CORRECTING FOR PHOTOBLEACHING IN SINGLE MOLECULE TRACKING EXPERIMENTS

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Single molecule tracking (SMT) has recently developed into a powerful technique for studying interactions of transcription factors (TF) with their chromatin response elements *in vivo*. However, loss of fluorescence due to photobleaching, both reversible and irreversible leads to a reduction in the lengths of some tracks, and can therefore cause an underestimation of residence times. With the aid of simulations, we have developed a new computational correction procedure that can account for reversible and irreversible photobleaching, and investigated the influence on the sample size on the need for such corrections. Finally, we have applied our correction method to the study of Ace1p and two other DNA-binding proteins, histone H3 (*HHT1*) and heat shock factor (*HSF1*) in the budding yeast *Saccharomyces cerevisiae*, and show that the non-specific residence times of these very different DNA-binding proteins are surprisingly similar.