

1. Set S as the sample of all peptide log-ratios $\{l_i\}_{i=1}^n$ from the experiment if the data does not require normalization.
 - a. If the data requires normalization, set S as the normalized sample $\{l_i - M\}_{i=1}^n$ or $\{l_i - \bar{l}\}_{i=1}^n$ where $M = \text{median}(\{l_i\}_{i=1}^n)$ and $\bar{l} = \sum_{i=1}^n \frac{l_i}{n}$ to normalize by the median or the mean respectively.
2. For protein j in the set of proteins one to m :
 - a. Calculate the number of peptides $n_j = \#\{l_i | p_i = j\}$ in the subsample of protein j .
 - b. Calculate the protein log-ratio $L_j = \sum_{\{l_i | p_i = j\}} \frac{l_i}{n_j}$ for protein j .
 - c. If $n_j = 1$:
 - i. Estimate the p-value of protein j by evaluating $\widehat{\text{p-value}}_j = \frac{\sum_{i=1}^n I\{|L_j| > |l_j|\} + 1}{n+1}$ where $I\{|L_j| > |l_j|\} = 1$ if $|L_j| > |l_j|$ is true and $I\{|L_j| > |l_j|\} = 0$ if $|L_j| > |l_j|$ is false.
 - d. If $n_j > 1$:
 - i. For b from one to B :
 - A. Randomly sample without replacement n_j numbers between one and n to obtain the set $\{k_a\}_{a=1}^{n_j}$ where k_a is a number between one and n .
 - B. For the random peptide log-ratio subsample $S_b = \{l_{k_a}\}_{a=1}^{n_j}$ using the random sample $\{k_a\}_{a=1}^{n_j}$.
 - C. Compute the protein log-ratio of the random subsample by evaluating $L'_b = \sum_{a=1}^{n_j} \frac{l_{k_a}}{n_j}$.
 - ii. Estimate the p-value by evaluating $\widehat{\text{p-value}}_j = \frac{\sum_{b=1}^B I\{|L_j| > |L'_b|\} + 1}{B+1}$ where $I\{|L_j| > |L'_b|\} = 1$ if $|L_j| > |L'_b|$ is true and $I\{|L_j| > |L'_b|\} = 0$ if $|L_j| > |L'_b|$ is false.