

Below is a **list of publications** that represent both past and current work in math/computational biology:

1. Sakhanenko, N.A. and Galas, D.J., “Markov Logic Networks in the Analysis of Genetic Data”, J Comp Biol, 17(11): 1491-1508 (2010).
2. Galas, D.J., Nykter, M., Carter, G.W., Price, N. and Shmulevich, I., “Biological Information as Set-based Complexity”, IEEE Transactions on Information Theory, 56(2): 667-677 (2010).
3. Cho, J-H., Wang, K., and Galas, D.J., “An integrative approach to inferring biologically meaningful gene modules”, BMC Systems Biology, 5:117 (2011).
4. Sakhanenko, N.A. and Galas, D.J., “Complexity of Networks I: The Set-complexity of Binary Graphs”, Complexity, 17:51-64 (2011).
5. Ignac, T.M., Sakhanenko, N.A., Galas, D.J., “Relation Between the Set-Complexity of a Graph and its Structure”, *Proceedings of the 8th International Workshop on Computational Systems Biology (WCSB; 2011)*.
6. Sakhanenko N.A., and Galas D.J, “Interaction information in the discretization of quantitative phenotype data”, *Proceedings of the 8th International Workshop on Computational Systems Biology (WCSB; 2011)*, H. Koepl, et al. (eds.), TICSP Series 57, 2011, p.161–164.
7. Ignac, T.M., Sakhanenko, N.A., Galas, D.J., “On the Set-Complexity of a Graph”, EURASIP Journal on Bioinformatics and Systems Biology, 1:(13). [Epub ahead of print] PubMed PMID: 22995062 (2012).
8. Ignac, T.M., Sakhanenko, N.A. and Galas, D.J., “Complexity of Networks II: The Set-complexity of a Class of Edge-colored Graphs”, Complexity (2012).
9. Sakhanenko, N. and Galas, D.J., “Probabilistic logic methods and some applications to biology and medicine”, J Comp Biol, 19(3): 316-336 (2012).

10. Shannon, P.T., Grimes, M., Kutlu, B., Bot, J.J., and Galas, D.J., "RCytoscape: Tools for Exploratory Network Analysis", BMC Bioinformatics, 9;14(1):217 (2013).
11. Ignac, T., Skupin, A., Sakhanenko, N.A., Galas, D.J., "Discovering pair-wise genetic interactions: An information theory-based approach", PLoS One, 9(3):e92310 (2014).
12. Galas DJ, Sakhanenko N.A., Skupin A, Ignac T., "Describing the Complexity of Systems: Multivariable 'Set Complexity' and the Information Basis of Systems Biology", J Comp Biol, 21(2):118-40 (2014).
13. Sakhanenko, N.A. and Galas, D.J., "Biological data analysis as an information theory problem: Multivariable dependence measures and the Shadows algorithm", J Comp Biol, 22(11):1-20. doi: 10.1089/cmb.2015.0051 (2015).
14. Galas, D.J. and Sakhanenko, N.A., "Unifying formalism for multivariate information-related measures: Möbius operators on subset lattices" arXiv1601.06780 (2016).
15. Kunert-Graf, J., Sakhanenko, N.A., Galas, D.J. "Complexity and Vulnerability Analysis of the *C. elegans* Gap Junction Connectome", Entropy: Complexity, 19(3), 104; doi:10.3390/e19030104 (2017).
16. Galas, D.J., Dewey, Kunert-Graf, J., Sakhanenko, N.A., "Expansion of the Kullback-Leibler Divergence, and a new class of information metrics", Axioms, 6(2), 8; doi:10.3390/axioms6020008 (2017).
17. Sakhanenko, N.A., Kunert-Graf, J. and Galas, D. J., "The Information Content of Discrete Functions and Their Application to Genetic Data Analysis", J Comp Biol, 24, 1153-1178 (2017).
18. Kunert-Graf, J.M., Eschenburg, K.M., Galas, D.J., Kutz, J.N., Rane, S.D., Brunton, B.W., "Extracting Reproducible Time-Resolved Resting State Networks using Dynamic Mode Decomposition", bioRxiv. doi.org/10.1101/343061 (in press, 2018).

19. Sakhanenko, N.A., Galas, D.J., "Symmetries among multivariate information measures explored using Möbius operators", Entropy, 21(1), 88; <https://doi.org/10.3390/e21010088> (2019).
20. Uechi, L., Galas, D.J., Sakhanenko, N.A., "Multivariate analysis of data sets with missing values: an information theory-based reliability function", J Comp Biol, 26(2), 152-171; <https://doi.org/10.1089/>
21. Galas, D. J., Sakhanenko, N.A., and Kunert-Graf, J., "Towards an information theory of quantitative genetics", J Comp Biol (2020). Waterman, M., Arratia, R. and Galas, D., "Pattern Recognition in Several Sequences: Consensus and Alignment," Bull Math Biol, 46:515-527 (1984).
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31. Carter, G.W., Rush, C.G., Uygun, F., Sakhanenko, N.A., Galas, D.J., Galitski, T., "A Systems-Biology Approach to Genetic Complexity: Modular Analysis of Genetic-Interaction Networks", *Chaos*, 20(2):026102 (2010).
32. Roach, J.C., Glusman, G., Smit, A.F.A., Huff, C.D., Hubley, R., Shannon, P.T., Rowen, L., Pant, K.P., Goodman, N., Bamshad, M., Shendure, J., Drmanac, R., Jorde, L.B., Hood, L., and Galas, D.J., "Analysis of Genetic Inheritance in a Family Quartet by Whole Genome Sequencing", *Science*, 328(5978): 636-639 (2010).
33. Roach, J.C., Glusman, G., Hubley, R., Montsaroff, S.Z., Holloway, A.K., Srivastava, D., Garg, V., Pollard, K.S., Galas, D.J., and Smit, A.F.A., "Chromosomal Haplotypes by Genetic Phasing of Human Families", *Amer Journ Human Genetics* (2011).
34. Bousquet, J., Anto, J.M., Sterk, P.J., et al., "Systems medicine and integrated care to combat chronic noncommunicable diseases", *Genome Medicine*, 3(43): doi:10.1186/gm259 (2011).
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37. Wu, X., Kim, T-K, Baxter, D., Scherler, K., Gordon, A., Fong, O., Etheridge, A., Galas, D.J., Wang, K., “sRNAlyzer - A flexible and customizable small RNA sequencing data analysis pipeline”, *Nucleic Acids Research*, (2017).
38. Sakhanenko, N.A., Cromie, G., Dudley, A., Galas, D.J., “Computational Inference Software for Tetrad Assembly from Randomly Arrayed Yeast Colonies”, *G3: Genes | Genomes | Genetics* (April 2019).
39. Murillo, O.D. et al. [as part of the NIH Extracellular RNA Communication Consortium (ERCC)], “exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids”, *Cell*, 177, 463-477; <https://doi.org/10.1016/j.cell.2019.02.018> (April 2019).