

Macroevolution of Genome Size in Amphibians

H. Christoph Liedtke¹, David Gower², Mark Wilkinson², Ivan Gomez-Mestre¹

¹Estación Biológica de Doñana, Seville, Spain

²Natural History Museum, London, UK

/GENOME SIZES

Genomes conspicuously vary in size across the tree of life. Genome size is not directly linked to organismal complexity and in eukaryotes the differences are mostly due to non-coding DNA. Differences in genome size across taxa are due to changes in insertion-deletion ratios, intron number and length, gene duplication events and differential proliferation of transposable elements. Resulting variation in genome size is thought to be adaptive, link to biological traits or complexity of life cycles. Homing in on such causal relationships has proven difficult because many of these components are inter-correlated and biological traits often show strong phylogenetic signal. Emerging comparative phylogenetic methods allow us to test evolutionary hypotheses on the mode and rates of genome sizes evolution as well as evolutionary correlations with life history traits. Amphibians constitute the group of vertebrates with the largest variation in genome size, and due their global distribution are exposed to a large array of environmental conditions and selective pressures. Moreover, they have the greatest diversity of reproductive modes of all tetrapods. We ask the following questions:

What are the patterns of genome size evolution in amphibians?

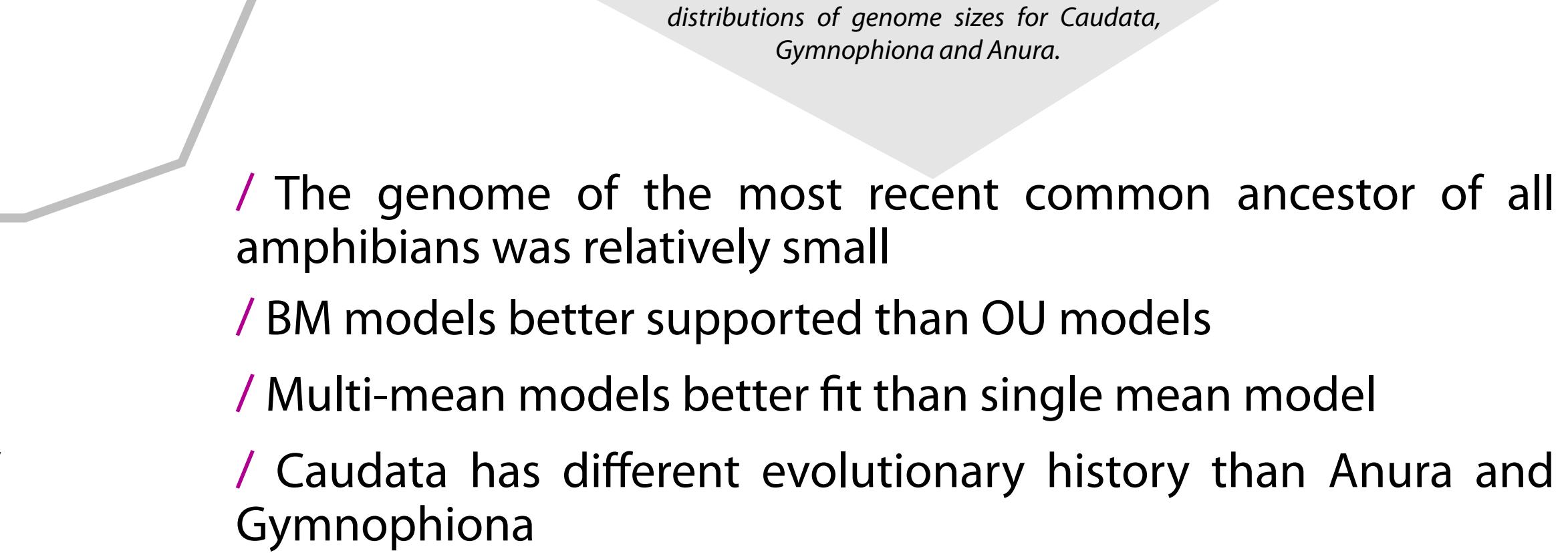
Are evolutionary changes in genome size correlated to life history evolution?

/MODE OF EVOLUTION

We complemented existing measures of genome sizes (www.genomesize.com) with our own measurements for several species, especially for Gymnophiona, a group of amphibians that has largely been ignored in previous studies. We used macroevolutionary methods to test whether genome sizes evolved stochastically as a function of time (adhering to a Brownian motion [BM] model) or whether genomes are pulled towards one or more selective optima (Ornstein-Uhlenbeck [OU] model). We also tested whether genome size evolution is best described by a single process across all amphibians or whether different lineages evolved towards different optima, using the hypothesis-driven model comparison algorithms implemented in mvMORPH (Clavel et al. 2015).

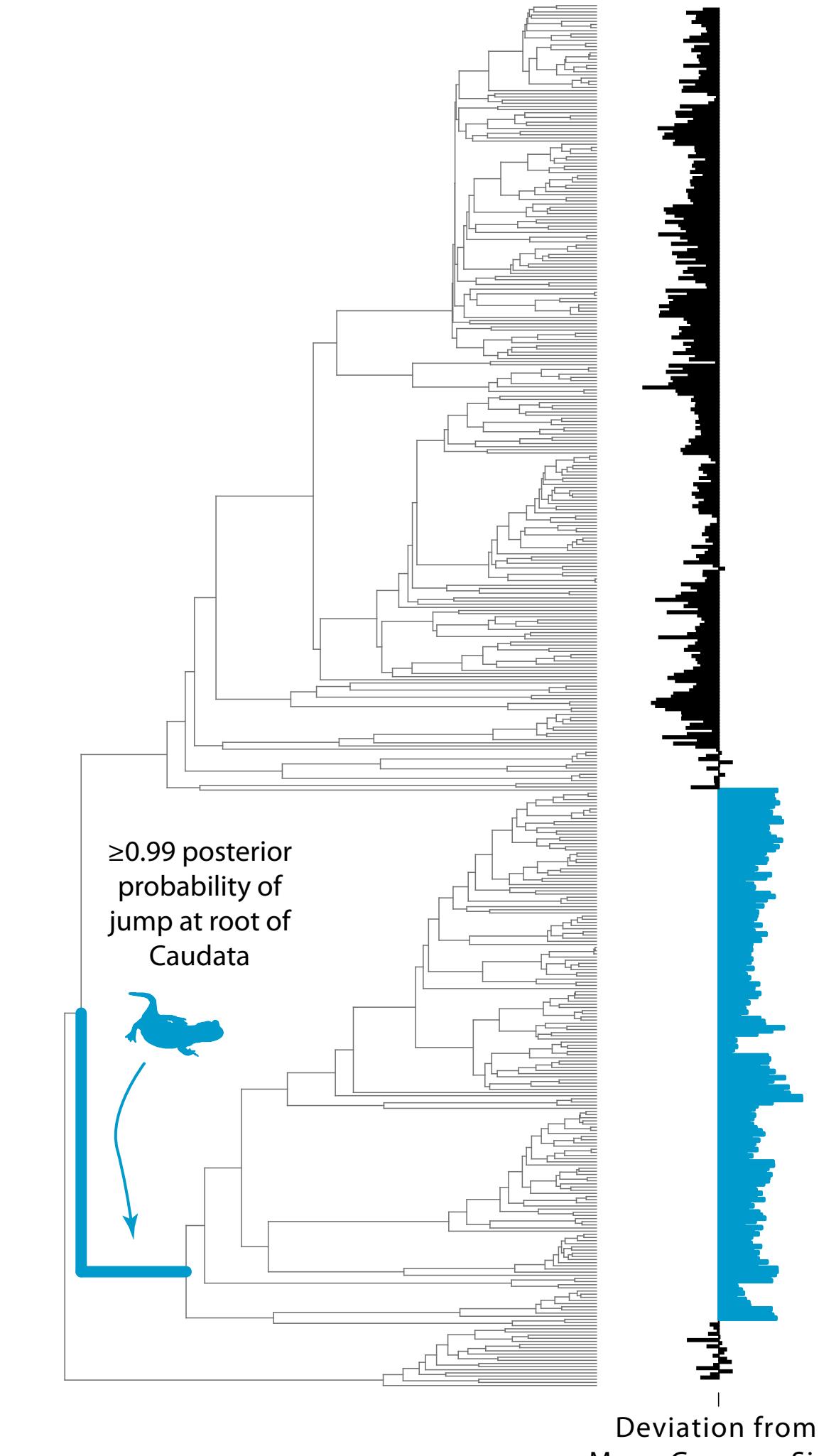
Evolutionary Hypotheses:

	AIC	dAIC
Brownian motion		
Single mean	-530.2	37.2
Salamander shift	-567.5	
Shift at root of every order	-564.6	2.8



- / The genome of the most recent common ancestor of all amphibians was relatively small
- / BM models better supported than OU models
- / Multi-mean models better fit than single mean model
- / Caudata has different evolutionary history than Anura and Gymnophiona

/RATE OF EVOLUTION



- / Genome size evolved gradually in amphibians, but...
- / Large genomes of Caudata are the result of a punctuated shift

Punctuated vs Gradual Evolution

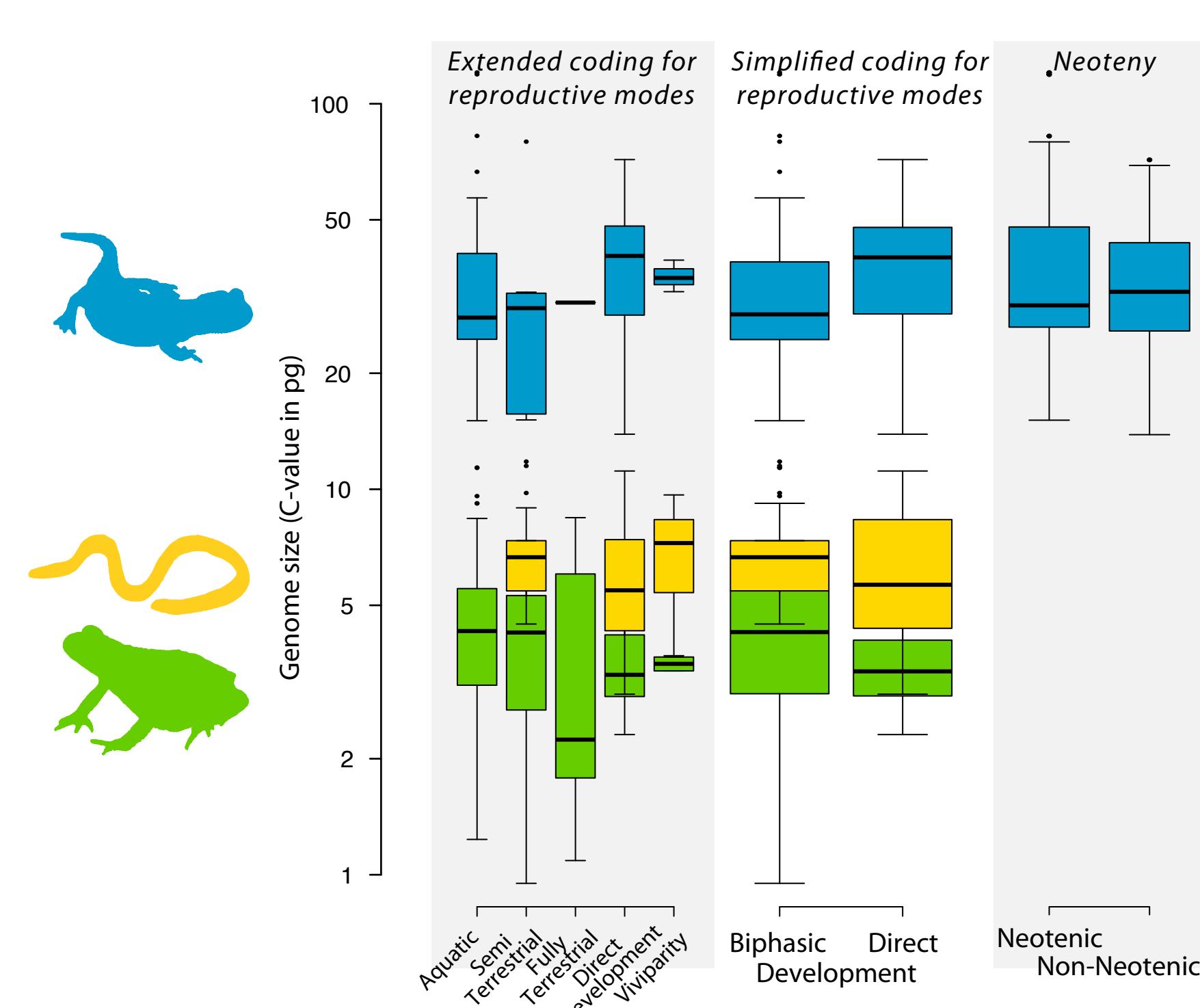
Rates of trait evolution need not be constant over time nor across clades and evolution can be gradual or punctuated. Using 'levolution' (Duchén et al. 2017) we compare the model-fit of a gradual change-only rate model with a 'random-jump' model that allows a trait to experience saltational deviations from the gradual background process along any given branch of the phylogeny (Lévy process).

The Lévy model was a significantly better fit (LRT: 193.19; p>0.001; dAIC 189.19), recovering a single 'jump' event at the stem of all Caudata (posterior probability >0.99).

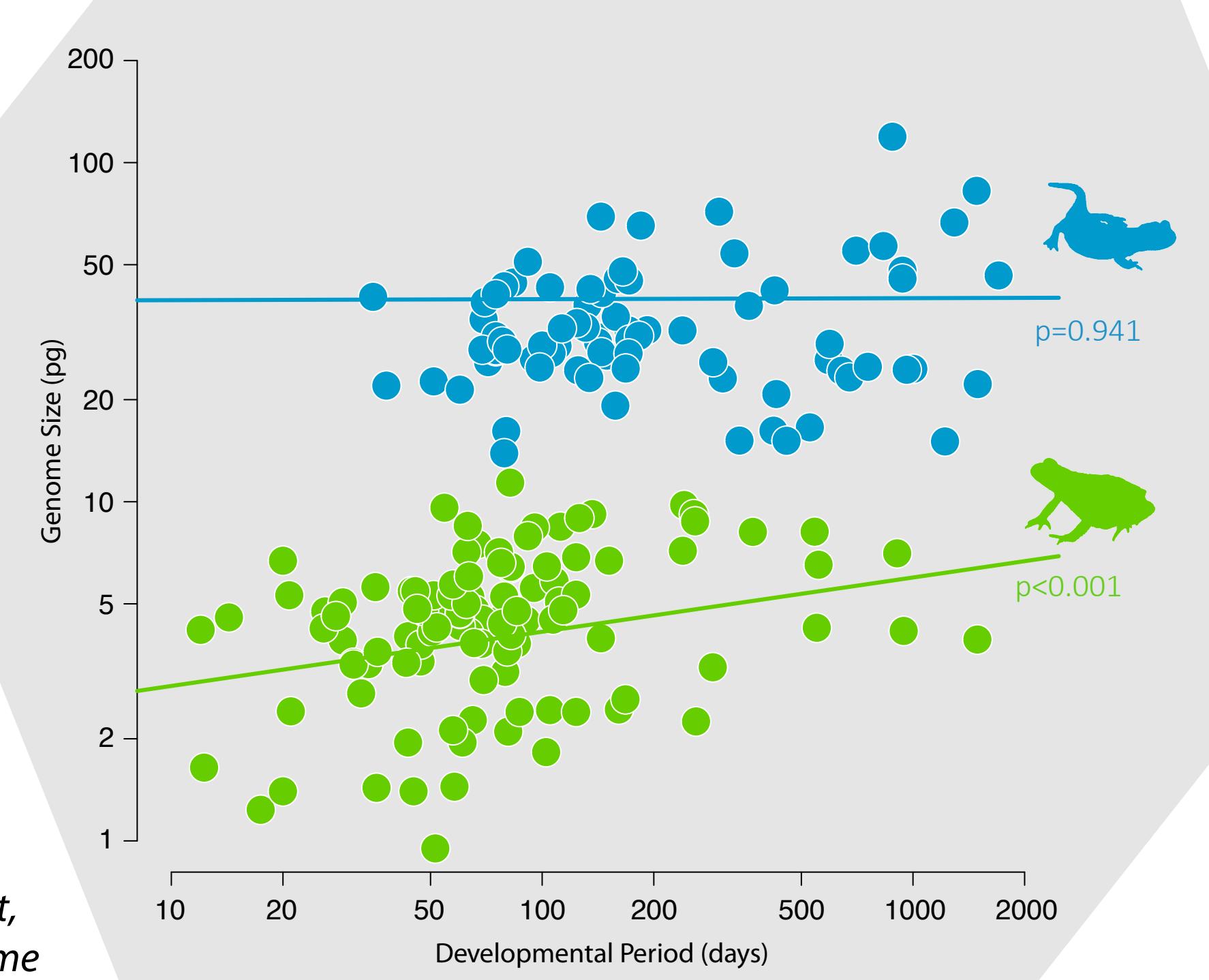
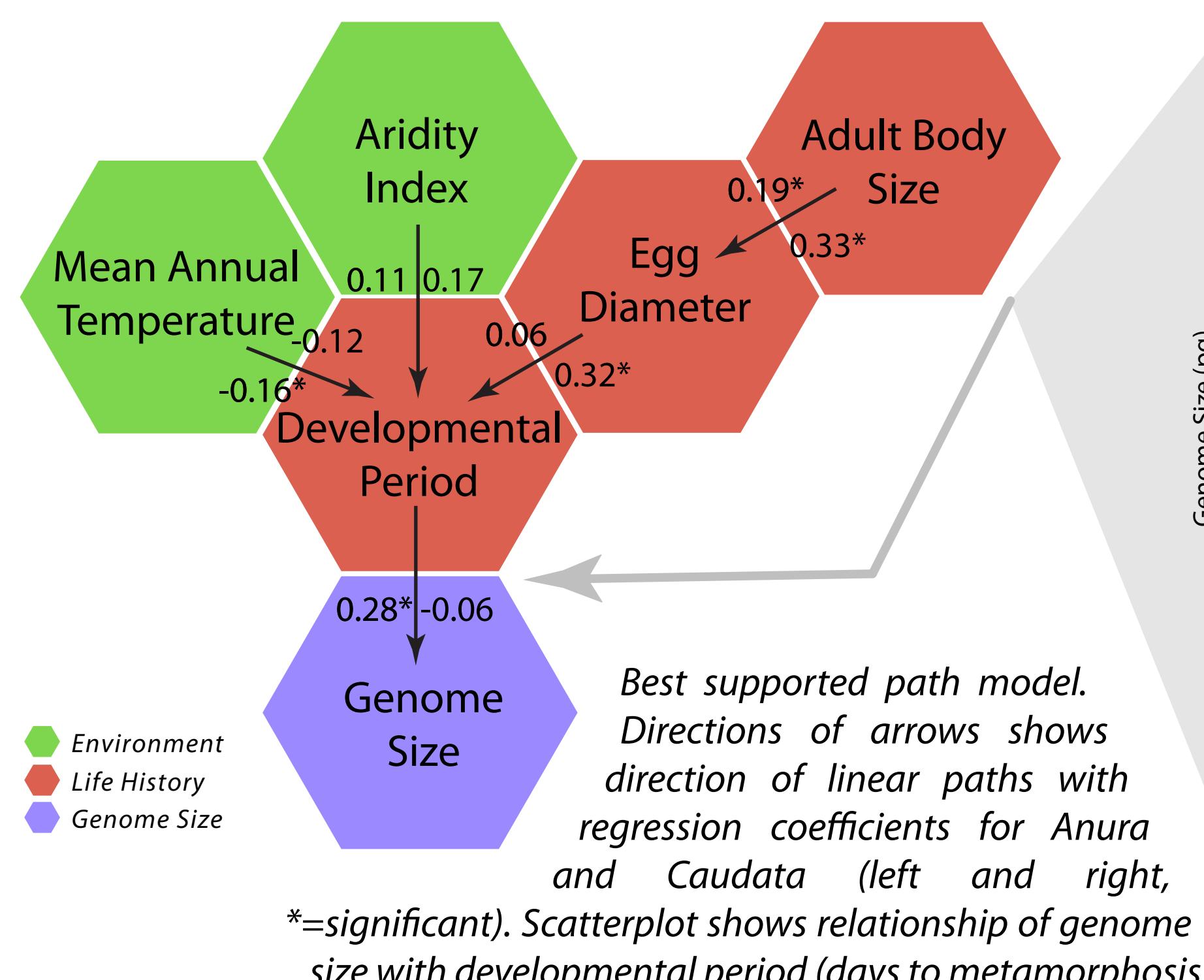
/EVOLUTIONARY CORRELATIONS WITH LIFE HISTORY

Complex life cycles and genome size

The ancestral amphibian life cycle was biphasic (aquatic larvae, terrestrial adults), but many species have lost either the larval (direct development or viviparity) or adult (neoteny) stage. It has been suggested that maintaining drastically distinct life stages requires additional genomic architecture. We tested this using a pANOVA.



- / There are no differences in genome sizes of amphibians with broadly different life cycles



Effects of intercorrelated life history and environmental variables on genome size

It is unclear whether genome size, due to its inverse relationship with cell replication rates, can indirectly be limited by climate and/or selection acting on life history traits. We used phylogenetic path analysis (Hardenberg and Gonzalez-Voyer 2012), a hypothesis driven framework for comparing models with multiple, complex variable interactions, to test direct and indirect effects of life history and environment on genome size.

- / Best model: Only developmental period has a direct effect on genome size, and developmental period is determined both by the environment (temperatures and aridity) and other life history traits (egg size corrected for body size)

/CONCLUSIONS

- / The ancestral amphibian had a moderately sized genome, whose size evolved stochastically over time following a Brownian motion process, with a distinct set of parameters for Caudata and for Anura + Gymnophiona
- / Genome size evolves gradually following a BM process, but with rare saltations in trait space. A statistically supported, punctuated event of this nature led to the genome gigantism in Caudata
- / Contrary to previous claims, there is no evidence for associations of life cycle complexity with genome size
- / Fast developmental rates are favourable in hot, dry environments where breeding periods are short, which indirectly select for smaller genomes in Anura (but seemingly not in Caudata)

/FIND OUT MORE



www.christophliedtke.com