BRC Science Highlight
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Bayesian Confidence Intervals for Multiplexed Proteomics Integrate Ion-Statistics with Peptide Quantification Concordance

Background/objective

Proteomics data have powerful implications for metabolic engineering. While the field has experienced significant advances in recent years, one shortcoming has been the inability to rigorously assign confidence to these measurements. Here, researchers developed a novel, mathematically rigorous method, BACIQ (Bayesian Approach to Confidence Intervals for protein Quantitation) for computing and uncertainty around quantitative multiplexed proteomics measurements.

Approach

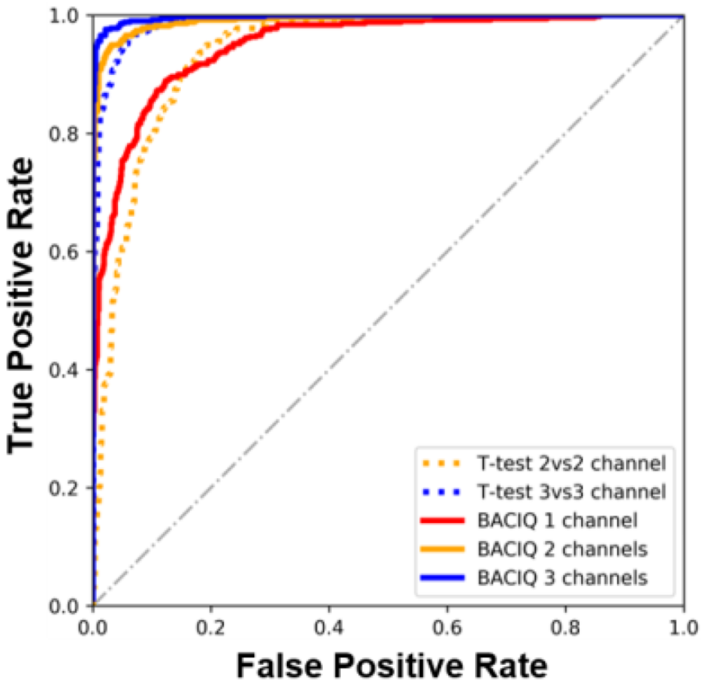
- The team developed a Bayesian Beta-Binomial model to rigorously compute uncertainty of quantitative multiplexed proteomics measurements.
- Researchers validated the approach on samples of known protein content and by reanalyzing previously published proteomics data.

Results

- BACIQ appropriately interprets information from low signal peptides, increasing measurement sensitivity.
- BACIQ added sensitivity to detection of small changes.

Significance

BACIQ will increase sensitivity of proteomics methods. Assigning confidence in measurements is important because it allows one to assess the significance of changes — enabling more accurate data generation to improve metabolic engineering and modeling efforts.



BACIQ outperformed the t-test when the same number of samples were used. The t-tests require multiple samples to detect statistically significant differences; BACIQ does not.

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