## Installation

```
   - Install the bioconductor package 'affy'
   # within R
     source("http://bioconductor.org/biocLite.R")
     biocLite("affy")

   - Install the "pvac" and "pvacExampleData" source packages
   # on command line
     R CMD INSTALL pvac
     R CMD INSTALL pvacExampleData

   - [Optional] install pbapply (from CRAN) for viewing progress bar
```

## Example

```
       # within R
       library(affy)
       library(pvac)
       library(pvacExampleData)
       data(pvacExampleData)          # pvacExampleData is a raw
AffyBatch object

       myeset = rma(pvacExampleData)  # eset summarized using RMA

       res = pvacFilter(pvacExampleData)   # perform pvac filtering

       res$aset                            # names of probesets that have
passed the filter

       myeset.filtered = myeset[res$aset,] # eset object after filtering

       # statistical tests within R ...,
       #  or output a  tab-delimited file of probeset level data
       write.exprs(myeset.filtered,'out.txt')
```