# XCAT phantom parameter file

This is an example parameter file for the XCAT phantom, using photon energies corresponding to SPECT.

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mode = 4        # program mode (0 = phantom, 1 = heart lesion, 2 = spherical lesion, 3 = plaque, 4 = vectors, 5 = save anatomical variation) SEE NOTE 0
act_phan_each = 1   # activity_phantom_each_frame (1=save phantom to file, 0=don't save)
atten_phan_each = 0 # attenuation_coeff_phantom_each_frame (1=save phantom to file, 0=don't save)
act_phan_ave = 0    # activity_phantom_average    (1=save , 0=don't save) see NOTE 1
atten_phan_ave = 1  # attenuation_coeff_phantom_average  (1=save, 0=don't save) see NOTE 1

motion_option = 0   # motion_option  (0=beating heart only, 1=respiratory motion only, 2=both motions) see NOTE 2

out_period = 5      # output_period (SECS) (if <= 0, then output_period=time_per_frame*output_frames)
time_per_frame = 0  # time_per_frame (SECS) (**IGNORED unless output_period<=0**)
out_frames = 16     # output_frames (# of output time frames )

hrt_period = 5          # hrt_period (SECS) (length of beating heart cycle; normal = 1s) see NOTE 3
hrt_start_ph_index = 0.0    # hrt_start_phase_index (range=0 to 1; ED=0, ES=0.4) see NOTE 3
heart_base = vmale50_heart.nrb  # basename for heart files (male = vmale50_heart.nrb; female = vfemale50_heart.nrb)
heart_curve_file = heart_curve.txt  # name for file containing time curve for heart

apical_thin = 0.0   # apical_thinning (0 to 1.0 scale, 0.0 = not present, 0.5 = halfway present, 1.0 = completely thin)
uniform_heart = 0   # sets the thickness of the LV (0 = default, nonuniform wall thickness; 1 = uniform wall thickness for LV)

hrt_v1 = 0.0        # sets the LV end-diastolic volume (0 = do not change); see NOTE 3A
hrt_v2 = 0.0        # sets the LV end-systolic volume (0 = do not change); see NOTE 3A
hrt_v3 = 0.0        # sets the LV volume at the beginning of the quiet phase (0 = do not change); see NOTE 3A
hrt_v4 = 0.0        # sets the LV volume at the end of the quiet phase (0 = do not change); see NOTE 3A
hrt_v5 = 0.0        # sets the LV volume during reduced filling, before end-diastole (0 = do not change); see NOTE 3A

hrt_t1 = 0.5        # sets the duration from end-diastole to end-systole, hrt_v1 to hrt_v2 (default = 0.5s); see  NOTE 3A
hrt_t2 = 0.192      # sets the duration from end-systole to beginning of quiet phase, hrt_v2 to hrt_v3 (default = 0.192s); see NOTE 3A
hrt_t3 = 0.115      # sets the duration of quiet phase, hrt_v3 to hrt_v4 (default = 0.115s); see NOTE 3A
hrt_t4 = 0.193      # sets the duration from end of quiet phase to reduced filling, hrt_v4 to hrt_v5 (default = 0.193s); see NOTE 3A

resp_period = 5                 # resp_period (SECS) (length of respiratory cycle; normal breathing = 5s) see NOTE 3
resp_start_ph_index = 0.0   # resp_start_phase_index (range=0 to 1, full exhale= 0.0, full inhale=0.4) see NOTE 3
max_diaphragm_motion = 2.0  # max_diaphragm_motion  (extent in cm's of diaphragm motion; normal breathing = 2 cm ) see NOTE 4
max_AP_exp = 0.5        # max_AP_expansion  (extent in cm's of the AP expansion of the chest; normal breathing =  1.2 cm) see NOTE 4
dia_filename = diaphragm_curve.dat  #name of curve defining diaphragm motion during respiration
ap_filename = ap_curve.dat          #name of curve defining chest anterior-posterior motion during respiration

hrt_motion_x = 0.0      #hrt_motion_x (extent in cm's of the heart's lateral motion during breathing; default = 0.0 cm)
hrt_motion_y = 0.5      #hrt_motion_y (extent in cm's of the heart's AP motion during breathing; default = 1.2 cm)
hrt_motion_z = 2.0      #hrt_motion_z (extent in cm's of the heart's up/down motion during breathing; default = 2.0 cm)

hrt_motion_rot_xz = 0.0     #hrt_motion_rot_xz (extent in degrees of the heart's xz rotation during breathing; default = 0.0 ) SEE NOTE 4 and NOTE 8
hrt_motion_rot_yx = 0.0     #hrt_motion_rot_yx (extent in degrees of the heart's yx rotation during breathing; default = 0.0 ) SEE NOTE 4 and NOTE 8
hrt_motion_rot_zy = 0.0     #hrt_motion_rot_zy (extent in degrees of the heart's zy rotation during breathing; default = 0.0 ) SEE NOTE 4 and NOTE 8

vessel_flag = 0         # vessel_flag (1 = include arteries and veins, 0 = do not include)
coronary_art_flag = 0           # coronary artery flag (1 = include coronary arteries, 0 = do not include)
coronary_vein_flag = 0           # coronary vein flag (1 = include coroanry veins, 0 = do not include)
papillary_flag = 0      # papillary_flag (1 = include papillary muscles in heart, 0 = do not include)
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arms_flag = 1       # arms_flag (0 = no arms, 1 = arms at the side)
gender = 1      # male or female phantom (0 = male, 1 = female), be sure to adjust below accordingly
organ_file = vfemale50.nrb  # name of organ file that defines all organs (male = vmale50.nrb, female - vfemale50
    ↪ .nrb)

phantom_long_axis_scale = 1.0       # phantom_long_axis_scale (scales phantom laterally - scales everything but
    ↪ the heart) SEE NOTE 5
phantom_short_axis_scale = 1.0      # phantom_short_axis_scale (scales phantom AP - scales everything but the
    ↪ heart) SEE NOTE 5
phantom_height_scale = 1.0      # phantom_height_scale (scales phantom height - scales everything but the heart)
    ↪  SEE NOTE 5

head_cir_scale = 1.0            # head_circumference_scale (scales head radially - scales everything in head)
    ↪ SEE NOTE 5
head_height_scale = 1.0                 # head_height_scale (scales head height - scales everything in head) SEE
    ↪  NOTE 5
head_skin_cir_scale = 1.0       # head_skin_circumference_scale (scales head radially - scales only outer skin)
    ↪ SEE NOTE 5

torso_long_axis_scale = 1.0     # torso_long_axis_scale (sets torso, chest and abdomen, transverse axis - scales
    ↪  everything but the heart) SEE NOTE 5
torso_short_axis_scale = 1.0        # torso_short_axis_scale (sets torso, chest and abdomen, AP axis - scales
    ↪ everything but the heart) SEE NOTE 5

chest_skin_long_axis_scale = 1.0        # chest_skin_long_axis_scale (sets chest transverse axis - scales only
    ↪ body outline) SEE NOTE 5
chest_skin_short_axis_scale = 1.0       # chest_skin_short_axis_scale (sets chest AP axis - scales only body
    ↪ outline) SEE NOTE 5

abdomen_skin_long_axis_scale = 1.0      # abdomen_skin_long_axis_scale (sets abdomen transverse axis - scales
    ↪ only body outline) SEE NOTE 5
abdomen_skin_short_axis_scale = 1.0     # abdomen_skin_short_axis_scale (sets abdomen AP axis - scales only body
    ↪  outline) SEE NOTE 5

pelvis_skin_long_axis_scale = 1.0       # pelvis_skin_long_axis_scale (sets pelvis transverse axis - scales only
    ↪  body outline) SEE NOTE 5
pelvis_skin_short_axis_scale = 1.0      # pelvis_skin_short_axis_scale (sets pelvis AP axis - scales only body
    ↪ outline) SEE NOTE 5

arms_cir_scale = 1.0            # arms_circumference_scale (scales arms radially - scales everything in arms)
    ↪ SEE NOTE 5
arms_length_scale = 1.0         # arms_length_scale (scales arms length - scales everything in arms) SEE NOTE 5
arms_skin_cir_scale = 1.0       # arms_skin_circumference_scale (scales arms radially - scales only outer skin)
    ↪ SEE NOTE 5

legs_cir_scale = 1.0            # legs_circumference_scale (scales legs radially - scales everything in legs)
    ↪ SEE NOTE 5
legs_length_scale = 1.0                 # legs_length_scale (scales legs length - scales everything in legs) SEE
    ↪  NOTE 5
legs_skin_cir_scale = 1.0       # legs_skin_circumference_scale (scales legs radially - scales only outer skin)
    ↪ SEE NOTE 5

bones_scale = 1.0   # bones_scale (scales all bones in 2D about their centerlines, makes each bone thicker)  SEE
    ↪  NOTE 5

head_torso_muscle_scale = 1.0   # head_torso_muscle_scale (compresses/expands the muscles radially)  SEE NOTE 5
arms_muscle_cir_scale = 1.0 # arms_muscle_cir_scale (compresses/expands the muscles radially)  SEE NOTE 5
legs_muscle_cir_scale = 1.0 # legs_muscle_cir_scale (compresses/expands the muscles radially)  SEE NOTE 5

hrt_scale = 1.0     # hrt_scale  (scales heart in 3D)

breast_type = 1     # breast_type (0=supine, 1=prone)
which_breast = 1    # which_breast (0 = none, 1 = both, 2 = right only, 3=left only )

rbreast_long_axis_scale = 1.0   # right breast_long_axis (sets the breasts lateral dimension) SEE NOTE 5
rbreast_short_axis_scale = 1.0  # right breast_short_axis (sets the breasts antero-posterior dimension) SEE NOTE
    ↪  5
rbreast_height_scale = 1.0  # right breast_height (sets the breasts height)  SEE NOTE 5

vol_rbreast = 0.0               # sets rbreast volume by scaling in 3D, will over-rule above scalings

rbr_theta = 10.0        # theta angle of the right breast (angle the breast is tilted transversely (sideways)
    ↪ from the center of the chest SEE NOTE 5
rbr_phi = 0.0       # phi angle of the right breast (angle the breast is tilted up (+)  or down (-) SEE NOTE 5
r_br_tx = 0.0       # x translation for right breast
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r_br_ty = 0.0       # y translation for right breast
r_br_tz = 0.0       # z translation for right breast

lbreast_long_axis_scale = 1.0   # left breast_long_axis (sets the breasts lateral dimension) SEE NOTE 5
lbreast_short_axis_scale = 1.0  # left breast_short_axis (sets the breasts antero-posterior dimension) SEE NOTE
    ↪ 5
lbreast_height_scale = 1.0      # left breast_height (sets the breasts height)  SEE NOTE 5

vol_lbreast = 0.0       # sets lbreast volume by scaling in 3D, will over-rule above scalings

lbr_theta = 10.0                # theta angle of the left breast (angle the breast is tilted transversely (
    ↪ sideways) from the center of the chest SEE NOTE 5
lbr_phi = 0.0           # phi angle of the left breast (angle the breast is tilted up (+)  or down (-) SEE NOTE
    ↪ 5
l_br_tx = 0.0       # x translation for left breast
l_br_ty = 0.0       # y translation for left breast
l_br_tz = 0.0       # z translation for left breast

rdiaph_liv_scale = 1.0      # height of right_diaphragm/liver dome (0 = flat, 1 = original height, > 1 raises
    ↪ the diaphragm)  SEE NOTE 5
ldiaph_scale = 1.0      # height of left diaphragm dome (0 = flat, 1 = original height, > raises the diaphragm)
    ↪  SEE NOTE 5

frac_H2O = 0.5  # fraction (by weight) of water in wet bone and wet spine (used to calc. atten coeff)

marrow_flag = 1         # render marrow (0 = no, 1 = yes)
thickness_sternum = 0.4     # thickness sternum  (cm)
thickness_scapula = 0.35    # thickness scapulas (cm)
thickness_ribs = 0.3        # thickness ribs     (cm)
thickness_backbone = 0.4    # thickness backbone (cm)
thickness_pelvis = 0.4      # thickness pelvis (cm)
thickness_collar = 0.35     # thickness collarbones (cm)
thickness_humerus = 0.45    # thickness humerus (cm)
thickness_radius = 0.45     # thickness radius (cm)
thickness_ulna = 0.45       # thickness ulna (cm)
thickness_hand = 0.35       # thickness hand bones (cm)
thickness_femur = 0.5       # thickness femur (cm)
thickness_tibia = 0.6       # thickness tibia (cm)
thickness_fibula = 0.5      # thickness fibula (cm)
thickness_patella = 0.3     # thickness patella (cm)
thickness_foot = 0.4        # thickness foot bones (cm)

thickness_si = 0.6  # thickness of small intestine wall (cm)
thickness_li = 0.6  # thickness of large intestine wall (cm)
si_air_flag = 1     # 0 = do not include air and 1 = include air in small intestine
li_air_flag = 5     # location of air in the large intestine see NOTE 6
thickness_esoph = 0.3   # thickness of the esophagus wall (cm)

vol_prostate = 0.0  # set the volume of the prostate; (0 = do not change)
vol_testes = 0.0    # set the volume of the testes; (0 = do not change)
vol_liver = 0.0     # set the volume of the liver; (0 = do not change)
vol_stomach = 0.0   # set the volume of the stomach; (0 = do not change)
vol_pancreas = 0.0  # set the volume of the pancreas; (0 = do not change)
vol_spleen = 0.0    # set the volume of the spleen; (0 = do not change)
vol_gall_bladder = 0.0  # set the volume of the gall_bladder; (0 = do not change)
vol_rkidney = 0.0   # set the volume of the right kidney; (0 = do not change)
vol_lkidney = 0.0   # set the volume of the left kidney; (0 = do not change)
vol_radrenal = 0.0  # set the volume of the right adrenal; (0 = do not change)
vol_ladrenal = 0.0  # set the volume of the left adrenal; (0 = do not change)
vol_small_intest = 0.0  # set the volume of the small intestine; (0 = do not change)
vol_large_intest = 0.0  # set the volume of the large intestine; (0 = do not change)
vol_bladder = 0.0   # set the volume of the bladder; (0 = do not change)
vol_thyroid = 0.0   # set the volume of the thyroid; (0 = do not change)
vol_thymus = 0.0    # set the volume of the thymus; (0 = do not change)
vol_salivary = 0.0  # set the volume of the salivary glands; (0 = do not change)
vol_pituitary = 0.0 # set the volume of the pituitary gland; (0 = do not change)
vol_eyes = 0.0      # set the volume of the eyes; (0 = do not change)
vol_rovary = 0.0    # set the volume of the right ovary; (0 = do not change)
vol_lovary = 0.0    # set the volume of the left ovary; (0 = do not change)
vol_ftubes = 0.0    # set the volume of the fallopian tubes; (0 = do not change)
vol_uterus = 0.0    # set the volume of the uterus; (0 = do not change)
vol_vagina = 0.0    # set the volume of the vagina; (0 = do not change)
vol_larynx = 0.0    # set the volume of the larynx/pharynx; (0 = do not change)
vol_trachea = 0.0   # set the volume of the trachea (total); (0 = do not change)
vol_esoph = 0.0     # set the volume of the esophagus (total); (0 = do not change)
vol_epidy = 0.0     # set the volume of the epididymus; (0 = do not change)
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pixel_width = 0.3125    # pixel width (cm);  see NOTE 7
slice_width = 0.3125    # slice width (cm);
array_size = 128    # array size
subvoxel_index = 2  # subvoxel_index (=1,2,3,4 -> 1,8,27,64 subvoxels/voxel, respectively)
startslice = 360        # start_slice;
endslice = 459      # end_slice;

d_ZY_rotation = 0   # change in zy_rotation (beta) in deg. (0); see NOTE 8
d_XZ_rotation = -63 # change in xz_rotation ( phi) in deg. (0);
d_YX_rotation = -45 # change in yx_rotation ( psi) in deg. (0);
X_tr = 0.0  # x translation in mm ;
Y_tr = 0.0  # y translation in mm ;
Z_tr = 0.0  # z translation in mm ;

activity_unit = 0   # activity units (1= scale by voxel volume; 0= don't scale) NOTE 11

myoLV_act = 75      # hrt_myoLV_act - activity in left ventricle myocardium
myoRV_act = 75      # hrt_myoRV_act - activity in right ventricle myocardium
myoLA_act = 75      # hrt_myoLA_act - activity in left atrium myocardium
myoRA_act = 75      # hrt_myoRA_act - activity in right atrium myocardium
bldplLV_act = 2     # hrt_bldplLV_act - activity in left ventricle chamber (blood pool)
bldplRV_act = 2     # hrt_bldplRV_act - activity in right ventricle chamber (blood pool)
bldplLA_act = 2     # hrt_bldplLA_act - activity in left atria chamber (blood pool)
bldplRA_act = 2     # hrt_bldplRA_act - activity in right atria chamber (blood pool)
body_activity = 2       # body_activity (background activity) ;
muscle_activity = 2     # muscle activity;
brain_activity = 2      # brain activity;
sinus_activity = 2      # sinus activity;
liver_activity = 2.0        # liver_activity;
gall_bladder_activity = 2   # gall_bladder_activity;
r_lung_activity = 4     # right_lung_activity;
l_lung_activity = 4             # left_lung_activity;
esophagus_activity = 50     # esophagus_activity;
laryngopharynx_activity = 2 # laryngopharynx_activity
st_wall_activity = 2        # st_wall_activity;  (stomach wall)
st_cnts_activity = 2        # st_cnts_activity;   (stomach contents)
pancreas_activity = 2       # pancreas_activity;
r_kidney_cortex_activity = 75   # right_kidney_cortex_activity;
r_kidney_medulla_activity = 75  # right_kidney_medulla_activity;
l_kidney_cortex_activity = 75   # left_kidney_cortex_activity;
l_kidney_medulla_activity = 75  # left_kidney_medulla_activity;
adrenal_activity = 2        # adrenal_activity;
r_renal_pelvis_activity = 2 # right_renal_pelvis_activity;
l_renal_pelvis_activity = 2     # left_renal_pelvis_activity;
spleen_activity = 75        # spleen_activity;
rib_activity = 5        # rib_activity;
cortical_bone_activity = 5  # cortical_bone_activity;
spine_activity = 6      # spine_activity;
spinal_cord_activity = 2    # spinal_cord_activity;
bone_marrow_activity = 2    # bone_marrow_activity;
art_activity = 2        # artery_activity;
vein_activity = 2       # vein_activity;
bladder_activity = 2        # bladder_activity;
prostate_activity = 30      # prostate_activity;
asc_li_activity = 2     # ascending_large_intest_activity;
trans_li_activity = 2       # transcending_large_intest_activity;
desc_li_activity = 2        # desc_large_intest_activity;
sm_intest_activity = 2      # small_intest_activity;
rectum_activity = 2     # rectum_activity;
sem_activity = 2        # sem_vess_activity;
vas_def_activity = 2        # vas_def_activity;
test_activity = 2       # testicular_activity;
epididymus_activity = 2     # epididymus_activity;
ejac_duct_activity = 2      # ejaculatory_duct_activity;
pericardium_activity = 2        # pericardium activity;
cartilage_activity = 2      # cartilage activity;
intest_air_activity = 2.0   # activity of intestine contents (air);
ureter_activity = 2.0       # ureter activity;
urethra_activity = 2.0      # urethra activity;
lymph_activity = 2.0        # lymph normal activity;
lymph_abnormal_activity = 2.0   # lymph abnormal activity;
airway_activity = 2.0       # airway tree activity
uterus_activity = 60        # uterus_activity;
vagina_activity = 50        # vagina_activity;
right_ovary_activity = 40   # right_ovary_activity;
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left_ovary_activity = 30    # left_ovary_activity;
fallopian_tubes_activity = 20   # fallopian tubes_activity;
parathyroid_activity = 2    # parathyroid_activity;
thyroid_activity = 2        # thyroid_activity;
thymus_activity = 2     # thymus_activity;
salivary_activity = 2       # salivary_activity;
pituitary_activity = 2      # pituitary_activity;
eye_activity = 2        # eye_activity;
lens_activity = 2       # eye_lens_activity;
lesn_activity = 2       # activity for heart lesion, plaque, or spherical lesion

energy  = 140   # radionuclide energy in keV (range 1 - 40MeV, increments of 0.5 keV) ; for attn. map only

#---------------------Regional Heart Motion Defect---------------------------
motion_defect_flag = 0  # (0 = do not include, 1 = include) regional motion abnormality in the LV as defined by
    ↪ heart lesion parameters see NOTE 9
#---------------------------------------------------------------------------

#----------------------Heart lesion parameters------------------------------SEE NOTE 9
ThetaCenter = 0.0       # theta center in deg. (between 0 and 360)
ThetaWidth = 100.0      # theta width in deg., total width (between 0 and 360 deg.)
XCenterIndex = .5       # x center (0.0=base, 1.0=apex, other fractions=distances in between)
XWidthIndex = 60        # x width, total in mm's
Wall_fract = 1.0        # wall_fract, fraction of the outer wall transgressed by the lesion
motion_scale = 0.0      # scales the motion of the defect region (1 = normal motion, < 1 = reduced motion),
    ↪ altered motion blends with normal

border_zone_long = 10       # longitudinal width (in terms of number of control points) of transition between
    ↪ abnormal and normal motion
border_zone_radial = 5      # radial width (in terms of number of control points) of transition between abnormal
    ↪  and normal motion
#--------------------------------------------------------------------------

#----------------------Spherical lesion parameters--------------------------SEE NOTE 10
x_location = 103        # x coordinate (pixels) to place lesion
y_location = 129        # y coordinate (pixels) to place lesion
z_location = 63         # z coordinate (pixels) to place lesion
lesn_diameter = 5.0     # Diameter of lesion (mm)
tumor_motion_flag = 1       # Sets tumor motion (0 = default motion based on lungs, 1 = motion defined by user
    ↪ curve below)
tumor_motion_filename = tumor_curve.dat     # Name of user defined motion curve for tumor
#--------------------------------------------------------------------------

#----------------------Heart plaque parameters------------------------------SEE NOTE 11
p_center_v = 0.2        # plaque center along the length of the artery (between 0 and 1)
p_center_u = 0.5        # plaque center along the circumference of the artery (between 0 and 1)
p_height = 1.0          # plaque thickness in mm.
p_width = 2.0           # plaque width in mm.
p_length = 5.0          # plaque length in mm.
p_id = aorta            # vessel ID to place the plaque in
#--------------------------------------------------------------------------

#----------------------Vector parameters------------------------------------SEE NOTE 12
vec_factor = 2      # higher number will increase the precision of the vector output
#--------------------------------------------------------------------------

#--------------------------------------------------------------------------
#--------------------------------------------------------------------------
#This is a general parameter file for the DYNAMIC XCAT phantom, version 2.0
#--------------------------------------------------------------------------
#THE PARAMETERS CAN BE IN ANY ORDER. THE PROGRAM WILL SORT THEM.
#--------------------------------------------------------------------------
#                             NOTES:
#--------------------------------------------------------------------------
#NOTE 0: The phantom program can be run in different modes as follows.
#  Mode 0: standard phantom generation mode that will generate phantoms of the
#          body.
#  Mode 1: heart lesion generator that will create phantoms of only the user
#          defined heart lesion. Subtract these phantoms from those of mode 0
#          to place the defect in the body.
#  Mode 2: spherical lesion generator that will create phantoms of only the
#          user defined lesion. Add these phantoms to those of mode 0 to place
#          the lesions in the body.
#  Mode 3: cardiac plaque generator that will create phantoms of only the
#          user defined plaque. Add these phantoms to those of mode 0 to place
#          the plaques in the body.
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#  Mode 4: vector generator that will output motion vectors as determined from
#          the phantom surfaces. The vectors will be output as text files.
#  Mode 5: anatomy generator will save the phantom produced from the user-defined anatomy
#          parameters. The phantom is saved as two files, the organ file and the heart_base
#          file. The names of these files can then be specified in the parfile for later runs
#          with the program not having to take the time to generate the anatomy again. In using
#      a saved anatomy, be sure to set all scalings back to 1; otherwise, the anatomy will be
#          scaled again.
#
#NOTE 1: The average phantom is the average ONLY OF THOSE FRAMES GENERATED. That is,
#  if you specify that only 2 frames be generated, then the average phantom is
#  just the average of those 2 frames.
#  ****************************************************************************
#  ** FOR A GOOD AVERAGE, generate at least 8-16 frames per 1 complete heart
#  ** cycle and/or per 1 complete respiratory cycle.
#  ****************************************************************************
#
#NOTE 2: Heart motion refers to heart BEATING or contraction, while resp.
#  motion refers to organ motion due to breathing. Note that the entire heart is
#  translated or rotated due to resp. motion, even if it is not contracting.
#  ** IF motion_option=1 , THE HEART WILL MOVE (TRANSLATE) BUT NOT BEAT.****
#
#NOTE 3:   Users sets the length and starting phase of both the heart
#          and respiratory cycles. NORMAL values for length of heart beat and
#          respiratory are cycles are 1 sec. and 5 secs., respectively,
#          BUT THESE CAN VARY AMONG PATIENTS and will increase if the patient
#          is under stress.
#
#          An index value between 0 and 1 is used the specify the starting phase
#          of the heart or resp cycles. IF NO MOTION IS SPECIFIED THEN THE STARTING
#          PHASE IS USED AS THE SINGLE PHASE AT WHICH THE PHANTOM IS GENERATED.
#          (see documentation for more details).
#
#NOTE 3A:  These parameters control the LV volume curve of the heart. The user can specify the LV
#      volume at 5 points in the cardiac cycle. Check the logfile to see what the default volumes
#          are.  The end-diastolic volume can only be reduced. The way to increase it would be to change
#          the overall heart scale.  The end-systolic volume can be increased or reduced. The other volumes
#          need to have values between the end-diastolic and end-systolic volumes.  The time durations for the
#          different portions of the cardiac cycle must add up to a total of 1.
#
#          Changing these parameters will alter the heart_curve.  The altered curve and heart files can be
    ↪ output using
#          mode = 5.
#
#NOTE 4:  These NORMAL values are for normal tidal breathing.
#  ** Modeling a deep inhale may require higher values. **
#
#  The AP_expansion parameter controls the anteroposterior diameter of the ribcage, body,
#  and lungs. The ribs rotate upward to expand the chest cavity by the amount indicated by the
#  AP_expansion parameter. The lungs and body move with the expanding ribs. There is maximum amount
#  by which the AP diameter can expand, due to the size of the ribs (some expansions are impossible
#  geometrically.) If the user specifies too great an expansion, the program will terminate with an
#  error message.
#
#  The diaphragm motion controls the motion of the liver, the left diaphragm, stomach, spleen and
#  all organs downstream from them.
#
#  The heart has its own parameters to control its motion. It can translate left or right (+/- values of
    ↪ hrt_motion_x respectively),
#  to the anterior/posterior (+/- values of hrt_motion_y respectively), or up/down (+/- values of hrt_motion_z
    ↪ respectively)
#  with the diaphragm motion. The heart can also rotate. The x-axis runs from the right side of the body to the
    ↪ left.
#  Changing the x-rot will tilt the heart up(+ values)/down (- values).  The y-axis runs from the front of the
    ↪ body to the back.
#  Changing the y-rot will tilt the heart from side to side.  The z-axis runs from the feet to the head.
#  The z-rot will spin the heart right or left.
#
#NOTE 5: The phantom program outputs statistics on these anatomical parameters in the logfile it generates.  The
    ↪  logfile is
#         named with the extension _log.  These statistics can be used to determine the amount of scaling
    ↪ desired. Be aware
#     the phantom scaling parameters scale the entire phantom; therefore, any body, heart or breast scalings
    ↪ will
#         be additional to this base scaling.
#
```

```
#NOTE 6:  Location of air in the large intestine and rectum
#          5 = air visible in the entire large intestine and rectum
#          4 = air visible in ascending, transverse, descending, and sigmoid portions of the large intestine
#          3 = air visible in ascending, transverse, and descending portions of the large intestine
#          2 = air visible in ascending and transverse portions of the large intestine
#          1 = air visible in ascending portion of the large intestine only
#          0 = no air visible (entire large intestine and rectum filled with contents)
#
#
#NOTE 7:
#        - The phantom dimensions do not necessarily have to be cubic. The array_size parameter
#          determines the x and y dimensions of the images.  The number of slices in the z dimension
#          is determined by the start_slice and end_slice parameters.  The total number of slices is
#          end_slice - start_slice + 1.
#
#NOTE 8:
#        - rotation parameters determine
#          initial orientation of beating (dynamic) heart LV long axis
#        - d_zy_rotation : +y-axis rotates toward +z-axis (about x-axis) by beta
#          d_xz_rotation : +z-axis rotates toward +x-axis (about y-axis) by phi
#          d_yx_rotation : +x-axis rotates toward +y-axis (about z-axis) by psi
#
#        - Based on patient data, the mean and SD heart orientations are:
#                zy_rot = -110 degrees (no patient data for this rotation)
#                xz_rot = 23 +- 10 deg.
#                yx_rot = -52 +- 11 deg.
#
#    - Phantom will output total angles for the heart orientation in the logfile
#
#NOTE 9: Creates lesion (defect) for the LEFT VENTRICLE ONLY.
#
#--------------------------------
#  theta_center: location of lesion center in circumferential dimension
#
#  theta center =    0.0  => anterior wall
#  theta center =  +90.0  => lateral   "
#  theta center = +180.0  => inferior  "
#  theta center = +270.0  => septal    "
#--------------------------------
#  theta_width : lesion width in circumferential dimension
#
#  TOTAL width of defect in degrees. So for example a width of 90 deg.
#  means that the width is 45 deg. on either side of theta center.
#--------------------------------
#  x center :   lesion center in long-axis dimension
#
#  x center = 0    -> base of LV
#  x center = 1.0  -> apex of LV
#--------------------------------
#  x width:  lesion width in long-axis dimension
#
#  total width. Defect extend half the total width on either side of the
#  x_center.
#
#  NOTE: if the specified width extends beyond the boundaries of the LV
#        then the defect is cut off and the effective width is less than the
#        specified width. So for example...
#
#--------------------------------
#  Wall_fract : fraction of the LV wall that the lesion transgresses
#  Wall_fract = 0.0 => transgresses none of the wall
#  Wall_fract = 0.5 => transgresses the inner half of the wall
#  Wall_fract = 1.0 => trangresses the entire wall
#--------------------------------
#
#
#NOTE 10: Creates a spherical lesion in the XCAT phantom. Depending on where the lesion is placed, it will move
    ↪ with
#         the respiratory motion. Location of the lesion is specified in pixel values. Initial location of the
    ↪ lesion
#         needs to be with respect to end-expiration.
#
#
#
#NOTE 11: Creates a plaque in the coronary vessel tree that will move with the cardiac/respiratory motion
#
```

```
#--------------------------------------------------------------------------
#  plaque_center: location of plaque along the length of the specified artery
#    center = 0    -> base of artery
#    center = 1.0  -> apex of artery
#
#-------------------------------------------
#  plaque_thickness : plaque thickness in mm.
#
#-------------------------------------------
#  plaque_width :   plaque width in mm.
#
#-------------------------------------------
#  plaque_length :  plaque length in mm.
#
#------------------------------------------------------
#  plaque_id  :  vessel to place the plaque in
#
#        aorta
#        rca1
#        rca2
#        lad1
#        lad2
#        lad3
#        lcx
#------------------------------------------------------
#
#
#NOTE12:  Using mode = 4, vectors are output for each voxel of frame 1 to the current frame. The vectors show
    ↪ the motion
#         from the 1st frame to frame N. The vectors are output as text files with the format of
#         output_name_vec_frame1_frameN.txt.
#         The output vectors are a combination of known sampled points from the phantom objects and vectors
    ↪ interpolated
#         from these sampled points.  The known vectors are designated as such in the vector output.  You can
    ↪ increase
#         the number of known points (and accuracy of the vector output) by increasing the parameter vec_factor.
```