

Table 1S  
Parameters used in synthetic signal generator

Parameter	description
$nn$	The number of nucleosomes we want to add to the synthetic signal. Signals with 200 nucleosomes have been used. Note that higher values of $nn$ requires higher computational cost when using the <i>HMM</i> .
$nl$	The length of a nucleosome (we know that in real case a nucleosome is 150 base pairs long). Nucleosome length has been set to 150 because this value corresponds to the real length of a nucleosome.
$\lambda$	Mean of the poisson distribution used to model the expected distances between adjacent nucleosomes. This value has been set to 200 in order to avoid nucleosomes overlap for the final purpose of making a more precise comparison by using only well positioned nucleosomes.
$r$	The resolution of a single microarray probe. The resolution of microarray has been set to 50, this value is the same of the <i>Saccharomyces cerevisiae</i> microarray dataset.
$o$	The length in base pairs of the overlapping zone between two consecutive probes. The overlap of microarray has been set to 20, this value is the same of the <i>Saccharomyces cerevisiae</i> microarray dataset.
$nr$	The number of spotted copies (replicates) of nucleosomal and genomic DNA on each probe of the microarray. It has been set to 100, because higher values don't give more realistic signals.
$dp$	The percentage of the delocalized nucleosomes over the total number of nucleosomes. It has been set to 0 because we are interested on the performance over the well positioned nucleosomes class.
$dr$	It represents the range (in base pairs) which limit the delocalization of a nucleosome in each copy of $nr$ . This parameter is useless in all the performed experiments because we have generate only well positioned nucleosomes.
$nsv$	The variance of the green signal in each probe, even in absence of nucleosomes due to the cross hybridization. This variance follows a normal distribution with mean 0.1. This value is set to 0.01 to guarantee a low but existence of green intensity in each spot even in absence of nucleosomes due to the cross hybridization.
$pur$	The percentage of DNA purification, which is the probability that each single DNA fragment of the $nr$ copies appears in the microarray hybridization. It has been set to 0.8 by biological consideration.
$ra$	Relative abundance between nucleosomal and genomic DNA. It has been set to 4, this value arises by looking min and max value of the real signal. In particular, it results that green intensity in the maxima point of the real signal is 4 times greater then red intensity.
$SNR$	The linear signal to noise ratio of the synthetic signal to generate. Note that the noise is assumed to be gaussian. It has been set to 1,2,4,6,8,10 on each experiment respectively.