Subject: Realigning command in IDL.
Posted by mph522 on Thu, 18 Feb 1999 08:00:00 GMT

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Dear all,

I was just wondering whether there was a simple command in IDL/wave to realign two images together. I have two 3D MR datasets from the same subject which were taken six months apart, from which I'm trying to detect changes in brain volume (looking for voxels whose intensities have changed by a certain amount).

However, even after realigning and normalising the images using SPM96, the images are still not perfectly matched and this is leading to errors in my results.

Thanks in advance,

Carol.

Subject: Re: Realigning command in IDL.
Posted by David Foster on Mon, 22 Feb 1999 08:00:00 GMT

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Carol Docherty wrote:

>
> Dear all,
>
> I was just wondering whether there was a simple command in IDL/wave to realign two images together. I have two 3D MR datasets from the same subject which were taken six months apart, from which I'm trying to detect changes in brain volume (looking for voxels whose intensities have changed by a certain amount).
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Carol -

2D images can be manipulated using POLYWARP() and WARP_TRI(), but since
your data is 3D you may want to try either:

1) AIR (Automated Image Registration) by Dr. Roger Woods of
   the Laboratory of Neuro Imaging at UCLA:

http://bishopw.loni.ucla.edu/AIR3/

Source code is freely available, and it's supposed to work
fairly well.

2) You might want to get AFNI (Analysis of Functional Neuro Images)
by registering with the author, Dr. Robert Cox, at:

http://varda.biophysics.mcw.edu/~cox/index.html

This package is really meant for functional MRI, but it has a 3D registration program that is supposed to be much faster than AIR and produce nearly identical results. It's free, but you must register before downloading the software.

If neither of these solutions work for you or don't provide needed functionality then email me and I'll explain what we've done here. We're basically using a method similar to that used in AIR (known as the Woods algorithm, using SVD to compute translations, rotations and scaling required to align two series of tie-points).

Feel free to call me if you have any questions. Good luck! You might consider segmenting your volumes into gray/white/csf and looking at the totals of those compartments; this method would be less susceptible to misregistration errors than trying to do a voxel-by-voxel comparison.

Dave
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David S. Foster   Univ. of California, San Diego
Programmer/Analyst   Brain Image Analysis Laboratory
foster@bial1.ucsd.edu Department of Psychiatry
(619) 622-5892   8950 Via La Jolla Drive, Suite 2240
La Jolla, CA 92037
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