Maturation and mammalian longevity: sensitivity to taxonomic adjustment in AnAge

A reproducible comparative analysis of 801 mammalian species

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Abstract

Background: developmental timing and longevity covary across mammals, but the size of an association can depend strongly on taxonomic adjustment. Hypothesis: later female maturity is associated with greater maximum longevity after adjustment for adult mass and mammalian order. Methods: we analyzed a frozen official AnAge export using a locally recorded prospective plan, complete-case filters, family-clustered inference and family-blocked internal prediction checks. Results: 801 species from 116 families and 24 orders were eligible. A doubling of maturity age was associated with 18.20% greater maximum longevity (95% CI 13.44% to 23.16%; log coefficient 0.241, two-paper Holm-adjusted $p = 1.66 \times 10^{-12}$). The coefficient fell to 0.118 with family intercepts. In 760 species eligible for prediction assessment, adding maturity reduced log-scale RMSE from 0.366 to 0.328. The high-quality-only estimate was imprecise and its interval included zero. Conclusion: the known maturation-longevity relationship persists in this export but its magnitude depends on taxonomic resolution. These comparative associations do not establish that delaying maturation extends life.

Background and hypothesis

AnAge provides curated life-history and longevity records for comparative research [1,2]. The developmental-timing hypothesis is not new: de Magalhães, Costa and Church analyzed developmental schedules with phylogenetic independent contrasts in 2007 [3]. This paper asks a narrower reproducibility question: how stable is the maturity association to different taxonomic controls, record-quality restrictions and prediction across held-out families in a later downloadable snapshot? The contribution is an auditable robustness analysis, not a novel biological mechanism or an independent replication in newly collected animals.

We specified a positive association between log female maturity age and log maximum longevity, conditional on log adult mass and order. Female maturity provides one consistently defined sex-specific predictor; maximum longevity is generally a species record and is not necessarily female-specific. The outcome represents observed longevity, not a direct estimate of biological aging rate.

Methods

Data and provenance. The official AnAge ZIP was acquired on 5 September 2026 at 08:07:32 UTC from the www.genomics.senescence.info host. Its SHA-256 is e3ddb66e32e973a79932859ba53013e8f60d957c6ec01c6eb573e3ea3018d630. The enclosed release notes identify build 15, released 3 July 2023. The export parses to 4,645 records, whereas the release page states 4,671 entries [4]; the discrepancy remains unresolved and no missing records were synthesized. The included manifest records the hashes of the ZIP and extracted files. HAGR permits attributed reuse under CC BY 3.0 [5].

Eligibility and quality control. We retained Mammalia records with positive finite female maturity in days, adult mass in grams and maximum longevity in years; nonmissing order and family; and acceptable or

high longevity quality. Missing values were not imputed. There were no duplicated HAGRIDs. All 801 eligible species had maturity age below their longevity record. Species names, original source rows, fields, eligibility flags, Cook distances and leverage are provided. The quality indicator concerns longevity evidence and does not independently validate every maturity or mass measurement. According to HAGR, some life-history traits derive from compilations rather than original measurements [6].

Primary analysis. We fitted ordinary least squares: log(longevity) = intercept + β log(female maturity) + γ log(adult mass) + order intercepts. Each species received equal weight. Standard errors use a family-clustered sandwich covariance with correction G/(G-1) × (N-1)/(N-K), and confidence limits and two-sided tests use a t distribution with G-1 degrees of freedom. Here G is the number of families, N the number of species and K the model rank. The interpretable effect for a doubling of maturity is 100 × (2^β-1). The two primary p values from this paper and the accompanying DrugAge paper were adjusted together with Holm's method [7]. Confidence intervals are pointwise 95% intervals, not simultaneous intervals.

Robustness. Planned alternatives were unadjusted and mass-only models, family intercepts, exclusion of humans, exclusion of bats and primates, high-quality-only and captivity-only subsets, and leave-one-order-out refits. An adjustment for sample-size category and specimen origin was documented after schema inspection but before fitting. These categories address recorded observation effort without measuring its exact value. The analysis did not use a phylogenetic tree; order or family controls and clustered uncertainty cannot replace a phylogenetic comparative model or remove all shared-ancestry dependence.

Internal prediction assessment. Families were assigned to five shared folds within order with seed 20260905. Only orders with at least two families were eligible, ensuring the test data never contained an order absent from training. Mass-plus-order and maturity-plus-mass-plus-order models were evaluated on the same held-out species. This evaluates prediction for unseen families within represented orders, not for new orders or independently collected data. A post-hoc bootstrap resampled held-out families 10,000 times for uncertainty in the pooled paired squared-error difference; this conditional interval does not capture the variation from repeating the fold allocation or refitting each bootstrap sample.

Verification. Base R 4.6.1 performed the analyses. A Python/NumPy implementation independently read the raw file and reproduced the primary coefficient and clustered standard error within 10^{-10}; direct numerical integration verified the t-tail probabilities. The first, middle and last eligible species alphabetically were checked against live HAGR pages. These checks agreed on maturity, mass and longevity for Acinonyx jubatus, Macaca sinica and Zapus hudsonius. Original source monographs were not re-extracted; the checks verify export-to-database consistency only. The plan was committed locally before download (commit 7aaad8b), not registered in an independent registry.

Results

Of 1,349 mammalian records, 1,003 had acceptable/high quality, 1,021 had positive maturity, 1,337 had positive adult mass and 1,029 had positive longevity. These counts overlap and must not be added as sequential exclusions. Their intersection with taxonomic completeness contained 801 species (59.38% of mammals). Complete-case availability therefore limits the target population.

Table 1. Log maturity associations. Intervals use family clustering. Sensitivity models estimate different conditional associations and are not independent replications.

Model / subset	Species	β (95% CI)
primary	801	0.241 (0.182, 0.301)
unadjusted	801	0.584 (0.536, 0.632)

Model / subset	Species	β (95% CI)
mass adjusted	801	0.443 (0.366, 0.520)
family intercepts	801	0.118 (0.055, 0.180)
no humans	800	0.239 (0.179, 0.298)
no bats primates	620	0.232 (0.166, 0.298)
high quality	99	0.273 (-0.009, 0.555)
captivity	732	0.228 (0.165, 0.291)
effort origin adjusted	801	0.245 (0.190, 0.300)

The primary coefficient was 0.241 (SE 0.030; 95% CI 0.182 to 0.301), corresponding to an 18.20% longevity difference per doubling of maturity. The unadjusted coefficient was 0.584 and the mass-adjusted coefficient 0.443, showing substantial attenuation when taxonomic context was added. With family intercepts, β was 0.118 (95% CI 0.055 to 0.180), equivalent to an 8.49% difference per doubling. These contrasts show that a single species-wide coefficient is sensitive to what between-group variation the model removes.

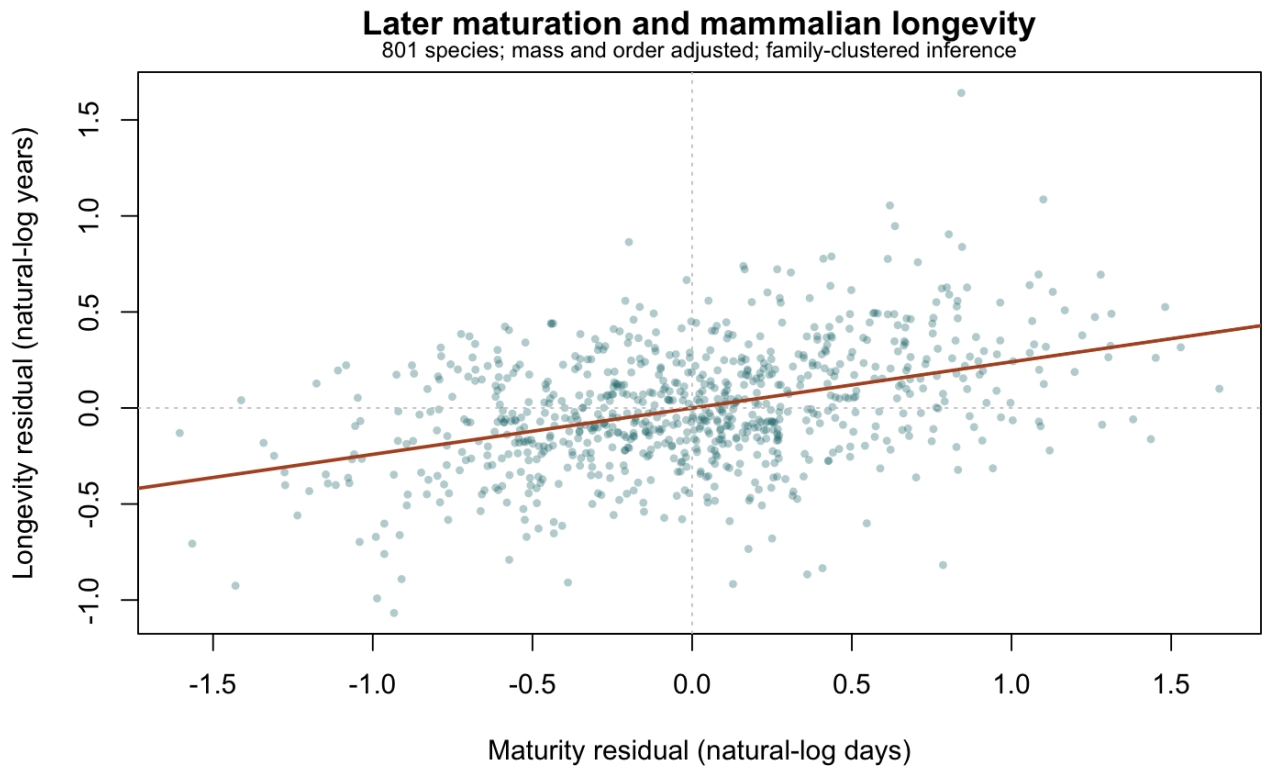

Figure 1. Residual association after removing adult mass and order from both log maturity and log longevity. Each point is a species; the line has the primary regression slope. The display does not remove fine-scale phylogenetic dependence.

Excluding humans or both bats and primates changed β to 0.239 and 0.232, respectively. The observation-effort/origin model yielded 0.245. Leave-one-order-out estimates ranged from 0.204 to 0.259. The high-quality-only subset contained 99 species in 33 families and yielded β = 0.273 with a wide interval (-0.009 to 0.555); it does not independently exclude a null association. No record was discarded because of Cook distance or an unfavorable effect direction.

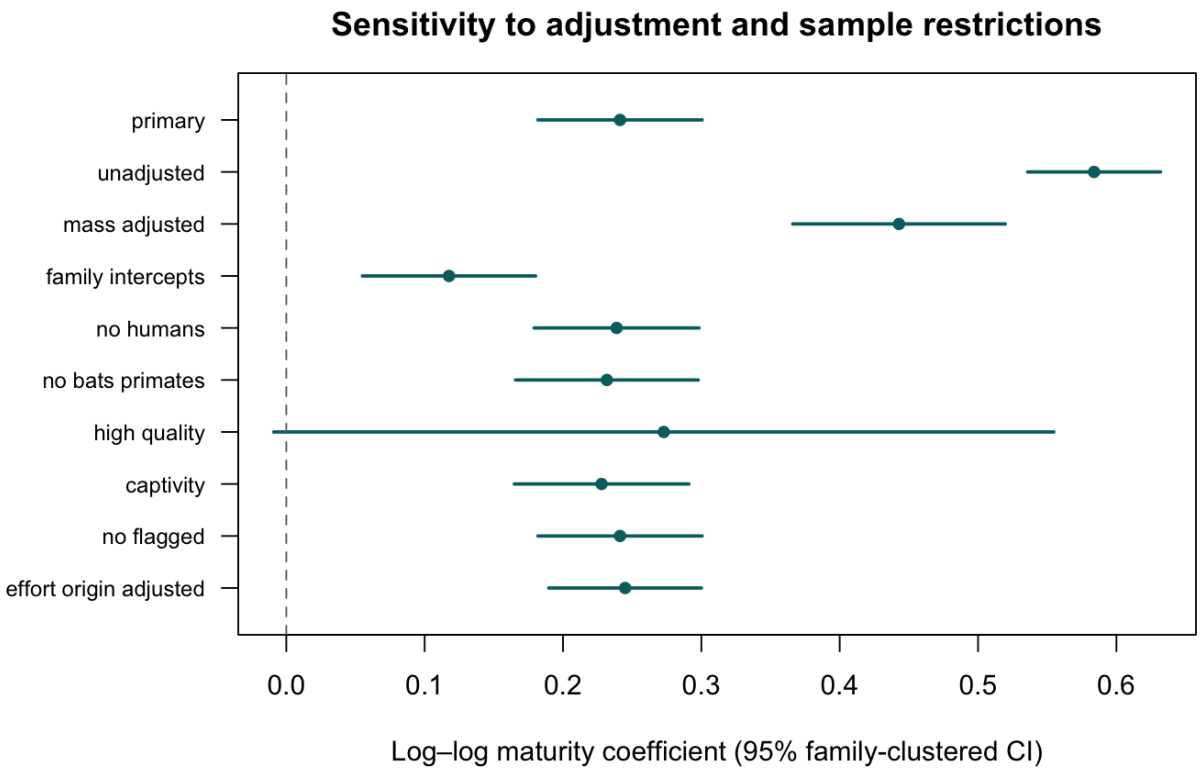

Figure 2. Planned models and sample restrictions, plus the pre-fitting observation-effort adjustment. The no-flagged result is identical to primary because no species failed the maturity-versus-longevity check. High-quality-only uncertainty crosses zero.

Internal prediction included 760 species, 107 families and 15 orders, excluding 41 species from nine orders with only one represented family. Log-longevity RMSE declined from 0.3664 to 0.3275, a 10.60% relative reduction, after adding maturity. The mean paired squared-error difference was -0.02695 squared natural-log units (post-hoc family-bootstrap 95% interval -0.04579 to -0.01030). This is evidence of internal predictive information, not external validation or a guarantee for an unobserved lineage.

Discussion and limitations

The results are consistent with the previously reported relationship between developmental timing and longevity [3]. They also show why adjustment matters: the coefficient is less than half as large with family intercepts as with order intercepts. Neither coefficient should be interpreted as an intervention effect. A taxonomic comparison cannot distinguish correlated ecological strategies, inherited biology, or measurement practices from a causal effect of maturation.

Several limitations materially restrict interpretation. The data are a curated convenience sample rather than a random sample of mammal species. Longevity records depend on numbers observed and captive conditions; coarse categories can only partially address that bias. Maximum recorded age does not directly measure mortality acceleration, and the maturity predictor is not measured in the same individuals. Body mass, maturity and longevity contain measurement error. The study uses no dated phylogeny and may retain correlated errors across families. Family fixed effects also change the estimand toward within-family contrasts. Missing traits can select distinctive species, and source compilations overlap earlier comparative studies. Consequently this is neither independent biological validation nor evidence that a molecular pathway has been identified.

The prediction result supports including developmental context in exploratory comparative bioinformatics. A stronger follow-up would use a reconciled dated mammal tree, multiple phylogenetic realizations, independently curated traits and predeclared external taxa. Those analyses were not performed here. No result supports deliberately delaying human maturation or predicts a benefit from a longevity treatment.

Data, code and research transparency

The accompanying reproduction archive contains the original public exports, CC BY 3.0 attribution, hashes, prospective plan and deviations, R scripts, independent Python verifier, every included record, fold assignments, coefficient tables, plots and environment information. Run Rscript scripts/robustness.R and then python3 scripts/verify.py (NumPy 2.3.5). The main R analysis requires only base/recommended R packages. Run from the archive root; no network access is needed for frozen-data reproduction. Reference retrieval and refresh are separate optional scripts. Data acquisition involved no private participant records or new animal experiments. No ethics approval was obtained or asserted for this secondary analysis.

Prepared using OpenAI Codex for Australis Biogenetics. AI assistance covered question selection, literature retrieval, programming, numerical checks, drafting and formatting. No human scientific author, institutional affiliation, ethics approval, external peer review or expert endorsement is asserted. Numerical cross-checks were performed by a second implementation, not by an independent human reviewer. Publication on a company website is not scientific peer review. The commercial website requested the work; no funding award, outside sponsor, or investigator conflict-of-interest declaration has been supplied. HAGR’s curators and cited authors did not participate in or endorse this analysis.

References

[1] de Magalhães JP, Abidi Z, Dos Santos GA, Avelar RA, Barardo D, Chatsirisupachai K, Clark P, De-Souza EA, Johnson EJ, Lopes I, Novoa G, Senez L, Talay A, Thornton D, To PKP. Human Ageing Genomic Resources: updates on key databases in ageing research. Nucleic Acids Research. 2024;52(D1):D900-D908. https://doi.org/10.1093/nar/gkad927

[2] de Magalhães JP, Costa J. A database of vertebrate longevity records and their relation to other life-history traits. Journal of Evolutionary Biology. 2009;22(8):1770-1774. https://doi.org/10.1111/j.1420-9101.2009.01783.x

[3] de Magalhães JP, Costa J, Church GM. An analysis of the relationship between metabolism, developmental schedules, and longevity using phylogenetic independent contrasts. Journals of Gerontology A. 2007;62(2):149-160. https://doi.org/10.1093/gerona/62.2.149

[4] Human Ageing Genomic Resources. AnAge build 15 release notes. 3 July 2023; accessed 5 September 2026. https://genomics.senescence.info/species/release.html

[5] Human Ageing Genomic Resources. Disclaimers, credits, and copyright: CC BY 3.0. Accessed 5 September 2026. https://genomics.senescence.info/legal.html

[6] Human Ageing Genomic Resources. Using HAGR: AnAge documentation. Accessed 5 September 2026. https://genomics.senescence.info/help.html

[7] Holm S. A simple sequentially rejective multiple test procedure. Scandinavian Journal of Statistics. 1979;6(2):65-70. https://www.jstor.org/stable/4615733