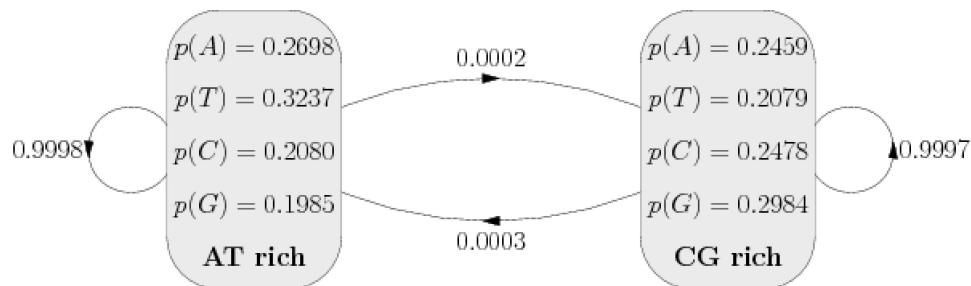


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## Tutorial 2: Week 3-5

- This will be marked in the lab session in week 5 by me
- 1. Write a program to implement Needleman-Wunsch for proteins
  - You will need the [blosum50](#) scoring matrix
  - You can use any programming language
  - Run this on HEAGAWGHEE versus PAWHEAE
  - Compare this to page 23 in [lecture 5](#)
  - Match the protein sequence SALPQPTTPVSSFTSGSMLGRTDTALTNTYSAL with PSPTMEAVTSVEASTASHPHSTSSYFATTYYHLY
- 2. Modify your program to implement the Smith-Waterman algorithm
  - Again run this on HEAGAWGHEE versus PAWHEAE
  - Compare this to page 5 in [lecture 6](#)
  - Find the best local match between MQNSHSGVNQLGGVFNVRPLPDSTRQKIVELAHSGARPCDISRILQVSNGCVSKILGRY and TDDECHSGVNQLGGVFNVRPLPDSTRQKIVELAHSGARPCDISRI
- 3. We are going to test the BLAST algorithm
  - Download the Pax6 protein for the mouse by going to <http://www.uniprot.org/uniprot/P63015> choose the "Format" tab and choose the FASTA (canonical) format
  - Do the same for the eyeless protein for the fruit fly <http://www.uniprot.org/uniprot/O96791>
  - Perform a BLAST sequence comparison using the web service at <https://blast.ncbi.nlm.nih.gov>
- 4. Program the following HMM to generate CG rich regions



- 5. Write a viterbi algorithm for finding the most likely CG regions and find a way of drawing this
- 6. Run this on the genome for the [phase lambda](#) or [here](#)

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