

Inheritance and inequality under communal land tenure: convergence on cultural–evolutionary regimes

Nicolas Montalva  0000-0001-8612-663X^{1*},
Francisca Vásquez-Estay  0009-0006-8013-1693^{1,2},
Margarita Reyes-Madrid  00000-0003-1521-0994^{1,3},
Pablo Varas-Enríquez  0000-0003-1521-0994^{4,5,6}

^{1*}Society and Health Research Center, Universidad Mayor, José Toribio Medina 29, Santiago, 8340589, Región Metropolitana, Chile.

²Escuela de Salud Pública, Facultad de Medicina, Universidad de Chile, Av. Independencia 1027, Santiago, 8380453, Región Metropolitana, Chile.

³Núcleo Interdisciplinario de Biología y Genética, Instituto de Ciencias Biomédicas (ICBM), Facultad de Medicina, Universidad de Chile, Av. Independencia 1027, Santiago, 8380453, Región Metropolitana, Chile.

⁴Department of Social and Behavioral Sciences, Toulouse School of Economics, Université Toulouse Capitole, 1, Esplanade de l'Université, Toulouse, 31000, France.

⁵BirthRites Lise Meitner Research Group, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig, 04103, Germany.

⁶Department of Human Behavior, Ecology, and Culture, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig, 04103, Germany.

Contributing authors: nicolas.montalva@umayor.cl;
fran.vasquez.e@gmail.com; ma.reyesmadrid@gmail.com;
pablo.varas-enriquez@tse-fr.eu;

Bayesian Zero-inflated Beta phylogenetic regression

Here we present a full description of the Bayesian zero-inflated beta phylogenetic regression model used in our analyses.

The model was defined as as:

$$G_i \sim \text{ZIBeta}(\mu_i, \phi, \pi_{zi}), \quad (1)$$

Where G_i represents landholding inequality among right-holders for observation i , μ_i denotes the conditional mean of the continuous Beta component (the expected inequality when inequality is present), ϕ represents the precision parameter of the Beta distribution, and π_{zi} is the zero-inflation probability (the probability that observation i is a structural zero).

μ_i was modelled with a logit-link linear predictor incorporating fixed effects and a phylogenetic random effect:

$$\text{logit}(\mu_i) = \beta_0 + \beta_M M_i + \beta_A A_i + \beta_S S_i + u_{\text{community}[i]}, \quad (2)$$

where β_0 is a global intercept, β_M , β_A , and β_S are coefficients for multigeniture (M_i), agnatic bias (A_i), and surname diversity (S_i), respectively. The term $u_{\text{community}[i]}$ represents a phylogenetic random effect for the community of observation i , accounting for shared cultural and evolutionary history among communities.

The phylogenetic random effects were modeled as drawn from a multivariate normal distribution:

$$u \sim \mathcal{N}(0, \Sigma_{\text{phylo}}). \quad (3)$$

Where Σ_{phylo} is the phylogenetic covariance matrix derived from the community phylogeny.

The precision and zero-inflation parameters were modelled as:

$$\log(\phi) = \alpha_\phi, \quad \text{logit}(\pi_{zi}) = \alpha_{zi}. \quad (4)$$

where α_ϕ is the log of the precision parameter and α_{zi} is the log-odds of the zero-inflation probability.

Priors were defined as:

$$\begin{aligned} \beta_0 &\sim \mathcal{N}(0, 1.5), \\ (\beta_M, \beta_A, \beta_S) &\sim \mathcal{N}(0, 1), \\ \sigma_{\text{phylo}} &\sim \text{Exp}(2), \\ \alpha_\phi &\sim \mathcal{N}(\log 5, 1), \\ \alpha_{zi} &\sim \mathcal{N}(\text{logit}(0.1), 1.5). \end{aligned} \quad (5)$$

Models were run in four chains with 12,000 iterations and 4,000 warmup. Convergence was assessed using $\hat{R}$, ESS, and inspection of trace plots.