

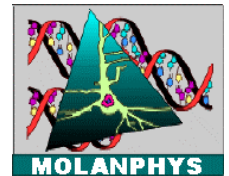
Tim Hulsen

10-08-1979

1997-2001 student in Biology at the University of Nijmegen

'stages':

02/2000-08/2000:  
Molecular Animal Physiology  
(Prof. Dr. Gerard Martens)



10/2000-04/2001  
Centre for Molecular and Biomolecular Informatics  
(Prof. Dr. Gert Vriend)



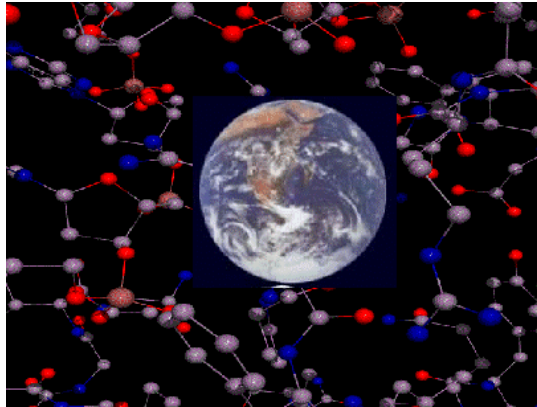
2001-2002 Bioinformatician at NV Organon, Oss



2002-? PhD student in Bioinformatics at the CMBI  
Computational Genomics ("Comics")  
(Prof. Dr. Martijn Huynen)  
in cooperation with Organon

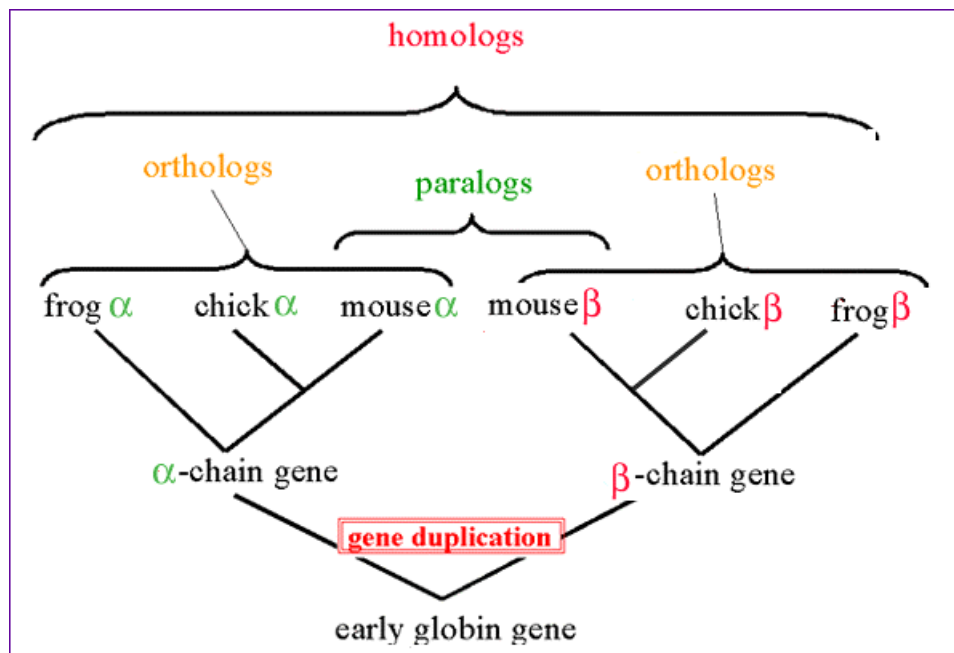


## PhD project: “Protein World”



- Large scale computation at SARA (Amsterdam) carried out by GENE-IT and Organon
- Sequence comparison of all currently known and predicted proteins (106 organisms; >400,000 proteins; ~90 billion pairwise comparisons)
- Algorithm used: not the commonly used BLAST and FASTA, but Smith-Waterman: slower but more reliable!
- Z-values calculated for the best-matching proteins to test the statistical significance
- Updated ~ 2 times a year with ‘new’ proteomes (e.g. rat, rice)
- Made available to the community through BioASP ([www.bioasp.nl](http://www.bioasp.nl)) the new Dutch bioinformatics portal
- My job: using these data to define orthologous and paralogous relations as good as possible and combine this information with expression data, chromosomal position data, etc.

## Orthology / paralogy



Orthologous proteins: proteins in different species that derive from a common ancestor, after a speciation. Often have the same function!

Paralogous proteins: proteins within a single species that diverged by gene duplication.

Especially orthology can be very important in sequence annotation:  
Function of human protein unknown?

Check its mouse ortholog -> its function is **probably** the same

Orthologous relations between 9 eukaryotes (Human, mouse, fly, worm, yeast, etc.) already defined through a method using multiple alignments and phylogenetic trees

By combining orthology with things like expression data, gene order data, etc. the **probability** mentioned above can be made higher