Evolución de familias multigénicas 2020

- Consecuencias funcionales de la duplicaciones génicas
- Evolución Molecular

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Turning a hobby into a job: How duplicated genes find new functions

Gavin C. Conant and Kenneth H. Wolfe‡*

Abstract | Gene duplication provides raw material for functional innovation. Recent advances have shed light on two fundamental questions regarding gene duplication: which genes tend to undergo duplication? And how does natural selection subsequently act on them? Genomic data suggest that different gene classes tend to be retained after single-gene and whole-genome duplications. We also know that functional differences between duplicate genes can originate in several different ways, including mutations that directly impart new functions, subdivision of ancestral functions and selection for changes in gene dosage. Interestingly, in many cases the 'new' function of one copy is a secondary property that was always present, but that has been co-opted to a primary role after the duplication.

DOI: 10.1038/nrg2689 · Corpus ID: 7382546

The evolution of gene duplications: classifying and distinguishing between models

Hideki Innan, Fyodor A. Kondrashov · Published 2010 · Biology, Medicine · Nature Reviews Genetics

Gene duplications and their subsequent divergence play an important part in the evolution of novel gene functions. Several models for the emergence, maintenance and evolution of gene copies have been proposed. However, a clear consensus on how gene duplications are fixed and maintained in genomes is lacking. Here, we present a comprehensive classification of the models that are relevant to all stages of the evolution of gene duplications. Each model predicts a unique combination of evolutionary... CONTINUE READING

Review > J Hered. Sep-Oct 2009;100(5):605-17. doi: 10.1093/jhered/esp047. Epub 2009 Jul 13.

Distinguishing Among Evolutionary Models for the Maintenance of Gene Duplicates

Matthew W Hahn [1]

Affiliations + expand

PMID: 19596713 DOI: 10.1093/jhered/esp047

Abstract

Determining the evolutionary forces responsible for the maintenance of gene duplicates is key to understanding the processes leading to evolutionary adaptation and novelty. In his highly prescient book, Susumu Ohno recognized that duplicate genes are fixed and maintained within a population with 3 distinct outcomes: neofunctionalization, subfunctionalization, and conservation of function. Subsequent researchers have proposed a multitude of population genetic models that lead to these outcomes, each differing largely in the role played by adaptive natural selection. In this paper, I present a nonmathematical review of these models, their predictions, and the evidence

Evolution by gene duplication: an update

Jianzhi Zhang

DOI: https://doi.org/10.1016/S0169-5347(03)00033-8

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Abstract

The importance of gene duplication in supplying raw genetic material to biological evolution has been recognized since the 1930s. Recent genomic sequence data provide substantial evidence for the abundance of duplicated genes in all organisms surveyed. But how do newly duplicated genes survive and acquire novel functions, and what role does gene duplication play in the evolution of genomes and organisms? Detailed molecular characterization of individual gene families, computational analysis of genomic sequences and population genetic modeling can all be used to help us uncover the mechanisms behind the evolution by gene duplication.

Review > Genetics. 1999 Apr;151(4):1531-45.

Preservation of Duplicate Genes by Complementary, Degenerative Mutations

A Force [1], M Lynch, F B Pickett, A Amores, Y L Yan, J Postlethwait

Affiliations + expand

PMID: 10101175 PMCID: PMC1460548

Free PMC article

Abstract

The origin of organismal complexity is generally thought to be tightly coupled to the evolution of new gene functions arising subsequent to gene duplication. Under the classical model for the

What Is the Role of Genome Duplication in the Evolution of Complexity and Diversity? FREE

Karen D. Crow ✉, Günter P. Wagner

Molecular Biology and Evolution, Volume 23, Issue 5, May 2006, Pages 887–892,
https://doi.org/10.1093/molbev/msj083

Published: 20 December 2005 **Article history** ▾

Published: July 2003

Functional Divergence in Protein (Family) Sequence Evolution

Xun Gu

Genetica **118**, 133–141(2003) | Cite this article

Abstract

As widely used today to infer 'function', the homology search is based on the neutral theory

Published: 28 May 2002

Extensive genomic duplication during early chordate evolution

Aoife McLysaght, Karsten Hokamp & Kenneth H. Wolfe

Nature Genetics **31**, 200–204(2002) | Cite this article

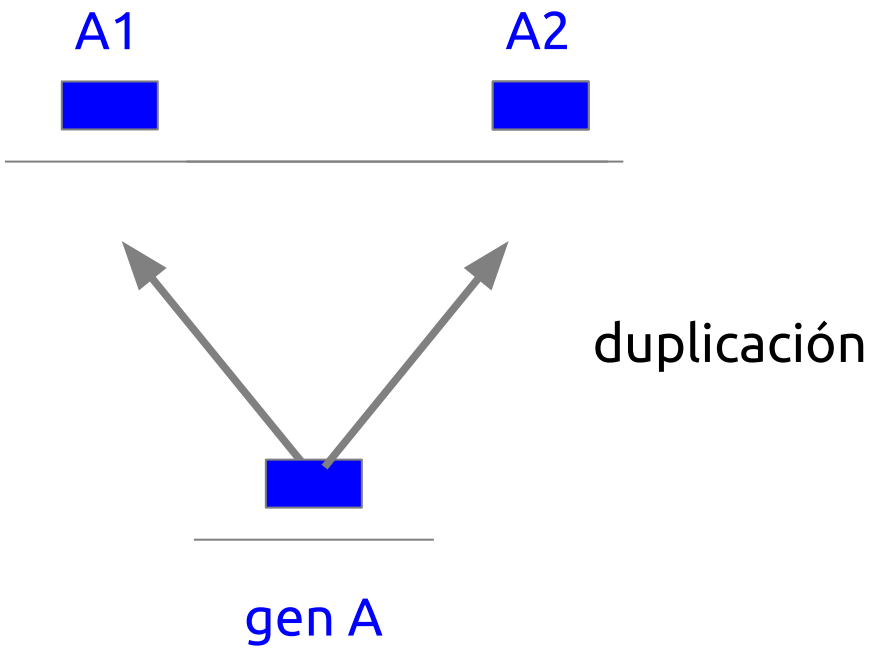
Destino de genes duplicados?

Perder su función (pseudogenes)

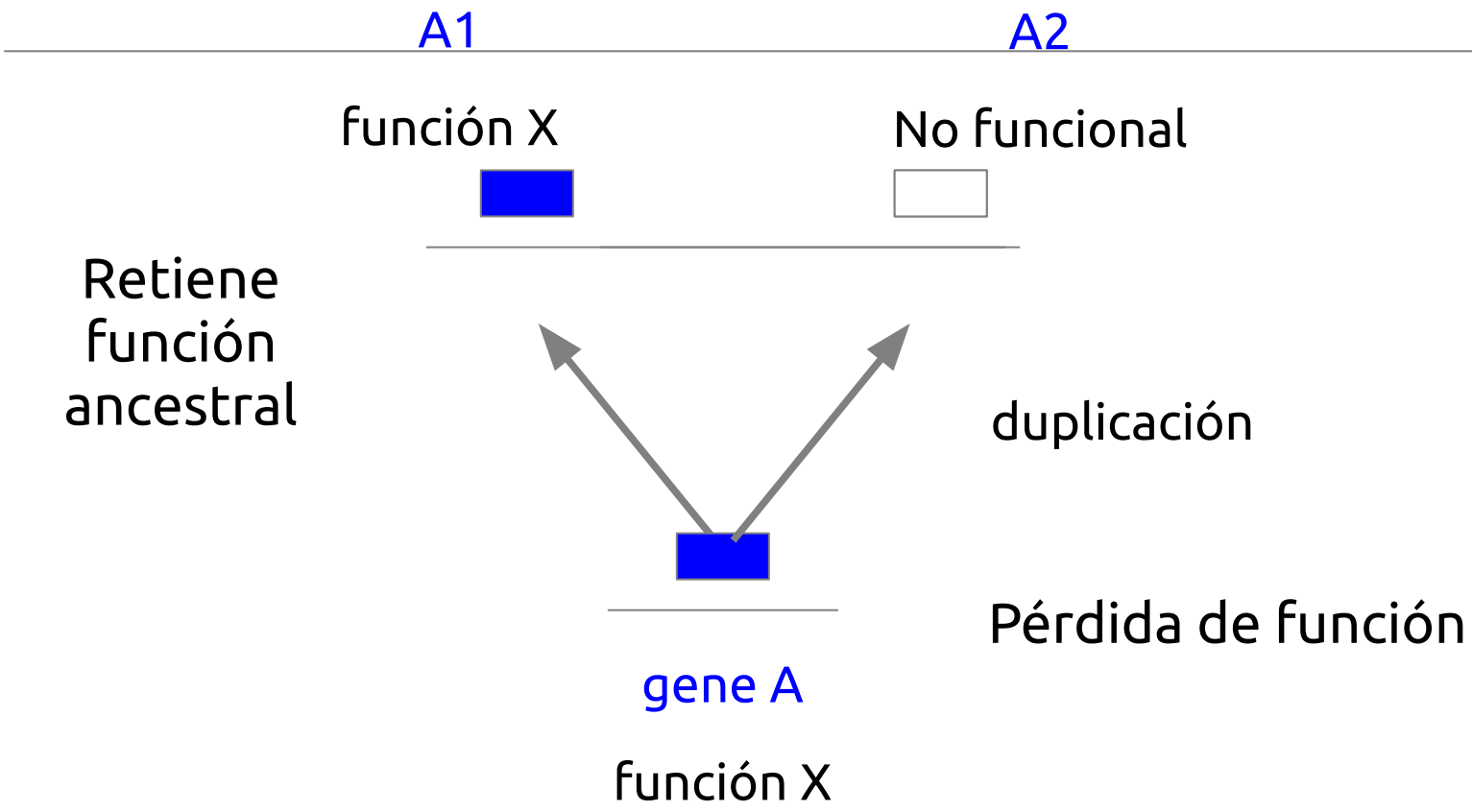
Mantener la misma función (copias redundantes)

Adquirir una nueva función (Neofuncionalización)

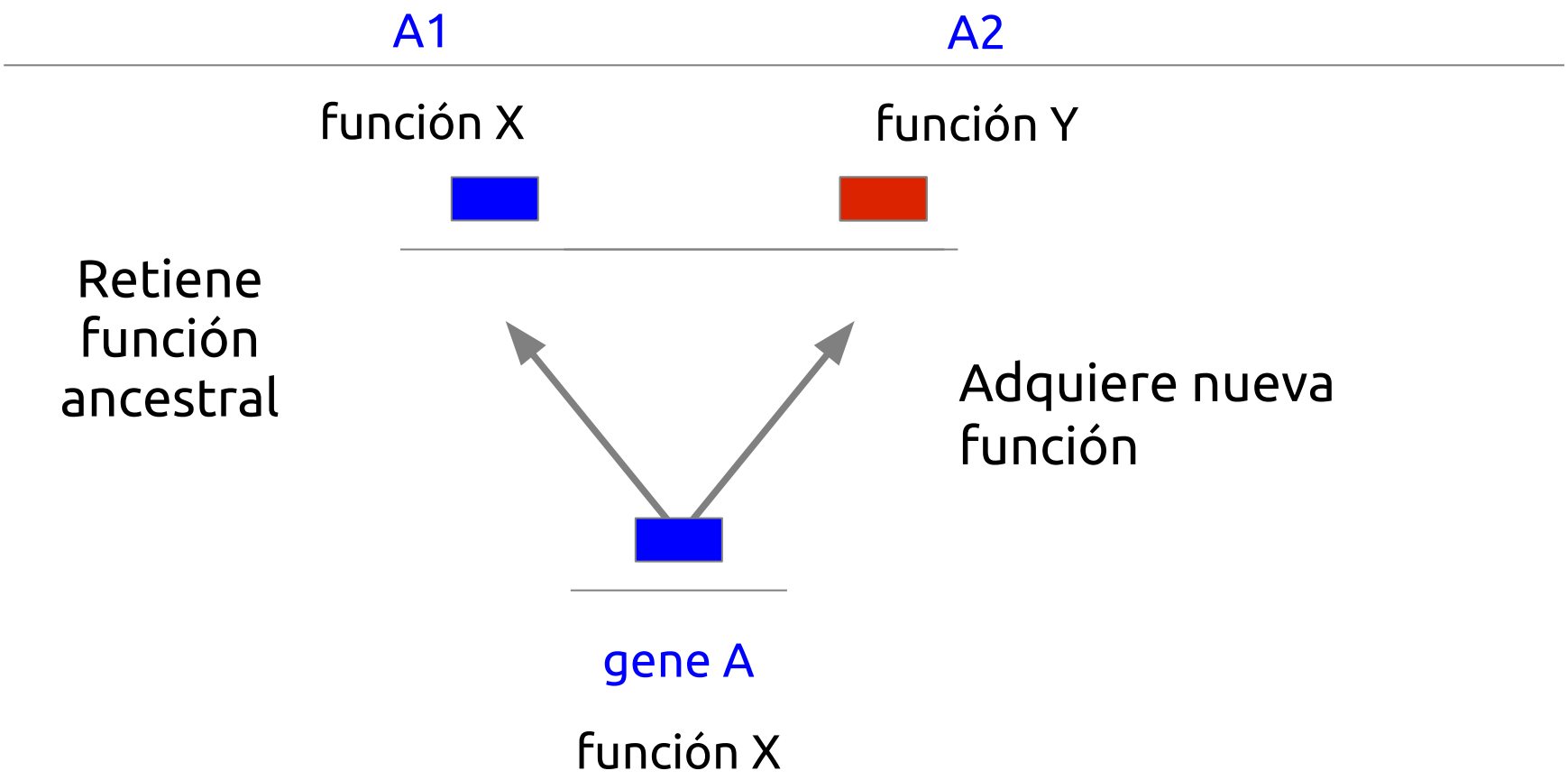
Destino de genes duplicados?



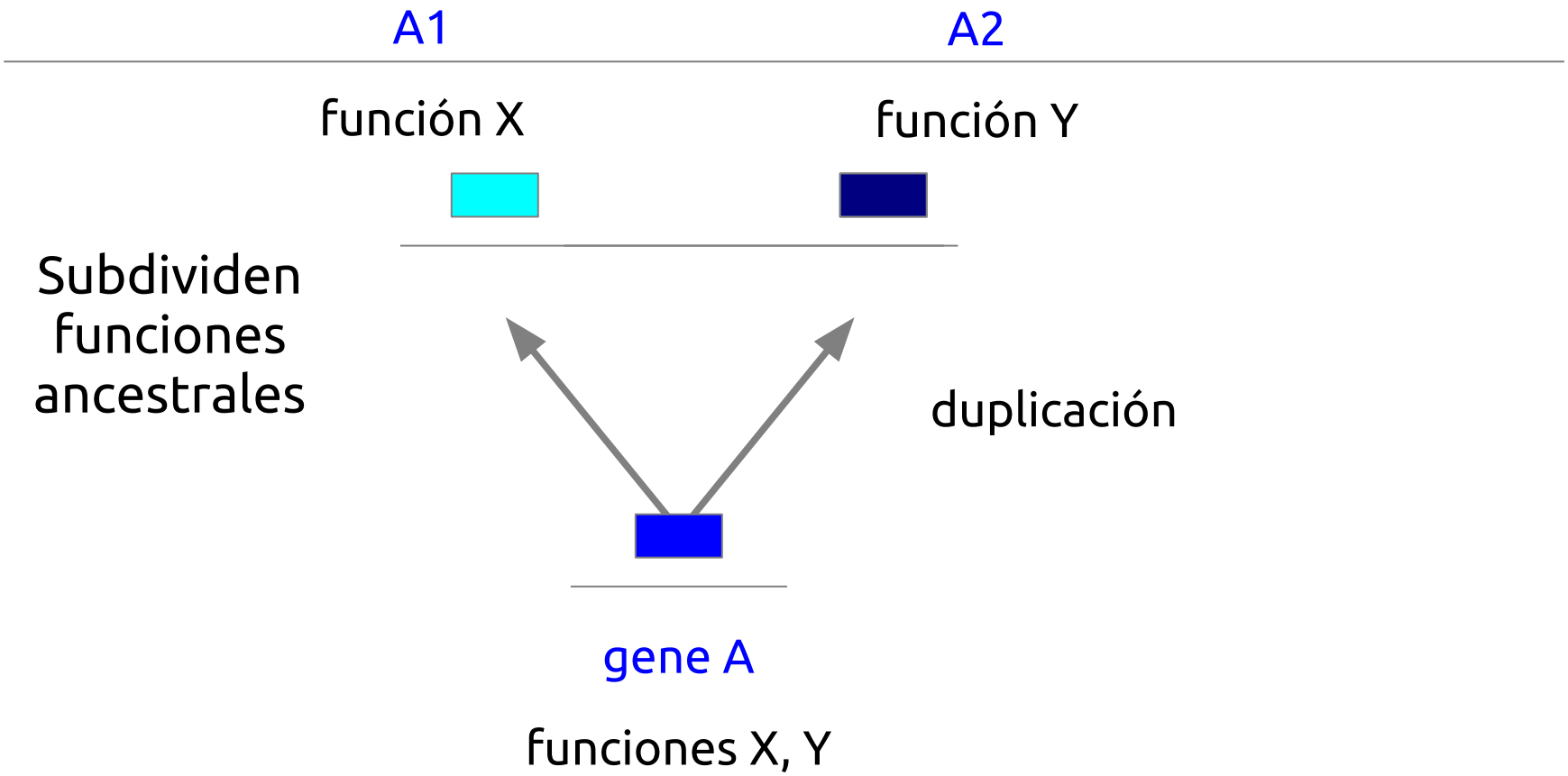
Pseudogenización



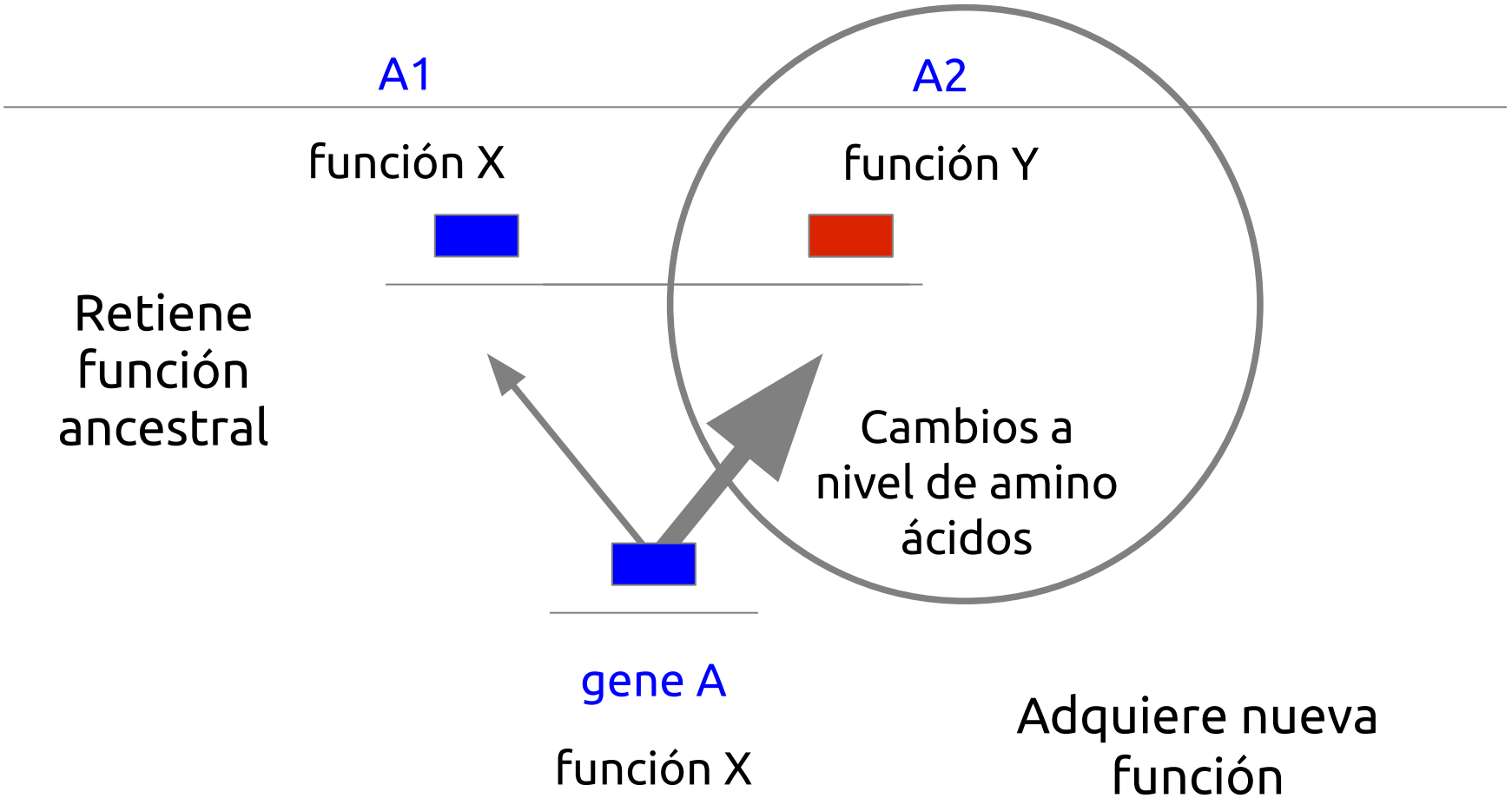
Neofuncionalización



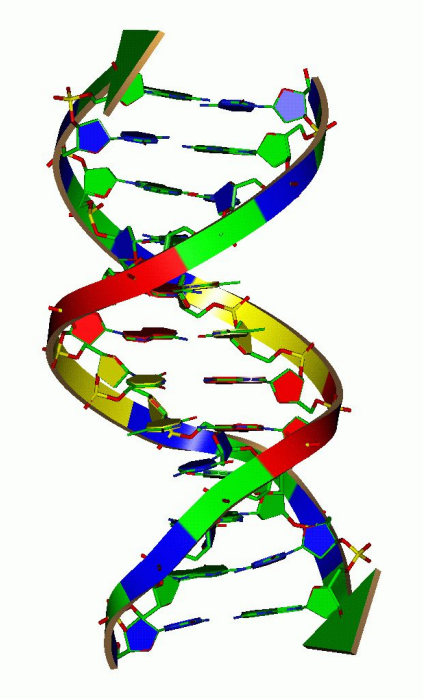
Subfuncionalización



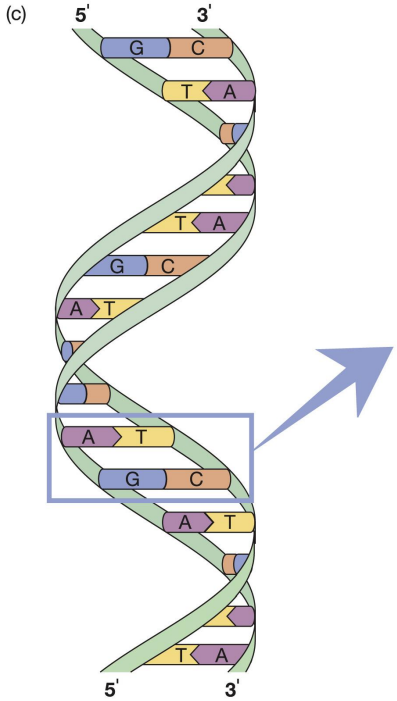
Neofuncionalización

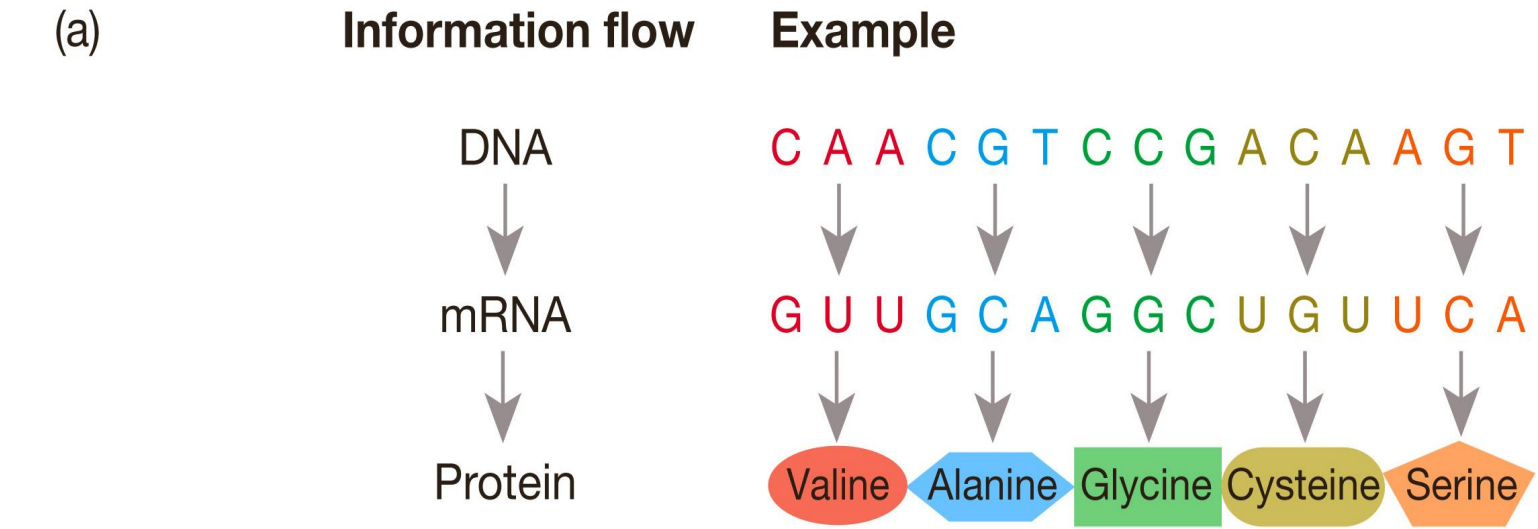


Evolución Molecular

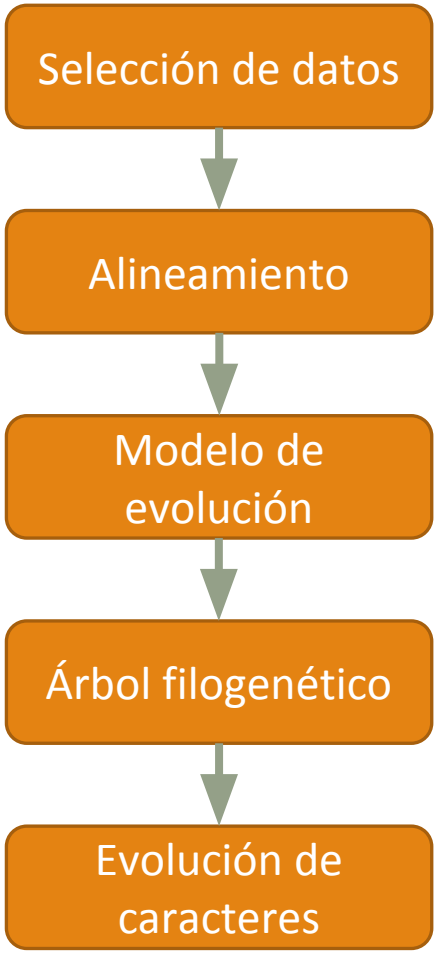


Dogma Central de la Biología Molecular





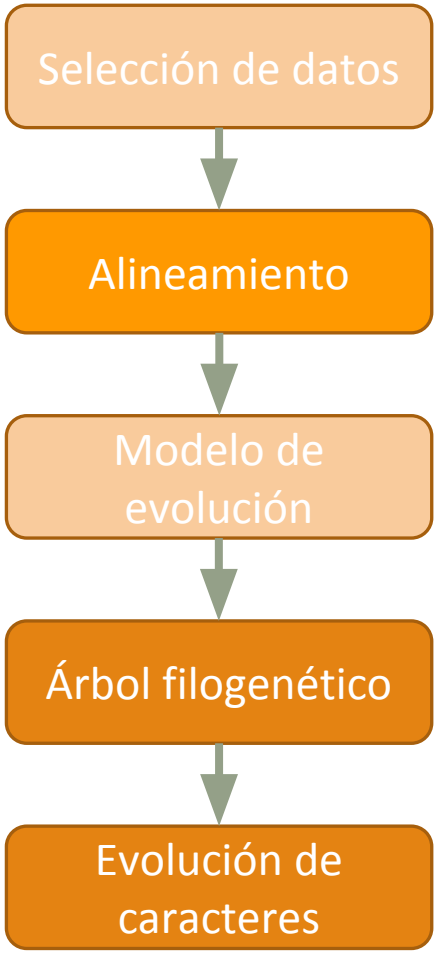
Un esquema más general



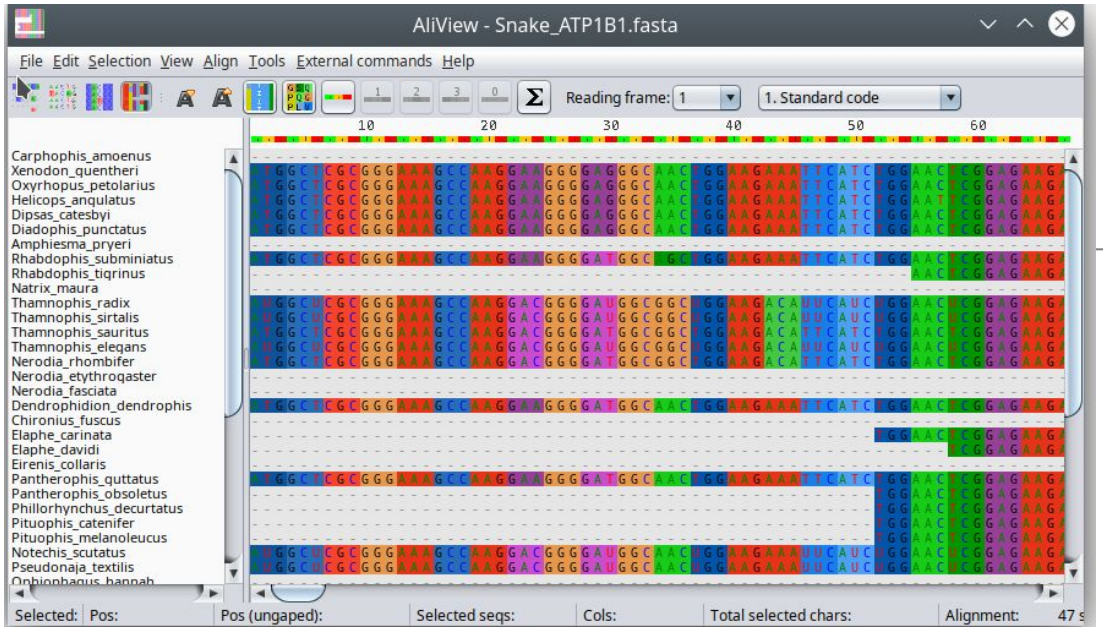
Como primera aproximación, podemos considerar que estos son pasos ordenados linealmente.

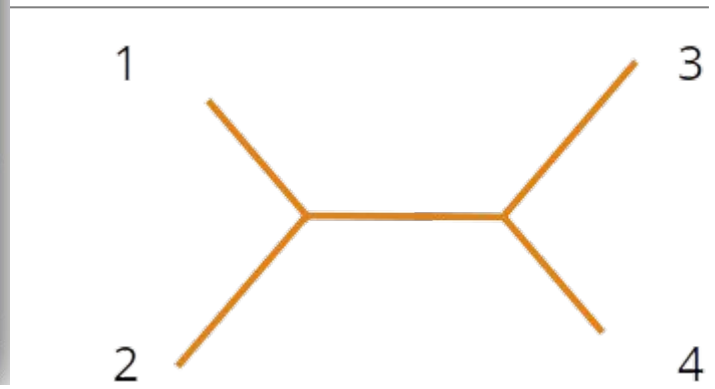
Pero, como vimos en el taller de selección de datos y alineamiento, es un proceso de iteración entre fases más complejo (“de ida y vuelta”).

Evolución Molecular



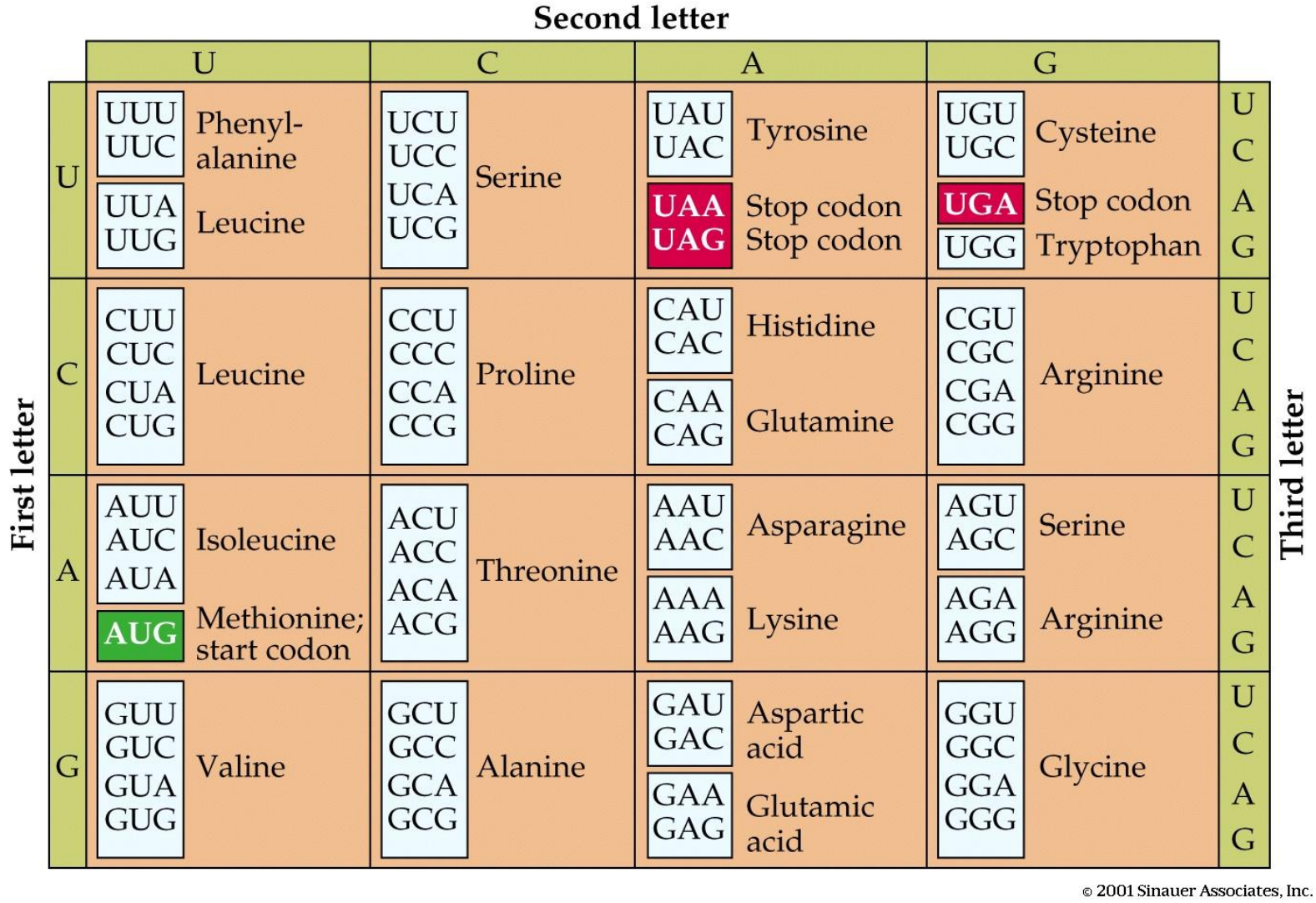
Dado un alineamiento y árbol filogenético, podemos reconstruir los cambios a nivel de codones, y a partir de allí hacer inferencias sobre el rol de la selección natural en la evolución de esas secuencias.





$$q_{ij} = \begin{cases} 0, & \text{if the two codons differ at more than one position,} \\ \pi_j, & \text{for synonymous transversion,} \\ \kappa\pi_j, & \text{for synonymous transition,} \\ \omega\pi_j, & \text{for nonsynonymous transversion,} \\ \omega\kappa\pi_j, & \text{for nonsynonymous transition,} \end{cases}$$

Código genético



Código genético

Redundancia: en las secuencias codificantes, podemos distinguir entre cambios a nivel de ADN que no modifican la secuencia de aminoácidos, tambien llamados **cambios sinónimos**, y cambios a nivel de ADN que modifican la correspondiente secuencia de aminoácidos, tambien llamados **cambios no sinónimos**.

sinónimos	TT**T** (Phe) → TT**C** (Phe)
no sinónimos	TT**T** (Phe) → TT**A** (Leu)

Podemos definir dos tasas de sustitución:

dS: tasa de sustituciones sinónimas por sitio sinónimo

dN: tasa de sustituciones no sinónimas por sitio no sinónimo

ω = dN/dS, un estimador de la presión de selección a nivel de amino ácidos

Teoría Neutral de la Evolución Molecular

La mayoría de las mutaciones a nivel de amino ácidos son deletéreas, y tienden a ser eliminadas por la selección purificadora, mientras que la mayoría de las sustituciones observadas son funcionalmente equivalentes (neutrales).

Teoría Neutral de la Evolución Molecular

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La teoría neutral provee un marco teórico sólido para analizar la influencia de la selección natural en los cambios a nivel de ADN, y también nos da la hipótesis nula con respecto a los patrones de sustitución sinónima y no sinónima.

Comparar las dos tasas de sustitucion (ω =dN/dS)

ω = 1: cambios a nivel de amino ácidos son selectivamente neutros

ω < 1: cambios a nivel de amino ácidos son deletéreos (selección purificadora)

ω > 1: cambios a nivel de amino ácidos son positivos (selección positiva)

> Trends Ecol Evol. 2000 Dec 1;15(12):496-503. doi: 10.1016/s0169-5347(00)01994-7.

Statistical Methods for Detecting Molecular Adaptation

Z Yang, JP Bielawski

PMID: 11114436 PMCID: PMC7134603 DOI: 10.1016/s0169-5347(00)01994-7

Free PMC article

Abstract

The past few years have seen the development of powerful statistical methods for detecting adaptive molecular evolution. These methods compare synonymous and nonsynonymous substitution rates in protein-coding genes, and regard a nonsynonymous rate elevated above the synonymous rate as evidence for darwinian selection. Numerous cases of molecular adaptation are being identified in various systems from viruses to humans. Although previous analyses averaging rates over sites and time have little power, recent methods designed to detect positive selection at individual sites and lineages have been successful. Here, we summarize recent statistical methods for detecting molecular adaptation, and discuss their limitations and possible improvements.

Journal of Structural and Functional Genomics **3:** 201–212, 2003.

Maximum likelihood methods for detecting adaptive evolution after gene duplication

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Department of Biology, University College London, Darwin Building, Gower Street, London WCIE 6BT, United Kingdom
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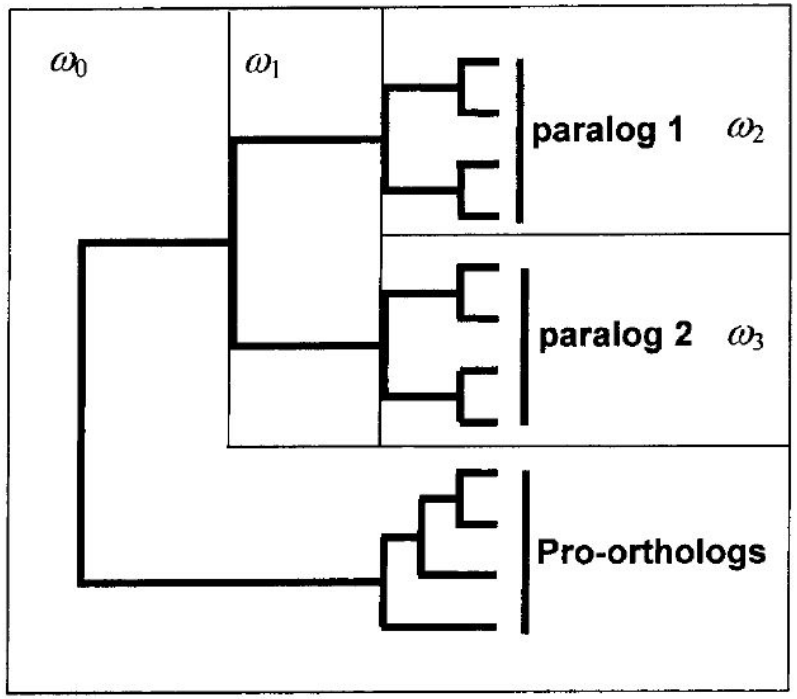
Received 24.01.2002; Accepted in final form 29.08.2002

Key words: codon model, ECP, EDN, gene family, maximum likelihood, positive selection, Troponin C



Comparative Study > J Mol Evol. 2004 Jul;59(1):121-32. doi: 10.1007/s00239-004-2597-8.

A Maximum Likelihood Method for Detecting Functional Divergence at Individual Codon Sites, With Application to Gene Family Evolution

Joseph P Bielawski [1], Ziheng Yang

Affiliations + expand

PMID: 15383915 DOI: 10.1007/s00239-004-2597-8

Abstract

The tailoring of existing genetic systems to new uses is called genetic co-option. Mechanisms of

Hudson-Kreitman-Aguadé test en genómica poblacional

Hudson-Kreitman-Aguadé test

Compara los niveles de divergencia interespecífica (D) y polimorfismo intraespecífico (P) entre dos loci.

	Adh	Locus de referencia
Polimorfismo	0.101	0.022
Divergencia	0.056	0.052
P/D	1.800	0.420
x^2	6.09	
p-value	0.016	

HKA-like test en genómica poblacional

Comparación del número de genes y pseudogenes de receptores olfativos entre humanos y chimpancés

	Funcionales	Pseudogenes
CNV en humanos	116	143
Diferencias	16	11
P/D	7.3	13
x^2	2.06	
p-value	0.15	

Zhang J. 2007. The drifting human genome PNAS 104 (51) 20147-2014.

Nozawa M, Kawahara Y , Nei M. 2007. Genomic drift and copy number variation of sensory receptor genes in humans. PNAS 104:20421–20426.