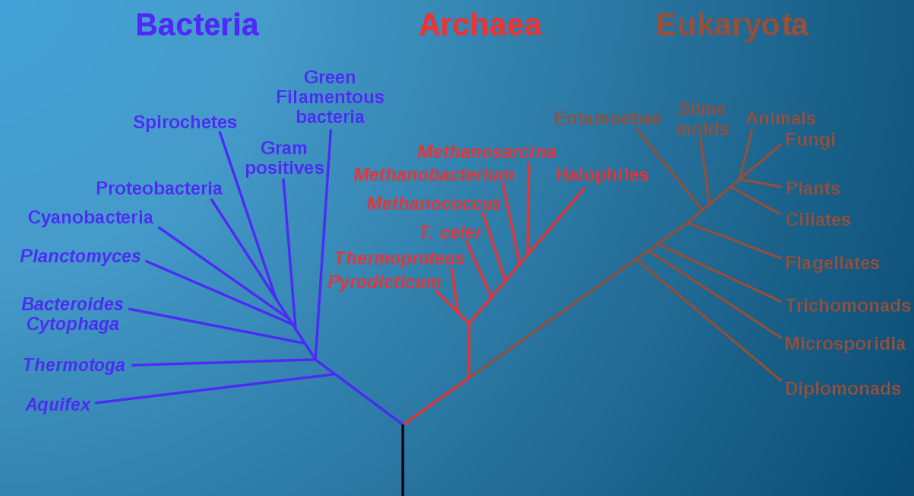
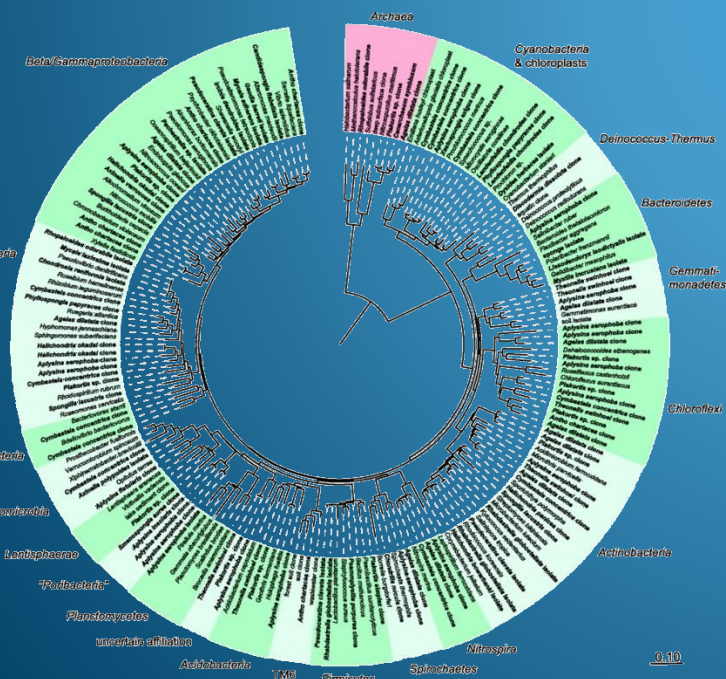
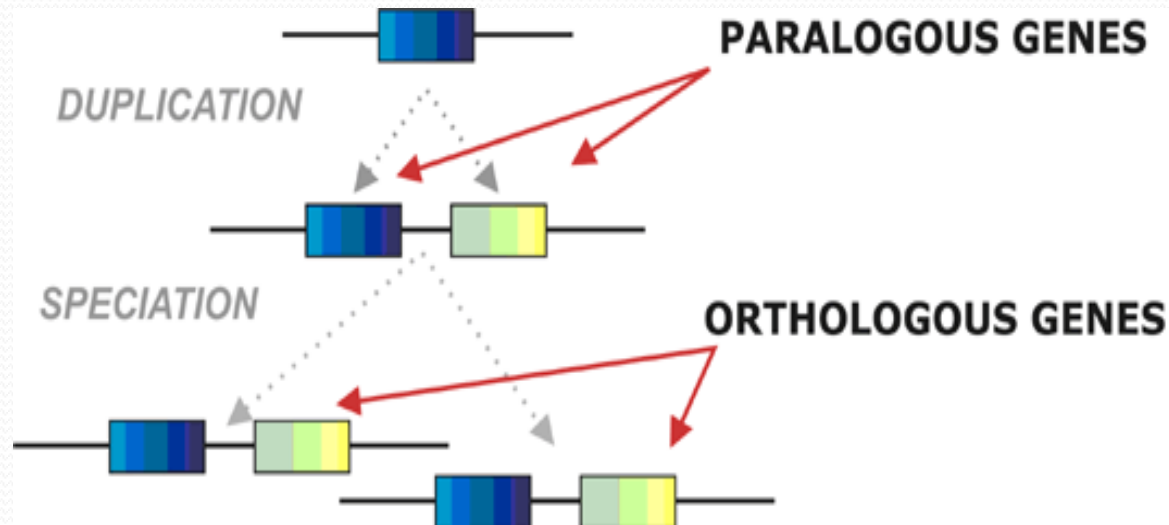


Application of bioinformatics in evolutionary analyzes



- The genes identification of different species occurs most often by searching for homologues.
- Orthologes are genes that share a common ancestor, and are the most commonly sought homologs for genes in single copy.
- Paralogs result from duplication events.

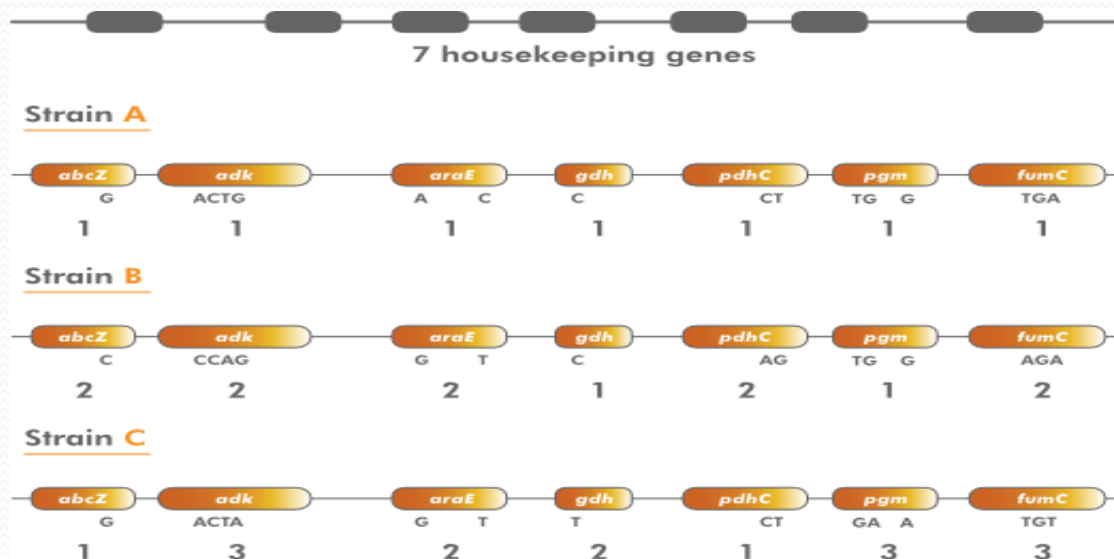


- Many of the problems with the identification of orthologs arise from the difficulties in predicting genes / annotating genomes.
- Typically, 3 approaches are used to identify and annotate genes in the genome:
 1. cis – alignment;
 1. trans – alignment;
 1. *de novo* predictions (programmes like GENSCAN, N-SCAN –in USCS browser (<http://genome.uscs.edu>)).

- The identification of orthologs occurs mainly through homology and gene synteny.
- The orthologes require complete information.
- Traditionally, the classification of orthologes is either by reciprocal best fit or reciprocally of the least distance.
- The main procedure involves collecting all genes from two species and comparing them.

- Monophylic group; monophylic alignment - based on 16S rRNA gene sequence assays.
- As an alternative to 16S, the rRNA genes are those for the 23S rRNA.
- There are alternative protein tags that could be used to reveal genealogy. For instance, the products of the genes *rpoB*, *dnaJ*, *recN*, *recA*, *dnaK*, *hsp60*, *gyrB*, *cpn60* and others.

- An alternative approach is to use individual housekeeping genes for genealogy in multilocus sequence analysis (MLSA).
- MLSA directly measures the variations of the DNA sequence in a set of housekeeping genes and characterizes the strains in their unique allele profiles.



- Evolutionary relationships between different species can be represented by phylogenetic / evolutionary tree. It is based on similarities and differences in their physical or genetic characteristics.

