Let the groups be indexed by $0, 1, \ldots, \ell$, where 0 corresponds to the reference group. For each $i = 0, \ldots, \ell$, let $t_i$ be the number of replicate experiments in the $i$-th group. Let $x_{g,i,k}$ be the (cleansed and normalized) intensity of gene tag $g$ in the $k$-th experiment in the $i$-th group, when defined. Finally, let $t_{g,i}$ be the number of replicate values for gene tag $g$ in group $i$ (note that $t_{g,i} = t_i$ whenever tag $g$ has a value in each of the experiments for group $i$). Let $(n_0, n_1, \ldots, n_\ell)$ be the minimum presence list, i.e. list of minimum number of values a tag should have for each group in order to be considered. Let $s$ (between 0 and 1) be the desired false positive rate.

1. Eliminate from further consideration any tag $g$ such that $t_{g,i} < n_i$ for some $i = 0, 1, \ldots, \ell$.

2. For each tag $g$ and for each $i = 0, \ldots, \ell$, let $x_{g,i}$ be the average of the (available) values for tag $g$ in group $i$.

3. If shift is provided, go to 5. Else, let $m = \min_{g,i} \frac{x_{g,i}}{n_i}$ and $\varsigma = \max_{g,i} \frac{x_{g,i} - m}{\sqrt{\frac{1}{n_i} \frac{n_i}{t_{g,i}}}}$ where $x_{g,i}$ is the sample standard deviation of the $x_{g,i,k}$. Let $\text{shift} = \max \{ 0, (\text{shift.par} - m) \varsigma \}$, where $\text{shift.par}$ is as provided by the user (default is 3).

4. For each tag $g$ and for each $i = 0, \ldots, \ell$ and $k = 1, \ldots, t_i$, let $x_{g,i,k} = x_{g,i,k} + \text{shift}$ (if $x_{g,i,k}$ is defined) and $x_{g,i} = x_{g,i} + \text{shift}$.

5. Eliminate from further consideration any tag $g$ for which $x_{g,0} = 0$.

6. For each tag $g$ and for each $i = 1, \ldots, \ell$, let $r_{g,i} = \frac{x_{g,i}}{x_{g,0}}$. Then the list of ratios associated to gene tag $g$ is $(r_{g,1}, r_{g,2}, \ldots, r_{g,\ell})$.

7. For each $i = 1, \ldots, \ell$, let $\min_i$ (resp. $\max_i$) be the minimum (resp. maximum) of $r_{g,i}$ over all tags.

8. For each $i = 1, \ldots, \ell$, let $f_i$ be the empirical distribution of $\frac{x_{g,i,k}}{\sqrt{\frac{1}{n_i} \frac{n_i}{t_{g,i}}}}$, for $g$ varying over the gene tags and $k$ varying over the replicates for gene tag $g$ in group $i$ and 0 respectively. (If $t_{g,i} = 1$ replace the numerator by $x_{g,i,k}$; similarly if $t_{g,0} = 1$.) This distribution is computed by dividing the range of the values into 100 bins.

9. For each $i = 1, \ldots, \ell$, compute the smallest $C_i$ such that

$$\sum_{j=\text{bin containing } C_i} f_i(j) < s$$

through a binary search. In a similar fashion compute $c_i$.

10. For each $i = 1, \ldots, \ell$, the level cutoff list is obtained by taking all successive powers of $C_i$ which are strictly less than $\max_i$ and all successive powers of $c_i$ which are strictly greater than $\min_i$ and for which there is at least one smaller non-zero $r_{g,i}$. Let $0 < a_{i,1} < a_{i,2} < \cdots < a_{i,n_i}$ be the level cutoff list thus obtained. Let $B_i = \left[ a_{i,0}, a_{i,1} \right], \left[ a_{i,1}, a_{i,2} \right], \ldots, \left[ a_{i,n_i}, \infty \right)$, where $B_i = \left[ a_{i,0}, a_{i,1} \right]$ is the interval containing $1$.

11. For each $g$ and for each $i = 1, \ldots, \ell$, let $j_i$ be such that $r_{g,i} \in B_{i,j_i}$. The pattern attached to $g$ is then $(j_1, j_2, \ldots, j_\ell)$.