GE Healthcare

GE Essential Simulation Guidelines

Date/Author	Revision Summary
4 April 2013 Milioni De Carvalho, Pablo (GE Healthcare)	Description of CatSim simulation package for GE Essential (Mammography and Tomosynthesis geometry)

NOTES:

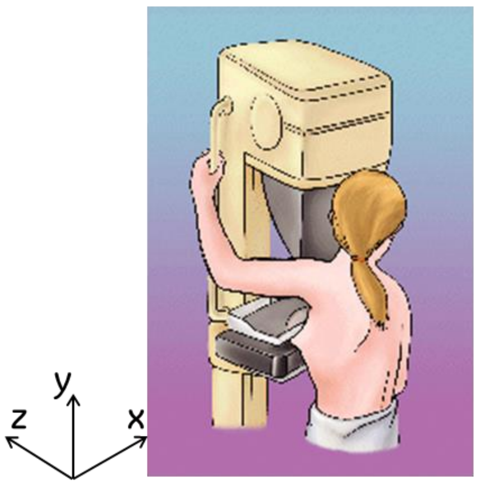
Version 1.0 (April 2013):

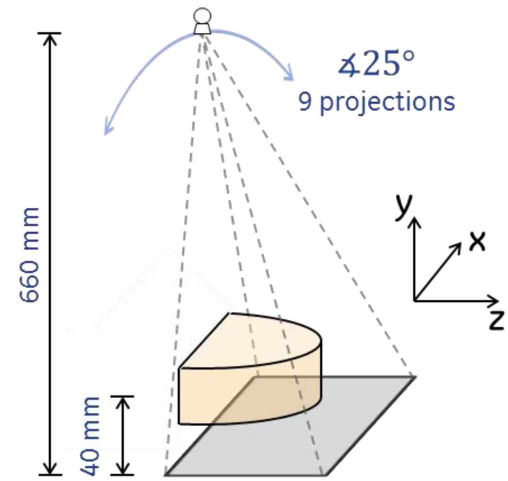
- Based on CatSim version 5.3 (03-Apr-2013)
- Description of the bucky composition is missing. Not sure if needs to be included, and if it can be disclosure
- Not sure about the electronic noise values
- DAS offset needs to be taken from system. It depends on the spectra and calibration
- Spectrum files need to be scaled in order to match real systems. This can be done by measuring the x-ray tube output (mGy/mAs)

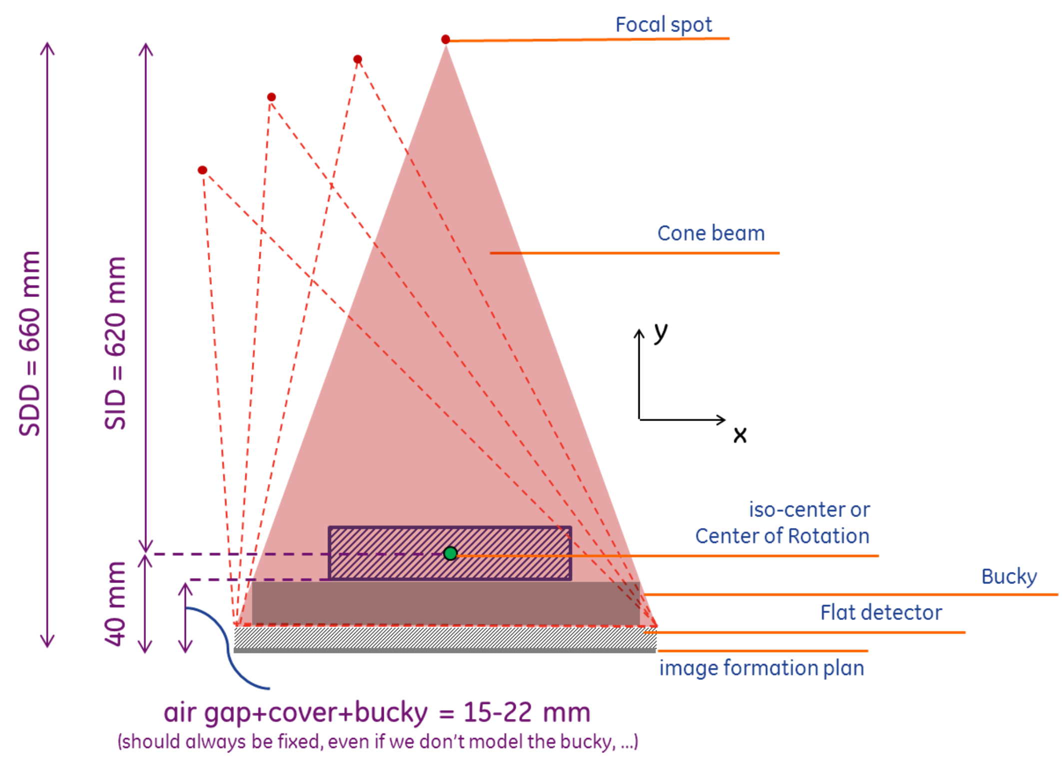
Pablo Milioni (GE Healthcare)

Contents

1. Geometry


y
z
x


∡25°
9 projections
660 mm
40 mm
y
x
z


Focal spot
Cone beam
y
x
SDD = 660 mm
SID = 620 mm
40 mm
iso-center or
Center of Rotation
Bucky
Flat detector
image formation plan
air gap+cover+bucky = 15-22 mm
(should always be fixed, even if we don't model the bucky, ...)

2. Committed folders

MX/materials --> set of materials composing the breast + flat filters + miscellaneous

A good simplification for the breast composition is to mix *breast_adipose*, *breast_glandular* and *skin*. Other files such as breast25, breast50, breast75 are linear combinations of *breast_adipose* and *breast_glandular*, which provide homogeneous mixtures at 25, 50 and 75% fibroglandular-equivalent materials, as defined by Hammerstein *et al.* [1, 2]

MX/mfiles --> Gantry and LUT ramp

Gantry_Tomo.m: it is basically the same as a helical gantry. The difference is that the detector does not rotate around the z-axis. The possibility of either translating the source independently of the detector (*cfg.source_z_offset*, useful to put the source over the chest wall side) or both source and detector at the same time (*cfg.start_z*) in the z-direction was included.

Detection_DAS_Tomo.m: make the truncation from electrons to counts, instead of the default rounding. IMPORTANT!!!! Note that cfg.das_lsb is the slope of the linear part of the so-called LUT ramp. The function itself is very complicated and non-linear close to 14-bit limits (0 counts, and specially 16383 counts). Nevertheless, it will work just fine in the middle range.

MX/phantoms --> phantom samples

MX/samples --> configurations files for Mammography (single projection) and/or Tomosynthesis (multiple projections over limited angular arc). Mammo cfg file can be seen as a particular case of Tomo cfg file, for example by selecting to project only the 0° view. However, Matlab version of CatSim has a default verification blockage that does not allow selecting the views we want to project. It is not true for Freemat version, which runs well.

MX/spectrum --> spectrum files for Molybdenum (Mo) and Rhodium (Rh) targets

- ✓ speXim_**Mo**26.dat corresponds to **Mo** target and **26** kV
- ✓ speXim_**Rh**30.dat corresponds **Rh** target and **30** kV

3. Configuration file

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% GEOMETRY AND DETECTOR (GE Essential) %
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
cfg.sid = 660-40;                                    % Source-to-isocenter distance (mm)
cfg.sdd = 660;                                       % Source-to-detector distance (mm)
cfg.callback_detector = 'DetectorThirdgenCurved';    % Build a curved fs-centered detector
cfg.binning = 1;                % easy way to perform binning (useful for faster simulations)
cfg.cols_per_mod = 1500/cfg.binning; % (full size is 3062) Number of detector columns per module
cfg.rows_per_mod = 1500/cfg.binning; % (full size is 2394) Number of detector rows per module
cfg.col_offset = 0.0;               % Lateral shift of detector (in cols, along positive X-axis)
cfg.row_offset = 0.0;         % Longitudinal shift of detector (in rows, along positive z-axis)
cfg.col_size = 0.100*cfg.binning;                    % Detector column size or x-pitch (mm)
cfg.row_size = 0.100*cfg.binning;                    % Detector row size or z-pitch (mm)
cfg.col_fillfraction = 0.8;        % Fill fraction of detector cells in the column direction
cfg.row_fillfraction = 0.8;        % Fill fraction of detector cells in the row direction
```

The true size of the detector matrix is 3062 (columns – x axis) vs. 2394 (rows – z axis). Since it is quite a big matrix to keep in memory (especially when using full poly-chromatic spectra), a binning option was included, which will keep the geometry and allow faster simulations.

```
%%%%%%%%%%%%%%%%%
% SCAN PROTOCOL %
%%%%%%%%%%%%%%%%%
cfg.callback_gantry = 'Gantry_Tomo';               % Ideal 3rd gen gantry behavior

%%%%%% tomosynthesis protocol %%%%%%
cfg.source_z_offset = -cfg.rows_per_mod*cfg.row_size/2;% translate only the source in z-direction
cfg.start_angle = -12.5;                               % Rotation angle for first view (degrees)
cfg.end_angle = 12.5;                                  % Rotation angle for last view (degrees)
cfg.total_n_views = 9;                       % Set this number explicitly to do partial rotations
cfg.views_per_rotation = (cfg.total_n_views-1)*360/(cfg.end_angle - cfg.start_angle);    % Number of
views in a rotation
cfg.mAs = 200;                                   % mAs per view
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
```

Typical tomosynthesis acquisition involves 9 images with 25° angular span. Specific view angles can be projected using *cfg.start_view* and *cfg.stop_view*. (Note that this manipulation works fine in FreeMat version, but in Matlab the function *Config_Check.m* will not allow free manipulation of the first and last views).

Exposure control is performed using *cfg.mAs*, corresponding to mAs levels of each view.

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% SPECTRUM & BOWTIE & FILTRATION %
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
cfg.callback_spectrum = 'GetSpectrum';          % Spectrum reader callback
cfg.spectrum_filename = 'speXim_Rh30.dat';      % Filename of spectrum to use (includes kVp)
cfg.recompute_spectrum=0;                            % Re-compute spectrum every view ?
cfg.spectrum_scale_mm = 0;
cfg.spectrum_scale_mA = 0;

cfg.callback_bowtie = 'GetBowtie';                   % Bowtie reader callback
cfg.bowtie_filename = 'VCTair.txt';                  % Name of the bowtie file cfg.recompute_bowtie=0;
% Recompute (dynamic) bowtie every view

cfg.callback_filtration = 'GetFilter';               % Filtration calculation callback
cfg.flat_filters = {'rh', sprintf('%f',0.025/cos(cfg.target_angle*pi()/180))};
cfg.recompute_filtration=0;                           % Recompute filtration every view
```

Spectrum files speXim_XXYY.dat files model the anode XX — Molybdenum (Mo) or Rhodium (Rh) — at YY tube voltage (in KV). Note that the x-ray tube output (mGy/mAs) may vary. Therefore, air kerma measurements should be compared to these simulated spectra, and a final scaling included in mAs values to match the data.

There is no bowtie!

Flat filters available in GE Essential are:

- ✓ Mo 0.030 mm
- ✓ Rh 0.025 mm
- ✓ Cu 0.3 mm, always with additional Aluminum (Al) 0.3 mm layer

They must always be divided by the cosine of the target angle (22.5°).

```
%%%%%%%
% DAS %
%%%%%%%
cfg.callback_DAS = 'Detection_DAS_Tomo';                            % DAS callback
cfg.callback_DAS_air = 'Detection_DAS_Tomo';                        % DAS callback
cfg.callback_DAS_offset = 'Detection_DAS_Tomo';                     % DAS callback
cfg.das_offset = 0;                                  % Channel offset
cfg.das_gain = (1000/2.1)*0.15*0.7*0.72/(0.8^2);     % Conversion factor to DAS units (photons-
>electrons)
cfg.das_enoise = 0;                                  % Std of electronic noise
cfg.das_lsb = 4400;               % slope of linear part LUT ramp (550 for tomosynthesis mode)
cfg.das_minvalue = 0;
```

There is a non-zero offset which depends on the system calibration and the used spectra.

DAS gain provides the absorption efficiency (x to light photons + some other things) after scintillator absorption (given by the CsI thickness). Some validation experiments with GE Senographe DS demonstrated good agreement in SI values for Mo/Mo, Mo/Rh and Rh/Rh, which are quasi-monochromatic spectra. For high-energy broad spectra (Cu filtration), other effects such as fluorescence, come into play and are not modeled herein. Therefore, agreement is drastically worse in these cases (*Additional work needs to be done here !!*)

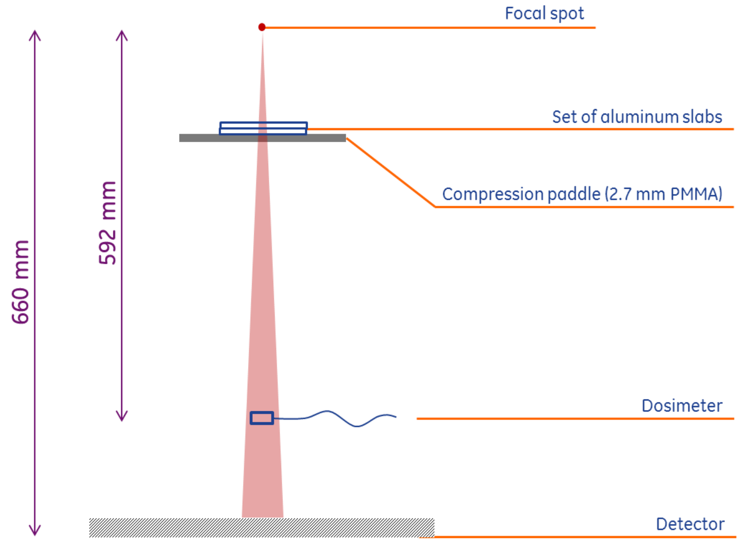
To transform absorbed light photons into counts, a non-linear function is used. The parameter *cfg.das_lsb* denotes the slope of the linear part of this function, and will work well for count values not too close to zero or saturation (16383).

In general, noise is modeled in CatSim as quantum noise (Poisson distribution) and additive electronic noise (Gaussian distribution). Noise values will deviate from experiments since the detector's MTF is not fully modeled. In order to match spatial resolution and noise properties, the scintillator blur can be convolved to the sampling sinc [3].

4. Validation (CatSim 3.22 + FreeMat 3.6)

Air kerma, Tube Output, HVL

- ✓ GE Senographe DS system
- ✓ Follows HVL calibration procedure



Mo/Mo 26 kV 100 mAs

spectrum source: SpeXim	CatSim	Measurement	CatSim error to meas (%)
Air Kerma @ 592 mm (mGy)	8.425	8.156	3.30
Tube Yield @ 592 mm (µGy/mAs)	84.25	81.56	3.30
HVL (mm)	0.339	0.327	3.65
1/4 VL (mm)	0.752	0.748	0.57
1/8 VL (mm)	1.225	1.235	-0.86
1/10 VL (mm)	1.385	1.382	0.24

Mo/Rh 28 kV 100 mAs

spectrum source: SpeXim	CatSim	Measurement	CatSim error to meas (%)
Air Kerma @ 592 mm (mGy)	9.524	8.508	11.95
Tube Yield @ 592 mm (µGy/mAs)	95.24	85.08	11.95
HVL (mm)	0.417	0.415	0.53
1/4 VL (mm)	0.921	0.925	-0.44
1/8 VL (mm)	1.493	1.499	-0.46
1/10 VL (mm)	1.691	1.679	0.72

Rh/Rh 30 kV 100 mAs

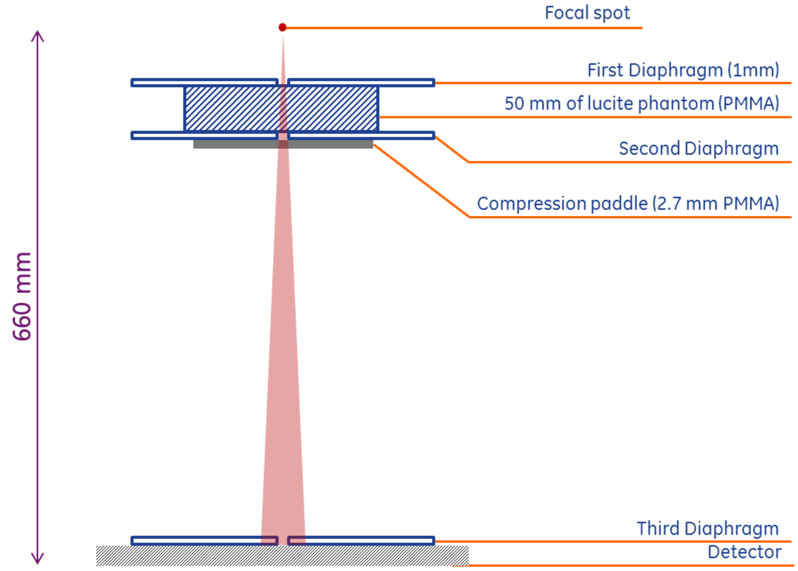
spectrum source: SpeXim	CatSim	Measurement	CatSim error to meas (%)
Air Kerma @ 592 mm (mGy)	10.670	9.899	7.79
Tube Yield @ 592 mm (µGy/mAs)	106.70	98.99	7.79
HVL (mm)	0.446	0.441	1.05
1/4 VL (mm)	1.019	1.020	-0.12
1/8 VL (mm)	1.700	1.642	3.53
1/10 VL (mm)	1.935	1.875	3.19

Mo/Cu 49 kV 100 mAs

spectrum source: SpeXim	CatSim	Measurement	CatSim error to meas (%)
Air Kerma @ 592 mm (mGy)	0.492	0.418	17.66
Tube Yield @ 592 mm (µGy/mAs)	4.92	4.18	17.66
HVL (mm)	3.469	3.415	1.59
1/4 VL (mm)	7.288	6.831	6.68
1/8 VL (mm)			
1/10 VL (mm)			

Signal Intensity

- ✓ Rh/Rh 28kV
- ✓ Experiment geometry built to attenuate scatter
- ✓ GE Senographe DS system

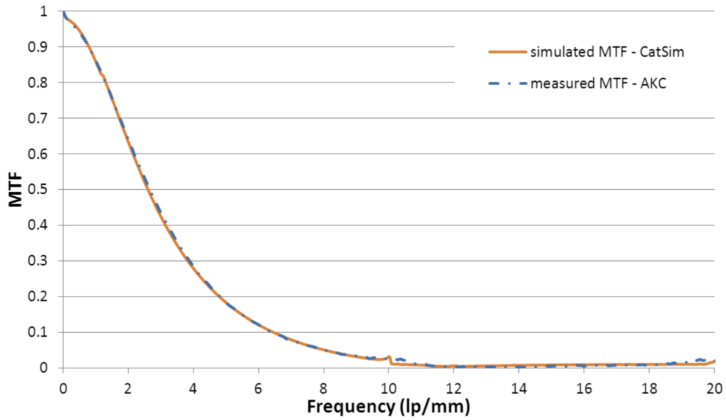


spectrum source: SpeXim	CatSim	Measurement (mean SI)	std dev (σ)	CatSim error to meas (%)	ΔSI/σ
Mo/Mo 28kV 200 mAs	2000	1958	16	2.15	2.55
Mo/Mo 26kV 200 mAs	1264	1261	13	0.23	0.22
Mo/Rh 28kV 200 mAs	2880	2432	20	18.40	22.37
Rh/Rh 30kV 200 mAs	5028	4421	36	13.72	16.68
Rh/Cu 49kV 200 mAs	14405	8047	57	79.01	110.79

Note that the error in SI values can still be decrease, since the simulated spectra and the real spectra have different tube outputs (mGy/mAs), as described in the previous table.

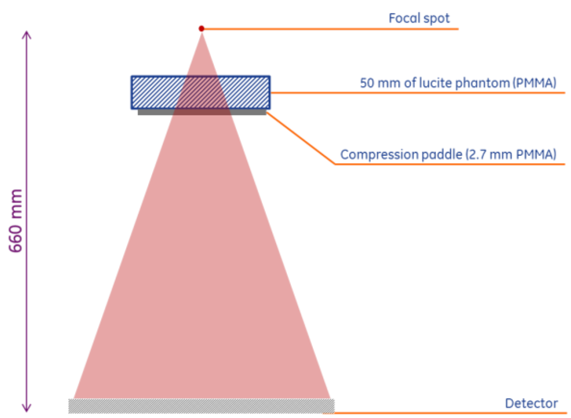
MTF

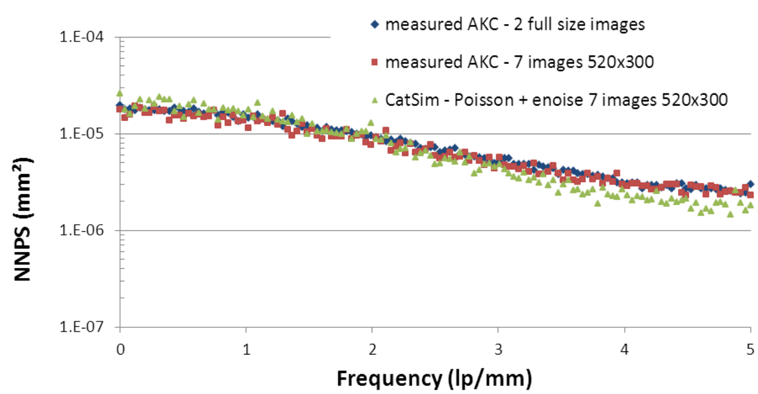
- ✓ Rh/Rh 28kV
- ✓ Simulation included scintillator blur model derived from measurement
- ✓ GE Essential system
- ✓ MTF calculated using tilted slit method



NPS

- ✓ Rh/Rh 30kV
- ✓ Simulation included scintillator blur model derived from measurement
- ✓ GE Essential system, including the MTF





5. References

1. Hammerstein, G.R., Miller, D.W., White, D.R., Masterson, M.E., Woodard, H.Q., Laughlin, J.S.: Absorbed radiation dose in mammography. Radiology. 130, 485–91 (1979).

2. Boone, J.: Glandular Breast Dose for Monoenergetic and High-Energy X-ray Beams: Monte Carlo Assessment. Radiology. 23–37 (1999).

3. Saunders, R.S., Samei, E.: A method for modifying the image quality parameters of digital radiographic images. Medical Physics. 30, 3006 (2003).