

# Machine Learning E16 - Handin 3

## Hidden Markov Model for Gene Finding in Prokaryotes

Group 22

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Table 1: *text*

validation	Approximate correlation coefficient		
	C	R	Both
Genome 1			
Genome 2			
Genome 3			
Genome 4			
Genome 5			
Average			

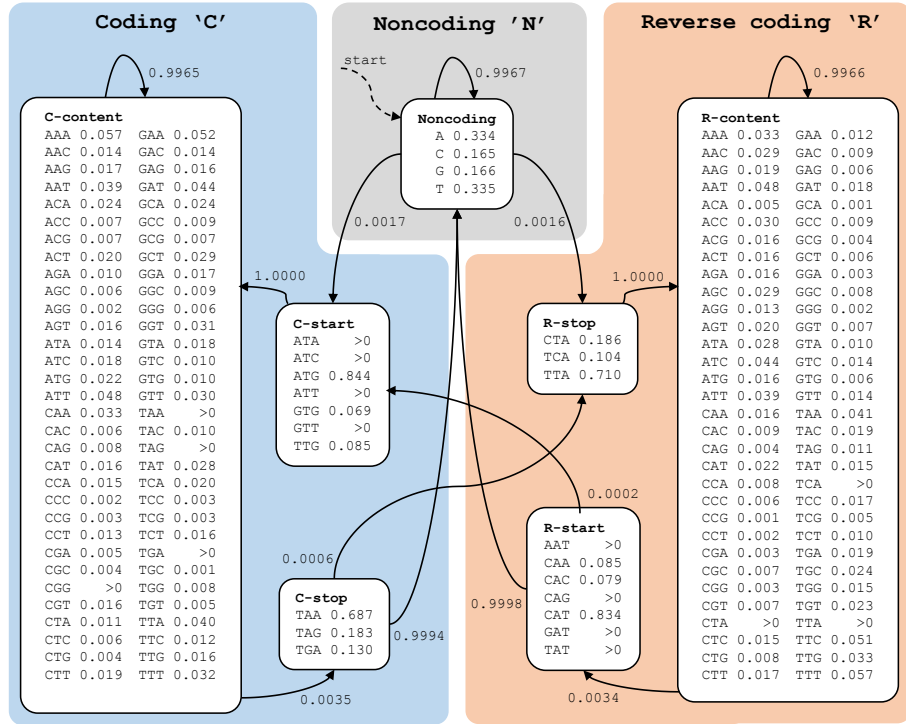


Figure 1: *State graph for out HMM for genome annotation by explicitly matching codons within coding areas, and enforcing certain start and stop codons. Transition and emission probabilities gained by counting annotated data.*