Modeling trait values (with analysis of fossil)

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What do we know?

FAMILY CANIDAE
Coyote, Fox, Jackal, Wild Dog, and Wolf Species of the World
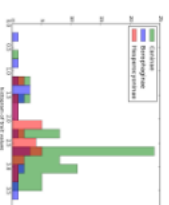

log Kg
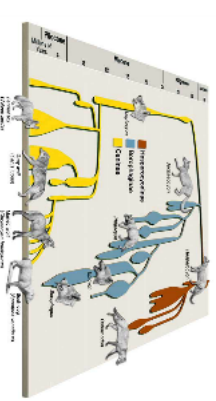
I. Hesperocyoninae
II. Borophaginae
III. Caninae
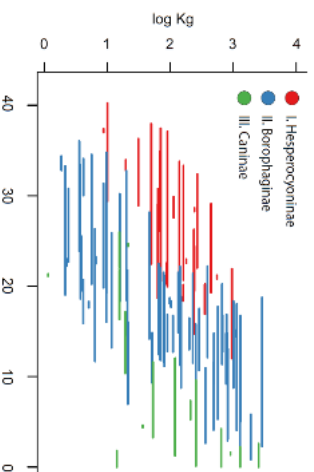
time of origination
time of extinction
body mass

Goals

understand the process,
that govern trait evolution

do not use
phylogenetic three
(information about
connection between
species)

achieve with
incomplete fossil data

Methods

statistics & random processes

Estimation of parameters:
- max likelihood
- Bayesian (MCMC)

tested on simulations and applied to real data

Main results and conclusions

- approaches (Bayesian and max-likelihood) agrees

- results of three subfamilies separated are different that from the whole family

- there exist positive trend in mass , limited by some optimal value(thus agrees with biological prediction)

- evolution in this case is not random