



Methods for Estimating Extinction and Diversification Rates

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Motivation

- Phylogenetic estimation
- How do we gauge a model's applicability at evolutionary timescales?
 - Fossil records
 - Environmental events

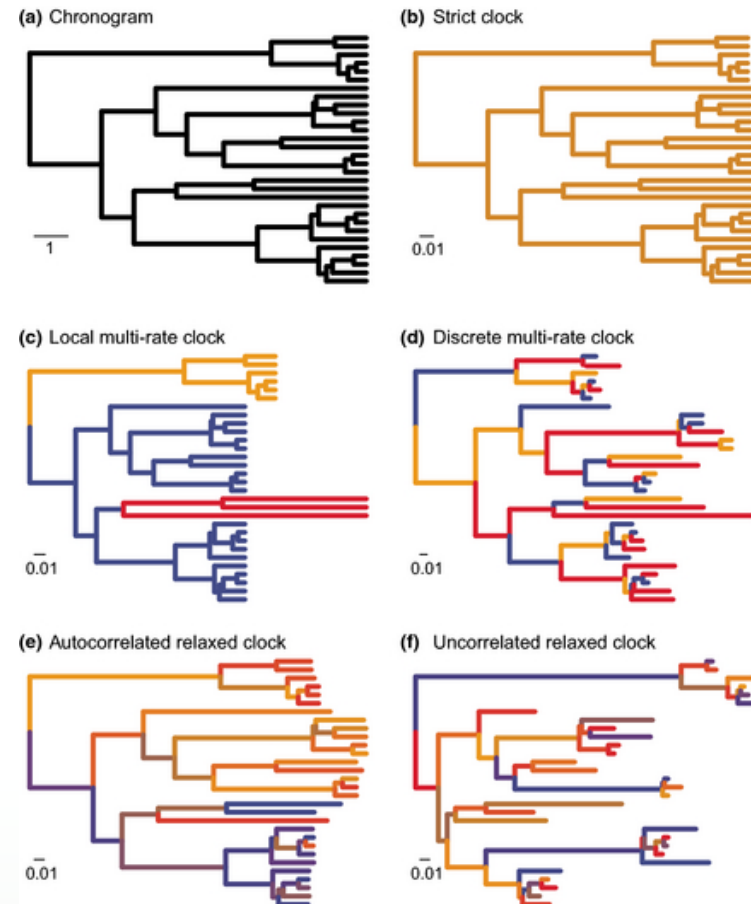


Current Methods

- BAMB (Bayesian)
- MEDUSA (Maximum Likelihood)
- TreePar (Maximum Likelihood)
- CoMET (Bayesian)

Considerations

- Molecular Clock
 - Strict
 - Relaxed
- Extinction Type
 - Global
 - Lineage-Specific





Goals

- Comprehensive exploration of the field
 - Pros/Cons of each method
 - Major roadblocks
- State of the field going forward
 - New directions
 - Predictive efficacy



References

Ho, S. Y. W. and Duchêne, S. (2014), Molecular-clock methods for estimating evolutionary rates and timescales. *Mol Ecol*, 23: 5947–5965. doi:10.1111/mec.12953

Laurent, S., Robinson-Rechavi, M., Salamin, N. Are we able to detect mass extinction events using phylogenies? bioRxiv 004572; doi: <https://doi.org/10.1101/004572>

Laurent, S./ Robinson-Rechavi, M., Salamin, N. (2015). Detecting patterns of species diversification in the presence of both rate shifts and mass extinctions. *BMC Evolutionary Biology*, 15:157. doi: 10.1186/s12862-015-0432-z.

May, M. R., Höhna, S. and Moore, B. R. (2016). A Bayesian approach for detecting the impact of mass-extinction events on molecular phylogenies when rates of lineage diversification may vary. *Methods Ecol Evol*, 7: 947–959. doi:10.1111/2041-210X.12563.

May, M. R., & Moore, B. R. (2016). How Well Can We Detect Lineage-Specific Diversification-Rate Shifts? A Simulation Study of Sequential AIC Methods. *Systematic Biology*, 65(6), 1076–1084. <http://doi.org/10.1093/sysbio/syw026>

Vitti, J.J., Grossman, S.R., and Sabeti, P.C. (2013). Detecting natural selection in genomic data. *Annual Review of Genetics*, 47, 97–120.