Change in normalization processes

I have done some changes in anatomical normalization processes, and I am about do perform more changes, since I need to integrate normalizaton processes in the T1 pipeline. I hope it will not cause any perturbations, but... this is a warning... I am working on the stable version since I don't know which part of trunk is to be merged with stable or not.

- builtin databases to access FSL and SPM templates: a small database it setup on the fly (with an ad-hoc ontology) to allow access to the FSL templates within its own installation for FSL normalization. I am doing the same for SPM. The problem with SPM is to determine the main SPM installation directory without actually running Matlab (I want to avoid it to save startup time and licenses).
- FSL normalization output matrix type was wrong: it was using a SPM type.
- SPM normalization matrix type: the normalization processes were using a "SPM transformation parameters" type (defined in the t1mri toolbox), whereas a "SPM2 normalization matrix" type was already existing in axon, and was used in SPM normalization conversion processes. So I will get rid of the duplicate "SPM transformation parameters" type and replace it in the fmri toolbox.
- some processes were declaring unused parameters ('voxel_size', 'anat_voxel_size'...): I will comment them out
- some parameters links were building attributes dictionaries from a diskitem, wich were picking explicit ontology attributes ("subject", "protocol"...), before passing it to findValue(). It is simpler and cleaner to just pass the input diskitem, so I will change it.

If there are any side effect in the next few days, just tell me...

Denis (2009/12/21)