# Persistent homology analysis of type 2 diabetes genome-wide association studies in protein-protein interaction networks

Authors: Euijun Song

Summary:  
Genome-wide association studies (GWAS) involving increasing sample sizes have  
identified hundreds of genetic variants associated with complex diseases, such  
as type 2 diabetes (T2D); however, it is unclear how GWAS hits form unique  
topological structures in protein-protein interaction (PPI) networks. Using  
persistent homology, we explore the evolution and persistence of the  
topological features of T2D GWAS hits in the PPI network with increasing  
P-value thresholds. The largest connected component of the T2D GWAS hits is  
significantly detected in the PPI network (196 nodes and 235 edges, P$<$0.05).  
In the 1-dimensional homology group analysis, all 18 1-dimensional holes  
(loops) of the T2D GWAS hits persist over all P-value thresholds. The  
1-dimensional persistent T2D disease module (59 nodes and 83 edges) comprising  
these 18 persistent 1-dimensional holes is significantly larger than that  
expected by chance (P$<$0.001), indicating a significant topological structure  
in the PPI network. Our computational topology framework potentially possesses  
broad applicability to other complex phenotypes in identifying topological  
features that play an important role in disease pathobiology.

Published: 2023-07-31 11:17:30+00:00

PDF URL: http://arxiv.org/pdf/2307.16575v1

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# On the use of associative memory in Hopfield networks designed to solve propositional satisfiability problems

Authors: Natalya Weber, Werner Koch, Ozan Erdem, Tom Froese

Summary:  
Hopfield networks are an attractive choice for solving many types of  
computational problems because they provide a biologically plausible mechanism.  
The Self-Optimization (SO) model adds to the Hopfield network by using a  
biologically founded Hebbian learning rule, in combination with repeated  
network resets to arbitrary initial states, for optimizing its own behavior  
towards some desirable goal state encoded in the network. In order to better  
understand that process, we demonstrate first that the SO model can solve  
concrete combinatorial problems in SAT form, using two examples of the Liars  
problem and the map coloring problem. In addition, we show how under some  
conditions critical information might get lost forever with the learned network  
producing seemingly optimal solutions that are in fact inappropriate for the  
problem it was tasked to solve. What appears to be an undesirable side-effect  
of the SO model, can provide insight into its process for solving intractable  
problems.

Published: 2023-07-31 16:25:37+00:00

PDF URL: http://arxiv.org/pdf/2307.16807v1

Downloaded Time: 2023-07-31

# LASSO extension: using the number of non-zero coefficients to test the global model hypothesis

Authors: Carsten Uhlig, Steffen Uhlig

Summary:  
In this paper, we propose a test procedure based on the LASSO methodology to  
test the global null hypothesis of no dependence between a response variable  
and $p$ predictors, where $n$ observations with $n < p$ are available. The  
proposed procedure is similar to the F-test for a linear model, which evaluates  
significance based on the ratio of explained to unexplained variance. However,  
the F-test is not suitable for models where $p \geq n$. This limitation is due  
to the fact that when $p \geq n$, the unexplained variance is zero and thus the  
F-statistic can no longer be calculated. In contrast, the proposed extension of  
the LASSO methodology overcomes this limitation by using the number of non-zero  
coefficients in the LASSO model as a test statistic after suitably specifying  
the regularization parameter. The method allows reliable analysis of  
high-dimensional datasets with as few as $n = 40$ observations. The performance  
of the method is tested by means of a power study.

Published: 2023-07-31 02:38:34+00:00

PDF URL: http://arxiv.org/pdf/2307.16374v1

Downloaded Time: 2023-07-31

# Semi-Quantitative Group Testing for Efficient and Accurate qPCR Screening of Pathogens with a Wide Range of Loads

Authors: Anantham Nambiar, Chao Pan, Vishal Rana, Mahdi Cheraghchi, João Ribeiro, Sergei Maslov, Olgica Milenkovic

Summary:  
Pathogenic infections pose a significant threat to global health, affecting  
millions of people every year and presenting substantial challenges to  
healthcare systems worldwide. Efficient and timely testing plays a critical  
role in disease control and transmission prevention. Group testing is a  
well-established method for reducing the number of tests needed to screen large  
populations when the disease prevalence is low. However, it does not fully  
utilize the quantitative information provided by qPCR methods, nor is it able  
to accommodate a wide range of pathogen loads. To address these issues, we  
introduce a novel adaptive semi-quantitative group testing (SQGT) scheme to  
efficiently screen populations via two-stage qPCR testing. The SQGT method  
quantizes cycle threshold ($Ct$) values into multiple bins, leveraging the  
information from the first stage of screening to improve the detection  
sensitivity. Dynamic $Ct$ threshold adjustments mitigate dilution effects and  
enhance test accuracy. Comparisons with traditional binary outcome GT methods  
show that SQGT reduces the number of tests by $24$% while maintaining a  
negligible false negative rate.

Published: 2023-07-31 00:18:18+00:00

PDF URL: http://arxiv.org/pdf/2307.16352v1

Downloaded Time: 2023-07-31