Kukka taeoe puch'ae kwalli ŭi kaeyo mit hyanghu puch'ae kwalli sisŭt'em kuch'uk panghyang

Han'guk Kaebal Yŏn'guwŏn - Bioinformatics and Genomics @ CRG

Description: -

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Health risk assessment.
Cancer -- Environmental aspects -- Colorado.
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Rocky Flats Plant (U.S.)
West Indies, British -- Politics and government.
Psychotropic drugs -- Poisoning -- Handbooks.
Poisoning -- Therapy -- Handbooks.
Poison control centers -- United States -- Directories.
Emergencies -- Handbooks.
Poison control centers -- United States -- Directories.
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This first published genome of a basal hemimetabolous insect, provides an out-group for comparison with other sequenced insects, and pavesthe way to elucidate molecular mechanisms in Negative selection prevents the fixation of deleterious alleles. We have launched MetaPhOrs, a meta-method to predict orthology and paralogy from multiple phylogenetic evidence.

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Thus, although some deleterious alleles can segregate in the population, conventional wisdom holds that deleterious mutations are evolutionary dead ends.

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In an letter to Nature published today we show that for mt-tRNAs this is not always the case. 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. The Groups at CRG's Bioinformatics and Genomics Program have strong collaborations with the CRG's Bioinformatics core and with other experimental groups at the CRG.

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We believe that it is at the intersection between Experimentation and Computation that the Biology of the XXIst century will be edificated, and at the program we have our own experimental laboratory. New features have been added to the user's front end, including fully interactive tree images and link outs to external information. In addition we built maximum likelihood trees for orthologous gene families in OrthoMCL, COG, and EggNOG.

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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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