Abstract

Association between causal genes and their genetic diseases is an important problem concerning human health. Linkage analysis is such a method that can identify which unknown disease genes are located in chromosomal region out of hundreds of candidate genes according to their functions, interactions, and pathways which is good identification of genes associated with general/hereditary disorders. Here, we used method for prioritization of candidate genes of Dementia by the use of a global network distance measure, Random Walk Analysis, which detects neurological disorder been associated with distribution of sub-network among the genes.

References

- Gaulton, K. J. et al. A computational system to select candidate genes for complex human traits.
Protein Network for Associating Genes with Dementia

Bioinformatics, 23, 1132–1140.
- Perez-Iratxeta, C. et al.
- Update of the G2D tool for prioritization of gene candidates to inherited diseases.

- Aerts, S. et al.
- Sam, L. et al.
- Radivojac, P. et al.
- Karni, S. et al.
- Ma, X. et al.
- George, R. A. et al.
- Analysis of protein sequence and interaction data for candidate disease gene prediction.

- Ozgur, A. et al.
- van Driel, M. A. et al.
- Perez-Iratxeta, C., Bork, P., and Andrade, M. A.
- Lopez-Bigas, N., and Ouzounis, C. A.
- Genome-wide identification of genes likely to be involved in human genetic disease.

Nucleic Acids Res. 32, 3108–3114.
- Oti, M., Snel, B., Huynen, M., and Brunner, H. G.
- Huynen, M., Snel, B., Lathe, W. 3rd and Bork, P.
- Eisenberg, D., Marcotte, E. M., Xenarios, I., and Yeates, T. O.
- Moreau, Y. and Tranchevent, L. C.
Protein Network for Associating Genes with Dementia

- Piro, R. M. and Di Cunto, F.
- McKusick, V.
- Kohler, S., Bauer, S., Horn, D., and Robinson, P. N.
- Kamburov, A., Pentchev, K., Galicka, H., Wierling, C., Lehrach, H. and Herwig, R.
- Niu, Y., Otasek, D. and Jurisica, I.
- Evaluation of linguistic features useful in extraction of interactions from PubMed; application to annotating known, high-throughput and predicted interactions in I2D. Bioinformatics, 26, 111–119.
- Patil, A., Nakai, K. and Nakamura, H.
- Balaji, S., McClendon, C., Chowdhary, R., Liu, J. S. and Zhang, J.
- Saric, J., Jensen, L. J., Ouzounova, R., Rojas, I. and Bork, P.
- Skrabaneck, L., Saini, H. K., Bader, G. D. and Enright, A. J.
Protein Network for Associating Genes with Dementia

- Harrington, E. D., Jensen, L. J. and Bork, P.
- Jensen, L. J., Julien, P., Kuhn, M., von Mering, C., Muller, J., Doerks, T. and Bork, P.
- Kuhn, M., von Mering, C., Campillos, M., Jensen, L. J. and Bork, P.
- Brohee, S., Faust, K., Lima-Mendez, G., Sand, O., Janky, R., Vanderstocken, G., Deville, Y. and van Helden, J.

**Index Terms**

Computer Science            Applied Sciences

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Genetic diseases; Dementia; Random Walk Analysis; Neurological disorder.