CLONALITY, RICHNESS, AND MULTINOMIAL PARAMETERS

RICHARD A. OLSHEN
STANFORD UNIVERSITY

The B cells and T cells of the adaptive immune system undergo rearrangements of antigen receptor genes in their genomes, and undergo clonal expansion in response to antigenic stimuli. Modern DNA sequencing enables study of molecular populations. The vector of frequencies of particular rearrangements is of interest in quantifying the decline of the immune system with age, and also in quantifying responses to vaccines. The cited vector and various functionals of it recall statistical concerns, including but not limited to problems of estimating non-centrality parameters and of estimating covariance matrices in as few dimensions as one. One such functional, clonality, is the squared length of the vector. Another, richness, is the number of rearrangements. Without some but not all sources of error in estimation, one is led to study estimation of multinomial parameters.

I will report on problems mentioned and “solutions” proposed. All work is collaborative with others, who will be mentioned (blamed?) as instances arise.