

# Package ‘digitalPCR’

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**Type** Package

**Title** Estimate Copy Number for Digital PCR

**Version** 1.1.0

**Depends** stats

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**Description** The assay sensitivity is the minimum number of copies that the digital PCR assay can detect. Users provide serial dilution results in the format of counts of positive and total reaction wells. The output is the estimated assay sensitivity and the copy number per well in the initial dilute.

**License** GPL-2

**NeedsCompilation** no

**Repository** CRAN

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## R topics documented:

digitalPCR . . . . .	1
digitalPCR-internal . . . . .	3

<b>Index</b>	<b>4</b>
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digitalPCR	<i>Estimate copy number and assay sensitivity from dPCR serial dilution</i>
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## Description

The assay sensitivity is the minimum number of copies that the digital PCR assay can detect. Users provide serial dilution results in the format of counts of positive and total reaction wells. The output is the estimated assay sensitivity and the copy number per well in the initial dilute.

**Usage**

```
digitalPCR(pos, neg, dilution, Nboot, single.copy = c("FALSE", "TRUE"), upper.copy=100)
```

**Arguments**

pos	a numeric vector of number of positive reactions in the order of dilutions
neg	a numeric vector of number of negative reactions in the order of dilutions
dilution	a numeric vector of folds of dilutions relative to the initial dilution
Nboot	number of bootstrapping
single.copy	character tells whether the assay is assumed single-copy sensitive. default "FALSE"
upper.copy	the upper bound of copy number in highest concentration

**Details**

the pos, neg and dilution vector must be in the same order from high to low concentrations.

**Value**

The returned value is a list of four components:

mean copy number	mean copy number
sd copy number	standard deviation of copy number
copy numbers	bootstrapped copy number estimates
thresholds	bootstrapped assay sensitivity estimates

**Author(s)**

Xutao Deng

**Examples**

```
#dilution at 1,2,4,8 fold
pos=c(221,97,39,14)
dilution=c(1,2,4,8)
neg=384-pos
#note in practice, set this 100 or larger
Nboot=10

result1=digitalPCR(pos, neg, dilution, Nboot)
print(paste(result1$"mean copy number", result1$"sd copy number"))
hist(result1$"thresholds",xlim=c(-2,10))

#the following example contains only 1 dilution
result2=digitalPCR(230, 355, 1, Nboot, "TRUE")
```

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digitalPCR-internal    *Internal functions*

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**Description**

Internal functions

**Author(s)**

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# Index

`bootstrapping (digitalPCR-internal)`, 3

`digitalPCR`, 1

`digitalPCR-internal`, 3

`likelihood (digitalPCR-internal)`, 3

`maximum.likelihood`

`(digitalPCR-internal)`, 3

`poisson.param (digitalPCR-internal)`, 3

`TL (digitalPCR-internal)`, 3