Respiratory motion modelling group project for CMBI course

Overview

This coursework will get you to fit and evaluate various different correspondence models that relate the internal respiratory motion, as represented by deformable registrations, to a respiratory surrogate signal, measured from the patient's skin surface.

The Problem

Knowing how the internal anatomy moves with respiration can be very useful for both planning and guiding radiotherapy treatment. However, it can be very difficult to directly measure this motion during treatment. Therefore respiratory motion models have been proposed, which use a correspondence model to relate the motion of the internal anatomy to an easily measured respiratory surrogate signal, such as the height of the patient's chest/abdomen. These models are built prior to treatment from synchronised imaging and surrogate data, and can then be used to estimate the motion during treatment from just the surrogate data.
For this project the internal motion is determined from Cine CT data (thin CT volumes with only 12 slices) using deformable image registration. The registration result is stored as displacements of a regular control point grid. The correspondence models relate each of the control point displacements to the surrogate signal. The surrogate signal was generated from the average height of the patient's skin surface over the chest and abdomen. As well as using the measured surrogate signal, the rate of change (i.e. temporal gradient) of the surrogate signal and the respiratory phase (calculated from the peaks and troughs of the surrogate signal trace) will be used for some of the correspondence models in the advanced tasks.

The Model

For the core tasks the correspondence model will relate the displacements of the control points to the surrogate signal using either a linear model [1], a 2nd order polynomial model [2], or 3rd [3] order polynomial model.

$$x = c_1 s + c_0 \quad [1]$$

$$x = c_2 s^2 + c_1 s + c_0 \quad [2]$$

$$x = c_3 s^3 + c_2 s^2 c_1 s + c_0 \quad [3]$$

where x is the CP displacement, s is the surrogate signal value, and c_n are the model coefficients that need to be fit to the data.

The Data

You will be provided with data from one patient. Please remember that this is data from a real patient, and you should only use it for the purpose of

completing this coursework. All data will be from the same patient. Data will come from 5 different couch positions (i.e. different sections of the anatomy), and there will be 40 Cine CT volumes (and associated data) from each couch position. You will be given the following data:
Full CT volume (4DCT_ref_lungs.nii): end-exhale 4DCT volume - the lungs have already been segmented

Cine CT volumes (ct_couch_pos*_cine**.nii): These are for visually assessing the registrations and model estimates so you will just be given 10 (out of 40) volumes - the lungs will already have been segmented in each volume.

Registration results, images (reg*_couch_pos*_cine**_image.nii): two sets of registrations have been run (using different registration parameters). You will be given the resulting deformed volumes from both sets corresponding to the 10 Cine CT volumes you have been given. These are for comparing the registration results.

Registration results, transformations (reg_couch_pos*_cine**_cpg.nii): These contain the displacements of the Control Point Grids, CPGs, that define the registration results. These are used for building the motion models.

Respiratory surrogate data (resp_surr_couch_pos*.mat): a MATLAB file containing the value of the surrogate signal, the gradient of the surrogate signal, and the respiratory phase, corresponding to every Cine CT (note - only the surrogate signal is needed for the core tasks, the gradient and phase are needed for some of the advanced tasks).

Anatomical landmarks (landmarks_couch_pos*.mat): the co-ordinates of an anatomical landmark in every Cine CT volume and of the corresponding landmark in the full CT volume.

MATLAB Code

I will provide you with some MATLAB code for reading in the images and transformations, for displaying the images, and for applying the transformations (although you are welcome to use your own code if you prefer). You will need to write all your own code to fit the models and to generate new transformations from the models.
To load the data use the load_nii function (found in the NIFTI_20110921 folder – this function was originally downloaded from the matlab file exchange) – this is used to load both the images and the transformations (they are both saved in nifti format)
To display a slice from a volume use the dispNiiSlice function. To display slices from two volumes using a colour-overlay use the dispNiiSliceColourOverlay function.

To deform a volume with a B-spline transformation use the deformNiiWithCPG function, and to transform one or more points with a B-spline transformation use the transPointsWithCPG function.
If you have any questions about the matlab code, or need any help running it, ask me in the tutorial sessions or email me. You are welcome to re-use the code for your own research, but if you do please acknowledge that the code came from me, and definitely do not try and pass it off as your own code!

Core Tasks

1) Decide which set of registrations best aligns the full volume with the Cine CT volumes

To do this you will need to read each Cine CT volume and the corresponding registration result volumes into MATLAB, and display slices from these volumes to visually assess the results and determine which result best aligns the data.
Note, because of the 'slab like' nature of the data, only some of the axial slices contain the lungs, depending on which couch position the data comes from. The slices with lungs in them are:
couch position 1: slices 66-76
couch position 2: slices 55-65
couch position 3: slices 44-54
couch position 4: slices 34-43
couch position 5: slices 23-33
You should compare the registrations and Cine CT volumes at several different slices and over all 10 volumes. This should enable you to see which set of registrations best aligned the volumes. It should also enable you to get a feel for how much respiratory motion there is and how well the registrations can recover it. Comment on how the motion varies across the different couch positions, and how well the registrations can recover the motion.

2) Fit a linear correspondence model

The CPG for each registration result can be read in to MATLAB using the provided code. The CPG is stored in a 5D array – but the 4^{th} dimension is ‘redundant’ (i.e. there is only 1 element along the 4^{th} dimension – in the nifti format the 4^{th} dimension is used for time, and each registration result is from a single time), and the 5^{th} dimension has 3 elements for the displacement in the x, y, and z directions. The surrogate signal values can be loaded into MATLAB by opening the surrogate data file. You should then plot the value of one of the CP displacements on the vertical axis against the value of the surrogate signal on the horizontal axis. You should plot the values for all 40 registration results. You should make a plot for each couch position – the indexes into the 5D arrays that should be used for each couch position are:

couch position 1: (30,40,33,1,3)
couch position 2: (30,40,28,1,3)
couch position 3: (30,40,23,1,3)
couch position 4: (30,45,18,1,3)
couch position 5: (30,45,13,1,3)

You should then fit a 1D linear model [1] to this CP displacement. Once you have fit the 1D model you should plot the model fit over the plot of the CP displacement. See my lecture slides for a similar plot using a 3rd order polynomial model.
Once you know you have successfully fit the model to the CP displacement specified above you should proceed to fit a separate model to every CP displacement. This can be done by looping through every CP displacement, putting the values from all 40 registration results into a vector, and fitting the model for that CP displacement. Alternatively it can be done by forming a large matrix containing all 40 registration results for every CP displacement, and fitting all the models simultaneously. See my slides for a hint on how to do this, and ask me or the lab assistants if you need help.

3) Fit the polynomial correspondence models

Follow the approach in the previous task but fit the 2^{nd} and 3^{rd} order polynomial models instead of the linear model. Plot the model fits for the same CP displacement as before. Comment on how well each of the models fit the CP displacement data. What limitations are there on the type of motion that can be modelled using the linear and polynomial correspondence models?

4) Evaluate the motion models

To evaluate the motion models you should use the leave-one-out method. Fit the models as above but only using 39 of the 40 registration results. Use each model to estimate the transformation (CP displacements) for the surrogate signal value corresponding to the left out registration result. In order to assess the estimated transformation you will need to store it in a nifti structure like the registrations – this can be done by copying the header from the registration result, reshaping the estimated CPG into a 5D array, and assigning it to the .img in the nifti structure. Assess the model estimates using the three techniques below. Repeat this process for all 40 registrations.

Visual assessment. Use the transformation estimated by the model to deform the full volume, then visually compare the result in the same way as you did for the registration results. The provided matlab code can be used to read in the full volume and deform it using the estimated transformations (if you need help applying the transformation to the full volume ask me or the lab assistants). Note - as you only have the first 10 Cine CT volumes you can only visually assess the model estimates corresponding to these Cine CT volumes.

Calculate the deformation field error: the difference between the deformation field resulting from your estimated transformation and the deformation field resulting from the left-out registration result. The deformation fields can also be calculated with the deformNiiWithCPG function. Find the mean and standard deviation of the 3D Euclidean deformation field error for each Cine CT. The deformation fields outside the lungs will not be well constrained so should be ignored when evaluating the models. Note – voxels in the Cine CTs which are outside the lungs are set to -1.

Find the landmark error: you should do this for the original registration results as well as the model estimates. The landmark locations in the Cine CT and full volumes can be loaded from the data file. The landmarks in the Cine CT volumes can be transformed into the full volume space using the transformPointsWithCPG function - note, the Cine CT landmark coordinates are transformed into the full CT space, and not the other way around, as you are transforming point coordinates rather than forming an image. The landmark error is the 3D Euclidean distance between the transformed landmark and the landmark in the full volume. Note, for some couch positions (e.g. 5) it was not possible to locate the landmark point in all Cine CT volumes (as there was too much motion) - in these cases the landmark coords will be given as NaN in the data file.

What are the advantages and disadvantages of the three different methods of assessing the models? Do the results from the three methods agree with each other? How do the results for the different models compare to each other and is this what you would expect? Why was the leave one out method used and do you think this was the best approach for this data? Can you think of any criticisms against using the leave one out method to assess the models ability to estimate respiratory motion?

Also calculate the AIC and BIC for each of the different models. Which is the ‘best’ model according to these measures? Does this agree with your results above?

5) Estimate the uncertainty in the models

Use a bootstrapping method to estimate the distribution of model parameters and their uncertainty for each of the three models. Plot the results for the same CP displacement used in tasks 2 and 3 for each model parameter from the three different models. Comment on the similarities and differences between the results for the different models and parameters. Comment on which bootstrapping method you used and why.

Advanced tasks

Complete one or more advanced tasks

Experiment with separating the registrations into those that are from inhalation (respiratory phase < 0.5) and those that are from exhalation

(phase >= 0.5), and fitting a separate model to each. Evaluate the model estimated transforms using the leave one out methods in the same way as for the previous models. Does fitting separate models for inhalation and exhalation give better results and why?

Try fitting different correspondence models, e.g.:

a cyclic B-spline model relating the CP displacements to the respiratory phase (see references for the equation for the B-spline model),

a 2D linear model relating the CP displacements to both the signal value and the signal gradient,

a 2D polynomial and/or a 2D B-spline model relating the CP displacements to both the signal value and the signal gradient,

any other models you think appropriate.

Think carefully about whether it makes sense to split the data into inhalation and exhalation for the B-spline and 2D (and your own) models. Evaluate the models using the same methods as before. How do the results for the different models compare to each other and what does this tell us about the models and the types of motion and variation seen in the data?

Experiment with different fitting methods, e.g. using pinv instead of the mldivide (\) operator, or using MATLABS inbuilt functions for model fitting). How do the models from the different fitting methods compare to each other. How does the computation time vary for the different fitting methods?

Apply Principal Components Analysis (PCA) to the registration results, and then fit a model relating the PCs to the surrogate signal (see Ref 4). How do the results compare to the other models?

References

Ref 1: McClelland et al, 'Respiratory motion models: A review' Medical Image Analysis, 2013

Ref 2: McClelland, 'Estimating internal respiratory motion from respiratory surrogate signals using correspondence models,' chapter in book: '4D Motion Modeling: Estimation of Respiratory Motion for Radiation Therapy,' editors Ehrhardt and Lorenz, in press.

Ref 3: McClelland et al, 'Inter-fraction variations in respiratory motion models' Physics Medicine and Biology 2011

Ref 4: Zhang et al, 'Correction of motion artifacts in cone-beam CT using a patient specific respiratory motion model' Medical Physics 2010

Ref 5: Rueckert et al, ‘Nonrigid registration using free-form deformations: application to breast MR images’ TMI 1999

Ref 6: McClelland et al, ‘Combining image registration, respiratory motion modelling, and motion compensated image reconstruction’ WBIR 2014