

1. Set the proportion of changed proteins 2π .
2. Set the mean deviation in the expression of peptide log-ratios μ .
3. Set the variance of the changed log-ratio distributions σ^2 .
4. Set the parameter ϕ for generating the size of each protein subsample.
5. Set the number of proteins to simulate m .
6. For protein j in the set of proteins from one to m :
 - a. Randomly generate a protein subsample of size n_j from the geometric distribution $f(n_j) = (1 - \phi)^{(n_j-1)}\phi$.
 - b. Randomly Draw R from a uniform distribution in the interval of zero and one.
 - c. If $0 \leq R \leq 1 - 2\pi$:
 - i. Randomly generate n_j peptide log-ratios from the density $f_G(l; 0, 1)$.
 - d. If $1 - 2\pi < R \leq 1 - \pi$:
 - i. Randomly generate n_j peptide log-ratios from the density $f_G(l; -\mu, \sigma^2)$.
 - e. If $1 - \pi < R \leq 1$:
 - i. Randomly generate n_j peptide log-ratios from the density $f_G(l; \mu, \sigma^2)$.