

Question	Response
When do you see standards being developed for ranging - and how does that work?	The APT community does have a standards group and we have consulted professional standards community, the first steps are to define terms, it is a slow process, the next steps are to publish procedures and once they get accepted, you can then consider actually joining the standards organization and publish standards. We look forward to very soon having working algorithms in AP Suite for automatic ranging - we can then get feedback from the community as to what the default settings should be. Of course with the large variation in local background, peak shapes etc. there will need to be a few different definitions - Please support the community and consider joining the IFES standards efforts.
You mentioned the noise metric and efficiency, can you cover that again	The noise metric in ppm/nsec can be used as a measure of how good the data is, and can give indication of what data you might be missing because it is not in peaks. If run conditions are not correct, you can get ions evaporating in-between pulses. The noise metric divided by the pulse rate in kHz is the fraction of data contained in the noise floor, so if the metric is 50, which is a pretty noisy run, and you are pulsing at 500kHz, this means that 10 % of the data is in the background
Can the peak ID feature be trusted - it looks like it makes many suggestions that don't make sense	Yes, Peak ID does actually work well, but with all the elements in the periodic table it will find groups of ions that randomly match your peaks - so, you do need to use logic. There are several parameters to minimize this, like not allowing more than 2 or 3 ions per molecule, and you can exclude as many elements in the periodic table as you want - Seeing the list that is created, you do need to sift through it, but I have been pleased with the list of the proposed ions in general.
Why is H not good for mass calibration? Wouldn't it give you a good point at that end of the spectrum?	As it is the lightest ion its TOF is very short and any electrostatic perturbations will affect it more, so these ions may not be as precisely placed in the mass spectrum - if you mass calibration is way off due to a recent detector calibration/service that is not complete, using hydrogen is a way to get a rough calibration, but it should not be used for the final calibration generally speaking
Sorry, what the issue on slide 29? The composition didn't seem very different.	Sloppy ranging can often be ignored for the large peaks in the spectrum, APT SNR is so high that yes, the major peaks can be ranged with less care and still give accurate results, but the minor species in this analysis, B, P were off by as much as 30%
The result of Currie (slide 23 I think) has been discussed in a recent publication (which also includes a detailed mathematical look at background subtraction) https://doi.org/10.1017/S1431927620024290	THANK YOU - I missed this publication somehow. Dr. Haley does a nice job of explaining an improved background calculation and how the Curie calculations are a bit conservative due to the set of assumptions. Haley, D., London, A. J. & Moody, M. P. Processing APT Spectral Backgrounds for Improved Quantification. <i>Microscopy and Microanalysis</i> 26, 964–977 (2020). **Note, there are some subtleties in this next reference, Alvarez that Haley cites that have been challenged by other others, so use with care! Alvarez JL. Poisson-based detection limit and signal confidence intervals for few total counts. <i>Health Phys.</i> 2007 Aug;93(2):120-6. doi: 10.1097/01.HP.0000261331.73389.bd. PMID: 17622816. Bramlitt ET, Shonka JJ. Comment on poisson-based detection limit and signal confidence intervals for few total counts. <i>Health Phys.</i> 2008 Jan;94(1):86-7; author reply 87-8. doi: 10.1097/01.HP.0000290608.68386.5e. PMID: 18091156.
What would be a good reference for learning the first step: determining the background levels?	the Haley reference above has a great overview
With major peaks with long tails, the tails can cover up smaller peaks, is there a good strategy for finding them?	Optimizing specimen preparation and run conditions are a first good start, and whenever possible, removing non-Region of Interest data from the analysis volume.
If background subtraction is not accurate when the isotopes are ranged separately, then how one can trust pick decomposition?	So, if isotope values are not correct due to multits, etc. YES, that will affect the decomposition work, the algorithm takes into effect all the ratios of all the isotopes, it will optimize the correction as best it can.