Applying mean filter to smooth microarray data

   To reduce irrelevant details of expression patterns in MGED so that a trend across time can emerge, we applied a mean filter (Gonzalez and Woods, 2002), in the discrete signal processing area, to smooth microarray data.   In general, if the underlying noise follows a Gaussian distribution, a simple mean filter will suffice. A mean filter with kernel size $r \times c$ can be viewed as a window of size $r \times c$ centered at an original datum, and replacing the datum (pixel) with the average of all pixels in the window. Thus the larger the kernel, the smoother the image produced by the filtering. A mean filter with kernel size 1×3 was applied in our study, and its effect is demonstrated in Fig. 2. The expression patterns of TC gene pairs (*CSM3* and *HST3*) before and after the filtering are plotted in Fig. 1, where the thin solid green (thin dotted blue) line depicts the original expression levels of *CSM3* (*HST3*), while the bold solid green (bold dotted blue) line the expression levels of *CSM3* (*HST3)* after the filtering. Before the filtering, it was hard to observe any pattern from these curves, whereas a CP emerged after the filtering.
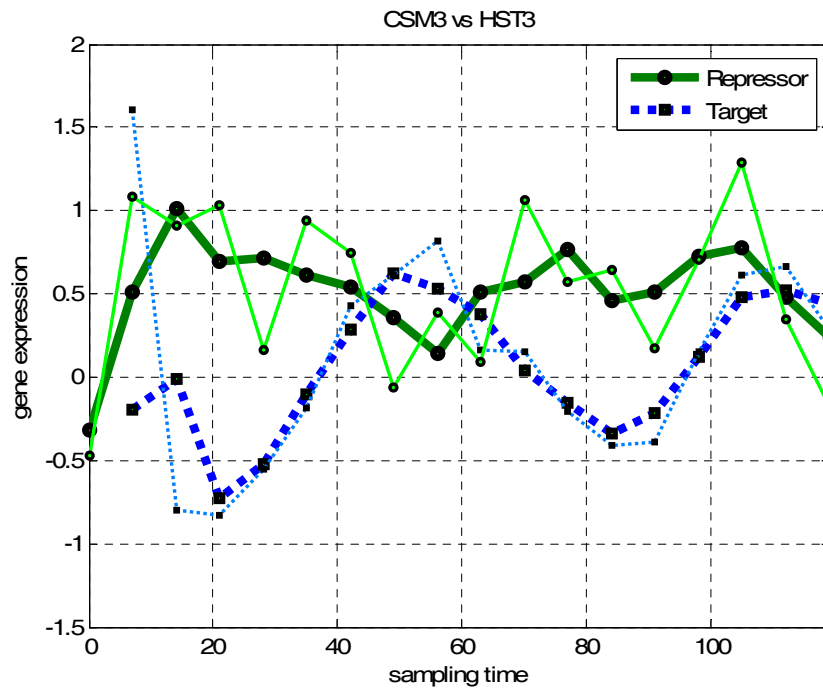

Fig. 2. Paired gene expression patterns before (thin lines) and after (bold lines) the filtering (kernel size
      1×3).