

Assessing potential miRNA targets based on a Markov model

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ABSTRACT. At present, studies on microRNA mainly focus on the identification of microRNA genes and their mRNA targets. Although researchers have identified many microRNA genes, relatively few microRNA targets have been identified by experimental methods. Computational programs designed for predicting potential microRNA targets provide numerous targets for experimental validation. We used a Markov model to examine base-pairing binding patterns of known microRNA targets. Using this model, potential microRNA targets in human species predicted by four well-known computational programs were assessed. Each potential target was assigned a score reflecting consistency with known target binding patterns. Targets with scores higher than the cutoff value would be identified by our model. The predicted targets identified by our model have base-pairing binding pat-

terns consistent with known targets. This model was efficient for evaluating the extent to which a potential target was accurately predicted.

Key words: Markov chain model; Machine-learning method; MicroRNA target prediction; Maximum likelihood estimation; Potential target assessment