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CORRECTING NONLINEAR CALIBRATION IN MASS SPECTROMETRY

DIAGNOSTICS

Algorithms applied to mass spectrometric analysis data that enhance chromatographic performance by correcting bias in non-linear data.

TECHNOLOGY TYPE

Instrumentation
Software
Mass Spectrometry

STAGE OF DEVELOPMENT

Applied in a clinical reference laboratory setting.

IP PROTECTION

U.S. Utility Patent Pending

Mass Spectrometry Analyte Detection and Related Methods

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Reference Number: U-5603

Technology & Venture Commercialization

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TECHNOLOGY SUMMARY

Stable isotope labeled internal standards are widely used in mass spectrometry. Isotopic interference between signals of the internal standard and the analyte, however, causes nonlinear calibration, which limits the dynamic range and produces inaccurate assessments of analyte concentration.

Application of two equations to mass spectrometry expands the range of analysis by generating a more accurate fit and correcting the inherent bias for many analyte/internal standard pairs. This process allows for corrections to nonlinear data, enabling the use of analyte/internal standard combinations that would otherwise be impractical. This approach removes much of the difficulty associated with use of stable labeled internal standards, such as labeling, isotope effects, and cost.

FEATURES AND BENEFITS

- Increases accuracy across a broader range of concentrations.
- Corrects for nonlinear data.
- Extends dynamic range.
- Improves chromatographic performance.
- Provides better fitting regressions and eliminates a source of bias in clinical and bioanalytical assays.

RECENT PUBLICATIONS

Rule, G.S., Clark, Z.D., Yue, B., Rockwood, A.L. (2013). Correction for isotopic interferences between analyte and internal standard in quantitative mass spectrometry by a nonlinear calibration function. *Analytical Chemistry*. 85(8): 3879-3885. doi: [10.1021/ac303096w](https://doi.org/10.1021/ac303096w)

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