



# Award Details

## Rigidity in enveloping algebras

### Research Details

Competition Year:	2019	Fiscal Year:	2020-2021
Project Lead Name:	Usefi, Hamid	Institution:	Memorial University of Newfoundland
Department:	Mathematics	Province:	Newfoundland and Labrador
Award Amount:	19,000	Installment:	4 - 5
Program:	Discovery Grants Program - Individual	Selection Committee:	Mathematics and Statistics
Research Subject:	Lie theory	Area of Application:	Mathematical sciences
Co-Researchers:	No Co-Researcher	Partners:	No Partners

### Award Summary

My research in a broad sense falls in algebra. Lie algebras and enveloping algebras are active and important research areas both within algebra and in other fields such as Mathematical Physics, Particle Physics, String Theory, Geometry, Hyperplane Arrangement, etc. Lie theory methods used by the Fields medallist Efim Zelmanov led him to solve the Bounded Kurosh Problem in Group Theory. Lie algebras are non-commutative and non-associative objects. What is "non-commutativity"? Consider the action where we pour two chemicals in a flask. Here, it doesn't matter which product we pour first into the flask. In other words, the action is commutative. In comparison "non-associativity" involves three objects. For example, consider a chemical product obtained by mixing three different chemicals A, B, and C in a flask. So the recipe is to add together A and B first and then add C. In Mathematics formulation, we can summarize this procedure as  $(A+B)+C$ . Instead, if we first add C and A and then add B we could possibly get a different product. In other words,  $C+(A+B)$  may not be the same as  $(C+A)+B$ . We can interpret this experience and say that the action of adding chemicals is commutative but not associative. My expertise in Algebra has led me to broaden my research program. For example, we use Artificial Intelligence and machine learning to detect and prevent abnormal access in privacy sensitive organizations like Healthcare System or TAX system. We are also developing new methods in face detection and recognition. My research program also contributes to vital problems such as Cancer diagnoses and immunotherapy. In genome-wide association study (GWAS), partial or all of the human genome is sequenced for discovering the associations between genetic factors and a disease. In GWAS the genetic variants under consideration are single nucleotide polymorphisms (SNPs), the most common type of variation among people. The number of SNPs usually goes over one million in a dataset; therefore, a set of powerful data mining and machine learning methods are needed in order to investigate genetic data to reveal the most significant genetic variants that cause a disease. In machine learning and pattern recognition, feature selection is the process of selecting the most important features of a problem while removing unnecessary ones. The use of feature selection in microarray datasets or gene expression for detecting cancer is widely investigated. Golub et al. were the first to identify a subset of 50 genes that can discriminate acute myeloid leukemia from acute lymphoblastic leukemia, and subsequently predict class membership of new leukemia cases. As part of our research program, we investigate a new feature selection method based on perturbation theory. The effectiveness of our method is verified by performing a series of comparisons with conventional and novel feature selection methods in the literature on some Cancer datasets.