Assignment 4.1

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

((((((((((dmel<5>_52:5,(dsec<1>_51:1,dsim<0>_53:1)<4>_52:4)<7>_52:8,(dyak<3>_55:10,
dere<2>_50:10)<6>_52:3)<11>_52:31,dana<10>_50:44)<15>_50:11,(dpse<9>_45:1,dper<8>_45:1)
<14>_45:54)<19>_49:7,dwil<18>*_62:62)<21>_49:1,((dmoj<13>_43:31,dvir<12>_41:31)<17>_44:12,
dgri<16>_46:43)<20>_46:20)<23>_49:187,agam<22>*_83:250)<25>_44:10,bmor<24>_46:260)
<27>_43:20,tcas<26>_49:280)<31>_40:20,amel<30>_21:300)<33>_36:50,(phum<29>*_5:260,
apis<28>_18:260)<32>*_21:90)<34>_30;

The ancestral state (34) has a size of 30.

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

Overall, the size of gene families across Hexapoda is changing because the p value is significant so we can reject the null hypothesis that there is no change across the branches. 6 species out of 18 are expanding, 7 species are contracting and 5 species do not change size.

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?

Yes, there is a difference since the 2 lambda model has a higher base family likelihood than the single lambda model. The birth-and-death process is different between the two groups since the 2 lambda model finds two different lambda values for them.

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

The ratio is 0.2284, so there are functional constraints among the copies. Duplicates of a gene can have different functional constraints on them. For example, if the structure of a protein created by a gene is crucial, as long as as one of the duplicate genes does not mutate and maintains its structure, the other can mutate a lot since the original function of the gene is preserved from the first duplicate.

Is there any specific site under positive selection?

Codon 72 is under positive selection