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Alice C. U. Schwarze* (alice.schwarze@maths.ox.ac.uk), Mathematical Institute, University of Oxford, Woodstock Road, Oxford, OX2 7GG, United Kingdom, and **Mason A. Porter** and **Jonny Wray**. *Structural and Functional Redundancy in Biological Networks*.

Several scholars of evolutionary biology have suggested that functional redundancy (also known as biological “degeneracy”) is important for robustness of biological networks. Structural redundancy indicates the existence of structurally similar subsystems that can perform the same function. Functional redundancy indicates the existence of structurally different subsystems that can perform the same function. For networks with Ornstein–Uhlenbeck dynamics, Tononi et al. [Proc. Natl. Acad. Sci. U.S.A. **96**, 3257–3262 (1999)] proposed measures of structural and functional redundancy that are based on mutual information between subnetworks. For a network of n vertices, an exact computation of these quantities requires $O(n!)$ time. We derive expansions for these measures that one can compute in $O(n^3)$ time. We use the expansions to compare the contributions of different types of motifs to a network’s structural and functional redundancy. We compute structural and function redundancy for protein-interaction networks and find that these networks have larger functional redundancy than corresponding realisations of several random-graph models. (Received September 26, 2017)