Artifacts Induced by Selective Blanking of Time-Domain Data in Fourier Transform Mass Spectrometry

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Results and Discussion

Fourier transform mass spectrometry (FTMS) of the isolated isotopic distribution for a highly charged biomolecule produces time-domain signal containing large amplitude signal "beats" separated by extended periods of much lower signal magnitude. Signal-to-noise ratio for data sampled between beats is low, due to destructive interference of the signals induced by members of the isotopic distribution. Selective blanking of the data between beats has been used to increase spectral signal-to-noise ratio. However, blanking also eliminates signal components, and thus can potentially distort the resulting FT spectrum. Here, we simulate the time-domain signal from a truncated isotopic distribution for a single charge state of an antibody. Comparison of the FT spectra produced with or without blanking and with or without added noise clearly show that blanking does not improve mass accuracy and introduces spurious peaks (see Figure 1) at both ends of the isotopic distribution (thereby making it more difficult to identify posttranslational modifications and/or adducts). Although the artifacts are reduced by use of multiple Gaussian (rather than square wave) windowing, blanking appears to offer no advantages for identifying true peaks or for mass measurement.

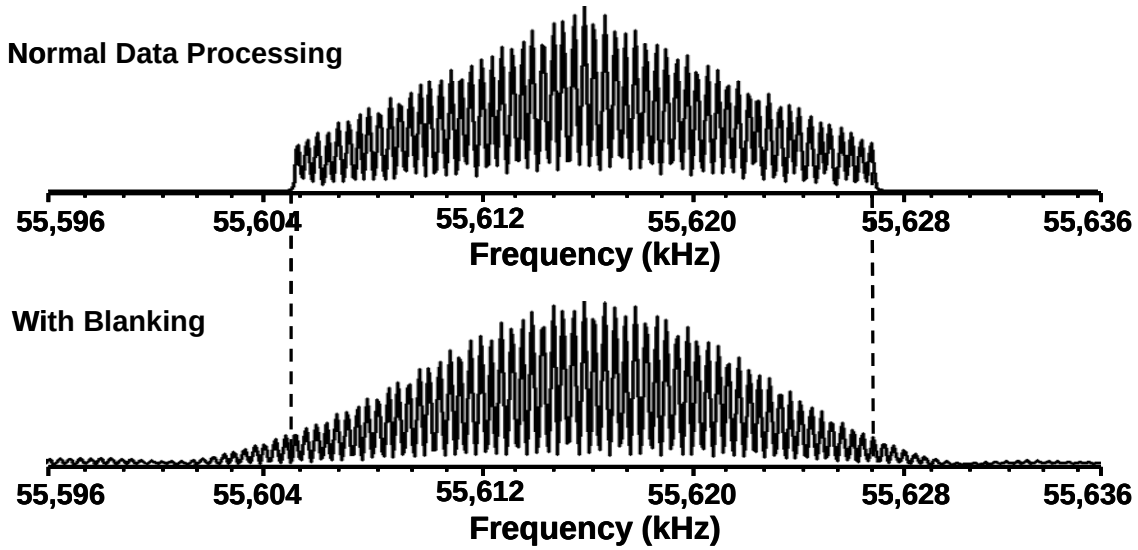

Figure 1. Simulated noiseless magnitude-mode FT-ICR mass spectra. Note the spurious signals at both ends of the bottom spectrum due to blanking of the time-domain segments between "beats" (see text).

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References

[1] Xian, F., *et al*., J. Am. Soc. Mass Spectrom.**24**, 1722-1726 (2013).