README file for the **DATASETS/IMAGES/Mammography\_masses** folder

The single .pgm images in the subfolders show the mass lesions in an almost central position.

**Legend for the mass file names.**

Lesions are malignant if the file name ends with “\_1.pgm”, benign if it ends with “\_2.pgm”, e.g.:

0007p1\_1\_1.pgm contains a malignant mass

0003f1\_1\_1\_2.pgm contains a benign mass

**Folder content.**

- small\_sample/ with 8 mass examples (4 benign and 4 malignant)

- large\_sample/ with 177 mass examples (104 benign and 73 malignant).

The large\_sample/ includes the small\_sample/

The output of the segmentation algorithm are also provided as a reference in:

- small\_sample\_Im\_segmented\_ref/ contains the resampled and the mass mask for each example of the small\_sample/

- large\_sample\_Im\_segmented\_ref/ contains the resampled and the mass mask for each example of the large\_sample/

**Segmented masses.**

The folders

small\_sample\_Im\_segmented\_ref/

large\_sample\_Im\_segmented\_ref/

Contain for each original IMAGE the IMAGE\_resized.pgm and the IMAGE\_mass\_mask.pgm (of the same size of the MAGE\_resized.pgm).

These segmentations have been generated with segmentation code developed in Lecture6 (mass\_segment.m)

General information on the dataset collection can be found in the reference paper: Delogu et al, Characterization of mammographic masses using a gradient-based segmentation algorithm and a neural classifier, Comput Biol Med. 2007 Oct;37(10):1479-9, <https://www.ncbi.nlm.nih.gov/pubmed/17383623>