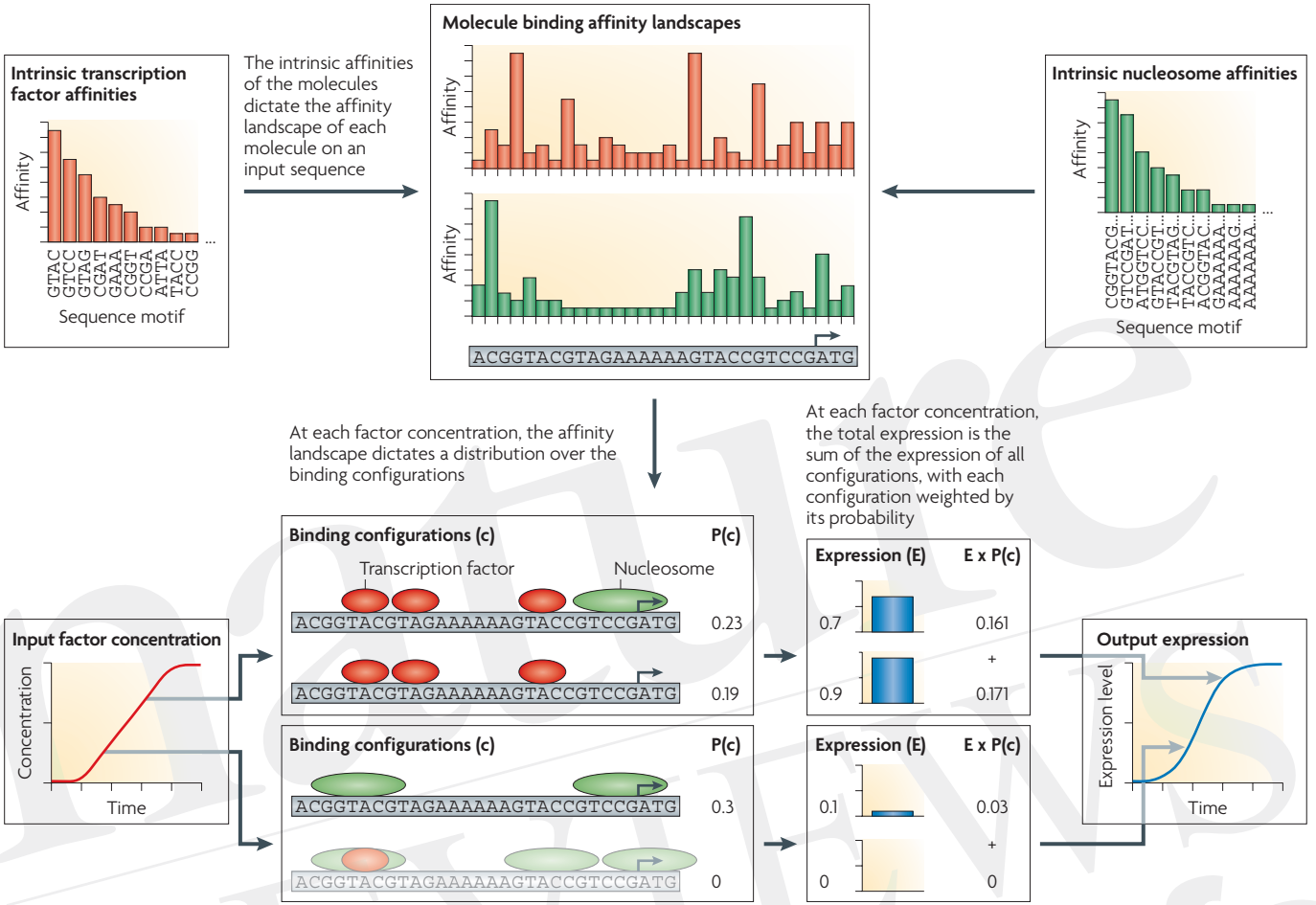

Figure 1 | **Overview of quantitative models for computing expression from DNA sequences.** Flow diagram of the computational approach for a simplified regulatory sequence with nucleosomes and one transcription factor as the input binding molecules. Each of the input molecules has intrinsic binding affinities for every possible sequence of length *k* (top panels, left and right), in which *k* is the number of base pairs recognized by the binding molecule. These intrinsic molecule affinities dictate how every DNA sequence is 'translated' into a unique binding affinity landscape for each molecule along the sequence (top panel, centre). For each factor concentration (c; bottom panel, left), the model uses these binding affinity landscapes to compute a probability (P) distribution over configurations of bound molecules (see BOX 1 for details); a small subset of these configurations is illustrated (bottom panel, centre). Configurations in which two bound molecules overlap are not allowed owing to steric hindrance constraints, thereby modelling binding competition between molecules (see the bottom configuration, which has a probability of zero). Finally, each configuration results in a particular transcriptional output (bottom panel, right); the final expression is then the sum of the expression contribution of each configuration, weighted by their probability.