**DECLARATION**

We hereby declare that the Capstone Project Phase - 1 entitled **“Title of the project”** has been carried out by us under the guidance of <Prof. Guide Name, Designation> and submitted in partial fulfilment of the course requirements for the award of degree of **Bachelor of Technology** in **Computer Science and Engineering** of **PES University, Bengaluru** during the academic semester January – May 2021. The matter embodied in this report has not been submitted to any other university or institution for the award of any degree.

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| **<SRN 1>** | **<Name 1>** | **<Signature>** |
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**ABSTRACT**

With the advent of the sphere of bioinformatics, of there is a new confluence engineering and biology that has led to remarkable changes in the way researches approach difficult and time consuming problems. The pharmaceutical industry has highly benefitted from this. Research and opened new gates with regards to how we look at drugs and their applications. With this window of opportunity, comes a big challenge: information on these drugs are not computationally friendly. In this work we take advantage of the structural and functional aspects of a drug to generate a drug embedding, an accurate representation which will serve as a gateway to other bio informatic applications like drug discovery, drug target interactions, drug reprofiling and drug repositioning. We employ machine learning techniques to learn the embeddings of the drugs and validate their efficacy by testing against a known biological classification. Additionally, we are aiming to solve an important bioinformatic application which is: early and accurate identification of potential adverse drug reactions (ADRs) for combined medication which is vital for public health. Since most clinical trials focus on a single drug and its therapeutic effects, most drug-drug interaction induced ADRs go unnoticed until the drugs are actually approved. This has been one of the top 10 reasons on death in United States according to the studies. To solve the same problem we employ various machine learning models to predict drug-drug induced ADRs using the structural and functional characteristics of drugs.