Models for teardrop spots in 2-DE gels

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Background and Objective: Spot detection and spot matching across multiple sets of gel images are essential first steps for proteomics investigations based on two-dimensional gel electrophoresis (2-DE). Although a 3-dimensional Gaussian distribution is a widely accepted modeling assumption for protein spots (Garrels 1989; Appel et al. 1997; Bettens 1996) it is clear from our 2-D gels that many spots exhibit reproducible intensity patterns resembling a “teardrop” shape that do not fit a Gaussian model. Up to now, most spot detection algorithms assume a Gaussian spot shape and have problems identifying teardrop spots.

Methods: We investigated different spot models for these teardrop spots and developed a parametric algorithm that uses a variety of different models for spot intensity distribution. We concentrated on investigating spot models that offer explanations for the cause of the teardrop shape. The spot detection algorithm identifies a “seed” set of possible spot locations, and then attempts to fit multiple spot models to each location.

Results: Our teardrop spot models are generally superior to Gaussian models in fitting teardrop spots. In contrast to the typical Gaussian assumption, it appears that better teardrop models can be developed when the pI-axis and the molecular weight axis are not assumed to be independent.

Discussion and Conclusions: Many 2-DE gels exhibit teardrop spots that cannot be modeled by current analysis software packages. Our investigations offer the first attempt at modeling and explaining this phenomenon.

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