

## HIVcDNAvantWout03 data

This data represents the first block from the first microarray slide image from van't Wout et al. (2003). The encoded image data from the two channels for this block are provided as datasets `hiv1raw` and `hiv2raw`, and can be obtained via the `data` command.

```
> data(hiv1raw)
> data(hiv2raw)
```

Because the data are encoded for compact storage, they need to be transformed as follows in order to extract the intensities:

```
> hiv1 <- (256*256-1-matrix(hiv1raw,nrow=450,ncol=1000))^2*4.71542407E-05
> hiv2 <- (256*256-1-matrix(hiv2raw,nrow=450,ncol=1000))^2*4.71542407E-05
```

Note that this transformation is specific to this data; in general stored image data must be converted as needed to image intensities. Figure 1 shows the image data for the two channels in reverse gray scale. The gray scale is calibrated using the square roots of the intensities for better contrast. These plots can be obtained with the `spotSegmentation` package (Li et al. 2005) in R/Bioconductor using the following commands:

```
> plotBlockImage(sqrt(hiv1))
> plotBlockImage(sqrt(hiv2))
```

## References

- [1] Q. Li, C. Fraley, R. E. Bumgarner, K. Y. Yeung, and A. E. Raftery. Donuts, scratches, and blanks: Robust model-based segmentation of microarray images. *Bioinformatics*, 21:2875–2882, 2005.
- [2] A. B. van't Wout, G. K. Lehrman, S. A. Mikeeva, G. C. O'Keefe, M. G. Katze, R. E. Bumgarner, G. K. Geiss, and J. I. Mullins. Cellular gene expression upon human immunodeficiency type 1 infection of CD4(+)-T-cell lines. *Journal of Virology*, 77(2):1392–1402, January 2003.

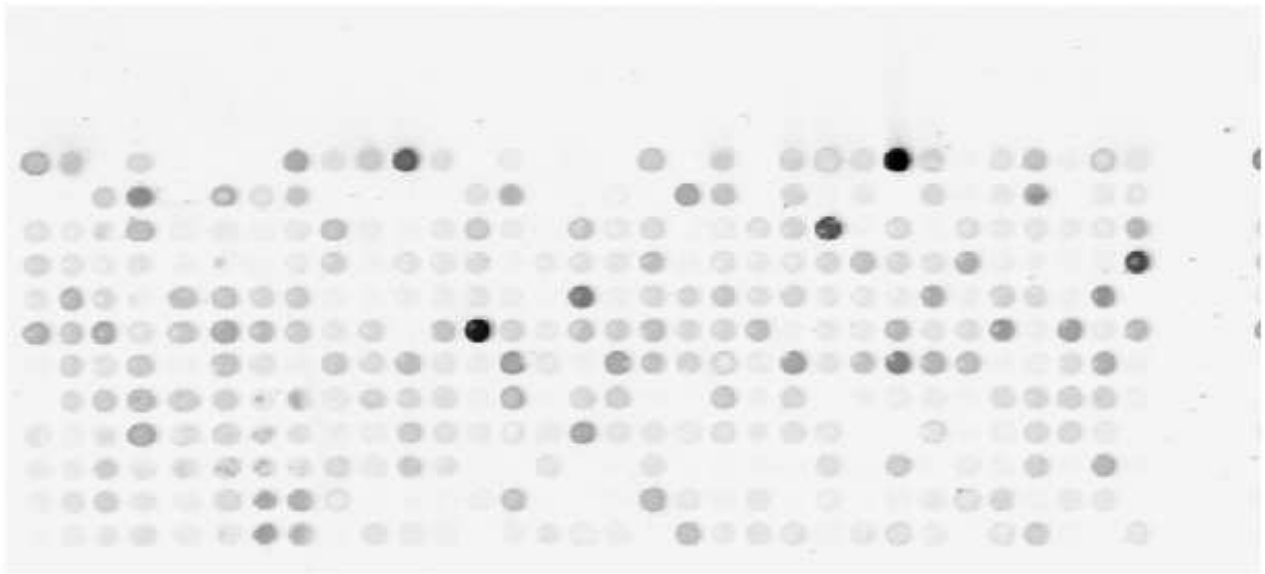


Figure 1: Reverse gray-scale plot of image intensities from channel 1 (Cy3 green) and channel 2 (Cy5 red) of the first block from the first slide of HIV data from van't Wout et al. (2003).