

# 4.4.2 - PCR Amplification

## Parameter

Parameter Name	Variable	Default Value	Parameter Range	Description
PCR_DISTRIBUTION		default	{default, none, file}	parameter specifies the name of a PCR distribution file, or 'default' to use a distribution with 15 rounds and 20 bins. A value of 'none' disables PCR amplification.
PCR_PROBABILITY	<div>Unknown macro: 'mathinline'</div>	0.7	<div>Unknown macro: 'mathinline'</div>	duplication probability in each step of the simulated PCR. The parameter value is only taken into account if GC_MEAN is 'NaN'.
GC_MEAN	$mean_{GC}$	0.5	NaN, $0 < mean_{GC} < 1$	mean of duplication probability distribution with respect to GC content; the distribution is approximated by a normal distribution. A value of 'NaN' disables the GC-dependency of PCR and employs the (constant) probability PCR_PROBABILITY
GC_SD	$SD_{GC}$	0.1	$0 < SD_{GC} < 1$	standard deviation of duplication probability distribution with respect to GC content

## Algorithm

The efficiency of the polymerase chain reaction (PCR) amplification is either specified by an universal success rate

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, or, by a normal distribution 

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 parameterized to capture GC preferential biases (default  $mean_{GC}=0.5$  and  $SD_{GC}=0.1$ ). Given  $p$ , the number of copies produced from a certain fragment is determined by random sampling under the cumulative binomial:

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with  $S$  denoting the PCR cycle and  $N$  the number of molecules. As default, we assume 15 PCR cycles ( $S=15$ ), and sample randomly the number of duplicates yielded by PCR amplification under the corresponding probability distribution  $P_{15}(N)$  for all possible values of  $N=[1;2^{15}]$ . The recursion terminates by

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