

# Permutation goodness of fit test for Poisson distribution

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*Radarweg 29, Amsterdam*

*Elsevier Inc<sup>a,b</sup>, Global Customer Service<sup>b,\*</sup>*

*<sup>a</sup>1600 John F Kennedy Boulevard, Philadelphia*

*<sup>b</sup>360 Park Avenue South, New York*

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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:

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

5 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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<sup>\*</sup>Corresponding author

*Email address:* `support@elsevier.com` (Global Customer Service)

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10 probabilities are used to perform a Chi Square test and the test statistic  $\chi_R$  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  
15  $\hat{\lambda}_P$ , estimate probabilities of negative and positive partitions and finally perform the Chi square test to obtain test statistic  $\chi_P$ .

The p-value of permutation test is defined as:

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

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

In case of very low  $\hat{\lambda}_R$ , sometimes the  $\hat{\lambda}_P$  may be exactly zero. In this case the Chi square test has 0 degrees of freedom.

## 20 References

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