

Assignment 4: Comparative Genomics

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

Answer:

From the 5 run of the CAFE5 commands, below the chosen lowest lnL:

Model Base Final Likelihood (-lnL): 81.0423

Lambda: 0.003333333059575

In addition, from the treefile, the ancestral state was inferred to have 30 copies of OBP genes

2. Which is the general mode of evolution of the OBP gene family across Hexapoda? Has it undergone different dynamics across the surveyed species (i.e.: Is the OBP gene family expanded or contracted in any specific lineage)?

Answer:

The global evolution rate across Hexapoda (lambda) is 0.003.

However, if we see carefully, amel, phum and aphs have contraction on the gene count while others (drossophila) expanded

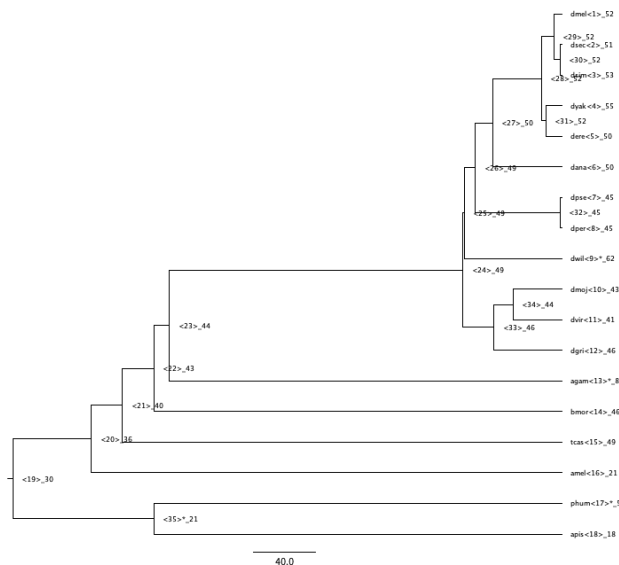


Figure 1: Inferred .tre File

3. 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?

Answer:

From the 5 run of the CAFE5 commands, below is the lowest lnL:

Model Base Final Likelihood (-lnL): 79.898

Lambda: 0.0053475325429573, 0.003333194129154

From the result above, we can see that the birth-and-death rate is not constant across *Drosophila* and the others. In addition, *Drosophila* tend to have higher birth-and-death rate which is expected.

4. Which is the dN/dS ratio in the three duplicated OBP genes (OBP56f, OBP56g and OBP56h)? Are there different functional constraints among these copies? Which is the most likely reason of this observation?

Answer:

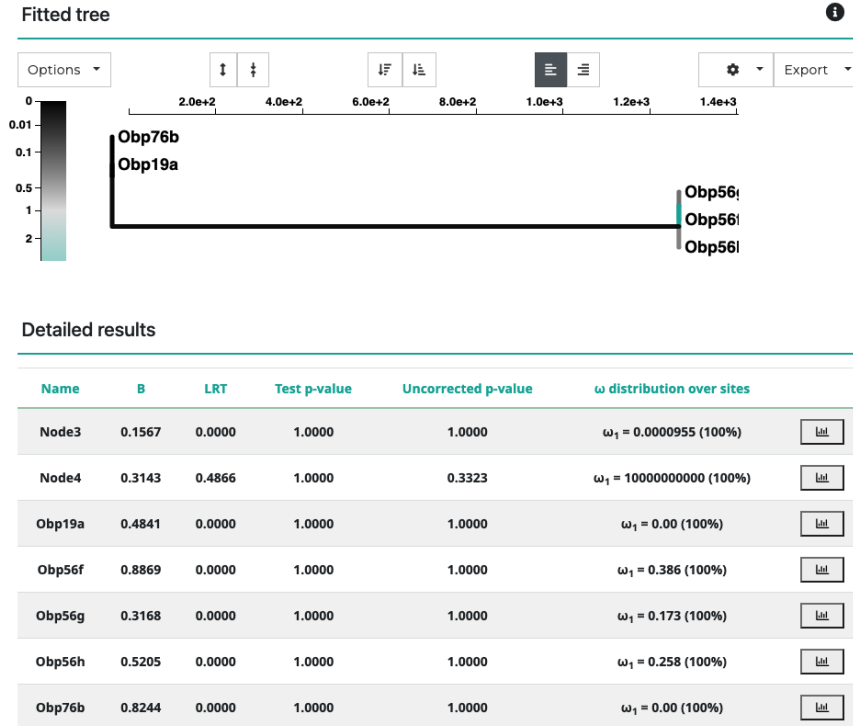


Figure 2: aBSREL Result

Based on the aBSREL analysis, the three duplicated genes have (ω) values of 0.386, 0.173, and 0.258, respectively. Furthermore, the available evidence does not sufficiently support the notion that these genes have undergone positive evolution (p-value=1), potentially attributable to various functional constraints. One potential explanation for this phenomenon could be attributed to different functions of these genes in the food perception but they bind into the same ligand.

5. Is there any specific site under positive selection?

Answer:

Yest there is. Figure 3 shows four sites that which exhibit positive selection at significant level of 10%.

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Export Table to CSV

Site ↕	Partition ↕	α ↕	β^1 ↕	p^1 ↕	β^+ ↕	p^+ ↕	LRT ↕	p-value ↕	# branches under selection ↕	Total branch length ↕	MEME LogL ↕	FEL LogL ↕	FEL α ↕	FEL β ↕
72	1	0.00	0.00	0.13	353.55	0.87	5.19	0.03	0.00	0.00	-21.63	-19.04	0.07	1.36
171	1	0.00	0.00	0.47	69.19	0.53	3.61	0.08	0.00	0.00	-12.18	-10.34	0.16	1.13
95	1	0.19	0.19	0.67	94.49	0.33	3.23	0.09	1.00	0.00	-16.78	-15.19	0.20	0.61
109	1	0.00	0.00	0.26	162.80	0.74	3.41	0.09	0.00	0.00	-16.99	-15.39	0.20	0.00
67	1	0.00	0.00	0.57	63.16	0.43	3.03	0.11	2.00	0.00	-17.39	-15.20	0.11	1.38
99	1	0.66	0.00	0.79	156.20	0.21	2.71	0.12	1.00	0.00	-17.07	-14.04	0.05	1.37
53	1	0.00	0.00	0.16	35.40	0.84	2.27	0.16	0.00	0.00	-20.03	-19.19	0.43	8.20
160	1	0.00	0.00	0.00	2.62	1.00	2.20	0.16	0.00	0.00	-18.45	-18.45	1.00	0.00
81	1	0.00	0.00	0.00	12.24	1.00	1.73	0.21	0.00	0.00	-19.76	-19.39	0.69	0.00
156	1	0.00	0.00	0.00	0.43	1.00	1.73	0.21	0.00	0.00	-11.75	-11.75	1.00	0.00
21	1	0.00	0.00	0.00	610.95	1.00	1.65	0.22	0.00	0.00	-20.76	-19.94	0.44	1.36
68	1	0.66	0.00	0.74	5.15	0.26	1.65	0.22	1.00	0.00	-15.82	-14.10	0.18	0.58
124	1	0.00	0.00	0.03	4.38	0.97	1.61	0.22	0.00	0.00	-9.11	-8.95	0.85	0.00
167	1	0.00	0.00	0.00	2.02	1.00	1.68	0.22	0.00	0.00	-13.80	-13.80	1.00	0.00
97	1	0.00	0.00	0.07	4.90	0.93	1.61	0.23	0.00	0.00	-13.65	-13.12	0.59	0.00

Figure 3: MEME Result