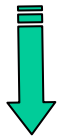
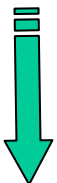


Genomic data



Functional genomics



Comparative genomics



Horizontal comparative genomics: comparing the same type of data in multiple species



Vertical comparative genomics: comparing different types of genomic data from a single species

Interpreting the functional content of a given genomic sequence is one of the central challenges of biology today. The rapid development of freely available genomic databases promises to transform every field of biology.

Functional genomics data derived from transcriptomics and proteomics enable us to have an unexpected view of global cellular activities. However, these data still miss a lot of information because protein annotation is still limited and the information on protein function remains unreliable.

The overlap of information from various genomics datasets increases the reliability of the gene function prediction. In simple organisms it is more easy to verify the function of newly predicted protein sequences.

Problems for horizontal genomics are:  
Which species should we compare? Which tools should we use?

Problems for vertical genomics are: which genome structures should we compare ? Which tools should we use?

Comparative genomics already gave good results using bacterial genomes because of their simplicity and the large number of sequence available. Also the few known mammalian genomes have been studied by comparative genomics, however many genes still remain with unknown function and protein interactions are still unknown.

Now many unicellular eukaryotes besides yeasts have been sequenced and they can provide a lot of new information. Most of them are parasitic protozoa like: Trypanosoma, Leishmania, Plasmodium, Toxoplasma etc. Others are free living protozoa, such as: Dictyostelium, Tetrahymena, Paramecium. They are very helpful for comparison and for validation of data by gene manipulation approach.

The parasites genome projects revealed important metabolic pathways which can be targeted to develop antiparasite drugs and antigens for potential vaccines. However, many other fruitful results can be obtained using comparative genomics in this field, for example regulation of transcription is still quite unknown in these organisms.