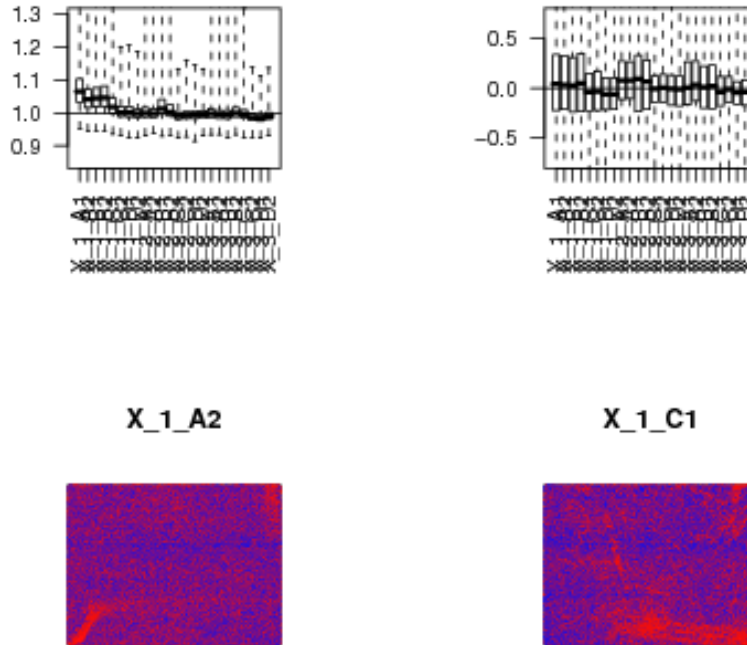


The affyPLM package fits probe-level robust regressions to obtain probe-set summaries.

```
> library(affyPLM)
> splm = fitPLM(afxsub)

> png(file = "doim.png")
> par(mar = c(7, 5, 5, 5), mfrow = c(2, 2), las = 2)
> NUSE(splm, ylim = c(0.85, 1.3))
> RLE(splm)
> image(splm, which = 2, type = "sign.resid")
> image(splm, which = 5, type = "sign.resid")
```

In the following graphic, we have the NUSE distributions (upper left), the RLE distributions (upper right), and second and fifth chips in signed residuals displays.



These chips seem to have adequate quality, although there is some indication that the first four are a bit different with respect to variability.

4.2 Outlier detection using diagnostics

Let's apply the diagnostic-dimension reduction-multivariate outlier procedure `ArrayOutliers`.

```
> AO = ArrayOutliers(afxsub, alpha = 0.05, qcOut = afxsubQC, plmOut = splm,
+   degOut = afxsubDEG)
> nrow(AO[["outl"]])
```

```
[1] 0
```

We see that there are no outliers declared. This seems a reasonable result for arrays that were hybridized in the context of a QC protocol. Let us apply the `mdqc` procedure. As input this takes any matrix of quality indicators. The third component of our `ArrayOutliers` result provides these as computed using `simpleaffy qc()`, `affy AffyRNAdeg`, and `affyPLM NUSE` and `RLE`. The QC measures for the first two chips are:


```
> AO[[3]][1:2, ]
```

```
      avgBG      SF Present  HSAC07  GAPDH  NUSE      RLE
X_1_A1 60.05505 1.1765695 52.42250 1.245477 1.065898 1.064069 0.04163564
X_1_A2 52.42248 0.9459093 54.63009 1.273977 1.094208 1.040718 0.03253112
      RLE_IQR RNAslope
X_1_A1 0.5626532 3.141527
X_1_A2 0.5459847 3.210157
```

We now use the `mdqc` package with MVE robust covariance estimation.

```
> library(mdqc)
> mdq = mdqc(AO[[3]], robust = "MVE")
> mdq
```

```
Method used: nogroups      Number of groups: 1
Robust estimator: MVEMDs exceeding the square root of the 90 % percentile of the Chi-S
[1] 6 16 17 18 21 24
MDs exceeding the square root of the 95 % percentile of the Chi-Square distribution
[1] 6 16 17 18 21 24
MDs exceeding the square root of the 99 % percentile of the Chi-Square distribution
[1] 6 16 17 18 21 24
```

We see that a number of the arrays are determined to be outlying by this procedure according to several thresholds.

5 Intensity contamination in the spikein data

We begin with a simple demonstration of a contamination procedure that simulates severe blobby interference with hybridization.

The code below is unevaluated to speed execution. Set `eval=TRUE` on all chunks to see the actual process.

```
> require(mvoutData)
> data(s12c)

> image(s12c[, 1])
```

12_13_02_U133A_Mer_Latin_Square_Expt1_R1



For this AffyBatch instance, we have contaminated the first two arrays in this way. We now apply the ArrayOutliers procedure:

```
> aos12c = ArrayOutliers(s12c, alpha = 0.05)
```

```
> aos12c[[1]]
```

| | samp | avgBG | SF | Present | | |
|---|--|------------|----------|--------------|------------|-------------|
| 1 | 12_13_02_U133A_Mer_Latin_Square_Expt1_R1 | 7205.48413 | 5.494978 | 19.05381 | | |
| 2 | 12_13_02_U133A_Mer_Latin_Square_Expt2_R1 | 7205.12544 | 5.801398 | 17.62332 | | |
| 8 | 12_13_02_U133A_Mer_Latin_Square_Expt8_R1 | 31.23121 | 1.181946 | 45.47982 | | |
| | HSAC07 | GAPDH | NUSE | RLE | RLE_IQR | RNAslope |
| 1 | 9.488671 | 8.6364494 | 1.578471 | -0.514913919 | 1.33150311 | -0.05195296 |
| 2 | 8.517500 | 9.7475845 | 1.579164 | -0.514617696 | 1.37213796 | -0.07638096 |
| 8 | 1.042255 | 0.8965249 | 1.000006 | 0.001987620 | 0.09164597 | 1.53050152 |

We find three arrays declared to be outlying. At the different candidate significance levels we have:

```

> aos12c[[4]]

[[1]]
[[1]]$inds
[1] 1 2

[[1]]$vals
          PC1          PC2          PC3
[1,] -6.345625  0.08184738  0.05419247
[2,] -6.485447 -0.07281758 -0.05421514

[[1]]$k
[1] 5

[[1]]$alpha
[1] 0.01

[[2]]
[[2]]$inds
[1] 8 1 2

[[2]]$vals
          PC1          PC2          PC3
[1,]  1.104062 -0.18796407 -0.008319271
[2,] -6.345625  0.08184738  0.054192469
[3,] -6.485447 -0.07281758 -0.054215145

[[2]]$k
[1] 5

[[2]]$alpha
[1] 0.05

[[3]]
[[3]]$inds
[1] 8 1 2

[[3]]$vals
          PC1          PC2          PC3
[1,]  1.104062 -0.18796407 -0.008319271
[2,] -6.345625  0.08184738  0.054192469

```

```
[3,] -6.485447 -0.07281758 -0.054215145
```

```
[[3]]$k  
[1] 5
```

```
[[3]]$alpha  
[1] 0.1
```

So at the 0.01 level we have identified only the contaminated arrays.

We apply `mdqc` in the same manner.

```
> mdqc(aos12c[[3]], robust = "MVE")
```

```
Method used: nogroups          Number of groups: 1  
Robust estimator: MVEMDs exceeding the square root of the 90 % percentile of the Chi-S  
[1] 2  
MDs exceeding the square root of the 95 % percentile of the Chi-Square distribution  
[1] 2  
MDs exceeding the square root of the 99 % percentile of the Chi-Square distribution  
[1] 2
```

We see that only one of the contaminated arrays is identified by this procedure. This may be an instance of masking.

6 Appendix: Sources and text for statically computed sections with `eval set to false`

Manual work with the MAQC subset

All the code following has had evaluation turned off because execution times are slow.

We consider an `AffyBatch` supplied with the Bioconductor `MAQCsubset` package. Marginal boxplots of raw intensity data are provided in the next figure. Sample labels are decoded `AFX _ [lab] _ [type] [replicate] .CEL` where `[lab] ∈ (1, 2, 3)`, `[type]` denotes mixture type (A = 100% USRNA, B = 100% Ambion brain, C = 75% USRNA, 25% brain, D = 25% USRNA, 75% brain), and `replicate ∈ (1, 2)`.

```
> library(arrayMvout)  
> library(MAQCsubset)  
> if (!exists("afxsub")) data(afxsub)  
> sn = sampleNames(afxsub)  
> if (nchar(sn)[1] > 6) {  
+   sn = substr(sn, 3, 8)
```

```

+   sampleNames(afxsub) = sn
+ }

> opar = par(no.readonly=TRUE)
> par(mar=c(10,5,5,5), las=2)
> boxplot(afxsub, main="MAQC subset",
+   col=rep(c("green", "blue", "orange"), c(8,8,8)))
> par(opar)

```

QA diagnostics

Of interest are measures of RNA degradation:

```

> #afxsubDEG = AffyRNAdeg(afxsub)
> #save(afxsubDEG, file="afxsubDEG.rda")
> library(arrayMvout)
> data(afxsubDEG)
> plotAffyRNAdeg(afxsubDEG,
+   col=rep(c("green", "blue", "orange"), c(8,8,8)))

```

and the general ‘simpleaffy’ QC display:

```

> #afxsubQC = qc(afxsub)
> #save(afxsubQC, file="afxsubQC.rda")
> data(afxsubQC)
> plot(afxsubQC)

```

The affyPLM package fits probe-level robust regressions to obtain probe-set summaries.

```

> library(affyPLM)
> #if (file.exists("splm.rda")) load("splm.rda")
> #if (!exists("splm")) splm = fitPLM(afxsub)
> splm = fitPLM(afxsub)
> #save(splm, file="splm.rda")

> png(file="doim.png")
> par(mar=c(7,5,5,5),mfrow=c(2,2),las=2)
> NUSE(splm, ylim=c(.85, 1.3))
> RLE(splm)
> image(splm, which=2, type="sign.resid")
> image(splm, which=5, type="sign.resid")

```

These chips seem to have adequate quality, although there is some indication that the first four are a bit different with respect to variability.

Outlier detection using diagnostics

Let's apply the diagnostic-dimension reduction-multivariate outlier procedure `ArrayOutliers`.

```
> AO = ArrayOutliers(afxsub, alpha=0.05, qcOut=afxsubQC,  
+   plmOut=splm, degOut=afxsubDEG)  
> nrow(AO[["out1"]])
```

We see that there are no outliers declared. This seems a reasonable result for arrays that were hybridized in the context of a QC protocol. Let us apply the `mdqc` procedure. As input this takes any matrix of quality indicators. The third component of our `ArrayOutliers` result provides these as computed using `simpleaffy qc()`, `affy AffyRNAdeg`, and `affyPLM NUSE` and `RLE`. The QC measures for the first two chips are:

```
> AO[[3]][1:2, ]
```

We now use the `mdqc` package with MVE robust covariance estimation.

```
> library(mdqc)  
> mdq = mdqc( AO[[3]], robust="MVE" )  
> mdq
```

We see that a number of the arrays are determined to be outlying by this procedure according to several thresholds.

Intensity contamination in the spikein data

We begin with a simple demonstration of a contamination procedure that simulates severe blobby interference with hybridization.

The code below is unevaluated to speed execution. Set `eval=TRUE` on all chunks to see the actual process.

```
> require(mvoutData)  
> data(s12c)  
  
> image(s12c[,1])
```

For this `AffyBatch` instance, we have contaminated the first two arrays in this way. We now apply the `ArrayOutliers` procedure:

```
> aos12c = ArrayOutliers(s12c, alpha=0.05)  
> aos12c[[1]]
```

We find three arrays declared to be outlying. At the different candidate significance levels we have:

```
> aos12c[[4]]
```

So at the 0.01 level we have identified only the contaminated arrays.

We apply `mdqc` in the same manner.

```
> mdqc(aos12c[[3]], robust="MVE")
```

We see that only one of the contaminated arrays is identified by this procedure. This may be an instance of masking.

```
> sessionInfo()
```

```
R version 4.2.0 RC (2022-04-19 r82224)
```

```
Platform: x86_64-pc-linux-gnu (64-bit)
```

```
Running under: Ubuntu 20.04.4 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.15-bioc/R/lib/libRblas.so
```

```
LAPACK: /home/biocbuild/bbs-3.15-bioc/R/lib/libRlapack.so
```

```
locale:
```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_GB             LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8   LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C              LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
attached base packages:
```

```
[1] tools      stats      graphics  grDevices  utils      datasets  methods
[8] base
```

```
other attached packages:
```

```
[1] arrayMvout_1.54.0  affy_1.74.0          Biobase_2.56.0
[4] BiocGenerics_0.42.0  parody_1.54.0
```

```
loaded via a namespace (and not attached):
```

```
[1] colorspace_2.0-3      rjson_0.2.21
[3] ellipsis_0.3.2        siggenes_1.70.0
[5] mclust_5.4.9          XVector_0.36.0
[7] GenomicRanges_1.48.0  base64_2.0
[9] affyio_1.66.0         bit64_4.0.5
[11] AnnotationDbi_1.58.0  fansi_1.0.3
[13] xml2_1.3.3            codetools_0.2-18
```

| | | |
|------|---------------------------|-----------------------------|
| [15] | splines_4.2.0 | sparseMatrixStats_1.8.0 |
| [17] | cachem_1.0.6 | scrime_1.3.5 |
| [19] | methylumi_2.42.0 | Rsamtools_2.12.0 |
| [21] | annotate_1.74.0 | cluster_2.1.3 |
| [23] | dbplyr_2.1.1 | png_0.1-7 |
| [25] | HDF5Array_1.24.0 | readr_2.1.2 |
| [27] | BiocManager_1.30.17 | compiler_4.2.0 |
| [29] | httr_1.4.2 | assertthat_0.2.1 |
| [31] | Matrix_1.4-1 | fastmap_1.1.0 |
| [33] | limma_3.52.0 | cli_3.3.0 |
| [35] | prettyunits_1.1.1 | glue_1.6.2 |
| [37] | GenomeInfoDbData_1.2.8 | dplyr_1.0.8 |
| [39] | doRNG_1.8.2 | rappdirs_0.3.3 |
| [41] | Rcpp_1.0.8.3 | bumphunter_1.38.0 |
| [43] | vctrs_0.4.1 | Biostrings_2.64.0 |
| [45] | rhdf5filters_1.8.0 | multtest_2.52.0 |
| [47] | nlme_3.1-157 | preprocessCore_1.58.0 |
| [49] | rtracklayer_1.56.0 | iterators_1.0.14 |
| [51] | DelayedMatrixStats_1.18.0 | stringr_1.4.0 |
| [53] | lifecycle_1.0.1 | restfulr_0.0.13 |
| [55] | rngtools_1.5.2 | XML_3.99-0.9 |
| [57] | beanplot_1.3.1 | nleqslv_3.3.2 |
| [59] | zlibbioc_1.42.0 | MASS_7.3-57 |
| [61] | hms_1.1.1 | MatrixGenerics_1.8.0 |
| [63] | parallel_4.2.0 | SummarizedExperiment_1.26.0 |
| [65] | GEOquery_2.64.0 | minfi_1.42.0 |
| [67] | rhdf5_2.40.0 | RColorBrewer_1.1-3 |
| [69] | yaml_2.3.5 | curl_4.3.2 |
| [71] | memoise_2.0.1 | biomaRt_2.52.0 |
| [73] | reshape_0.8.9 | stringi_1.7.6 |
| [75] | RSQLite_2.2.12 | genefilter_1.78.0 |
| [77] | S4Vectors_0.34.0 | BiocIO_1.6.0 |
| [79] | foreach_1.5.2 | lumi_2.48.0 |
| [81] | GenomicFeatures_1.48.0 | filelock_1.0.2 |
| [83] | BiocParallel_1.30.0 | GenomeInfoDb_1.32.0 |
| [85] | rlang_1.0.2 | pkgconfig_2.0.3 |
| [87] | matrixStats_0.62.0 | bitops_1.0-7 |
| [89] | nor1mix_1.3-0 | lattice_0.20-45 |
| [91] | purrr_0.3.4 | Rhdf5lib_1.18.0 |
| [93] | GenomicAlignments_1.32.0 | bit_4.0.4 |
| [95] | tidyselect_1.1.2 | plyr_1.8.7 |
| [97] | magrittr_2.0.3 | R6_2.5.1 |

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| [99] | IRanges_2.30.0 | generics_0.1.2 |
| [101] | DelayedArray_0.22.0 | DBI_1.1.2 |
| [103] | mgcv_1.8-40 | pillar_1.7.0 |
| [105] | survival_3.3-1 | KEGGREST_1.36.0 |
| [107] | RCurl_1.98-1.6 | tibble_3.1.6 |
| [109] | crayon_1.5.1 | KernSmooth_2.23-20 |
| [111] | utf8_1.2.2 | BiocFileCache_2.4.0 |
| [113] | tzdb_0.3.0 | progress_1.2.2 |
| [115] | locfit_1.5-9.5 | grid_4.2.0 |
| [117] | data.table_1.14.2 | blob_1.2.3 |
| [119] | digest_0.6.29 | xtable_1.8-4 |
| [121] | affyContam_1.54.0 | tidyr_1.2.0 |
| [123] | illuminaio_0.38.0 | mdqc_1.58.0 |
| [125] | openssl_2.0.0 | stats4_4.2.0 |
| [127] | quadprog_1.5-8 | askpass_1.1 |