MetAssimulo	SimulateSpectrum				
		readParamFile	Read in Parameters when run in 'batch mode'.		
		SetUpPeakShiftInput	Read in peak shift data and convert to NSSD names	**Converter**	
		PeakShiftInput	Read in peak shift data		
		ReadInConcs	Read in Concentration data		
		MainConverter	Convert synonyms to NSSD names	**Converter**	
		SimulationOfConcs	Simulate Concentrations	**NormalDisCDF**	
				InverseNormalDis	
		CorrConcs	Simulate Correlated Concentrations	**SimulationOfConcs**	Sim uncorrelated metabolites
				SimCorrelated	Sim correlated metabolites
		ReadInExp	Read in Experiment #		
		ReadInProtons	Read in Proton data		
		RemoveWaterAndStandard	Pre-Processing	Set Exclusion Regions to zero	
		BaselineCorrectionWithSplines		Correct baseline using splines	
		RemoveArtifacts		Remove negative artifacts	
		KernelSmootherFinal		Kernel Smoother	
		SimulateSpectrumWithShift	Construct final spectrum with peak shift	**PeakDetection**	Detect peaks and identify multiplets
				FinalSpectrumShift	Calculate shift
		FinalSpectrumNoShift	Construct final spectrum	**KernelSmoothThresh**	Smooth spectrum
		Display Results	Display Results		

SynonymConverter

SynonymConverter

Cov_Matrix	Calculate Covariance Matrix

IndivPeakDetection	Find Peaks	**IndivPeakSetBoundaries**	Find Peak edges
FindingPeaksToShiftTogether	Find multiplet peaks	**FindCorrespondingPeaks**	Link multiplet peaks together
GenerateAcidBaseLimits2	Generate AB Limits		
CalculateShift			
KernelSmoothThresh	Smooth spectrum	**conv_fft**	Convolution using FFT method
conv_fft	Convolution using FFT method		