



Dpto. Biología Molecular e Ingeniería Bioquímica  
Centro Andaluz de Biología del Desarrollo

# Análisis bioinformático de la lucha entre bacterias y bacteriófagos mediante sistemas CRISPR-Cas

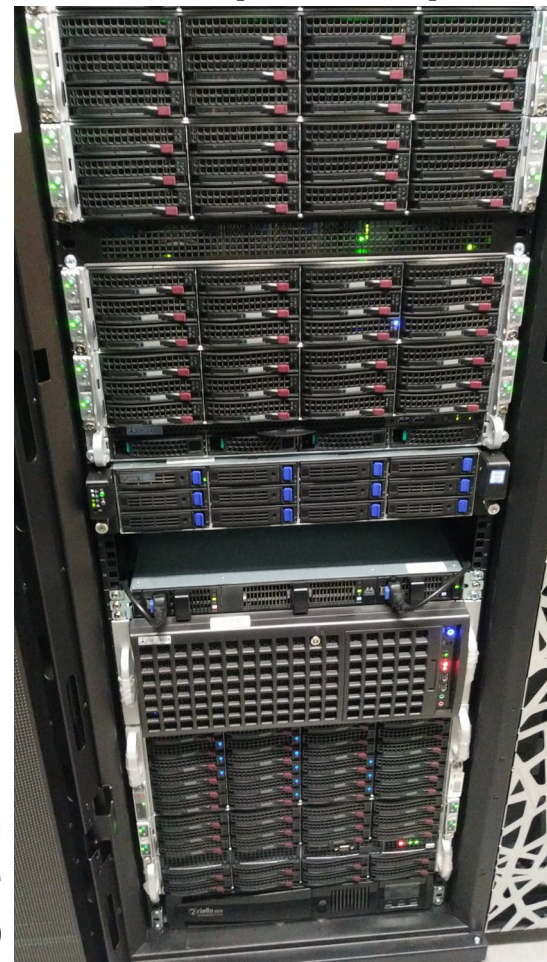
Antonio J. Pérez-Pulido  
Grupo UPOBioinfo

<http://www.bioinfocabd.upo.es>

## Lugar físico de realización: Unidad de Bioinformática

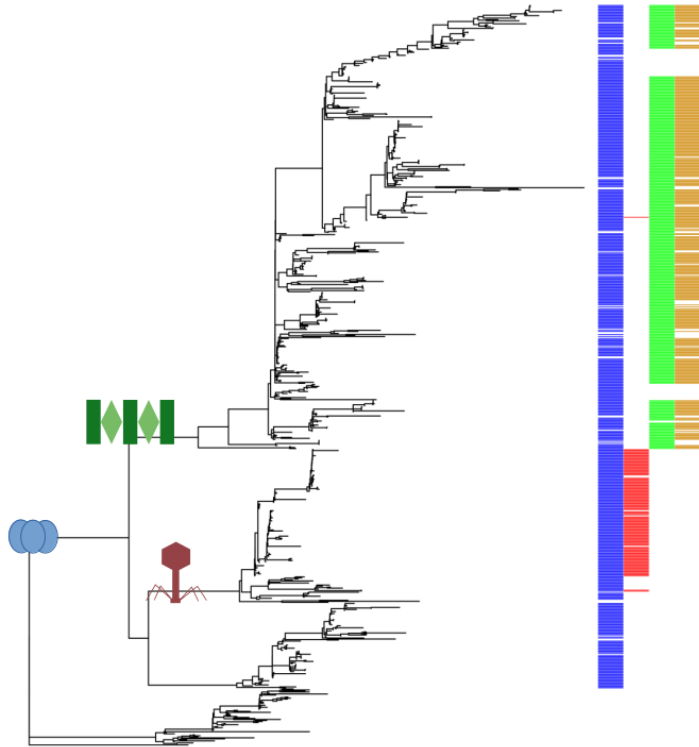
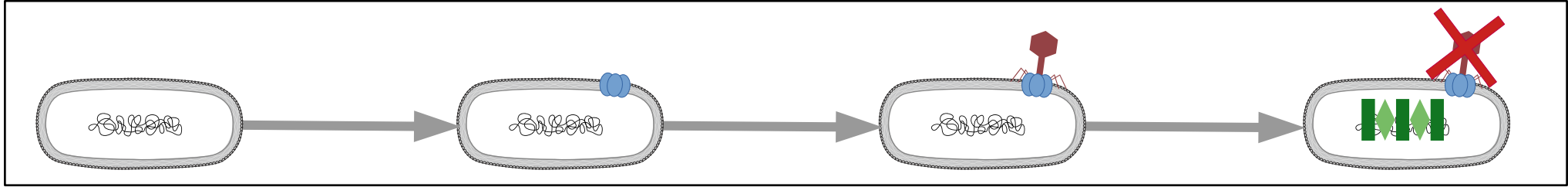


## Centro de Cálculo Científico de la UPO (C3UPO)



Equipo a usar:  
45 nodos con  
1.704 cores de  
cálculo

# Trabajaremos con pangenomas bacterianos y de fagos



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## MICROBIOLOGY

### Analysis of bacterial pangenomes reduces CRISPR dark matter and reveals strong association between membranome and CRISPR-Cas systems

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CRISPR-Cas systems are prokaryotic acquired immunity mechanisms, which are found in 40% of bacterial genomes. They prevent viral infections through small DNA fragments called spacers. However, the vast majority of these spacers have not yet been associated with the virus they recognize, and it has been named CRISPR dark matter. By analyzing the spacers of tens of thousands of genomes from six bacterial species, we have been able to reduce the CRISPR dark matter from 80% to as low as 15% in some of the species. In addition, we have observed that, when a genome presents CRISPR-Cas systems, this is accompanied by particular sets of membrane proteins. Our results suggest that when bacteria present membrane proteins that make it compete better in its environment and these proteins are, in turn, receptors for specific phages, they would be forced to acquire CRISPR-Cas.



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