**Cerebral Blood Flow Processing (John Hood - 11/5/2012)**

1. Get PET data from pet archives (**rlogin light**, **arcfind** pXXXX, **arcget** pXXXX).
2. Use **betawel** to determine calibration factor (will need Beta Probe Cal Sheet from patient study and a \*.crv file).
   1. Create a pXXXX.wel file in the directory
   2. Enter data. Make sure to press enter after each number was entered.
   3. Note well calibration factor (approximately around 20)
3. Check experimental log sheet for any unusual events.
4. Get plasma/whole blood data sheet taken during the study
5. Get the following Arterial Blood Gas
   1. Get the following data:
      1. Mean hematocrit (Hct)
      2. Mean arterial oxygen content = Hb (approx. 13) x 0.951 (on sheet, it normally is 95.1) x 1.39
6. Use **headstart** to determine the start of frame 3 for non-dynamic studies (and note it) (**headstart** pXXXXoc1.r), usually 16.1
7. Run **betadcv** for water studies (betadcv pXXXXho1)
   1. Enter well calibration factor
   2. Y
   3. 1
   4. 2 – extension
   5. Hct value
   6. 2
   7. 2
   8. Y
   9. 12
   10. Dry syringe weight
   11. Wet syringe weight
   12. Time sampled
   13. Time counted
   14. Total counts
   15. Background counts
   16. Correction factor – 1.02379
   17. N
8. Run **betadcv** for CO studies (betadcv pXXXXco1)
   1. Enter well calibration factor
   2. Y
   3. 1
   4. 2 – extension
   5. Hct value
   6. 2
   7. 2
   8. Y
   9. 12
   10. Dry syringe weight
   11. Wet syringe weight
   12. Time sampled
   13. Time counted
   14. Total counts
   15. Background counts
   16. Correction factor – 1.02379
   17. N
9. Check each plot using **plotcrv** (plotcrv pXXXXho1.crv)
10. Open pXXXXho1\_g3.v file using vidi
    1. In vidi, open \*\_g3.v file (first frame, all planes)
    2. Get x value by going to middle frame (press middle button) and noting the x value in the bottom left side of the vidi window. Then switch orientation from transverse to sagittal view. Pick a point in the brain that is sort of the middle (but a smidgeon biased closer to the occipital lobe) and get the corresponding y and z values from it. Note these x, y, and z coordinates.
11. Determine the dynamic start times for ho studies using **sumdyn40** (sumdyn40 . p XXXX ho 1 v) (unsure about this a bit) ….
    1. Enter x coordinate
    2. Enter y coordinate
    3. Enter z coordinate
    4. Y
    5. 0
    6. Note which frame update was observed on graph that comes out
    7. Enter this frame as first frame of 40-sec integration (i.e. 13-32)
    8. Run **makedta** to determine shifts in ho and co curves
       1. p7861
       2. 2 (ho and co)
       3. 2 (ho)
       4. Ho1
       5. 0
       6. Enter, enter again
       7. 22
       8. Vidi
       9. Enter
       10. Zoom
       11. 0
       12. 40
       13. Shift
       14. Move curves so their uptake is really close to each other. Typical value will be -8 or so
       15. Enter
       16. Continue
       17. 3 (co1)
       18. Oc1
       19. Enter
       20. Value from headstart on oc curve
       21. 3
       22. Enter
       23. Enter (no shift needed)
12. Smooth co images using gauss of 0.3 (**gauss** p7861oc1.v 0.3)
13. Run metproc on all emission studies (**metproc** p7861)
    1. enter
    2. \_g3.v
    3. N
    4. Enter pie slope (which is 4.88 right now for 3D, but might change)
    5. Enter
    6. Enter
    7. Enter
14. Use vidi to get global CBF and CBV values
    1. Open pXXXXho1\_g3.v as image 1
    2. Open Viewer (to determine top most and bottom most slices to be included in the brain mask, example would be 14 to 37)
    3. Make mask (press mask, enter 14 on top, and 37 on bottom, for example. Press enter after entering numbers to make sure they “register” in the program)
    4. Create Mask
    5. Apply Mask
    6. Open Processing
       1. Image 1
       2. CBF
       3. Choose corresponding \*hdr file
    7. Open Mask
       1. Press Statistics
    8. Do the same for co
    9. Typical CBF values are ~46 while typical CBV values are ~2.82
    10. All of these statistics will be saved in a “vidi\_stats\_XXXXXXXX.log “ file