What's going on in my fMRI processing?

Step 1, **Slice Timing**:
The fMRI images you collected are made up of 42 axial slices, each of which was collected one after the other. This step interpolates the signal between scans in an attempt to recreate images that would have been collected simultaneously.

Step 2, **Coregister:Estimate**:
The algorithm that will stretch the anatomical scan into a "normalized" size so that it can be directly compared to other brains assumes that the image is roughly in line with a template supplied by SPM; this step helps line the two images up.

Step 3, **Segment**:
This step normalizes the anatomical scan so that it is in the common space used by other investigators. This way, we can localize activity in common atlases, compare activity between groups of subjects, and make sure our results fit into the pretty display options in SPM. The same math will be used in Step 6 to normalize our functional images. The step is called "Segment" because it also creates tissue-specific images that include only our subjects' grey matter, white matter, bone, or CSF.

Step 4, **Realign:Estimate and Reslice**:
This step automatically lines up all of the fMRI images one on top of the other so that the same voxel represents the same place in the brain across time, even if the subject moved a little or if "drift" caused a change in localization of the signal.

Step 5, **Coregister:Estimate**:
This time, we are lining up the fMRI images as best we can to the anatomical scan. After having done so, we can then use the normalization parameters (created in Step 3) to warp the functional images into common atlas space.

Step 6, **Normalize: Write**:
This step writes out the fMRI images in common atlas space.

Step 7, **Smooth**:
This step 'blurs' the images in 3 dimensions to remove high frequency spatial noise and satisfy the normal distribution requirement for residuals in parametric hypothesis testing. When analyzing groups of subjects, this step also allows for combining activity between subjects that have slightly different anatomical locations.

Step 8, **fMRI Model Specification**:
In this step, we build a General Linear Model of the expected timecourse of activity for voxels that significantly correlate with our task.

Step 9, **Model Estimation**:
Math math math. Here, our model is fitted to the observed activity at each voxel. Estimations of the effect size (the magnitude of activity that is correlated with our expected timecourse) at each voxel are calculated.

Step 10, **Contrast Manager**:
In this step, we decide which effects we want to test for significant activity (i.e., we indicate that we want to test the increase in effect size between the 2-Back and 1-Back conditions in our task).

Step 11, **Results Report**:
Gives a quick and dirty printout of voxel locations that have significantly increased activity from 1-Back to 2-Back in our subject's brain during this task.