

*Who Are Those Strangers in the Latin Square*

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We approach the Affy Latin Square data from a classical parametric statistical modeling perspective. A first stage is to formulate a reasonable model for the probe-level data based on extant knowledge of the experimental design and technology. We present some options for this and settle on a linear mixed model for the log<sub>2</sub> perfect match data. Upon applying this model to data for every gene in turn, we discover that not only do the fourteen spiked-in genes appear highly significant, but that a few additional, unexpected, genes display profiles remarkably similar to those of the fourteen. We investigate each of these genes in more detail and provide explanations for their appearance.