
breastMass Documentation

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Welcome to the VICTRE breastMass software documentation!

This documentation provides information regarding how to download, install, and use the VICTRE breastMass software which generates breast cancer masses with random sizes and shape properties. These mass models can be inserted into anthropomorphic voxelized whole-breast phantoms generated by the VICTRE software package breastPhantom to create virtual patients.

This software is an independent reimplement of the model described in

Sisternes, L. , Brankov, J. G., Zysk, A. M., Schmidt, R. A., Nishikawa, R. M. and Wernick, M. N. (2015), *A computational model to generate simulated three-dimensional breast masses*. Med. Phys., 42: 1098-1118.



doi:10.1118/1.4905232

This software was developed as part of the Virtual Imaging Clinical Trials for Regulatory Evaluation (VICTRE) project at the U. S. Food and Drug Administration.

The VICTRE tools provide a complete simulated imaging chain for mammography and digital breast tomosynthesis and are available as [open source software](#)

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CHAPTER 1

Overview

This software defines a breast mass in terms of a three dimensional binary mask where 1 represents a voxel inside the mass and 0 represents a voxel outside the mass. Masses are randomly generated, with the main body of the mass defined via a Gaussian random sphere technique. Random branching spicules are grown out from the mass surface. See the paper by de Sisternes, et al. (doi.org/10.1118/1.4905232) for more details on theory of the mass model.

Note: This software was independently developed and may not exactly represent the models represented in the work cited above due to differences in implementation.

The breastMass source code is available [here](#). It is written in C++ and therefore must be compiled for your system before use.

2.1 Operating System

This software has been developed and tested on Debian and Red Hat based Linux distributions. Compilation is via cmake and should be possible on any UNIX-like operationg system (including MacOS) with minimal modification to the build configuration in the provided CMakeLists.txt file, however the following distributions are recommended:

- Ubuntu 16.04
- Centos 7.x

The following build instructions are based on Ubuntu 16.04.

2.2 Compilation

First, install the packages necessary to compile the software (reminder: instructions are specific to Ubuntu, consult your operating system documentation for analagous package names and installation procedures) From a terminal command prompt:

```
> sudo apt-get install cmake vtk6 libvtk6-dev \  
                        libblas-dev liblapack-dev \  
                        libboost-dev libboost-program-options-dev \  
                        libproj-dev
```

Next, clone the git repository:

```
> git clone https://github.com/DIDSR/breastMass
```

From a suitable build directory generate a Makefile using cmake and run make:

```
> cmake <path to repository>
> make
```

where <path to repository> is the directory containing the cloned repository.

Note: When running cmake you may receive an error message related to references to files “/usr/lib/x86_64-linux-gnu/libvtkRenderingPythonTkWidgets.so” and “/usr/bin/vtk”. This is a known Ubuntu VTK bug but since we are not linking to these files, the error can safely be ignored.

2.3 Finish

If the previous steps were successful, the executable breastMass should be present in the build directory. This file can be copied to a convenient location in your path, or the build directory can be added to \$PATH. No additional installation steps are required. Consult the next section which describes how to run the executable.

Running the Software

3.1 Command line options

breastMass is run from the command line and requires that a single command line options be specified:

```
> breastMass -c <configFile>
```

required command line argument

-c configFile a configuration file specifying all mass parameters

optional command line argument

-h print a help message

3.2 Operating Mode

breastMass is run from the command line. A configuration file must be provided as in the following example:

```
> breastCrop -c mass.cfg
```

See subsequent sections of this documentation for the output file formats and configuration file details.

3.3 Sample Configuration Files

The /cfg directory contains several sample configuration files

testMass.cfg A random 20mm diameter mass without spicules generated at 0.1 mm resolution

testSpiculated.cfg A random 20mm diameter mass with spicules generated at 0.1 mm resolution

VICTREMass.cfg The 5mm diameter spiculed mass used in the VICTRE study with specific random number seed (0.05 mm voxel resolution)

breastMass outputs a 3-dimensional voxel volume consisting of binary values (1 for inside mass and 0 for outside mass). Three output files are generated:

mass_XXXXXXXX.vti The voxel volume stored in VTK image format (XML with zlib-compressed data element). This is a file format native to the Visualization Toolkit. See <https://www.vtk.org> for more information. This file can be opened in Paraview, an open-source, multi-platform data analysis and visualization application available for download at <https://www.paraview.org/> The integer *XXXXXXXX* appearing in the filename is the random number seed that was used to generate the phantom.

mass_XXXXXXXX_mmm.raw The voxel volume stored in raw binary format. The integer *XXXXXXXX* appearing in the filename is the random number seed that was used to generate the phantom. The integer *mmm* is the number of voxels in each dimension (all voxel volumes are cubes).

mass_XXXXXXXX.cfg A copy of the configuration file used to generate the mass.

Configuration File Parameters

The configuration file contains all the parameters necessary to generate a breast mass. They are divided into several categories, primarily by tissue type. In the following tables each parameter is given a brief description.

5.1 base parameters

Name	Type	Notes
base.imgRes	float (mm)	voxel size
base.seed	integer	random number seed (chosen randomly if not specified)

5.2 mass parameters

Name	Type	Notes
mass.lMax	integer	maximum spherical harmonic order
mass.alpha	double (mm)	mean mass radius (mm)
mass.meanSigma2	double (mm ²)	mean mass surface irregularity variance
mass.stdSigma2	double (mm ²)	mass surface irregularity standard deviation
mass.powerLaw	double	covariance power law index
mass.meanLF	double	mean number of low freq. modifications
mass.stdLF	double	std. deviation of number of low freq. modifications
mass.meanShape	double	mean LF shape distribution 0=spike, 1=bump
mass.stdShape	double	std. deviation of LF shape 0=spike, 1=bump
mass.meanLFRad	double	mean relative LF radius
mass.stdLFRad	double	std. deviation of LF radius
mass.meanLFLen	double	mean relative LF length
mass.stdLFLen	double	std. deviation of LF length
mass.meanFuzzAlpha	double	mean fuzzy alpha
mass.stdFuzzAlpha	double	std. deviation of fuzzy alpha

5.3 spicule parameters

Name	Type	Notes
spicule.meanInitial	double	mean number of initial segments
spicule.stdInitial	double	std. deviation number of initial segments
spicule.meanNeigh	double	mean max number of neighbor segments
spicule.stdNeigh	double	std. deviation max number of neighbor segments
spicule.meanInitRad	double	mean initial relative radius
spicule.stdInitRad	double	std. deviation initial relative radius
spicule.meanRadDec	double	mean radius decrease
spicule.stdRadDec	double	std. deviation radius decrease
spicule.meanInitLen	double	mean initial relative radius
spicule.stdInitLen	double	std. deviation initial relative radius
spicule.meanLenDec	double	mean length decrease
spicule.stdLenDec	double	std. deviation length decrease
spicule.meanContProb	double	mean continue prob.
spicule.stdContProb	double	std. deviation continue prob.
spicule.meanBranchAng	double	mean asymmetric bifurcation prob.
spicule.stdBranchAng	double	std. deviation asymm bif. prob.