

Transcription unit organization in Prokaryotes

Gabriel Moreno-Hagelsieb¹ and Warren F. Lamboy²

Keywords: genome organization, operons, inter-genic distances

1 Abstract.

Here we show that a lot can be learned of the transcription unit (TU) organization of prokaryotes by analyzing the number of genes of directons, stretches of genes in the same strand with no intervening gene in the opposite strand, and of the inter-genic distances. We give a detailed study of *Escherichia coli* K12, compared with data on experimentally determined TUs available through RegulonDB [1]. We use *E. coli* K12 as a basis to compare the tendencies in TU organization of other prokaryotes.

References

- [1] Salgado, H., et al., *RegulonDB (version 4.0): transcriptional regulation, operon organization and growth conditions in Escherichia coli K-12*. 2004. *Nucleic Acids Res* **32 Database issue**: p. D303-6.

¹ Program of Computational Genomics, CIFN-UNAM, Apdo Postal 565-A, Cuernavaca, Morelos, 62100 Mexico.

² Center for Agricultural Bioinformatics, USDA-ARS, Cornell Theory Center, Cornell University, Ithaca, NY 14853.