Using methods of computational topology, we have developed a new method of analysis of CT-SPECT images of experimentally induced solid tissue tumors in mice. Using concepts from Morse theory, we extract and analyze critical points on each image, and represent each tumor image by labeled contour trees. Leaf and branch lengths are determined either by changes in intensity or volume between critical values. To quantify the differences between treated tumors and control-group tumors we utilize a phylogenetic metric, principal component analysis, and k-means clustering on the collection of binary tree representations of the images. With these methods we are able to distinguish treatment and control groups, and identify structural differences between the tumors in these groups. Algorithmic development was carried out in MATLAB. Mouse images and image extraction software have been provided courtesy of inviCRO. (Received September 16, 2014)