

## BIOS 741, week 11, discussion questions

- Dujon et al. (2004) found that, in each of the four yeast genomes that they sequenced, the GC content of the protein coding sequences was correlated with the GC content of the genome, but was also more GC-rich than the genome. What is the most likely explanation for this result?
- Dujon et al. (2004) found that, in some cases orthologous proteins in yeast species shared < 60% amino acid identity, but paralogous proteins shared > 60% amino acid identity. What is the most likely explanation for this result?
- King et al. (2008) reported that the *M. brevicollis* genome contained many peptide motifs previously thought to be specific to metazoans (EGF repeats, ankyrin repeats, immunoglobulin repeats, etc) but did not have these motifs in the same combinations in individual proteins, nor did they have the cellular functions with which these motifs are associated in metazoans. What is the most likely explanation for this result?
- King et al. (2008) concluded that intron gain in many genes preceded the origin of the metazoans. How can homologous introns be identified within homologous genes? How can intron gain be distinguished from intron loss? How can introns be gained (plausible molecular mechanisms)?