Integrating the massive amount of new genomic information into medical practice will require new approaches to knowledge management. This need is particularly acute in surgical pathology where the evaluation of diagnostic tissue sections now requires assessment of the location and staining intensity for a wide range of proteins that are identified through the use of labeled antibodies. The possible combinations of visual features that may be observed threaten to exceed the limits of the human intellect.

Research was undertaken to construct a knowledge-based decision support system for this task. An algorithm written in MATLAB® and employing fuzzy logic was designed to interpret the staining results of eight antibodies that are used to classify lymphoid tumors. Testing with all possible combinations of antibody results (256) was consistent with the expected diagnoses. It appears that this method may be helpful in solving the information overload problem and may significantly improve the accuracy and consistency of disease diagnoses.