more\_turing\_biology.docx

to explore new models of computation in biology

Alternative Splicing (see http://localhost/Archives/Alternative\_Splicing\_Notes.txt)

Alternative splicing might skip, shuffle, or shift exons and might retain introns from pre-mRNA. It has major (99%) and minor (1%) pathways, differentiated by slightly different splicosomes. Trans-splicing in C. elegans adds 22 nt fragments, SL1 (57%) and SL2 (15%) to the 5' end of mRNA precursers. Polyadenylation mirrors trans-splicing, but always adds a 3' poly-A tail.

How can I combine these transformations to form useful algorithms? What are the conditions, rates, and fidelities of shuffling, skipping, shifting and so on? How can we inject and extract strands from this process?