1 Program 3ddup

1.1 Purpose

Program 3ddup will make a 'Warp-on-demand' duplicate copy of a given 3D dataset. The new dataset will consist only of a .HEAD file. There are two applications for this capability:

- It is possible to change the dataset type with 3ddup. This means that the original dataset can be anatomical and the new dataset functional (-fim type). The only disk space penalty will be a few Kbytes for the new .HEAD file—there is no need to duplicate the .BRIK file. In this way, for example, it is possible to gather Magnetic Resonance Angiograms (MRA data) and view the 3D dataset either as anatomy (gray background) or as function (overlaid in color).

- This is the only way to get *AFNI* to write out a resampled version of a dataset in the +orig view. *AFNI* will not overwrite a .BRIK file unless the dataset is warped from another dataset. (This is to prevent destruction of data that cannot easily be recreated by 'Warp-on-demand'.) With 3ddup, the new dataset can be overwritten at whatever resolution desired (creating a new .BRIK file), using the 'Define Datamode' controls. (Of course, after it is resampled and overwritten, it is no longer a perfect duplicate of the original.)

Note that when resampling a functional dataset (using the button 'Write Function Brick'), it will be written out onto the grid corresponding to the current anatomical dataset, at the currently chosen grid size. This grid will have cubical voxels if Warp-on-demand is chosen; however, if View-data-brick is chosen in *AFNI*, then the output grid will conform to the anatomy data brick grid, which is not necessarily cubical.

If the function is not defined on parts of the anatomy, then zeros are written in those locations. If the original function brick extends outside the domain of the anatomy brick, then the newly resampled function brick will be clipped to fit the anatomy brick.

1.2 Usage

3ddup [options] dataset

1.3 Options

-type Convert to the given 'type', which must be chosen from the same list as in to3d.

-session dirname Write output into given directory (default=./).

-prefix pname Use 'pname' for the output directory prefix (default=dup).

N.B.: Even if the new dataset is anatomical, it will not contain any markers, duplicated from the original, or otherwise.