

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	Unknown macro: 'mathinline'	0.7	Unknown macro: 'mathinline'	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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