In all validations of new code, use finger tapping data sets:

There is a folder "TestDatasets" to the SPM svn. In it, there are 2 different data sets: a single block session (FingerTapping\_B\_Dataset.rar) and a 2 sessions data set with the same block data and also the event-related data (FingerTapping\_BE\_Dataset.rar).  
  
We will use this as a standard dataset to validate the NIRS toolbox. In general, let's use this folder on the svn to put small datasets for testing.

OVERALL TO VALIDATE END RESULTS:

1. Run NIRS\_SPM data sets on NIRS\_SPM toolbox and on nirs10, and  
   compare results.

ISSUES TO ADDRESS IN SPECIFIC MODULES:

When you look at one issue: Please report results in this file with details so that once a problem is solved, we do not go back to it. The goal is to try to get some closure on some of these interrogations.

1. Module OD to HbO/HbR:
   1. Check calculation, e.g. is the order of wavelengths consistent throughout the code (all the modules)? what happens if 830 is wavelength 2 instead of 1?

Michèle, June 14th 2012

For module nirs\_run\_ODtoHbOHbR, the order of wavelengths is consistent and, no matter the number or order\*\*\* of the wavelengths (specified by "NIRS.Cf.dev.wl(NIRS.Cf.H.C.wl)" for each channel), the output is still of the form

[ conc\_HbO\_pair1(time1) conc\_HbO\_pair1(time2) ...;

conc\_HbO\_pair2(time1) conc\_HbO\_pair2(time2) ...;

...

conc\_HbR\_pair1(time1) conc\_HbR\_pair1(time2) ...;

... ];

\*\*\*However it is important that the order of the channels is such that wavelengths are grouped and not alternated. For example :

ch1 = 830

ch2 = 830

ch3 = 830

ch4 = 690

ch5 = 690

ch6 = 690

is OK

but

ch1 = 830

ch2 = 690

ch3 = 830

ch4 = 690

ch5 = 830

ch6 = 690

is NOT OK

The index for the wavelengths for each channel can be checked in NIRS.Cf.H.C.wl (this field should be something like 2,2,2,1,1,1 and NOT 1,2,1,2,1,2).

Also, if values for DPF and PVF are entered as an option in the module (job.DPF.DPFval and job.PVF.PVFval), they must be entered in an order corresponding to that in NIRS.Cf.dev.wl, that is the order of the wavelengths of the device used (i.e. for CW6, wavelength1 = 690, wavelength2 = 830 : NIRS.Cf.dev.wl = [690 830].)

I have not checked the other modules.

One might want to try and run this module on data acquired at 3 or more wavelengths in order to double-check the validity of the module.

* 1. Is the order of filtering of the data, and the nature of the filters, similar or different to other standards, such as Homer or NIRS\_SPM?

1. Module coregistration:
   1. For about 10% of Claudine/Michele's patients, the positioning of the optodes is quite wrong. What is this due to? How can this be fixed? (If it is a problem with the input brainsight files that were wrong, then this should not be fixed in the toolbox code)
   2. There are several other coregistration modules (manual, coreg with T1, with template). Do these modules work? Are they useful or should they be removed?
2. Some modules have not been maintained: module to exclude channels based on stdev, module for heart rate, module for detecting movement, validate that they still work properly.
3. Averaging module: needs validation (use tapping data above)
4. GLM:
   1. PCA option not working
   2. The two high pass filters should be combined into one option
   3. option “filter design matrix” should be removed
   4. option “units for design” should be removed
5. Group module, and 1-anova, 2-anova (and eventually mixed 2-anova) modules:
   1. Improve the documentation on these modules. Explain what each module is designed to do. Specifically:
      1. Group: does averaging over the contrasts defined in the contrast module
      2. 1-anova: does a between-subject 1-anova
      3. 2-anova: does a within-subject repeated measures 2-anova where 1 factor is sessions and the other is conditions (i.e. stimulus type)
      4. Mixed 2-anova: when coded, will do a mixed 2-anova, between-subject on one factor, and within subject on conditions on the other factor
   2. Large arrays of responses (betas from the 1st level of the GLM or averaging module) are constructed. Is the correct data being put there for each of the many options? The way these arrays are filled is a mess, and needs to be cleaned up.
   3. Check that the following options do what they should:
      1. Group: FFX is really a fixed effect study
      2. Group: RFX is really a random effect study
      3. Contrast: the “group\_multi\_session” option: is it correctly implemented at the group of subject level?
6. Is NIRS\_SPM code for EC and other corrections implemented correctly in nirs10?  
   What about the fixes to the calc\_EC function needed due to Inf obtained when calculating exponentials? To test for that, one needs results following the GLM that are identical between nirs10 and NIRS\_SPM (possibly simulated data) and check that the results of the topographic reconstructions are the same.
7. Contrast module: Spatial\_LPF option: does it work?
8. Contrast and group modules: correction based on tube formula. Does it still work? Should all the code (several functions, often labeled “old”) pertaining to tube formula be removed?

NICE TO HAVE:

1. GLM estimation: this module is a mess, needs good clean up
   1. remove subsessions?
2. contrasts and further modules (group, anovas):
   1. Remove option to show only activations or deactivations but not both
   2. Remove option “ do not combine colorbars”
3. 3D: all needs validation; reml not quite working
4. Add\_test\_stimuli and ROC: this module needs to be documented and simplified.

SPECIFIC PROBLEMS TO EPILEPSY OR SPECIFIC STUDIES:

1. Does the module nirs\_boxy work correctly for the 1st epilepsy patient, 101LH?  
   The issue is multiplexing with fewer sources. Even if the code runs, it may not be reading  
   the ISS Imagent files correctly. Verify.
2. read\_nirs\_onsets for epilepsy onsets. This module removes some types of onsets. This should be documented so that users know how to use it. Also, the permute\_onsets module does not work correctly.
3. Find out why Claudine's study initially gave positive results but not anymore