Permutation goodness of fit test for Poisson distribution

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Abstract

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1. Methods

The permutation goodness of fit test for Poisson distribution (further called PGoF) is based on Chi Square test. The $\hat{\lambda}$ is calculated from counts of positive and negative partitions using following relationship:

$$\hat{\lambda} = -\ln\left(1 - \frac{k}{n}\right) \qquad (1)$$

According to the MIQUE Guidelines for Digital PCR, k is number of positive partitions and n is a total number of partitions. To perform the permutation test, we firstly compute $\hat{\lambda}_R$ for data vector. Next, from the density of Poisson distribution we estimate the chance of having negative partition (no template molecules) or positive partition (more than zero template molecules). Obtained

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probabilities are used to perform a Chi Square test and the test statistic χ_R is preserved.

Further, we use the $\hat{\lambda}_R$ to generate a large number of n-long sample from Poisson distribution. Each sample is binarized to positive and negative partitions and we perform the exactly the same procedure as for the real sample: we $\hat{\lambda}_P$, estimate probabilities of negative and positive partitions and finally perform the Chi Square test to obtain test statistic χ_P.

The p-value of permutation test is defined as:

$$\text{p-value} = \frac{N_{\chi_P > \chi_R}}{N} \tag{2}$$

where $N_{\chi_P > \chi_R}$ is number of times when χ_P was more extreme than χ_R.

In case of very low $\hat{\lambda}_R$, sometimes the $\hat{\lambda}_P$ may be exactly zero. In this case we assume, that $\chi_P = 0$, that's how Chi test behaves ;)

References

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