Optimized data analysis pipeline for MALDI MSI based tumor typing from FFPE tissue samples evaluated on six benchmark classification tasks

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Goals
- Develop optimized pre-processing pipeline for MALDI MSI based tumor typing
- Consider different clinical tumor typing and subtyping tasks
- Consider intra- and inter-lab scenarios and different instrument types

Data
- Benchmark panel acquired from 25 TMAs, 2031 cores and 1410 patients total

m/z range
- Non-linear intensity profile normalization (IPN, bottom row) improves comparability across different acquisitions (Boskamp et al, ASMS 2018)

Normalization
- Mild Gaussian kernel spatial denoising (right) increases signal-to-noise ratio as compared to original data (left)

Alignment
- Dimensionality reduction by downsampling to peak areas over 0.4 Da intervals (Boskamp et al, ASMS 2018)

Spatial denoising
- Mass calibration based on statistical peptide mass model reduces misalignment (Boskamp et al, ASMS 2018)

Downsampling
- log transform with appropriate scaling results in more symmetric intensity distributions – beneficial for subsequent LDA classification

Transformation
- Balanced accuracy 82% and 92%
- Performance gain over baseline (TIC only) 9.5 ... 39.8% pts. for five of six tasks
- Mass alignment / downsampling alone yields 5 ... 18.5% pts. for five of six tasks

Classification
- Systematic investigation of six benchmark problems yields an optimized pre-processing pipeline for MALDI MSI tumor typing applications
- Significant performance gains achieved in intra- and inter-lab scenarios
- Improved robustness towards SOP variations and technical variability

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