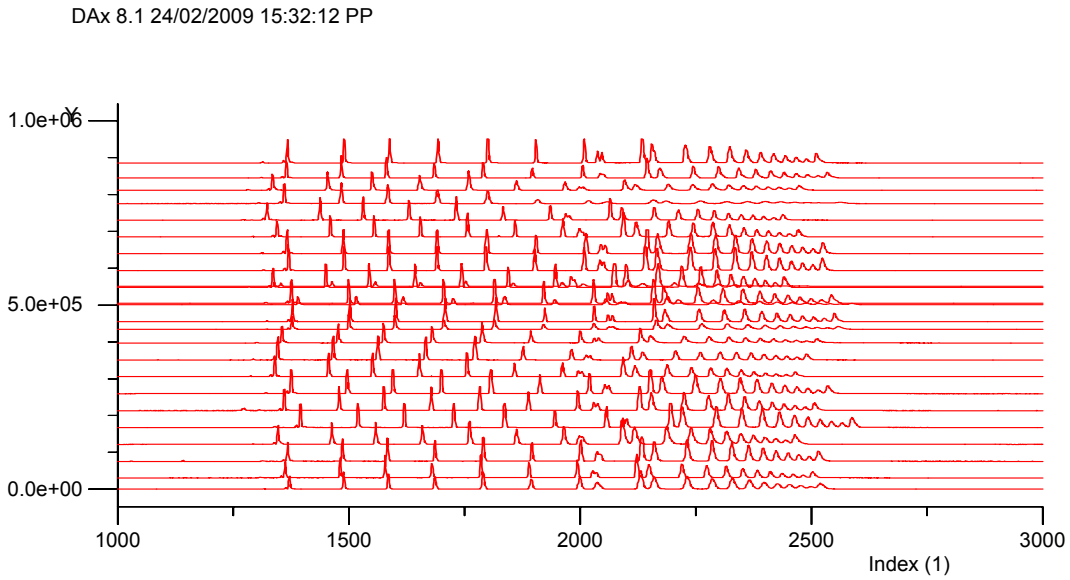
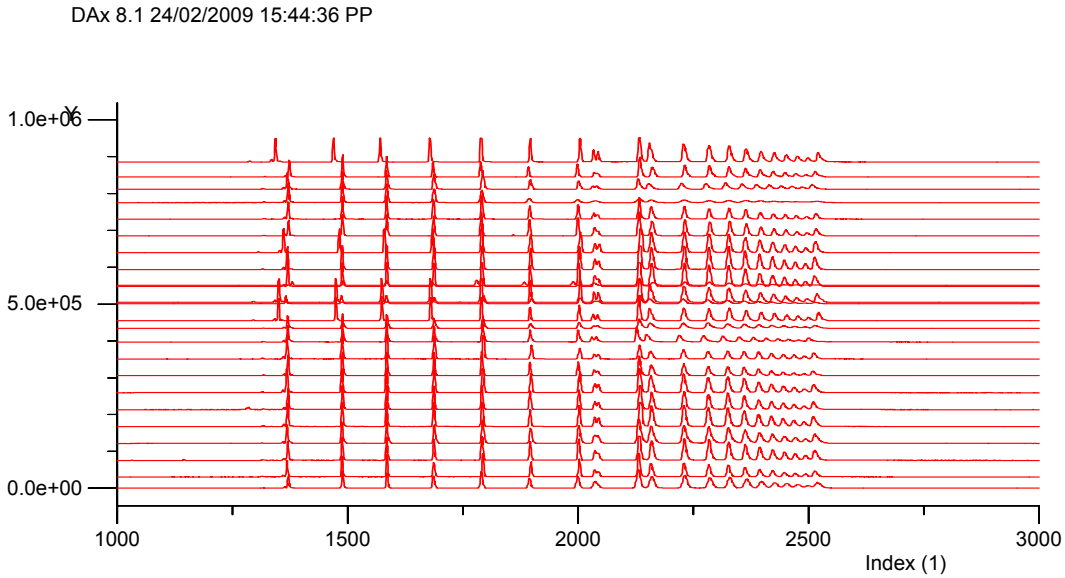
Using Horizontal Overlay “Match Curve Shapes” to Align Data from a Single Well Plate

24 traces were run on a single well plate on a MegaBACE system. The traces are not ideally aligned:

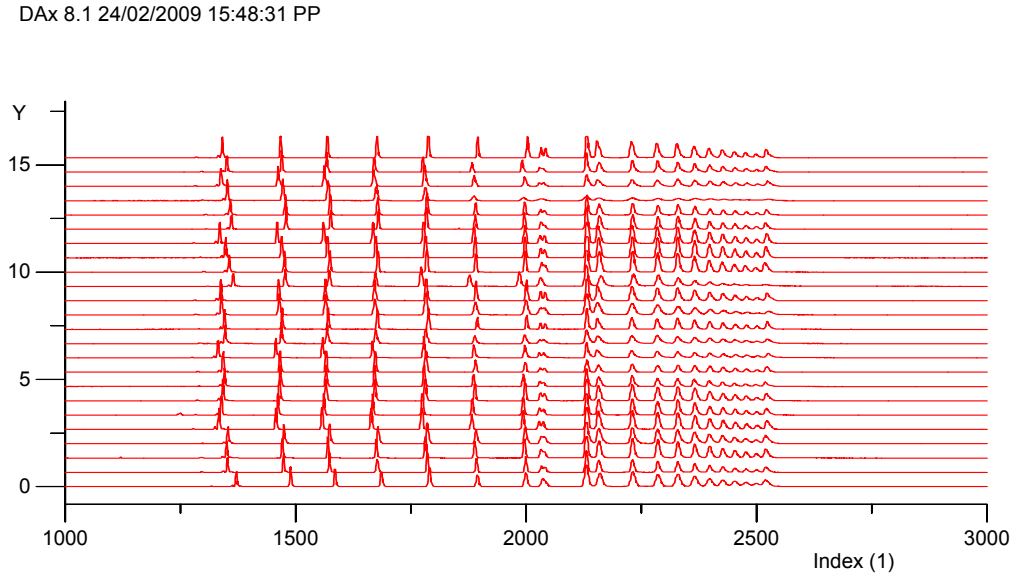


Overlaying the traces, specifying a maximum stretch factor of 5%, and no interval, aligns the traces almost perfectly:

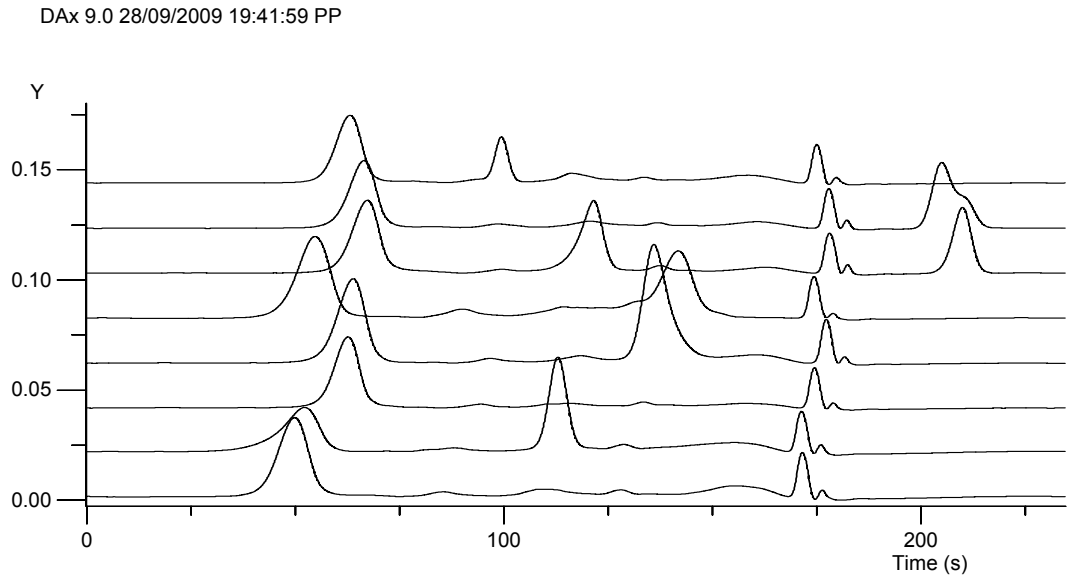


No baselines were constructed, nor were peaks detected: unlike other overlay techniques, shape overlay does not use peaks.

Limiting the overlay interval to the range of interest, 2100 - 2600, gives even better results:

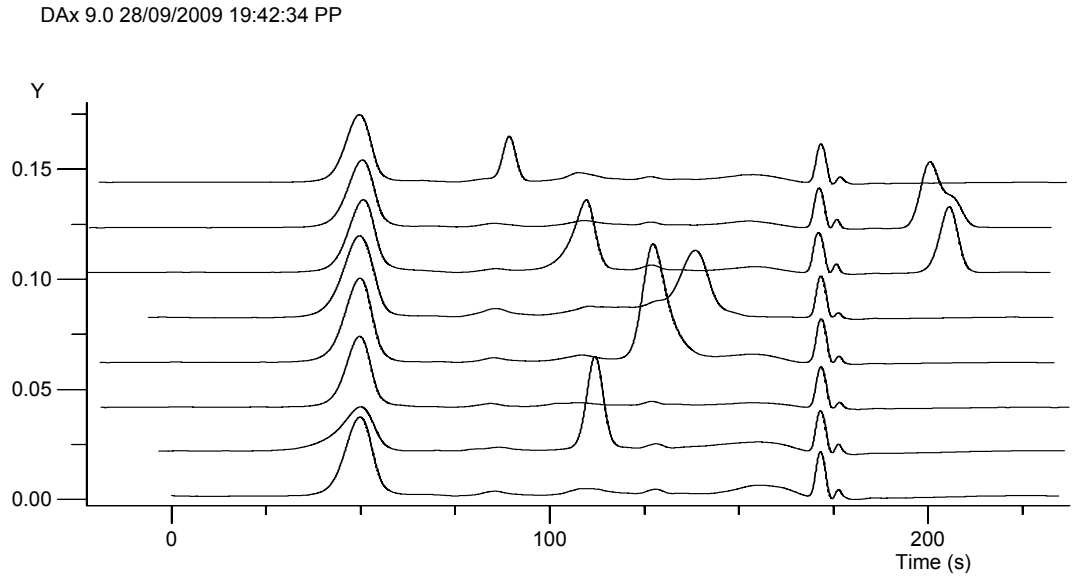


Another example compares capillary electrophoresis measurements of serum proteins:

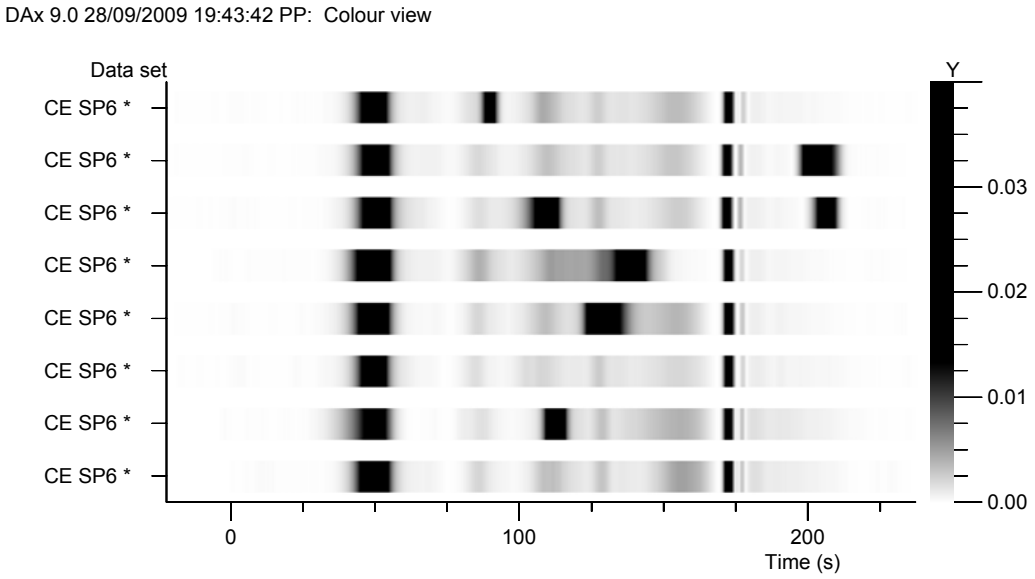


Each measurement contains two especially prominent peaks: an albumin peak at the start and a marker peak towards the end. Various abnormal peaks are also present.

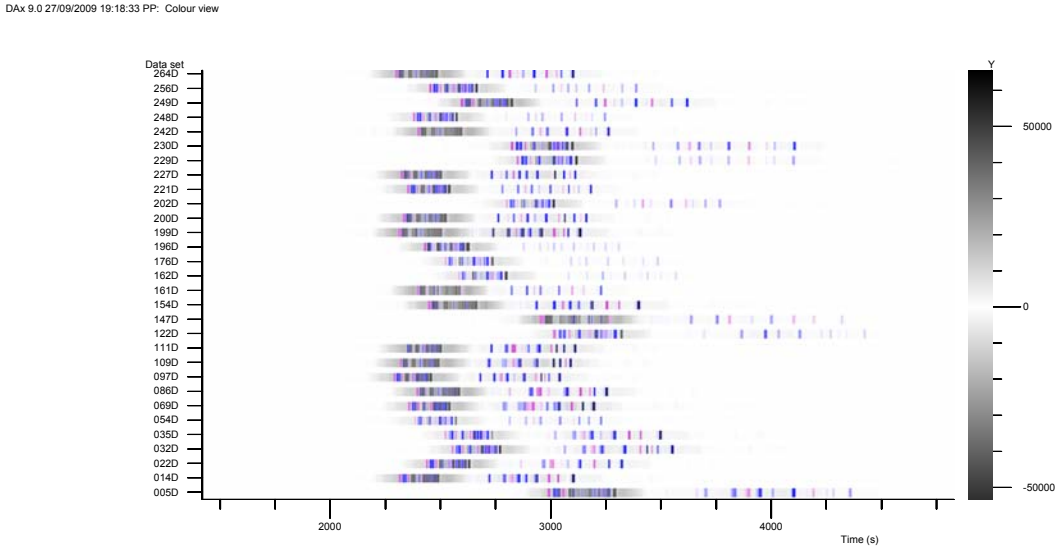
After overlaying:



Displayed as a colour view:

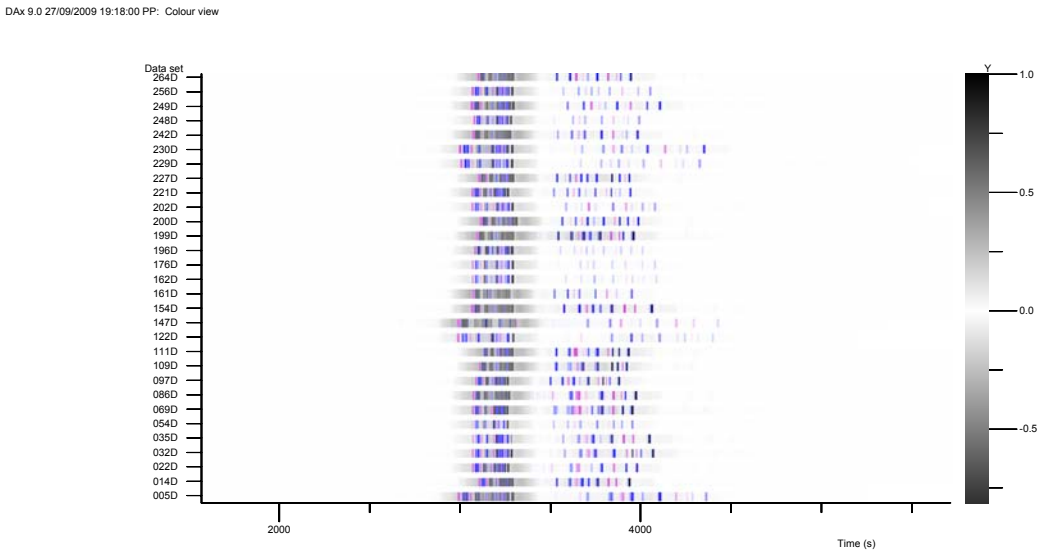


Another example of poorly aligned measurements, this time displayed as a colour view:



Each lane in this graph contains a HEX, FAM and TET trace. The colour displayed is the most intense value at each point, with HEX displayed as black, FAM as purple and TET as blue.

After aligning on the HEX traces[1]:



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[1] The FAM and TET traces are scaled in the same way as the HEX traces from the same well. The vertical scale was normalised also.