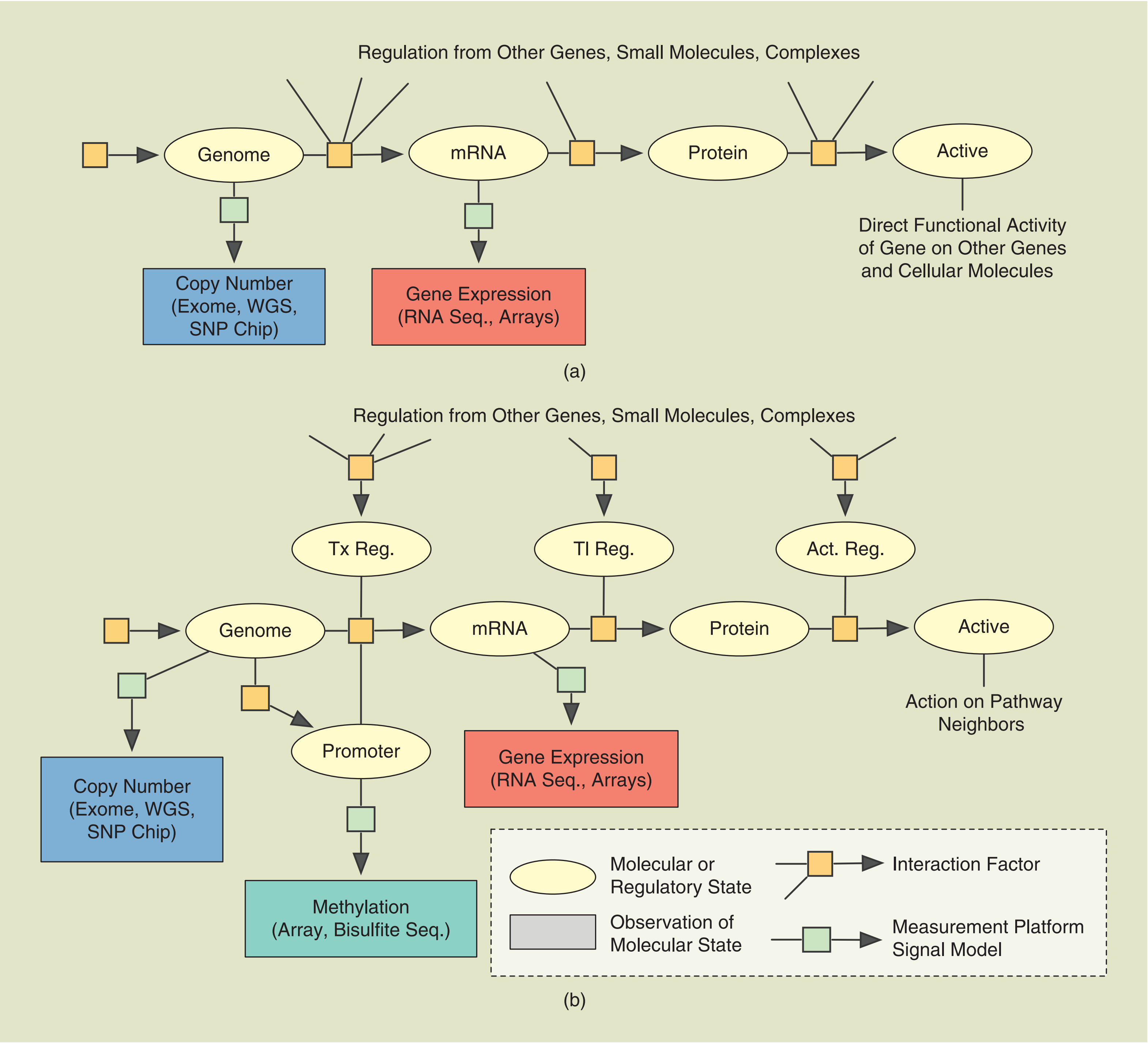

[FIG7] **The Paradigm model was meant to integrate many types of functional genomic information with a pathway structure. Multiple information states of each gene are modeled via a probabilistic graphical model representation of the central dogma of molecular biology. Interactions between genes, complexes, and small molecules are modeled with factors that connect separate gene dogmas. Each factor describes the relationship between connected variables, with the arrow indicating the directionality of the conditional probability table. (a) The simplest dogma, used for aCGH and transcriptomic data. (b) A more complex dogma that includes methylation information.**