2017).
34. M. J. Li, B. Yan, P. C. Sham and J. Wang, Exploring the function of genetic variants in the non-coding genomic regions: approaches for identifying human regulatory variants affecting gene expression, *Brief Bioinformatics* **16**, 393 (2015).
35. D. L. Nicolae, E. Gamazon, W. Zhang, S. Duan, M. E. Dolan and N. J. Cox, Trait-Associated SNPs Are More Likely to Be eQTLs: Annotation to Enhance Discovery from GWAS, *PLOS Genet* **6**, p. e1000888 (2010).
36. T. Chen and C. Guestrin, XGBoost: A scalable tree boosting system, *arXiv.org* **1603.02754**, 1 (2016).
37. L. Buzdugan, M. Kalisch, A. Navarro, D. Schunk, E. Fehr and P. Bühlmann, Assessing statistical significance in multivariable genome wide association analysis, *Bioinformatics* **32**, 1990 (2016).
38. M. Hess, S. Lenz, T. J. Blätte, L. Bullinger and H. Binder, Partitioned learning of deep boltzmann machines for snp data, *Bioinformatics* **33**, 3173 (2017).
39. I. Lee, U. M. Blom, P. I. Wang, J. E. Shim and E. M. Marcotte, Prioritizing candidate disease genes by network-based boosting of genome-wide association data, *Genome research* **21**, 1109 (2011).
40. B. Linghu, E. S. Snitkin, Z. Hu, Y. Xia and C. DeLisi, Genome-wide prioritization of disease genes and identification of disease-disease associations from an integrated human functional linkage network, *Genome biology* **10**, p. R91 (2009).
41. P. Jia, S. Zheng, J. Long, W. Zheng and Z. Zhao, dmgwas: dense module searching for genome-wide association studies in protein–protein interaction networks, *Bioinformatics* **27**, 95 (2010).
42. Y. Moreau and L.-C. Tranchevent, Computational tools for prioritizing candidate genes: boosting disease gene discovery, *Nature Reviews Genetics* **13**, p. 523 (2012).
43. L. Gao, Y. Uzun, P. Gao, B. He, X. Ma, J. Wang, S. Han and K. Tan, Identifying noncoding risk variants using disease-relevant gene regulatory networks, *Nature communications* **9**, p. 702 (2018).
44. A. Grover and J. Leskovec, node2vec: Scalable feature learning for networks, in *Proceedings of the 22nd ACM SIGKDD international conference on Knowledge discovery and data mining*, 2016.
45. L. Teng, B. He, J. Wang and K. Tan, 4dgenome: a comprehensive database of chromatin interactions, *Bioinformatics* **31**, 2560 (2015).
46. C. Stark, B.-J. Breitkreutz, T. Reguly, L. Boucher, A. Breitkreutz and M. Tyers, Biogrid: a general repository for interaction datasets, *Nucleic acids research* **34**, D535 (2006).
47. S. Yang, C. Y. Kim, S. Hwang, E. Kim, H. Kim, H. Shim and I. Lee, Coexpedia: exploring biomedical hypotheses via co-expressions associated with medical subject headings (mesh), *Nucleic acids research* **45**, D389 (2016).
48. S. Hwang, C. Y. Kim, S. Yang, E. Kim, T. Hart, E. M. Marcotte and I. Lee, Humannet v2: human gene networks for disease research, *Nucleic acids research* **47**, D573 (2018).
49. B. He, C. Chen, L. Teng and K. Tan, Global view of enhancer–promoter interactome in human cells, *Proceedings of the National Academy of Sciences* **111**, E2191 (2014).
50. Y. Goldberg and O. Levy, word2vec explained: deriving mikolov et al.'s negative-sampling word-embedding method, *arXiv preprint arXiv:1402.3722* (2014).
51. J. Bergstra and Y. Bengio, Random search for hyper-parameter optimization, *Journal of Machine Learning Research* **13**, 281 (2012).
52. L. D. Ward and M. Kellis, Interpreting noncoding genetic variation in complex traits and human disease, *Nature Biotechnol* **30**, 1095 (2012).