4.4.2 - PCR Amplification

Parameter

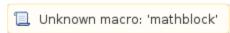| Parameter Name	Variable	Default Value	Parameter Range	Description
PCR_DISTRIBUTION		default	{default, none, file}	parameter specifies the name of a PCR distribution file, or 'default' to use a distribution with 15 rounds and 20 bins. A value of 'none' disables PCR amplification.
PCR_PROBABILITY	Unknown 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 distribuiton 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 distribuiton with respect to GC content

Algorithm

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

Unknown macro: 'mathinline' , or, by a normal distribution Unknown macro: 'mathinline' 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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