

TREND ANALYSIS

The trend analysis method is as follows:

Algorithm 1: The trend analysis method

- 1: Input: smoothed expression data X_i .
 - 2: Fit X_i to a linear function $L_i \times s + C_i$. Here, the estimated coefficient is denoted as L_i and the constant is denoted as C_i .
 - 3: Calculate the standard deviation of the detrended expression data, and denote as V_i . The detrended expression data $H_i(s)$ is obtained as $H_i(s) = X_i(s) - (L_i \times s + C_i)$, which means that removes the best straight-line fit linear trend from X_i . Therefore, $V_i = std(H_i(s))$.
 - 4: A score is defined, $R_i = |L_i/V_i|$.
 - 5: Output: score R_i .
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Linear trend represents a systematic increase or decrease in data over time. By removing the linear trend from the data, the fluctuation of the detrended data was considered, and such fluctuation is not caused by time change. Therefore, we believe that the higher the score R_i , the most likely the expression of the corresponding alternative splicing event i (RNA-binding protein i) changes significantly in the EM transition process.

An example is given to further illustrate. Consider the following data,

s	0.0200	0.0233	0.0267	0.0300	0.0333	...	0.9767	0.9800	0.9833
X_1	3.1424	3.1370	3.1372	3.1414	3.1523	...	3.0517	3.1227	3.1827

Fit X_i to a linear function $L_i \times s + C_i$. Here, we get $L_1 = 0.5195$ and $C_1 = 2.9909$, i.e., the linear trend is $0.5195 \times s + 2.9909$. Then the detrended expression data $H_1(s) = X_i(s) - (0.5195 \times s + 2.9909)$. We have the score $R_1 = 3.5771$. The figure is as follows,

