

A note on esApply

ExpressionSets are complex objects. `exprs(ExpressionSet)` produces $G \times N$, where G is the number of genes on a chip and N is the number of tissues analyzed, and `pData(ExpressionSet)` produces $N \times p$, where p is the number of phenotypic or demographic, etc., variables collected.

Abstractly, we are often interested in evaluating functions $f(y; x)$ where y is an N -vector of expression results for a specific gene and x is an N -dimensional structure, coordinated with y , that distinguishes elements of y for processing in the function f . A basic problem is to guarantee that the j th element of y is correctly associated with the j th component of x .

As an example, let's consider `sample.ExpressionSet`, which is an *ExpressionSet* supplied with Biobase. We will print a little report, then the first N -vector of gene expressions and some covariate data:

```
> print(sample.ExpressionSet)
```

```
ExpressionSet (storageMode: lockedEnvironment)
assayData: 500 features, 26 samples
  element names: exprs, se.exprs
protocolData: none
phenoData
  sampleNames: A B ... Z (26 total)
  varLabels: sex type score
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
Annotation: hgu95av2
```

```
> print(exprs(sample.ExpressionSet)[1,])
```

	A	B	C	D	E	F	G
192.7420	85.7533	176.7570	135.5750	64.4939	76.3569	160.5050	
	H	I	J	K	L	M	N
65.9631	56.9039	135.6080	63.4432	78.2126	83.0943	89.3372	
	O	P	Q	R	S	T	U
91.0615	95.9377	179.8450	152.4670	180.8340	85.4146	157.9890	
	V	W	X	Y	Z		
146.8000	93.8829	103.8550	64.4340	175.6150			

```
> print(pData(sample.ExpressionSet)[1:2,1:3])
```

	sex	type	score
A	Female	Control	0.75
B	Male	Case	0.40

Now let's see how expressions and a covariate are related:

```
> print(rbind(exprs(sample.ExpressionSet[1,]),
+ sex <- t(pData(sample.ExpressionSet))[1,]))
```

	A	B	C	D	E
AFFX-MurIL2_at	"192.742"	"85.7533"	"176.757"	"135.575"	"64.4939"
	"Female"	"Male"	"Male"	"Male"	"Female"
	F	G	H	I	J
AFFX-MurIL2_at	"76.3569"	"160.505"	"65.9631"	"56.9039"	"135.608"
	"Male"	"Male"	"Male"	"Female"	"Male"
	K	L	M	N	O
AFFX-MurIL2_at	"63.4432"	"78.2126"	"83.0943"	"89.3372"	"91.0615"
	"Male"	"Female"	"Male"	"Male"	"Female"
	P	Q	R	S	T
AFFX-MurIL2_at	"95.9377"	"179.845"	"152.467"	"180.834"	"85.4146"
	"Female"	"Female"	"Male"	"Male"	"Female"
	U	V	W	X	Y
AFFX-MurIL2_at	"157.989"	"146.8"	"93.8829"	"103.855"	"64.434"
	"Male"	"Female"	"Male"	"Male"	"Female"
	Z				
AFFX-MurIL2_at	"175.615"				
	"Female"				

A function that evaluates the difference in median expression across strata defined using an abstract covariate *x* is

```
> medContr <- function( y, x ) {
+   ys <- split(y,x)
+   median(ys[[1]]) - median(ys[[2]])
+ }
```

We can apply this to a small *ExpressionSet* that gives back the data listed above:

```
> print(apply(exprs(sample.ExpressionSet[1,,drop=F]), 1,
+   medContr, pData(sample.ExpressionSet)[["sex"]]))
```

AFFX-MurIL2_at
-12.7935

That's a bit clumsy. This is where `esApply` comes in. We pay for some simplicity by following a strict protocol for the definition of the statistical function to be applied.

```

> medContr1 <- function(y) {
+   ys <- split(y,sex)
+   median(ys[[1]]) - median(ys[[2]])
+ }
> print(esApply( sample.ExpressionSet, 1, medContr1)[1])

```

```

AFFX-MurIL2_at
-12.7935

```

The manual page on `esApply` has a number of additional examples that show how applicable functions can be constructed and used. The important thing to note is that the applicable functions *know* the names of the covariates in the `pData` dataframe.

This is achieved by having an environment populated with all the variables in `phenoData(ExpressionSet)` put in as the environment of the function that will be applied. If that function already has an environment we retain that but in the second position. Thus, there is some potential for variable shadowing.

1 Session Information

The version number of R and packages loaded for generating the vignette were:

```

R Under development (unstable) (2020-10-17 r79346)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.1 LTS

```

```

Matrix products: default
BLAS: /home/biocbuild/bbs-3.13-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.13-bioc/R/lib/libRlapack.so

```

```

locale:
 [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8      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] parallel stats graphics grDevices utils datasets
 [7] methods base

```

```

other attached packages:

```

```
[1] Biobase_2.51.0      BiocGenerics_0.37.0
```

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

```
[1] compiler_4.1.0 tools_4.1.0
```