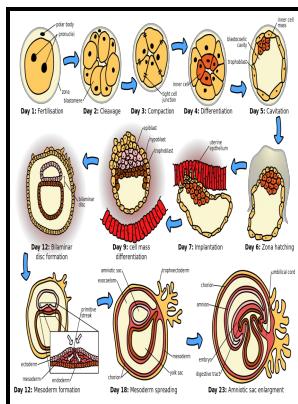


Ontophaneia

Roptron - Bioinformatics and Genomics @ CRG



Description: -

-Ontophaneia

-Ontophaneia

Notes: Poems.

This edition was published in 1988



Filesize: 62.55 MB

Tags: #Bioinformatics #and #Genomics #@ #CRG

Bioinformatics and Genomics @ CRG

Two of the groups in our programme Gabaldón and Guigó have participated in the analysis of the genomic sequence of the pea aphid *Acyrtosiphon pisum*, published this week in PLoS Biology. In this article we present the modern state of the theory of duplicated genes and provide concrete recommendations for future experiments that may do a better job at elucidating the selective mechanisms at work in the evolution of duplicated genes.

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To maximize reliability and coverage, we retrieved gene trees from PhylomeDB, Ensembl, TreeFam and Orthogroups. Thus, although some deleterious alleles can segregate in the population, conventional wisdom holds that deleterious mutations are evolutionary dead ends. A review article detailing and contrasting different theories on the evolution of gene duplications has been in Nature Reviews Genetics.

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We have launched MetaPhOrs, a meta-method to predict orthology and paralogy from multiple phylogenetic evidence. We believe that it is at the intersection between Experimentation and Computation that the Biology of the XXIst century will be edified, and at the program we have our own experimental laboratory.

Bioinformatics and Genomics @ CRG

In an letter to Nature published today we show that for mt-tRNAs this is not always the case. .

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. This first published genome of a basal hemimetabolous insect, provides an out-group for comparison with other sequenced insects, and pave the way to elucidate molecular mechanisms in Negative selection prevents the fixation of deleterious alleles.

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We use computation as a means both to interrogate and to model biological phenomena.

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- [Narodnoe khozyaistvo SSSR v gody Velikoi Otechestvennoi voyny, iyun 1941-Mai 1945gg. - bibliograficheskii](#)