

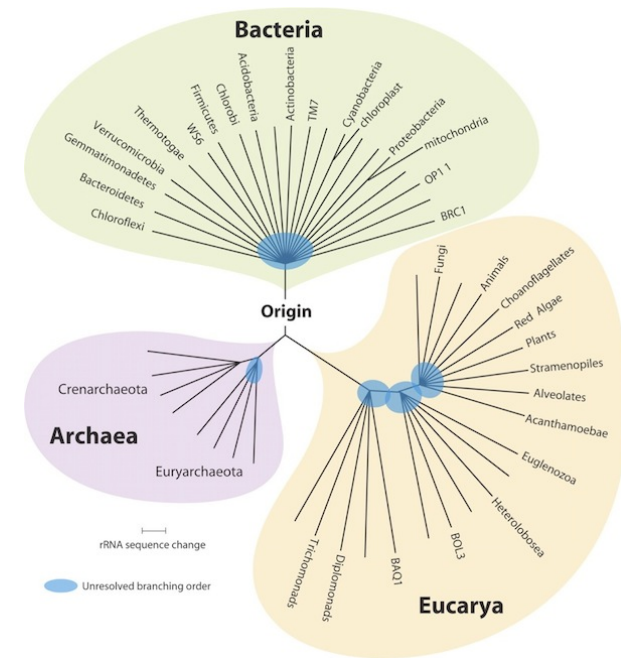
Curso de Evolución 2022

Facultad de Ciencias

Montevideo, Uruguay

<http://evolucion.fcien.edu.uy/>

<http://eva.fcien.udelar.edu.uy/>



Tema 2. Las filogenias como contexto de análisis de la evolución. **Aplicaciones del análisis filogenético.** Análisis filogenético según el principio de parsimonia. Métodos basados en distancias y en modelos de evolución molecular.

**Métodos filogenéticos comparativos.**

# Finalidad de esta presentación breve

- Presentar aplicaciones adicionales de las filogenias.
- En particular, para comparar y estudiar asociaciones de características de los organismos y su entorno en un marco filogenético.
- Servir como introducción y material de apoyo al Práctico 2 del curso.

# Un artículo que cambió la forma de hacer comparaciones entre especies

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The American Naturalist

January 1985

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## PHYLOGENIES AND THE COMPARATIVE METHOD

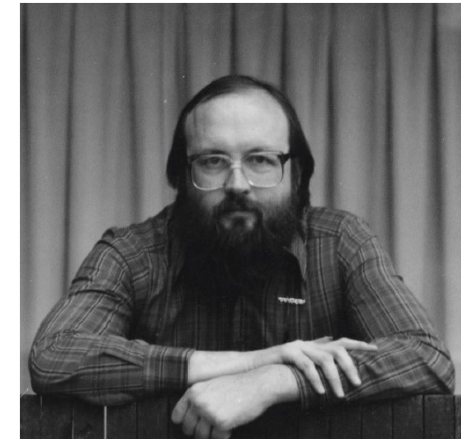
JOSEPH FELSENSTEIN

VOL. 193, NO. 6 THE AMERICAN NATURALIST JUNE 2019

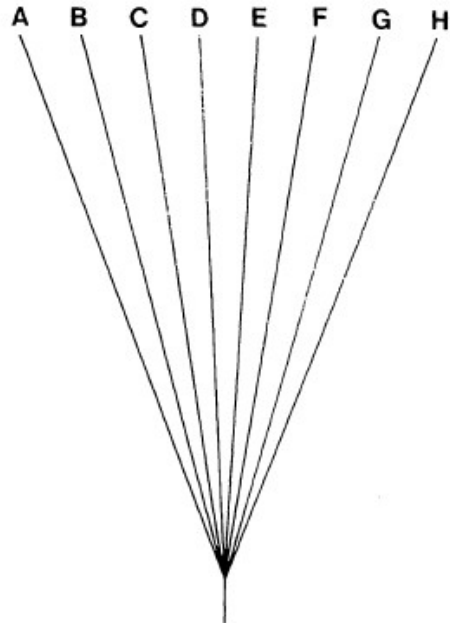
HISTORICAL COMMENT

## Revisiting a Key Innovation in Evolutionary Biology: Felsenstein's "Phylogenies and the Comparative Method"

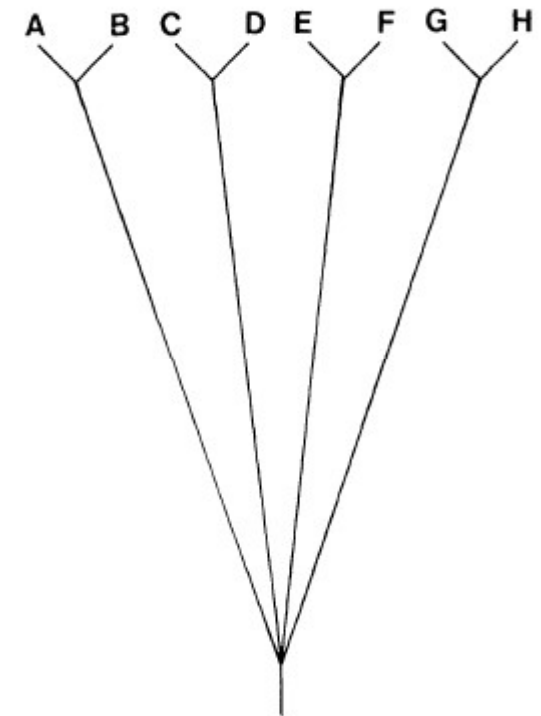
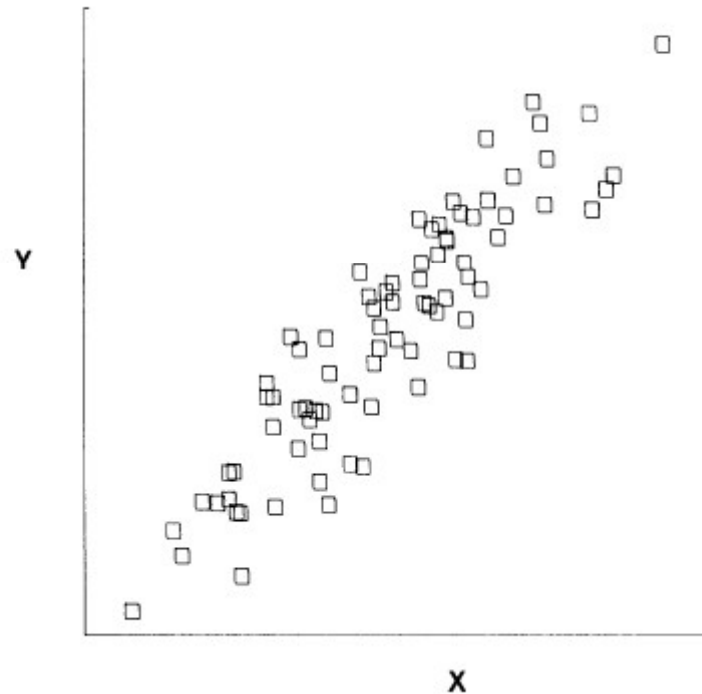
Raymond B. Huey,<sup>1,\*</sup> Theodore Garland Jr.,<sup>2</sup> and Michael Turelli<sup>3</sup>



# El problema

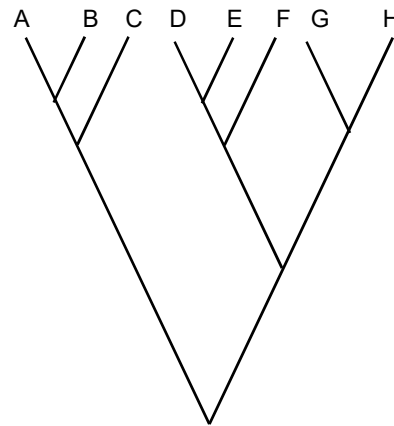
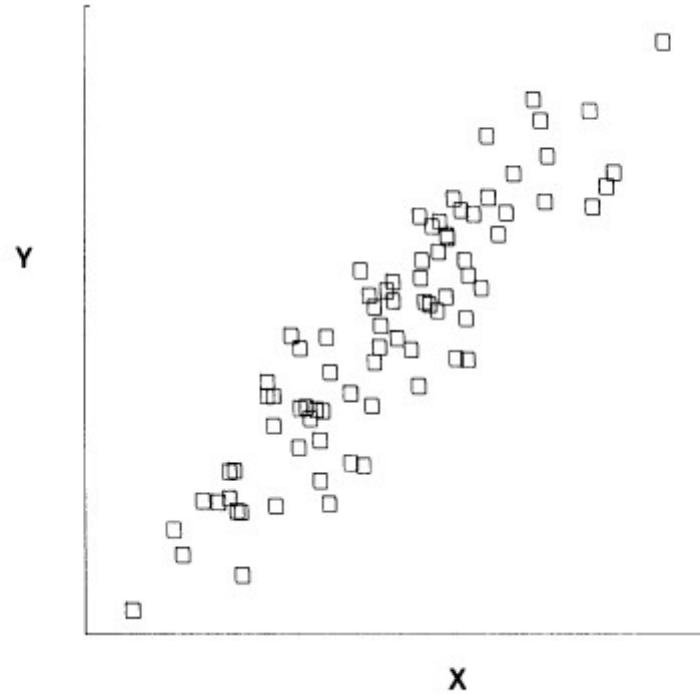
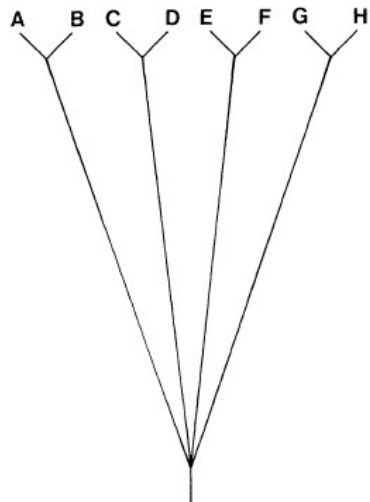
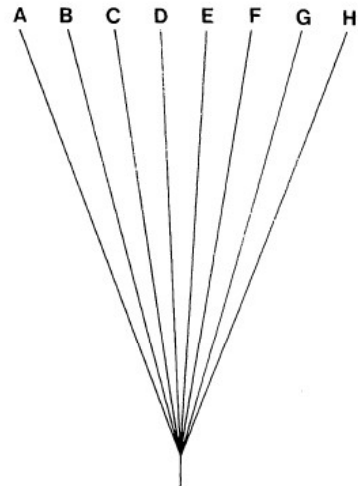


No tenemos 50  
observaciones  
independientes, sino  
8 (c/u con varias  
réplicas)



4 líneas  
independientes; y  
asociados a c/u de  
ellos 4 pares, c/u  
independiente de los  
restantes

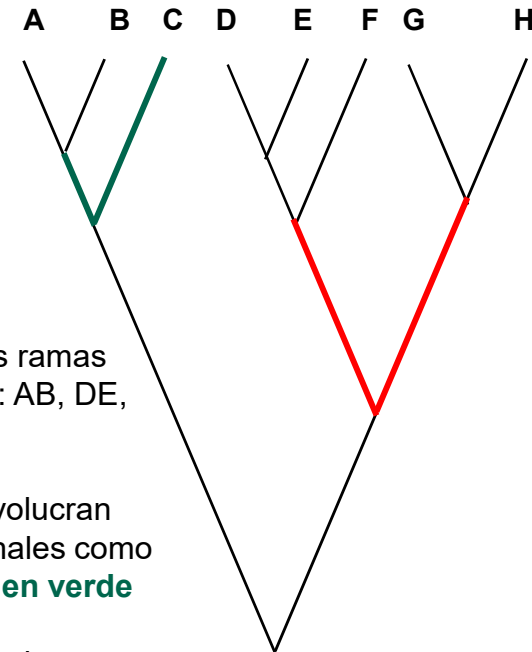
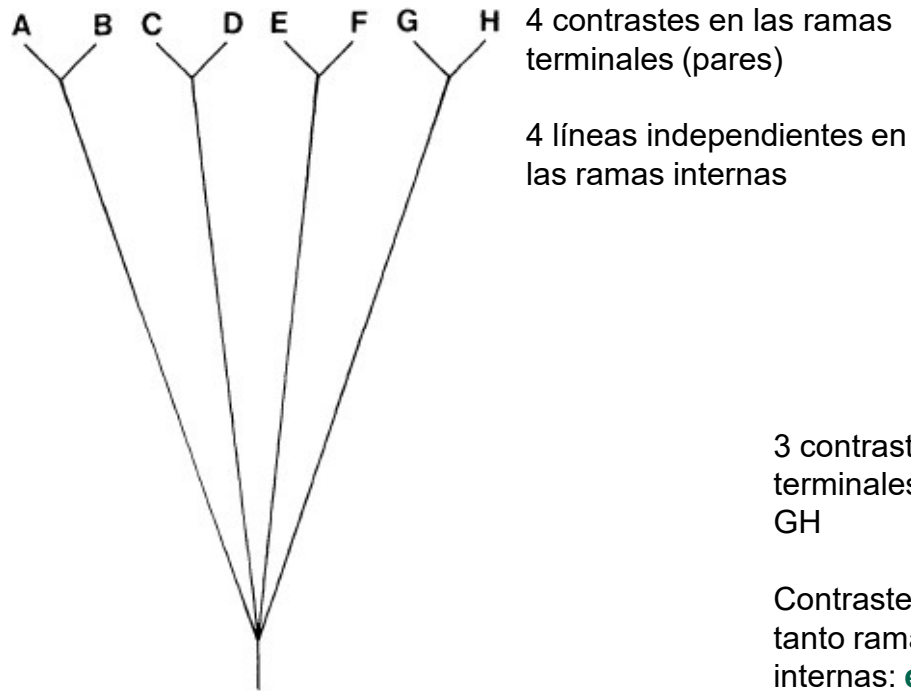
# Generalizando



El número de árboles relevantes posibles (con raíz, completamente dicotómicos) es  $> 135.000$ .

Y deberíamos considerar también variaciones en la longitud de las ramas (a lo largo de las cuales ocurre la divergencia).

# Una solución posible: contrastes independientes

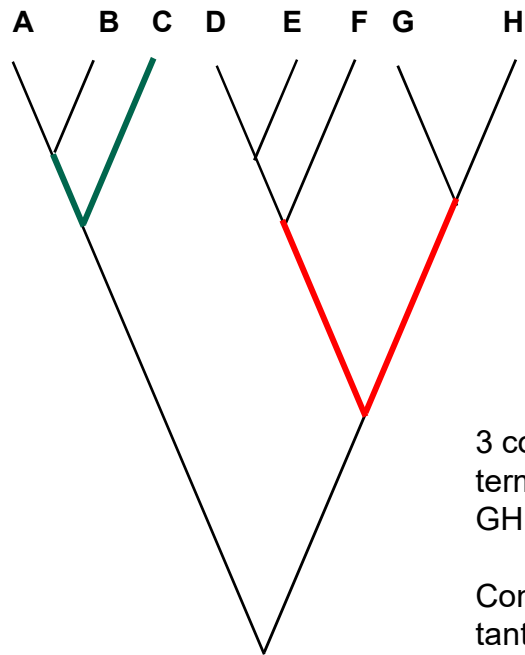


3 contrastes en las ramas terminales (pares): AB, DE, GH

Contrastes que involucran tanto ramas terminales como internas: **ejemplo en verde**

Contrastes que involucran ramas internas: **ejemplo en rojo**

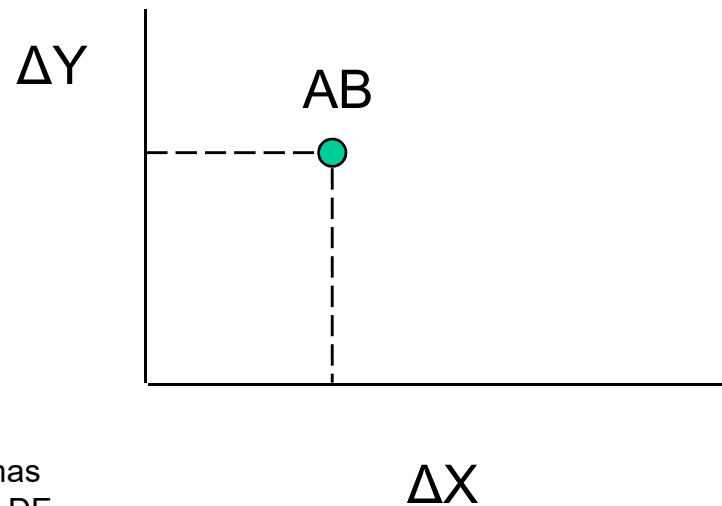
# El objetivo es evaluar cómo se asocian los cambios en dos variables a lo largo de las ramas del árbol



3 contrastes en las ramas terminales (pares): AB, DE, GH

Contrastes que involucran tanto ramas terminales como internas: **ejemplo en verde**

Contrastes que involucran ramas internas: **ejemplo en rojo**



## COMPARATIVE METHOD

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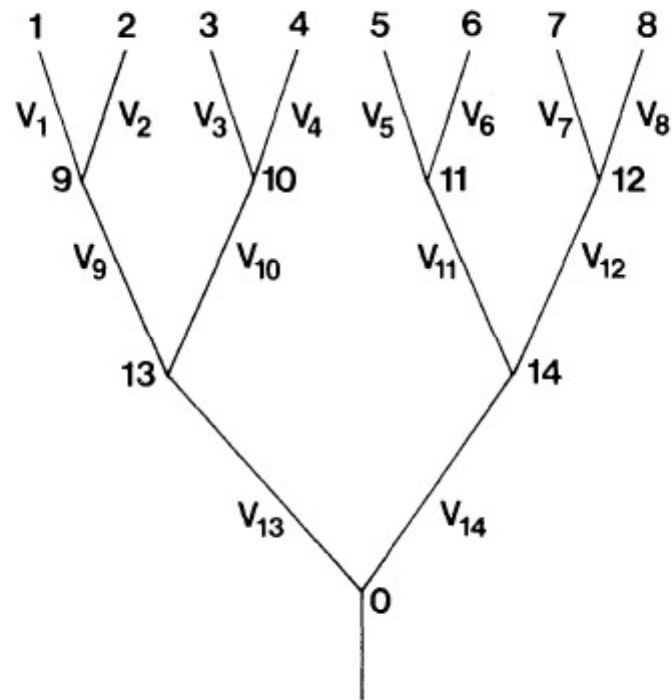


FIG. 8.—An example of a phylogeny, assumed known, from which we can define independent contrasts between taxa. This tree is highly symmetric, so that  $v_1 = v_2 = v_3 = v_4 = v_5 = v_6 = v_7 = v_8$ ,  $v_9 = v_{10} = v_{11} = v_{12}$ , and  $v_{13} = v_{14}$ .

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The preceding computation of contrasts depended on the phylogeny having a particular, and very unlikely, symmetric structure. Fortunately a more general procedure exists, of which the above was a special case. I have discussed its elements elsewhere (Felsenstein 1973) as part of a computational method for obtaining the likelihood of a given phylogeny. The general prescription for computing these contrasts is repeated applications of the following steps: (1) Find two tips on the phylogeny that are adjacent (say nodes  $i$  and  $j$ ) and have a common ancestor, say node  $k$ . (2) Compute the contrast  $X_i - X_j$ . This has expectation zero and variance proportional to  $v_i + v_j$ . (3) Remove the two tips from the tree, leaving behind only the ancestor  $k$ , which now becomes a tip. Assign it the character value

$$X_k = \frac{(1/v_i) X_i + (1/v_j) X_j}{1/v_i + 1/v_j}. \quad (3)$$

the weighted average of  $X_i$  and  $X_j$ , the weights being proportional to the inverses of the variances  $v_i$  and  $v_j$ . (4) Lengthen the branch below node  $k$  by increasing its length from  $v_k$  to  $v_k + v_i v_j / (v_i + v_j)$ . This lengthening occurs because the weighted average that computes  $X_k$  in equation (3) does not compute the phenotype of the ancestor but only estimates it, and does so with an error that is statistically indistinguishable from an extra burst of evolution after node  $k$ .

After one pass through steps 1–4, we have found one contrast and reduced the number of tips on the tree by one. We continue to repeat steps 1–4 until there is only one tip left on the tree. This will extract  $n - 1$  contrasts if there were originally  $n$  species. Each contrast can be divided by the square root of its variance to bring them to a common variance. Since the  $v_i$  are arbitrary, this procedure can be used on a phylogeny of any shape whatsoever, even on ones that contain multifurcations, since those can always be represented as a series of bifurcations having some branch lengths zero.