IMAGE PROCESSING PIPELINE FOR MULTIPLE IMAGES WITH SPM

The following manual provides a detailed list of steps to segment, register and smooth multiple images in a given folder without having to manually select each file.

1. Run SPM in Matlab command window

>> spm

Three different windows may be opened:

1. Menu
2. Graphics
3. 7219
4. In the Menu window, select Batch. A new window (Batch Editor) will open.
5. In the upper bar, select BasicIO 🡪 File/Dir Operations 🡪 File selector (Batch Mode). You will see “File Selector (Batch Mode)” appear in the Module List section at the left.
6. In Current Module: File Selector (Batch Mode):
   1. Directory: Select the desired folder with the images
   2. Filter: Double click on <-X and write, for example, “sub”
   3. Descend into subdirectories: Select No.

We are now finished with the File Selector section.

1. Back again at the upper bar, from SPM, select Spatial 🡪 Segment. In the Module List section, Segment will appear under File Selector (Batch Mode).
2. In Current Module: Segment
   1. Data: Clicking here allows more channels of images to be deﬁned. This is useful for multi-spectral segmentation (eg if there are T2-weighted and PD-weighted images of the same subjects), but as we will just be working with a single image per subject, we just need one channel
      1. Channel
         1. Volumes: Here you specify all the IXI scans to be segmented. Click and select “Dependency” on the lower right. A “Volumes” window will open, select “File Selector…” And ok.
         2. Bias regularisation: Leave this as it is. It works reasonably well for most images.
         3. Bias FWHM: Again, leave this as it is.
         4. Save Bias Corrected: This gives the option to save intensity in homogeneity corrected version of the images, or a ﬁeld that encodes the inhomogeneity. Leave this at Save nothing because we don’t have a use for them here.
   2. Tissues: This is a list of the tissues to identify
      1. Tissue: The ﬁrst tissue usually corresponds to grey matter.
         1. Tissue probability map: Leave this at the default setting, which points to a volume of grey matter tissue probability in one of the images released with SPM12.
         2. Num. Gaussians: This can usually be left as it is.
         3. Native Tissue: We want to save Native + Dartel imported. This gives images of grey matter at the resolution of the original scans, along with some lower resolution “imported” versions that can be used for the Dartel registration.
         4. Warped Tissue: Leave this at None, as grey matter images will be aligned together with Dartel to give closer alignment.
      2. Tissue: The second tissue is usually white matter.
         1. Tissue probability map: Leave alone, so it points to a white matter tissue probability map.
         2. Num. Gaussians: Leave alone.
         3. Native Tissue: We want Native + Dartel imported.
         4. Warped Tissue: Leave at None.
      3. Tissue: The third tissue is usually CSF.
         1. Tissue probability map
         2. Num. Gaussians
         3. Native Tissue: Just chose Native Space. This will give a map of CSF, which can be useful for computing total intra-cranial volume.
         4. Warped Tissue: Leave at None
      4. Tissue: Usually skull.
         1. Tissue probability map
         2. Num. Gaussians
         3. Native Tissue: Leave at None.
         4. Warped Tissue: Leave at None
      5. Tissue: Usually soft tissue outside the brain
         1. Tissue probability map
         2. Num. Gaussians
         3. Native Tissue: Leave at None.
         4. Warped Tissue: Leave at None
      6. Tissue: Usually air and other stuff outside the head
         1. Tissue probability map
         2. Num. Gaussians
         3. Native Tissue: Leave at None.
         4. Warped Tissue: Leave at None
   3. Warping & MRF
      1. MRF Parameter: This tries to remove isolated mis-classiﬁed voxels, and generally tidy up the tissue classes. It’s probably best to leave this at the default setting of 1.
      2. CleanUp: This is a bit of an ad hoc procedure that tries even harder to eliminate mis-classiﬁed tissues outside the brain6. Again, the default settings should work reasonably well.
      3. Warping regularisation: This is a penalty term to keep deformations smooth. Leave alone.
      4. Sampling distance: A speed/accuracy balance. Sampling every few voxels will speed up the segmentation, but may reduce the accuracy. Leave alone
      5. Deformation ﬁelds: Not needed here, so leave at None

Once everything is set up (and there are no “<-” symbols, which indicate that more information is needed), then you could click the Run button (the green triangle) - and wait for a while as it runs. This is a good time for questions. If there are hundreds of images, then it is chance to spend a couple of days away from the computer.

After the segmentation is complete, there should be a bunch of new image ﬁles generated. Files containing “c1” in their name are what the algorithm identiﬁes as grey matter. If they have a “c2” then they are supposed to be white matter. The “c3” images, are CSF. The ﬁle names beginning with “r” (as in “rc1”) are the Dartel imported versions of the tissue class images, which will be aligned together next

Now we are done with the Segmentation.

1. In the upper bar, in SPM select Tools 🡪 Dartel tools 🡪 Run Dartel (create template), and Run Dartel (create template) will appear under Segment in the Module List.
2. In Current Module: Run Dartel (create template):
   1. Images: Two channels of images need to be created. Click on Images and in the lower section Curent Item: Images, select New: Images twice.
      1. Images: Select “Dependency” in the lower right corner and select Segment: rc1 Images.
      2. Images: Select “Dependency” in the lower right corner and select Segment: rc2 Images.
   2. Settings: There are lots of options here, but they are set at reasonable default values. Best to just leave them as they are.

Now we are done creating the templates. It will generate u\_rc1 files and a series of template images.

1. In the upper bar, in SPM select Tools 🡪 Dartel tools 🡪 Normalise to MNI space, and Normalise to MNI space will appear under Run Dartle (create template) in the Module List.
2. In Current List Module: Normalise to MNI space:
   1. Dartel Template: Select “Dependency” in the lower right corner and select “Run Dartel (create Templates): Template (Iteration 6)”.
   2. Select according to: Choose Many Subjects, as this allows all ﬂow ﬁelds to be selected at once, and then all grey matter images to be selected at once.
      1. Many Subjects
         1. Flow ﬁelds: Select all the ﬂow ﬁelds created by the previous step (u\_\*.nii). Select “Dependency” and select “Run Dartel (create Templates): Flow Fieds”.
         2. Images: Need one channel of images if only analysing grey matter. Select “Dependency” and select “Segment: c1 Images”. Create 2 new images and again, select “Dependency” and then select “Segment: c2 Images” and “Segment: c3 Images” respectively.
         3. Voxel Sizes: Specify voxel sizes for spatially normalised images. Leave as is (NaN NaN NaN), to have 1.5mm voxels.
         4. Bounding box: The ﬁeld of view to be included in the spatially normalised images can be speciﬁed here. For now though, just leave at the default settings.
         5. Preserve: For VBM, this should be set to Preserve Amount (“modulation”), so that tissue volumes are compared.
         6. Gaussian FWHM: Specify the size of the Gaussian (in mm) for smoothing the processed data by. This is typically between about 4mm and 12mm. Use 10mm for now.

Then hit run.