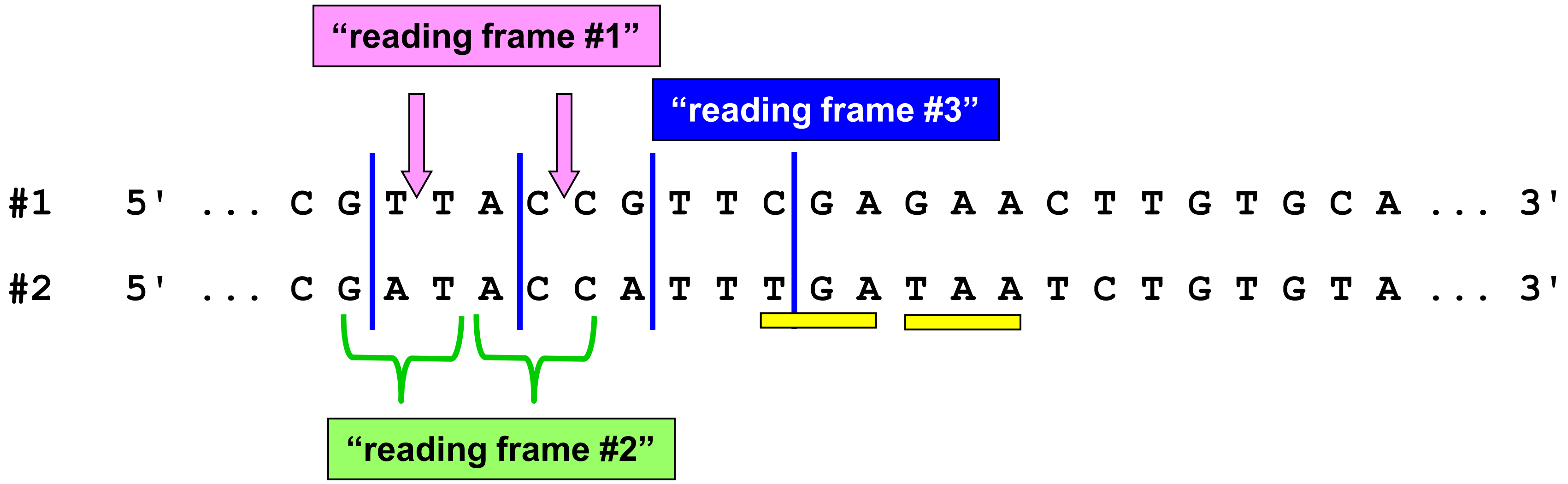
Practice question #1



If protein-coding sequence under strong functional constraint…

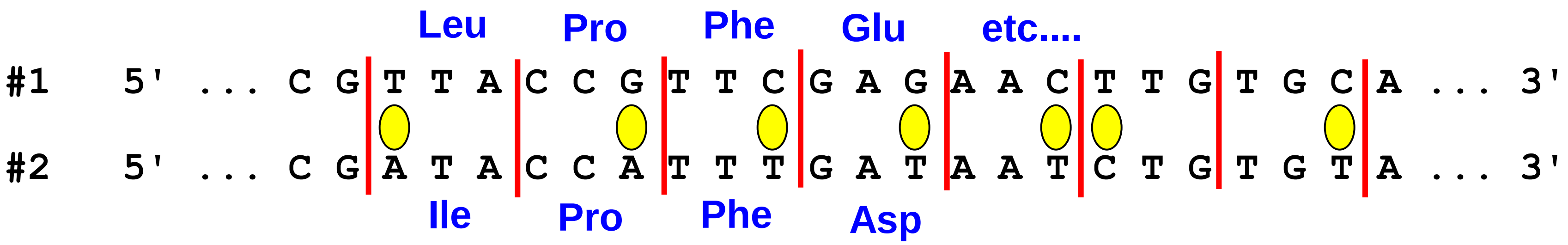
might expect (mostly) silent nt substitutions between #1 and #2…

and conservative amino acid substitutions…

Could look for an initiation codon, but it might be further upstream….

So divide into possible reading frames…

Any potential stop codons (to exclude any frames)??



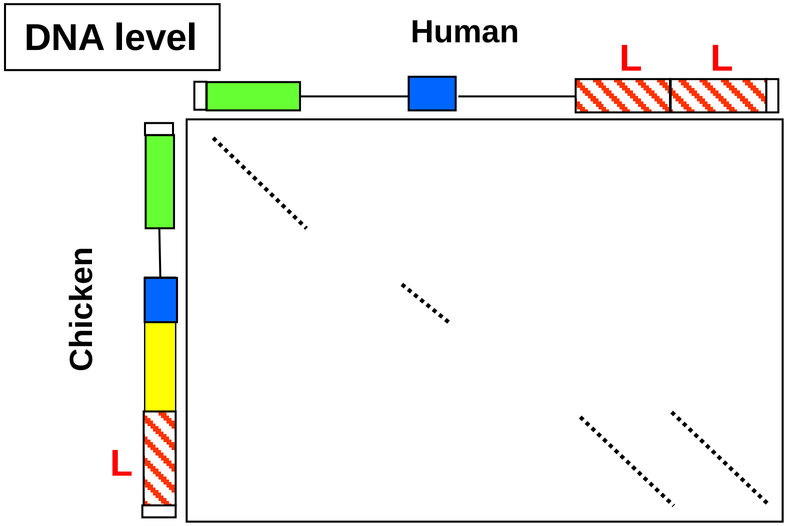
Practice question #3

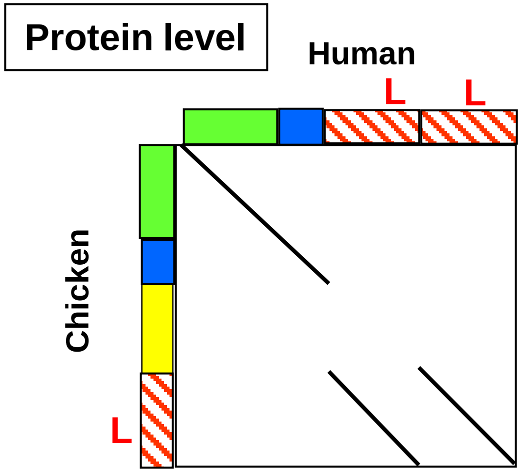
Approximately 450 non-synonymous sites

Practice question #4

About 52% amino acid identity

Practice question #5



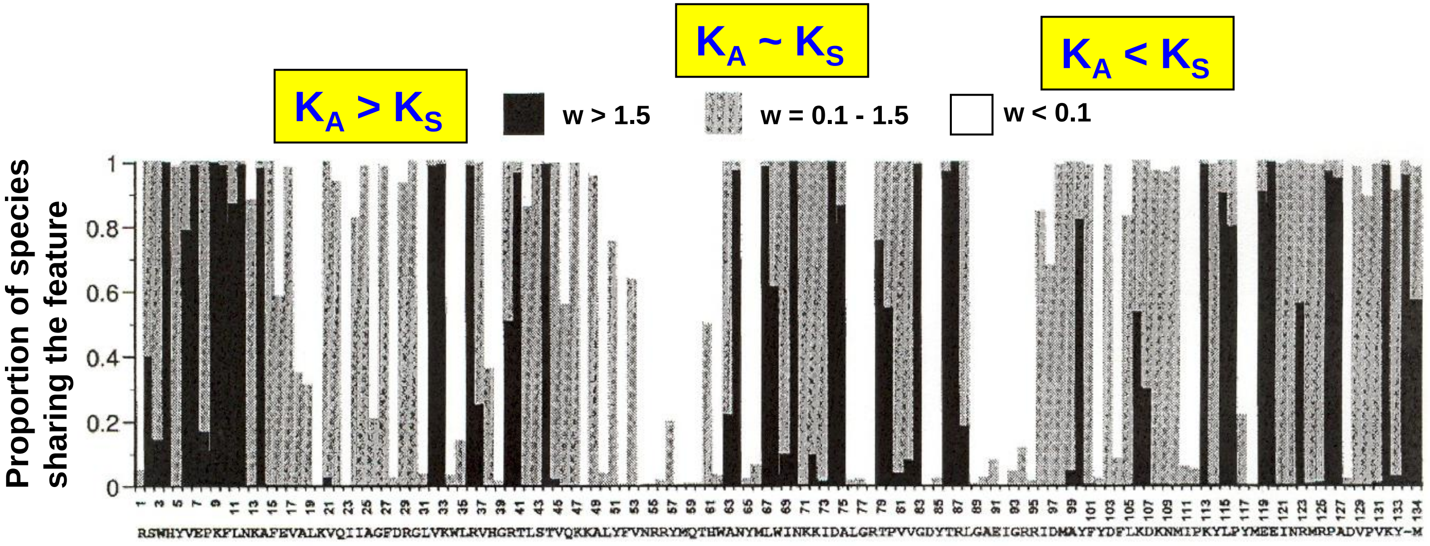


Assumption: human exon 2 closely related to 5’ end of (longer) chicken exon 2. What if this was not the case?

Note: white boxes represent UTR regions & coloured blocks are coding regions

Practice question #6

As mentioned in class, this figure is taken from a paper dealing with positive selection seen for abalone sperm cell lysin evolution (see p.123 in text)



Comparison of amino acid sequences of protein E (actually lysin) from 25 abalone species

Yang et al. *Mol Biol Evol* 17:1446, 2000

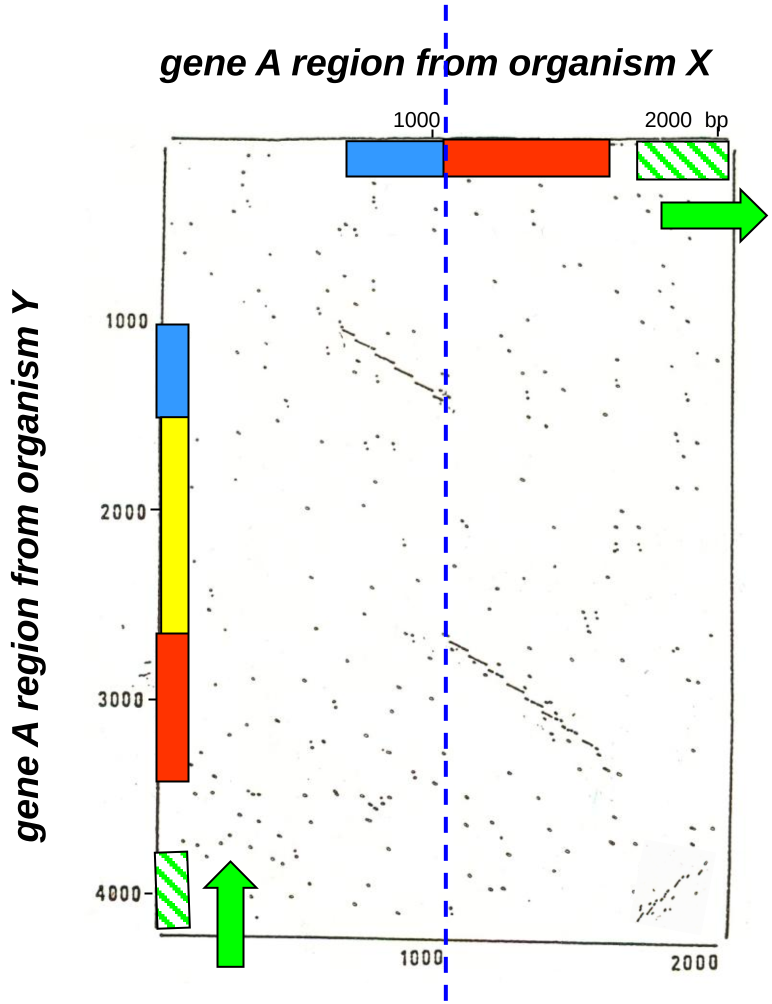
- **wide variation seen in selective pressure on amino acid sites along length of protein**

> Many amino acid sites are clearly under strong purifying selection, with the nonsynonymous rate close to 0, while some other sites are under diversifying selection, with the nonsynonymous rate elevated to more than three times the synonymous rate.

- **N-terminal region shows cluster of sites undergoing rapid change (adaptive evolution)**

vs. several other regions (eg. amino acid positions 54-60) which show strong functional constraint (important for structural or enzymatic activity of protein?)

Practice question #7



What might yellow region be?

additional protein domain...?

or ***intron*** *…?*