



Notes Towards a Network Approach to Gene Orientation

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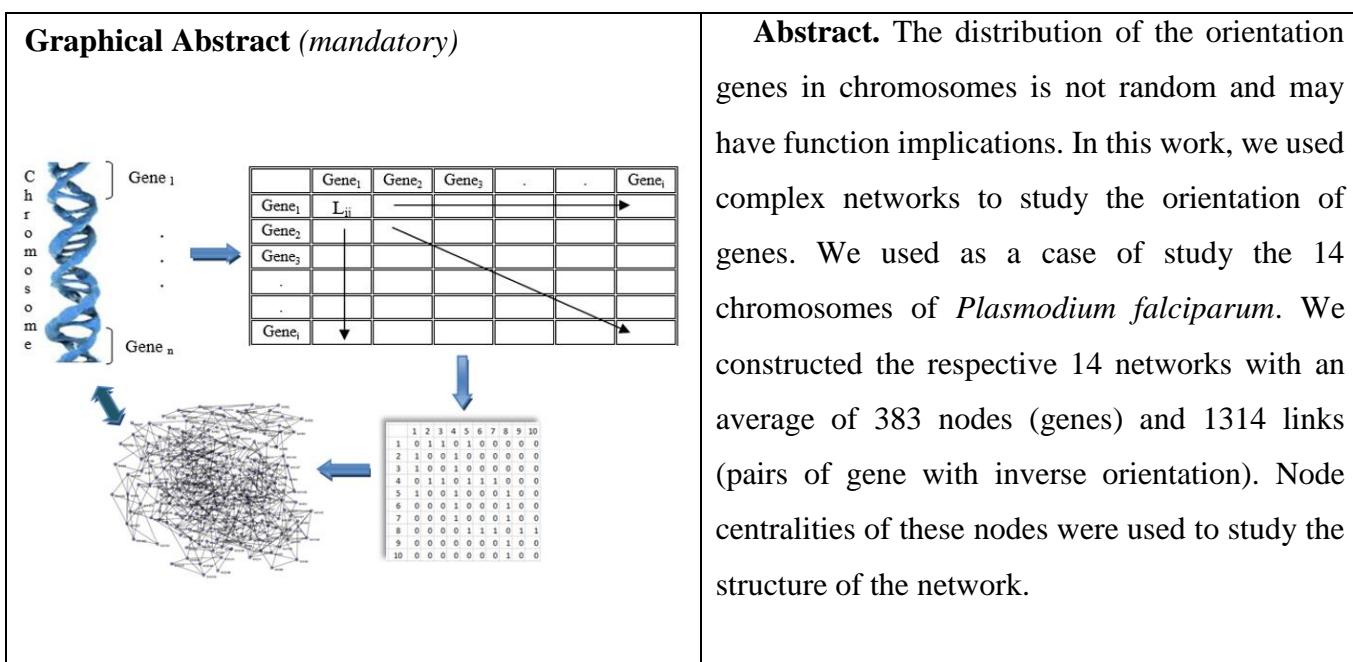
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References

1. Hurst, L. D.; Williams, E. J.; Pal, C., Natural selection promotes the conservation of linkage of co-expressed genes. *Trends Genet* 2002, 18, (12), 604-6.
2. Kustatscher, G.; Grabowski, P.; Rappaport, J., Pervasive coexpression of spatially proximal genes is buffered at the protein level. *Mol Syst Biol* 2017, 13, (8), 937.
3. Newman, M., The Structure and Function of Complex Networks. *SIAM Review* 2003, 56, 167-256.
4. Lin, H. H.; Zhang, L. L.; Yan, R.; Lu, J. J.; Hu, Y., Network Analysis of Drug-target Interactions: A Study on FDA-approved New Molecular Entities Between 2000 to 2015. *Sci Rep* 2017, 7, (1), 12230.