

# **Student Talks**

## **Presentation Abstract**

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# Abstract

In medical image analysis it is often useful to register images from different individuals so that equivalent structures are aligned. This provides a common frame of reference in which different individuals can be compared or change in one individual over time can be highlighted.

Registration comprises data transformations and a measure of similarity. Similarity is optimised by applying spatial transformation to images and these transformation can be rigid – or more usefully – non rigid. A common approach to solving this problem is to select one image (the reference) and transform all the other images to fit it. This approach leads to an arbitrary solution and we contend that the problem should be solved in a group-wise manner, without relying on this choice of a reference.

By registering images, one can identify the corresponding points and this correspondence is dense. These correspondences can then be used to *automatically* construct a statistical model which encapsulates variation in the images. It is of high value to 3-D models where manual mark-up of correspondences becomes laborious.

The experiments thus far employed clamped-plate splines for transformations. The similarity measure of interest approximates description length of a model representation of all data. It does so by constructing a model of the data and calculating the determinant of this model. The advantages of a group-wise algorithm were investigated in 1-D before attempting similar 3-D registrations.

Results show that registration is practical using these criteria and models can be constructed automatically, without prior data annotation. Although it is unclear whether the group-wise approach leads to a better solution, it does provide a unique one.