

Table S1. Reparametrization and baseline values of NPCE OSMOSE model parameters used for the UA

Parameters type	Anchovy (sp1)	Peruvian hake (sp2)	Sardine (sp3)	Jack mackerel (sp4)	Chub mackerel (sp5)	Mesopelagics (sp6)	Munida (sp7)	Humboldt squid (sp8)	Euphausiids (sp9)
predation accessibility of prey to predator	Reparametrization: $p_{1,sp1} = A(sp_1, sp_2)$ $p_{2,sp1} = A(sp_1, sp_3)$ $p_{3,sp1} = A(sp_1, sp_4)$ $p_{4,sp1} = A(sp_1, sp_5)$ $p_{5,sp1} = A(sp_1, sp_6)$ $p_{6,sp1} = A(sp_1, sp_7)$ $p_{7,sp1} = A(sp_1, sp_8)$ $p_{8,sp1} = A(sp_1, sp_9)$ Baseline value (x): $p_{1,sp1} = 0.10$ $p_{2,sp1} = 0.90$ $p_{3,sp1} = 0.90$ $p_{4,sp1} = 0.90$ $p_{5,sp1} = 0.55$ $p_{6,sp1} = 0.05$ $p_{7,sp1} = 0.60$ $p_{8,sp1} = 0.60$	Reparametrization: $p_{1,sp2} = A(sp_2, sp_1)$ $p_{2,sp2} = A(sp_2, sp_3)$ $p_{3,sp2} = A(sp_2, sp_4)$ $p_{4,sp2} = A(sp_2, sp_5)$ $p_{5,sp2} = A(sp_2, sp_6)$ $p_{6,sp2} = A(sp_2, sp_7)$ $p_{7,sp2} = A(sp_2, sp_8)$ $p_{8,sp2} = A(sp_2, sp_9)$ Baseline value (x): $p_{1,sp2} = 0.20$ $p_{2,sp2} = 0.20$ $p_{3,sp2} = 0.15$ $p_{4,sp2} = 0.15$ $p_{5,sp2} = 0.45$ $p_{6,sp2} = 0.02$ $p_{7,sp2} = 0.65$ $p_{8,sp2} = 0.50$	Reparametrization: $p_{1,sp3} = A(sp_3, sp_1)$ $p_{2,sp3} = A(sp_3, sp_2)$ $p_{3,sp3} = A(sp_3, sp_4)$ $p_{4,sp3} = A(sp_3, sp_5)$ $p_{5,sp3} = A(sp_3, sp_6)$ $p_{6,sp3} = A(sp_3, sp_7)$ $p_{7,sp3} = A(sp_3, sp_8)$ $p_{8,sp3} = A(sp_3, sp_9)$ Baseline value (x): $p_{1,sp3} = 0.90$ $p_{2,sp3} = 0.15$ $p_{3,sp3} = 0.90$ $p_{4,sp3} = 0.90$ $p_{5,sp3} = 0.60$ $p_{6,sp3} = 0.05$ $p_{7,sp3} = 0.60$ $p_{8,sp3} = 0.60$	Reparametrization: $p_{1,sp4} = A(sp_4, sp_1)$ $p_{2,sp4} = A(sp_4, sp_2)$ $p_{3,sp4} = A(sp_4, sp_3)$ $p_{4,sp4} = A(sp_4, sp_5)$ $p_{5,sp4} = A(sp_4, sp_6)$ $p_{6,sp4} = A(sp_4, sp_7)$ $p_{7,sp4} = A(sp_4, sp_8)$ $p_{8,sp4} = A(sp_4, sp_9)$ Baseline value (x): $p_{1,sp4} = 0.90$ $p_{2,sp4} = 0.15$ $p_{3,sp4} = 0.90$ $p_{4,sp4} = 0.90$ $p_{5,sp4} = 0.60$ $p_{6,sp4} = 0.90$ $p_{7,sp4} = 0.60$ $p_{8,sp4} = 0.50$	Reparametrization: $p_{1,sp5} = A(sp_5, sp_1)$ $p_{2,sp5} = A(sp_5, sp_2)$ $p_{3,sp5} = A(sp_5, sp_3)$ $p_{4,sp5} = A(sp_5, sp_4)$ $p_{5,sp5} = A(sp_5, sp_6)$ $p_{6,sp5} = A(sp_5, sp_7)$ $p_{7,sp5} = A(sp_5, sp_8)$ $p_{8,sp5} = A(sp_5, sp_9)$ Baseline value (x): $p_{1,sp5} = 0.90$ $p_{2,sp5} = 0.15$ $p_{3,sp5} = 0.90$ $p_{4,sp5} = 0.90$ $p_{5,sp5} = 0.90$ $p_{6,sp5} = 0.90$ $p_{7,sp5} = 0.60$ $p_{8,sp5} = 0.60$	Reparametrization: $p_{1,sp6} = A(sp_6, sp_1)$ $p_{2,sp6} = A(sp_6, sp_2)$ $p_{3,sp6} = A(sp_6, sp_3)$ $p_{4,sp6} = A(sp_6, sp_4)$ $p_{5,sp6} = A(sp_6, sp_5)$ $p_{6,sp6} = A(sp_6, sp_7)$ $p_{7,sp6} = A(sp_6, sp_8)$ $p_{8,sp6} = A(sp_6, sp_9)$ Baseline value (x): $p_{1,sp6} = 0.55$ $p_{2,sp6} = 0.45$ $p_{3,sp6} = 0.60$ $p_{4,sp6} = 0.60$ $p_{5,sp6} = 0.90$ $p_{6,sp6} = 0.50$ $p_{7,sp6} = 0.95$ $p_{8,sp6} = 0.90$	Reparametrization: $p_{1,sp7} = A(sp_7, sp_1)$ $p_{2,sp7} = A(sp_7, sp_2)$ $p_{3,sp7} = A(sp_7, sp_3)$ $p_{4,sp7} = A(sp_7, sp_4)$ $p_{5,sp7} = A(sp_7, sp_5)$ $p_{6,sp7} = A(sp_7, sp_6)$ $p_{7,sp7} = A(sp_7, sp_8)$ $p_{8,sp7} = A(sp_7, sp_9)$ Baseline value (x): $p_{1,sp7} = 0.90$ $p_{2,sp7} = 0.025$ $p_{3,sp7} = 0.90$ $p_{4,sp7} = 0.90$ $p_{5,sp7} = 0.90$ $p_{6,sp7} = 0.50$ $p_{7,sp7} = 0.50$ $p_{8,sp7} = 0.55$	Reparametrization: $p_{1,sp8} = A(sp_8, sp_1)$ $p_{2,sp8} = A(sp_8, sp_2)$ $p_{3,sp8} = A(sp_8, sp_3)$ $p_{4,sp8} = A(sp_8, sp_4)$ $p_{5,sp8} = A(sp_8, sp_5)$ $p_{6,sp8} = A(sp_8, sp_6)$ $p_{7,sp8} = A(sp_8, sp_7)$ $p_{8,sp8} = A(sp_8, sp_9)$ Baseline value (x): $p_{1,sp8} = 0.60$ $p_{2,sp8} = 0.65$ $p_{3,sp8} = 0.60$ $p_{4,sp8} = 0.70$ $p_{5,sp8} = 0.60$ $p_{6,sp8} = 0.95$ $p_{7,sp8} = 0.50$ $p_{8,sp8} = 0.95$	Reparametrization: $p_{1,sp9} = A(sp_9, sp_1)$ $p_{2,sp9} = A(sp_9, sp_2)$ $p_{3,sp9} = A(sp_9, sp_3)$ $p_{4,sp9} = A(sp_9, sp_4)$ $p_{5,sp9} = A(sp_9, sp_5)$ $p_{6,sp9} = A(sp_9, sp_6)$ $p_{7,sp9} = A(sp_9, sp_7)$ $p_{8,sp9} = A(sp_9, sp_8)$ Baseline value (x): $p_{1,sp9} = 0.60$ $p_{2,sp9} = 0.50$ $p_{3,sp9} = 0.60$ $p_{4,sp9} = 0.60$ $p_{5,sp9} = 0.60$ $p_{6,sp9} = 0.90$ $p_{7,sp9} = 0.55$ $p_{8,sp9} = 0.95$
minimum predator:prey size ratio for each species stage (θ_{stage})	Reparametrization: $p_{9,sp1} = f(\theta_{stage1})$ $p_{10,sp1} = f(\theta_{stage2})$ Baseline value (x): $p_{9,sp1} = 0.0008$ $p_{10,sp1} = 0.0032$	Reparametrization: $p_{9,sp2} = f(\theta_{stage1})$ $p_{10,sp2} = f(\theta_{stage2})$ Baseline value (x): $p_{9,sp2} = 0.0127$ $p_{10,sp2} = 0.0127$	Reparametrization: $p_{9,sp3} = f(\theta_{stage1})$ $p_{10,sp3} = f(\theta_{stage2})$ Baseline value (x): $p_{9,sp3} = 0.0006$ $p_{10,sp3} = 0$	Reparametrization: $p_{9,sp4} = f(\theta_{stage1})$ $p_{10,sp4} = f(\theta_{stage2})$ Baseline value (x): $p_{9,sp4} = 0.0021$ $p_{10,sp4} = 0.0032$	Reparametrization: $p_{9,sp5} = f(\theta_{stage1})$ $p_{10,sp5} = f(\theta_{stage2})$ Baseline value (x): $p_{9,sp5} = 0.0021$ $p_{10,sp5} = 0.0032$	Reparametrization: $p_{9,sp6} = f(\theta_{stage1})$ Baseline value (x): $p_{9,sp6} = 0.0064$	Reparametrization: $p_{9,sp7} = f(\theta_{stage1})$ Baseline value (x): $p_{9,sp7} = 0.0042$	Reparametrization: $p_{9,sp8} = f(\theta_{stage1})$ $p_{10,sp8} = f(\theta_{stage2})$ $p_{11,sp8} = f(\theta_{stage2})$ Baseline value (x): $p_{9,sp8} = 0.0182$ $p_{10,sp8} = 0.0116$ $p_{11,sp8} = 0.0091$	Reparametrization: $p_{9,sp9} = f(\theta_{stage1})$ $p_{10,sp9} = f(\theta_{stage2})$ Baseline value (x): $p_{9,sp9} = 0.0002$ $p_{10,sp9} = 0.0003$
maximum predator:prey size ratio for each species stage (α_{stage})	Reparametrization: $p_{11,sp1} = f(\alpha_{stage1})$ $p_{12,sp1} = f(\alpha_{stage2})$ Baseline value (x): $p_{11,sp1} = 0.0784$ $p_{12,sp1} = 0.1023$	Reparametrization: $p_{11,sp2} = f(\alpha_{stage1})$ $p_{12,sp2} = f(\alpha_{stage2})$ Baseline value (x): $p_{11,sp2} = 0.1946$ $p_{12,sp2} = 0.2325$	Reparametrization: $p_{11,sp3} = f(\alpha_{stage1})$ $p_{12,sp3} = f(\alpha_{stage2})$ Baseline value (x): $p_{11,sp3} = 0.0248$ $p_{12,sp3} = 0.0042$	Reparametrization: $p_{11,sp4} = f(\alpha_{stage1})$ $p_{12,sp4} = f(\alpha_{stage2})$ Baseline value (x): $p_{11,sp4} = 0.0297$ $p_{12,sp4} = 0.0393$	Reparametrization: $p_{11,sp5} = f(\alpha_{stage1})$ $p_{12,sp5} = f(\alpha_{stage2})$ Baseline value (x): $p_{11,sp5} = 0.0297$ $p_{12,sp5} = 0.0393$	Reparametrization: $p_{10,sp6} = f(\alpha_{stage1})$ Baseline value (x): $p_{10,sp6} = 0.1719$	Reparametrization: $p_{10,sp7} = f(\alpha_{stage1})$ Baseline value (x): $p_{10,sp7} = 0.2922$	Reparametrization: $p_{12,sp8} = f(\alpha_{stage1})$ $p_{13,sp8} = f(\alpha_{stage2})$ $p_{14,sp8} = f(\alpha_{stage2})$ Baseline value (x): $p_{12,sp8} = 0.2282$ $p_{13,sp8} = 0.2869$ $p_{14,sp8} = 0.4954$	Reparametrization: $p_{11,sp9} = f(\alpha_{stage1})$ $p_{12,sp9} = f(\alpha_{stage2})$ Baseline value (x): $p_{11,sp9} = 0.0422$ $p_{12,sp9} = 0.0632$
predator:prey stage threshold (S_{thr} in cm)	Reparametrization: $p_{13,sp1} = f(S_{thr})$ Baseline value (x):	Reparametrization: $p_{13,sp2} = f(S_{thr})$ Baseline value (x):	Reparametrization: $p_{13,sp3} = f(S_{thr})$ Baseline value (x):	Reparametrization: $p_{13,sp4} = f(S_{thr})$ Baseline value (x):	Reparametrization: $p_{13,sp5} = f(S_{thr})$ Baseline value (x):	-	-	Reparametrization: $p_{15,sp8} = f(S_{thr})$ $p_{16,sp8} = f(S_{thr})$	Reparametrization: $p_{13,sp9} = f(S_{thr})$ Baseline value (x):

	$p_{13,sp1} = 0.5128$	$p_{13,sp2} = 0.2647$	$p_{13,sp3} = 0.3358$	$p_{13,sp4} = 0.2451$	$p_{13,sp5} = 0.4926$			Baseline value (x): $p_{15,sp8} = 0.6316$ $p_{16,sp8} = 0.5$	$p_{13,sp9} = 0.2308$
maximum starvation mortality rate ($M_{\epsilon_{max}}$ in y^{-1})	Reparametrization: $p_{14,sp1} = f(A)$ Baseline value (x): $p_{14,sp1} = 0.10$	Reparametrization: $p_{14,sp2} = f(A)$ Baseline value (x): $p_{14,sp2} = 0.05$	Reparametrization: $p_{14,sp3} = f(A)$ Baseline value (x): $p_{14,sp3} = 0.10$	Reparametrization: $p_{14,sp4} = f(A)$ Baseline value (x): $p_{14,sp4} = 0.15$	Reparametrization: $p_{14,sp5} = f(A)$ Baseline value (x): $p_{14,sp5} = 0.05$	Reparametrization: $p_{11,sp6} = f(A)$ Baseline value (x): $p_{11,sp6} = 0.5$	Reparametrization: $p_{11,sp7} = f(A)$ Baseline value (x): $p_{11,sp7} = 0.1$	Reparametrization: $p_{17,sp8} = f(A)$ Baseline value (x): $p_{17,sp8} = 0.1$	Reparametrization: $p_{14,sp9} = f(A)$ Baseline value (x): $p_{14,sp9} = 0.5$
von Bertalanffy threshold (a_{thr} in y)	Reparametrization: $p_{15,sp1} = f(a_{thr})$ Baseline value (x): $p_{15,sp1} = 0.1167$	Reparametrization: $p_{15,sp2} = f(a_{thr})$ Baseline value (x): $p_{15,sp2} = 0.0417$	Reparametrization: $p_{15,sp3} = f(a_{thr})$ Baseline value (x): $p_{15,sp3} = 0.0625$	Reparametrization: $p_{15,sp4} = f(a_{thr})$ Baseline value (x): $p_{15,sp4} = 0.0625$	Reparametrization: $p_{15,sp5} = f(a_{thr})$ Baseline value (x): $p_{15,sp5} = 0.05$	$p_{12,sp6} = f(a_{thr})$ Baseline value (x): $p_{12,sp6} = 0.175$	$p_{12,sp7} = f(a_{thr})$ Baseline value (x): $p_{12,sp7} = 0.125$	$p_{18,sp8} = f(a_{thr})$ Baseline value (x): $p_{18,sp8} = 0.6667$	Reparametrization: $p_{15,sp9} = f(a_{thr})$ Baseline value (x): $p_{15,sp9} = 0.10$
egg size (cm)	Reparametrization: $p_{16,sp1} = f(A)$ Baseline value (x): $p_{16,sp1} = 0.10$	Reparametrization: $p_{16,sp2} = f(A)$ Baseline value (x): $p_{16,sp2} = 0.10$	Reparametrization: $p_{16,sp3} = f(A)$ Baseline value (x): $p_{16,sp3} = 0.10$	Reparametrization: $p_{16,sp4} = f(A)$ Baseline value (x): $p_{16,sp4} = 0.10$	Reparametrization: $p_{16,sp5} = f(A)$ Baseline value (x): $p_{16,sp5} = 0.10$	Reparametrization: $p_{13,sp6} = f(A)$ Baseline value (x): $p_{13,sp6} = 0.10$	Reparametrization: $p_{13,sp7} = f(A)$ Baseline value (x): $p_{13,sp7} = 0.10$	Reparametrization: $p_{19,sp8} = f(A)$ Baseline value (x): $p_{19,sp8} = 0.10$	Reparametrization: $p_{16,sp9} = f(A)$ Baseline value (x): $p_{16,sp9} = 0.10$
critical threshold of predation efficiency (ϵ_{crit})	Reparametrization: $p_{17,sp1} = f(A)$ Baseline value (x): $p_{17,sp1} = 0.57$	Reparametrization: $p_{17,sp2} = f(A)$ Baseline value (x): $p_{17,sp2} = 0.57$	Reparametrization: $p_{17,sp3} = f(A)$ Baseline value (x): $p_{17,sp3} = 0.57$	Reparametrization: $p_{17,sp4} = f(A)$ Baseline value (x): $p_{17,sp4} = 0.57$	Reparametrization: $p_{17,sp5} = f(A)$ Baseline value (x): $p_{17,sp5} = 0.57$	Reparametrization: $p_{14,sp6} = f(A)$ Baseline value (x): $p_{14,sp6} = 0.57$	Reparametrization: $p_{14,sp7} = f(A)$ Baseline value (x): $p_{14,sp7} = 0.57$	Reparametrization: $p_{20,sp8} = f(A)$ Baseline value (x): $p_{20,sp8} = 0.57$	Reparametrization: $p_{17,sp9} = f(A)$ Baseline value (x): $p_{17,sp9} = 0.57$
maximum rate of predation ingestion (I_{max} in $g\ bodyg^{-1}y^{-1}$)	Reparametrization: $p_{18,sp1} = f(A)$ Baseline value (x): $p_{18,sp1} = 3.5$	Reparametrization: $p_{18,sp2} = f(A)$ Baseline value (x): $p_{18,sp2} = 3.5$	Reparametrization: $p_{18,sp3} = f(A)$ Baseline value (x): $p_{18,sp3} = 3.5$	Reparametrization: $p_{18,sp4} = f(A)$ Baseline value (x): $p_{18,sp4} = 3.5$	Reparametrization: $p_{18,sp5} = f(A)$ Baseline value (x): $p_{18,sp5} = 3.5$	Reparametrization: $p_{15,sp6} = f(A)$ Baseline value (x): $p_{15,sp6} = 3.5$	Reparametrization: $p_{15,sp7} = f(A)$ Baseline value (x): $p_{15,sp7} = 3.5$	Reparametrization: $p_{21,sp8} = f(A)$ Baseline value (x): $p_{21,sp8} = 3.5$	Reparametrization: $p_{18,sp9} = f(A)$ Baseline value (x): $p_{18,sp9} = 3.5$
natural mortality rate (M in y^{-1})	Reparametrization: $p_{19,sp1} = f(A)$ Baseline value (x): $p_{19,sp1} = 0.9177$	Reparametrization: $p_{19,sp2} = f(A)$ Baseline value (x): $p_{19,sp2} = 0.2102$	Reparametrization: $p_{19,sp3} = f(A)$ Baseline value (x): $p_{19,sp3} = 0.1624$	Reparametrization: $p_{19,sp4} = f(A)$ Baseline value (x): $p_{19,sp4} = 0.1853$	Reparametrization: $p_{19,sp5} = f(A)$ Baseline value (x): $p_{19,sp5} = 0.2136$	Reparametrization: $p_{16,sp6} = f(A)$ Baseline value (x): $p_{16,sp6} = 0.7108$	Reparametrization: $p_{16,sp7} = f(A)$ Baseline value (x): $p_{16,sp7} = 0.2322$	Reparametrization: $p_{22,sp8} = f(A)$ Baseline value (x): $p_{22,sp8} = 1.8466$	Reparametrization: $p_{19,sp9} = f(A)$ Baseline value (x): $p_{19,sp9} = 0.2879$
larval mortality rate (M_0 in $month^{-1}$)	Reparametrization: $p_{20,sp1} = f(A)$ Baseline value (x): $p_{20,sp1} = 9.5821$	Reparametrization: $p_{20,sp2} = f(A)$ Baseline value (x): $p_{20,sp2} = 9.8035$	Reparametrization: $p_{20,sp3} = f(A)$ Baseline value (x): $p_{20,sp3} = 13.2393$	Reparametrization: $p_{20,sp4} = f(A)$ Baseline value (x): $p_{20,sp4} = 12.5882$	Reparametrization: $p_{20,sp5} = f(A)$ Baseline value (x): $p_{20,sp5} = 13.1210$	Reparametrization: $p_{17,sp6} = f(A)$ Baseline value (x): $p_{17,sp6} = 2.0804$	Reparametrization: $p_{17,sp7} = f(A)$ Baseline value (x): $p_{17,sp7} = 6.7572$	Reparametrization: $p_{23,sp8} = f(A)$ Baseline value (x): $p_{23,sp8} = 8.9452$	Reparametrization: $p_{20,sp9} = f(A)$ Baseline value (x): $p_{20,sp9} = 1.5779$
fishing mortality multiplier (f_m)	Reparametrization: $p_{21,sp1} = f(A)$ Baseline value (x): $p_{21,sp1} = 1$	Reparametrization: $p_{21,sp2} = f(A)$ Baseline value (x): $p_{21,sp2} = 1$	Reparametrization: $p_{21,sp3} = f(A)$ Baseline value (x): $p_{21,sp3} = 1$	Reparametrization: $p_{21,sp4} = f(A)$ Baseline value (x): $p_{21,sp4} = 1$	Reparametrization: $p_{21,sp5} = f(A)$ Baseline value (x): $p_{21,sp5} = 1$	-	-	Reparametrization: $p_{24,sp8} = f(A)$ Baseline value (x): $p_{24,sp8} = 1$	-

sex ratio ($Frac_{fem}$)	Reparametrization: $p_{22,sp1} = f(A)$ Baseline value (x): $p_{22,sp1} = 0.5$	Reparametrization: $p_{22,sp2} = f(A)$ Baseline value (x): $p_{22,sp2} = 0.5$	Reparametrization: $p_{22,sp3} = f(A)$ Baseline value (x): $p_{22,sp3} = 0.5$	Reparametrization: $p_{22,sp4} = f(A)$ Baseline value (x): $p_{22,sp4} = 0.5$	Reparametrization: $p_{22,sp5} = f(A)$ Baseline value (x): $p_{22,sp5} = 0.5$	Reparametrization: $p_{18,sp6} = f(A)$ Baseline value (x): $p_{18,sp6} = 0.5$	Reparametrization: $p_{18,sp7} = f(A)$ Baseline value (x): $p_{18,sp7} = 0.5$	Reparametrization: $p_{25,sp8} = f(A)$ Baseline value (x): $p_{25,sp8} = 0.5$	Reparametrization: $p_{21,sp9} = f(A)$ Baseline value (x): $p_{21,sp9} = 0.5$
$L_t = 0$ (von Bertalanffy growth parameter in cm)	Reparametrization: $p_{23,sp1} = f(A)$ Baseline value (x): $p_{23,sp1} = 0.1009$	Reparametrization: $p_{23,sp2} = f(A)$ Baseline value (x): $p_{23,sp2} = 0.0537$	Reparametrization: $p_{23,sp3} = f(A)$ Baseline value (x): $p_{23,sp3} = 0.2553$	Reparametrization: $p_{23,sp4} = f(A)$ Baseline value (x): $p_{23,sp4} = 0.0457$	Reparametrization: $p_{23,sp5} = f(A)$ Baseline value (x): $p_{23,sp5} = 0.0203$	Reparametrization: $p_{19,sp6} = f(A)$ Baseline value (x): $p_{19,sp6} = 0.0667$	Reparametrization: $p_{19,sp7} = f(A)$ Baseline value (x): $p_{19,sp7} = 0.1157$	Reparametrization: $p_{26,sp8} = f(A)$ Baseline value (x): $p_{26,sp8} = 0.0943$	Reparametrization: $p_{22,sp9} = f(A)$ Baseline value (x): $p_{22,sp9} = 0.2998$
k (von Bertalanffy growth parameter in y^{-1})	Reparametrization: $p_{24,sp1} = f(A)$ Baseline value (x): $p_{24,sp1} = 0.76$	Reparametrization: $p_{24,sp2} = f(A)$ Baseline value (x): $p_{24,sp2} = 0.205$	Reparametrization: $p_{24,sp3} = f(A)$ Baseline value (x): $p_{24,sp3} = 0.22$	Reparametrization: $p_{24,sp4} = f(A)$ Baseline value (x): $p_{24,sp4} = 0.1670$	Reparametrization: $p_{24,sp5} = f(A)$ Baseline value (x): $p_{24,sp5} = 0.41$	Reparametrization: $p_{20,sp6} = f(A)$ Baseline value (x): $p_{20,sp6} = 1.15$	Reparametrization: $p_{20,sp7} = f(A)$ Baseline value (x): $p_{20,sp7} = 0.375$	Reparametrization: $p_{27,sp8} = f(A)$ Baseline value (x): $p_{27,sp8} = 1.1$	Reparametrization: $p_{23,sp9} = f(A)$ Baseline value (x): $p_{23,sp9} = 1.8$
L_∞ (von Bertalanffy growth parameter in cm)	Reparametrization: $p_{25,sp1} = f(A)$ Baseline value (x): $p_{25,sp1} = 19.50$	Reparametrization: $p_{25,sp2} = f(A)$ Baseline value (x): $p_{25,sp2} = 68$	Reparametrization: $p_{25,sp3} = f(A)$ Baseline value (x): $p_{25,sp3} = 38.71$	Reparametrization: $p_{25,sp4} = f(A)$ Baseline value (x): $p_{25,sp4} = 81.6$	Reparametrization: $p_{25,sp5} = f(A)$ Baseline value (x): $p_{25,sp5} = 40.60$	Reparametrization: $p_{21,sp6} = f(A)$ Baseline value (x): $p_{21,sp6} = 8$	Reparametrization: $p_{21,sp7} = f(A)$ Baseline value (x): $p_{21,sp7} = 4.2$	Reparametrization: $p_{28,sp8} = f(A)$ Baseline value (x): $p_{28,sp8} = 95$	Reparametrization: $p_{24,sp9} = f(A)$ Baseline value (x): $p_{24,sp9} = 2.6$
size at maturity (s_{mat} in cm)	Reparametrization: $p_{26,sp1} = f(s_{mat})$ Baseline value (x): $p_{26,sp1} = 0.5722$	Reparametrization: $p_{26,sp2} = f(s_{mat})$ Baseline value (x): $p_{26,sp2} = 0.4872$	Reparametrization: $p_{26,sp3} = f(s_{mat})$ Baseline value (x): $p_{26,sp3} = 0.3856$	Reparametrization: $p_{26,sp4} = f(s_{mat})$ Baseline value (x): $p_{26,sp4} = 0.3245$	Reparametrization: $p_{26,sp5} = f(s_{mat})$ Baseline value (x): $p_{26,sp5} = 0.7084$	Reparametrization: $p_{22,sp6} = f(s_{mat})$ Baseline value (x): $p_{22,sp6} = 0.2634$	Reparametrization: $p_{22,sp7} = f(s_{mat})$ Baseline value (x): $p_{22,sp7} = 0.3807$	Reparametrization: $p_{29,sp8} = f(s_{mat})$ Baseline value (x): $p_{29,sp8} = 0.6630$	Reparametrization: $p_{25,sp9} = f(s_{mat})$ Baseline value (x): $p_{25,sp9} = 0.0113$
constant of proportionality of the allometric length- weight relationship (c in $g\ cm^{-3}$)	Reparametrization: $p_{27,sp1} = f(A)$ Baseline value (x): $p_{27,sp1} = 0.0065$	Reparametrization: $p_{27,sp2} = f(A)$ Baseline value (x): $p_{27,sp2} = 0.007$	Reparametrization: $p_{27,sp3} = f(A)$ Baseline value (x): $p_{27,sp3} = 0.0089$	Reparametrization: $p_{27,sp4} = f(A)$ Baseline value (x): $p_{27,sp4} = 0.0135$	Reparametrization: $p_{27,sp5} = f(A)$ Baseline value (x): $p_{27,sp5} = 0.0086$	Reparametrization: $p_{23,sp6} = f(A)$ Baseline value (x): $p_{23,sp6} = 0.0083$	Reparametrization: $p_{23,sp7} = f(A)$ Baseline value (x): $p_{23,sp7} = 0.174$	Reparametrization: $p_{30,sp8} = f(A)$ Baseline value (x): $p_{30,sp8} = 0.005$	Reparametrization: $p_{26,sp9} = f(A)$ Baseline value (x): $p_{26,sp9} = 0.0093$

Text S1: NPCE OSMOSE model re-parametrization

We briefly describe the NPCE OSMOSE parameters selected for the UA in this study.

- Predation parameters: The predation accessibilities are used in the model to describe the accessibility of prey to predators. These parameters reflect the vertical overlap of predators and prey in the water column. Predation accessibilities take values between 0 and 1 and determine the total accessible biomass (P_{tot_s}) for the predator school (s):

$$P_{tot_s} = \sum_{p=1}^{p=N} A(pred_s, prey_p) B_{prey_p} \quad (s.1)$$

where p is the prey school (p from 1 to N) available for school s , $A(pred_s, prey_p)$ is the accessibility of each prey p to the predator school s and, B_{prey_p} the corresponding biomass of each prey p . In addition, the total biomass that a predator school can eat ($P_{eatable_s}$) depends on the biomass of the predator (B_{pred_s}) and the maximum rate of ingestion of the predator species (I_{max}):

$$P_{eatable_s} = B_{pred_s} I_{max} \quad (s.2)$$

We decided to run the UA on the $A(pred_s, prey_p)$ parameters (predation accessibilities parameters, in Table 2 the parameter N°1). These values are proportions that $\in [0,1]$, so we chose a logit scale for these parameters. We also run the UA on the I_{max} (in Table 2, the parameter N° 9). Since the only constraint is to keep positive the parameter value, we used the logarithmic scale for I_{max} .

- Feeding size ranges: In OSMOSE, the predation is controlled by the minimum (R_{min}) and maximum (R_{max}) size ratios (in Table 2, parameters N° 2 and N° 3). Predator schools can only feed on prey schools whose lengths meet these thresholds:

$$R_{min} \leq \frac{L_{pred}}{L_{prey}} \leq R_{max} \quad (s.3)$$

where the ratios (R_{min} and R_{max}) are the threshold values for predator length (L_{pred}) over prey length (L_{prey}) ratio. When information is available, a split around the size threshold (s_{thr}) allows specifying different feeding size ranges between species stages (the parameter called predator-prey stage threshold, N° 4 in Table 2). Predator-prey stage threshold (s_{thr}) is part of the UA. However, we re-parameterized it by s_{thr}/L_{∞} in logit scale (with values from 0 to 1). It ensures that s_{thr} will always be smaller or equal to L_{∞} .

Likewise, R_{min} should never be higher than R_{max} . Therefore, manipulations of R_{min} and R_{max} separately for the UA are risky and should be avoided for model consistency. We thus decided to re-parametrize the equation of this process and implement the UA using angles in polar coordinates. Users should think carefully about the potential consequences of changing parameter values that are interdependent in the model equations and re-parametrize them when necessary. Using equation s.3 in cartesian coordinates (predator size in abscissa and prey size

in ordinate), we transformed it into polar coordinates calculating angles between the abscissa, minimum and maximum prey length:

$$g(m_1, m_2) = \tan^{-1} \left(\frac{m_2 - m_1}{1 + m_1 m_2} \right) \quad (\text{s.4})$$

where $g(m_1, m_2)$ is the angle (in degrees) between the slopes (m_1 and m_2), m_2 being always greater than m_1 . Using equation s.4, we calculated two angles: i) the angle between the horizontal axis and the minimum prey length ($\theta = g(0, m_1)$), and the angle between the minimum and maximum prey length ($\alpha = g(m_1, m_2)$). The parameters m_1 and m_2 were re-parameterized as the angles θ and α for each species (see Table S.1, e.g., $\theta_{stage\ 1}$ and $\alpha_{stage\ 1}$, and $\theta_{stage\ 2}$ and $\alpha_{stage\ 2}$ for the first and second anchovy stages). The new parameterization of R_{min} and R_{max} (as function of θ_{stage} , and θ_{stage} and α_{stage} respectively) physically restricts the parameter values to the first quadrant, representing all the possibilities for the predator-prey size ratios ($\pi/4$ means predator and prey size can be equal while $\pi/2$ means there is no limit on the prey size for a predator). Besides, to ensure $R_{max} > R_{min}$, R_{max} is restricted to the first quadrant minus θ_{stage} . The re-parameterized values are presented in Table S.1, and for the UA they use a logit scale.

- Starvation mortality: When the predation efficiency (ε_i) is below the critical threshold (ε_{crit} , parameter N° 8 in Table 2), schools do not have enough food to fulfill their requirements undergoing starvation mortality (M_{ε_i} of school i , see equation s.5). This process is controlled by the maximum starvation mortality rate ($M_{\varepsilon_{max}}$) of the species as follows:

$$M_{\varepsilon_i} = -\frac{M_{\varepsilon_{max}}}{\varepsilon_{crit}} \varepsilon_i + M_{\varepsilon_{max}} \quad (\text{s.5})$$

We implemented the UA using $M_{\varepsilon_{max}}$ (parameter N° 5 in Table 2) on a logarithmic scale since its values are positive. ε_{crit} is also part of the UA, but we use a logit scale because its values accept only numbers between 0 and 1.

- Growth: Individuals of a given school are assumed to grow in size and weight (at time t) only when the food ingested fulfills their maintenance requirements. A simple linear model is used below the threshold age (a_{thr} , parameter N° 6 in Table 2). Above a_{thr} , the von Bertalanffy model is used to determine the average mean length increase, as follows:

$$L_t = L_{\infty}(1 - \exp(-k(t - t_0))) \quad (\text{s.6})$$

where L_{∞} is the asymptotic size (parameter N° 16 in Table 2), k the growth coefficient (parameter N° 15 in Table 2), and t_0 the theoretical age when size is 0. The UA is implemented using L_{∞} , k , $L_{t=0}$ (the length at $t = 0$, parameter N° 14 in Table 2, abbreviated as L_0). These parameters are manipulated individually and on a logarithmic scale for L_{∞} and k since the only constraint is to keep the parameter value positive. For the UA we decided to re-parameterized L_0 as a rate of L_0/L_{∞} on a logit scale. This ensures that L_0 will never be greater than L_{∞} . a_{thr} is also part of the UA on a logit scale. However, we re-parameterized it by a_{thr}/a_{max} on a logit

scale (with values from 0 to 1), where a_{max} is the longevity (in years). It ensures that a_{thr} will always be smaller or equal to a_{max} , but never bigger than a_{max} .

The weight of a school is calculated using the allometric relationship:

$$W = cL^b \quad (s.7)$$

where b is the exponent and c the constant of proportionality of the allometric length-weight relationship. We chose to constrain the UA to the constant of proportionality (c , in Table 2 the parameter N° 18) in logarithmic scale, leaving b fixed.

- Size and weight of eggs: The life cycle of each species is modelled starting with the egg stage. Egg size is part of the UA (parameter N° 7 in Table 2) and it co-varies with egg weight. For each UA simulation, we calculated the corresponding egg weight as a function of egg size, keeping the mean density constant as follows:

$$egg_{weight} = \frac{4}{3} \pi \left(\frac{egg_{size}}{2} \right)^3 mean_{density} \quad (s.8)$$

The $mean_{density}$ is calculated using the baseline egg size and weight values. Then each time that the egg_{size} takes a new value due to the UA, the egg_{weight} should be recalculated, meaning that both parameters are changing together. The only mathematical constraint for these parameters is to obtain a positive numerical value, so we used the logarithmic scale.

- Sources of mortality: The abundance of a school i at time $t + \Delta t$, ($N_{i,t+\Delta t}$), is modeled as a function of abundance at time t ($N_{i,t}$) and the following sources of mortality:

$$N_{i,t+\Delta t} = N_{i,t} e^{-\Delta t(F_s(t) + M_s(t) + M_{\epsilon_i}(t) + P_i(t))} \quad (s.9)$$

where F_s is the fishing mortality rate and M_s the natural mortality rate of species s . M_{ϵ_i} is the starvation mortality rate and P_i the predation mortality rate, both related to the fish school i .

The natural mortality rate (parameter N° 10 in Table 2) and starvation mortality (already described in equation s.5) are part of the UA. The fishing mortality rate used in the NPCE OSMOSE model varies with time (t) and species size. We decided to include the fishing mortality in the UA by creating a fishing mortality multiplier f_m (parameter N° 12 in Table 2). It is a positive value with a baseline value equal to 1. The fishing multiplier is used in the UA by multiplying the fishing mortality rate (matrix of fishing mortalities, time vs. species size). Another source of mortality is the larval mortality rate ($M_{0,s}$). This parameter controls the number of eggs and larvae for species s , at age 0 and at time $t + \Delta t$, ($N_{s,0,t+\Delta t}$), as follows:

$$N_{s,0,t+\Delta t} = N_{s,0,t} e^{-\Delta t M_{0,s}} \quad (s.10)$$

where $N_{s,0,t}$ represents the number of eggs and larvae in the system at time t , and $M_{0,s}$ is the larval mortality rate by species (parameter N° 11 in Table 2). This parameter is a vector (one larval mortality rate by time step) in the NPCE OSMOSE model. The UA takes this parameter using the mean of the vector (mean over time).

Baseline values of natural mortality rate, larval mortality, and fishing mortality were estimated by a calibration process following a logarithmic scale. We chose the same scale to perform the experiments as part of the UA.

- **Reproduction:** any school whose length is greater than the size at sexual maturity (s_{mat} , parameter N° 17 in Table 2) enters the reproduction process at the end of the time step. This allows the generation of a new school at the egg stage. For a given species:

$$N_{eggs} = Frac_{fem} \alpha season B_{mat} \quad (s.11)$$

where $Frac_{fem}$ is the fraction of females (also called sex ratio, parameter N° 13 in Table 2), α is the relative fecundity. This parameter indicates the number of eggs per gram of mature females. The *season* is a file that provides the spawning distribution within a year, and B_{mat} is the sum of the biomass of the schools that reached sexual maturity.

$Frac_{fem}$ is part of the UA. We chose the logit scale because this parameter only takes values from 0 to 1.

The size at sexual maturity (s_{mat} , parameter N° 17 in Table 2) is also part of the UA. However, we re-parameterized it by $L_0 + s_x(L_\infty - L_0)$, then we used s_x for the UA in logit scale (with values from 0 to 1). It ensures that s_x will always be smaller of L_∞ , but also bigger than L_0 .