

Samples	Source	#samples	#OTUs	best-fit $m$	$R^2$		AIC		Reference
					neutral	neutral	neutral	binomial	
<i>Caenorhabditis elegans</i>									
natural samples	natural	22	193	0.03	0.37	-673.2	-452.5		[1]
lab samples	lab	34	106	0.01	0.33	-330.0	-208.2		
<i>Ircinia oros</i>									
Spain, Barcelona	natural	11	1121	0.41	0.6	-5391.47	-4966.26		[2]
<i>Sarcotragus fasciculatus</i>									
Spain, Barcelona	natural	12	735	0.83	0.81	-3552.82	-3165.09		[2]
<i>Carteriospongia foliascens</i>									
Australia, Davies Reef	natural	15	939	0.36	0.6	-5435.40	-5007.39		[2]
Australia, Fantome Island	natural	14	728	0.81	0.79	-3740.45	-3336.08		
Australia, Orpheus Island	natural	15	750	0.86	0.8	-3987.01	-3539.84		
Australia, Green Island	natural	13	774	0.47	0.59	-3846.0	-3542.79		
Australia, Torres Strait	natural	7	336	0.78	0.58	-1410.75	-1244.0		
<i>Mus musculus</i>									
natural samples	natural	69	281	0.11	0.84	-1217.97	-998.15		[3]
lab samples	lab	54	136	0.18	0.82	-536.30	-452.48		
<i>Nematostella vectensis</i>									
1 day post fertilization (dpf)	lab	6	226	0.23	0.46	-738.68	-655.06		[4]
4 dpf	lab	15	149	0.33	0.67	-521.62	-479.29		
40 dpf	lab	12	155	0.09	0.59	-502.39	-413.96		
123 dpf	lab	12	195	0.39	0.69	-678.72	-623.49		
385 dpf	lab	20	225	0.17	0.58	-766.93	-679.74		
401 dpf	lab	8	120	0.7	0.74	-446.34	-402.59		
<i>Hydra vulgaris</i>									
0.5 weeks after hatching (wah)	lab	8	699	0.6	0.54	-2527.91	-2289.35		[5]
2.5 wah	lab	8	248	0.28	0.44	-820.92	-756.19		
5 wah	lab	8	242	0.53	0.45	-1129.85	-1041.28		
9 wah	lab	8	257	0.5	0.43	-833.46	-765.88		
15 wah	lab	8	140	0.45	0.59	-466.20	-432.55		
<i>Aurelia aurita</i>									
control	lab	5	163	0.91	0.69	-624.96	-538.45		[6]
quorum quenching (QQ)	lab	18	391	0.62	0.85	-1716.09	-1532.6		
Environment									
Compost	natural	65	587	0.48	0.87	-2690.26	-2491.77		[1]
Seawater	natural	16	2518	0.62	0.7	-12345.33	-11113.17		[2]
Sediment	natural	12	3796	0.77	0.47	-16658.27	-14665.48		[2]

## References

- [1] Dirksen P, Marsh SA, Braker I, Heitland N, Wagner S, Nakad R, et al. The native microbiome of the nematode *Caenorhabditis elegans*: gateway to a new host-microbiome model. *BMC Biology*. 2016;14(1):38.
- [2] Thomas T, Moitinho-Silva L, Lurgi M, Björk JR, Easson C, Astudillo-García C, et al. Diversity, structure and convergent evolution of the global sponge microbiome. *Nature Communications*. 2016;7:11870.
- [3] Wang J, Kalyan S, Steck N, Turner LM, Harr B, Künzel S, et al. Analysis of intestinal microbiota in hybrid house mice reveals evolutionary divergence in a vertebrate hologenome. *Nature Communications*. 2015;6:6440.
- [4] Mortzfeld BM, Urbanski S, Reitzel AM, Künzel S, Technau U, Fraune S. Response of bacterial colonization in *Nematostella vectensis* to development, environment and biogeography. *Environmental Microbiology*. 2016;18(6):1764–1781.
- [5] Franzenburg S, Fraune S, Altröck PM, Kuenzel S, Baines JF, Traulsen A, et al. Bacterial colonization of Hydra hatchlings follows a robust temporal pattern. *ISME Journal*. 2013;7:781–790.
- [6] Weiland-Bräuer N, Fischer MA, Pinnow N, Schmitz RA. Potential role of host-derived quorum quenching in modulating bacterial colonization in the moon jellyfish *Aurelia aurita*. *Scientific Reports*. 2019;9(1):34.