This feature is for correcting reference patterns between different mass spectrometer tunings. In practice, it is for 'correcting' ones own mass spectrometer's tuning with the assumption that the NIST tuning is 'correct'. The feature compares some data collected on your spectromer to that with data from NIST, then corrects for your spectrometer’s tuning factor during the analysis. This can improve quantitative accuracy.

**Suggested Procedure for How to use the Tuning Factor Correction Feature:**

1. Make two directories. A directory named “\TuningCorrection\” and a directory named “\Analysis\”. Fill the two directories to be identical (with the same files you plan to use during a regular MSRESOLVE analysis).
   1. In both directories, you will have made a reference file intended for analysis (the one that goes in referenceFileNamesList). Name this file “ReferenceForAnalysisBeforeTuningCorrection”
      1. It is assumed that this file will have some ‘self-measured’ reference patterns, and possibly also some ‘NIST/Standard’ reference patterns. (thus, it is some kind of mixed reference file where different molecules have patterns from different sources).
2. In the directory named \TuningCorrector\ , add two *more* reference files, give the csvs names as below:
   1. UserChoices['measuredReferenceYorN']['referenceMeasuredFileName'] =['ReferenceCollected.csv','xyyy'] 🡨 this has at least one molecule and contains *only* patterns collected from your instrument.
   2. UserChoices['measuredReferenceYorN']['referenceLiteratureFileName'] =['ReferenceLiterature.csv','xyyy'] 🡨 this has at least one molecule and contains *only* patterns from NIST or other standard reference.
   3. There must be *at least one* molecule that appears in both patterns. Fragmentation patterns that span a large range (like Hexane and Heptane) are ideal.
3. In directory named \TuningCorrection\ directory, open UserInput.py (or the GUI) and turn on the feature TuningCorrector feature, also called measuredReferenceYorN, to yes.
   1. Run MSRESOLVE in this directory with whatever settings you want, but DataAnalysis must be on. While it is intended to work with pre-processing, at present, this feature only works with DataAnalysis on.
   2. There will be a file created named Exported…TuningCorrector.csv Open this file. (if there is more than one, then open the one with the highest number).
      1. Copy the patterns for the molecules which were measured on your instrument: they have now been tuning corrected to match NIST etc.
      2. You are only copying out the molecules collected by your instrument. For any molecules that were collected by NIST, leave them!
         1. the program may have put out tuning corrected patterns from NIST also, but those one are garbage, those are like having the tuning correction applied twice.
4. In the directory named \Analysis\ open the file named ReferenceForAnalysisBeforeTuningCorrection
   1. Paste in the Tuning Corrected patterns you’ve copied in the previous step
      1. You are only pasting over the molecules collected from your instrument.
      2. (you will be pasting over all or some of the fragmentation patterns – it is fine if the ones are pasting will be standardized to 100 while the old ones are not).
      3. For any patterns collected by NIST, leave them as they are! Just as they were when they started, don’t mess with them!
   2. In this analysis directory, turn off the feature TuningCorrector feature, also called measuredReferenceYorN, by setting it to “no”. Your Tuning correction has already been done, so the feature needs to be off.
5. Run your analysis with your new corrected or mixed reference file!