1. Functionally linked genes in bacterial and archaeal genomes are often organized into operons. However, the composition and architecture of operons are highly variable and frequently differ even among closely related genomes. Therefore, to efficiently extract reliable functional predictions for uncharacterized genes from comparative analyses of the rapidly growing genomic databases, dedicated computational approaches are required.  
     
   Last year group of scientists developed a protocol ICITY which use to systematically and automatically identify genes that are likely to be functionally associated with a ‘bait’ gene or locus by using relevance metrics. Given a set of bait loci and a genomic database defined by us, this protocol compares the genomic neighborhoods of the baits to identify genes that are likely to be functionally linked to the baits by calculating the abundance of a given gene within and outside the bait neighborhoods and the distance to the bait.   
     
   We used the ICITY protocol to determine the existence of a functional relationship between the recently discovered DGR operons and the bacterial immune system.