AM Regression - 1

- **AM** = **A**mplitude **M**odulated (or Modulation)
  - ★ Have some extra data measured about each response to a stimulus, and maybe the BOLD response amplitude is modulated by this
  - ★ Reaction time; Galvanic skin response; Pain level perception; Emotional valence (happy or sad or angry face?)
- Want to see if some brain activations vary proportionally to this **ABI** (**A**uxiliary **B**ehaviorial **I**nformation)

- Discrete levels (2 or maybe 3) of ABI:
  - ★ Separate the stimuli into sub-classes that are determined by the ABI ("on" and "off", maybe?)
  - ★ Use a GLT to test if there is a difference between the FMRI responses in the sub-classes

```
3dDeconvolve ...                                                    \
 -stim_times 1 regressor_on.1D  'BLOCK(2,1)' -stim_label 1 'On'   \
 -stim_times 2 regressor_off.1D 'BLOCK(2,1)' -stim_label 2 'Off' \
 -gltsym 'SYM: +On | +Off' -glt_label 1 'On+Off'                   \
 -gltsym 'SYM: +On -Off'   -glt_label 2 'On-Off' ...
```

  - "`On+Off`" tests for any activation in *either* the "on" or "off" conditions
  - "`On-Off`" tests for differences in activation *between* "on" and "off" conditions
  - Can use `3dcalc` to threshold on ***both*** statistics at once to find a **conjunction**

AM Regression - 2

- Continuous (or several finely graded) ABI levels
  - ★ Want to find active voxels whose activation level also depends on ABI
  - ★ `3dDeconvolve` is a linear program, so must make the assumption that the change in FMRI signal as ABI changes is linearly proportional to the changes in the ABI values
- Need to make 2 separate regressors
  - ★ One to find the mean FMRI response (the usual `-stim_times` analysis)
  - ★ One to find the variations in the FMRI response as the ABI data varies
- The second regressor should have the form

$$r_{\mathrm{AM2}}(t) = \sum_{k=1}^{K} h(t-\tau_k)\cdot(a_k - \bar{a})$$

  - ★ Where a_k = value of k^{th} ABI value, and $\bar{a}$ is the average ABI value
- Response (β) for first regressor is standard activation map
- Statistics and β for second regressor make activation map of places whose BOLD response changes with changes in ABI
  - ★ Using 2 regressors allows separation of voxels that are active but are *not* detectably modulated by the ABI from voxels that *are* ABI-sensitive

AM Regression - 3

- New feature of **3dDeconvolve**: **-stim_times_AM2**
- Use is very similar to standard **-stim_times**
  - ★ **-stim_times_AM2 1 times_ABI.1D 'BLOCK(2,1)'**
  - ★ The **times_ABI.1D** file has time entries that are "married" to ABI values:

```
10*5 23*4 27*2 39*5
17*2 32*5
*
16*2 24*3 37*5 41*4
```

  - ★ Such files can be created from 2 standard ASCII **.1D** files using the new **1dMarry** program
    - o The **-divorce** option can be used to split them up
- **3dDeconvolve** automatically creates the two regressors (unmodulated and amplitude modulated)
  - ★ Use **-fout** option to get statistics for activation of the pair of regressors (i.e., testing null hypothesis that *both* β weights are zero: that there is no ABI-independent ***or*** ABI-proportional signal change)
  - ★ Use **-tout** option to test each β weight separately
  - ★ Can **1dplot** $\mathbf{X}$ matrix columns to see each regressor

AM Regression - 4

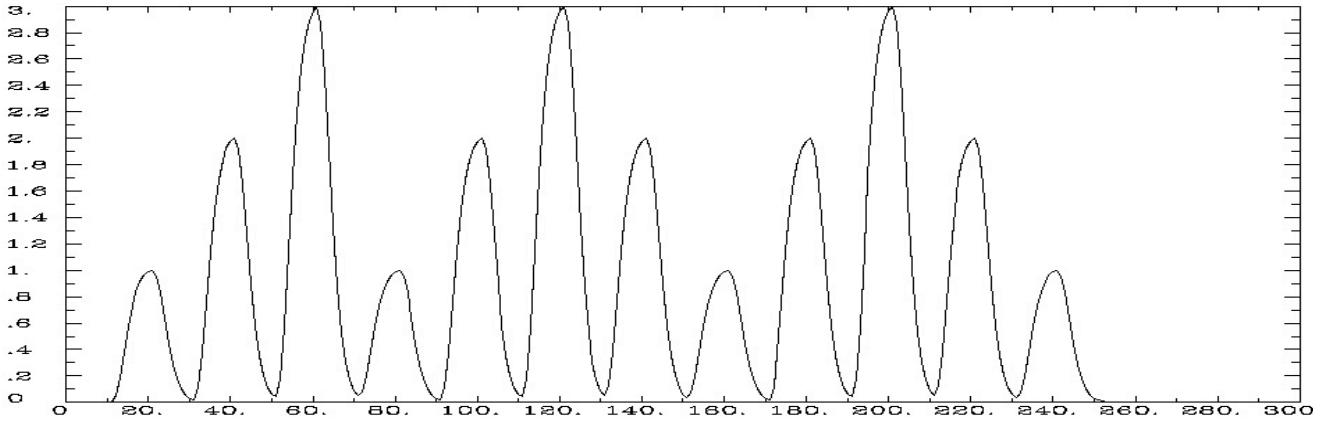
- The AM feature is new, and so needs some practical user experiences before it can be considered "standard practice"
  - ★ In particular: don't know how much data or how many events are needed to get good ABI-dependent statistics
  - ★ You could also use AM regression to *remove* potential confounds in FMRI responses that co-vary with some external parameter
- If you want, **`-stim_times_AM1`** is also available
  - ★ It only builds the regressor proportional to ABI data directly, with no mean removed: $r_{\mathrm{AM1}}(t) = \sum_{k=1}^{K} h(t-\tau_k)\cdot a_k$
  - ★ Can't imagine what value this option has, but you never know … (if you can think of a good use, let me know)
- Future directions:
  - ★ Allow more than one amplitude to be married to each stimulus time (insert obligatory polygamy/polyandry joke here)
    - o How many ABI types at once is too many? I don't know.
  - ★ How to deal with unknown nonlinearities in the BOLD response to ABI values? I don't know. (Regress each event separately, then compute MI?)
  - ★ Deconvolution with amplitude modulation? Requires more thought.

AM Regression - 5

Timing: **AM.1D** = 10*1 30*2 50*3 70*1 90*2 110*3 130*2 150*1 170*2 190*3 210*2 230*1

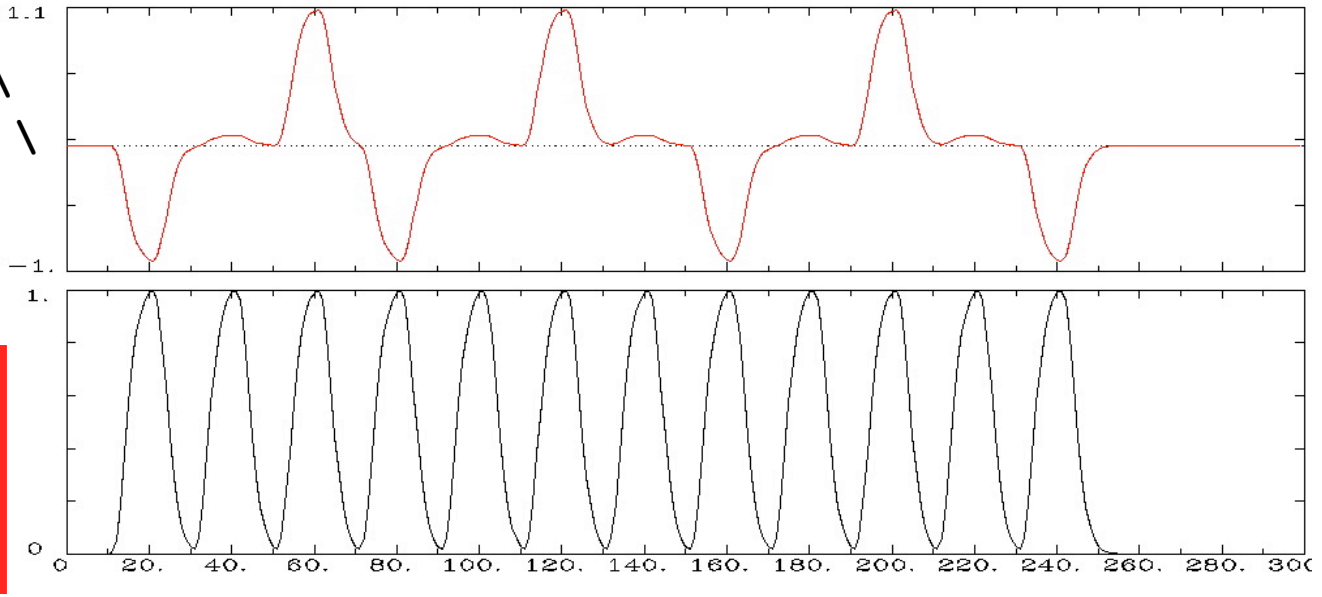
- **3dDeconvolve -nodata 300 1.0 -num_stimts 1 **
  -stim_times_AM1 1 AM.1D 'BLOCK(10,1)' -x1D AM1.x1D
- **1dplot AM1.x1D'[2]'**

AM1 model of signal (modulation = ABI)



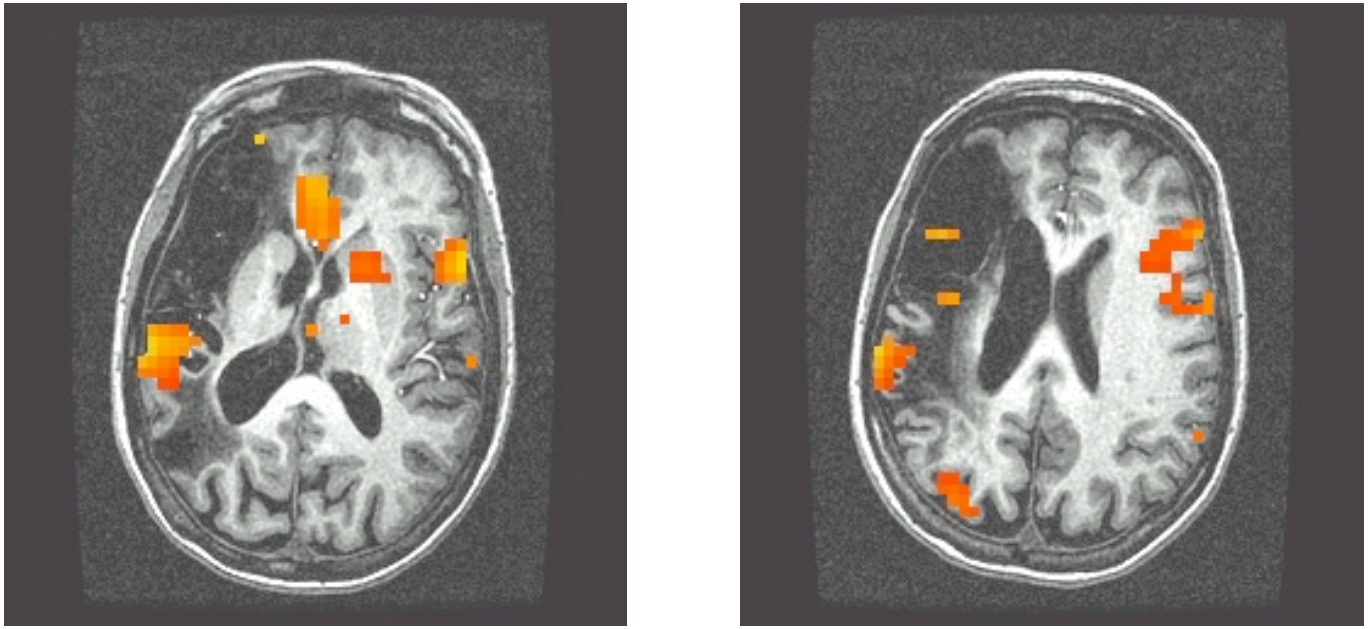
- **3dDeconvolve -nodata 300 1.0 **
  **-num_stimts 1 **
  **-stim_times_AM2 1 **
  **AM.1D 'BLOCK(10,1)' **
  -x1D AM2.x1D
- **1dplot -sepscl **
  AM2.x1D'[2,3]'

AM2 model of signal: is 2D sub-space spanned by these 2 time series



AM Regression - 6

- First actual user: Whitney Anne Postman (NIDCD; PI=Al Braun)
- Picture naming task in aphasic stroke patient
- ABI data = number of alternative names for each image (e.g., "balcony" & "porch" & "veranda", vs. "strawberry"), from 1 to 18
  - 8 imaging runs, 144 stimulus events
- 2 slices showing activation map for BOLD responses proportional to ABI (β_{AM2})
  - What does this mean about the brain and aphasia? Don't ask me!

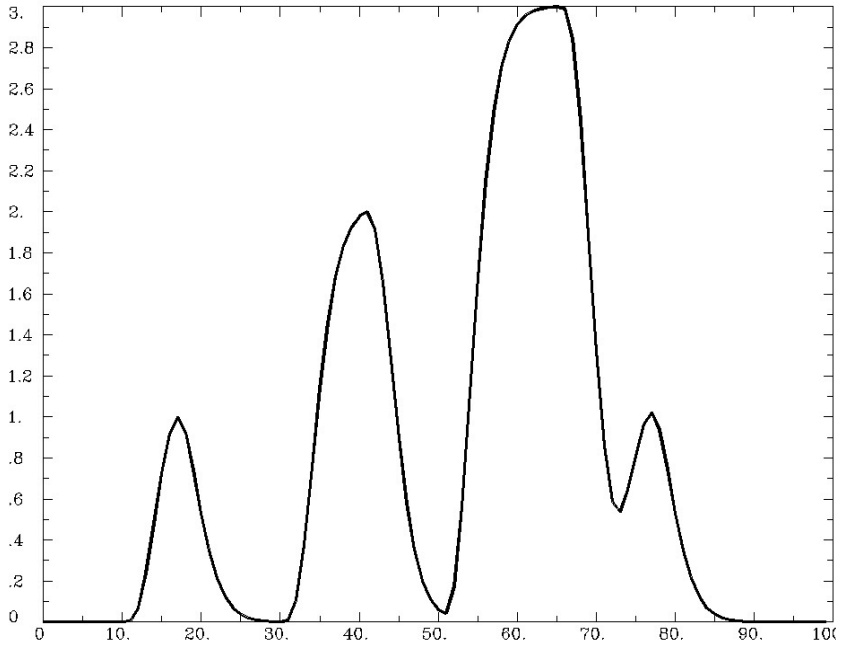


AM Regression - Updates: Dec 2008

- The **-stim_times_AM*** options (and program **1dMarry**) have been modified to allow the input of multiple amplitudes with each time
- For example:
  - **37.2*1,2,3 42.6*-1,7,4 53.7*2,-6,1**
  - 3 extra amplitudes per time point
  - **-stim_times_AM2** will generate 4 regressors
  - 1 regressor for the constant magnitude FMRI response
  - 1 regressor for each of the extra amplitudes
- **-stim_times_AM1** still builds only 1 regressor, as before
  - Amplitude of each **BLOCK** (say) is modulated by sum of all extra amplitudes provided
- You can use **-stim_times_AMx** as a synonym for -**stim_times_AM2**, if you prefer

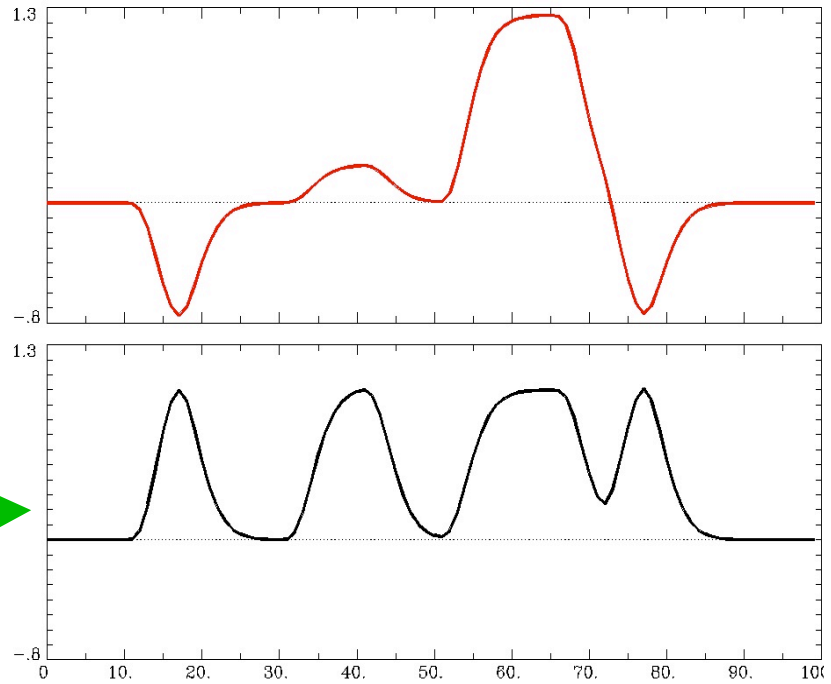
DM Regression - Dec 2008

- For use with **-stim_times_AM*** a new variant of the **BLOCK** response model function is available: **dmBLOCK**
  - "duration modulation" instead of (or on top of) amplitude modulation
- Example:
  - File **A1.1D** = **10*1:5 30*2:10 50*3:15 70*1:5**
    - 2 extra parameters per time: amplitude modulation:duration
    - Last parameter always duration
      - Use '**:**' as the separator
    - Previous = amplitude modulation
  - **3dDeconvolve **
    **-nodata 100 1.0 **
    **-num_stimts 1 **
    **-polort -1 **
    **-stim_times_AM1 1 A1.1D **
    dmBLOCK -x1D A1dm.x1D
  - **1dplot A1dm.x1D**



DM Regression - 2

- Same thing, but with **AM2** model
  - **3dDeconvolve **
    **-nodata 100 1.0 **
    **-num_stimts 1 **
    **-polort -1 **
    **-stim_times_AM2 1 A1.1D **
    dmBLOCK -x1D A2dm.x1D
  - **1dplot A2dm.x1D**



- **dmBLOCK** doesn't require an amplitude modulation parameter, but will use one (or more) if present
  - Duration parameter is always the ***last*** parameter married to the time, and is separated by a '**:**' character
- Future dream: may have more nonlinearly modulated response model functions — any ideas?