bt_ascii2avg	this function takes an ascii file and converts contents to
	  1) a Neuroscan-format .avg file, and
	  2) a text file containing the marked latencies
	Both resulting files will retain the same base filename
	as the ASCII file with extensions of .avg and .mrk,
	respectively.
	
	Usage: bt_ascii2avg('filename.txt')

bt_biologic2avg	this function takes a Bio-logic ascii file and converts its
	contents to:
	  1) a Neuroscan-format .avg file, and
	  2) a text file containing the marked latencies
	Both resulting files will retain the same base filename
	as the ASCII file with extensions of .avg and .mrk,
	respectively.
	
	Usage: bt_biologic2avg('filename.txt')

bt_fft2	this function computes frequency-domain amplitudes of
	three user-defined frequency bins of brainstem
	response. Results are not scaled to peak µV.
	
	Usage: [F0 F1 HF] =
	bt_fft2('filename.avg',10,40,100,150,300,350,600,800);
	
	over the range of 10 to 40 ms, finds average frequency
	amplitude of 100-150 Hz, 300-350 Hz and 600-800 Hz.
	
	Three variables are returned the workspace:
	  (1) Freq1: mean amplitude over F0_Lo-F0_Hi Hz
	  (2) Freq2: mean amplitude over F1_Lo-F1_Hi Hz
	  (3) Freq3: mean amplitude over HF_Lo to HF_Hi Hz

bt_fftbiomap	this function computes frequency-domain amplitudes of
	F0, F1 and high-freqency bins of BioMAP response.
	
	Usage: [F0 F1 HF] =
	bt_fftbiomap('filename.avg',start_latency,stop_latency);
	
	Note, BioMAP default latencies are 11.38, 40.58.
	
	Three variables are returned the workspace:
	  (1) F0: mean amplitude over F0_Lo-F0_Hi Hz
	  (2) F1: mean amplitude over F1_Lo-F1_Hi Hz
	  (3) HF: mean amplitude over HF_Lo to HF_Hi Hz

bt_fftsc	this function computes frequency-domain amplitudes of three user-defined frequency bins of Brainstem response. Results are scaled to peak µV.
	
	Usage: [F0 F1 HF] = bt_fftsc('filename.avg',10,40,100,150,300,350,600,800);
	
	over the range of 10 to 40 ms, finds average frequency amplitude of 100-150 Hz, 300-350 Hz and 600-800 Hz.
	
	Three variables are returned the workspace:
	  (1) Freq1: mean amplitude over F0_Lo-F0_Hi Hz
	  (2) Freq2: mean amplitude over F1_Lo-F1_Hi Hz
	  (3) Freq3: mean amplitude over HF_Lo to HF_Hi Hz

bt_qncorr	this function compares two files via correlation. Typically this is used to compare a response recorded in background noise with a response to the same stimulus in quiet.
	
	Usage: [StraightCorr CrossCorr Lag]=bt_qncorr(Qfile, Nfile, start, stop);
	
	Requires 4 input arguments:
	  Qfile, Nfile: quiet and noise .avg files.
	  start, stop: latency, in ms., over which the correlations
	  are run
	
	3 variables are returned to the workspace:
	  (1) StraightCorr: Simple Pearson's r over desired latency range
	  (2) CrossCorr: Maximum correlation, allowing noise response to lag quiet by up to 2 ms.
	  (3) Lag: Amount of timeshift (in ms.) to achieve CrossCorr
	
	In cases where the best correlation occurs with no shift, Lag will be 0 and StraightCorr will equal CrossCorr.
	
	Dependancies:
	  openavg.m
	  xcorrelation.m

bt_rms	this function computes RMS amplitude of response period (selectable), of prestim period, and the resulting SNR.
	
	Usage: [RMS RMSprestim SNR] = bt_rms('filename.avg',start_latency,stop_latency);
	
	Note, if start,stop omitted, BioMARK default latencies (11.38, 40.58) are used.
	
	Three variables returned to workspace are
	  RMS: RMS amplitude of selected latency range
	  RMSprestim: RMS amplitude of prestimulus activity
	  SNR: The quotient of RMS/RMSprestim

bt_srcorr	Compares brainstem file to the evoking stimulus using cross correlation
	
	Usage: [PosCorr PosLag NegCorr NegLag] = bt_srcorr('file.avg', start, stop);
	
	A typical brainstem response, when cross-correlated with the stimulus, exhibits two major correlogram maxima: one positive, one negative. This function returns both and their respective lags.
	
	INPUT ARGUMENTS:
	'file.avg': BioMARK data file (in .avg format)
	start, stop: latency, in ms., over which the correlation is run
	
	OUTPUT ARGUMENTS:
	PosCorr, NegCorr: maximum/minimum r-values found at lags corresponding to onset response.
	
	PosLag, NegLag: lags corresponding to above.
	
	Dependancies:
	  filtered_stimulus.avg
	  openavg.m
	  xcorrelation.m

bt_xcorrelation	this function calculates the maximum correlation (maxmincor) value and its respective lag (LAG) over an imputted lag range, for a specified portion of a response. The user must specify whether to find the max positive or max negative correlation value