

MSstatsPTM: Statistical relative quantification of post-translational modifications in bottom-up mass spectrometry-based proteomics

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Abstract

Liquid chromatography coupled with bottom up mass spectrometry (LC-MS/MS)-based proteomics is increasingly used to detect changes in post-translational modifications (PTMs) in samples conditions. Analysis of data from such experiments faces numerous statistical challenges. These include the low abundance of modified proteoforms, the small number of observed peptides that span modification sites, and confounding between changes in the abundance of PTM and the overall changes in the protein abundance. Therefore, statistical approaches for detecting differential PTM abundance must integrate all the available information pertaining to a PTM site, and consider all the relevant sources of confounding and variation. In this manuscript we propose such a statistical framework, which is versatile, accurate, and leads to reproducible results. The framework requires an experimental design, which quantifies, for each sample, both peptides with post-translational modifications and peptides from the same proteins with no modification sites. The proposed framework supports both label-free and tandem mass tag (TMT)-based LC-MS/MS acquisitions. The statistical methodology separately summarizes the abundances of peptides with and without the modification sites, by fitting separate linear mixed effects models appropriate for the experimental design. Next, model-based inferences regarding the PTM and the protein-level abundances are combined to account for the confounding between these two sources. Evaluations on computer simulations, a spike-in experiment with known ground truth, and three biological experiments with different organisms, modification types and data acquisition types demonstrate the improved fold change estimation and detection of differential PTM abundance, as compared to currently used approaches. The proposed framework is implemented in the free and open-source R/Bioconductor package *MSstatsPTM*.

Introduction

Signaling mechanisms allow cells to mount a fast and dynamic response to a multitude of biomolecular events. Signaling is facilitated by the modification of proteins at specific residues, acting as molecular on/off switches [1, 2, 3]. Characterizing relative abundance of a modification site’s occupancy repertoire across experimental conditions provides important insights [4]. For example, meaningful patterns of changes in post-translational modifications (PTMs) abundance can serve as biomarkers of a disease [5]. Alternatively, distinguishing the quantitative changes in a PTM from the overall changes of the protein abundance helps gain insight into biological and physiological processes operating on a very short timescale [6][7]. This helps to distinguish between relative site occupancy changes at steady-state protein levels, typical for short time-scale signaling events, and observed relative changes of PTMs as a result of underlying gene expression or protein abundance levels.

Bottom-up liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS) is a tool of choice for unbiased and large-scale identification and quantification of proteins and their PTMs [8, 9]. However, LC-MS-based interrogation of the modified proteome is challenging, for a number of reasons. First, the relatively lower abundance of modified proteoforms dictates that a global interrogation can only be achieved through large-scale enrichment protocols with modification-specific antibodies or beads [10]. Variability in the enrichment efficiency inevitably affects the reproducibility of the number of spectral features (e.g., peptide precursor ions or their fragments) and their intensities. Second, contrary to the often large number of identified peptides that can be used to quantify protein abundance, there are relatively few representative peptides that span a modification site, and there may be multiple modified sites on a single peptide [4]. Third, unless early signaling events are interrogated, the interpretation of the relative changes in modification occupancy are inherently confounded with changes in the overall protein abundance, complicating the interpretation of the results [11][12]. Finally, technological aspects of bottom-up MS experiments, such as presence of labeling by tandem mass tag (TMT), introduce additional sources of uncertainty and variation.

The technological difficulties in PTM identification and quantification increase the uncertainty and the variation in the data, and challenge the downstream statistical analyses. Frequently data from these experiments are analyzed using statistical methods that were not originally designed for this task. Researchers use methods such as *t*-test[13], Analysis of Variance[14], or Limma[15], by taking as input the intensity ratios of modified and unmodified peptide features, and comparing the mean abundance of different PTM sites. Such approaches do not fully account for all the sources of uncertainty. As the result, these approaches are either not directly applicable to experiments with non-trivial designs (such as experiments with multiple conditions, paired and time course designs, and experiments with labeling), or require the analysts to exercise non-trivial statistical expertise.

This manuscript proposes a versatile statistical analysis framework that accurately detects relative changes in post-translational modifications. The framework requires an experimental design, which quantifies, for each sample, both the peptides with post-translational modifications, and peptides from the same proteins with no modification sites. The framework supports data-dependent acquisitions (DDA) that are label-free or tandem mass tag (TMT)-based. The statistical methodology separately summarizes the abundances of peptides with and without the modification sites, and fits separate linear mixed effects models that reflect the biological and technological aspects of the experimental design. Next, model-based inferences regarding the PTM and the protein-level abundances are combined to account for the confounding between these two sources.

We evaluated the proposed framework on two datasets from computer simulations, one benchmark controlled mixture, and three biological investigations. The datasets illustrate a diverse set of organisms, modification types, acquisition methods and experimental designs, showing the applicability of the framework to a variety of situations. By appropriately leveraging the information from the unmodified peptides, the proposed approach improved the accuracy of the estimates of PTM fold changes, and produced a better calibrated false positive rate of detecting differentially abundant PTMs as compared to existing methods. In particular, accounting for the confounding from protein abundance allowed us to characterize the true effect of the modification, avoiding the need for more manual and time intensive follow-up investigation.

The proposed approach is implemented as a freely available open source R package *MSstatsPTM*, as part of the *MSstats* family of packages [16, 17], and is available on Bioconductor.

Experimental procedures

Data overview and availability

Table 5.1 summarizes the experiments. Two computer simulations had known ground truth, and varied in experimental realism. The first simulation produced a perfectly clean dataset, with many replicates and no missing values. The second simulation introduced real-world characteristics, such as limited modified features and missing values. Details of computer simulations are available in Supplementary Section 2.1 and on GitHub (https://github.com/devonjkohler/MSstatsPTM_simulations).

One spike-in experiment also had known changes in modified spike-in peptides, but had real-world experimental characteristics. Finally, three biological experiments demonstrated the applicability of the proposed approach across different biological organisms, modifications, experimental designs and acquisition strategies. The experimental data, R scripts with *MSstatsPTM* analysis, and results of the statistical analysis are available in MassIVE.quant (<https://massive.ucsd.edu/ProteoSAFe/static/massive-quant.jsp>) [18].

Dataset 1: Computer simulation 1 - Label-free

Simulation design: The simulation represented an idealistic case. 24 synthetic label-free datasets were generated with different experimental designs and different biological variation. In each dataset, 1,000 proteins had 10 unmodified features per protein. Each of the 1,000 proteins had one PTM. Each PTM was represented by 10 modified features. The PTMs of 500 proteins had a differential fold change between conditions, while the other 500 proteins were generated with no changes in abundance between conditions. Furthermore, the fold changes of half of the 500 differential PTMs were fully masked by changes in the unmodified protein. Finally, the fold change of half the 500 non-differential PTMs was entirely due to changes in the unmodified protein. All the differential PTMs were generated with an expected log base 2 fold change of 0.75 between conditions.

Each simulation was generated with random biological variation. The observed peptide abundances were simulated by adding random noise $\mathcal{N}(0, \sigma^2)$ to the deterministic abundances described above. Two values $\sigma^2 = \{.2, .3\}$ were motivated by the experimental datasets in this manuscript.

Evaluation: We evaluated the ability of the statistical methods to correctly detect differentially abundant PTMs. We gauged the methods ability to avoid false positives (i.e. specificity), accurately estimate the fold change between conditions, and analyzed the sensitivity of detecting differentially abundant PTMs. The evaluation was performed both in the presence of confounding with changes in the unmodified protein and after applying adjustment to correct for the confounding.

Dataset 2: Computer simulation 2 - Label-free missing values and low features

Simulation design: The data were simulated as above, while providing a more realistic representation of the experiments. The feature counts and the proportion of missing values were as observed on average over all the the experimental datasets in this manuscript. Specifically, PTMs were simulated with 2 modified peptide features, and unmodified proteins were simulated with 10 features. Additionally, 20% of observations for both modified and unmodified peptides were missing completely at random.

Evaluation: The methods were evaluated as above. We evaluated their ability to correctly detect PTM’s specificity, fold change estimation, and sensitivity. These statistics were analyzed both in the presence of, and without, confounding with the overall changes in protein abundance.

Dataset 3: Spike-in benchmark - Ubiquitination - Label-free

Experimental design: Figure 1(a) overviews the experimental design. Four mixtures (i.e., conditions) were created with varying amounts of human lysate [which cell line?], background *E. Coli* lysate, and human spike-in ub-peptide mixture. Unmodified peptides from human lysate were viewed as the global proteome. Background *E. coli* lysate were used to equalize total protein levels. 50 heavy-labeled KGG motif peptides from 20 human proteins were spiked into the mixed background of the lysates. Quantitative changes in

protein and site abundance of these 20 human proteins were the target of the benchmark. In particular, we distinguished the unadjusted changes (i.e. changes in the abundances of the modified peptides) and the protein-level adjusted changes of (i.e., changes in the abundances of the modified peptides relative to the changes in the abundances of the human lysate). The true log-fold changes between the relevant components of the relevant mixtures are summarized in **Figure 1(b)**. Two replicate mixtures were created per condition.

Data acquisition: Each mixture was analyzed with KGG enrichment, and without KGG enrichment (i.e., in a global profiling run), with label-free LC-MS/MS. There was a 90.2% overlap of protein identifications between the identified background modified peptides and proteins quantified in the global profiling run.

Evaluation: We expect the relative abundances of the spike-in peptides to change as in **Figure 1(b)**. The changes in peptide abundances in all the comparisons except Mix 1 vs Mix 4 were distinct from changes in the global proteome abundances and distinct from zero, and were viewed as positive controls. In the comparison of Mix1 vs Mix 4 both the modified peptides and the global proteome background changed two-fold, and as the result the peptides in this comparison were viewed as a negative control. Since the background *E. Coli* lysate peptides were not expected to change in abundance in any comparison [in any, or in 3 vs 4?], they were viewed as additional (unadjusted) negative controls. We evaluated the statistical methods ability to avoid false positives, as well as their sensitivity in detecting the differentially abundant spike-in peptides and accurately estimate their expected fold change.

Dataset 4: Human - Ubiquitination - 1mix-TMT

Experimental Design: Luchetti et al. [19] profiled human epithelial cells engineered to express IpaH7.8 under a dox inducible promoter. Uninfected cells were measured at 0 and 6 hours, while cells infected with *Shigella Flexneri* (*S. Flexneri*) bacteria were measured at 1, 2, 4, and 6 hour increments, resulting in six total conditions. 11 samples were allocated to 1 TMT mixture in an unbalanced repeated measure design. All conditions had two biological replicates except for the Dox1hr condition, which was allocated one replicate.

Data acquisition: The ubiquitinated peptides, and the total proteome (i.e., global profiling) were each conducted in a single LC-MS/MS run. There was a 95% overlap between the identified modified peptides and proteins that were quantified in the global profiling run.

Evaluation: We evaluated the ability of the statistical methods to detect changes in the abundance of modified peptides both before and after adjusting for changes in global protein abundance. The six condition were labeled Dox1hr, Dox2hr, Dox4hr, Dox6hr, NoDox0hr, and NoDox6hr. All conditions were compared with each other, resulting in 15 pairwise comparisons. Since the dataset was a biological investigation, the true positive modifications were unknown. Shigella ubiquitin ligase IpaH7.8 was shown to function as an inhibitor of the protein Gasdermin D (GSDMD). GSDMD was actively degraded when IpaH7.8 expression was induced by dox treatment in human cells. We expect IpaH7.8 to function as an inhibitor of GSDMD in the global profiling run.

Dataset 5: Mouse - Phosphorylation - 2mix-TMT

Experimental Design: Maculins et al. [20] studied primary murine macrophages infected with *S. Flexneri*. The experiment quantified the abundance of total protein and of phosphorylation in wild type (WT), and in ATG16L1-deficient (cKO) samples, uninfected and infected with *S. Flexneri*. The abundance of total protein and post-translation modifications were quantified at three time points, uninfected, early infection (45-60 minutes), and late infection (3-3.5 hours). 22 biological samples were allocated to 2 TMT mixtures in an unbalanced repeated measure design, with 11 samples allocated to each mixture. 16 replicates were spread equally between the early and late WT and cKO conditions, resulting in four replicates per condition. Both the uninfected WT and cKO contained 3 replicates, with mixture one allocating one replicate to uninfected WT and two replicates to uninfected cKO. Conversely, mixture two contained one replicate of uninfected cKO and two uninfected WT.

Data acquisition: This experiment included a total proteome (i.e., a global profiling run) and a phosphopeptide enrichment run. There was a 90% overlap between the identified modified peptides and proteins that were quantified in the global profiling run.

Evaluation: We evaluated the ability of the statistical methods to detect changes in the abundance of modified peptides both before and after adjusting for changes in global protein abundance. The six conditions were labeled KO_Uninfected, KO_Early, KO_Late, WT_Uninfected, WT_Early, and WT_Late. 9 total comparisons were made, namely KO_Early-WT_Early, KO_Late-WT_Late, KO_Uninfected-WT_Uninfected, KO_Early-KO_Uninfected, KO_Late-KO_Uninfected, WT_Early-WT_Uninfected, WT_Late-WT_Uninfected, Infected-Uninfected, and KO-WT. Since the dataset was a biological investigation, the true positive modifications were unknown.

Dataset 6: Human - Ubiquitination - Label-free no global profiling run

Experimental Design: Cunningham et al. [21] investigated the relationship between USP30 and protein kinase PINK1, and their association with Parkinson’s Disease. The experiment profiled ubiquitination sites, and analyzed changes in the modified site abundance. The experiment had four conditions, CCCP, USP30 over expression (USP30 OE), Combo, and Control. Cell lines were used to create two biological replicates per condition. The abundance of modified peptides was quantified with label-free LC-MS/MS.

Data acquisition: This experiment did not include a separate global profiling run to measure unmodified peptides. In addition to low feature counts for unmodified peptides, this lead to substantially fewer matches between modified and unmodified peptides. There was a 41.9% overlap between the identified background modified peptides and proteins that were quantified in the global profiling run.

Evaluation: We evaluated the ability of the statistical methods to detect changes in the abundance of modified peptides both before and after adjusting for changes in global protein abundance. All the conditions were compared with each other in a full pairwise comparison, resulting in 6 comparisons. Since the dataset is a biological investigation, the true positive modifications were unknown.

Background

Goals of PTM characterization, input to statistical analyses, and notation

Consider a label-free LC-MS/MS experiment in the special case of a balanced design with I conditions and J biological replicates per condition. For simplicity, we assume that the experiment has no technical replicates, such that each biological replicate corresponds to an LC-MS/MS run. Figure 2 schematically illustrates this data structure for one PTM site, in a special case of $I = 2$ conditions and $J = 2$ biological replicates per condition. For one protein, the PTM site is represented by K spectral features (i.e., peptide ions, distinguished by their cleavage residues and charge states). The number of modified and unmodified features typically varies across proteins. Some log-intensities may be outliers, and some spectral features can be missing. The log₂-intensity of Feature k , in Replicate j of Condition i is denoted by y_{ijk}^* . Conversely, the unmodified protein is represented by L spectral features, and the log-intensity of Feature l from the unmodified peptides in the same run is denoted by y_{ijl} . The features can be quantified as part of a same mass spectrometry run, or in separate enrichment and global proteome profiling runs.

The population parameter of interest is the difference between the abundances of a PTM site in Condition i and Condition i' , denoted by μ_i^* and $\mu_{i'}^*$ respectively. We are interested in testing the null hypothesis

$$H_0 : \Delta_{PTM} = \mu_i^* - \mu_{i'}^* = 0 \text{ vs } H_a : \Delta_{PTM} = \mu_i^* - \mu_{i'}^* \neq 0 \quad (1)$$

Unfortunately, the population parameter is inherently confounded with the overall changes in protein abundance. To account for this, it is advantageous to consider a different null hypothesis:

$$H_0 : \Delta_{adj} = (\mu_i^* - \mu_i) - (\mu_{i'}^* - \mu_{i'}) = 0 \text{ vs } H_a : \Delta_{adj} = (\mu_i^* - \mu_i) - (\mu_{i'}^* - \mu_{i'}) \neq 0 \quad (2)$$

where μ_i and $\mu_{i'}$ reflect the overall protein abundances in Condition i and Condition i' . These quantities are estimated using protein features without with and without the modification site.

Existing statistical methods for detecting differentially abundant PTMs

[OV: even though we say 't-test', the model that we describe is in fact an ANOVA (i.e., nothing limits us to 2 conditions. Should we change it to ANOVA directly?)]

Two-sample t -test based on modified \log_2 -intensities

The basic two-sample t -test [22] is based on the model

$$y_{ijk}^* = \hat{\mu}_i^* + \epsilon_{ij}^*, \epsilon_{ij}^* \stackrel{iid}{\sim} \mathcal{N}(0, \sigma^{*2}), i = 1, \dots, I, j = 1, \dots, J, k = 1, \dots, K \quad (3)$$

The model allows us to estimate $\hat{\Delta}$ and its standard error. Based on the model, the approach tests the null hypothesis in Eq. (1), by comparing the test statistic against the Student distribution with $df = 2J - 2$ degrees of freedom in balanced designs. Unfortunately, this approach is fundamentally flawed as it does not account for the confounding between changes in the PTM abundance and the overall changes in the abundance of the protein.

Two-sample t -test based on ratios of modified and unmodified \log_2 -intensities

The basic t -test can be extended to account for the confounding of changes in PTM abundance and overall changes in protein abundance [23, 24, 25]. Typically this is done by first summarizing the feature intensities in each run, separately for modified and unmodified features, e.g. with the sum on the original scale, dividing the summary of the PTM abundance by the summary of the protein abundance and then taking a log. Specifically, for condition i and biological replicate j , the approach calculates

$$u_{ij} = \log \left(\sum_{k=1}^K 2^{y_{ijk}^*} \right) - \log \left(\sum_{l=1}^L 2^{y_{ijl}} \right) \quad (4)$$

The approach then models these values as

$$u_{ij} = (\mu_i^* - \mu_i) + \epsilon'_{ij}, \text{ where } \epsilon'_{ij} \stackrel{iid}{\sim} \mathcal{N}(0, \sigma'^2), i \in \{1, 2\} \quad (5)$$

The model allows us to estimate $\hat{\Delta}_{adj}$ and its standard error. Based on this model, we can test the more relevant null hypothesis in Eq. (2), by comparing the test statistic against the Student distribution with $[df = 2J - 2]$ [this should be the same df as the previous section?] degrees of freedom in balanced designs.

Although effective, the approach is somewhat simplistic. It is not applicable to experimental designs with more complex sources of biological and technological variation, such as experiments with repeated measurements, experiments with multiple batches or experiments with multi-run multiplexing. Since Eq. (4) performs the adjustment on the replicate level, the experiment must contain a matching number of replicates in both the modified and unmodified runs. Technological artifacts such as missing values further undermine the calculation of u_{ij} in Eq. (4). Finally, there is no self contained, straightforward implementation of the method, such as in the form of a coding package, requiring a more challenging manual application.

Limma

[DK: Current plan is to follow what Ting did for MSstatsTMT and keep this part brief but expand on EB methods in the supplementary.] The two versions of t -test [OV: ANOVA?] above can be expanded with

Empirical Bayes moderation in Limma [15, 23, 26, 27, 28, 29]. In particular, the ratio-based version which models the ratios \hat{u}_{ij} in Eq. (4) can be used to answer the null hypothesis in Eq. (2). Limma uses the transformed inputs to fit a linear model with a fixed condition and run effect for each PTM.

$$u_{ij} = \mu + Condition_i + Run_j + \epsilon_{ij}, \quad (6)$$

where $\sum_{i=1}^I Condition_i = 0, \sum_{j=1}^J Run_j = 0, \epsilon_{ij} \stackrel{iid}{\sim} \mathcal{N}(0, \sigma^2)$

The method then uses Empirical Bayes moderation to combine the variance estimations across all PTMs modeled. This increases the degrees of freedom with which the individual PTM variances are estimated [15].

The goal of Limma is to increase the sensitivity of detection of differential abundance when the experiment has few biological replicates.

Since Limma only improves upon the methods above in estimation of variation, it has the same limitations in terms of the experimental designs. The method is only directly applicable to experiments with at most two variance components, meaning that in more complex experiments it cannot account for all sources of variation. Additionally, it still requires the same experimental design for the modified and unmodified features so that the ratio calculation can be performed. Finally, there is no self contained implementation of the methods to PTMs, requiring manual transformation and application by the user.

Isobar-PTM Isobar-PTM was also proposed for experiments with LC-MS/MS quantitative strategies that employ isobaric labels such as TMT or isobaric tag for relative and absolute quantification (iTRAQ)[30]. Isobar-PTM expresses MS measurements with a linear model and performs adjustment with respect to protein abundance using the difference between log-ratio of modified peptides in two channels and log-ratio of protein level. Unfortunately, this statistical modeling framework is not applicable to either label-free workflows or experiments with complex designs.

Statistical modeling and parameter estimation in MSstats

MSstats [16] and *MSstatsTMT* [17] are a series of R/Bioconductor packages designed for protein significance analysis and statistical relative quantification of proteins and peptides in global, targeted and data-independent proteomics. Models in these packages takes as input a list of \log_2 -intensities y_{ijk} . For each protein, the feature \log_2 -intensities are first summarized into a single value per protein per run using Tukey’s median polish [31]. These summarized values are then used as input to fit a flexible family of linear mixed-effects models [32, 33, 34]. The specific model instances depend on the experimental design and data acquisition. For example, to model the unmodified protein in **Figure 2** *MSstats* fits the following model

$$y_{ij} = \mu + Condition_i + Run_j + \epsilon_{ij}, \quad (7)$$

where $\sum_{i=1}^I Condition_i = 0$, $Run \sim^{iid} \mathcal{N}(0, \sigma_j^2)$, $\epsilon_{ij} \sim^{iid} \mathcal{N}(0, \sigma^2)$

Parameters of the model are estimated using restricted maximum likelihood (REML) [35]. In turn, the parameters allow us to estimate the relevant quantity $\hat{\Delta}_{Protein}$ and its standard error. Where $\hat{\Delta}_{Protein}$ is estimated as

$$\hat{\Delta}_{Protein} = \hat{\mu}_i - \hat{\mu}_{i'} \quad (8)$$

Similarly to *Limma*, *MSstatsTMT* includes an optional Empirical Bayes moderation of the standard error [17], which increases the sensitivity of the model when the number of biological replicates in each condition is small. Based on the model, the approach tests the null hypothesis in Eq. (1), by comparing the test statistic against the Student distribution.

The *MSstats* framework has a number advantages over the methods above. First, unlike [t-test (or ANOVA?) and *Limma*], the family of linear mixed effects models is applicable to many complex experimental designs, including designs with multiple sources of variation, and unbalanced designs. Second, the approach is applicable to various data acquisition types, including label-free DDA and DIA, and experiments with TMT labeling, and is compatible with various data processing tools such as Skyline, Spectronaut, MaxQuant, Progenesis, Proteome Discoverer, and OpenMS. Third, the run-level summarization has been shown to be more robust to outliers and missing values as compared to feature averages [16]. Finally, the custom *MSstats* and *MSstatsTMT* implementation accounts for potential data artifacts, and is numerically scalable and stable, and is available through both command line and a dedicated graphical user interface.

Unfortunately, MSstats estimates the difference in overall protein abundance and tests the null hypothesis in Eq. (1). It does not account for the confounding between the changes in PTM abundance and the overall changes in protein abundance. In other words, it cannot directly test the null hypothesis in Eq. (2).

Results

Statistical methods in MSstatsPTM

Detection of changes in PTMs in balanced design with one source of variation

We propose a statistical approach for detecting changes in PTMs. The method takes as input the modified spectral features y_{ijk}^* , and the corresponding unmodified features y_{ijk} . Ideally, the modified features are acquired separately, after an enrichment to maximize the information content in the resulting dataset, and the unmodified features are acquired separately as part of a global proteome profiling. However the method can also take as input a combination of modified and unmodified features acquired within a same run.

We leverage the existing methods in *MSstats* and *MSstatsTMT* and extend them to remove confounding between changes in the PTM and the overall changes in protein abundance. Each feature type is summarized separately using *MSstats* or *MSstatsTMT*, resulting in run level values for the PTM, \hat{y}_{ij}^* , and unmodified peptide. The estimated summaries of the modified features are then used as the input to the model, such as in Eq. (8), in *MSstats* or *MSstatsTMT*. Similarly, the estimated summaries of the unmodified features are used as the input to the corresponding model in *MSstats* or *MSstatsTMT*.

For the modified features, the model-based estimates in *MSstats* and *MSstatsTMT* include $\hat{\Delta}_{PTM} = \hat{\mu}_i^* - \hat{\mu}_{i'}$, and its standard error $\widehat{SE}(\hat{\Delta}_{PTM})$. Similarly, for the unmodified features, the model-based estimates in *MSstats* and *MSstatsTMT* include $\hat{\Delta}_{protein} = \hat{\mu}_i - \hat{\mu}_{i'}$, and its standard error $\widehat{SE}(\hat{\Delta}_{protein})$. Therefore, the adjusted difference $\hat{\Delta}_{adj}$ in Eq. (2) can be estimated as

$$\hat{\Delta}_{adj} = (\hat{\mu}_i^* - \hat{\mu}_i) - (\hat{\mu}_{i'}^* - \hat{\mu}_{i'}) = (\hat{\mu}_i^* - \hat{\mu}_{i'}^*) - (\hat{\mu}_i - \hat{\mu}_{i'}) = \hat{\Delta}_{PTM} - \hat{\Delta}_{protein} \quad (9)$$

Assuming that the unexplained by the model sources of variation in the modified features are independent from the corresponding sources of variation in the unmodified features, the standard error $\widehat{SE}(\hat{\Delta}_{adj})$ is obtained by combining the standard errors from the unmodified and modified model fits.

$$\widehat{SE}(\hat{\Delta}_{adj}) = \sqrt{\widehat{SE}(\hat{\Delta}_{PTM})^2 + \widehat{SE}(\hat{\Delta}_{protein})^2} \quad (10)$$

The estimated standard error is larger than the standard errors associated with each distinct feature type, reflecting the increased uncertainty inherent to combining the uncertainty in two estimators. Finally, the degrees of freedom associated with Eq. (10) are obtained via the Satterthwaite approximation [22, 36]

$$\left(\widehat{SE}(\hat{\Delta}_{PTM})^2 + \widehat{SE}(\hat{\Delta}_{protein})^2 \right)^2 \bigg/ \left(\frac{\widehat{SE}(\hat{\Delta}_{PTM})^4}{df(\widehat{SE}(\hat{\Delta}_{PTM}))} + \frac{\widehat{SE}(\hat{\Delta}_{protein})^4}{df(\widehat{SE}(\hat{\Delta}_{protein}))} \right) \quad (11)$$

To test the null hypothesis in Eq. (2), the test statistic $\hat{\Delta}_{adj}/\widehat{SE}(\hat{\Delta}_{adj})$ is compared with the Student distribution with the degrees of freedom in Eq. (11). The p-values of the comparison are adjusted for multiple testing using the approach by Benjamin and Hochberg [37].

By leveraging the implementations in *MSstats* and *MSstatsTMT*, the proposed approach is very versatile. It is applicable to a wide variety of experimental designs, including group comparison, paired designs, time course designs and unbalanced designs. It is applicable to label-free data acquisition strategies such as DDA and DIA and experiments with TMT labeling. The proposed approach is also applicable to experiments where the experimental designs for PTM profiling and global proteome profiling vary in properties such as number of biological replicates, data acquisition strategies and runs.

Design of balanced PTM experiments with one source of variation

The proposed statistical framework allows for design of PTM experiments in terms of sample size calculation and power analysis. Sample size calculation takes as input a) q , the desired false discovery rate, b) β , the average Type II error rate, c) Δ , the minimal log-fold change in adjusted PTM abundance that we would like to detect, d) $m_0/(m_0 + m_1)$, the fraction of truly differentially modified PTM sites in the comparison, and e) $\sigma_{\gamma^*}^2$ and σ_{γ}^2 , the anticipated variances associated to modified and unmodified peptide features, respectively.

The variances can be derived based on the dataset being analyzed, assuming similar quantitative properties and variations. With these values and a user-specified number of conditions, the corresponding number of technical replicates per condition can then be derived, as described in [22]. Given the above quantities, the minimal number of replicates J is determined by the variance of the estimated log-fold change $SE^2(\hat{\Delta})$ as [OV: hmm... For what design and what model? It is unclear where eq 11 came from. This will be quite specific to the model and the design. Maybe refer to the model in Eq 7? (Which we should probably simplify to reflect the experiment in Figure2, while keeping the general indexes)]

$$\widehat{SE}(\hat{\Delta})_{adj}^2 = \left[\frac{2}{J} (\hat{\sigma}_{\gamma^*}^2 + \hat{\sigma}_{\gamma}^2) \right] \leq \left(\frac{\Delta}{t_{1-\beta, df} + t_{1-\alpha/2, df}} \right)^2 \quad (12)$$

where

$$\alpha = (1 - \beta) \cdot \frac{q}{1 + (1 - q) \cdot m_0/m_1} \quad (13)$$

and $t_{1-\beta, df}$ and $t_{1-\alpha/2, df}$ are the $100(1 - \beta)^{th}$ and the $100(1 - \alpha/2)^{th}$ percentiles of the t distribution, with $df = I(J - 1)$ degrees of freedom in balanced designs.

Solving for J , the number of biological replicates per group is calculated as

$$J \geq \frac{(2\hat{\sigma}_{\gamma^*}^2 + 2\hat{\sigma}_{\gamma}^2)(t_{1-\beta, df} + t_{1-\alpha/2, df})^2}{\Delta^2} \quad (14)$$

Details on how the proposed method can be used to run sample size calculations and power analysis on experiments with complex design can be seen in **Supplementary Sec. 1.1**. More details on sample size calculation can be found in [38].

Implementation of MSstatsPTM

The proposed methods are implemented in the open source R package *MSstatsPTM*. An overview of the steps of the package are illustrated in Figure 3. *MSstatsPTM* includes converters for multiple spectral processing tools, including MaxQuant, Progenesis, and Spectronaut. Conversion is done separately for the modified peptide and global profiling runs. To identify the local modification site we require the tool to identify where in the sequence the modification occurred. If the global profiling information is not available, the package can still analyze the modified run, but will do so without adjusting for changes in unmodified protein abundance. This amounts to testing the null hypothesis in Eq. (1); which amounts to running the methods seen in *MSstats* on modified peptide level data.

The next step is peptide/protein summarization. Summarization is performed separately for the PTM and global protein in the same way as described above for *MSstats*. The package can optionally impute missing values using an Accelerated Failure Time (AFT) model [39]. Missing value imputation should be performed with care when applied to PTM data. PTMs generally exhibit low feature counts and may be missing due to reasons other than low abundance. These issues can cause the missing value imputation to be unstable. Finally, a separate model is fit to both the modified and global profiling runs. This model is automatically adjusted depending on the experimental design and acquisition method. If the base model is not applicable, a simplified model is fit. After modeling, the modified model is adjusted for changes in unmodified protein abundance, using the methods described above.

We include visualizations for QC and model assessment. In QC plots the PTM and global protein are shown side by side, allowing for easier interpretation and comparison across data. In the model plots this is further separated into PTM, global protein, and adjusted PTM visualizations, allowing users to see the affect of the adjustment.

The package relies on functionalities from the R packages *MSstats* [16] and *MSstatsTMT* [17]. The statistical modeling relies on the functionality from the R packages *lme4* [40] and *lmerTest* [41]. The code is available on Bioconductor, <http://www.bioconductor.org/packages/release/bioc/html/MSstatsPTM.html>, and Github, <https://github.com/Vitek-Lab/MSstatsPTM>.

Evaluation

We evaluated *MSstatsPTM* on simulated and spike-in datasets with known ground truth in terms of true positives (*TP*), false positives (*FP*), true negatives (*TN*), and false negatives (*FN*) differentially abundant PTM. The true positives were defined as PTMs with changes distinct from the overall changes in protein abundance. The true negatives were defined as PTM which, after accounting for the changes in the overall protein abundance, were not differentially abundant. Additional summaries were the false discovery rate $FDR = FP/(TP + FP)$, $Recall = TP/(TP + FN)$, and $Accuracy = (TP + TN)/(TP + TN + FP + FN)$. For biological experiments with unknown ground truth, we compared the differentially abundant PTM with and without adjusting for changes in unmodified protein abundance.

The evaluations were based on the *MSstatsPTM*, and were performed without imputing missing values and without using Empirical Bayes moderation. *MSstatsPTM* was compared with [t-test?] and Limma. We did not compare to IsobarPTM because it is only applicable to TMT experiments, meaning it could not be applied to our ground truth data. All the evaluations were done at the adjusted p-value cutoff of $\alpha = .05$. More details are in **Supplementary Sec. 2**.

[OV: Most of the following sections simply re-state the results that can already be read off the figures. The sections would have more value if in addition/instead of describing the figures, we could provide the reasons/insight into why we see this performance. Could you try? In general, no need to repeat what we see in the figure - this is what the figures are for.]

[OV: Also, maybe combine two sections that make a similar point?]

[OV: also avoid the terms 'significant'. Replace it with 'differentially abundant'. Instead of 'bias' and 'convolution', use 'confounding']

In clean simulations, MSstatsPTM corrected for high FDR of differentially abundant PTM

[OV: maybe say something about the fact that this is a group comparisons design that doesn't require many variance components, and as such is favorable to Limma and t-test? Later when you have repeated measurements, clarify that these situations are more challenging for the existing methods and therefore the difference in the results is more pronounced.]

Figure 4a illustrated the high FDR observed on the simulated datasets when not accounting for the overall changes in protein abundance. After the adjustment, the FDR of all methods improved. In a clean simulation, recall and accuracy of *MSstatsPTM* and *Limma* performed similarly. As expected when not using Empirical Bayes moderation in *MSstatsPTM*, *Limma* performed slightly better in simulations with fewer biological replicates. In contrast, the performance of the two-sample *t*-test method lagged behind. This was due to the fact that the *t*-test only uses data within the groups of interest while ignoring the remainder of the data. In contrast, *MSstatsPTM* and *Limma* leverage information across comparisons, resulting in improved power in simulations with more comparisons. Additionally, since this simulation is a group comparison design that doesn't require many variance components, it is favorable to *Limma* and *t*-test

In noisy simulations, MSstatsPTM better calibrated the true fold change over the existing methods

[This section just describes the figure. Could you emphasize why we see these results? What are the reasons for differences in performance?]

In simulations with missing values and few features, *MSstatsPTM* outperformed *t*-test and *Limma*. Changes in unmodified protein level still needed to be accounted for to control the FDR. Once controlling for changes in the unmodified protein, the proposed method outperformed the other methods, as seen in **Figure 4b**. The proposed method calibrated model accuracy and recall rate well, even when the number of replicates were low. The proposed approach can handle low feature counts due to using Tukey's Median Polish for summarization. The existing methods summation approach requires more observations to correctly summarize the intensities in the run, whereas TMP is robust to few measurements.

Additionally, when comparing the fold change estimation across all modified peptides, the proposed method showed a tighter distribution of estimated fold changes around the true fold change. Specifically, the inner quartile range (IQR) of the estimated fold change for the proposed method was on average 21.8% smaller than *Limma* IQR and 10.4% smaller than *t*-test's IQR. This means that while the mean of the

estimated fold changes was generally correct for all methods, the proposed approach correctly estimated the fold change more often across all PTMs. This fold change comparison can be seen in **Supplementary Figure S6**.

In the label-free benchmark experiment, MSstatsPTM had a higher sensitivity than the existing methods

In this experiment all models incorrectly estimated the fold change of the modified spike-in peptides before adjusting for changes in global protein abundance. After adjustment, the spike-in peptides' fold change was generally in line with expectation in all methods, however the distribution of estimated fold changes was visibly wider (**Figure 5a**). Of the three approaches, the proposed method showed the tightest distribution around the true log fold change. Comparing the IQR of the spike-in peptide's log fold change, the proposed method's IQR was 36.78% smaller than *Limma* and 32.98% smaller than *t*-test's. While *Limma* and *t*-test generally estimated the correct fold change, the proposed method's estimation was more consistent across all modifications.

In **Figure 5b** we can clearly see the fold change of the red labeled spike-in peptides was only correctly estimated when accounting for changes in the unmodified protein abundance. Additionally, the background peptides, serving as the null model, show many false positives before adjustment. After adjustment the number of false positives substantially decreased. Specifically, for the proposed method, the number of false positives went from 20.88% to 1.84% after adjustment was applied. While the proposed method and *Limma* both correctly estimated the fold change of the spike-in peptides, using *Limma* resulted in many large adjusted p-values. Using *Limma* would have resulted in missing the majority of differential PTMs.

This experiment introduced more variance components, which is challenging for the existing methods and therefore the difference in the results is more pronounced than in the simulations.

In two group comparison TMT experiments, MSstatsPTM corrected for confounding with the unmodified protein

[This section just describes the figure. Could you emphasize why we see these results? What are the reasons for differences in performance?]

The results of these experiments are summarized in **Figure 6** and **Figure 7**. **Figure 6a** and **Figure 7a** show the number of differentially abundant modified peptides before and after adjustment. In both cases, more peptides lost than gained differential abundance after the adjustment. A question that must be addressed is if the decrease in differentially abundant peptides is due to the increased variance that comes from adjustment. This was tested by looking for modified peptides whose adjusted log fold change was within 10% of the unadjusted log fold change but became statistically insignificant after adjustment. In other words, the fold change was the same between models but variance increased. When this test was applied on this experiment, only one peptide became statistically insignificant due to an increase in variance. Thus we can conclude that the drop off in differentially abundant peptides was due to changes in global protein abundance.

Interestingly, the global protein was more likely to drive changes in abundance rather than mask changes in the PTM, i.e. when the protein and PTM moved in opposite directions. This can be seen in **Figure 7b**, where the global protein *TTP* followed the same trend as the modification at *S178*. Originally the modification was shown to be differentially abundant between KO_Uninfected and KO_Early, however this was due to confounding with the global protein. The proposed method corrects for these changes automatically, allowing us to see the true fold change, without having to do a side by side comparison.

Conversely, cases where the PTM and global protein move in opposite directions are interesting and should be highlighted, as the modification and protein had contradictory abundance changes. One such case can be seen in **Figure 6b**. Luchetti et al. [19] showed that *GSDMD* was actively degraded when IpaH7.8 expression was induced by dox treatment. Our reanalysis confirmed this, with the global *GSDMD* protein being downregulated when Dox treatments reached the 4 and 6 hour marks. Conversely, the ubiquitination of *GSDMD* at site *K62* was actually upregulated between the same conditions. This upregulation was originally confounded by the downregulation of unmodified *GSDMD*, as can be seen in **Figure 6b**, appearing to have little change between no dox and dox 4 and 6 hour. The proposed approach accounted for this confounding and the modification was shown to be differentially abundant, with an absolute fold change of

1.415 between the Dox1hr and Dox4hr conditions. The proposed method allowed us to see modifications of interest, while filtering out those that would originally be false positives.

In label-free experiment without a separate global profiling run, MSstatsPTM eliminated the confounding due to changes in the unmodified protein, albeit less effectively than in the presence of a global profiling run

[This section just describes the figure. Could you emphasize why we see these results? What are the reasons for differences in performance?] As discussed in **Section 2**, there was no unmodified global profiling run performed in this experiment. Once identification and quantification of the Ubiquitination profiling was performed, peptides which were unmodified were extracted and used in place of a global profiling run. This resulted in a lack of overlap between modified and unmodified peptides. Any modified peptide without a corresponding unmodified protein could not be adjusted. Of the 10,799 ubiquitin sites identified, only 4,526 had a corresponding unmodified protein and could be adjusted. Additionally, the lack of a separate global profiling run resulted in low feature counts for the unmodified protein model compared to other experiments, seen in Table 5.1.

The results of this experiment are summarized in **Figure 8**. After adjusting for changes in the unmodified protein, there were fewer significant modified peptides. In total, 2709 modified peptides became insignificant, while only 547 became significant. However, this was mainly due to not having a global profiling run, resulting in a lack of overlap between modified and unmodified peptides. In the bottom plot, only modified peptides that could be adjusted are shown. Here there were much fewer peptides that became insignificant after adjustment. 726 modified peptides became insignificant, 547 became significant, and 1,078 were significant in both models. Only 25 PTMs became insignificant due to increased variance from adjustment.

Discussion

We proposed a general statistical modeling framework and implementation for PTM characterization. The framework is designed for bottom-up MS workflows, which are characterized with variations from multiple confounded sources, frequent missing data, and associated uncertainty in the conclusions. The framework is general and is applicable to a variety of experimental designs. It outperforms the ad-hoc methods underlying *t*-test and Limma, and yields accurate results in the broad type of experimental circumstances, including the presence of missing values, changes in protein abundance, few representative peptides, and different acquisition methods. The framework allows us to plan for subsequent experiments, and choose the appropriate number of replicates in consideration of adjustment with respect to protein abundance. The implementation allows for straightforward application of the methods discussed and allows for reproducible experimental analysis.

Our results show that the proposed approach for modeling and summarization leads to more sensitive PTM significance analysis and more accurate and precise quantification. The gain is due to a more efficient use of the data, and to a more accurate understanding of the systematic and random variations. The proposed framework can be extended beyond the experimental designs with variation from multiple sources discussed above. Although demonstrated here on DDA, is also applicable to DIA, SRM and PRM acquisitions. Additionally, the approach can handle experiments with modified peptides processed using label-free methods and unmodified peptides processed using TMT labeling, or vice versa. In this case summarization and modeling is still done separately for both the modified and unmodified data, and then combined after modeling.

A potential limitation of the proposed framework is the assumption that all the peptides are correctly mapped to the underlying proteins and PTM sites, and the features are informative of the abundances of underlying protein and PTM. Also, characterizing PTMs with current data-dependent acquisition workflows is prone to being under sampled, leading to a sparse dataset with a large number of missing values for the analysis. Statistical methods accounting for effects due to experimental units and missing values introduced in this manuscript help interpret the data in a more objective manner. The latest development of targeted acquisition and data-independent acquisition methods are expected to further alleviate these issues.

Additionally, abundance levels of PTM sites can be confounded with each other if there are multiple modification sites per peptide, or confounded with changes in the unmodified peptide (as opposed to the

unmodified protein). In the current implementation the effect of a specific modification in a peptide with multiple modifications cannot be quantified. One potential solution to this is to measure the abundance of peptides with one modification and use this to adjust the peptide with multiple sites to remove the confounding. However, this method would likely run into challenges due to sparsity of features for modified peptides with both a single and multiple modification sites. A more complex approach to addressing this problem is likely necessary.

Overall, the proposed approach balances accuracy and practicality, and enables the analysis of complex experiments in high throughput. Future work is to carry out the inference and testing for not only the relative change of PTM abundance, but also the fraction of the protein that is modified at the particular site (site occupancy, or stoichiometry), and attempt to remove the confounding of individual PTMs in peptides with multiple modifications.

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Tables

Experimental Datasets Overview

	Dataset	No. of Conditions	No. of bio. replicates	No. of mod. peptides	No. of mod. features/site	No. of unmod. features/protein	Data availability	Analysis
Known Ground Truth	Computer simulation 1 - Label-free	2/3/4	2/3/5/10	1,000	10	10	Github	
	Computer simulation 2 - Missing and low features	2/3/4	2/3/5/10	1,000	2	10	Github	
	SpikeIn benchmark - Ubiquitination - Label-free	4	2	12,137	1.37	10.17	MSV000088971	TBD
Biological Experiment	Human - Ubiquitination - 1mix-TMT	6	2 or 1	8,848	1.21	11.01	MSV000088966	RMSV0000000356
	Mouse - Phosphorylation - 2mix-TMT	6	4 or 3	26,433	1.67	11.61	MSV000085565	RMSV0000000357
	Human - Ubiquitination - Label-free	4	2	10,799	1.40	1.65	MSV000078977	RMSV0000000358

Table 5.1: Simulated and experimental datasets. “Dataset” is the dataset code name. “No. of bio. replicates” shows the number of biological replicates per condition. Simulations were generated with different numbers of replicates. The designs of two biological experiments were unbalanced with unequal replicates per condition. “No. of mod. features/site” is the number of features (i.e., peptide ions) used to estimate the abundance of a single modification. “No. of unmod. peptides/protein” is the number of peptide ions without modifications that were used to estimate the global protein abundance. “Data availability” is the ID of the MassIVE.quant repository or the GitHub repository. “Analysis” is the ID of the MassIVE.quant reanalysis container, containing analysis code and modeling results. All the experiments were conducted in data-dependent acquisition (DDA) mode.

Figures

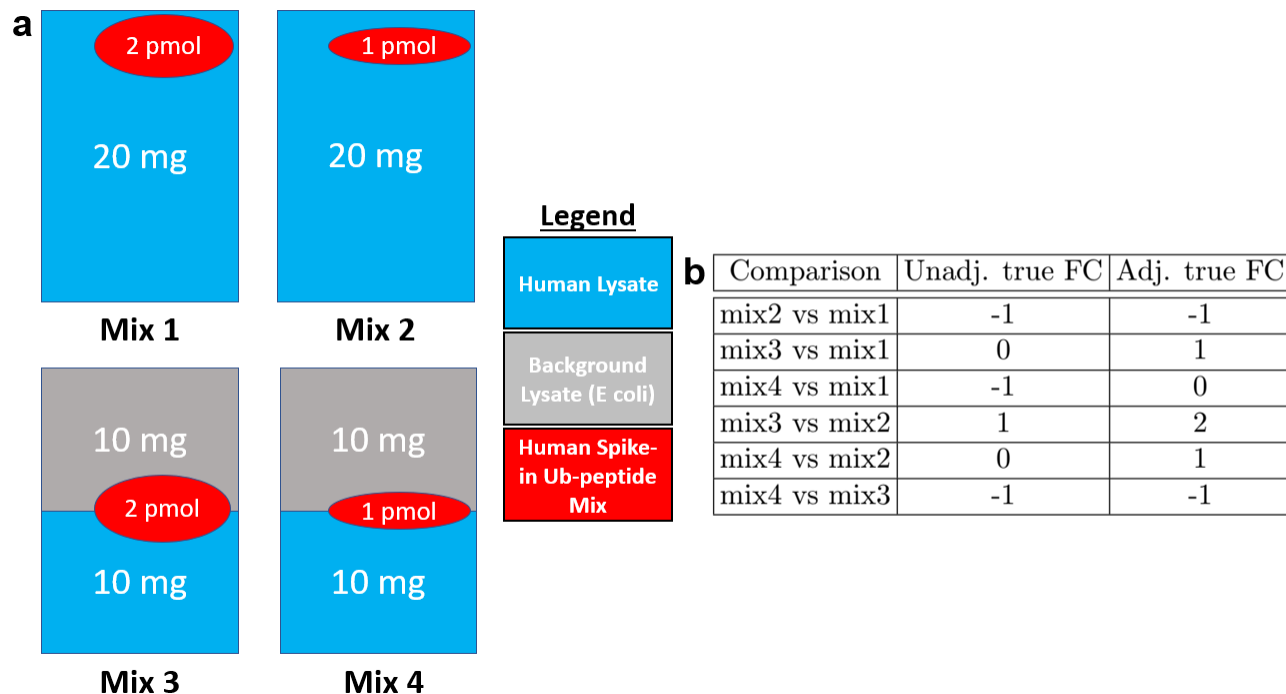


Figure 1: **Dataset 3: Spike-in benchmark - Ubiquitination - Label-free.** [In the legend, could you mark the blue box "Human lysate (global proteome)", the grey box "E. Coli lysate (background proteome)" and mark the red box as "50 spiked human ub-peptides". Check the capitalization] [In the table, could you change the headers to $\log_2\text{FC}$] (a) Four mixtures (i.e., conditions) were created with varying amounts of human lysate [which cell line?], background *E. Coli* lysate, and human spike-in ub-peptide mixture. Unmodified peptides from human lysate were viewed as the global proteome. Background *E. coli* lysate were used to equalize total protein levels. 50 heavy-labeled KGG motif peptides from 20 human proteins were spiked into the mixed background of the lysates. Quantitative changes in protein and site abundance of these 20 human proteins were the target of the benchmark. (b) We distinguished the unadjusted changes (i.e. changes in the abundances of the modified peptides) and the protein-level adjusted changes of (i.e., changes in the abundances of the modified peptides relative to the changes in the abundances of the human lysate). "Unadj. true $\log_2\text{FC}$ " are the log-ratios of the abundances of the spiked peptides between each condition. "Adj. true $\log_2\text{FC}$ " [Could you rephrase the calculation more precisely? Ratios of the ratios? I am wondering if a formula would be helpful?] was calculated by determining the ratio of spike-in peptides to human lysate in each mixture and then using the ratio to calculate the true fold change across comparisons.

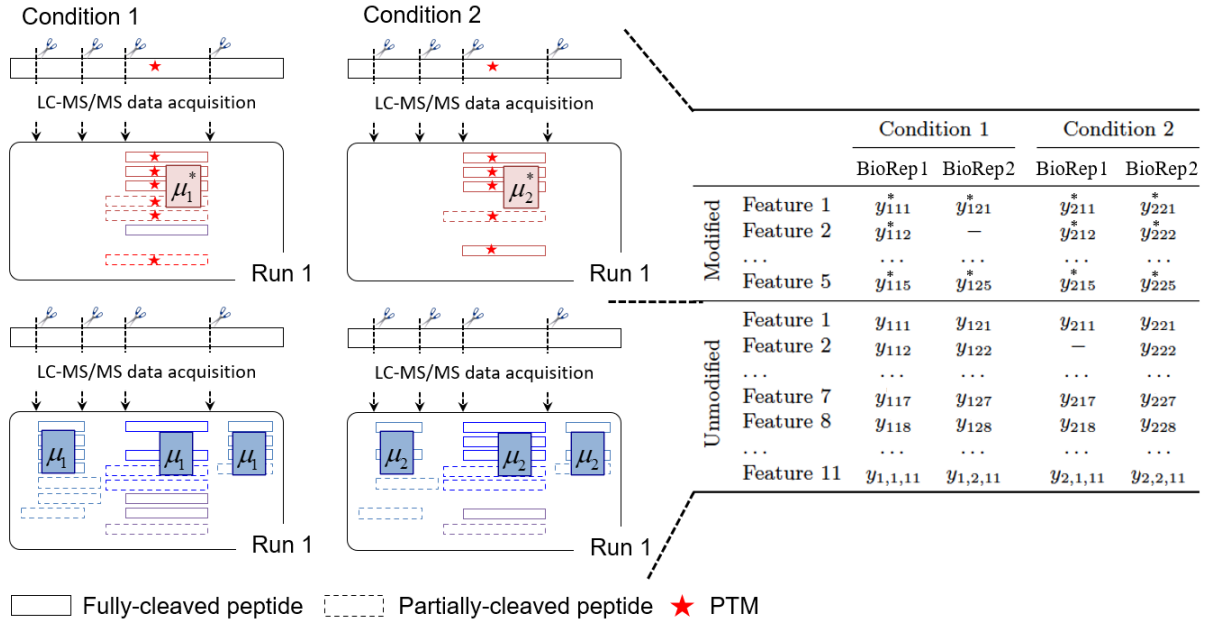


Figure 2: Schematic representation of one PTM site, in a special case of $I = 2$ conditions and $J = 2$ biological replicates per condition. We are interested in estimating the difference between the population-level PTM abundance between Condition 1 and Condition 2 (i.e., $\mu_1^* - \mu_2^*$), relative to the population-level difference of the overall protein abundance (i.e., $\mu_1 - \mu_2$). These quantities are characterized by the observed spectral Features (boxes), i.e. peptides of different charge states. The peptides can be fully cleaved (solid lines), or partially cleaved (dashed lines). The log₂-intensities of the modified peptides in Condition i , Run j , and Feature k are denoted by y_{ijk}^* . The log₂-intensities of Feature k corresponding to the unmodified peptide in Condition i and Run j are denoted by y_{ijk} .

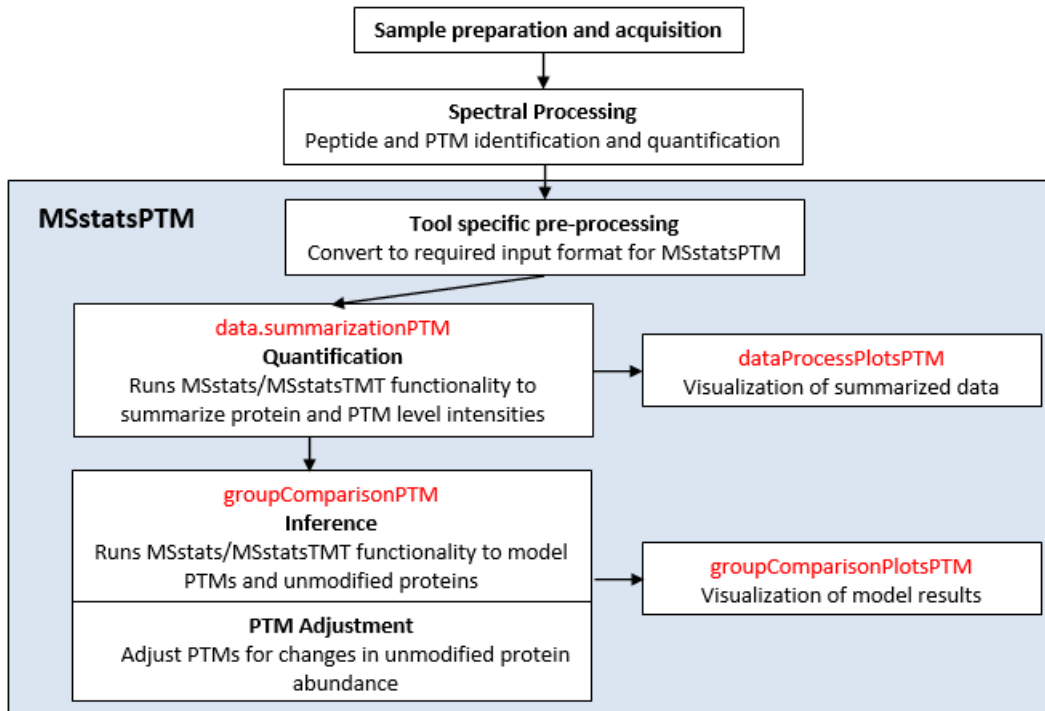


Figure 3: The workflow of *MSstatsPTM* and how it fits into the experimental pipeline. The name of the R functions used for each step are highlighted in red. The package's workflow starts after modified and unmodified peptide quantification. First tool specific pre-processing is performed, this includes modification site identification, general data cleaning, and formatting the data into the format needed for the package. The next step is feature level summarization, which summarizes features up to the modification level for the PTM data, and the protein level for the protein data. In the final step a model is fit to identify differential PTMs and unmodified proteins across conditions and the PTM model is adjusted for changes in the unmodified protein. After both the summarization and group comparison steps, plots can be created to summarize the results.

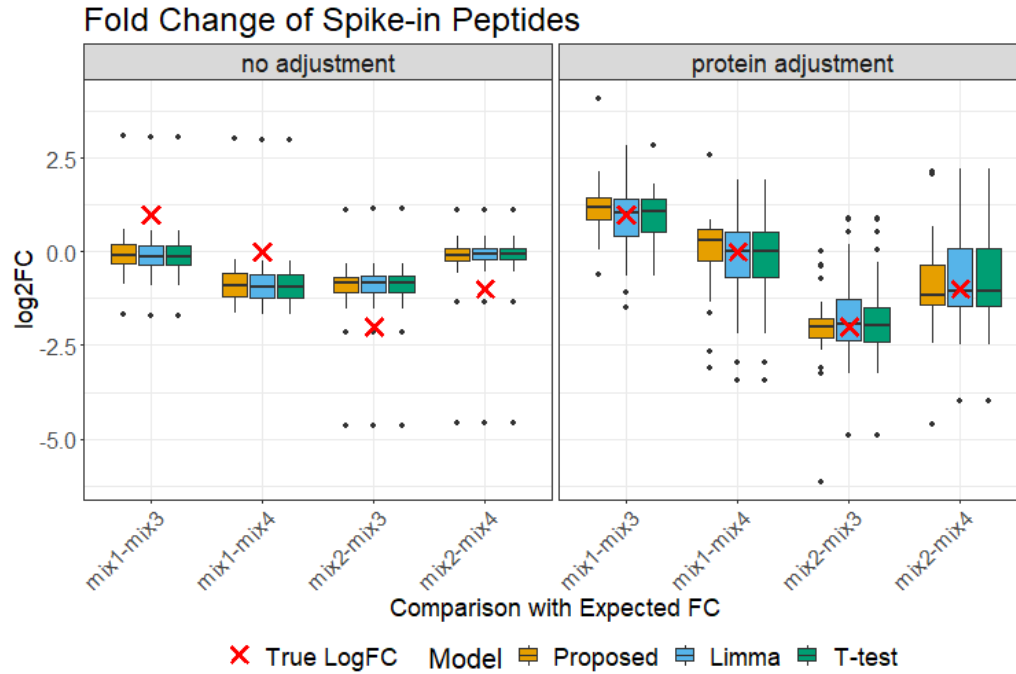


(a)

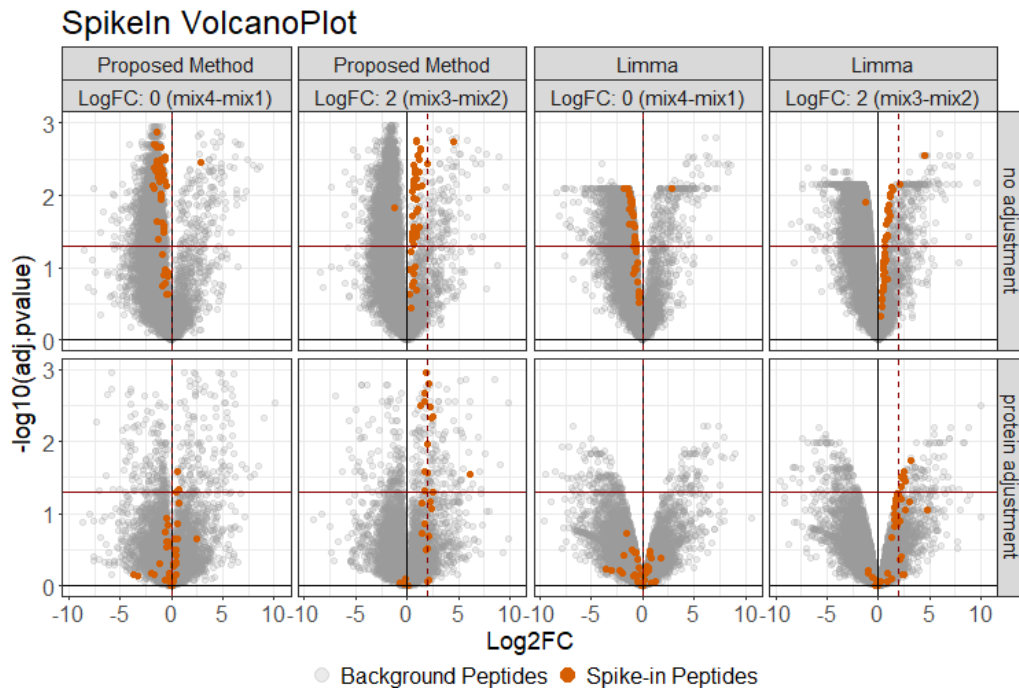


(b)

Figure 4: Dataset 1 & 2: Computer simulation. a) All the considered methods in the first computer simulation correctly calibrated FDR when adjusting for changes in protein abundance. In comparison, the methods without accounting for the protein-level changes resulted in off-target, high false positive rates. b) The advantage of using the proposed approach was apparent when including limited observations and missing values. Looking at accuracy, the proposed method outperformed Limma and *t*-test in nearly every model.



(a)



(b)

Figure 5: Dataset 3: Spike-in benchmark - Ubiquitination - Label-free. a) Before adjustment the fold change of the spike-in peptides' were systematically different from the expected fold change in all models. After adjustment, this systemic difference was removed, however the inner quartile range of the Limma and *t*-test models was wider than the proposed method. b) Before adjustment the spike-in peptides (colored red) did not follow the expected log fold change; after adjustment, the spike-in peptides were more in line with expectation. Using Limma, the spike-in peptides followed the expected log fold change after adjustment, however the majority of spike-in peptides did not have a significant adjusted p-value.

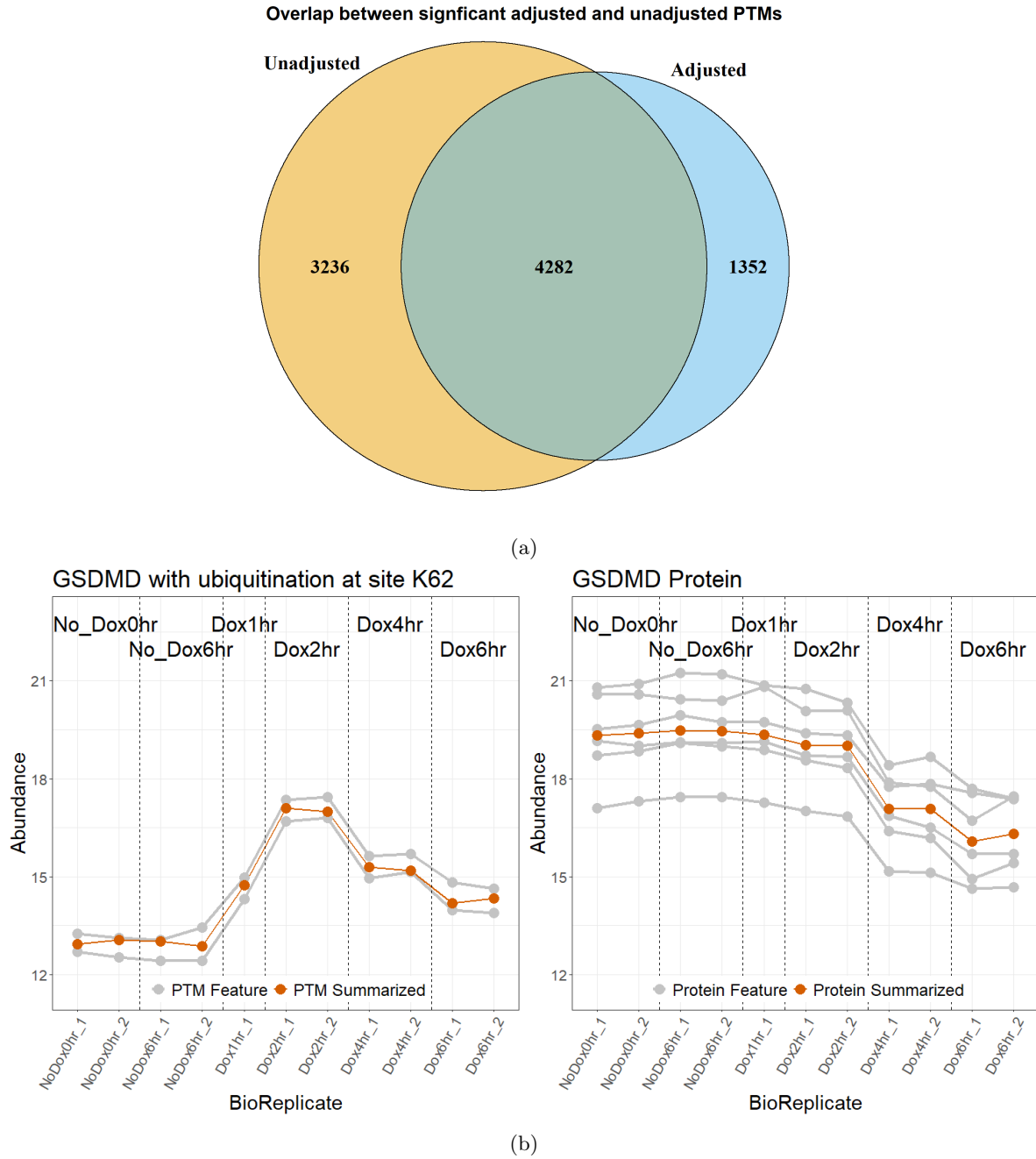


Figure 6: Dataset 4: Human - Ubiquitination - 1mix-TMT. a) The overlap of differential modified peptides for the PTM model with and without global protein level adjustment across all comparisons. 3,236 modified peptides became insignificant, 1,352 became significant, while 4,282 were significant in both models. b) Comparing the global profiling of protein *GSDMD* with the ubiquitination of the protein at site K62. When looking at the summary of the modification and global protein it was clear the conditions follow different trends. Specifically, there appeared to be no change in abundance between Dox1hr and Dox4hr in the modified plot, however there was a large negative change when looking at the unmodified plot. This indicated the modification was confounded with changes in the unmodified protein.

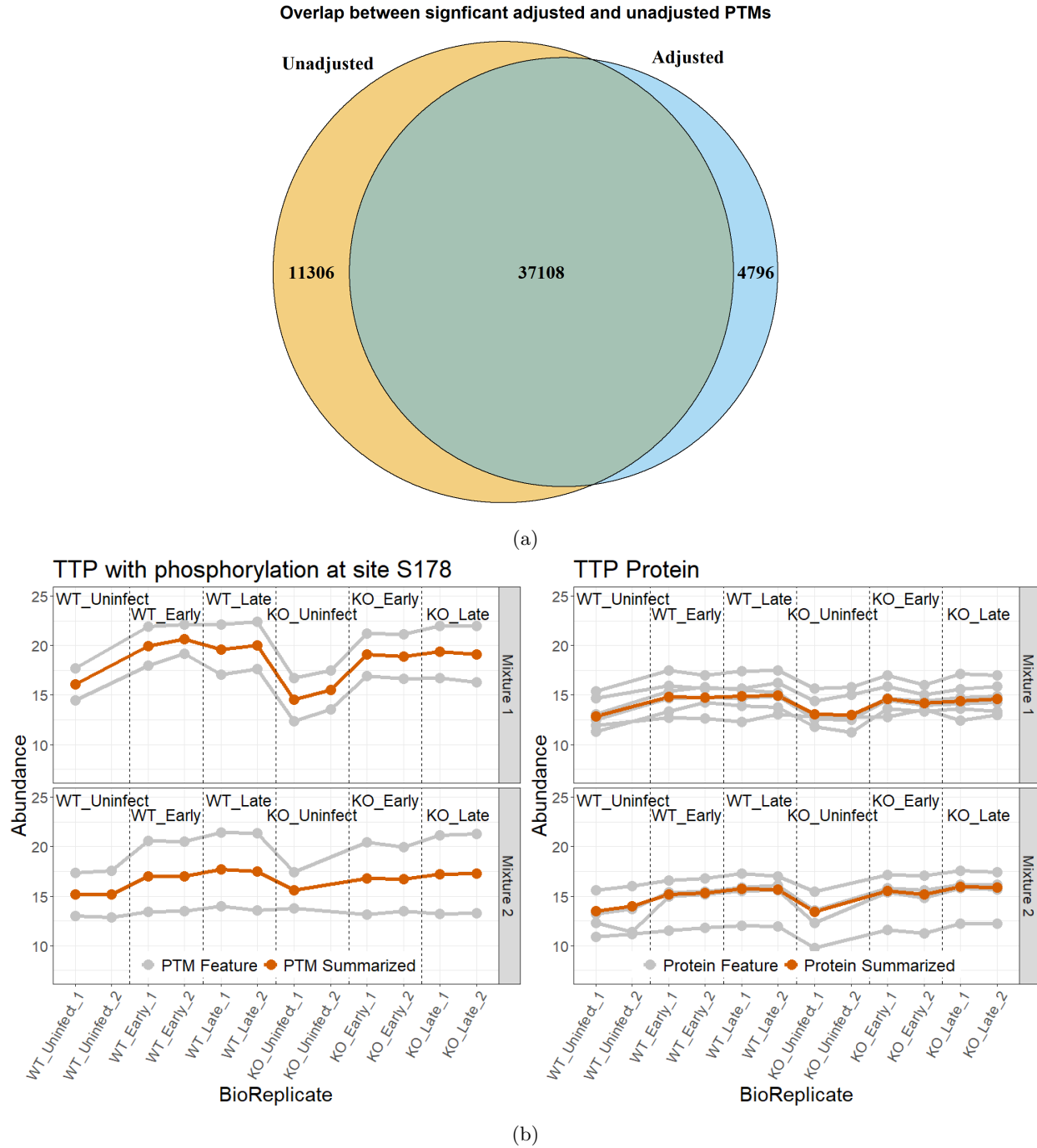
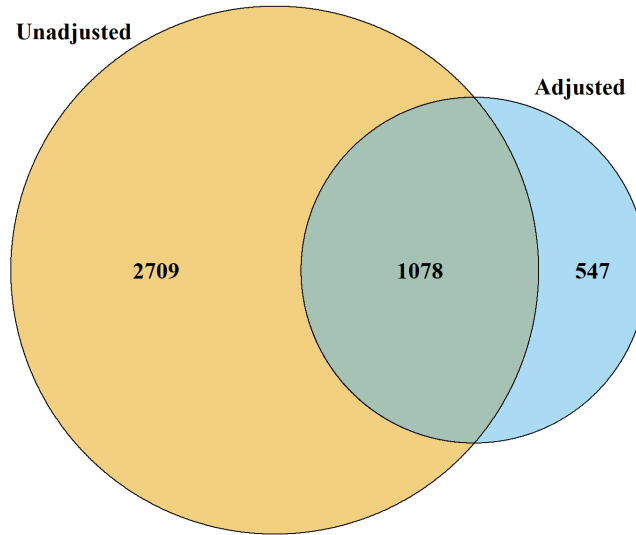
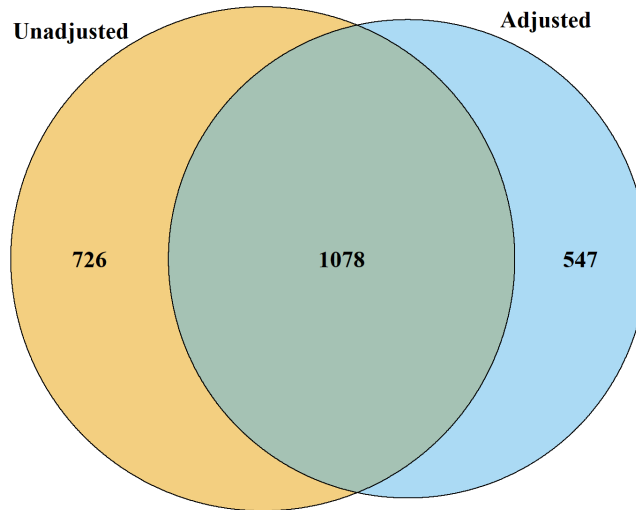


Figure 7: Dataset 5: Mouse - Phosphorylation - 2mix-TMT. a) The overlap of differentially modified peptides between the PTM model with and without global protein level adjustment across all comparisons. 19,286 peptides became insignificant, 4,947 became significant, and 41,552 were significant in both models. b) Comparing the global profiling of protein *TTP* with the modification of the protein at site *S178*. When looking at the summary of the modification and global protein it was clear the difference between conditions followed the same trend. Specifically, there was a positive adjustment in abundance when comparing WT.Uninfected to WT.Late in both the modification and global profiling run. This indicated the movement was driven by changes in global protein that was only accounted for in the model after adjusting for global protein abundance change.

Overlap between significant adjusted and unadjusted PTMs

(a)

Significant adjusted and unadjusted PTMs (matching only)

(b)

Figure 8: Dataset 6: Human - Ubiquitination - Label-free no global profiling run. a) The overlap of differential modified peptides for the PTM model with and without global protein level adjustment across all comparisons. More PTMs became insignificant than became significant after adjustment. This was due to not having a global profiling run, resulting in a lack of overlap between modified peptides and unmodified proteins. b) Here we made the same comparison but only looked at modified peptides where adjustment could be performed, ie they had a matching unmodified protein. In this case there were significantly less peptides that became insignificant after adjustment. This highlighted the need for a global profiling run.