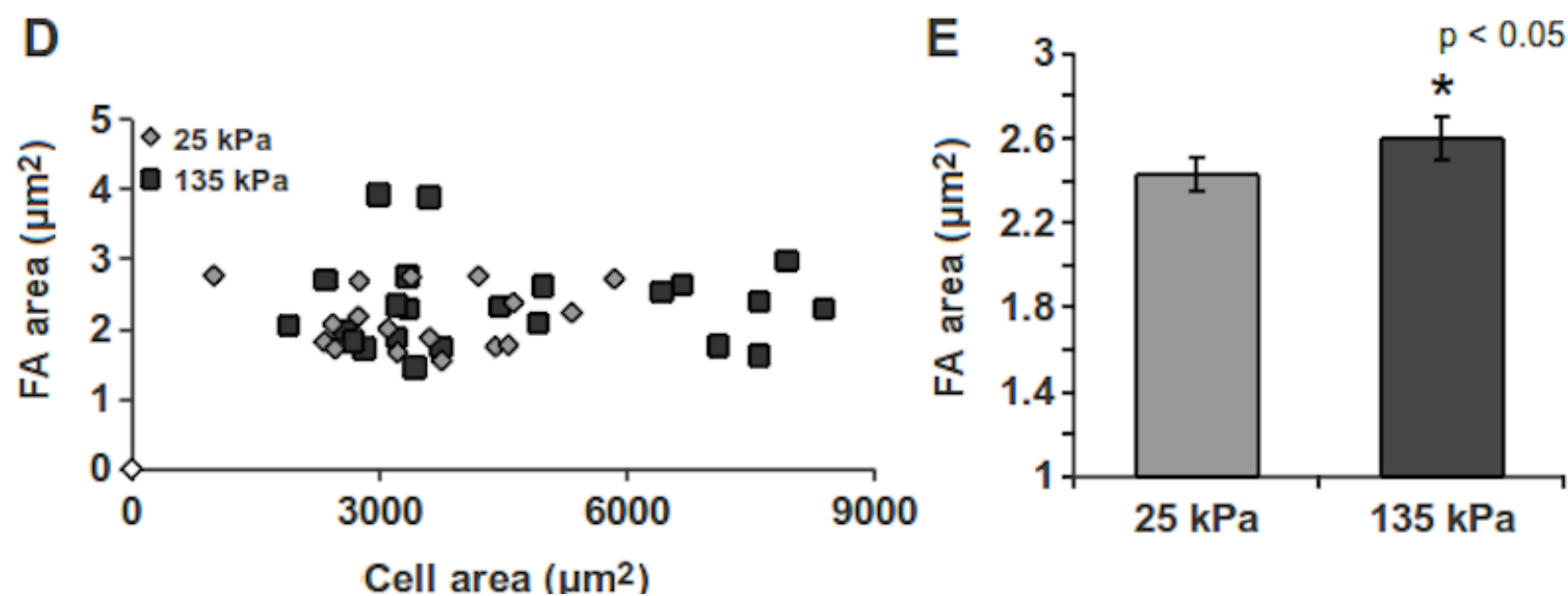


Protein clusters (green) in cells imaged on a confocal microscope can be computationally identified and analyzed for size, shape, intensity, etc. These features can then be studied as a function of any number of dependent variables.



For instance, I used this approach to find that while protein cluster size did not vary between smaller and bigger cells (D), protein clusters were ~10% bigger in cells cultured on a stiffer biomaterial (E)