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Functional Potential of Bacterial Communities using Gene Context Information

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Abstract

Estimation of the functional potential of a bacterial genome can be determined by accurate annotation of its metabolic pathways. Existing homology based methods for pathway annotation fail to account for homologous genes that participate in multiple pathways, causing overestimation of gene copy number. Mere presence of constituent genes of a candidate pathway which are dispersed on a genome often results in incorrect annotation, thereby leading to erroneous gene abundance and pathway estimation. Clusters of evolutionarily conserved coregulated genes are characteristic features in bacterial genomes and their spatial arrangement in the genome is constrained by the pathway encoded by them. Thus, in order to improve the accuracy of pathway prediction, it is important to augment homology based annotation with gene organization information. In this communication, we present a methodology considering prioritization of gene context for improved pathway annotation. Extensive literature mining was performed to confirm conserved juxtaposed arrangement of gene components of various pathways. Our method was utilized to identify and analyse the functional potential of all available completely sequenced bacterial genomes. The accuracy of the predicted gene clusters and their importance in metabolic pathways will be demonstrated using a few case studies. One of such case study corresponds to butyrate production pathways in gut bacteria where it was observed that gut pathogens and commensals possess a distinct set of pathway components. In another example, we will demonstrate how our methodology improves the prediction accuracy of carbohydrate metabolic potential in human microbial communities. Applicability of our method for estimation of functional potential in bacterial communities present in diverse environments will also be illustrated.

References

[1] Prakash, T. and Taylor, T.D (2012) Functional assignment of metagenomic data: challenges and applications. *Brief Bioinform* 13: 711–727. https://doi.org/10.1093/bib/bbs033

[2] Ballouz, S., Francis, A.R., Lan, R. and Tanaka, M.M (2010) Conditions for the evolution of gene clusters in bacterial genomes. *PLoS Comput Biol* 6: e1000672. https://doi.org/10.1371/journal.pcbi.1000672

[3] Andrianopoulos, K., Wang, L. and Reeves, P.R. (1998) Identification of the Fucose Synthetase Gene in the Colanic Acid Gene Cluster of Escherichia coli K-12. *J Bacteriol* 180: 998–1001.

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