Tutorial 5 Appendrun and quick measure programs

5.1 Combine two files

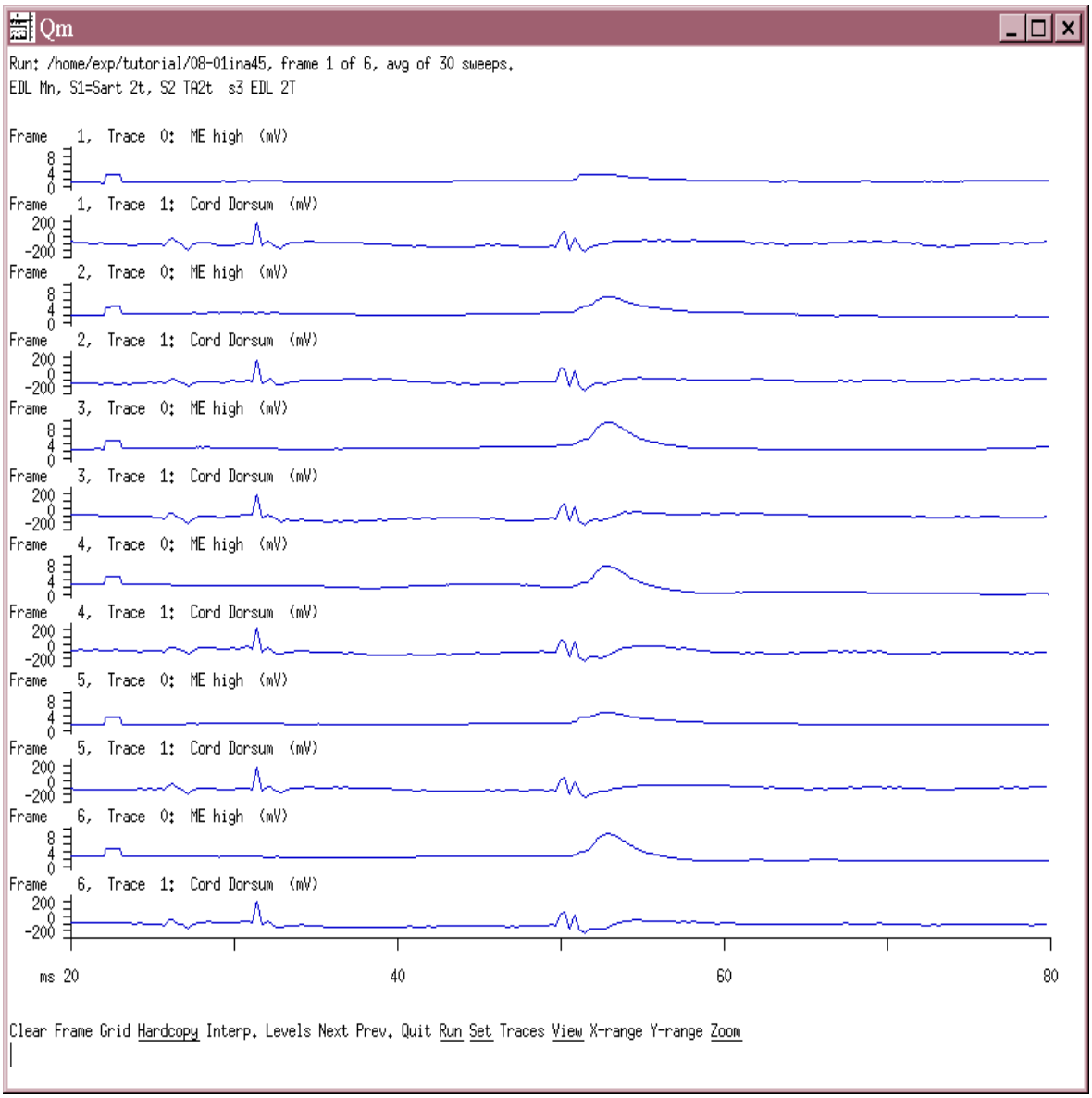
You have created two files (08-01ina45 and 08-01act45) that contain the trace-average separately for flexion and extension. You will use the *appendrun* program to combine these runfiles. The appendrun command is used by typing "*appendrun file1 file2*". The command puts file1 and file2 together and save the new file as file1. (Note that if you appendrun file1 and file2 you will loose your original file1 because it becomes the merged file but you still have file2 as it was originally).

After quitting Analysis, from the shell type appendrun 08-01-act45 08-01ina45. This way 08-01act45 will be the file that contains the merged data. After typing the command, you will be asked whether you want to appendrun these two files. Just answer yes. appendrun 08-01act28 08B02inact28, yes

5.2 Using the QuickMeasure (qm) program

Next you want to look at the appended file and determine the window for PSP amplitude analysis. Open quick measure by typing "qm c08-01act45" on your shell. You should see a window as shown in Fig 5.1.

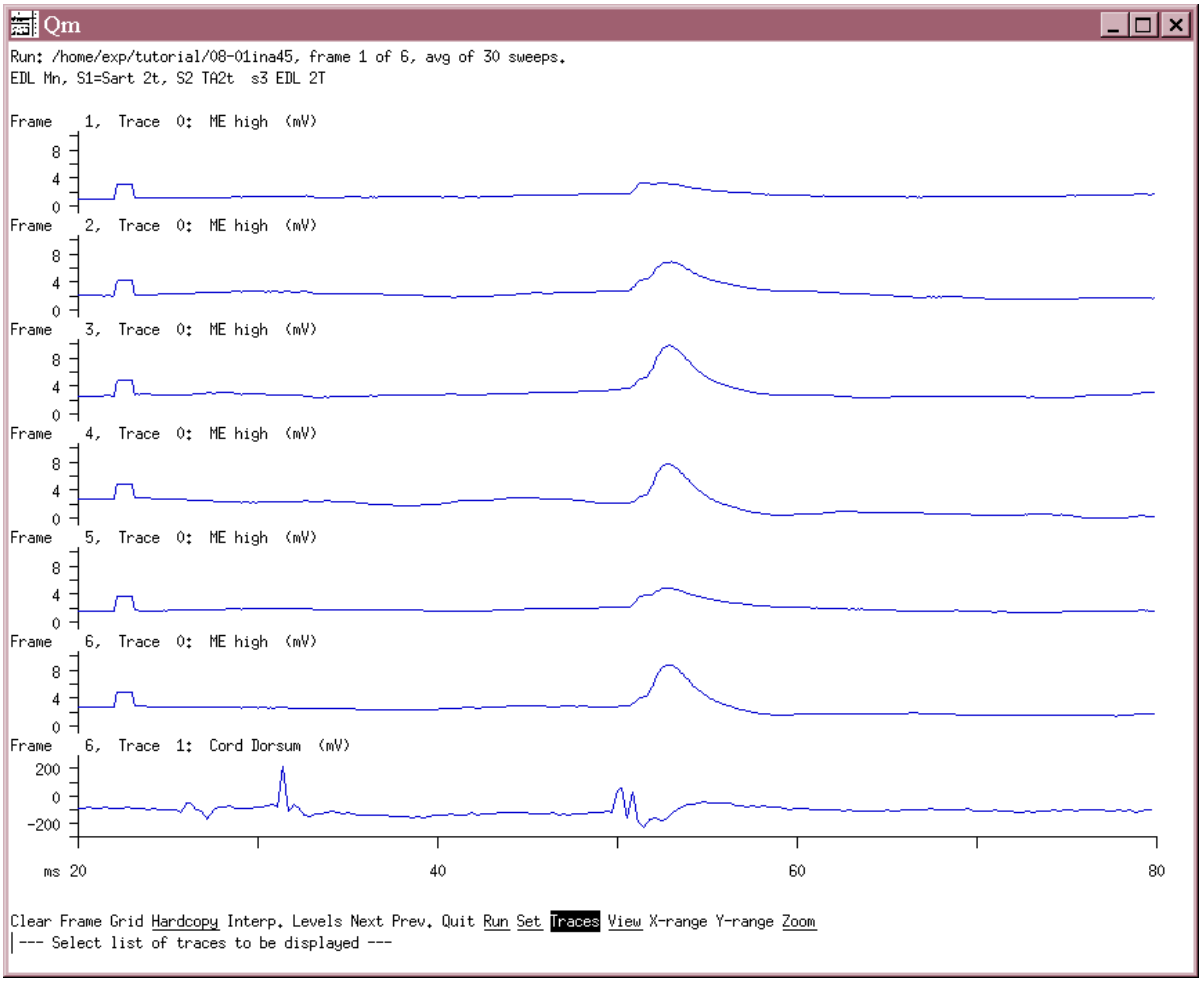
Fig 5.1



The top 4 lines (from Frame 1-4) are the 4 sets during the inactive (flexion) phase and underneath them are the 2 sets during the active (extension) phase. (You should remember that whenever you appendrun file1 and file2, the one displayed first (on the top) in the appended file is the data from file1.) You can adjust the number of frames

displayed in qm and also select which trace to display in each frame. If you select Frame from the Menu of qm and type 0;0;0;0;0;all then you will display trace 0 in frames 1-5 and both traces (0 and 1) in frame 6. Note that semicolon is used to discriminate between frames. Select Frame and enter “0;0;0;0;0;all” and you should see a window as show in Fig 5.2.

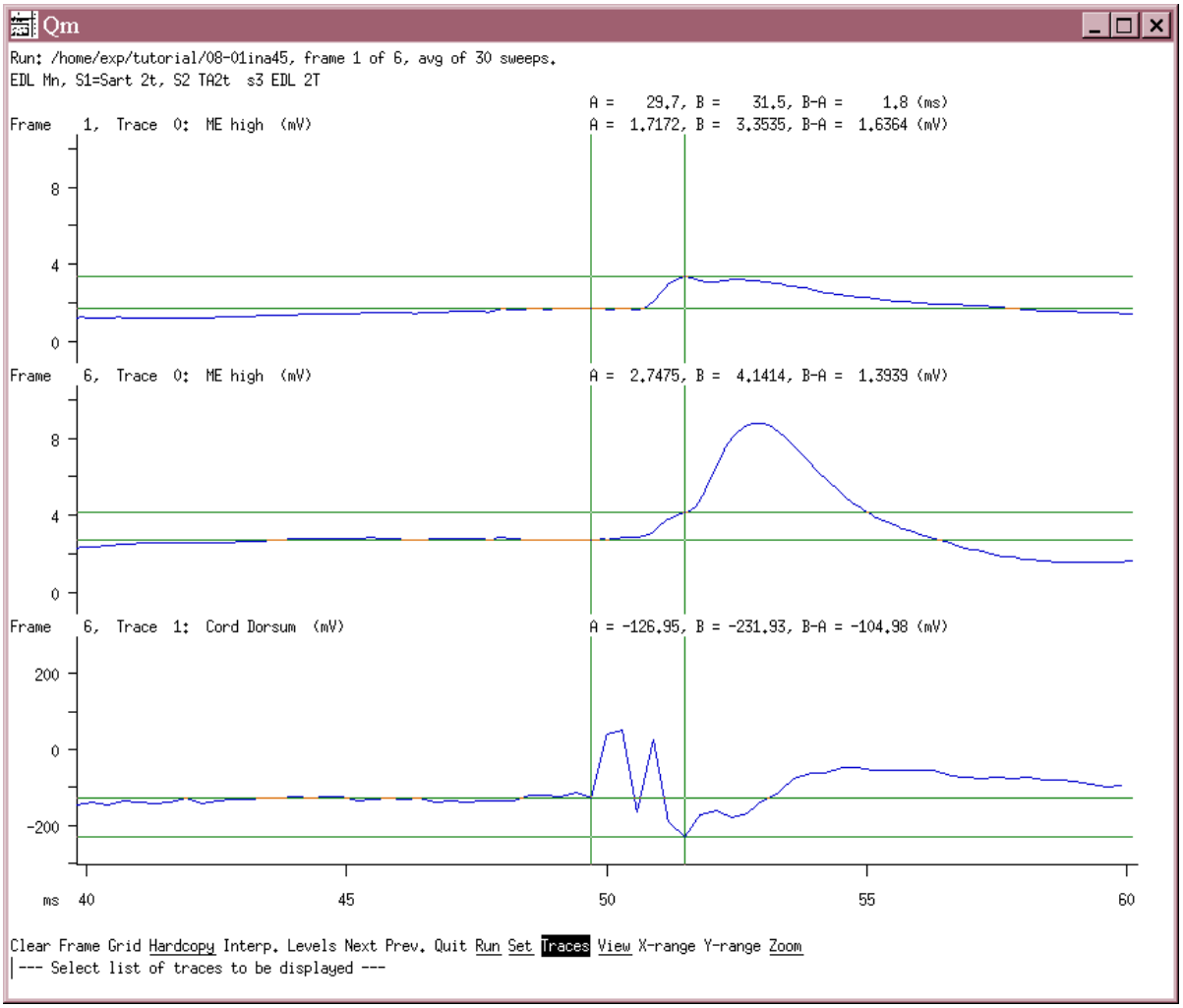
Fig 5.2



Place your cursor by left-clicking on the beginning of the evoked cord dorsum potential. Use the cord dorsum recording to locate this point. You can see in Fig 5.3 where the beginning is set. We placed the cursor at 29.7 ms. Then place your cursors

by middle-clicking to the top of the monosynaptic PSPs as seen in Fig 5.3. The place the cursor at the peak of the evoked monosynaptic PSPs, as seen in fig 5.2 it is at about 31.5 ms. With your rigth mouse button you should set the reference point for your measurements by moving your cursor to the left end of the screen, (lateral to the Y axis) and rigth-click with your mouse. After you set cursor A at the initiation of the cord dorsum potential and cursor B at the initiation of the monosynaptically evoked PSPs, write down the measurement read. (These values should be close to the ones seen in Fig 5.3).

Fig 5.3



Next you will determine the time for the peak of the disynaptic PSPs by placing the first cursor to the peak of the monosynaptic EPSP (as you did before for cursor B) and placing the second cursor on the point that you find as the peak of the disynaptically evoked PSPs. On Fig 5.4 you can see that the peak of the dysinaptic EPSPs was set at 32.7 ms.

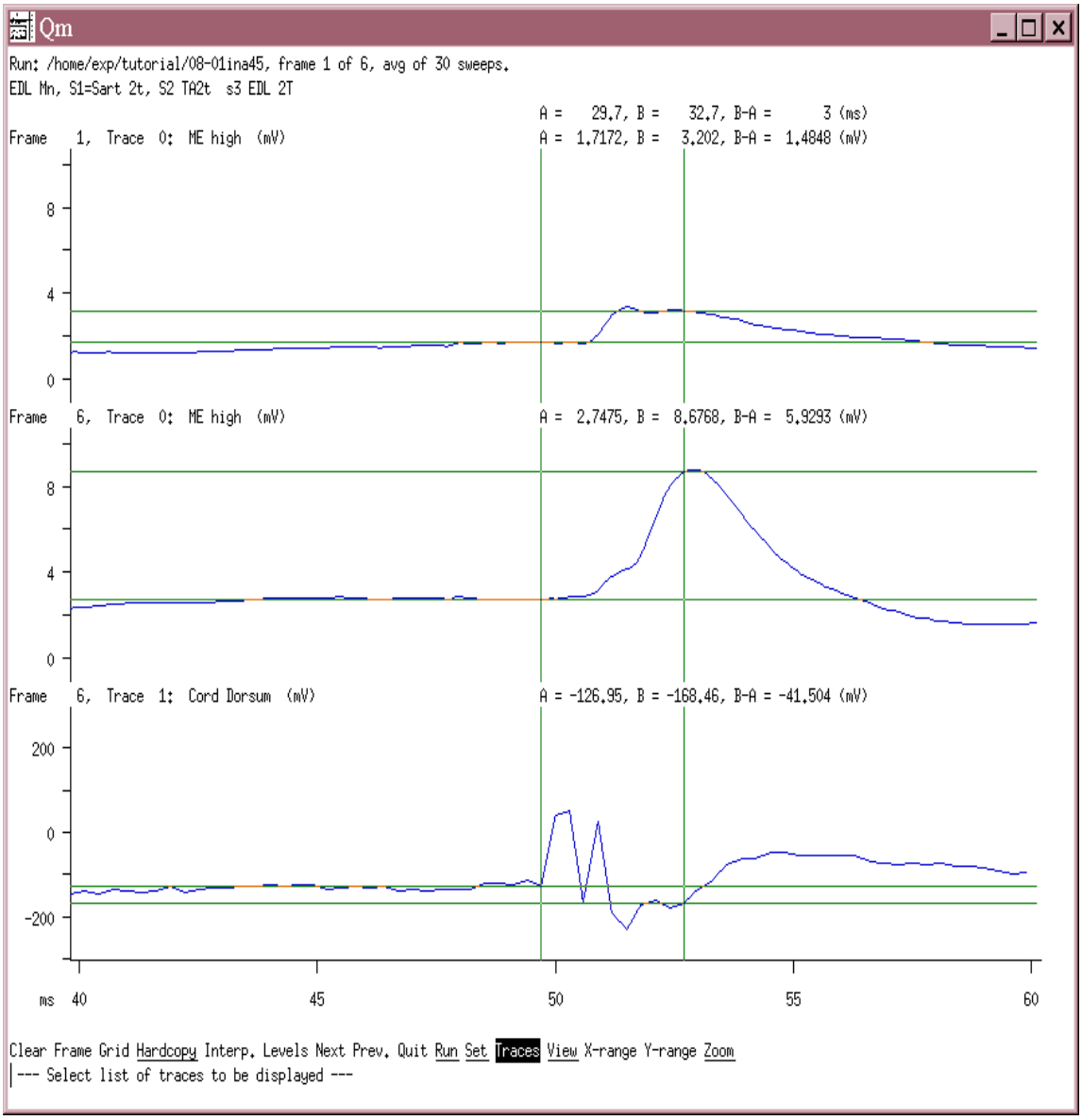


Fig 5.4

Determined the time when the maximal PSPs were evoked (peak of PSPs) you can select a window to analyze further the amplitude of the evoked PSPs. You can quit quick-measure by selecting Q and answer no to the prompt because you do not have to save the changes.