Universal scaling in phylogenetic branching

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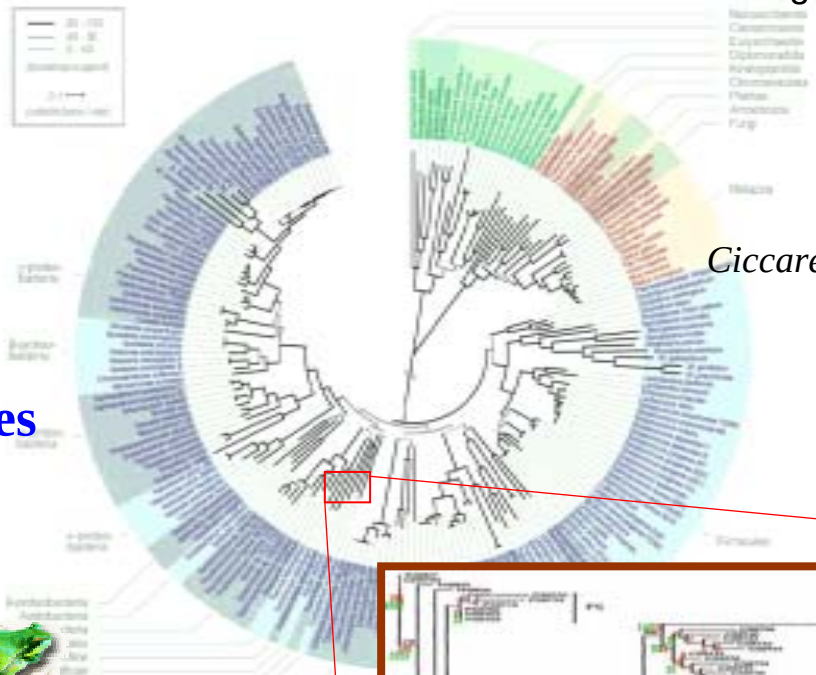
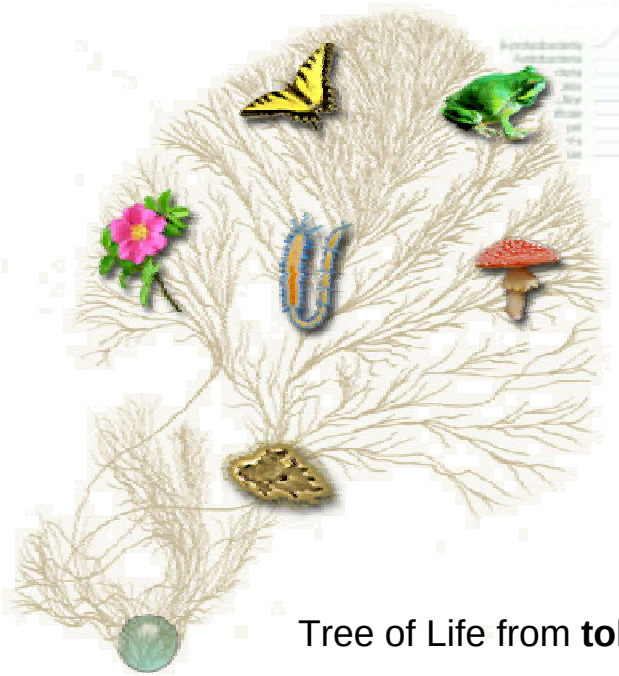


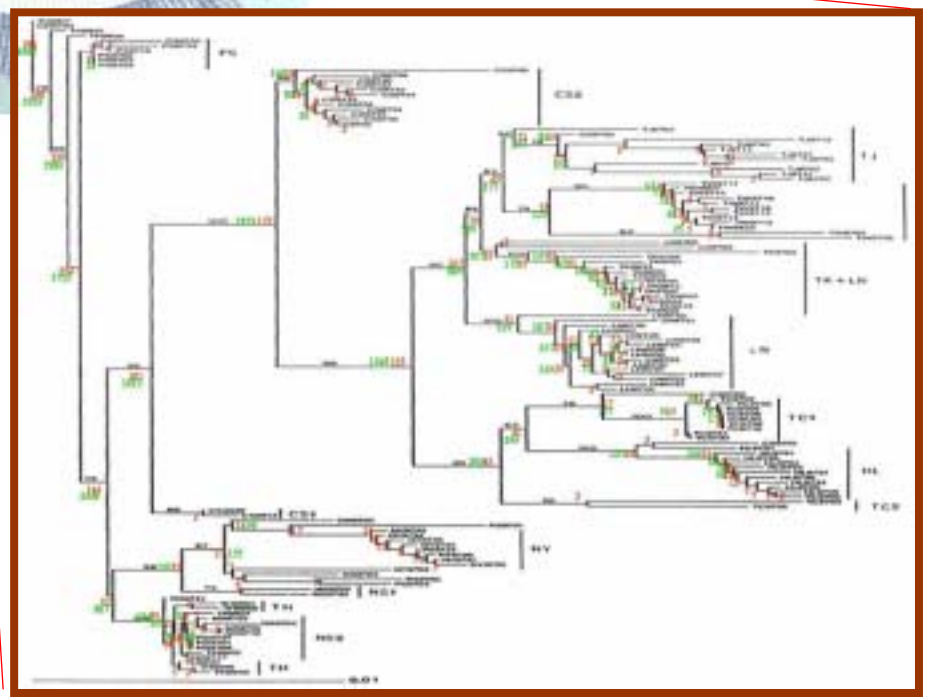
Ciccarelli, F. D. et al. Science (2006)

The “Tree of Life”

and phylogenetic trees



Tree of Life from **tolweb.org**



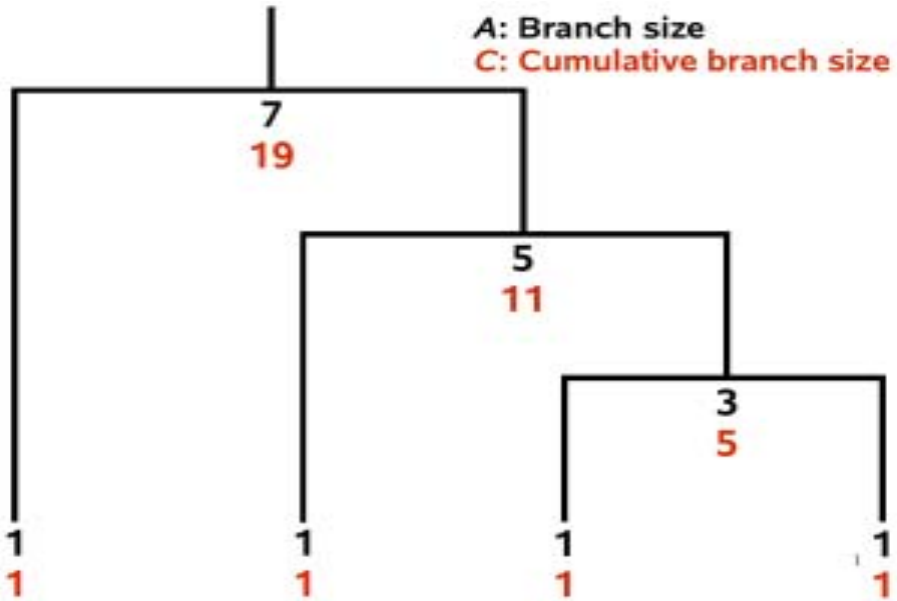
- Characterization of the topology of phylogenetic trees
- Is the branching the same at large (domains, kingdoms,…) and small evolutionary scales (genera, species), and inside the species level ?
- Is the branching the same in different organism groups (plants, animals, marine, terrestial, …) ?
- Can the observed branching properties by simple evolutionary models?

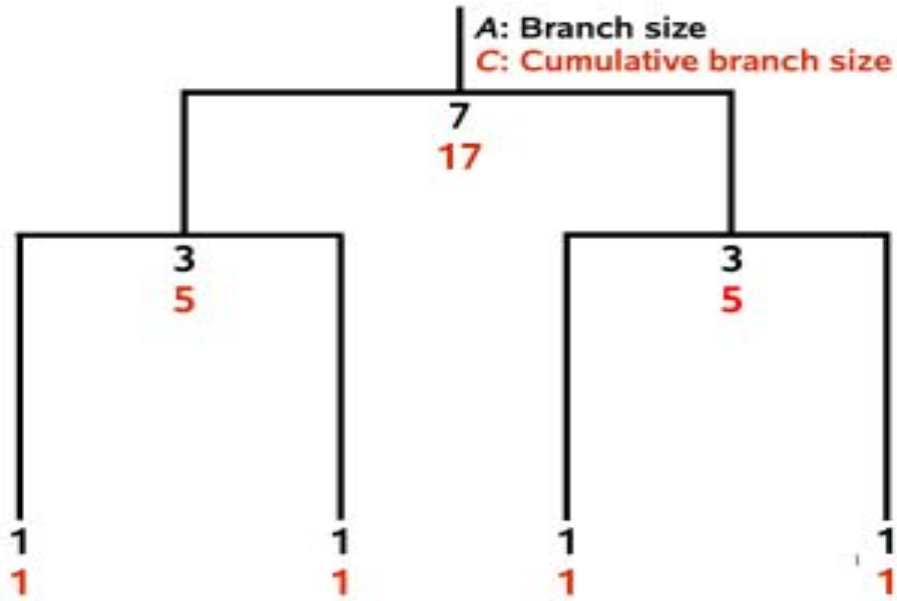
DATASET:

- 5212 **interspecific** phylogenetic trees from **TreeBASE**
- 67 **intraspecific** phylogenies, manually selected from published references, containing organisms from all kingdoms, and from different environments and climatic regions
- 67 manually published **interspecific** phylogenies, selected as before

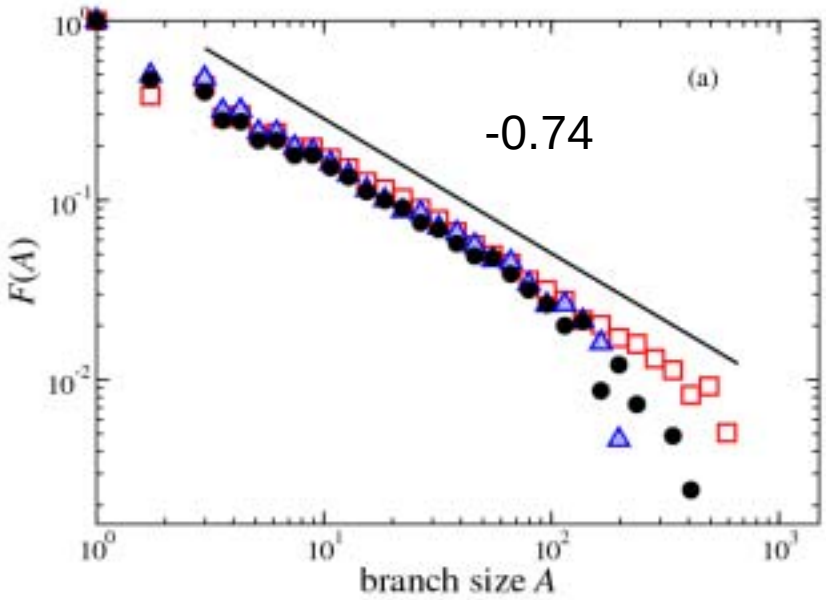
ALLOMETRIC SCALING ANALYSIS (on A's and C's)

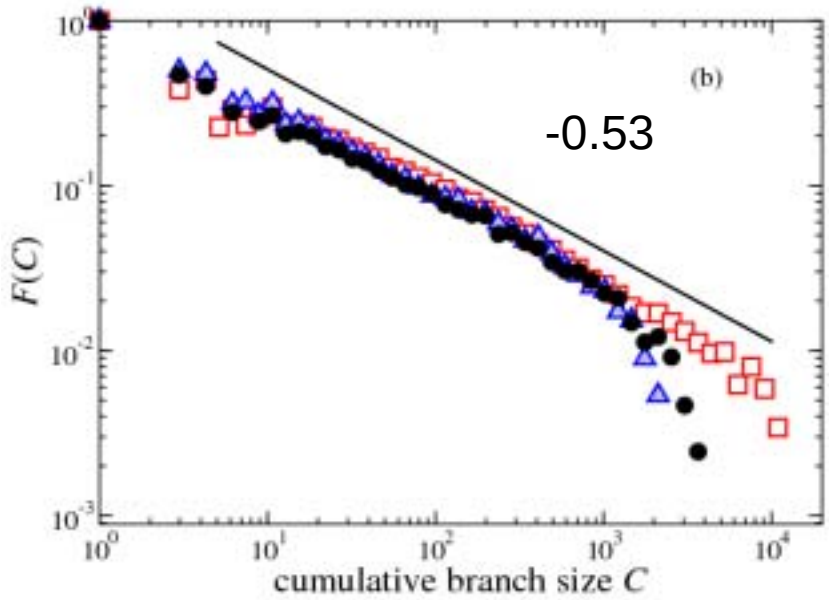
- For each node *i* of a tree, S_i is the subtree rooted at the node *i* containing all nodes bellow *i*.
- **Branch size**, A_i, is the number of nodes in the subtree S_i
- The **cumulative branch size**, $C_i = \Sigma_{k<i} A_k$, describes the shape of a subtree
- Borrowed from analysis of transportation networks, and from allometric scaling in physiology
- Allows to combine and extend classical results on size distributions and on unbalance





Cumulative complementary distribution functions of A and C

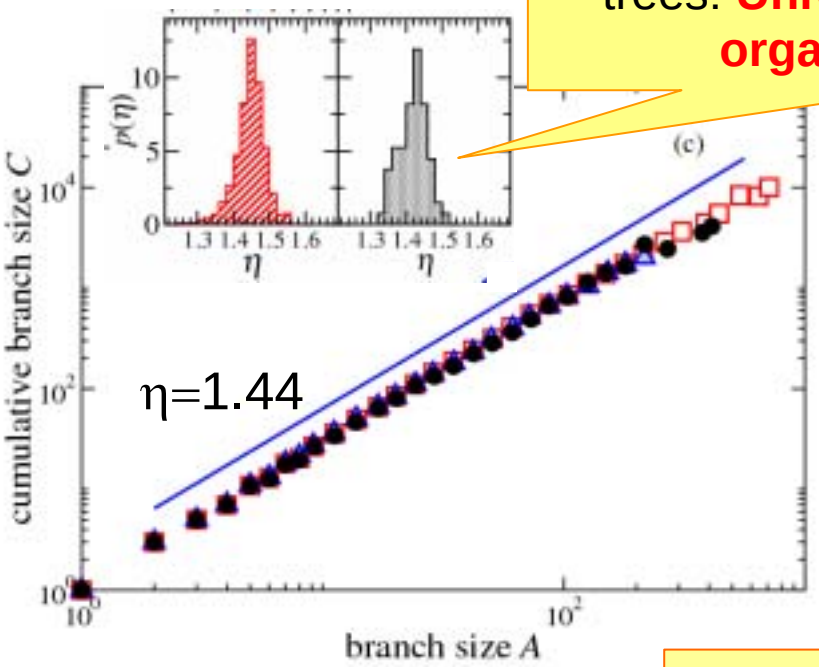




- TreeBASE (interspecific)
- INTERspecific
- INTRAspecific

Universality across evolutionary scales

Histograms of the exponents in different trees: **Universality among types of organisms and habitats**



C ~ A^{η} : Allometric scaling giving shape C vs size A

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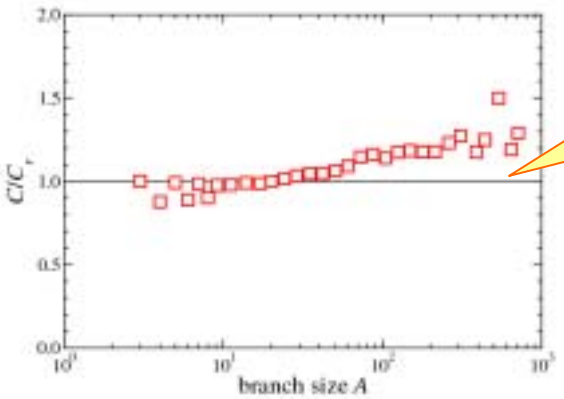
Universality across evolutionary scales



Prediction of the Makov Random Branching model

η=1 : Completely balanced (Cayley) tree
η=2 : Completely unbalanced