Mass cytometers can record tens of features for millions of cells in a sample, and in particular, for leukemic cells. Many methods consider how to cluster or identify populations of phenotypically similar cells within cytometry data, but there has yet to be a connection between cell activity and other features and these groups or clusters. We use differential geometric ideas and develop statistical tools to consider how cell cycle and signaling features vary as a function of the cell populations. This consideration leads to a better understanding of the nonlinear relationships that exist in the cytometry data.