Citation:

Xionglei He, Jianzhi Zhang, Rapid Subfunctionalization Accompanied by Prolonged and Substantial Neofunctionalization in Duplicate Gene Evolution, *Genetics*, Volume 169, Issue 2, 1 February 2005, Pages 1157–1164, https://doi.org/10.1534/genetics.104.037051

The claim for this article is stated directly in the abstract by the authors, Xionglei He and Jianzhi Zhang. They state that neither the neofunctionalization (NF) hypothesis nor the subfunctionalization (SF) hypothesis could properly explain the patterns shown between human gene expression and yeast protein interactions. In the abstract it is also stated that in their results it was determined that several new functions developed due to gene duplication. The authors then elaborate on the details of each hypothesis and how they interact. It is stated in the procedure that the Munich Information Center for Protein Sequences downloaded 6,402 open reading frames of *Saccharomyces cerevisiae* from the Comprehensive Yeast Genome Database. Out of that 6,402, it is stated that 4,362 of the sequences are encoded and named in the yeast databases. It is also documented that 625 duplicate pairs were found and 1022 confirmed nuclear genes were regarded as singletons. The article then further elaborates on the specific methods used throughout the procedure. The authors also include every genome database and any other databases used throughout the study. Along with the analysis of *Saccharomyces cerevisiae*, data of human gene expression using U95A arrays of Affymetrix were also studied and compared. Multiple tables and figures displaying symbol definitions and data analysis are also provided throughout the article.

In the final analysis the article begins with an analysis of *Saccharomyces cerevisiae* protein-protein interactions. The authors state that in order to reduce any possible errors, only the interaction data with high-confidence was analyzed. Then the mean shared partner data for singleton genes and non redundant pairs of duplicate genes for all of trials was thoroughly analyzed. It was concluded that there is no data that shows a statistically significant difference between the shared partners between duplicate genes when considering the amount of partners in yeast protein-protein interactions. It is also concluded that all three NF hypothesis models were rejected due to the presence of SF and that most of the genes that are considered duplicate genes go through NF and SF. This observation is what caused He and Zhang to come to their final conclusion, that since all of the NF and SF methods were not sufficient, then a new model would need to be proposed. Thus creating a new model termed "subneofunctionalizing"(SNF).