

Computer-extracted tumor segmentation from software: Chicago Dynamic MRI Explorer 2005 Version

This is what TICIA sends people who want to access the segmentation data:

“I understand that I am being granted preliminary access to the TCGA Breast Image Tumor Segmentation data set, and certify that I will not redistribute or use it any publications, abstracts or other work without the expressed permission of the TCGA-BRCA Phenotype Research Group.”

Here is the acknowledgement of the group's data in a publication:

“The authors would like to thank the TCGA Breast Phenotype Research Group for providing the computer-extracted tumor segmentation data used in this study. The tumor segmentation data comes from the University of Chicago lab of Maryellen Giger, whose lab members participated in the TCGA Breast Phenotype Research Group. In any presentation, poster, paper, etc, the segmentations should be identified as “Chicago Dynamic MRI Explorer 2005 Version”. We would also like to acknowledge The Cancer Imaging Archive and The Cancer Genome Atlas initiatives for making the imaging and the clinical data used in this study publicly available.”

Each of our tumor segmentation files is a binary file, consisting of the following format:

1. six uint16 values for the inclusive coordinates of the lesion's cuboid , relative to the image:

y_start y_end

x_start x_end

z_start z_end

2. the N int8 on/off voxels (0 or 1) for the above specified cube, where $N = (y_end - y_start + 1) * (x_end - x_start + 1) * (z_end - z_start + 1)$.

A voxel value of 1 denotes that it is part of the lesion, while a value of zero denotes it is not.