2-gVirtualXRay_vs_DRRs

September 21, 2022

```
[1]: from IPython.display import display
     from IPython.display import Image
     import os
     from utils import * # Code shared across more than one notebook
```

```
[2]: output_path = "2-output_data/"

     if not os.path.exists(output_path):
         os.mkdir(output_path)
```

1 gVirtualXray vs DRRs

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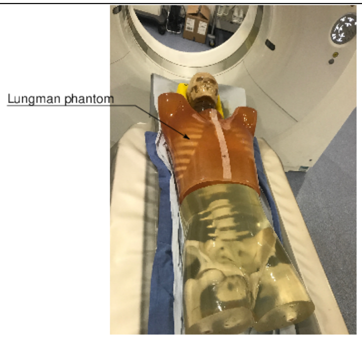
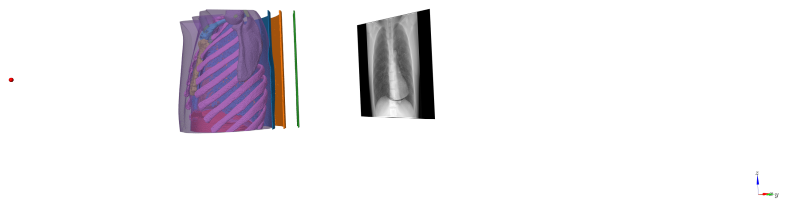
Purpose: In this notebook, we aim to demonstrate that gVirtualXRay is able to generate analytic simulations on GPU comparable to digitally reconstructed radiographs (DRRs) of a real CT scan computed with Plastimatch.

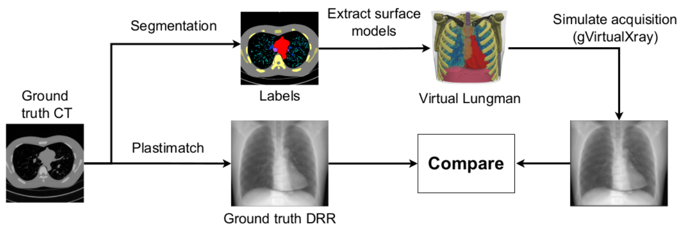
Material and Methods: For this experiment, we attempt to recreate a X-ray projections of the Lungman chest phantom with gVirtualXRay.

1. The CT of a chest phantom has been generated from a real scanner ahead of time.

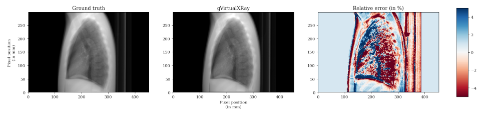
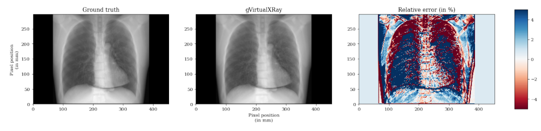
Lungman phantom	3D model of the phantom, source and detector
	

2. Structures in the reference CT have been segmented and labelled.
3. The resultant surfaces from the segmentations form a virtual lungman model.
4. We use gVirtualXRay to simulate X-ray projection on this model and

5. compare the result with Digitally Reconstructed Radiographs (DRRs) of the original CT scan.



Results: Images generated with gVirtualXray are very similar to DRRs computed with Plastimatch, despite the use of homogeneous materials in the simulation. MAPE is low in both cases (2.01% and 2.66%), ZNCC (99.65% and 99.36%) and SSIM (0.98 and 0.93) are high in both cases. It took 442 ms to compute the DRR images on GPU with Plastimatch compiled with CUDA, 29 ms with gVirtualXray. It corresponds to a 15x speedup.

	RL view	AP view
		
MAPE:	2.01%	2.66%
ZNCC:	99.65%	99.36%
SSIM:	0.98	0.92

The calculations were performed on the following platform:

```
[3]: printSystemInfo()
```

```
OS:
        Linux 5.3.18-150300.59.54-default
        x86_64

CPU:
        AMD Ryzen 7 3800XT 8-Core Processor

RAM:
        63 GB
GPU:
        Name: NVIDIA GeForce RTX 2080 Ti
        Drivers: 510.73.08
        Video memory: 11 GB
```

2 Import packages

[4]:
```
%matplotlib inline

import SimpleITK as sitk
import pandas as pd
import numpy as np
import numpy.ma as ma # Masking
from utils import *
from convertRaw import *
from gvxrPython3 import gvxr
from gvxrPython3 import json2gvxr
from gvxrPython3.utils import visualise

import matplotlib
import matplotlib.pyplot as plt

font = {'family' : 'serif'#,
        #'weight' : 'bold',
         # 'size'   : 22
       }
matplotlib.rc('font', **font)
# matplotlib.rc('text', usetex=True)

import plotly.express as px

from tifffile import imread, imwrite # Load/Write TIFF file

from sitk2vtk import *
from sklearn.metrics import mean_absolute_percentage_error as mape
from skimage.metrics import structural_similarity as ssim
import skimage

#import scipy
import os
import math
import zipfile
import datetime

import imageio

import random
import base64
from time import sleep
```

```
SimpleGVXR 2.0.2 (2022-09-14T19:31:53) [Compiler: GNU g++] on Linux
gVirtualXRay core library (gvxr) 2.0.2 (2022-09-14T19:31:52) [Compiler: GNU g++]
on Linux
```

[5]:
```
SAVE_DATA = True
GENERATE_NEW_DATA_ALWAYS = False
DO_K3D_PLOT = True
```

[6]:
```
DO_ARTEFACT_FILTERING_ON_GPU = True
DO_ARTEFACT_FILTERING_ON_CPU = False
number_of_projections = 1000
angular_step = 180 / number_of_projections
```

3 Configure gVirtualXRay environment

3.1 Create an OpenGL context and window

[7]:
```
json2gvxr.initGVXR("notebook-2.json", "OPENGL")
```

```
Create an OpenGL context: 512x512

Tue Sep 20 21:33:53 2022 ---- Create window (ID: -1)
Tue Sep 20 21:33:53 2022 ---- Initialise GLFW
Tue Sep 20 21:33:53 2022 ---- Create an OpenGL window with a 3.2 context.
Tue Sep 20 21:33:53 2022 ---- Make the window's context current
Tue Sep 20 21:33:53 2022 ---- Initialise GLEW
Tue Sep 20 21:33:53 2022 ---- OpenGL vendor: NVIDIA Corporation
Tue Sep 20 21:33:53 2022 ---- OpenGL renderer: NVIDIA GeForce RTX 2080
Ti/PCIe/SSE2
Tue Sep 20 21:33:53 2022 ---- OpenGL version: 3.2.0 NVIDIA 510.73.08
Tue Sep 20 21:33:53 2022 ---- Use OpenGL 4.5.
Tue Sep 20 21:33:53 2022 ---- Initialise the X-ray renderer if needed and if
possible
```

3.2 Create a parallel photon beam

[8]:
```
json2gvxr.initSourceGeometry()
```

```
Set up the beam
        Source position: [0, -500, 0, 'mm']
        Source shape: ParallelBeam
```

3.3 Create a monochromatic spectrum

[9]:
```
json2gvxr.initSpectrum();
```

Create a detector array.

[10]:
```
json2gvxr.initDetector()
```

```
Set up the detector
        Detector position: [0, 500, 0, 'mm']
        Detector up vector: [0, 0, 1]
        Detector number of pixels: [725, 426]
        Pixel spacing: [0.625, 0.7, 'mm']
```

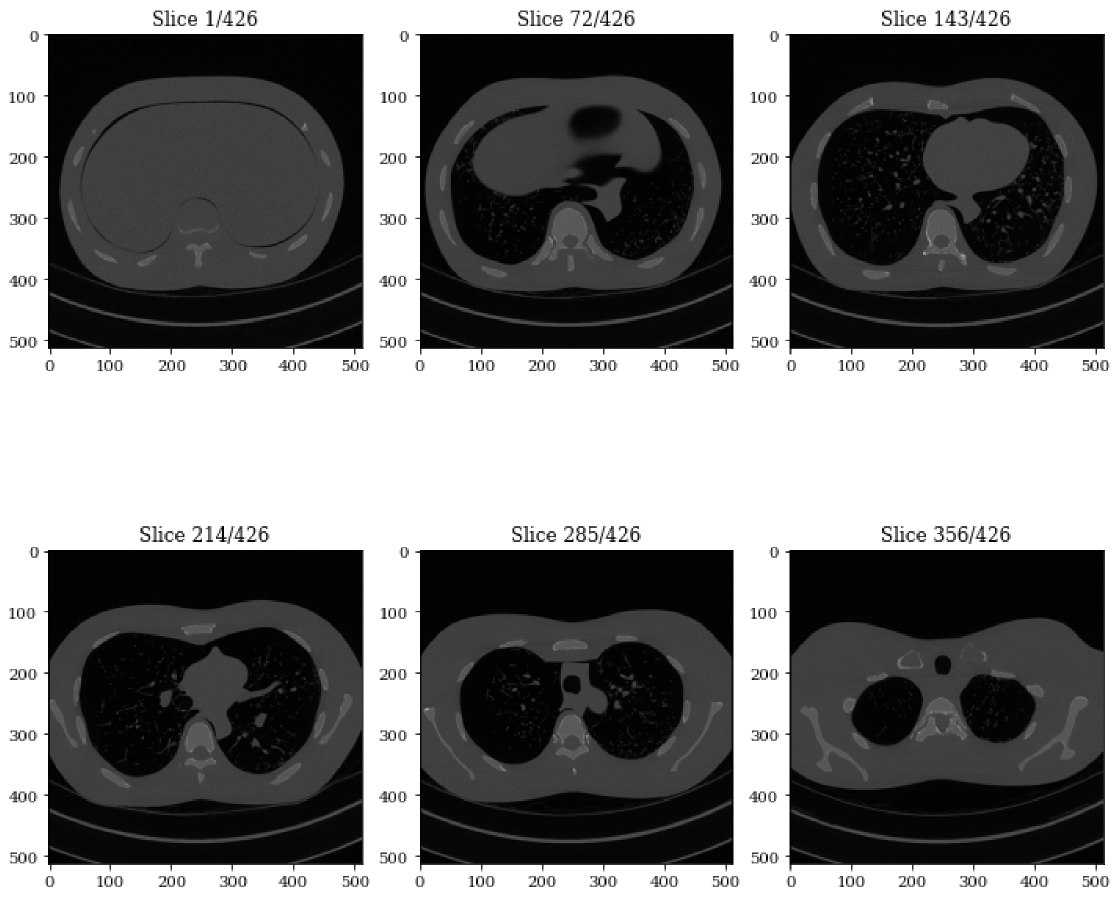
```
Tue Sep 20 21:33:53 2022 ---- Initialise the renderer
```

[11]:
```
nb_pixels = gvxr.getDetectorNumberOfPixels()
detector_size = gvxr.getDetectorSize("mm")
pixel_width = detector_size[0] / nb_pixels[0]
pixel_height = detector_size[1] / nb_pixels[1]
```

4 Load the CT scan

[12]:
```
# Read the reference CT
sitk_reader = sitk.ImageFileReader();
sitk_reader.SetImageIO("MetaImageIO");
sitk_reader.SetFileName("lungman_data/lungman.mha")
raw_ground_truth = sitk_reader.Execute()

# Make sure each volume has floating point precision
real_CT_in_HU = sitk.GetArrayFromImage(raw_ground_truth).astype(np.single)
del sitk_reader
del raw_ground_truth
```

[13]:
```
ncols = 3
nrows = 2

step = int(real_CT_in_HU.shape[0] / (ncols * nrows))
slices = range(0, int(real_CT_in_HU.shape[0]), step)

fig = plt.figure(figsize= (10,10))

ct_min_val = real_CT_in_HU.min()
ct_max_val = real_CT_in_HU.max()

for i in range(ncols):
    for j in range(nrows):
        index = j * ncols + i

        slice_id = slices[index]

        ax = fig.add_subplot(nrows, ncols, index + 1)
        ax.set_title("Slice " + str(slice_id + 1) + "/" + str(real_CT_in_HU.
 ↪shape[0]))
        ax.imshow(real_CT_in_HU[slice_id], cmap='gray', vmin=ct_min_val,␣
 ↪vmax=ct_max_val)

plt.tight_layout()
plt.savefig(output_path + '/lungman-real_CT_in_HU.pdf', bbox_inches = 'tight')
plt.savefig(output_path + '/lungman-real_CT_in_HU.png', bbox_inches = 'tight')
```



[14]:
```
def ShouldGenerateNew(*fnames):

    if (GENERATE_NEW_DATA_ALWAYS):
        return True

    for fname in fnames:
        if (not os.path.exists(fname)):
            return True

    return False
```

5 Convert ground truth from HU to

[15]:
```
fname = output_path + "/lungman-real_CT_in_mu.mha"

if ShouldGenerateNew(fname):

    #real_CT_in_mu = np.array(gvxr.convertHU2mu(real_CT_in_HU, ray_energy,␣
 ↪"keV"))
    mu_air  =gvxr.getMuFromHU(-1000.0, 72, "keV");
    mu_water  =gvxr.getMuFromHU(0.0, 72, "keV");
    real_CT_in_HU = real_CT_in_HU.astype(np.double);
    real_CT_in_mu = ((real_CT_in_HU / 1000.0 ) * (mu_water - mu_air)) +␣
 ↪mu_water;


    if SAVE_DATA:

        sitk_real_CT_in_mu = sitk.GetImageFromArray(real_CT_in_mu)
        sitk_real_CT_in_mu.SetSpacing([pixel_width, pixel_width, pixel_height])

        sitk_real_CT_in_mu.SetOrigin((-pixel_width * real_CT_in_mu.shape[2] / 2.
 ↪0,
                                      -pixel_width * real_CT_in_mu.shape[1] / 2.0,
                                      -pixel_height * real_CT_in_mu.shape[0] / 2.0))

        sitk.WriteImage(sitk_real_CT_in_mu, fname, useCompression=True)

else:
    sitk_real_CT_in_mu = sitk.ReadImage(fname)
    real_CT_in_mu = sitk.GetArrayFromImage(sitk_real_CT_in_mu)

del sitk_real_CT_in_mu
```

6 Extract data for this experiment

The labelled volumes are provided compressed in a zip file. Use this procedure to extract the surfaces and masks needed for this notebook.

[16]:
```
# Uncompress the labels
if (False == os.path.isfile("./lungman_data/segmentation-uncompressed/labels.
 ↪mha")):
    with zipfile.ZipFile(  "./lungman_data/segmentation-compressed.zip", 'r')␣
 ↪as myzip:
        myzip.extractall(  "./lungman_data/segmentation-uncompressed")

# Read the records for isovalue, average HU
```

```
mapHandle = open("./lungman_data/segmentation-uncompressed/map.dat");
bytes = mapHandle.read();
split_lines = bytes.split('\n');
bytes = None;
mapHandle.close();

# Read labels
label_rel_path = "./lungman_data/segmentation-uncompressed/labels.mha";
phantom = sitk.ReadImage(label_rel_path)
phantom_array = sitk.GetArrayFromImage(phantom)
```

[17]:
```
# rd = vtk.vtkMetaImageReader();
# rd.SetFileName(label_rel_path);
# rd.Update()
# vtkLabels = rd.GetOutput();

# Create threshold filter
# threshold = vtk.vtkImageThreshold();
# threshold.SetInputData(vtkLabels);
# threshold.SetReplaceOut(0);
# threshold.ReplaceOutOn()
# threshold.ReplaceInOff();

fname_HU = output_path + "/lungman-ground_truth2-CT-in_HU.mha"
fname_mu = output_path + "/lungman-ground_truth2-CT-in_mu.mha"

ref_data = {}

if ShouldGenerateNew(fname_HU, fname_mu):
    digital_phatom_in_HU = np.zeros(phantom_array.shape, dtype=np.int16) - 1000
    digital_phatom_in_mu = np.zeros(phantom_array.shape, dtype=np.single)
else:
    sitk_digital_phatom_in_HU = sitk.ReadImage(fname_HU)
    digital_phatom_in_HU = sitk.GetArrayFromImage(sitk_digital_phatom_in_HU)

    sitk_digital_phatom_in_mu = sitk.ReadImage(fname_mu)
    digital_phatom_in_mu = sitk.GetArrayFromImage(sitk_digital_phatom_in_mu)

for i in range(0, len(split_lines)):

    tuple_parts = split_lines[i].split('\t');

    structure_name = tuple_parts[2][0:-4]
    structure_isovalue = int(tuple_parts[0])

    print("Process", structure_name)
    # See if the surface already exists
    stl_rel_path = "./lungman_data/meshes/" + tuple_parts[2][0:-4] + ".stl";
    # if (True == os.path.isfile(stl_rel_path)): continue;

    # Threshold to get label
#     threshold.ThresholdBetween(structure_isovalue, structure_isovalue);
#     threshold.Update();
#     vtkIm = threshold.GetOutput();

#     # Extract surface and save
#     vtkSurface = extractSurface(vtkIm, structure_isovalue);
#     writeSTL(vtkSurface, stl_rel_path);
#     vtkSurface = None;
#     vtkIm = None;

    # Threshold the phantom
    binary_mask = (phantom == structure_isovalue)

    # Pad the image
    filt = sitk.ConstantPadImageFilter()
    filt.SetConstant (0)
    filt.SetPadLowerBound ([1, 1, 1])
    filt.SetPadUpperBound ([1, 1, 1])
    binary_image = filt.Execute(binary_mask)

    # Create a VTK image
    binary_array = sitk.GetArrayFromImage(binary_image)
    vtkimg = sitk2vtk(binary_image, centre=True)

    # binary_array = sitk.GetArrayFromImage(binary_image)
    min_val = binary_array.min()
    max_val = binary_array.max()

    threshold = min_val + 0.5 * (max_val - min_val)

    vtkmesh = extractSurface(vtkimg, threshold)
    del vtkimg

    writeSTL(vtkmesh, stl_rel_path)
    del vtkmesh


    # Get HU/mu

    if ShouldGenerateNew(fname_HU, fname_mu):

        kernel_radius = 2;
        # Sheets are too slim to be eroded so much
        if (structure_name.find("sheet") != -1):
            kernel_radius = 1;

        # Erode the mask
        erode = sitk.BinaryErodeImageFilter();
        erode.SetKernelRadius(kernel_radius);
        erode.SetForegroundValue(1);
        sitk_eroded_mask = erode.Execute(binary_mask);
        del erode

        eroded_mask = np.array(sitk.GetArrayFromImage(sitk_eroded_mask));
        del sitk_eroded_mask

        # Apply mask to simulated CT
        erored_test = (eroded_mask == 1)

        test = phantom_array == structure_isovalue
        avg_HU = np.mean(real_CT_in_HU[erored_test])
        avg_mu = np.mean(real_CT_in_mu[erored_test])

        # print("\t\t\"Material\": [\"HU\",", avg_HU, "]")

        ref_data[structure_name] = [avg_HU, avg_mu]
        digital_phatom_in_HU[test] = round(avg_HU)
        digital_phatom_in_mu[test] = avg_mu

del phantom
del real_CT_in_HU
```

```
Process bronchioles
Process bronchus
Process trachea
Process diaphram
Process skin
Process heart
Process ribs_spine
Process scapulas
Process sternum
Process clavicle
Process sheets_low
Process sheets_med
Process sheets_high
Process tumours_630HU
Process tumours_100HU
```

[18]:
```
if ShouldGenerateNew(fname_HU, fname_mu):

    if SAVE_DATA:
        sitk_digital_phatom_in_HU = sitk.GetImageFromArray(digital_phatom_in_HU)

        sitk_digital_phatom_in_HU.SetOrigin((-pixel_width *␣
↪digital_phatom_in_HU.shape[2] / 2.0,
                            -pixel_width * digital_phatom_in_HU.shape[1] / 2.0,
                            -pixel_height * digital_phatom_in_HU.shape[0] / 2.0))

        sitk_digital_phatom_in_HU.SetSpacing([pixel_width, pixel_width,␣
↪pixel_height])
        sitk.WriteImage(sitk_digital_phatom_in_HU, fname_HU,␣
↪useCompression=True)
        del sitk_digital_phatom_in_HU


        sitk_digital_phatom_in_mu = sitk.GetImageFromArray(digital_phatom_in_mu)

        sitk_digital_phatom_in_mu.SetOrigin((-pixel_width *␣
↪digital_phatom_in_mu.shape[2] / 2.0,
                           -pixel_width * digital_phatom_in_mu.shape[1] / 2.0,
                            -pixel_height * digital_phatom_in_mu.shape[0] / 2.0))

        sitk_digital_phatom_in_mu.SetSpacing([pixel_width, pixel_width,␣
↪pixel_height])
        sitk.WriteImage(sitk_digital_phatom_in_mu, fname_mu,␣
↪useCompression=True)
        del sitk_digital_phatom_in_mu

del digital_phatom_in_mu
del digital_phatom_in_HU
```

6.1 Create a phantom model from each mesh and its material

[19]:
```
json2gvxr.initSamples();
```

```
Tue Sep 20 21:36:12 2022 ---- file_name:
lungman_data/meshes/bronchioles.stl     nb_faces:       5338192 nb_vertices:
16014576        bounding_box (in cm):   (-12.625, -8.3125, -13.65)
(11.8125, 7.3125, 12.81)
Tue Sep 20 21:36:12 2022 ---- file_name:        lungman_data/meshes/bronchus.stl
nb_faces:       701200  nb_vertices:    2103600 bounding_box (in cm):
(-11.375, -8.0625, -11.97)      (11.75, 6.5, 10.57)
Tue Sep 20 21:36:12 2022 ---- file_name:        lungman_data/meshes/trachea.stl
nb_faces:       88328   nb_vertices:    264984  bounding_box (in cm):
(-2.8125, -6.625, -1.68)        (3.8125, 0.5, 14.84)
```

```
Tue Sep 20 21:36:13 2022 ---- file_name:        lungman_data/meshes/diaphram.stl
nb_faces:       507436  nb_vertices:    1522308 bounding_box (in cm):
(-12.625, -9, -14.84)   (11.875, 6.3125, -8.26)
Tue Sep 20 21:36:14 2022 ---- file_name:        lungman_data/meshes/skin.stl
nb_faces:       6416748 nb_vertices:    19250244        bounding_box (in cm):
(-15.9375, -11.75, -14.84)      (15.9375, 10.75, 14.84)
Tue Sep 20 21:36:14 2022 ---- file_name:        lungman_data/meshes/heart.stl
nb_faces:       440588  nb_vertices:    1321764 bounding_box (in cm):
(-2.6875, -8.375, -10.71)       (9.5625, 3.4375, 8.82)
Tue Sep 20 21:36:14 2022 ---- file_name:
lungman_data/meshes/ribs_spine.stl      nb_faces:       2225360 nb_vertices:
6676080 bounding_box (in cm):   (-14.5, -10.125, -14.84)        (13.625, 9.125,
14.84)
Tue Sep 20 21:36:14 2022 ---- file_name:        lungman_data/meshes/scapulas.stl
nb_faces:       568148  nb_vertices:    1704444 bounding_box (in cm):
(-15.9375, -3.8125, -2.8)       (15.9375, 8.1875, 14.84)
Tue Sep 20 21:36:14 2022 ---- file_name:        lungman_data/meshes/sternum.stl
nb_faces:       101856  nb_vertices:    305568  bounding_box (in cm):   (-3.75,
-9.5, -5.53)    (2.6875, -4.4375, 9.1)
Tue Sep 20 21:36:14 2022 ---- file_name:        lungman_data/meshes/clavicle.stl
nb_faces:       131804  nb_vertices:    395412  bounding_box (in cm):
(-12.375, -6.5625, 8.47)        (12.375, 4.0625, 14.84)
Tue Sep 20 21:36:14 2022 ---- file_name:
lungman_data/meshes/sheets_low.stl      nb_faces:       1160784 nb_vertices:
3482352 bounding_box (in cm):   (-15.9375, 6.1875, -14.84)      (15.9375,
11.1875, 14.84)
Tue Sep 20 21:36:15 2022 ---- file_name:
lungman_data/meshes/sheets_med.stl      nb_faces:       1120640 nb_vertices:
3361920 bounding_box (in cm):   (-15.9375, 9.4375, -14.84)      (15.9375, 14,
14.84)
Tue Sep 20 21:36:15 2022 ---- file_name:
lungman_data/meshes/sheets_high.stl     nb_faces:       467752  nb_vertices:
1403256 bounding_box (in cm):   (-15.9375, 13.3125, -14.84)     (15.9375,
15.9375, 14.84)
Tue Sep 20 21:36:15 2022 ---- file_name:
lungman_data/meshes/tumours_630HU.stl   nb_faces:       4952    nb_vertices:
14856   bounding_box (in cm):   (-10.625, -3.3125, -8.68)       (5.375, 2.375,
5.81)
Tue Sep 20 21:36:15 2022 ---- file_name:
lungman_data/meshes/tumours_100HU.stl   nb_faces:       3968    nb_vertices:
11904   bounding_box (in cm):   (-4.625, -4.75, -8.54)  (11.75, 2.9375, -0.14)
```

[20]:
```python
number_of_triangles = 0

for sample in json2gvxr.params["Samples"]:
    label = sample["Label"]
    number_of_triangles_in_mesh = gvxr.getNumberOfPrimitives(label)
    number_of_triangles += number_of_triangles_in_mesh

print("There are", f"{number_of_triangles:,}", "triangles in total")
```

```
There are 19,277,756 triangles in total
```

6.2 Visualise the virtual patient

[21]:
```
if (DO_K3D_PLOT):
    plot = visualise(use_log=True, use_negative=True, sharpen_ksize=2,␣
 ↪sharpen_alpha=1.0)
```

```
Output()
```

[22]:
```
fname = output_path + '/lungman_model.png'
if DO_K3D_PLOT and ShouldGenerateNew(fname):


    plot.fetch_screenshot() # Not sure why, but we need to do it twice to get␣
 ↪the right screenshot
    data = base64.b64decode(plot.screenshot)
    with open(fname,'wb') as fp:
        fp.write(data)
        fp.flush();
        fp.close();
```

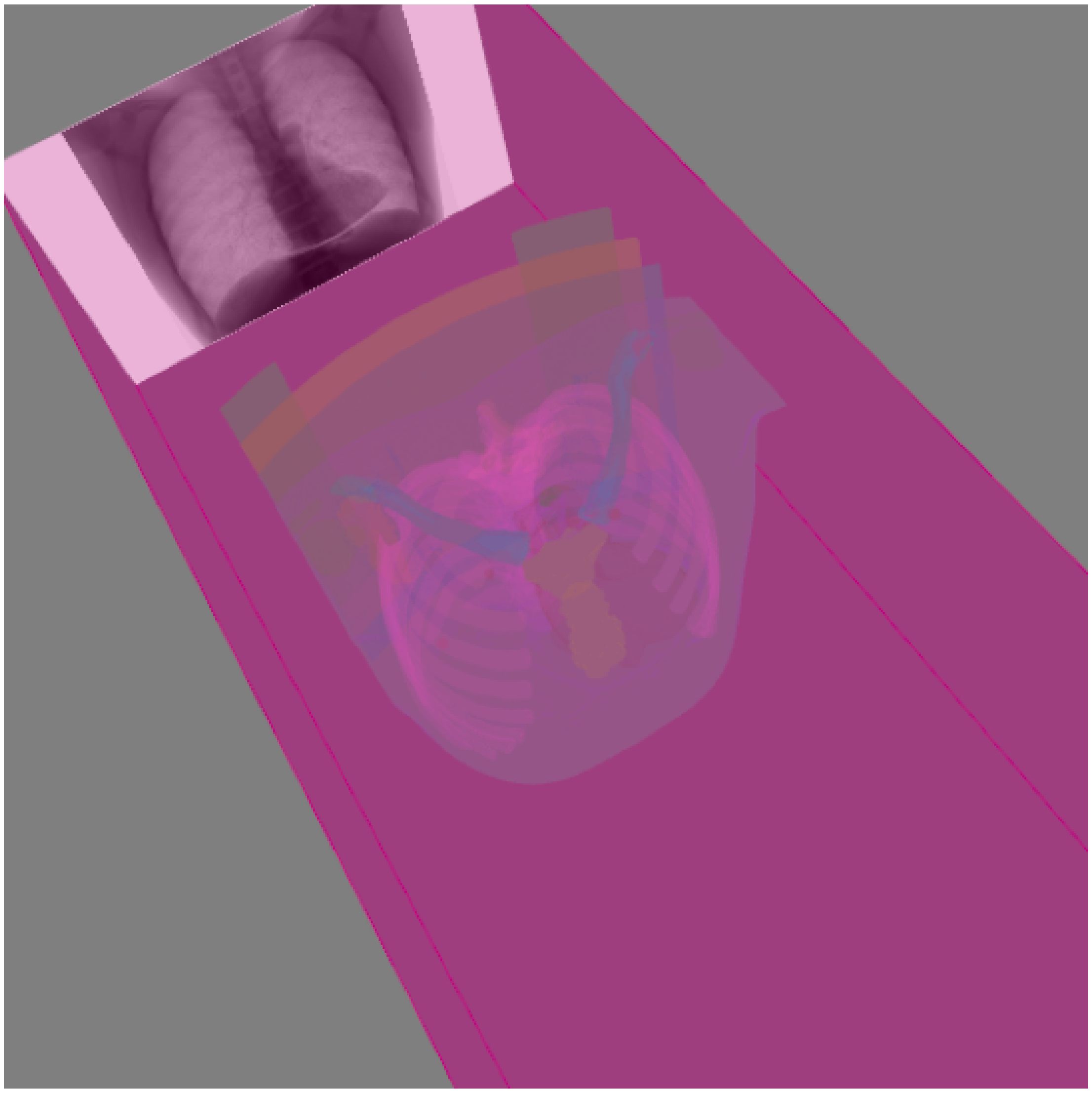
6.3 Visualise a single projection

[23]:
```
gvxr.computeXRayImage()
gvxr.displayScene()

# Give each mesh an alpha value
alpha = 0.2;
for i in range(gvxr.getNumberOfChildren('root')):
    label = gvxr.getChildLabel('root', i);
    pRGBA = gvxr.getAmbientColour(label);
    gvxr.setColour(label, pRGBA[0], pRGBA[1], pRGBA[2],alpha);

gvxr.useLighing(False)
gvxr.useWireframe(False)
gvxr.setZoom(1000)
gvxr.setSceneRotationMatrix([ 0.8535534,  0.5000000, -0.1464466,0,
  -0.5000000,  0.7071068, -0.5000000,0,
  -0.1464466,  0.5000000,  0.8535534,0,
                            0.0, 0.0, 0.0, 1.0])
gvxr.displayScene()
```

```
screenshot = gvxr.takeScreenshot()

plt.figure(figsize= (10,10))
plt.title("Screenshot")
plt.imshow(screenshot)
plt.axis('off')
```

```
[23]: (-0.5, 511.5, 511.5, -0.5)
```

Screenshot



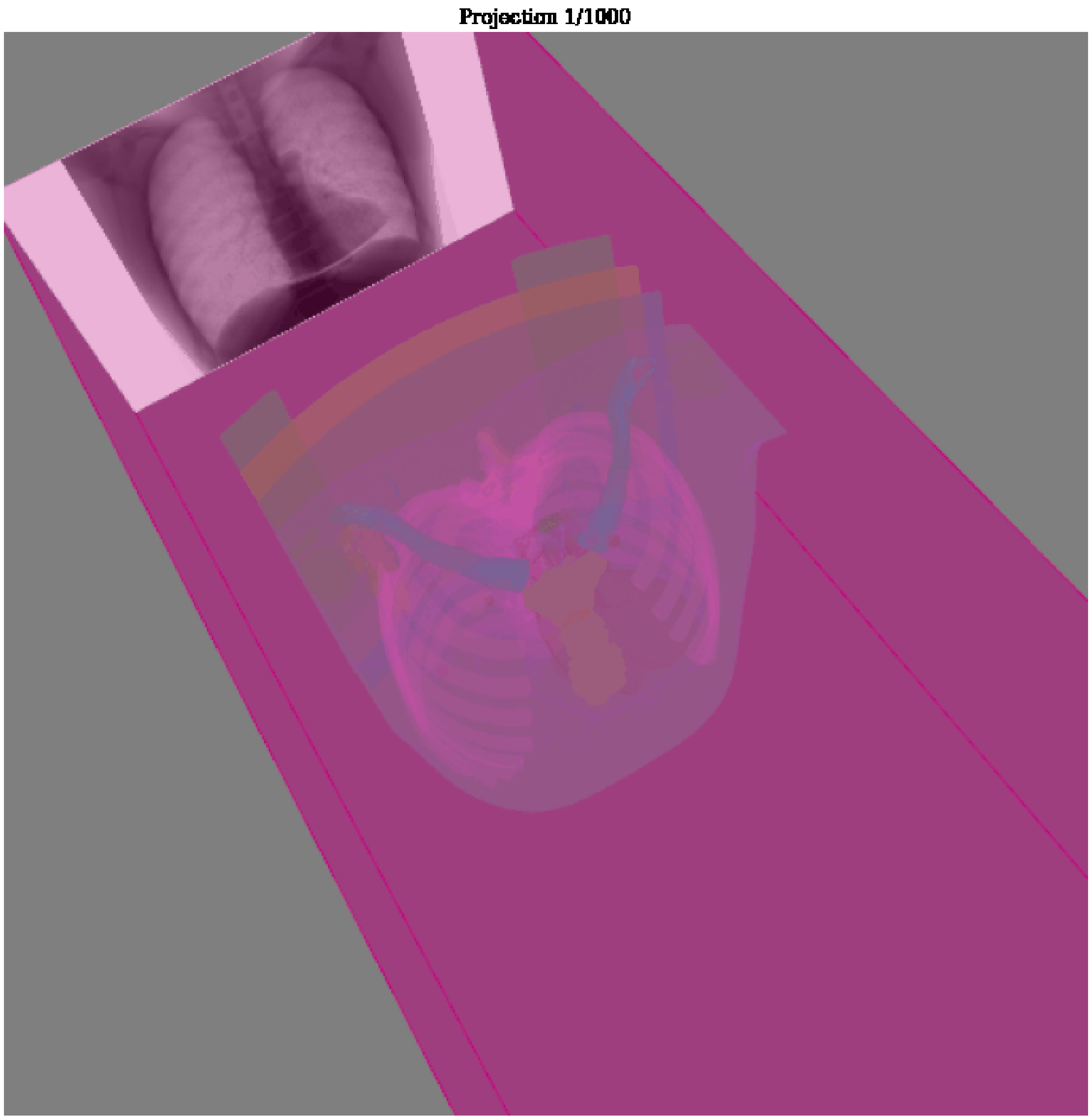
```
[24]: %%capture
runtimes = []
fname = output_path + "/lungman_flat.mha"
```

```python
if ShouldGenerateNew(fname):


    gvxr.disableArtefactFiltering()

    if DO_ARTEFACT_FILTERING_ON_GPU:
        gvxr.enableArtefactFilteringOnGPU()
    elif DO_ARTEFACT_FILTERING_ON_CPU:
        gvxr.enableArtefactFilteringOnCPU()

    temp = [];
    angles = [];
    runtimes = []

    # Create a GIF file
    writer = None
    fname_gif = output_path + "/lungman_acquisition.gif"

    if not os.path.exists(fname_gif):
        writer = imageio.get_writer(fname_gif, mode='I')

    # Save the transformation matrix
    transformation_matrix_backup = gvxr.getSceneTransformationMatrix()

    rotation_axis = json2gvxr.params["Detector"]["UpVector"]

    for angle_id in range(0, number_of_projections):

        # Add the rotation angle, starting from 0
        angles.append(angle_id * angular_step)

        # Compute an X-ray image
        # xray_image = np.array(gvxr.computeXRayImage());
        start_time = datetime.datetime.now()

        xray_image = np.array(gvxr.computeXRayImage()).astype(np.single)

        # if xray_image.shape != [208, 1062]:
        #     xray_image = resize(xray_image, [208, 1062])

        # xray_image = np.array(gvxr.computeXRayImage());

        end_time = datetime.datetime.now()
        delta_time = end_time - start_time
        runtimes.append(delta_time.total_seconds() * 1000)

        # Add to the set of projections
        temp.append(xray_image)

        # Update the rendering
        gvxr.displayScene();

        # Take a screenshot
        if writer is not None:
            if not angle_id % 30:
                screenshot = gvxr.takeScreenshot()

                plt.figure(figsize= (10,10))
                plt.title("Projection " + str(angle_id + 1) + "/" +␣
↪str(number_of_projections))
                plt.imshow(screenshot)
                plt.axis('off')

                plt.tight_layout()

                plt.savefig('temp.png', bbox_inches = 'tight')
                plt.close()


                image = imageio.imread("temp.png")
                writer.append_data(image)

        # Rotate the sample
        gvxr.rotateScene(angular_step, rotation_axis[0], rotation_axis[1],␣
↪rotation_axis[2])

    # We're done with the writer
    if writer is not None:
        writer.close()
        os.remove("temp.png")

    # Convert to numpy arrays
    raw_projections = np.array(temp).astype(np.single)
    del temp

    # Restore the transformation matrix
    gvxr.setSceneTransformationMatrix(transformation_matrix_backup)

    # Update the rendering
    gvxr.displayScene();
```

[25]:
```
if (len(runtimes) > 0):
    runtime_avg = round(np.mean(runtimes))
    runtime_std = round(np.std(runtimes))
```

```
else:
    runtime_avg = -1;
    runtime_std = 0;
```

```
[26]: with open(output_path + '/lungman_acquisition.gif','rb') as f:
    display(Image(data=f.read(), format='png', width=500))
```



7 Correct flat-field

Taking advantage of the detector response when there is no sample can help improve the quality of images when a sample is present. To elaborate, any variance between pixels when the detector is dark (X-Ray beam off) or full (X-Ray beam on) with no density will affect the quality of images

with a sample. Factoring for this systematic error is called flat-field correction.
N: corrected image
P: projection
D: dark field
F: full field
$N = \frac{P-D}{F-D}$
In this routine the projection data is flat-fielded.

[27]:
```
if ShouldGenerateNew(fname):

    corrected_projections = flatFieldCorrection(raw_projections)

    if SAVE_DATA:
        sitk_image = sitk.GetImageFromArray(corrected_projections)
        sitk_image.SetSpacing([pixel_width, pixel_height, angular_step])
        sitk.WriteImage(sitk_image, fname, useCompression=True)

else:
    temp = sitk.ReadImage(fname)
    corrected_projections = sitk.GetArrayFromImage(temp).astype(np.single)

    angles = np.linspace(0, angular_step * (number_of_projections - 1),␣
 ↪number_of_projections)

del raw_projections # Not needed anymore
```

8 Negative log normalisation

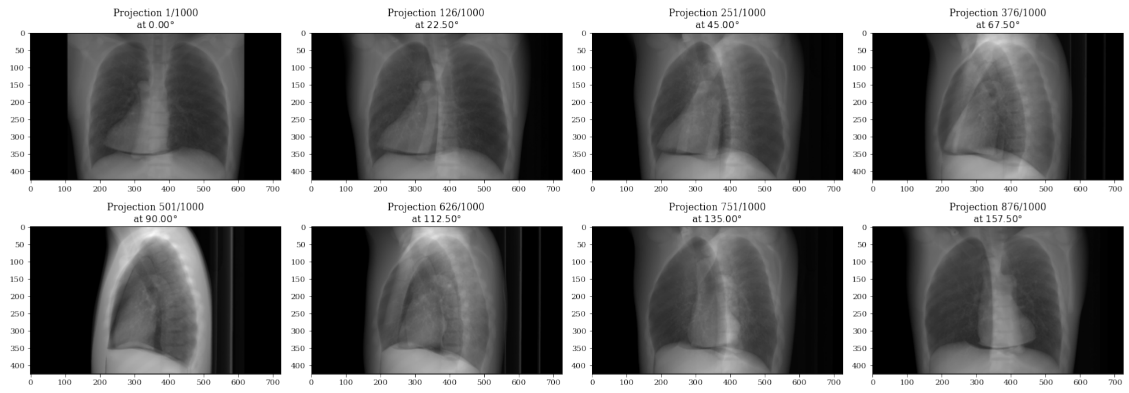
[28]:
```
fname = output_path + "/lungman_minus_log_projs.mha"

if ShouldGenerateNew(fname):

    minus_log_projs = minusLog(corrected_projections).astype(np.single)

    if SAVE_DATA:
        sitk_image = sitk.GetImageFromArray(minus_log_projs)
        sitk_image.SetSpacing([pixel_width, pixel_height, angular_step])
        sitk.WriteImage(sitk_image, fname, useCompression=True)

else:
    temp = sitk.ReadImage(fname)
    minus_log_projs = sitk.GetArrayFromImage(temp).astype(np.single)

del corrected_projections # Not needed anymore
```

Display the images

[29]:
```
proj_min = minus_log_projs.min()
proj_max = minus_log_projs.max()
```

Draw the projection

[30]:
```
ncols = 4
nrows = 2

step = int(minus_log_projs.shape[0] / (ncols * nrows))
slices = range(0, int(minus_log_projs.shape[0]), step)

fig = plt.figure(figsize= (20, 7))

for i in range(ncols):
    for j in range(nrows):
        index = j * ncols + i

        slice_id = slices[index]

        ax = fig.add_subplot(nrows, ncols, index + 1)
        ax.set_title("Projection " + str(slice_id + 1) + "/" +␣
 ↪str(minus_log_projs.shape[0]) + "\nat $" + "{:.2f}".format(angles[slice_id])␣
 ↪+ "\degree$")
        ax.imshow(skimage.transform.rotate(minus_log_projs[slice_id], 180),
                  cmap='gray',
                  vmin=proj_min,
                  vmax=proj_max)

plt.tight_layout()


plt.savefig(output_path + '/lungmand-simulated-projs.pdf', bbox_inches =␣
 ↪'tight')
plt.savefig(output_path + '/lungmand-simulated-projs.png', bbox_inches =␣
 ↪'tight')
```



8.1 Optimise Plastimatch centre

Use objective function to find optimimum centre. i.e. register the DRR onto the radiograph

[31]:
```
from pymoo.util.misc import stack
from pymoo.core.problem import Problem
from pymoo.core.problem import ElementwiseProblem
from threading import Thread
from sklearn.metrics import mean_absolute_percentage_error

def normImage(image_to_normalise):
    image_to_normalise -= np.mean(image_to_normalise);
    stddev = np.std(image_to_normalise);
    if (stddev == 0): stddev = 0.0001;
    image_to_normalise/= stddev;

def measure(truth, predict):
    N = 1.0;
    dims = np.shape(truth);
    for i in range(0, len(dims)):
        N *= dims[i];
    if (N == 0): return -1, -1, -1, -1, -1;

    zncc_denom = N * np.std(truth) * np.std(predict);
    if (zncc_denom == 0): zncc_denom = 0.00001;

    sub = truth - predict;

    mae_score = np.sum(np.abs(sub)) / N;
    zncc_score =  np.sum( (truth  - np.mean(truth)) *(predict - np.
↪mean(predict))) / zncc_denom;
    rmse_score =  np.sqrt(np.sum(np.power(sub, 2)) / N)
    mape_score = mean_absolute_percentage_error(truth, predict);
    ssim_score = ssim(truth, predict);
    return mae_score, zncc_score, rmse_score, mape_score, ssim_score

def objective(cx, cy):
        DRR = doLungmanDRRNumpy(g_NRM[0], g_NRM[1], g_NRM[2],
                                cx, cy,
                                 "DRR_",
                                 g_XRay.shape[1], g_XRay.shape[0]

                                );
        DRR = DRR.astype(np.single);
        normImage(DRR);
        mae, zncc, rmse, mape, ssim = measure(g_XRay, DRR);

        dzncc = (1.0 - zncc) / 2.0
        dssim = (1.0 - ssim) / 2.0


        row = []

        row.append(mae);
        row.append(dzncc);
        row.append(rmse);
        row.append(mape);
        row.append(dssim);
        return row;

class MyProblem(Problem):

    def __init__(self):
        super().__init__(n_var=2,
                         n_obj=5,
                         n_constr=0,
                         xl=np.array([0, -g_XRay.shape[0]]),
                         xu=np.array([g_XRay.shape[1],0])
                         )




    def _evaluate(self, X, out, *args, **kwargs):
            objs = []
            for tuple in X:
                objs.append(objective(tuple[0], tuple[1]));

            out["F"] = objs;


import time
from pymoo.factory import get_termination
from pymoo.algorithms.moo.nsga2 import NSGA2
from pymoo.factory import get_sampling, get_crossover, get_mutation

termination = get_termination("n_gen", 100)


algorithm = NSGA2(
    pop_size=40,
    n_offsprings=10,
    sampling=get_sampling("real_random"),
    crossover=get_crossover("real_sbx", prob=0.9, eta=15),
    mutation=get_mutation("real_pm", eta=20),
    eliminate_duplicates=False
)
#normImage(xray_AP);
#normImage(xray_RL);

from pymoo.optimize import minimize
```

Generate optimise result if not done so already

[32]:
```
import pymoo.core.result;

fname_nsga_rl_X = output_path + "/R-L-res-nsga2-X.dat";
fname_nsga_rl_F = output_path + "/R-L-res-nsga2-F.dat";
fname_nsga_ap_X = output_path + "/A-P-res-nsga2-X.dat";
fname_nsga_ap_F = output_path + "/A-P-res-nsga2-F.dat";

r_l_res_exists = not ShouldGenerateNew(fname_nsga_rl_X, fname_nsga_rl_F);

a_p_res_exists = not ShouldGenerateNew(fname_nsga_ap_X, fname_nsga_ap_F);

res_ap = pymoo.core.result.Result();
res_rl = pymoo.core.result.Result();

minus_log_proj_rl = np.copy(np.flip(minus_log_projs[(number_of_projections) //␣
 ↪2]));
minus_log_proj_ap = np.copy(np.flip(minus_log_projs[len(minus_log_projs) - 1]));
normImage(minus_log_proj_rl);
normImage(minus_log_proj_ap);
s="Time taken {t} seconds.";

if (r_l_res_exists):
    print("Getting R-L result from file");
    res_rl.X = np.loadtxt(fname_nsga_rl_X)
    res_rl.F = np.loadtxt(fname_nsga_rl_F)
else:
    print("Optimising R-L");
    g_NRM = [1, 0, 0]
    g_XRay = minus_log_proj_rl;

    problem = MyProblem();

    t_start = time.time();
    res_rl = minimize(problem,
                algorithm,
                termination,
                seed=1,
                save_history=True,
                verbose=True)

    t_end = time.time();
    print(s.format(t=(t_end - t_start)));

    np.savetxt(fname_nsga_rl_X, res_rl.X)
    np.savetxt(fname_nsga_rl_F, res_rl.F)

if (a_p_res_exists):
    print("Getting A-P result from file");
    res_ap.X = np.loadtxt(fname_nsga_ap_X)
    res_ap.F = np.loadtxt(fname_nsga_ap_F)
else:
    print("Optimising A-P");
    g_NRM = [0, -1, 0]
    g_XRay = minus_log_proj_ap;

    problem = MyProblem();

    t_start = time.time();
    res_ap = minimize(problem,
                algorithm,
                termination,
                seed=1,
                save_history=True,
                verbose=True)

    t_end = time.time();
    print(s.format(t=(t_end - t_start)));

    np.savetxt(fname_nsga_ap_X, res_ap.X)
    np.savetxt(fname_nsga_ap_F, res_ap.F)
```

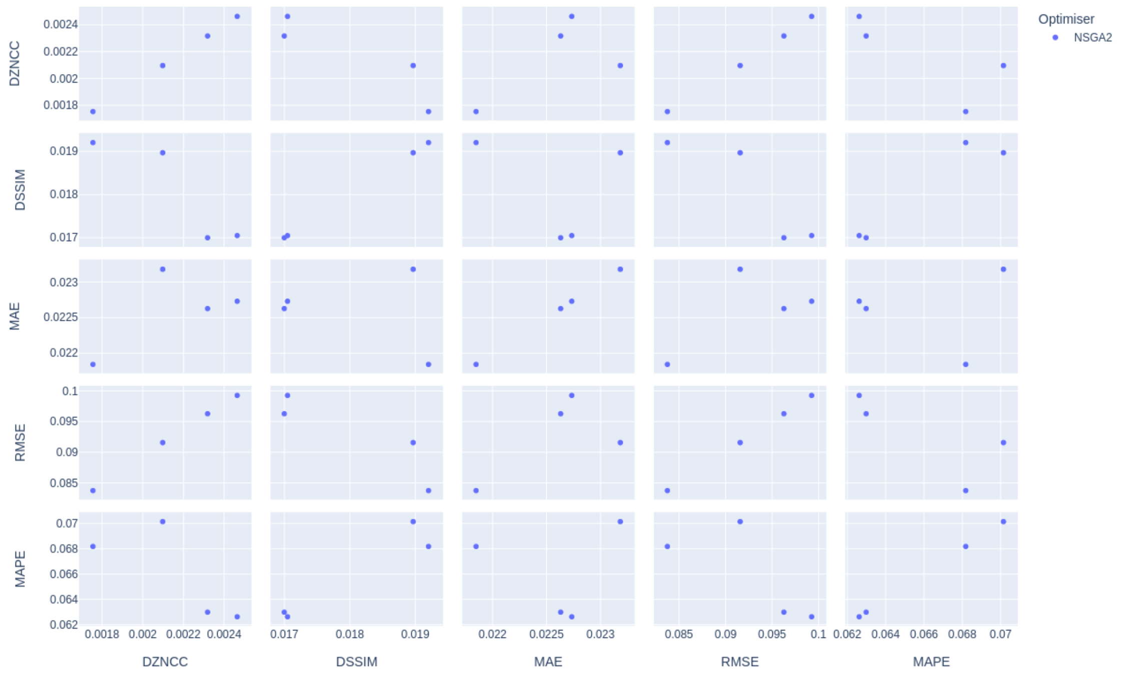
```
Getting R-L result from file
Getting A-P result from file
```

[33]:
```
del minus_log_projs
```

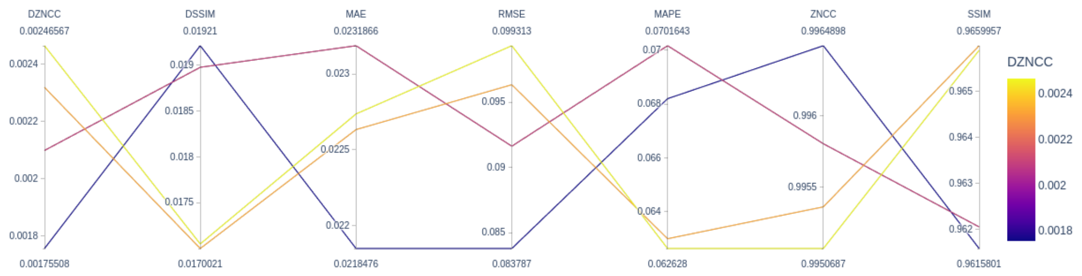
[34]:
```
df_RL = pd.DataFrame(data=np.append(res_rl.X, res_rl.F, axis=1),
                  columns=["cx", "cy", "MAE", "DZNCC", "RMSE", "MAPE", "DSSIM"])

df_RL["ZNCC"] = 1.0 - (df_RL["DZNCC"] * 2.0)
df_RL["SSIM"] = 1.0 - (df_RL["DSSIM"] * 2.0)
```

```
df_RL["Optimiser"] = "NSGA2"
df_RL.to_csv(output_path + "/RL-optimiser.csv")
```

[35]:
```
fig = px.scatter_matrix(df_RL,
    dimensions=["DZNCC", "DSSIM", "MAE", "RMSE", "MAPE"],
    color="Optimiser")

fig.update_layout(
    height=800,
    width=800
)

fig.show()

fig.write_image(output_path + "/RL-scatter_matrix.pdf", engine="kaleido")
fig.write_image(output_path + "/RL-scatter_matrix.png", engine="kaleido")
```

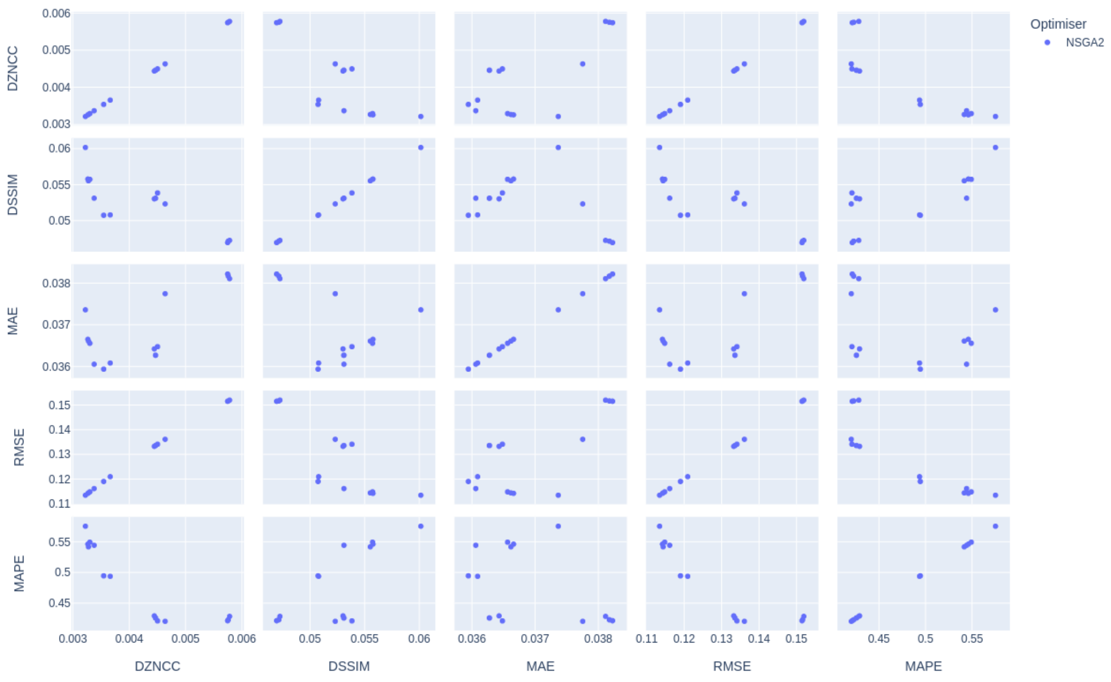


[36]:
```
fig = px.parallel_coordinates(df_RL[["DZNCC", "DSSIM", "MAE", "RMSE", "MAPE",␣
 ↪"ZNCC", "SSIM"]], color="DZNCC")
fig.show()

fig.write_image(output_path + "/rl-parallel_coordinates.pdf", engine="kaleido")
fig.write_image(output_path + "/rl-parallel_coordinates.png", engine="kaleido")
```

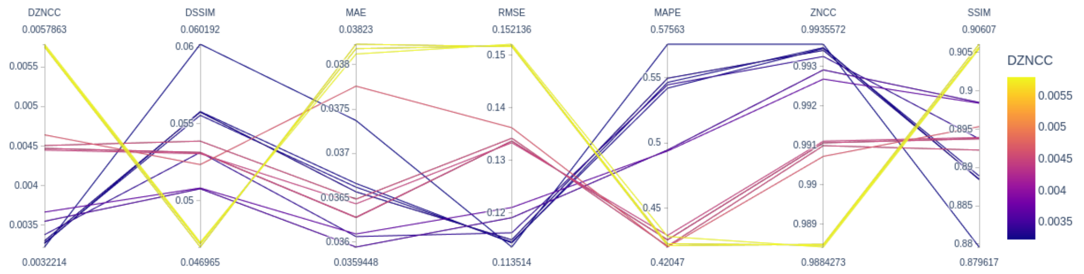


```
[37]: df_AP = pd.DataFrame(data=np.append(res_ap.X, res_ap.F, axis=1),
                          columns=["cx", "cy", "MAE", "DZNCC", "RMSE", "MAPE", "DSSIM"])

      df_AP["ZNCC"] = 1.0 - (df_AP["DZNCC"] * 2.0)
      df_AP["SSIM"] = 1.0 - (df_AP["DSSIM"] * 2.0)

      df_AP["Optimiser"] = "NSGA2"
      df_AP.to_csv(output_path + "/AP-optimiser.csv")
```

```
[38]: fig = px.scatter_matrix(df_AP,
          dimensions=["DZNCC", "DSSIM", "MAE", "RMSE", "MAPE"],
          color="Optimiser")

      fig.update_layout(
          height=800,
          width=800
      )

      fig.show()

      fig.write_image(output_path + "/AP-scatter_matrix.pdf", engine="kaleido")
      fig.write_image(output_path + "/AP-scatter_matrix.png", engine="kaleido")
```



[39]:
```
fig = px.parallel_coordinates(df_AP[["DZNCC", "DSSIM", "MAE", "RMSE", "MAPE",␣
↪"ZNCC", "SSIM"]], color="DZNCC")
fig.show()

fig.write_image(output_path + "/ap-parallel_coordinates.pdf", engine="kaleido")
fig.write_image(output_path + "/ap-parallel_coordinates.png", engine="kaleido")
```



[40]:
```
best_rl_id = np.argmin(res_rl.F[:,2])

best_ap_id = np.argmin(res_ap.F[:,2])
```

```
print("Optimum c for right to left", f"{res_rl.X[best_rl_id][0]:.2f}", ",", f"{␣
↪res_rl.X[best_rl_id][1]:.2f}")
print("Optimum c for anterior to posterior", f"{res_ap.X[best_ap_id][0]:.2f}",␣
↪",", f"{ res_ap.X[best_ap_id][1]:.2f}")

runtimes_drr_rl = []
runtimes_drr_ap = []

for i in range(50):
    start_time = datetime.datetime.now()

    DRR_RL = doLungmanDRRNumpy(1, 0, 0,
                              res_rl.X[best_rl_id][0], res_rl.X[best_rl_id][1],
                                "DRR_RL"
                               );

    end_time = datetime.datetime.now()
    delta_time = end_time - start_time
    runtimes_drr_rl.append(delta_time.total_seconds() * 1000)

    start_time = datetime.datetime.now()

    DRR_AP = doLungmanDRRNumpy(0, -1, 0,
                                 res_ap.X[best_ap_id][0], res_ap.
↪X[best_ap_id][1],
                                    "DRR_AP"
                                   );

    end_time = datetime.datetime.now()
    delta_time = end_time - start_time
    runtimes_drr_ap.append(delta_time.total_seconds() * 1000)

normImage(DRR_RL)
normImage(DRR_AP)
displayLinearPowerScales(DRR_RL,  "Lungman DRR (Right to left)", output_path +␣
↪"/R_L_lungman_radiograph");
displayLinearPowerScales(DRR_AP,  "Lungman DRR (Anterior to posterior)",␣
↪output_path + "/A_P_lungman_radiograph");
```

```
Optimum c for right to left 577.90 , -57.33
Optimum c for anterior to posterior 348.74 , -59.86
I/O time: 0.018244 sec
Total time: 0.0737641 secs
I/O time: 0.000760 sec
Total time: 0.0451169 secs
I/O time: 0.000759 sec
```

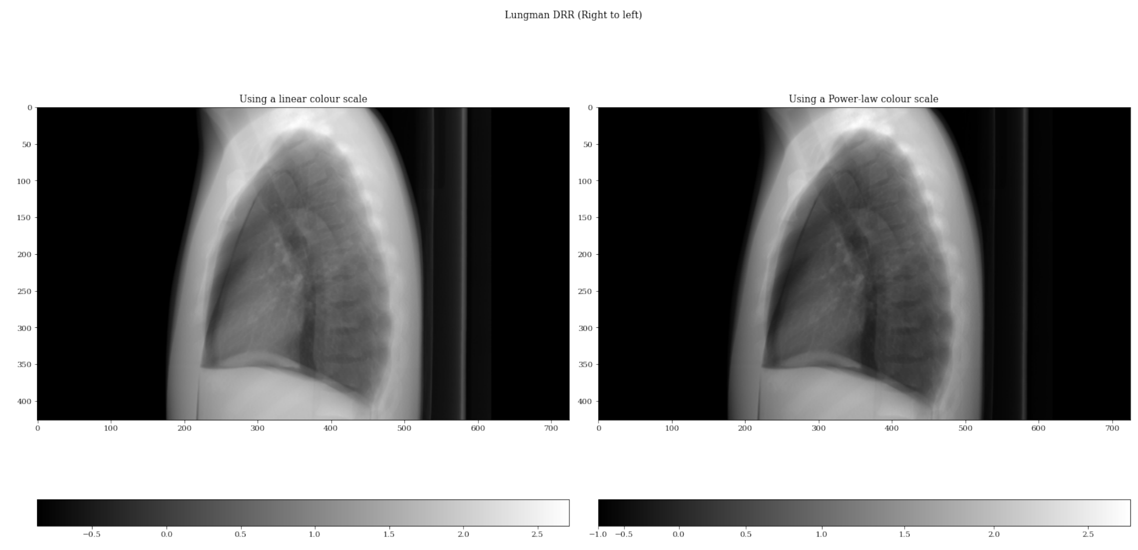
```
Total time: 0.0469489 secs
I/O time: 0.000748 sec
Total time: 0.057807 secs
I/O time: 0.000750 sec
Total time: 0.0531042 secs
I/O time: 0.000753 sec
Total time: 0.0483701 secs
I/O time: 0.000806 sec
Total time: 0.0465181 secs
I/O time: 0.000739 sec
Total time: 0.047421 secs
I/O time: 0.000913 sec
Total time: 0.059294 secs
I/O time: 0.000746 sec
Total time: 0.0499148 secs
I/O time: 0.000779 sec
Total time: 0.0458591 secs
I/O time: 0.000726 sec
Total time: 0.0460901 secs
I/O time: 0.000866 sec
Total time: 0.0479131 secs
I/O time: 0.000741 sec
Total time: 0.0431149 secs
I/O time: 0.000769 sec
Total time: 0.0472748 secs
I/O time: 0.000725 sec
Total time: 0.0456052 secs
I/O time: 0.000841 sec
Total time: 0.049746 secs
I/O time: 0.000770 sec
Total time: 0.043509 secs
I/O time: 0.000749 sec
Total time: 0.0485511 secs
I/O time: 0.000734 sec
Total time: 0.0441809 secs
I/O time: 0.000751 sec
Total time: 0.051239 secs
I/O time: 0.000737 sec
Total time: 0.0447822 secs
I/O time: 0.106299 sec
Total time: 0.152717 secs
I/O time: 0.000740 sec
Total time: 0.0490961 secs
I/O time: 0.091597 sec
Total time: 0.147803 secs
I/O time: 0.093439 sec
Total time: 0.138355 secs
I/O time: 0.046270 sec
```

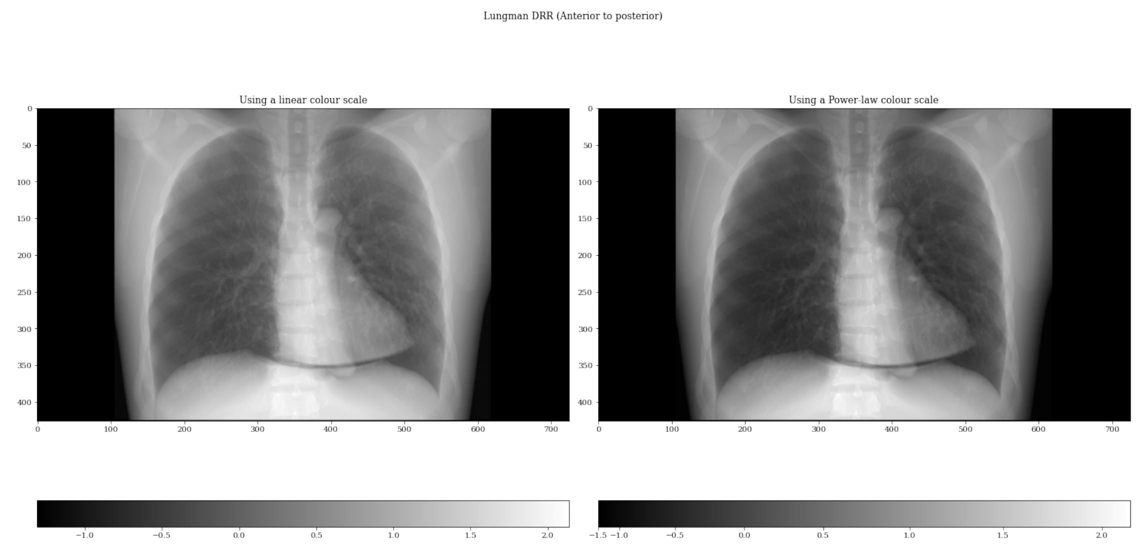
```
Total time: 0.0967321 secs
I/O time: 0.125970 sec
Total time: 0.167832 secs
I/O time: 0.053856 sec
Total time: 0.101283 secs
I/O time: 0.000861 sec
Total time: 0.046663 secs
I/O time: 0.028335 sec
Total time: 0.0781059 secs
I/O time: 0.000718 sec
Total time: 0.0430651 secs
I/O time: 0.537054 sec
Total time: 0.583241 secs
I/O time: 0.056161 sec
Total time: 0.100646 secs
I/O time: 0.000754 sec
Total time: 0.0480862 secs
I/O time: 0.093814 sec
Total time: 0.137293 secs
I/O time: 0.023076 sec
Total time: 0.0712631 secs
I/O time: 0.110715 sec
Total time: 0.154095 secs
I/O time: 0.139038 sec
Total time: 0.184701 secs
I/O time: 0.000754 sec
Total time: 0.049994 secs
I/O time: 0.088845 sec
Total time: 0.134505 secs
I/O time: 0.063166 sec
Total time: 0.110405 secs
I/O time: 0.000761 sec
Total time: 0.048589 secs
I/O time: 0.000747 sec
Total time: 0.0430689 secs
I/O time: 0.057039 sec
Total time: 0.104276 secs
I/O time: 0.000736 sec
Total time: 0.0437698 secs
I/O time: 0.000798 sec
Total time: 0.0507751 secs
I/O time: 0.000731 sec
Total time: 0.043416 secs
I/O time: 0.000721 sec
Total time: 0.0464649 secs
I/O time: 0.000722 sec
Total time: 0.04475 secs
I/O time: 0.000757 sec
```

```
Total time: 0.049186 secs
I/O time: 0.000762 sec
Total time: 0.0431399 secs
I/O time: 0.000827 sec
Total time: 0.047703 secs
I/O time: 0.000732 sec
Total time: 0.0445981 secs
I/O time: 0.000750 sec
Total time: 0.0498111 secs
I/O time: 0.000726 sec
Total time: 0.0595341 secs
I/O time: 0.138598 sec
Total time: 0.192656 secs
I/O time: 0.061419 sec
Total time: 0.106642 secs
I/O time: 0.178385 sec
Total time: 0.228104 secs
I/O time: 0.000705 sec
Total time: 0.059334 secs
I/O time: 0.000750 sec
Total time: 0.049866 secs
I/O time: 0.000742 sec
Total time: 0.040905 secs
I/O time: 0.000759 sec
Total time: 0.0481751 secs
I/O time: 0.000731 sec
Total time: 0.0423901 secs
I/O time: 0.000755 sec
Total time: 0.0472808 secs
I/O time: 0.000836 sec
Total time: 0.044852 secs
I/O time: 0.000755 sec
Total time: 0.0466731 secs
I/O time: 0.000753 sec
Total time: 0.0430391 secs
I/O time: 0.000751 sec
Total time: 0.049391 secs
I/O time: 0.000833 sec
Total time: 0.0441971 secs
I/O time: 0.000853 sec
Total time: 0.049762 secs
I/O time: 0.000745 sec
Total time: 0.0492032 secs
I/O time: 0.000758 sec
Total time: 0.048234 secs
I/O time: 0.000814 sec
Total time: 0.0444431 secs
I/O time: 0.000759 sec
```

```
Total time: 0.047219 secs
I/O time: 0.000847 sec
Total time: 0.044739 secs
I/O time: 0.000764 sec
Total time: 0.0461791 secs
I/O time: 0.000747 sec
Total time: 0.0430441 secs
I/O time: 0.000763 sec
Total time: 0.0469651 secs
I/O time: 0.000741 sec
Total time: 0.0444539 secs
I/O time: 0.000870 sec
Total time: 0.0475101 secs
I/O time: 0.000848 sec
Total time: 0.044795 secs
I/O time: 0.000766 sec
Total time: 0.047745 secs
I/O time: 0.000738 sec
Total time: 0.04408 secs
I/O time: 0.000751 sec
Total time: 0.0478711 secs
I/O time: 0.000761 sec
Total time: 0.043556 secs
I/O time: 0.000865 sec
Total time: 0.049355 secs
I/O time: 0.000763 sec
Total time: 0.044637 secs
I/O time: 0.000758 sec
Total time: 0.0483341 secs
I/O time: 0.000848 sec
Total time: 0.0447631 secs
I/O time: 0.000851 sec
Total time: 0.0480509 secs
I/O time: 0.000771 sec
Total time: 0.0430942 secs
I/O time: 0.000753 sec
Total time: 0.0479989 secs
I/O time: 0.000761 sec
Total time: 0.043932 secs
I/O time: 0.000754 sec
Total time: 0.0487309 secs
I/O time: 0.000747 sec
Total time: 0.0432129 secs
I/O time: 0.000875 sec
Total time: 0.0497971 secs
I/O time: 0.000758 sec
Total time: 0.0454919 secs
I/O time: 0.000806 sec
```

```
Total time: 0.0472479 secs
I/O time: 0.000741 sec
Total time: 0.0452471 secs
```


Lungman DRR (Right to left)
Using a linear colour scale
Using a Power-law colour scale


Lungman DRR (Anterior to posterior)
Using a linear colour scale
Using a Power-law colour scale

```
[41]: if (len(runtimes_drr_rl) > 0):
          runtimes_drr_rl_avg = round(np.mean(runtimes_drr_rl))
          runtimes_drr_rl_std = round(np.std(runtimes_drr_rl))
      else:
          runtimes_drr_rl_avg = -1;
          runtimes_drr_rl_std = 0;
```

[42]:
```
if (len(runtimes_drr_ap) > 0):
    runtimes_drr_ap_avg = round(np.mean(runtimes_drr_ap))
    runtimes_drr_ap_std = round(np.std(runtimes_drr_ap))
else:
    runtimes_drr_ap_avg = -1;
    runtimes_drr_ap_std = 0;
```

8.2 Comparison the analytic simulation with the ground truth data

8.2.1 Quantitative validation

Compute image metrics between the two simulated images:

1. zero-mean normalised cross-correlation (ZNCC), and
2. Structural Similarity Index (SSIM).

ZNCC can be expressed as a percentage, which eases the interpretation of the numerical values. SSIM is a number between 0 and 1. A good value of ZNCC is 100%, and SSIM 1.

Note than the mean absolute percentage error (MAPE), also known as mean absolute percentage deviation (MAPD), is not used due to 1) zero values in the ground truth, and 2) values are very smalls. Using the MAPE would lead to large errors for these reasons.

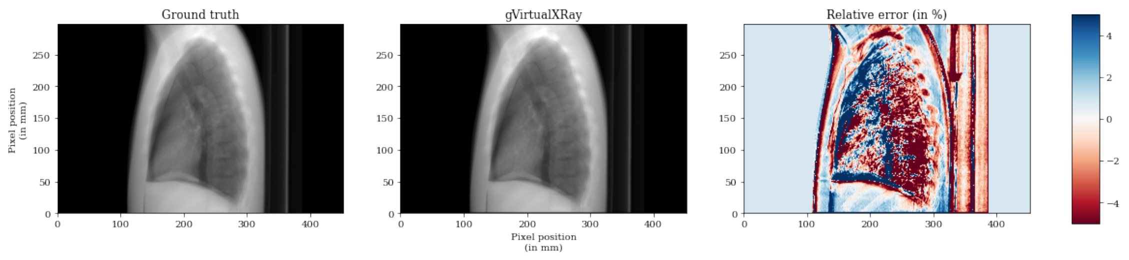
[43]:
```
def compare(ref_image, test_image):

    ZNCC = np.mean((ref_image - ref_image.mean()) / ref_image.std() *␣
 ↪(test_image - test_image.mean()) / test_image.std())
    print("ZNCC:", "{0:0.2f}".format(100 * ZNCC) + "%")

    offset1 = min(ref_image.min(), test_image.min())
    offset2 = 0.1 * (ref_image.max() - ref_image.min())
    MAPE = mape(ref_image.flatten() - offset1 + offset2, test_image.flatten() -␣
 ↪offset1 + offset2)
    print("MAPE:", "{0:0.2f}".format(100 * MAPE) + "%")

    SSIM = ssim(ref_image, test_image, data_range=ref_image.max() - ref_image.
 ↪min())
    print("SSIM:", "{0:0.2f}".format(SSIM))

    return ZNCC, MAPE, SSIM
```

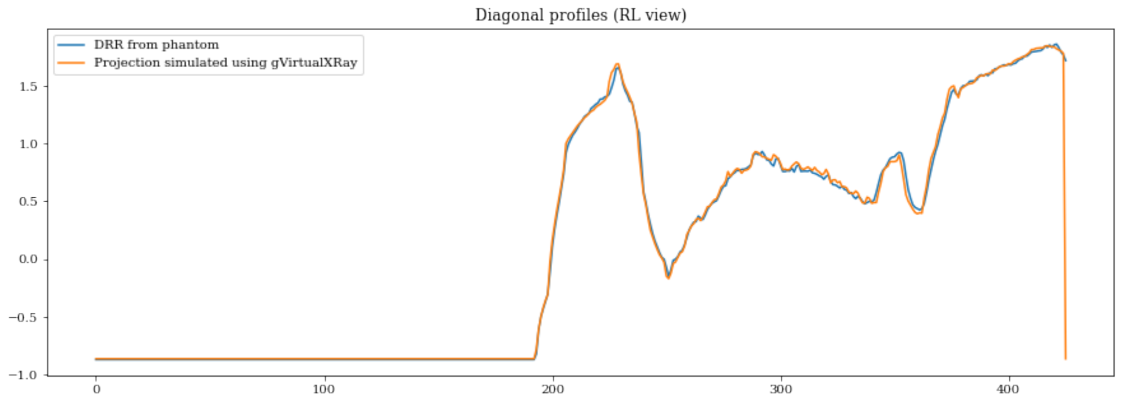
Medical orientations with plastimatch.

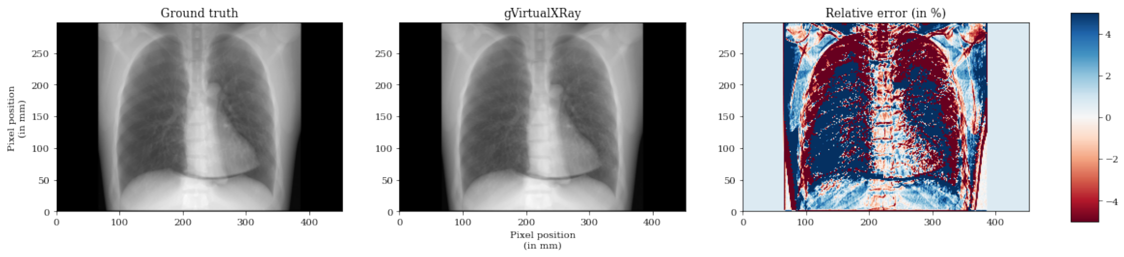
[44]:
```
spacing = json2gvxr.params["Detector"]["Spacing"]

print('R-L:')
ref_proj = DRR_RL
test_proj = minus_log_proj_rl
ZNCC_DRR_RL, MAPE_DRR_RL, SSIM_DRR_RL = compare(ref_proj, test_proj)
fullCompareImages(ref_proj,
                  test_proj,
                  "gVirtualXRay",
                  output_path + "/lungman-compare-projs-plastimatch-rl",
                  spacing,
                  False,
                  ref_proj.min(), ref_proj.max())

ref_diag = np.diag(ref_proj)
test_diag = np.diag(test_proj)

plt.figure(figsize=(15, 5))

ax = plt.subplot(111)

ax.set_title("Diagonal profiles (RL view)")

ax.plot(ref_diag, label="DRR from phantom")
ax.plot(test_diag, label="Projection simulated using gVirtualXRay")

ax.legend(loc='upper center', bbox_to_anchor=(0.5, 1.05),
          ncol=3, fancybox=True, shadow=True)

plt.legend()

plt.savefig(output_path + "/lungman-profiles-RL.pdf", bbox_inches = 'tight')
plt.savefig(output_path + "/lungman-profiles-RL.png", bbox_inches = 'tight')

print('\nA-P:')

ref_proj = DRR_AP
test_proj = minus_log_proj_ap
ZNCC_DRR_AP, MAPE_DRR_AP, SSIM_DRR_AP = compare(ref_proj, test_proj)
fullCompareImages(ref_proj,
                  test_proj,
                  "gVirtualXRay",
                  output_path + "/lungman-compare-projs-plastimatch-ap",
                  spacing,
                  False,
                  ref_proj.min(), ref_proj.max())

ref_diag = np.diag(ref_proj)
test_diag = np.diag(test_proj)

plt.figure(figsize=(15, 5))

ax = plt.subplot(111)
```

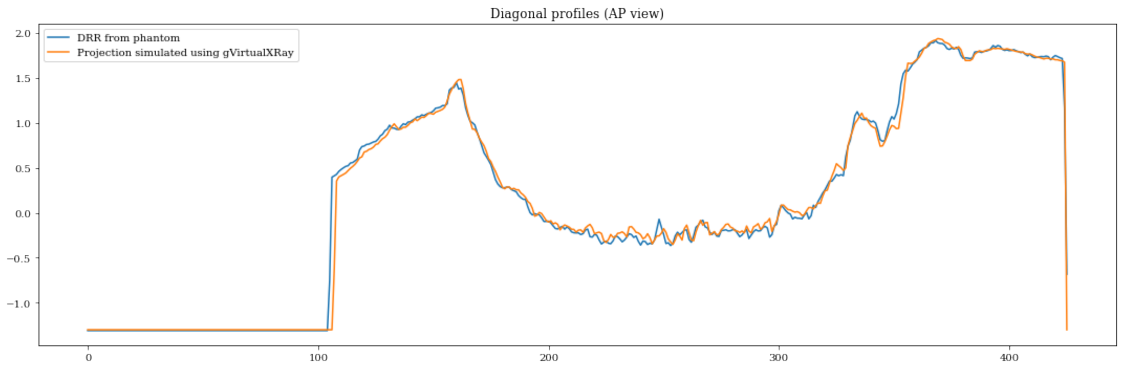
```
ax.set_title("Diagonal profiles (AP view)")

ax.plot(ref_diag, label="DRR from phantom")
ax.plot(test_diag, label="Projection simulated using gVirtualXRay")

ax.legend(loc='upper center', bbox_to_anchor=(0.5, 1.05),
          ncol=3, fancybox=True, shadow=True)

plt.legend()

plt.tight_layout()

plt.savefig(output_path + "/lungman-profiles-AP.pdf", bbox_inches = 'tight')
plt.savefig(output_path + "/lungman-profiles-AP.png", bbox_inches = 'tight')
```

```
R-L:
ZNCC: 99.65%
MAPE: 2.01%
SSIM: 0.98

A-P:
ZNCC: 99.36%
MAPE: 2.66%
SSIM: 0.92
```









Print a row of the table for the paper

[45]:
```
print("Lungman AP view & Plastimatch DRR & " +
      "{0:0.2f}".format(100 * MAPE_DRR_AP) + "\\%    &    " +
      "{0:0.2f}".format(100 * ZNCC_DRR_AP) + "\\%    &    " +
      "{0:0.2f}".format(SSIM_DRR_AP) + "    &    $" +
      str(DRR_AP.shape[1]) + " \\times " + str(DRR_AP.shape[0]) + "$    &    " +
      str(number_of_triangles) + "    &    " + str(runtimes_drr_ap_avg) + "␣
 ↪\\pm " + str(runtimes_drr_ap_std) + "    & " +
      "$" + str(runtime_avg) + " \\pm " + str(runtime_std) + "$ \\\\")
```

```
Lungman AP view & Plastimatch DRR & 2.66\%    &    99.36\%    &    0.92    &
$725 \times 426$    &    19277756    &    427 \pm 34    & $29 \pm 4$ \\
```

[46]:
```
print("Lungman RL view & Plastimatch DRR & " +
      "{0:0.2f}".format(100 * MAPE_DRR_RL) + "\\%    &    " +
      "{0:0.2f}".format(100 * ZNCC_DRR_RL) + "\\%    &    " +
      "{0:0.2f}".format(SSIM_DRR_RL) + "    &    $" +
      str(DRR_AP.shape[1]) + " \\times " + str(DRR_AP.shape[0]) + "$    &    " +
      str(number_of_triangles) + "    &    " + str(runtimes_drr_rl_avg) + "␣
 ↪\\pm " + str(runtimes_drr_rl_std) + "    & " +
      "$" + str(runtime_avg) + " \\pm " + str(runtime_std) + "$ \\\\")
```

```
Lungman RL view & Plastimatch DRR & 2.01\%    &    99.65\%    &    0.98    &
$725 \times 426$    &    19277756    &    456 \pm 101    & $29 \pm 4$ \\
```

9 All done

Destroy the window

[47]:
```
gvxr.destroyAllWindows()
```

```
Tue Sep 20 21:39:04 2022 ---- Destroy all the windows
Tue Sep 20 21:39:04 2022 ---- Destroy window 0(0x55558172f000)
```