SEMINARIO

BIOINFORMÁTICA

EXPOSITOR
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TITULO
Comparative genomics: form serendipity to reproducibility

Abstract:

The compact genomes of the hemiascomycete yeasts provide an ideal terrain for eukaryote comparative genomics: in the 450 Mya since their divergence from a common ancestor they have adapted to a wide range of ecological conditions, using a wide range of evolutionary mechanisms, while maintaining a relatively conserved gene repertoire. For these reasons yeasts present a unique opportunity for developing bioinformatic tools for comparative genomics, and since they play a considerable role in biotechnological applications, predictions made for the genome are often translated to useful experimental results.

What we find is that work on these species is not always hypothesis-driven, but serendipitous: the main results are often quite unexpected. I will present a number of concrete examples from large-scale comparative analyses, consider strategies for building useful bioinformatic tools, and conclude with a plea for reproducible science.

Lunes 29 de Julio del 2013 a las 17 : 00 hrs, Sala de Multimedia CMM, 6*to* piso.