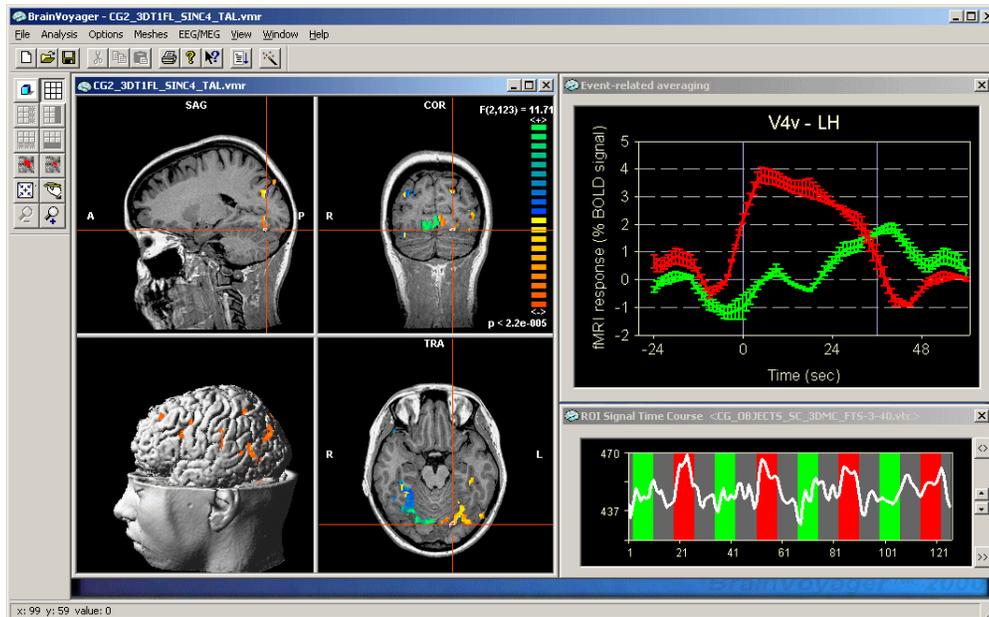




Institute for Imaging and Analytical Technologies

## *Brain Voyager Manual:*



## *Organizing, Processing and Analyzing fMRI data using Brain Voyager*

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## Preface

### *Is fMRI right for you?*

The average cost of performing an fMRI in the United States in 1998 was \$463.00 an hour. That cost reflects the use of the magnet and can be magnified by adding costs of research assistants, additional subject fees, experiment materials, etc. In addition, costs have risen, along with everything else. Compare the cost of doing an fMRI study with doing a thought study:

fMRI study  $\approx$  \$ 600.00/hour

Thought study  $\approx$  your salary  $\approx$  a whole lot less

Questions to ask yourself before committing to the expense and time of running an fMRI study:

- What do you hope to find?
- What would that tell you about the cognitive process involved?
- Would it add anything to what is already known from other techniques?
- Could the same question be asked more easily & cheaply with other techniques?
- Would fMRI add enough to justify the immense expense and effort?
- What would be the alternative outcomes (and/or null hypothesis)?
- Or is there not really any plausible alternative (in which case the experiment may not be worth doing)?
- If the alternative outcome occurred, would the study still be interesting?
- If the alternative outcome is not interesting, is the hoped-for outcome likely enough to justify the attempt?
- What would the headline be if it worked?
- What are the possible confounds?
- Can you control for those confounds?
- Has the experiment already been done?

Given that you have thought about these tough questions and are convinced that fMRI is the best way to answer your research question, let me tell you that you are not alone! The number of papers in the PubMed database reporting the use of fMRI methodology rose from 0 in 1990 to 746 in 2001. The current (2/2007) PubMed count is 165,405 ! The first psychology paper cited in PsycInfo to use fMRI occurred in 1993. As of February, 2007, peer reviewed journal articles using fMRI methodology counted over 2700!

### *Using this manual*

The purpose of the I<sup>2</sup>AT BV Manual is to provide a brief overview of fMRI in terms of both practical and analytical information. From a practical standpoint, the manual is composed of procedures and protocols for implementing human-subjects research in an fMRI environment. In addition, the manual attempts to provide a user-friendly procedural and help guide for doing fMRI processing using BrainVoyager.

The manual opens with a vocabulary list of terms that will be used throughout the manual. The next section provides an overview of types of fMRI designs and considerations for each. This section ends with the procedure for communicating your design to the MR technician. The third section addresses practical considerations, such as the equipment in the magnet, how to deal with head motion, how to organize your data, and particulars to doing neuroimaging at I<sup>2</sup>AT. In addition, this section includes information about screening and preparing participants for MRI.

The rest of the manual provides step-by-step instruction on preparing your data for analysis. This process is called pre-processing and involves at least four categories of operation from initial data assessment to creating functional and structural projects to linking your functional and structural scans to aggregating individual participant information into group data. The end goal is to guide researchers toward having data ready for statistical analysis. Particulars about analysis are not included in this manual.

Finally, the manual provides some links to resources and references to support information in the manual as well as to provide a start for further research. The Appendices include copies of required forms and a tutorial on finding the AC/PC points on a scan image.

What the guide won't do:

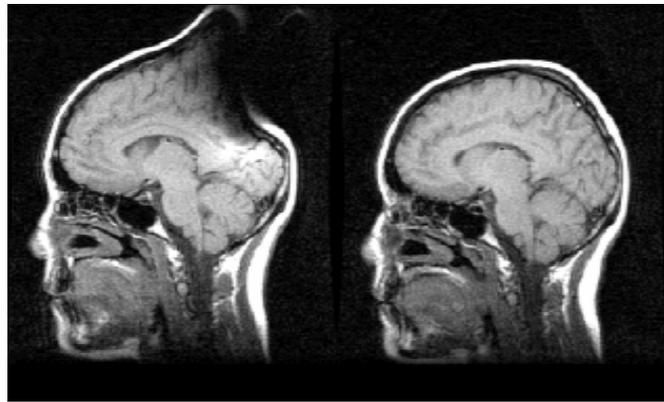
A caveat: there are limitations to the information that can be included in the guide. Some decisions that have to be made during the data analysis process are not clear-cut and depend on the individual study design, goals of the study, and convention within a specific field. The guide will focus on preprocessing, or the steps required to transition from the raw DICOM image files to a state required for general analysis. Individual statistical analyses will not be specified.

## About the Author

Dr. Deborah K. Eakin is an Assistant Professor in the Applied Cognitive Science Program at Mississippi State University. Her training in using fMRI started when she received a fellowship to attend the Summer Institute for Cognitive Neuroscience at Dartmouth College in 2002. She also received a fellowship to attend the American Psychological Association Advanced Training Institute in functional Magnetic Resonance Imaging (fMRI) at Massachusetts General Hospital in Charlestown, Massachusetts in 2004. In 2005, she completed a training course in BrainVoyager QX in Toronto.

During an NIA postdoctoral fellowship at the Georgia Institute of Technology, Dr. Eakin was instrumental in creating a liaison between the Biomedical Imaging Technology Center at Emory University and the School of Psychology at Georgia Tech. As a result, she conducted a 40-person fMRI study examining differential patterns of activation for various encoding strategies. In addition, the study examined whether the Hemispheric Asymmetry Reduction in Older Adults model was supported when strategy use was controlled for. Dr. Eakin is not an expert in fMRI or in analysis of fMRI data (n = 1 study!!). However, as a newly trained (and mostly self-taught) user of the methodology, she has a particular understanding of how to interact with participants in the magnet environment and the problems encountered by new users of the technology and of BrainVoyager.

## *I. Learning the vocabulary*



## Learning the Vocabulary

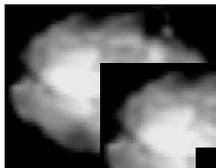
### MRI – *Magnetic Resonance Imaging*

- images brain anatomy
- high resolution, no temporal information



### fMRI – *functional MRI*

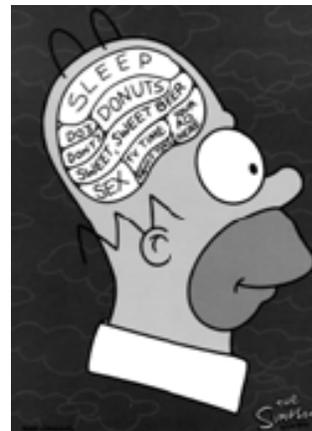
- images brain function
- low resolution, high temporal information



many images: e.g., collected

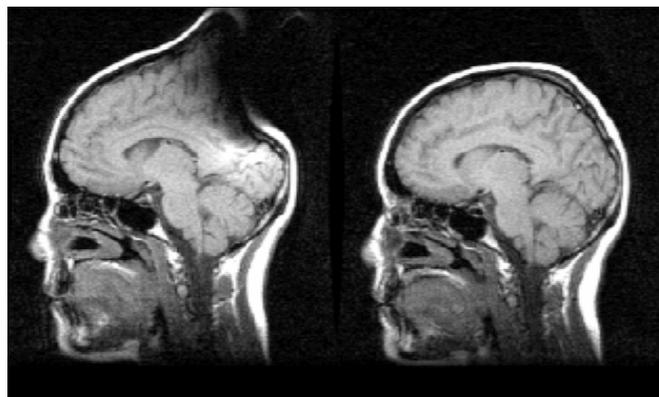
every 2 secs

over 5 minutes



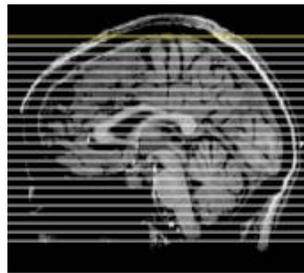
Basic TermsDefinition

fMRI	functional Magnet Resonance Imaging
BOLD	Blood oxygen level dependent
Anatomical or Structural	T1 data showing higher resolution images of the brain. [Usually collected at the beginning or end of an experiment. It takes about 5 minutes to collect 64x256x256 slices, or 20 minutes to collect 256x256x256 slices. 3-dimensional.]
Functional	T2* Data which has low spatial resolution containing time course information. [4-dimensional: 3 spatial, 1 temporal]
Slice Time Correction	If slices were collected in succession, the last functional slice would contain information from a later point in time than the first - this interpolates them in such a way as to minimize these differences.
Head Coil	Transmits and receives radio waves. This goes completely around the subjects' head.
Surface Coil	Focuses on a particular section of the head
Talairach	A standardized format for brains, in which the brain is fit into a box so that it can later be compared with other brains.
EPI	Echo-planar imaging
Shimming	Adjusting magnets to make magnetic field homogenous.
Artifacts	Areas in which activation/brain is not imaggable due to ghosts, interference and spikes from the magnet, and presence of metallic objects. Natural artifacts occur around sinuses and ear canals. Picture shows susceptibility artifacts around ear canal and due to tiny metal in hair elastic worn by participant.



Brain Vocabulary

Dorsal/Superior	Top of brain
Ventral/Inferior	Bottom of brain
Rostral/Anterior	Front of brain
Caudal/Posterior	Back of brain
Lateral	Outer areas – away from middle
Medial	Middle areas – toward middle
Slice	Single image of section of brain



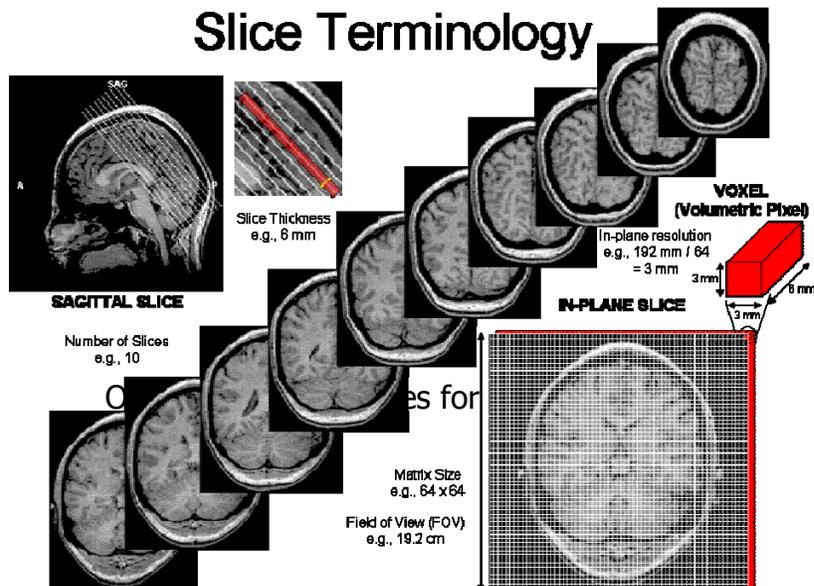
Figuratively speaking



Literally speaking

In-Plane Slice	Slice taken in the plane (e.g., coronal slice)
Slice Thickness	Measured in mm's (e.g., 6 mm)
Voxel	Volumetric pixel in mm's (e.g., 3mm), related to slice thickness

**Slice Terminology**

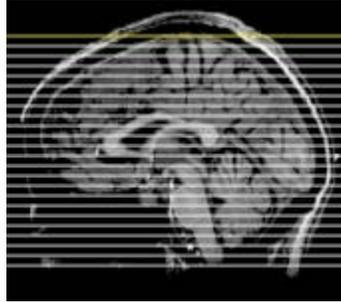


Volume

Axial

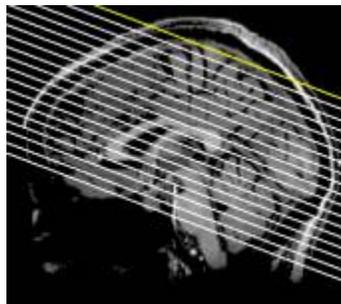
Orthogonal

Scans taken with slices oriented in parallel to axial plane (e.g., horizontal plane). NOTE: Axial Orthogonal is the preferred plane for the I<sup>2</sup>AT GE magnet.



Axial Oblique

Scans taken with slices oriented angled in relation to axial plane, usually along the AC-PC plane.

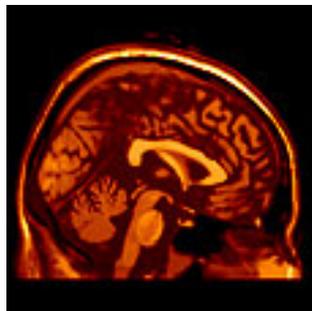


Field of View

Spatial extent of image from one edge to opposite edge in mm's

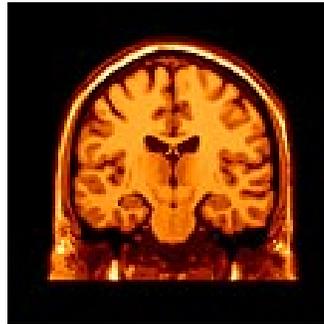
Midsagittal Plane

Slice along the midline from superior or dorsal (top) to inferior or ventral (bottom)



Coronal

Slice along the ear-to-ear line (laterally) from superior to inferior. Also called Frontal Plane



Horizontal (TRA)

Slice taken straight across the top (Hannibal-style) from rostral to caudal



fMRI DesignDefinition

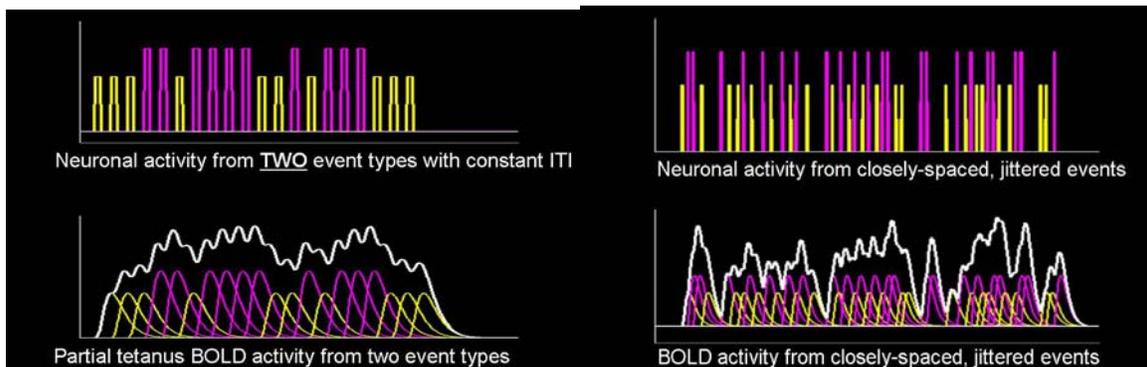
Run/Series	One continuous period of fMRI scanning (~5-7 mins)
Condition	One set of stimuli or one task.
Epoch	One Instance of a condition (Note: in block can include many trials/events)
Experiment	Set of conditions compared to each other. Consists of several runs.
Session	All scans collected from a subject in one day. Can consist of one or more experiments.
Trial/Event	One episode of the task involved in a run.
Paradigm	Set of conditions and order used in a run.
Block design	Multiple epochs of a condition are presented back-to-back
Event-related design	Epochs of a condition are interspersed "randomly" throughout a run
Disdaqs	Discarded data acquisitions – volumes collected at the beginning of a run before the magnet reaches steady state (n = 4 for I <sup>2</sup> AT GE magnet)

*Extensions in BV Definition*

DCM	The original DiCoM format saved by the magnet for both functional and anatomical scans.
SDT	The first level of conversion, allows data to be imported into BV.
POS	POS files are simple text files containing information about the position (e.g. of the subject in the fMRI scanner or of the slices relative to BV normal space).
SPR	Contains information about the scanner parameters for the corresponding .sdt (i.e., number of slices, thickness of slices, etc.)
AMR	The 2D format of the anatomical images. Each slice corresponds with the functional slices that were collected.
VMR	The 3D format of the anatomical images - will often encompass the entire brain.
V16	To keep file sizes down, brain voyager works in 8 bit format. To adjust contrast and brightness, you need the 16 bit information which is in this file.
FMR	The 2D functional data descriptor file. Can be opened in a word program. Contains information about the functional slices which were collected.
STC	The .stc, along with the .fmr, is the functional data. This file contains the function information for one slice, and there are .stc's for each slice.
VTC	The 3D functional data format. The .vtc is Talairached and aligned to the .vmr.
TRF	Transformation files that store information about any rotation/transformation you make to the .vmr (i.e., moving it to the AC-PC line or aligning the 2D and 3D data). These files are required to create the .vtc.
	IA.trf            Initial alignment file
	FA.trf            Final alignment file

TAL	Stores information about the size adjustment made to resize the brain into Talairach space. Also required for .vtc creation
PRT	The protocol file that you create that outlines the timing and conditions for each run.
RTC	The reference time course shows the optimal time course of your hypothesis.
ROI	The 2D region of interest outlines the area on your .amr for analysing.
VOI	3D region of interest outlining the voxels included in analysis.
SRF	The surface mesh which is the format for looking at surfaces.

## *II. Designing Your Study*



## Designing Your Study

Designing studies to implement fMRI methodology can be difficult. Not only are there challenges in terms of theoretical considerations. In addition, specifics of the fMRI environment present practical constraints in terms of the types of materials that can be presented, the types of responses that can be measured, and the length of the study. Mel Goodale, Professor of Neuroscience Psychology at the University of Western Ontario said, “fMRI is like trying to assemble a ship in a bottle – every which way you try to move, you encounter a constraint.” Jody Culham, an Assistant Professor in the Department of Psychology at the University of Western Ontario added, “That’s on a good day. On a bad day, it’s like trying to assemble a ship in a bottle blindfolded, drunk, and with one hand tied behind your back.”

If after much consideration you have determined that fMRI will provide information that no other methodology can provide regarding your research question, what do you need to know to design your study? The purpose of the section on designing your study is to provide a (very) brief overview of the different types of designs, to identify the considerations in designing an fMRI study, and to provide references for further study in research design using fMRI. Please refer to the Resources section for suggested readings on fMRI design.

### General Design Considerations

Decisions you make:

- Number of slices
- Slice orientation
- Slice thickness
- In-plane resolution (field of view, matrix size)
- Volume acquisition time
- Length of a run
- Number of runs
- Duration and sequence of epochs within run
- TR

Ask the physicist:

- Pulse sequence (e.g., gradient echo vs. spin echo)
- K-space sampling (e.g., echo-planar imaging or EPI vs. spiral imaging)
- Number of shots
- TR, TE, flip angle, etc.

NOTE: See section on *Communicating Your Design to the MR Tech* (p. 19) and fMRI Paradigm Information Sheet (Appendix A) at the end of the design chapter.

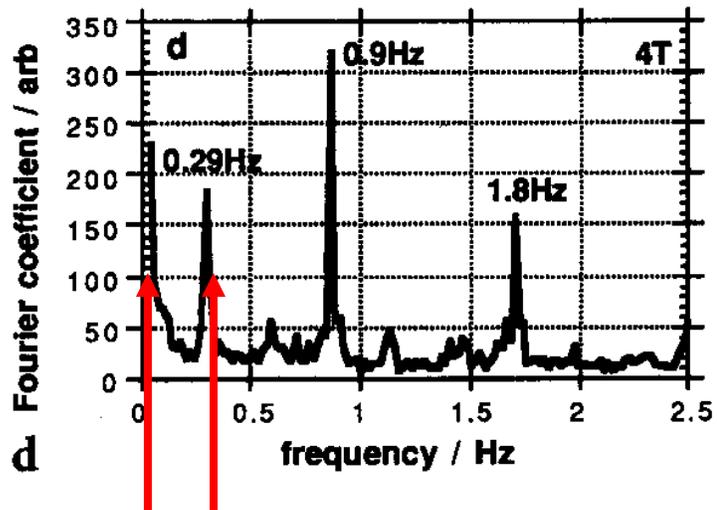
### Design Parameter Tradeoffs:

- Number of slices vs. volume acquisition time
  - the more slices you take, the longer you need to acquire them
  - e.g., 15 slices (4 shot) in 2 sec vs. 20 slices (4 shot) in 3 sec
- Number of slices vs. number of shots
  - 4 shot slices take longer than 2 shot slices
  - e.g., 15 slices (4 shot) in 2 sec vs. 18 slices (2 shot) in 2 sec
- Number of slices vs. in-plane resolution
  - the higher your in-plane resolution, the fewer slices you can acquire in a constant volume acquisition time
  - e.g., 128x128 matrix for 1 slice vs. a 64x64 matrix for 4 slices

### Power Issues:

- Statistical power
  - Probability of rejecting the null hypothesis when it is false
  - Ability to do so is result of effect size, sample size, and SNR
- Effect size
  - Bigger effects = more power
    - Require fewer subjects and fewer runs
- Sample size
  - Larger n = more power
    - More subjects
    - Longer runs
    - More runs
    - (all equal more \$\$\$\$)
- SNR or Signal-to-Noise Ratio
  - Better SNR = more power
    - Strong, clean magnet
    - Use of focal coils
    - Controlling for artifacts (e.g., physiological noise)
    - Use of more filtering during preprocessing
  - Physiological noise
    - Respiration
      - Every 4-10 sec (0.3 Hz)
      - Causes chest movement, distorts susceptibility
      - Don't set paradigm at respiration frequency

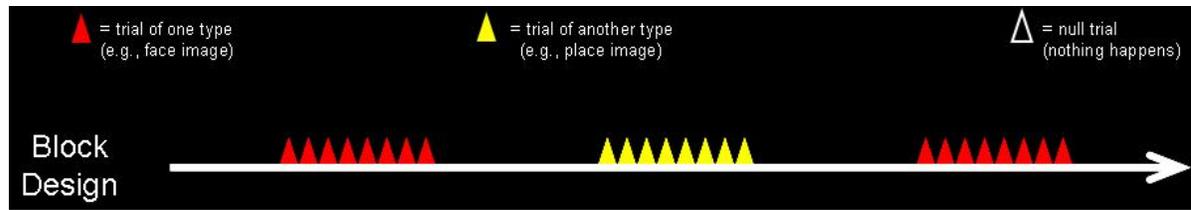
- Cardiac cycle
  - Every ~1 sec (0.9 Hz)
  - Pulsing motion, blood changes
  - Resolve by gating (Zhang et al., 2006)
  - Don't set paradigm at cardiac frequency



The "sweet spot" – avoid the noise!

## Types of Designs

### Block design



The block design is the foundation of neuroimaging research. Each block contains multiple trials of a single condition. Blocks of conditions are distributed across the run, interspersed with periods of baseline or null task blocks. Analyses use the subtraction method. For instance, if trial ▲ is presentation of pictures and trial ▲ is presentation of words, analysis would consist of the activation for pictures minus baseline activation as compared to activation for words minus baseline activation.

### Considerations for block design

*Appropriate baseline.* The baseline task might be as simple as a fixation cross in the middle of the screen, or even a blank screen. However, sometimes the appropriate fixation is more difficult to determine. For instance, if the process is something that happens during a resting state, a resting baseline would not be appropriate. In addition, sometimes the baseline is used to subtract out activation that occurs concurrently with the process of interest. For instance, if you wanted to determine whether there was differential activation for processing negative versus positive emotional words (e.g., death versus happy), some activation for simply reading the words would be present for both conditions. Therefore, an appropriate baseline might be to read neutral words (e.g., table).

*Designing the run.* Be sure to put conditions you want to compare within the same run. Extraneous variable can impact different runs differently. For instance, the attentional level of the participant can vary across runs and the noise level in the magnet can also vary across runs. You want that noise to vary non-systematically with the presentation of your conditions. Therefore, present the relevant comparison conditions within each run. Note: if you have more than four comparison conditions, a block design is probably not the best choice.

*Order of conditions in run.* It is good idea to counterbalance the order of presentation of conditions within the run in order to avoid order effects (e.g., condition B is influenced by processing of condition A). In addition, the order of conditions can be randomized across runs.

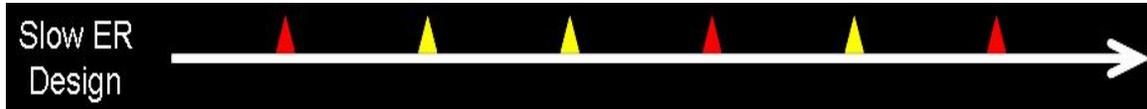
*Length of epoch.* In other words, how frequently should conditions change within the run? Of first consideration is the TR, which is the amount of time required for one complete brain volume to be collected. Consider a TR of 2 secs. If you use short epochs, for instance the condition changes every 4 seconds, only 2 volumes per condition will be collected and signal amplitude will be weak because there is not enough time for the signal to return to baseline. In addition, a 4 sec frequency is close to breathing frequency, resulting in respiratory artifacts. Such quick epochs could also be confusing to the subject. One solution could be to use short, but unequal epochs with the stimuli conditions of 4 seconds and baselines of 8 seconds; this solves only the weak signal problem. A better solution is to use medium epochs (e.g., every 16 secs). Note that the epoch length is a multiple of the TR, ensuring that complete sets of brain volumes (8 in the case of a 16 sec epoch) are collected during the epoch. If the TR is 3 secs, the epoch length would need to be adjusted to a multiple of 3 (e.g., 18 secs).

*Run duration.* At the beginning of a run, the time course of the stimuli presentation and the magnet are linked. As the run progresses, small lags occur and the linking of event to BOLD response is distorted. In addition, subjects can become fatigued during long scans. The optimal run length is ~ 5-7 minutes. Note: The entire run duration will be a multiple of your TR.

NOTE: The first four slices at the beginning of each run are disdaqs. Be sure to incorporate a null stimuli presentation during the disdaq times. In addition, after the disdaq presentation screens, be sure to start and end each run with a baseline condition.

## Event-related Design

In an event-related design, trials or events of a condition are presented in a random order rather than clustered in blocks.



*Slow event-related design.* Events are presented such that trials are separated in time by 12-14 seconds in order to allow the BOLD response to return to baseline before presenting another trial.

### Considerations for Slow ER designs

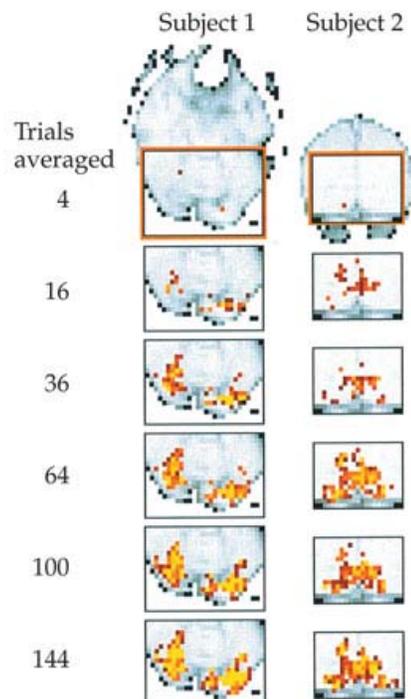
*Length of trial/event.* Each trial should be no less than the TR for the study in order to ensure at least one brain volume per event.

*Optimal trial spacing.* Optimal intertrial interval (ITI) depends on the duration of the trial. For a brief (< 2 sec) trial, the optimal ITI is 12 seconds. For longer trial durations, optimal ITI is determined by the following formula:

$$8 + (2 \times \text{stimulus duration})$$

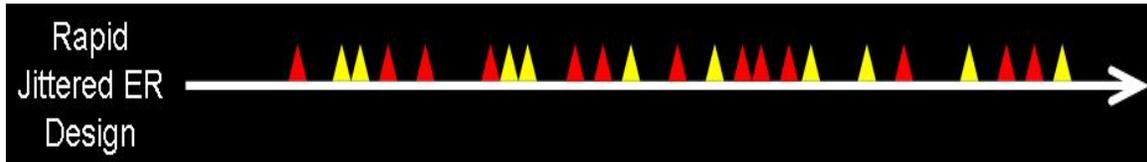
As such, if the trial duration is 4 secs, the ITI should be 16 secs.

*Number of trials.* Determined by effect size, the number of trials is a function of the standard error of the mean and the square root of the number of trials. The function asymptotes at around 15 trials. Below is a picture demonstrating the effect on your SNR of adding more trials:



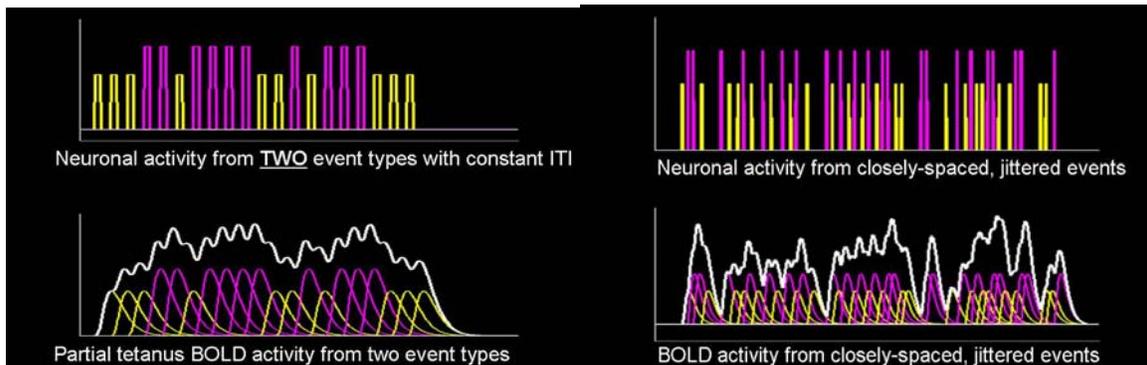
NOTE: Slow event-related designs can be cumbersome and time-consuming, and very boring for the subject.

*Rapid event-related design.* In a rapid ER design, trials of each condition are randomly mixed and presented rapidly (e.g., every 2 seconds).

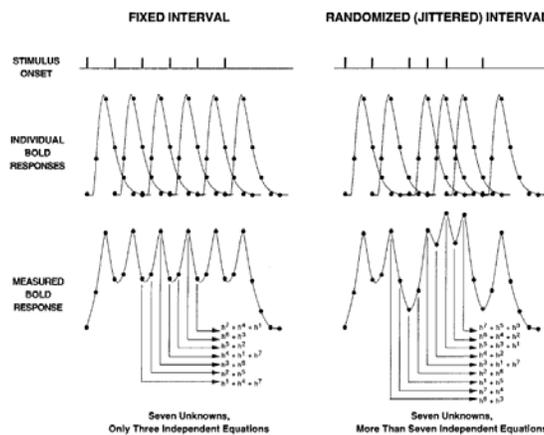


Considerations for Rapid ER designs

*Intertrial Interval (ITI).* The ITI in a Rapid ER design could be constant as in a Slow ER design, however *jittering*, or randomizing the ITI of the baseline allows for deconvolution of the fMRI signal (see Dale & Buckner, 1997 for a full explanation). Below is a comparison of neuronal activity and the BOLD activity for two events with a constant and a jittered ITI:



Note that the BOLD signal in the graph for jittered events is much more systematic and orthogonal with regard to the event. Jittering the ITI preserves the linear independence of the components of the hemodynamic response. Implications for jitter in deconvolution of the time-course will be discussed further in the analysis section.



*Determining the appropriate jitter.* There are two methods for determining the appropriate jitter of the ITI or baseline in a rapid ER design:

Do it yourself method: You could have ITIs of 2, 3, 4, 5 secs and have an equal number of each duration in a run. However, an exponential distribution of ITIs is recommended. Therefore, you might have 5 ITIs of 2 sec duration, 4 of 3 sec duration, 3 of 4 second duration, etc.

Optseq method: Optseq is a freeware program that can be obtained at <http://surfer.nmr.mgh.harvard.edu/optseq/>. Optseq runs either in a Linux or Mac OSX platforms. The program intakes the number and timing of events, the TR, number and timing of runs, and other parameters and outputs the optimal sequence of presentation of trials along with the optimal jitter of ITI.

*Determining event length.* The duration of each event is a function of the TR. The goal is to have at least one complete brain volume collected during each event. Therefore, for a TR of 2 secs, each event stimuli must be presented for at least 2 secs. If an event is presented longer, the duration should be a multiple of the TR. If your TR is 2 secs and you present your event for 3 secs, you do not have 2 complete brain volumes collected for that event. A better situation would be to increase the TR to 3 secs or to increase the duration of the event to 4 secs.

*Randomization of events.* As noted earlier, the optimal length of a run is ~5-7 minutes. In addition, ITI or baseline is jittered. Therefore, a study with several conditions which could take place across a 30 minute period of time in a behavioral study is now segmented into several short runs and trials of each condition are interleaved with ITIs of a variety of durations and frequency. Randomization of presentation of trials of different conditions across the entire study is not possible. A good solution is to randomize (or to allow Optseq to randomize for you) your conditions within a run, but to have particular stimuli assigned to each run. Then randomize the order in which the runs are presented. Each run will always have the same items presented in the same order within the run – this is required in order to optimize deconvolution. But the order in which runs are presented to a subject are randomized. For instance, in a study with 6 runs, run presentation order might look like:

S1	R1, R5, R3, R2, R6, R4	
S2	R5, R2, R1, R3, R4, R6	
S3	R6, R1, R5, R4, R2, R3	and so forth.

### *Communicating your design to the MR Tech*

Many of the parameters for collecting brain images are static and determined by the type of magnet used. However, some decisions depend on the interface between your design and the magnet. Spending time talking with the MR Tech about your study can increase the likelihood of getting good images – a MUST because of the expense of magnet time and the contribution by your participants.

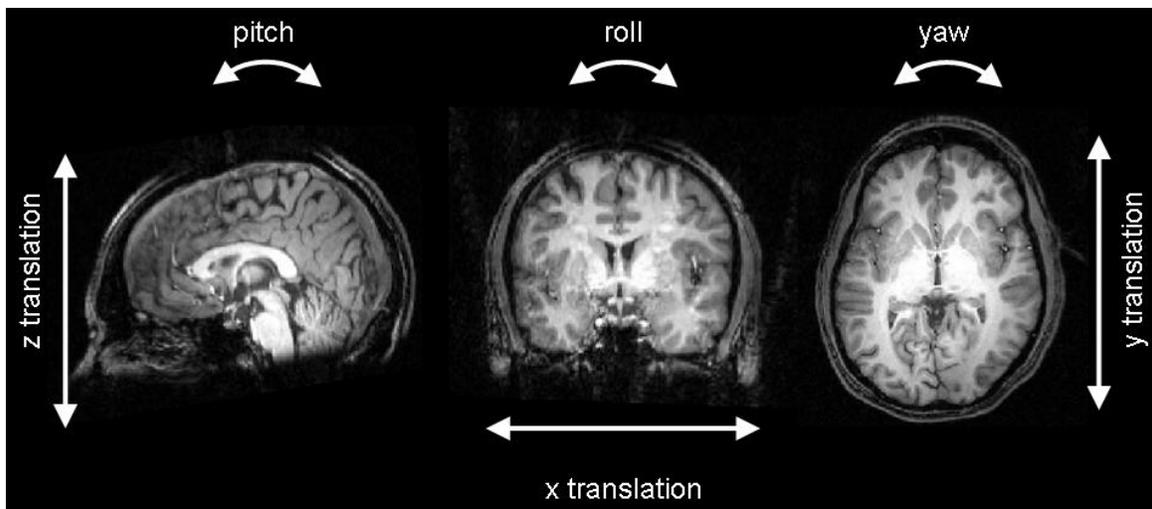
#### Before you scan

Generally, the MRI Tech needs to know your research question and how you want the brain images to contribute to answering the question. In addition, some specific information about TR, type of design, time of task, and the region of interest in the brain is required by the MRI Tech. Now is the time to take advantage of the expertise of the MRI Tech in optimizing your chance of decreasing SNR and having good, clean scans. Making a protocol sheet indicating the scan sequence, including number and type of runs/series, will help ensure good design communication.

#### At scan time

The MRI Tech will need to have some individual information about each participant as they come in. They will need to know the participant's weight, birth date, and subject identifier number. NOTE: Persons over 300 lbs cannot enter the magnet. They will also need to review the fMRI Screening form (complete online at [i2at.msstate.edu](http://i2at.msstate.edu)). Having in hand the scan sequence for the individual participant will also help eliminate communication errors. For instance, creating a subject log with the subject information mentioned above, as well as the randomization sequence of the runs/series will help you and the MRI Tech keep track of the session.

### *III. Practical Considerations*



## Practical Considerations

### Equipment

#### *Head coils*

Currently, the only type of head coil available is an 8-channel.



#### *Response collection*

Responses from participants can be collected in a variety of ways, including button presses, joy stick or track ball manipulation, and vocalization. Although collecting spoken responses from participants is possible (and sometimes necessary for the experiment), doing so is complicated and difficult. When the mouth moves, the head moves, and head motion critically reduces SNR.

The most common form of response collection is the response box, which has from 2 to four buttons of different colors that can be linked to particular responses in your experimental protocol. For instance, pressing a blue button can indicate a yes response; pressing a red button can indicate a no.

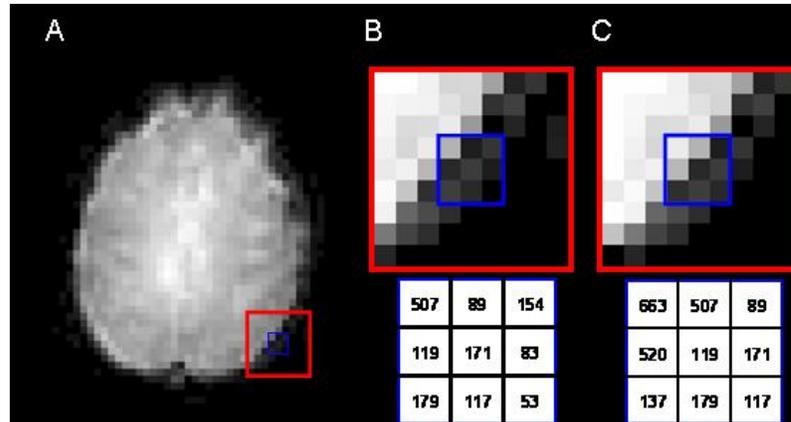


#### *Eyetrackers*

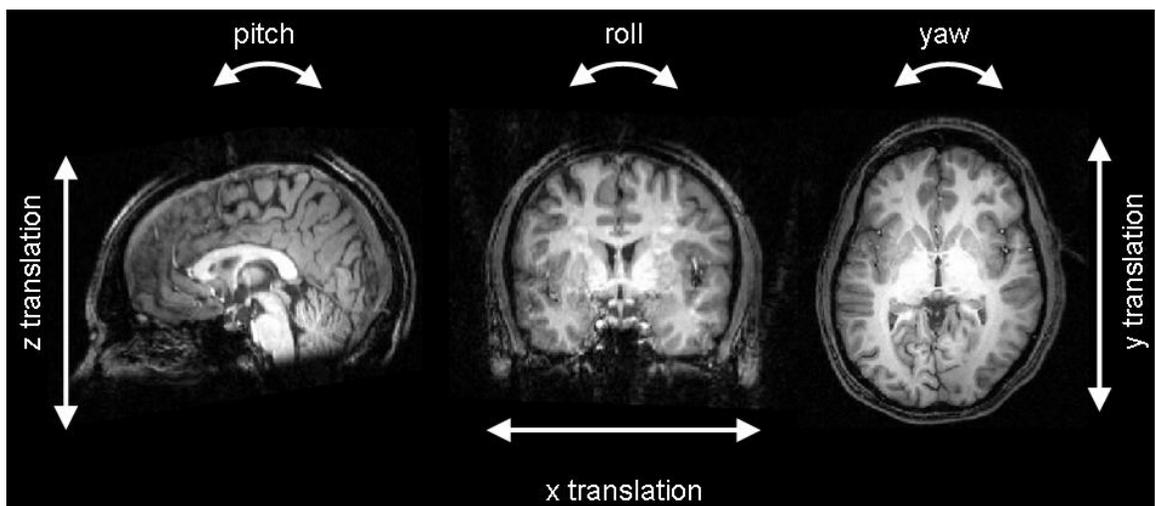
Additional information about processing in the brain can be gained by measuring eye movement using eyetracking equipment, which is available at I<sup>2</sup>AT. Eyetracking equipment can also be used to monitor participants for alertness in the scanner.

### Head Motion

Head motion is problematic for several reasons. First, activation due to head motion can be correlated with activation due to processing in response to an experimental condition. Second, head motion increases residuals, resulting in weaker statistical effects. Third, regions shift over time, within and across runs, and between the functional and structural scans. Finally, head motion can cause changes intensity of activation at the voxel level.



Heads can move along six different planes: three translations and three rotations.



Some motion can be corrected at the pre-processing stage, but there are costs to corrections, including loss of information from the top and bottom of the image. In addition, motion correction can lead to blurring of the image. Much information that can be addressed in the present manual is available, but how can it be avoided?

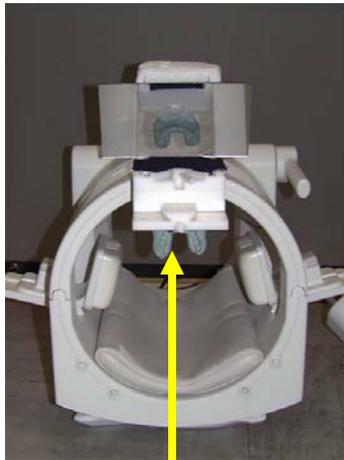


**Duct Tape?**



**Guillotine?**

Tempting, but neither duct tape nor the guillotine are practical solutions. Head motion is going to happen. Avoidance is not a reasonable goal, but minimizing it is. Some labs require participants to use a bite bar or thermoplastic masks:



**Bite Bar**



**Thermoplastic mask**

Neither procedure is used at I<sup>2</sup>AT. The best route to minimal head motion is training participants regarding the importance of holding still, even between runs. In addition, spend some additional time at the front end ensuring that the participant is comfortable and relaxed on the head cushion. Make sure they use the bathroom before entering the magnet room, and that their neck is in a comfortable position. Then use foam pieces to support the participant's head and neck within the head coil. Strips of paper, such as barber's neck strips, can be taped across the chin and forehead using medical tape (the barber strips prevents the tape from touching the skin) as physical reminders to hold still.

Organizing your data

**Experiment folder**

**Group folder**

**Scan data**

**Subject\_N**

***Localizer Folder***

*Raw Dicom Files*

***Run1 Folder*** (separate folder for each run)

Raw Data Folder

*Raw Dicom Files*

Project Files Folder

Slices Folder

*Renamed Dicom Files*

*Slice Time Correction Files*

*Motion Corrected Files*

*First Volume Files*

*FirstVol\_as\_anat File*

*Firstvol.fmr*

*POS File*

*VTC File*

*RTC File*

*IA. TRF File*

*FA. TRF File*

*POS File*

Motion Folder

*3D Motion correction snapshots*

*3D Motion correction data table*

*Time course movie*

PRTs Folder (Stimulation protocols)

*PRT Files*

***T1 Folder***

Raw Data Folder

*Raw Dicom Files*

Project Files Folder

*Renamed Dicom Files*

*VMR File (original)*

*TAL File*

*TRF File*

*VMR File (ACPC)*

*VMR File (TAL)*

*POS File*

*Snapshot of structural scan*

**Analysis**

***VTC Folder***

*VTC Files*

**CTR Folder**

*CTR Files*

**MDM Folder**

*MDM Files*

**GLM Design Matrix Files**

**Analyses**

## Neuroimaging at I<sup>2</sup>AT

First, a Research Project Application (found at [i2at.msstate.edu](http://i2at.msstate.edu)) must be completed for each study using the imaging equipment. NOTE: No research will be approved without prior IRB/IACUC approval. Information about IRB/IACUC research training and research applications can be found at <http://www.msstate.edu/dept/compliance/>

Second, all researchers must receive training in MRI safety annually.

Safety Training Directions:

Go to this link: <http://www.orc.msstate.edu/>

Click on the "Training" tab (left side)

Click on "General Safety", Tab 6

Scroll Down to "I<sup>2</sup>AT Safety Training II (non-medical)"

In order to use the magnet at I<sup>2</sup>AT, everyone involved with the project who intends to be in the magnet environment must complete the 3.0 T MRI Procedural Screening Form for Personnel (<http://www.I2AT.msstate.edu/>).

Scheduling MRI time is done online. View Scheduling directions at [i2at.msstate.edu](http://i2at.msstate.edu)

## Screening Participants

Participants must be carefully screened before placement in the magnet. Consideration of risk due to metal in the body is extremely important, especially for research. Minimal risk might be tolerable in a medical situation where the information gained from an MRI outweighs the risk. But in a research context, NO risk is acceptable. To assist in screening participants, I<sup>2</sup>AT has developed a participant screening form ([i2at.msstate.edu](http://i2at.msstate.edu)) that asks health questions about many different ways people can get metal in their bodies. This form should be included in any IRB application, and must be completed for every participant. Requiring this information from the participant will also require HIPPA language in your consent form.

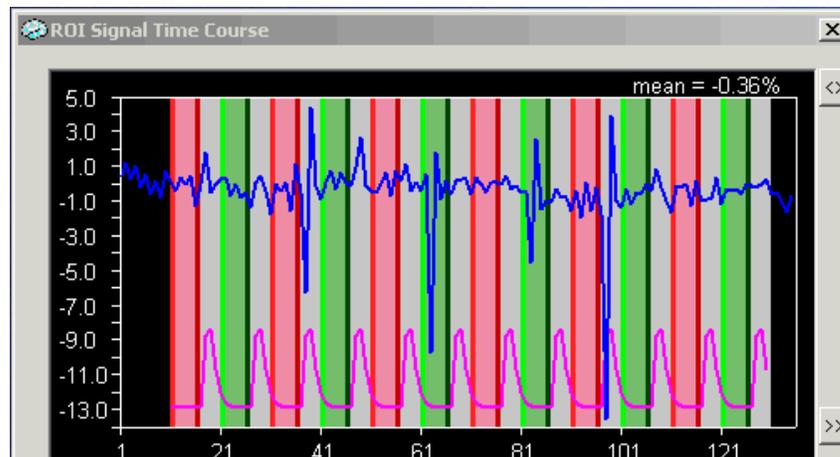
HINT: If your first interaction with a participant will be the neuroimaging portion of the study, you can ask for HIPPA waiver to ask the questions over the phone without recording any of the information in order to pre-screen potential participants.

## Preparing Participants

Appendix B is an example of a *Functional Magnetic Resonance Imaging Instruction Booklet* that can be edited and mailed to participants prior to their appointment for

the MRI. It includes information about appropriate clothing, directions to the facility, and procedure information.

## ***IV. Pre-processing-Initial Data Assessment***

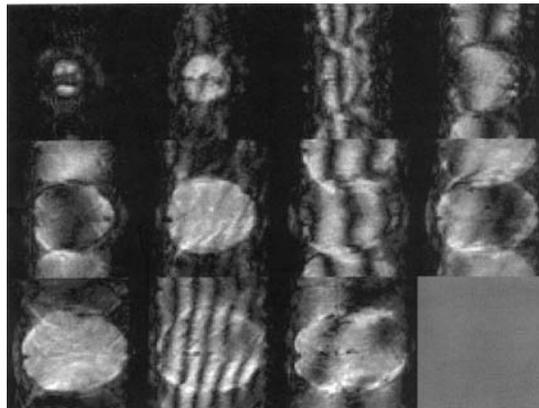


## Preprocessing – Initial Data Assessment

### Overview

One of the pros of BV (as compared to some other fMRI analysis packages) is that the program allows you to get “close” to your data. Before beginning the processing procedure, it is a good idea to get to know your data in the following ways:

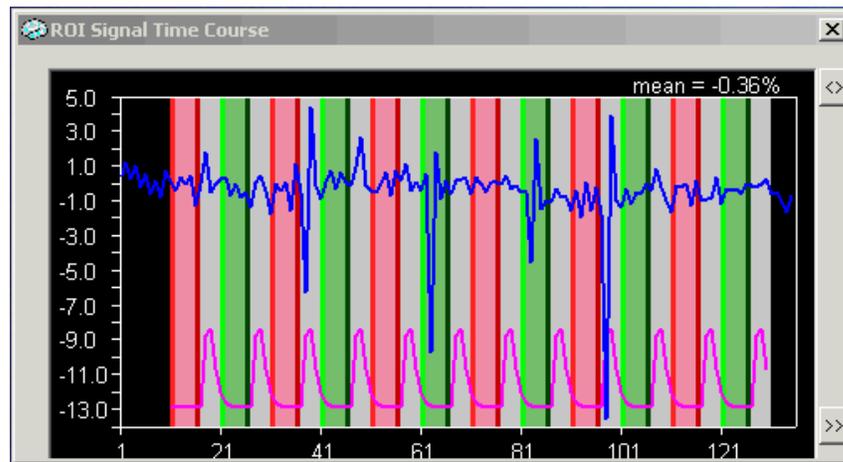
1. Look at the raw functional images. After constructing the anatomical and functional projects in BV, look closely at the images.
  - a. Where are the artifacts and distortions?
    - i. Expected = sinus artifacts
    - ii. Unexpected = dorsal cortical artifacts
  - b. How well do the functional and anatomical scans correspond?
    - i. This is an “eyeball” measure at this initial stage.
2. Look at the time course movies.
  - a. After creating the functional project (FMR)
    - i. Select Options, Time Course Movie
    - ii. Click on the Preload all button and play
    - iii. Watch for flashes (indicates “spikes”, or scanner artifacts)



**Scanner artifacts, such as those pictured above, are hardware malfunctions.**

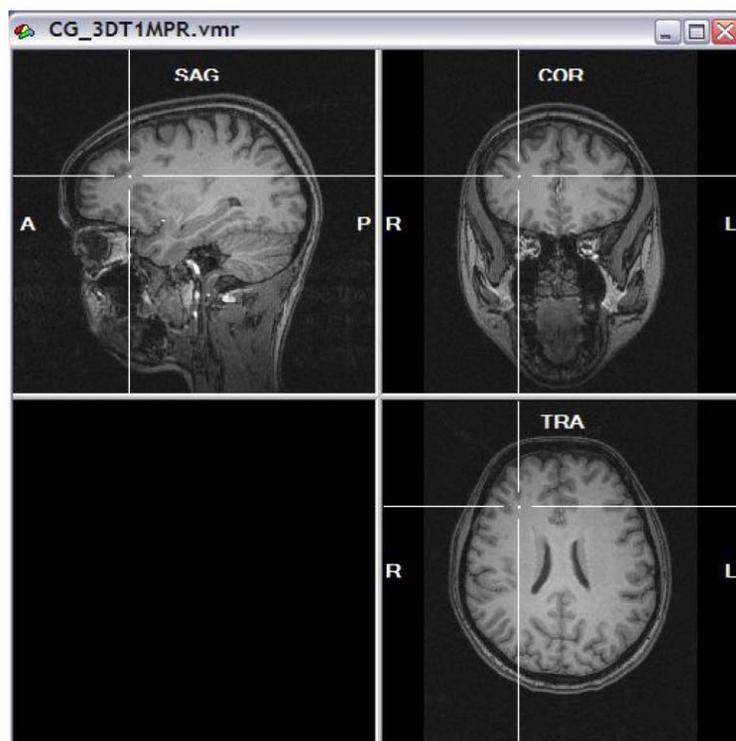
- iv. Watch for jumps across slices (indicates big head movement)
      - v. Watch generally for artifacts and distortions.

- b. NOTE: The movie resolution is not as crisp as the FMR resolution. Also, sometimes BV shows a shadowy image in the matrix in cells not relevant to the number of scan slices. This is a "feature" in BV and will not affect the data.
  3. Stop movie and zoom in on one or two cells of the FMR.
    - a. Click restore down box in top right-hand corner
    - b. Use the + magnify tool to increase magnification to the maximum possible. Select one or two adjacent slices showing the whole brain.
    - c. Pick a voxel just at the edge of the brain on which to focus.
    - d. Select Options, Time Course Movie
    - e. Click on the Preload all button and play
    - f. Watch for gross voxel changes
      - i. E.g., voxels that appear and disappear
      - ii. E.g., voxels that shift abruptly
    - g. Make a note of the time point that abrupt shifts occur and check to see if they correlate with presentation of stimuli.
    - h. Big shifts are usually evidence of head motion that will result in a decision not to use that particular participant.
      - i. Biggest problem = head motion that is correlated with experimental conditions
        1. E.g., always occurs when participant presses a button
    - i. NOTE: Can do this before and after motion correction and smoothing
4. Look at several ROI Signal Time Course graphs.
  - a. After creating the functional project (FMR)
    - i. Left-click anywhere in the cortical areas of any slice
    - ii. Look at the activation pattern for unexpected activation
      1. Abrupt signal change at the beginning of a run
      2. Spikes due to abrupt head motion
    - iii. Left-click anywhere in non-cortical areas of any slice (e.g., white matter, outside the head)
      1. Time courses should look different in these areas.
5. Look at individual runs, then individual subjects before aggregating the data.



**Spikes in signal, often due to abrupt head motion**

## V. Pre-Processing: Creating Projects



## Preprocessing – Creating Projects

### Overview

The end result of this course of preprocessing will be creation of the PRT, creation of a functional (FMR) and structural (VMR) projects, motion and time correction of the FMR project, and spatial smoothing and temporal filtering of the FMR project. When this stage of preprocessing is complete, the next step will be to link the functional and structural images together (see Preprocessing – Linking FMR to VMR).

NOTE: A \* indicates option selections that vary with each experiment.

FOR EACH RUN AND EACH PARTICIPANT DO:

Rename DICOM files

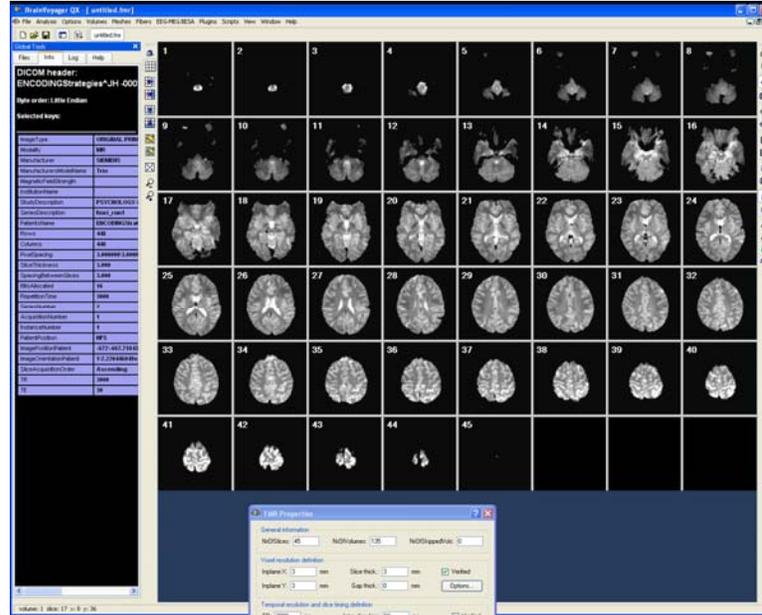
Go to the first run folder. Inside the Raw Data Folder should be the raw DICOM files associated with the first run. Copy (NOT move) the DICOM files into the Project Files Folder/Slices Folder.

1. Open Brain Voyager
2. Click File, Rename DICOM Files
3. Indicate path to Run folder/Slices Folder
4. Click on GO
5. BV will automatically rename files into BV convention
6. Repeat for each Run and the T1 structural scans.

This way the original raw DICOM files will be preserved. The renamed files will be in the Slices Folder.

## Creating functional projects

1. Open Brain Voyager
2. Click File, New Project
3. Select Functional MRI data set (FMR)
4. File type: DICOM
5. Click on Select First Source File
  - a. Select the first renamed DICOM file under the Run Folder/Slices Folder (the end of the file extension should be -0001.dcm)
  - b. The number of slices and number of volumes and X/Y resolution values should be automatically entered. BV reads this information from the header attached to the first DICOM file.
6. If you have DISDAT volumes (e.g., first four) enter that number as the number of slices to skip.
7. Create pseudo-AMR from first volume should be checked
8. Click on Advanced
9. Make sure the mosaic sequences is set to 64 x 64
10. Leave everything else as it is
  - a. Do not change the prefix of the STC files
11. Select Target directory
  - a. Should be Run Folder/Project Files Folder/Slices Folder
  - b. Hint: It is probably already selected automatically. You only need to change it if you want the STC files stored separately from the DICOM files
12. Select GO
13. Watch the head-stripping movie (rated PG)
14. Output should be a matrix of images of different slices, one cell for every slice – total number of cells = total number of slices



Sample VMR

15. Select File, Save As and name files with naming convention you choose.
  - a. A good convention is subject #, subject initials, scan session run number, presentation software run number (e.g., S11\_HM\_R1\_EPR3)
  - b. NOTE: If you do not save the project, the STC and FMR files will still be in the folder, but will be called "untitled" files.
16. Open Run Folder/Project Files Folder/Slices Folder and notice that the folder now contains:
  - a. Renamed DICOM files
  - b. STC Files
  - c. FMR File
  - d. POS File
  - e. First Volume as Anatomical File

FOR EACH RUN DO:

### Creating Stimulation Protocols (PRTs)

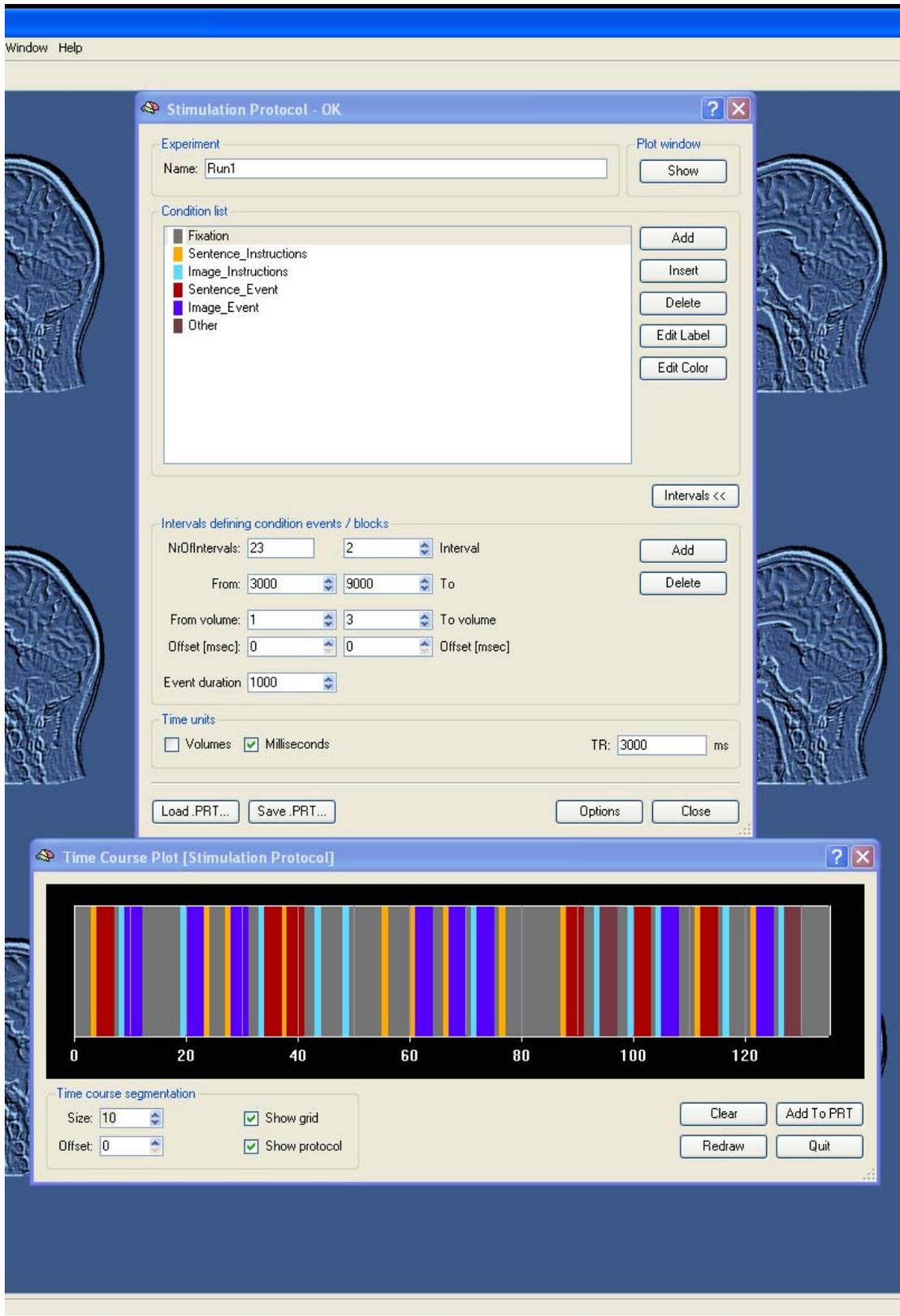
The PRT is the file BV uses to link the timing of stimuli presentation to the appropriate scan slice. A separate PRT will be needed for each run, because the order and timing of conditions should be different for each run. (NOTE: If you have a study in which the type of trial is participant-identified, a PRT will have to be created for each run *for each participant*). Creation of PRTs requires associating the timing indicated by the stimuli-presentation software (e.g., EPrime, Present, Superlab, etc.). You will have already calculated the cumulative onset time for each event. Armed with this information, PRTs are created in BV by:

Open the FMR for the run for which you are creating the PRT.

1. Select Analysis, Stimulation Protocol
2. Click on the Intervals button to expand the window to show intervals.
3. Click on the Show button to show the Plot Window.
  - a. Be sure both Show Grid and Show Protocol are checked
4. For each condition in the run (including fixation), you will need to add a condition event.
5. Click on Add. A condition will be added to the Condition list.
  - a. Click on Edit Label
    - i. Type in condition name.
  - b. Click on Edit Color
    - i. Select a color for the condition
    - ii. Suggestion: Use grey for fixation condition
  - c. NOTE: Keep a note on your selection! The condition name and color selected should be consistent across runs, across participants, and across groups.
6. Under the "Time units" section, click on Milliseconds

7. At the "Intervals defining condition events/blocks box"
  - a. Click Add once for each event of the condition
  - b. Notice that the NrOfIntervals is increasing with each click
  - c. Click on the Interval arrow to return to Interval 1
  - d. Enter the start time (in milliseconds) for the first event of the condition under From
  - e. Enter the end time for the first event of the condition under To
  - f. Continue until all of the events for that condition type is entered
8. Repeat the procedure until all events for all conditions are represented in the PRT
  - a. Be sure that the entire time course of the run is represented!
9. Notice that the conditions and events are being added pictorially in the Time Course Plot window. Use this window to help find problems and overlap in the From/To times for event intervals.
10. When the entire time course is correctly represented by the PRT, the Time Course Plot window will look "right" and the Stimulation Protocol window label will read OK (it read NOT OK if there is overlap in timing).
11. Change the Name at the top of the window to represent the run (or participant and run) the PRT represents (e.g., Run1)

NOTE: See screen shot of the PRT windows, next page.



Screen shot of the PRT windows

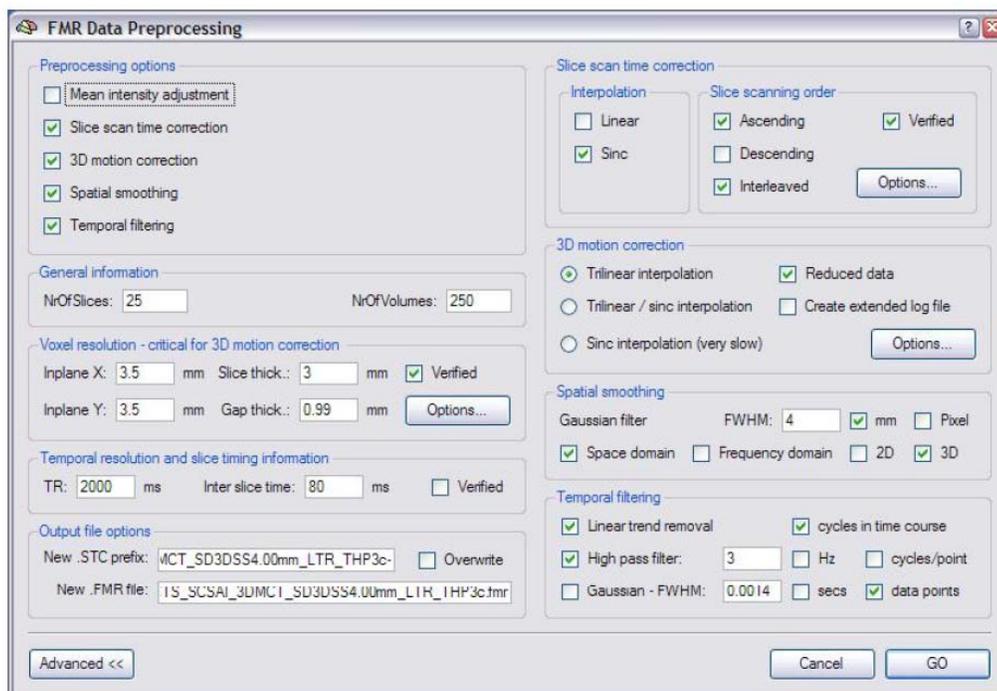
FOR EACH RUN DO:

Linking the PRT to the FMR

1. Open Brain Voyager
2. Open VMR
  - a. File, Open, Run Folder, Subject FMR
    - i. NOTE: not the \_firstvol.fmr
3. On the FMR Properties window, look under:
  - a. Referenced protocol (PRT) file
  - b. IF PRT is not already listed, use browse to go to Run Folder for that FMR and select the PRT file

Motion Correction

1. Select Analysis, FMR Data Preprocessing
2. The FMR Data Preprocessing window will pop up – Click on Advanced to expand the window
  - a. Select Slice scan time correction\*
  - b. Select 3D motion correction\*
  - c. Select Spatial smoothing\*
  - d. Select Temporal filtering\*



FMR Data Preprocessing Window

- NOTE: The parameters you select for each are unique to each study. Typically, the slice scan time correction can use the default options, as can the 3D motion correction. However, decisions about the amount of temporal and particularly spatial smoothing vary within the field. It is best to refer to convention within your area to make these determinations.
- NOTE: The Output file options designate the names of the new STC files and the new FMR file. It is best to go with the default labeling. The label has information in it regarding the type of preprocessing that was done on the original file as indicated in the example below:

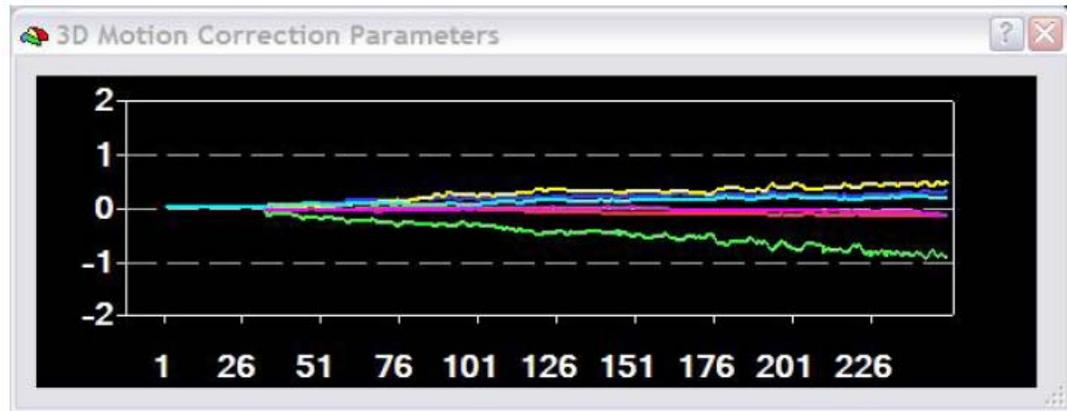
New file name:

S111\_ HM\_SCSAI\_3DMCT\_SD3DSS4.00mm\_LTR\_THP3c.fmr

SCSAI: Slice Scan time Correction, Slice scanning order Ascending Interleaved  
 3DMCT: 3 D Motion Correction with Trilinear estimation and interpolation  
 SD3DSS4.00mm: Space Domain 3D Spatial Smoothing with Gaussian filter of 4.00 mm  
 LTR: Linear Trend Removal  
 THP3c: Temporal High Pass with 3 cycles/points

3. Press GO
4. Process takes a while. You will see:
  - a. Head stripping movie
  - b. A graph showing the 3D Motion Correction Parameters
    - i. This is very important!
    - ii. Includes lines indicating motion from 0 for all 3 translations and all 3 rotations (see section on Head Motion, p. 30)
      1. Translations:
        - a. Red = X
        - b. Green = Y
        - c. Blue = Z
      2. Rotations:
        - a. Yellow = around X axis
        - b. Magenta = around Y axis
        - c. Cyan = around Z axis
    - iii. NOTE: Head motion, particularly abrupt motion that is greater than 1 or -1 is potentially problematic.

NOTE: See 3D motion correction plot (next page)



3D Motion Correction Plot

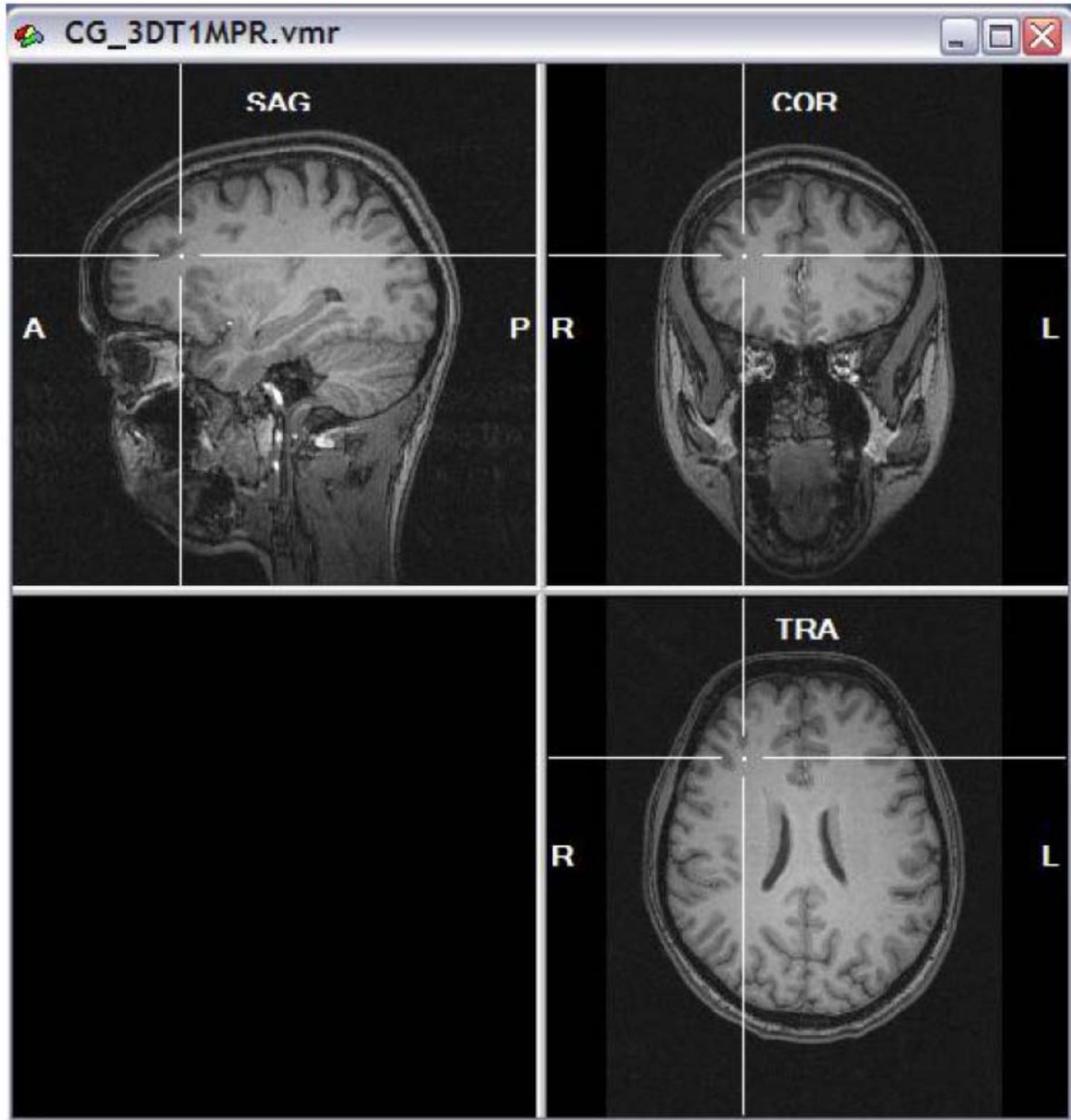
5. When the preprocessing is completed
  - a. Right-click inside the 3D Motion Correction Parameters box.
    - i. Select Show Options dialog
    - ii. Click on data table
    - iii. Save data table in Run Folder
      1. The parameters in the data table can be used later if you want to include head motion as a predictor in your analyses.
  - b. Close and right-click inside the 3D Motion Correction Parameters box.
    - i. Select save snapshot of plot
    - ii. Save plot snapshot in Run Folder

## FOR EACH PARTICIPANT DO:

## Creating anatomical projects

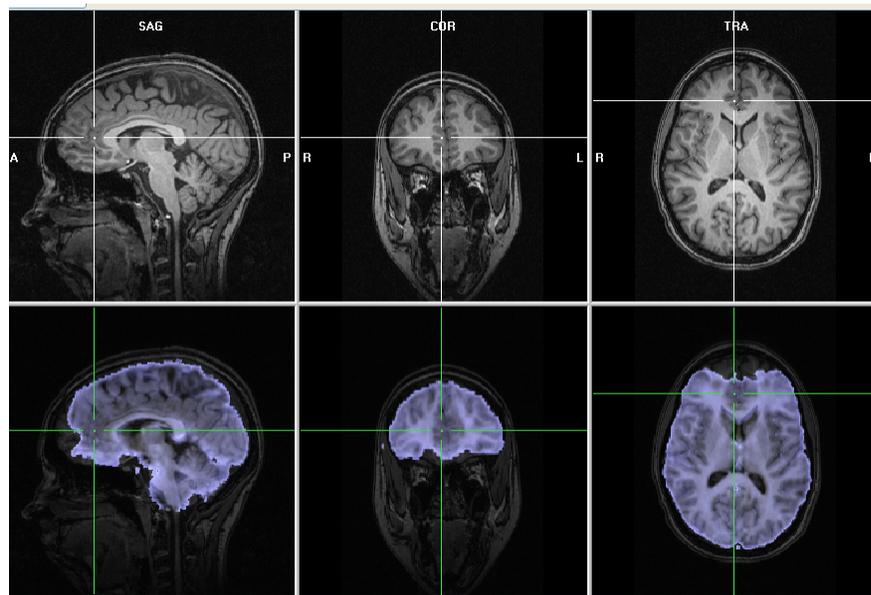
1. Open Brain Voyager
2. Click File, New Project
3. Select Anatomical 3D data set (VMR)
4. File type: DICOM
5. Click on Select First Source File
  - f. Select the first renamed DICOM file under the T1 Folder/Slices Folder (the end of the file extension should be -0001.dcm)
  - g. Change the number of slices to the number of DICOM files in your T1 folder.
6. Leave everything else as it is
7. Select Target directory
  - h. Should be T1 Folder/Project Files Folder/Slices Folder
  - i. Hint: It is probably already selected automatically. You only need to change it if you want the STC files stored separately from the DICOM files
8. Select GO
9. Watch the head-stripping movie (rated PG)
10. Output should be a very clear view of the brain structure from 3 different aspects: saggital, axial, and coronal (see next page for a screen shot).
11. Use the contrast and brightness tool to adjust and click OK.
12. Save VMR using naming convention you want.
  - a. E.g., S11\_HM\_T1
  - b. NOTE: the POS file will automatically be created and saved in the same folder
13. Use the crosshairs to move through the slices from the three aspects.

NOTE: Be sure you are aware of the convention in which the brain is being presented. Radiological convention: left and right are flipped. Neurological convention, left is left, right is right. BV should be able to use the information from the scan header to provide that information. Look under the Info tab.



VMR: Structural project

## **VI. Pre-Processing:** **Coregistration and Transformation**



## Preprocessing – Coregistration and Transformation

### Overview

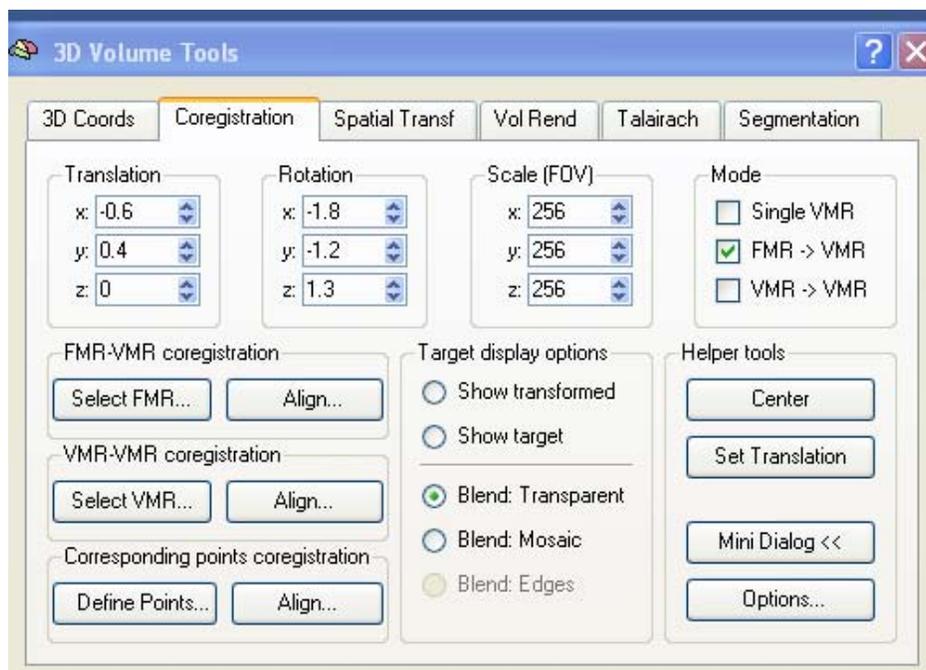
This stage of preprocessing is to coregister (or align) the functional and structural images (see Preprocessing – Aligning FMR to VMR) in order to be able to assign functional activation to a structure in the brain. In addition, the VMR will be transformed into AC/PC convention and Talairach space in order to aggregate runs and participants into group data for statistical analysis.

NOTE: A \* indicates option selections that vary with each experiment.

FOR EACH RUN AND EACH PARTICIPANT DO:

### Coregistration

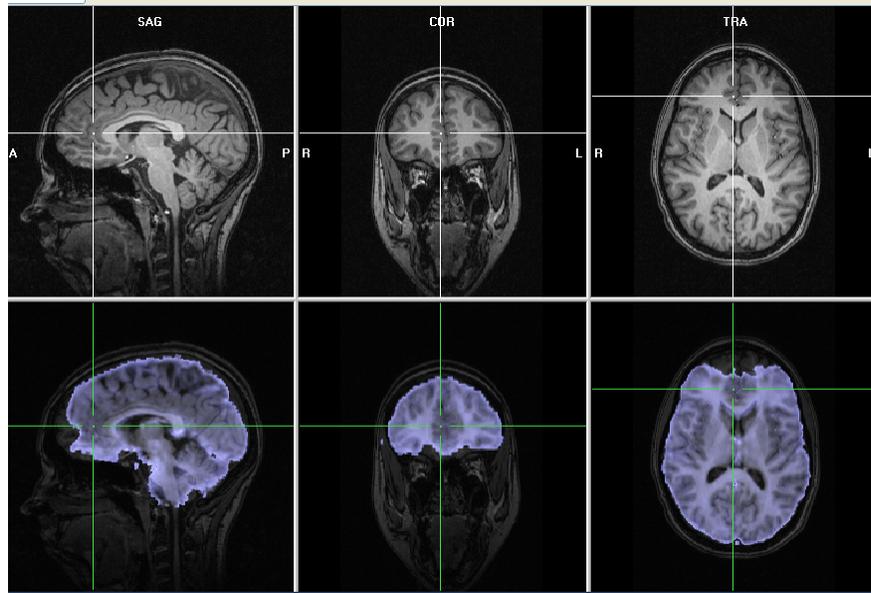
1. Open Brain Voyager
2. Select File, Open and go to the T1 Folder
3. Open the VMR file
4. The 3D Volume Tools window will open in front the anatomical images
5. Click on Full Dialog Box
6. Select Coregistration tab



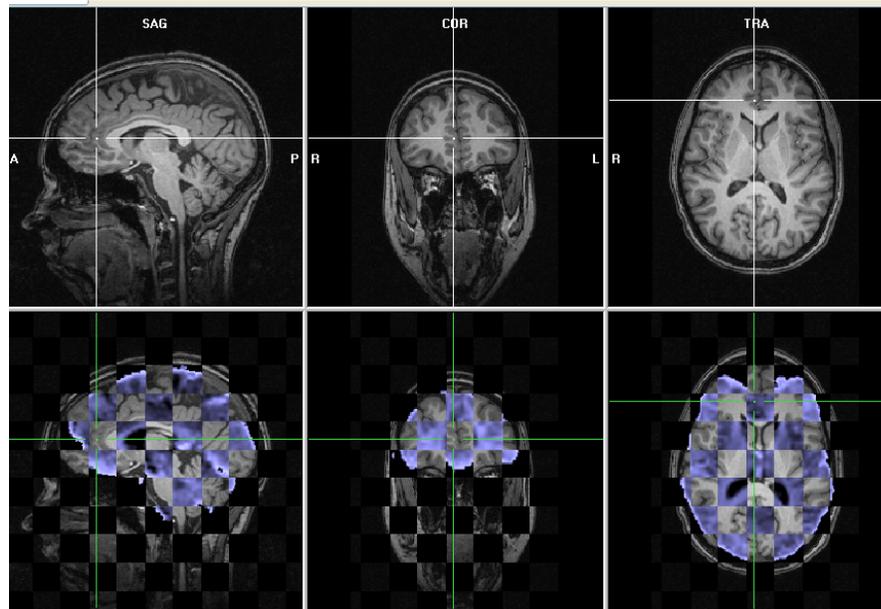
3D Volume Tools Window - Coregistration

7. Click on the Select FMR button
8. A browser window will open.
  - a. Go to the Run Folder for the first run.
  - b. ALWAYS select the pre-processed .fmr file. E.g.,:  
S111\_HM\_Run1\_EPR3\_3DMC\_SCSA\_SD3DSS4.00mm\_LTR\_THP3c.fmr
9. Click on the OPEN button.
10. NOTE that the project window now contains a 2x3 matrix with the T1 VMR images in the top row and corresponding functional images in the bottom row.
11. Click on the Align button next under the FMR-VMR coregistration heading.
12. NOTE that the aligned files are renamed and identified as .trf (transformation files).
13. DON'T run yet!
14. Select the Source options tab.
15. Make certain that the "Use linked AMR" is selected.
16. Click on Run IA (Initial Alignment)
  - a. Resultant file has extension of IA.TRF
17. Notice that the functional scans are now overlaid onto the structural scan.
18. Click on the Align button again.
19. Click on Run FA (Fine Alignment)
  - a. FA take a bit longer
  - b. Resultant file has extension of FA.TRF
20. Notice that the alignment of the functional and structural scans is better.
21. You can manually fine-tune the alignment (if you dare)
  - a. Use the system coordinates buttons (Translation, Rotation) to adjust the x, y, z orientation of the functional scan
  - b. You can change the view by clicking on the Target display options
    - i. Show transformed shows only the functional view
    - ii. Show target shows only the structural view

- iii. Blend: Transparent is the default and shows both
  - iv. Blend: Mosaic shows a checkerboard grid of both
    - 1. You can change the degree of transparency, block size, etc. using the Options button.
- c. NOTE: It is usually safe to do some minor Translation adjustments, but be cautious about Rotation adjustments.



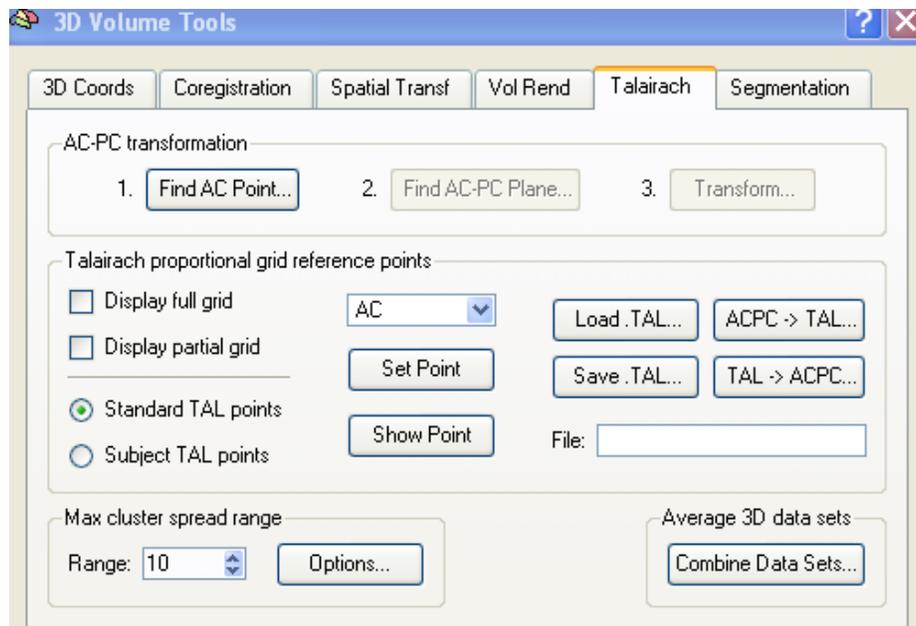
**Coregistration complete. Blend: Transparent view**



**Coregistration complete. Blend: Mosaic view**

## Transformation – AC/PC

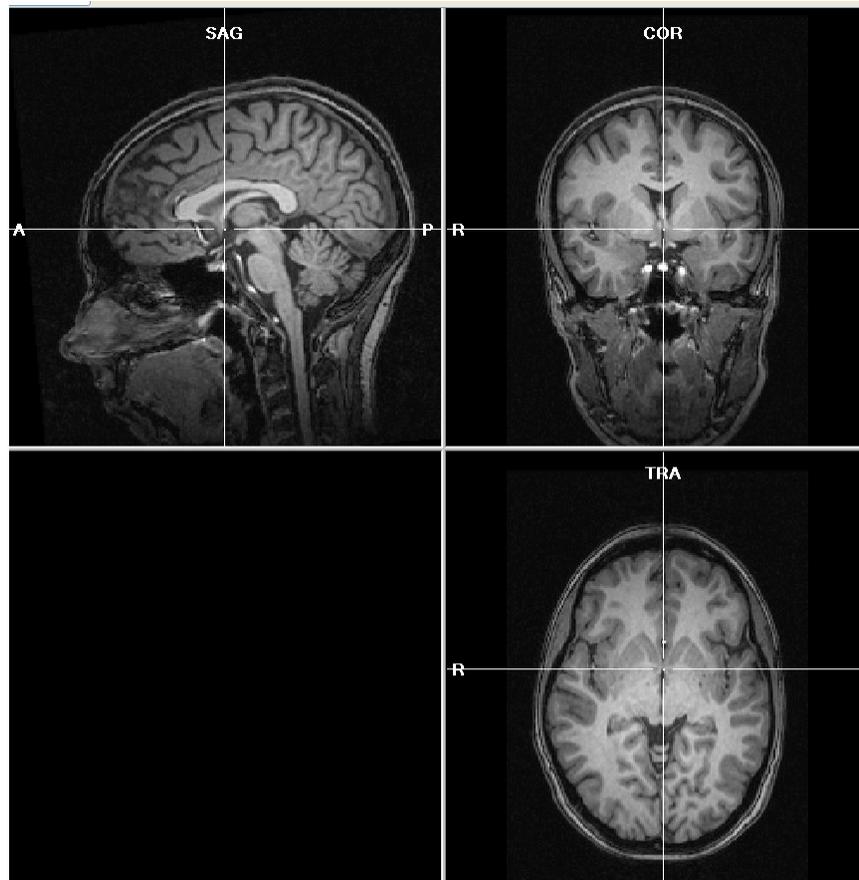
1. Open Brain Voyager
2. Select File, Open and go to the T1 Folder
3. Open the VMR file
4. The 3D Volume Tools window will open in front the anatomical images
5. Click on Full Dialog Box
6. Select Talairach tab



**3D Volume Tools Window - Talairach**

7. Select Click on the Find AC point button.
- NOTE: See the AC/PC Tutorial in Appendix C
8. Place cross-hairs on AC point using mouse or keyboard buttons – the arrows, plus SHIFT + arrows.
  9. When you are satisfied with having found the AC point, click OK.
  10. Select the Find ACPC plane button.
  11. Use up/down buttons in each plane to align the image so that the line falls along the ACPC plane.
  12. BE SURE TO CHECK ALL VIEWS: SAG, COR, TRA!!

13. When you are satisfied, click OK.
14. Click the Transform button.
15. The resultant file is a VMR that now has `_ACPC` added to the file name.



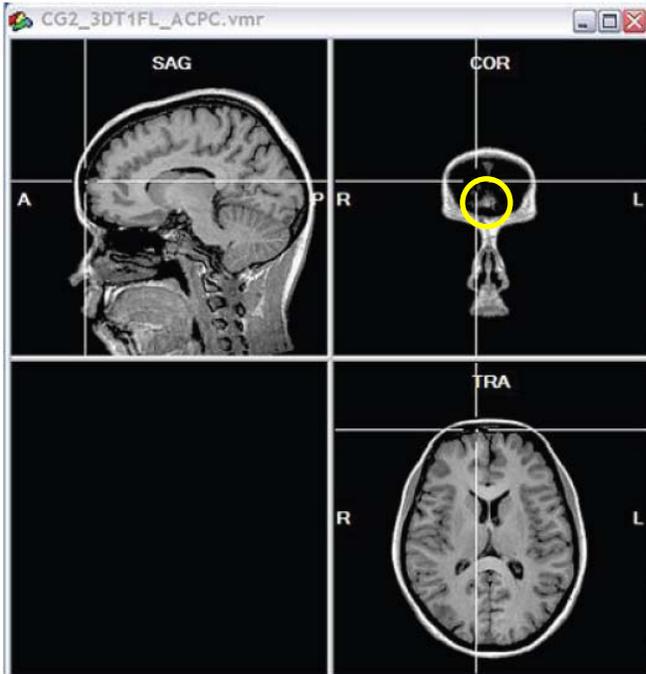
**Transformed VMR – AC/PC Aligned**

#### Transformation – Talairach

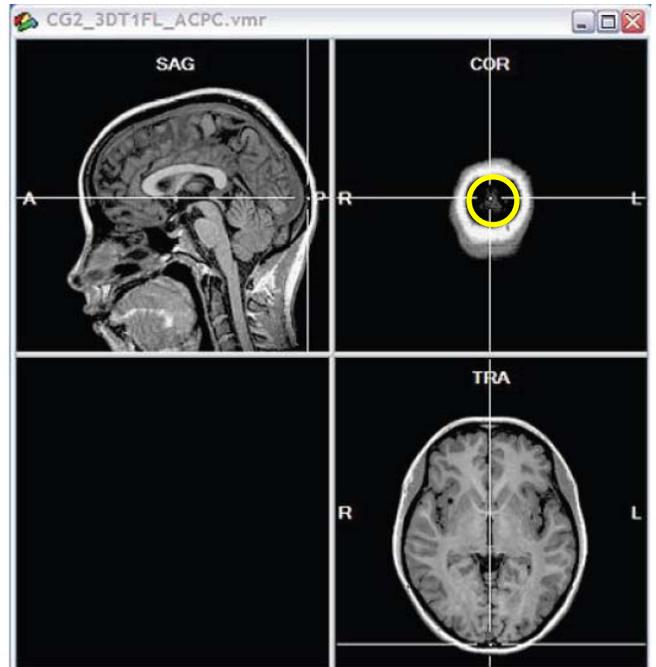
1. Using the same 3D Volume Tools Window, identify the Talairach proportional grid reference points on the participant VMR:
  - a. Select AC from the drop-down menu
  - b. Place crosshairs on the AC point and click OK
  - c. Select PC from the drop-down menu
  - d. Place crosshairs on the PC point and click OK

NOTE: See tutorial on locating the AC/PC points in Appendix C

- e. Select AP from the drop-down menu to set the anterior point
  - i. Find the most frontal point where you see cortex.
  - ii. Set the crosshairs on that point and then scroll through the various views until you are sure you have the point furthest front where the cortex begins.
  - iii. HINT: In the COR view, pull back until you just begin to see cortex in the slice image.
  - iv. When you have found the point, click Set Point
  
- f. Select PP from the drop-down menu to set the posterior point
  - i. Find the most back point where you see cortex.
  - ii. Set the crosshairs on that point and then scroll through the various views until you are sure you have the point furthest back where the cortex begins.
  - iii. HINT: In the COR view, pull back until you just begin to see cortex in the slice image.
  - iv. When you have found the point, click Set Point

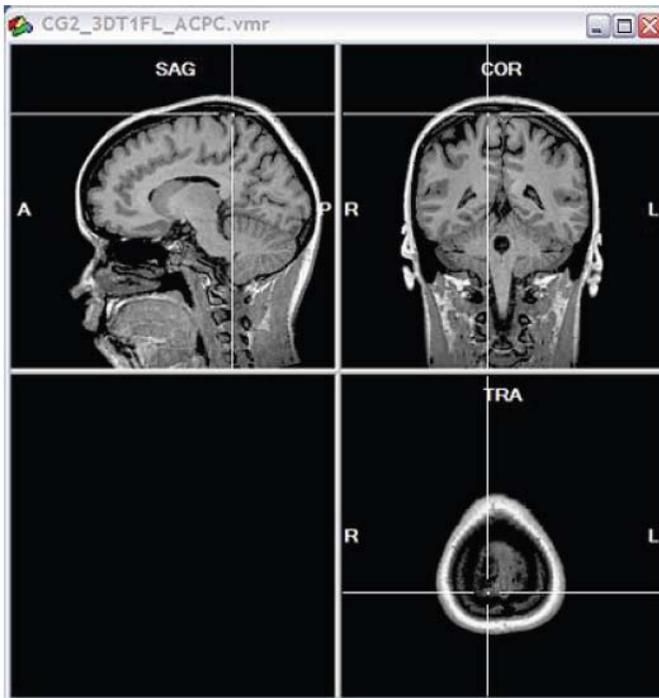


**Anterior point. Note: cortex just beginning to show in COR view.**

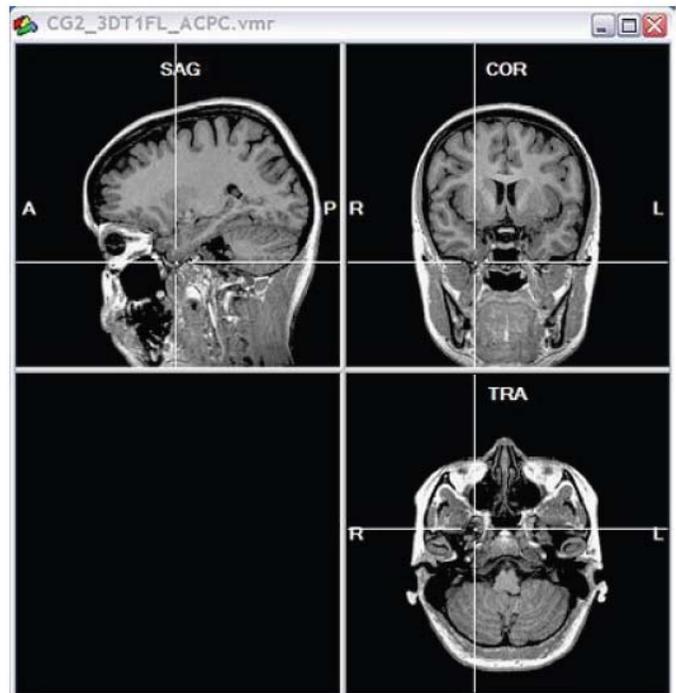


**Posterior point. Note: cortex just beginning to show in COR view.**

- g. Select SP from the drop-down menu to set the superior point
  - i. Find the topmost point where you see cortex.
  - ii. Set the crosshairs on that point and then scroll through the various views until you are sure you have the point at the top of the brain where the cortex begins.
  - iii. HINT: In the TRA view, pull back until you just begin to see cortex in the slice image.
  - iv. When you have found the point, click Set Point
  
- h. Select IP from the drop-down menu to set the inferior point
  - i. Find the bottommost point where you see cortex.
  - ii. Set the crosshairs on that point and then scroll through the various views until you are sure you have the point at the bottom of the brain where the cortex begins.
  - iii. This one is tougher – use all three views to help
  - iv. HINT: In the TRA view, pull back until you just begin to see cortex in the slice image in the cheek/sinus area.
  - v. When you have found the point, click Set Point

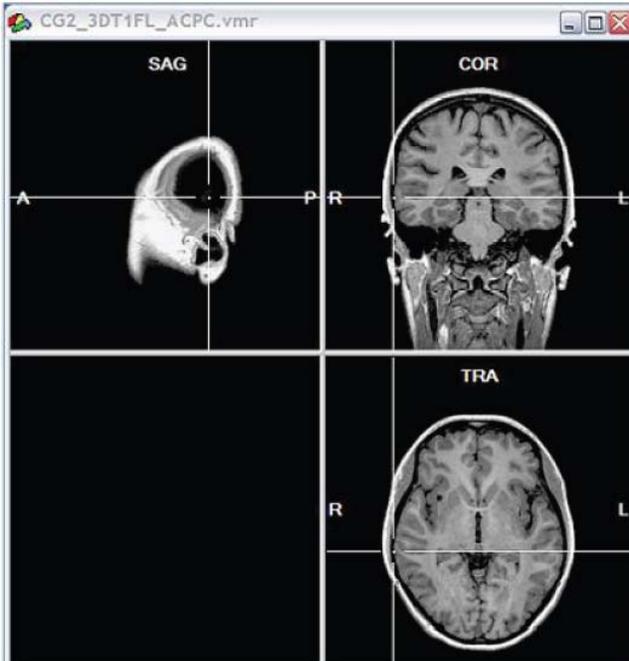


**Superior point. Note: cortex just beginning to show in TRA view.**

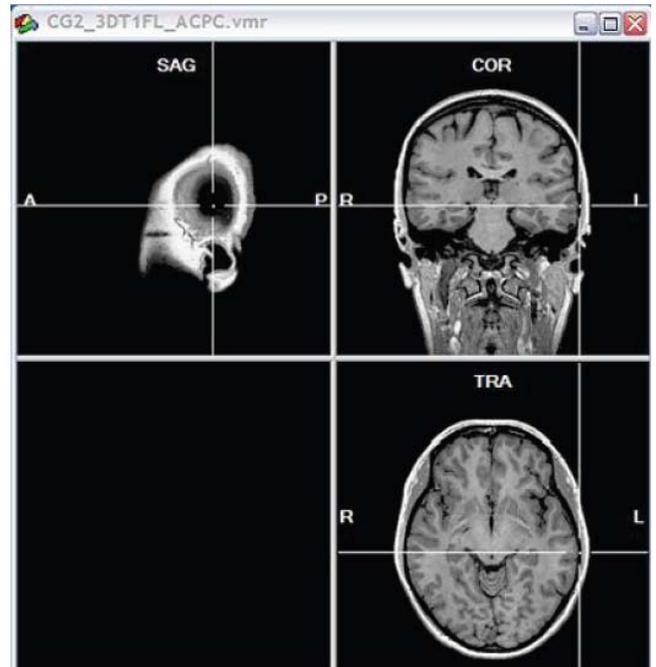


**Inferior point. Note: cortex just beginning to show in TRA view.**

- i. Select RP from the drop-down menu to set the right point
  - i. Find the furthest point on the right of the brain where you see cortex.
  - ii. Set the crosshairs on that point and then scroll through the various views until you are sure you have the point at the right of the brain where the cortex begins.
  - iii. HINT: In the SAG view, pull back until you just begin to see cortex in the slice image.
  - iv. When you have found the point, click Set Point
  
- j. Select LP from the drop-down menu to set the inferior point
  - i. Find the furthest point on the left of the brain where you see cortex.
  - ii. Set the crosshairs on that point and then scroll through the various views until you are sure you have the point at the left of the brain where the cortex begins.
  - iii. HINT: In the SAG view, pull back until you just begin to see cortex in the slice image.
  - iv. When you have found the point, click Set Point

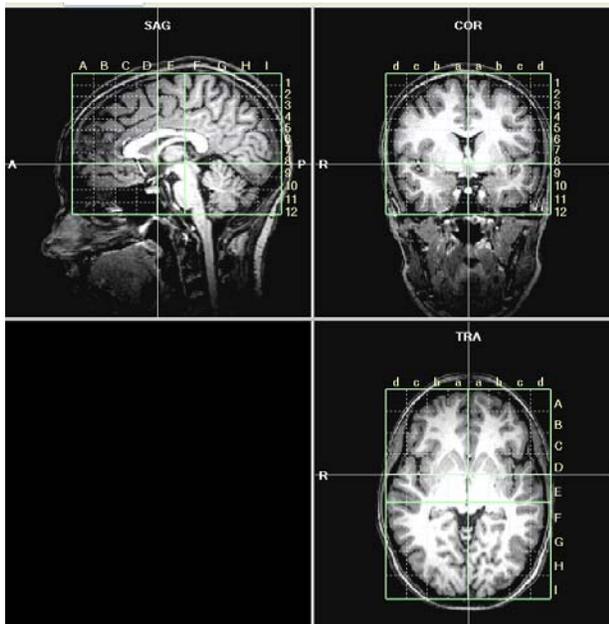


**Right point. Note: cortex just beginning to show in SAG view.**

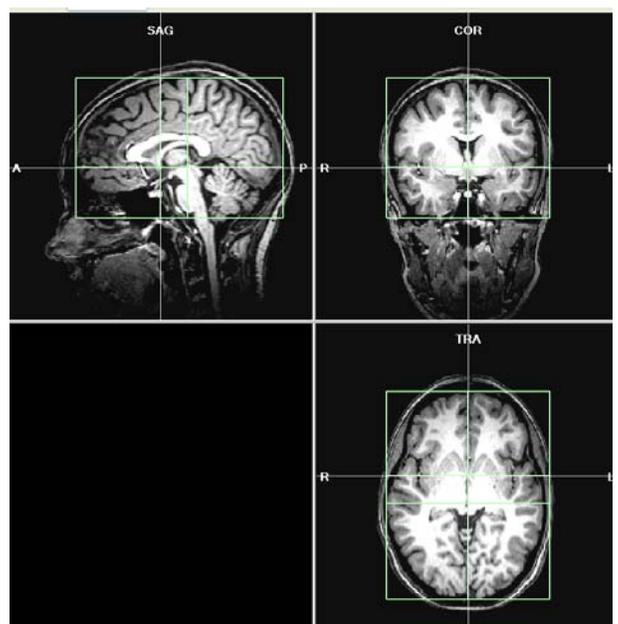


**Left point. Note: cortex just beginning to show in SAG view.**

2. Save the list of reference points
  - a. Click the Save.TAL button
  - b. Name file according to naming convention
  - c. Click Save
  
3. Warp the VMR from AC/PC space to Talairach space
  - a. Click ACPC → TAL button.
  - b. Click GO.
  - c. Click Save.
  
4. The resultant output is a view of VMR in Talairach space.
  - a. You can view the brain using the full grid
  - b. Or the partial grid.



Full Grid



Partial Grid

## **VII. Pre-Processing: Linking it all together**

**VTC File Creation**

Automatic detection of TRF files

To VMR     To ACPC     To TAL   

Functional slice-based data .file (FMR)

FMR -> VMR coregistration file 1, i.e. header-based (\_IA.TRF)

FMR -> VMR coregistration file 2, i.e. intensity-based fine-tuning (\_FA.TRF)

AC-PC translation/rotation file - Talairach, step 1 (\_ACPC.TRF)

Cerebrum border file for scaling - Talairach, step 2 (.TAL)

Resulting VTC file

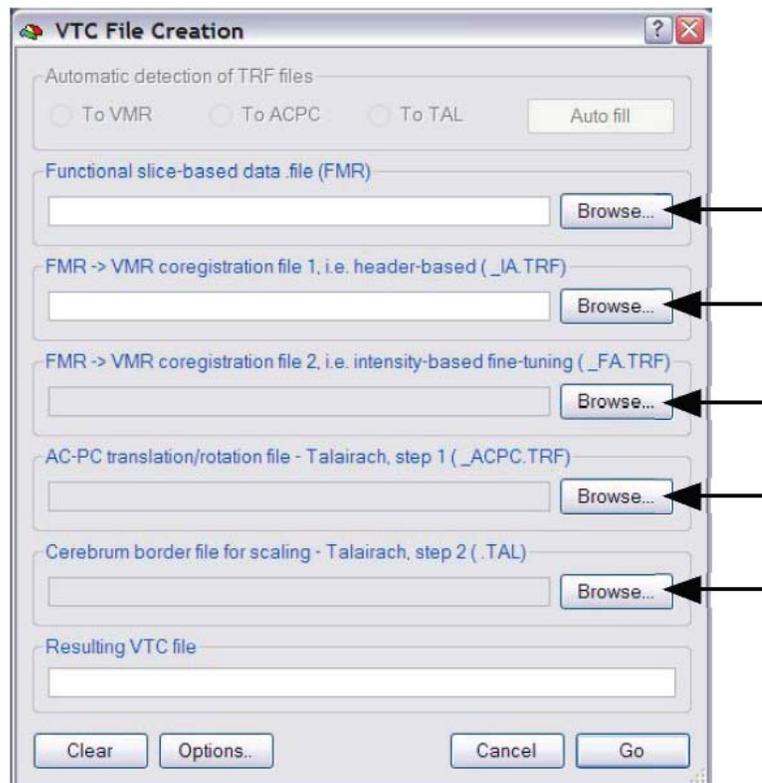
Preprocessing –  
Talairach transformation of functional data and VTC file creation

Overview: This stage of preprocessing is to register the functional data into Talairach space in order to aggregate the functional scans for multiple runs and multiple participants into group data.

FOR EACH RUN AND EACH PARTICIPANT DO:

Creating the VTC File

1. Open the original VMR file (not the AC/PC, not the TAL) to which the functional data has been coregistered for the participant
2. Click on Analysis, Create 3D time course (VTC) file
3. The VTC File Creation window will open



**VTC File Creation window**

4. Note that there are several blank slots to fill in file names that will be required to create the VTC:
  - a. Click Browse to find the file required for each slot
    - i. HINT: Much of the time, BV will locate the file automatically, but always double-check the path name to be certain!
  - b. For the Functional slice-based data file (FMR)
    - i. Select the preprocessed FMR file for the appropriate participant and run (e.g., the FMR with the motion correction, smoothing, etc. parameters in the file name)
  - c. For the FMR → VMR Coregistration File 1 (\_IA.TRF)
    - i. Select the TRF file for the initial alignment for the appropriate participant and run
  - d. For the FMR → VMR Coregistration File 2 (\_FA.TRF)
    - i. Select the TRF file for the fine alignment for the appropriate participant and run
  - e. For the AC-PC translation/rotation file – Talairach, step 1
    - i. Select the TRF file with ACPC in its file name for the appropriate participant and run
    - ii. Note: This file will come from the T1 folder
  - f. For the Cerebrum border file for scaling – Talairach, step 2
    - i. Select the TAL file
    - ii. Note: This file will come from the T1 folder
5. The name of the resultant VTC file will appear automatically. Press GO.
  - a. NOTE: This process takes the longest, and can take up to 4 minutes depending on your hardware.

## Linking the functional VTC file to the structural TAL.VMR

1. When the process is complete
  - a. Close the VMR that you had opened
  - b. Open the TAL.VMR for the appropriate participant
  - c. Click Analysis, Link 3D time course (VTC) file
  - d. In the Line 3D Volume Time Course (VTC) dialog window
    - i. Select the VTC file for the appropriate participant and run
    - ii. Be sure the Store reference to VTC file is checked
  - e. Click OK
2. Nothing happened! Or so it seems...
  - a. Right-click anywhere on the cerebrum
  - b. Select Show ROI time course
  - c. WOW – look at that! You will see the functional time course information linked now to the structural view!
3. From this point you can begin your statistical analyses

## **Resources and References**

### **Websites**

Official Brain Voyager Site: [www.brainvoyager.com](http://www.brainvoyager.com)

Whole Brain Atlas: <http://www.med.harvard.edu/AANLIB/home.html>

Learning Brain Anatomy the radiological way:  
[http://www.med.wayne.edu/diagRadiology/Anatomy\\_Modules/brain/brain.html](http://www.med.wayne.edu/diagRadiology/Anatomy_Modules/brain/brain.html)

Basics of MRI: <http://www.cis.rit.edu/htbooks/mri/>

MRI resource page: <http://www.rtstudents.com/mri/index.htm>

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- Grady CL, Horwitz B, Pietrini P, Mentis MJ, Ungerleider LG, Rapoport SI, Haxby JV, (1996): Effect of task difficulty on cerebral blood flow during perceptual matching of faces. *Human Brain Mapping* 4: 227-239.
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- Jennings JM, McIntosh AR, Kapur S, Tulving E, Houle S, (1997): Cognitive subtractions may not add up: the interaction between semantic processing and response mode. *Neuroimage* 5: 229-239.
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- Price CJ and Friston KJ, (1997): Cognitive conjunction: a new approach to brain activation experiments. *Neuroimage* 5: 261-270.
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## **Appendix A**

### **fMRI Paradigm Information Sheet**

This document is designed to help the MRI technologist at I<sup>2</sup>AT to build paradigms necessary for successful fMRI research. Please fill in the fields below completely. If you have any questions, please contact I<sup>2</sup>AT for assistance.

1) Please describe the experiment being conducted (i.e., what are the basic tasks, measures of interest, and expected results).

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2) Please fill in the values desired for the following parameters (detailed descriptions of each are given in the following pages):

TR (ms): \_\_\_\_\_

TE (ms): [default = 35] \_\_\_\_\_

Approximate timeframe for study: \_\_\_\_\_

Brain plane (sagittal, coronal, axial/transverse, oblique): \_\_\_\_\_

Slice thickness: \_\_\_\_\_

Spacing / gap: \_\_\_\_\_

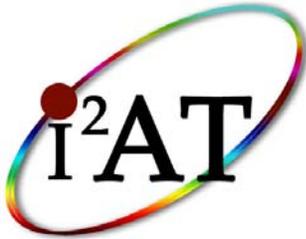
Field of view: \_\_\_\_\_

Area of brain: \_\_\_\_\_

Interleave/Sequential: \_\_\_\_\_

Design type (e.g., block, ER) \_\_\_\_\_

## Appendix B



### Institute for Imaging & Analytical Technologies Functional Magnetic Resonance Imaging Instruction Booklet

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On (date) \_\_\_\_\_ at (time) \_\_\_\_\_

you will be participating in the MRI portion of the \_\_\_\_\_ experiment. The following booklet contains important information concerning directions to I<sup>2</sup>AT, where the MRI will take place, reminders about the procedure/task, special instructions about doing the task inside the MRI magnet, and suggestions about how to prepare for the MRI phase. Please read all the instructions carefully and contact \_\_\_\_\_ if you have any questions.

#### Preparing for the MRI

You should be sure to wear comfortable, easy-to-change clothing for the MRI. You will be provided with “scrubs” to wear. Your clothing and personal items will be stored in a locked cabinet. Avoid shoes with metal. If you wear open-toed shoes or sandals, you might like to bring a pair of socks to keep your feet warm during the procedure. Avoid wearing an under-wire bra to the MRI or you will have to remove it. A “sports bra” or other bra with metal hooks and eyes are acceptable, but not under-wire.

Please do not wear any jewelry to the session. If you are wearing earrings, rings, watches, body jewelry (including piercings), barrettes, pony-tail elastic, wigs, hairpins, or other objects that could contain metal, you will be asked to remove them prior to the MRI. We will provide a safe place to store these items, but please consider leaving them in your car or at home.

Please do not wear makeup to the MRI. Some makeup contains small amounts of metal. Also, avoid using hair spray, hair gel, spray, lotions, and powders.

When you arrive, you will remove any metal containing objects as listed above, as well as hearing aids, glasses, wigs (with metal clips) and non-permanent dentures. You will also remove all objects from your pockets including your wallet, watch or timepiece. Again, please leave valuable items at home or in your car.

**Remember the procedure/task**

\*Here some information reminding them of the task (if you did a pre-training phase) could be inserted.\*

[Sample]

Remember that while you are in the MRI magnet, you will perform the same task that you learned during Phase I. You will be presented with a screen instructing you to either: “Generate a sentence” OR “Create an interactive image”. The instruction screen will be followed by a pair of unrelated words (e.g., CLOWN – SPOON). You should try to use the strategy in the instructions to link the two words together. You will indicate when you use the strategy instructed by pressing a button. Rather than use a keyboard, the following button press device will be used:

You will hold this button box on your lap and press the buttons using the fingers on your right hand. Just as with the keyboard, you press the appropriate button to tell us which strategy you used to link the two words together. Press the red button when you form a sentence, the yellow button when you generate an interactive image, the green button if you use another strategy, and the blue button if you cannot implement any strategy. Remember to try to use the instructed strategy, but the most important thing is to ACCURATELY report which strategy you actually used.



### **Inside the scanner**

There are three rules for doing a task in the scanner that are of the utmost importance. Brain scanning studies are very expensive and time consuming, so it is critical that we have the best data possible from each subject. We need you to be as conscientious as possible in performing the tasks, and following these three rules will help us tremendously.

Rule # 1 – When you see the small cross on the screen, ALWAYS keep your eyes focused on it. Devices in the scanner are able to follow your gaze to determine where you are looking on the screen. Your gaze location will be monitored throughout the study. Throughout the task, please maintain your gaze at the center of the screen where the cross is located. For the purposes of our brain scanning study, it is absolutely critical that you perform this task without moving your gaze off the center of the screen.

Rule # 2 – Once you are situated in the scanner, DO NOT move your head. The type of brain scanning we will be doing requires that all the brain images be aligned across all sessions and events. Moving has important negative implications. Imagine that half way through the study you move your head slightly. Once your head has moved, the images taken after this point will not be aligned with the images taken before you moved your head. As a result, data collected during the study might be unusable. To help keep your head steady throughout the study, we will ask you to lay your head on a small pillow and place foam wedges on each side of your head to support it. Additionally, your chin and/or forehead may be secured with tape (not applied to your skin). Participants usually find this to be a comfortable way to keep the head stationary. Also, occasionally between scanning runs you will see the computer screen change while we set up the computer program for the next scanning run. During this time feel free to relax and let your mind wander, but please do not move your head.

You are asked NOT to talk during the entire procedure so that your head will not move. However, you can communicate with us using the button box. When we ask you a question in the magnet, press the red button to indicate YES and the yellow button to indicate NO.

Rule # 3 – Do your best to remain focused on whatever task you are being asked to perform. When you perform a given task, do your best to only perform that task and nothing else. This is important if we are to identify the brain areas that underlie each task specifically. If you can follow this principle throughout the experiment, it will help us tremendously. If you only perform the critical task, we can identify the relevant brain areas. If you begin thinking about other things beside the task, we won't be able to tell them apart.

If at any time you begin to feel uncomfortable and do not wish to continue, press buttons on the button press box repeatedly and we will stop the scan immediately.

Here is a picture of the MRI scanner and how you will be positioned to enter the scanner.



**BE SURE YOU READ THIS:**

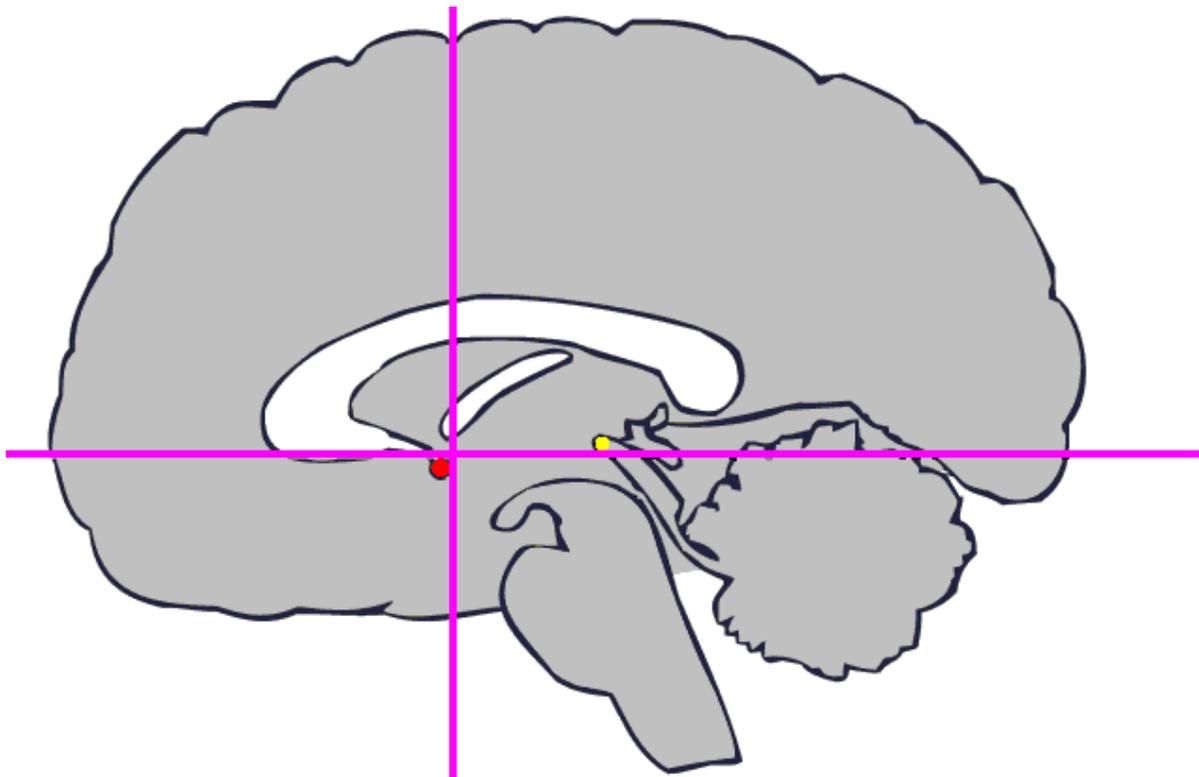
**Parking and Where to wait** – Enter your specifics here.

## Appendix C

### Finding the AC/PC points – A Tutorial

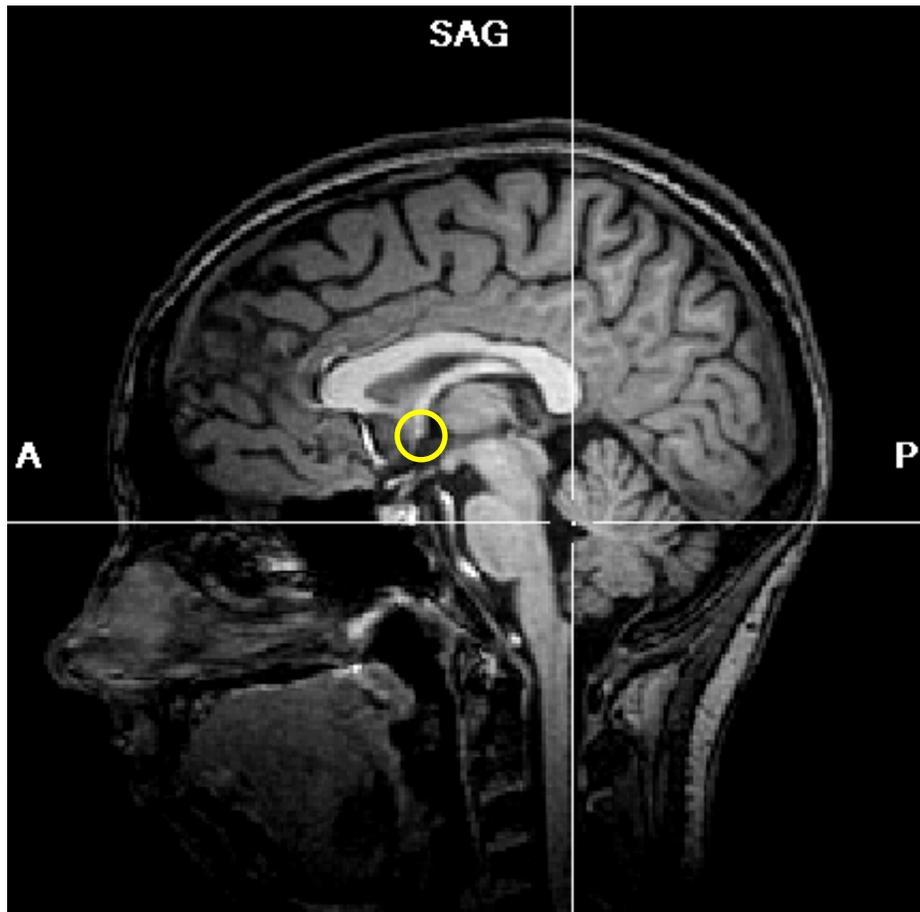
Overview: This tutorial is designed to help simplify the task of locating the AC and PC points. They can be difficult to locate until you see it done and then it is easy.

What are the AC/PC points? The AC is the anterior commissure and the PC is the posterior commissure. The commissures are bundles of fibre which connect the two hemispheres of the brain. The anterior commissure (AC) connects the middle and inferior temporal gyri of the two hemispheres, and runs across the midline just in front of the fornix. See red dot on stylized brain drawing below:



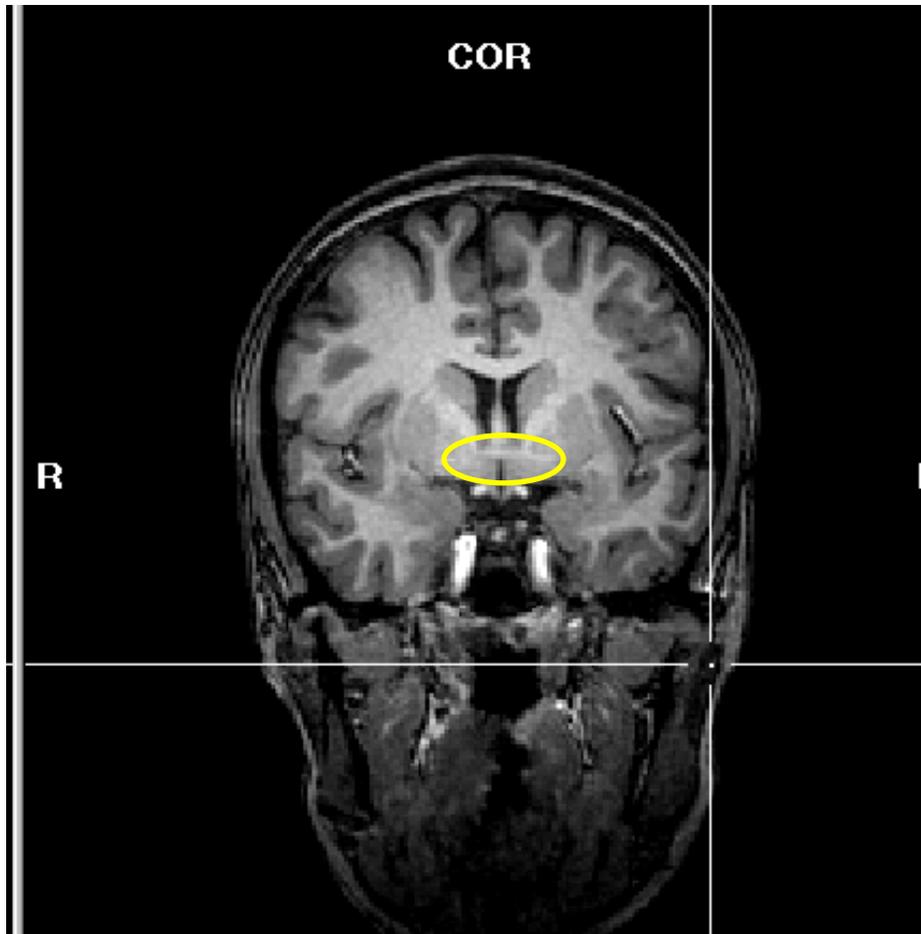
The posterior commissure connects midbrain and diencephalon structures. It is located just in front of and above the superior colliculi, below the pineal gland. It is represented by the yellow dot in the drawing above.

Finding the AC and PC points on a structural scan is easy once you know what you are looking for. To find the AC, look at the SAG view of the VMR, usually at the slice that is presented when you first open the VMR. The AC appears as a brighter white dot in the expected location. In this view, you are looking at the commissure as if you cut a straw and are looking directly into the end of the straw.



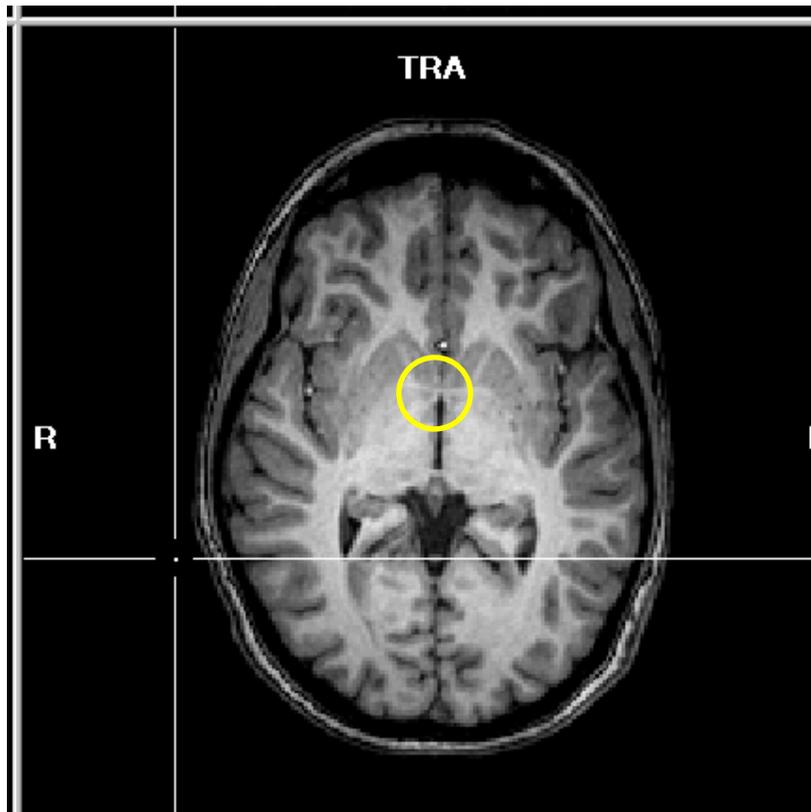
AC Point – SAG view

Once you locate the point on the SAG view, place it in your crosshairs on the SAG view. You can then fine-tune its location by using the COR and TRA views. On the COR view, you are looking from the back of the head at a slice that is cut from superior (top) to inferior (bottom) from ear to ear. So the AC is going to look like a little pathway connecting the left and right hemispheres together. You want your crosshairs to be right at the point that the two hemispheres separate.



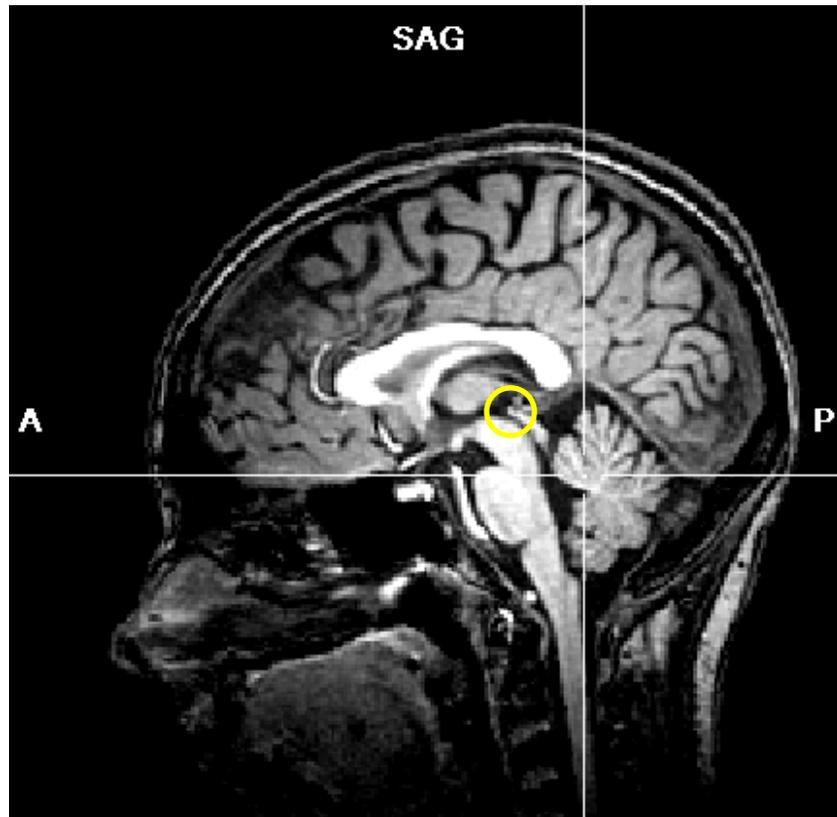
AC – COR View

For the TRA view, the AC commissure again looks like a connecting line, but now the view is a coronal slice from the superior view – looking down on the brain from above. Again, your crosshairs should be on the point along the AC that the two hemispheres diverge.



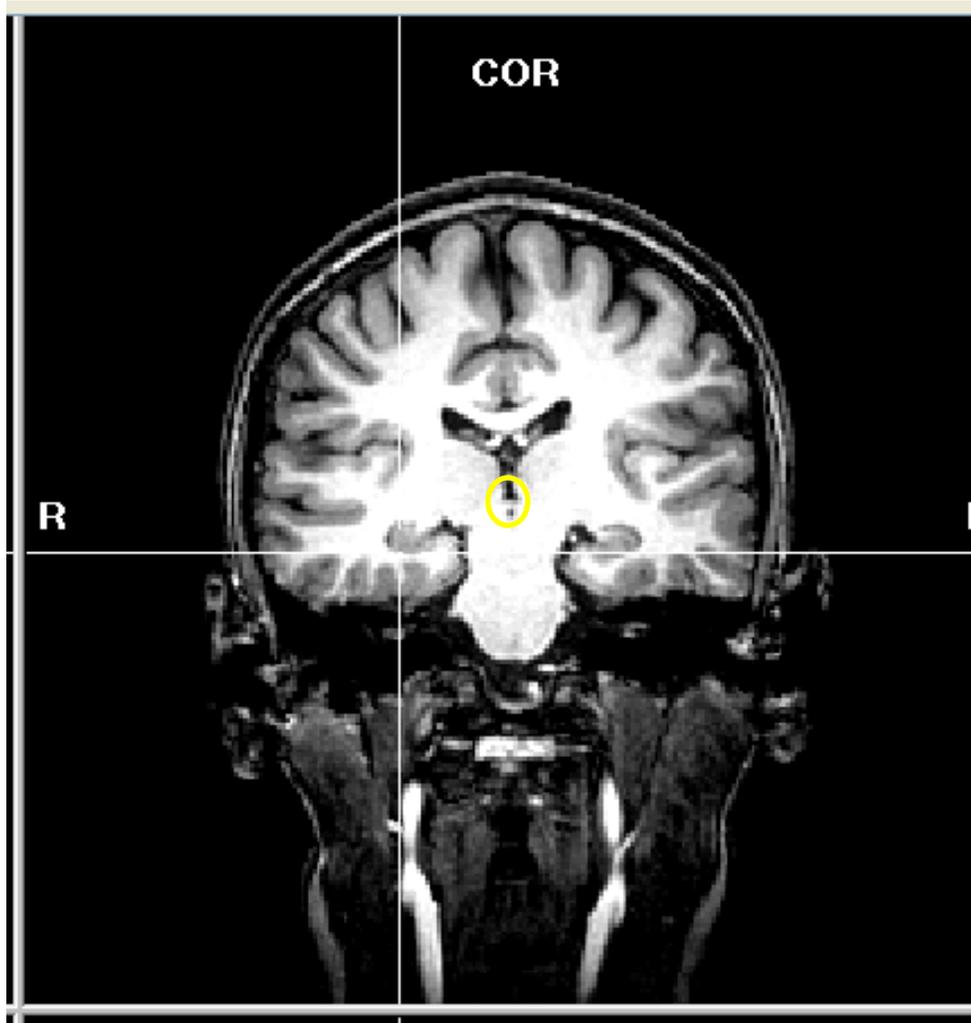
PC – TRA View

Finding the PC is a bit trickier, but still easy once you know what to look for. Start again with the SAG view. The PC appears as a white dot (often less bright than the AC), just at the tip of the superior colliculi.

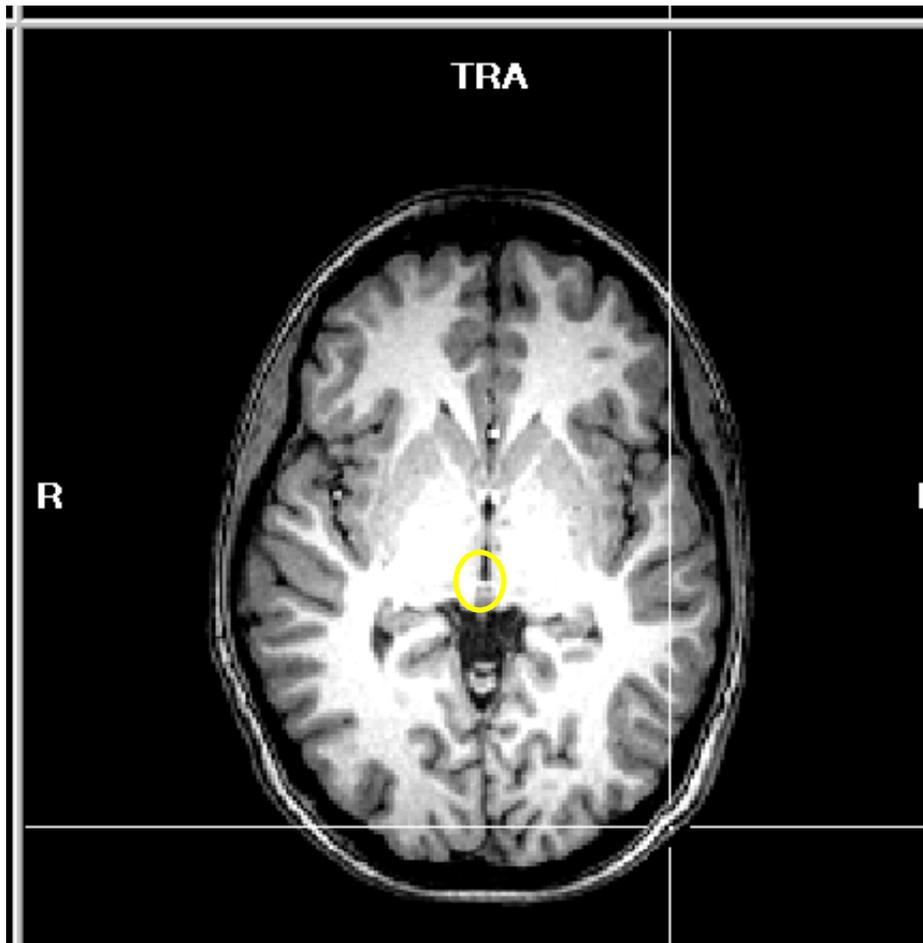


PC point – SAG view

Place the PC in your crosshairs. Once centered on the SAG view, use the COR and TRA views to fine-tune. The PC appears as a connecting fiber, just as the AC did, but it is in a posterior position, rather than an anterior position. The posterior position will be lower than the anterior position on the COR and TRA views, relative to the AC.

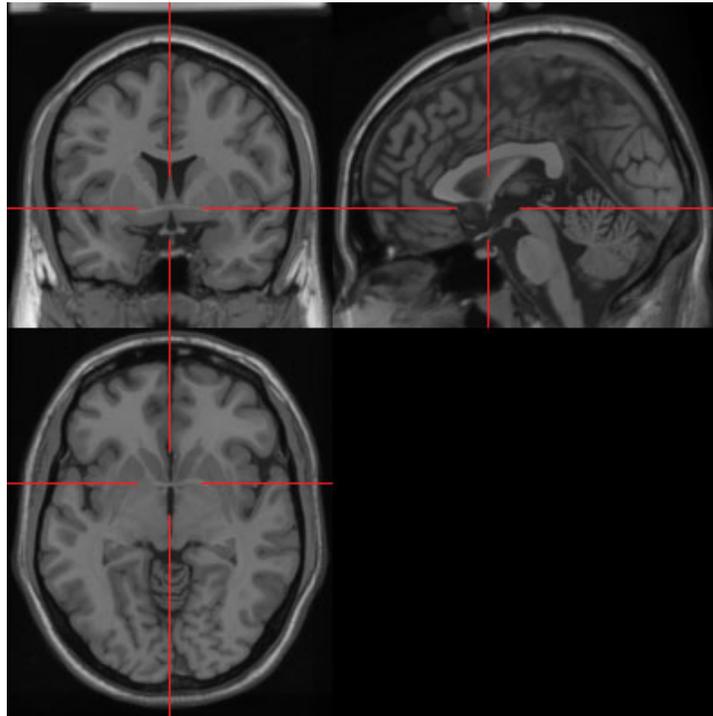


PC – COR view

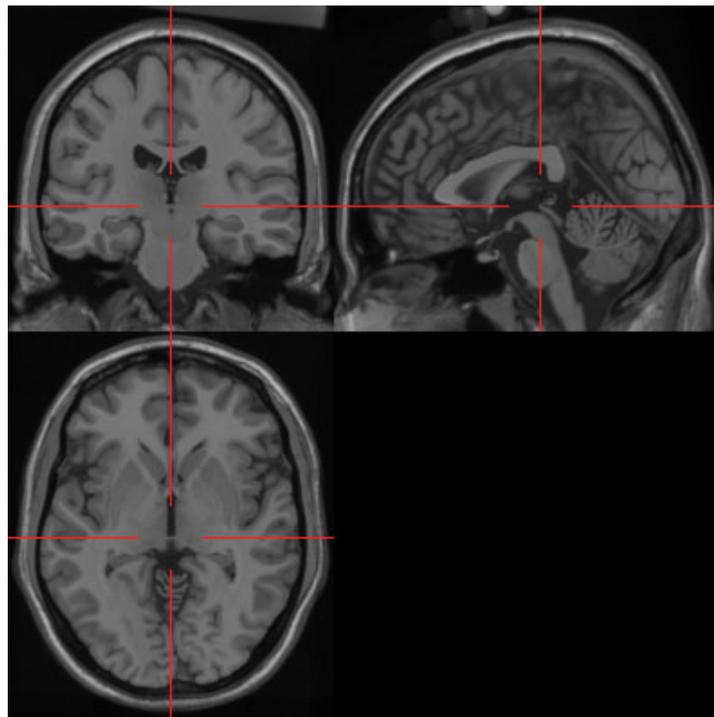


PC – TRA view

Here are some pictures from the web. They may be clearer my BV screen shots.



The AC is in the crosshairs for all three views



The PC is in the crosshairs for all three views