

MAKING SENSE OF TWO-DIMENSIONAL GEL IMAGES

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Two-dimensional polyacrylamide gel electrophoresis is currently one of the techniques of choice to separate and display all the proteins expressed in a tissue. In the resulting protein map, individual protein spots are identified and quantified. To this end, background noise and dust spikes are eliminated. A classification tree allows us to select regions containing spots. A multiple regression equation determines the gradient threshold above which features are selected. Images are aligned via a quadratic programming algorithm. Wavelets are utilized to summarize the two-dimensional gels. Within this framework, we seek to compare different gels by determining the strength and the location of the signal. This work is joint with A. Roy, F. Potra, Y. Zhang, V. Korostyshevskiy and Y. Hang.