**Exercise on comparative genomics analyses**

The datasets can be found at: https://drive.google.com/drive/folders/1AFOuRtZS5uJ0rpQHfntsKudjuIEtw5L8?usp=sharing

The main objective of this exercise is to reproduce by yourself the comparative genomics analyses learned during these sessions. First, you will estimate the birth-and-death rate and conduct evolutionary inferences of the Odorant Binding protein gene family in 18 Hexapoda species (Vieira and Rozas 2011) using the CAFE package. Using as input the table with OBP gene counts “obp\_all.hexapoda.tsv” and the phylogenetic tree “hexapoda.nwk”, answer the following questions:

Which is the ancestral state of the OBP gene family size in the phylogeny?

Which is the general mode of evolution of the OBP gene family across Hexapoda? Has it undergone different dynamics across the surveyed species?

Now, you can explore if the birth-and-death rate would differ under a two-model lambda with different rates for *Drosophila* and non-*Drosophila* hexapods. Using the previous files, in addition to the newick tree with the 2-lambda model “hexapoda\_2lambdamodel.nwk” you would be able to shed light into OBP evolution [Note: as an exploratory analysis, you only need to run the model and see the results, but there is no need to test for signification by using simulations]:

Are there differences in the OBP dynamics between *Drosophila* and the other Hexapoda species surveyed? Is the birth-and-death process constant across the phylogeny?

We have learnt that the OBP gene family follows a birth-and-death model of evolution where, in summary, new copies arise by tandem duplication and they can gain new functions or be lost by pseudogenization. Now you will explore the functional constraints in new duplicated copies by using a codon alignment of five *Drosophila melanogaster* copies (OBP56f, OBP56g and OBP56h are duplicated genes, OBP19a and OBP76b are used as outgroup sequences). Using HyPhy absrel and meme models in the “Obp\_aln.fas” and “Obp\_tree.nwk” files, you should be able to study the presence of functional constraints and positive selection in the codon alignments:

Which is the *d*N/*d*S ratio in the three duplicated OBP genes? Are there different functional constraints among copies? Which is the most likely reason of this observation?

Is there any specific site under positive selection?

**Bibliography**

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