Table S4. Log-likelihood ratio test (LLRT) results from IMa analyses. For each adjacent population pair, the likelihood of a simpler, alternative model where $\theta 1 = \theta 2 = \theta A$ is shown [log(P)], the degrees of freedom for the LLRT of the full and alternative model, results from the test (2LLR), and the probability of achieving the test statistic by chance under the null model (*P*-value) are shown. All alternative models where population size has not changed were rejected in favor of the full model at $\alpha = 0.05$.

Population Pair	Model	log(P)	d.f.	2LLR	P value
LAP-MAZ	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-29.43	2	40.94	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-20.38	3	22.84	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	903.11	< 0.0001
LAP-TAR	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	904.88	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	904.88	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	904.88	< 0.0001
LAP-SCA	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	908.00	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	908.00	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	908.00	< 0.0001
LAP-MAN	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	907.06	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	907.06	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	907.06	< 0.0001
MAZ-TAR	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	904.40	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	904.40	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	904.40	< 0.0001
MAZ-SCA	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	907.67	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	907.67	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	907.67	< 0.0001
MAZ-CEB	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	906.90	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	906.90	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	906.90	< 0.0001

Population Pair	Model	log(P)	d.f.	2LLR	P value
MAZ-MAN	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	907.76	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	907.76	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	907.76	< 0.0001
TAR-SCA	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	909.13	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	909.13	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	909.13	< 0.0001
TAR-CEB	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-65.15	2	114.86	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-69.59	3	123.74	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	905.59	< 0.0001
TAR-MAN	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	909.77	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	909.77	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	909.77	< 0.0001
SCA-CEB	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	905.55	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	905.55	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	905.55	< 0.0001
SCA-MAN	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-350.98	2	687.5	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-4.82	3	168.36	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-91.42	4*	906.58	< 0.0001
CEB-MAN	$\theta_1 = \theta_2 = \theta_A m_1 m_2$	-460.52	2	904.11	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2$	-460.52	3	904.11	< 0.0001
	$\theta_1 = \theta_2 = \theta_A m_1 = m_2 = 0$	-460.52	4*	904.11	< 0.0001

* Test distribution of 2LLR is a mixture