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Poster presentation

Exon level integration of proteomics and microarray data

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Background

Previous studies investigating the correspondence between mRNA expression level and protein abundance have generally reported low correlation. Complexities in the processes that regulate gene expression are often assumed to be a major cause of inconsistency between the two. We hypothesised that other factors, such as the reliability of the quantification technologies, the relative locations of the reporters with respect to the transcripts and proteins, and the supporting bioinformatics tools, might also contribute to the observed differences.

Results

Using the genome as a reference, and the mRNA/protein complement of a pair of steady state cell lines as source data, we successfully integrated iTRAQ quantitative protein mass spectrometry with Affymetrix Exon array data, at the level of individual exons. Upon integration, the Pearson correlation between the mRNA and protein data was significantly higher than previously observed ($r = 0.808$).

Conclusion

The application of enhanced bioinformatics filtering and peptide mapping techniques supports a tighter integration of quantitative proteomics and microarray data.

This is made possible by the advent of exon arrays, which enable a much finer-grained survey of the transcribed genome. This increased resolution not only improves the quantification of proteins and transcripts, but also enables the consideration of protein and mRNA expression at the level of individual exons. This may help further pursuit of processes such as alternative splicing.