1.	Title of the Project:		Bioinformatics approach for profiling antibiotic resistance genes from metagenomic DNA sequences
2.	Name and designation of the Project Director:		Dr. Shuvro Nandi Assistant Professor
3.	Name and designation of Associate Director(s) (for group project)		Not applicable
4.	Name of the Department/Institute:		Department of Microbiology
5.	Name of the Faculty:		Faculty of Life & Earth Science
6.	Brief description of the project:		
	(a) Project proposal with objectives and methodology (within 200 words):		
	Antibiotic resistance is a growing public health concerns in Bangladesh. The environment plays a key role as a reservoir of antibiotic resistance genes (ARGs) because ARGs can be transferred from environmental organisms to pathogens by horizontal gene transfer. Metagenomics, the sequencing of DNA from the entire community, helps to study ARGs in environmental organisms that consist of a complex group of possibly unculturable organisms. However, the challenges are how to analyze the metagenomics data, what information we can extract from the metagenomics and how to profile ARGs from these complex sequences. The main objective of this principally computational project will be to exploit a combination of newly available metagenome sequence data and novel bioinformatics techniques to profile and predict ARGs from environmental samples. The central methodology will be retrieval of metagenomic database sequences studied from Bangladesh, post processing to the raw sequences data, choosing the best approach to analyze metagenomic DNA sequence data and selection of the model for prediction of ARGs pool from metagenomic data. This will provide insights into the culture independent predication of antibiotic resistance patterns form metagenomes. Key words: Metagenomics, Bioinformatics, Antibiotic Resistance		
	(b) Review of literature on the subject matter of the project and rationale behind the present initiative (within 500 words):		
	The development of resistance to antibiotics by pathogens is one of the major issues face by human. It is estimated that the number of deaths due to antibiotic resistance will exceed 10 million annually by 2050 and cost approximately 100 trillion USD worldwide [1]. Antibiotic resistance arises when bacteria can survive an exposure to antibiotics that would normally kill or stop their growth. This process allows for the emergence of "*superbugs*" that are extremely difficult to treat with existing antibiotics. A few examples include methicillin-resistant *Staphylococcus aureus* (MRSA), which is an extremely drug-resistant bacterium associated with several infections [2], multidrug-resistant (MDR) *Mycobacterium tuberculosis*, which is resistant to rifampicin, fluoroquinolone, and isoniazid [3], and colistin-carbapenem-resistant *Escherichia coli*, which has gained resistance to last-resort drugs through the acquisition of the mcr-1 and blaNDM-1 antibiotic resistance genes (ARGs) [4]. The next generation DNA sequencing technology now provides a powerful tool to sequence genomes derived from DNA extracts obtained from a wide range of environmental samples. For example, the metagenomic DNA sequencing approaches in livestock manure, compost, wastewater treatment plants, soil, water, and other affected environments [5], could provide information about the complex microbial interaction. However, identification and profiling of the full complement of DNA, including ARGs, from these complex sequenced data are now a major challenge. Identification of ARGs from such samples can be done by using the bioinformatic principle of comparison of the		

	metagenomic DNA sequences against available online databases. Such comparison can be performed by aligning raw reads or predicted open reading frames (full gene length sequences) from assembled contigs to the database of choice, and then predicting or assigning the categories of ARGs present using a sequence similarity cutoff. In this approach we are going to use existing microbial resistance databases, to predict ARGs from metagenomic data. At the same time, we are going to use a deep learning approach to predict ARGs, considering the similarity distribution of sequences in the ARG database. At part of this process, we also going to develop, train, and evaluate deep learning model, to predict ARGs from metagenomic DNA sequences. **References:** 1. Review on Antimicrobial Resistance. *Tackling drug-resistant infections globally: final report and recommendations*. Review on antimicrobial resistance, 2016. 2. Vuong, Cuong, et al. "Investigational drugs to treat methicillin-resistant Staphylococcus aureus." *Expert opinion on investigational drugs* 25.1 (2016): 73-93. 3. Gandhi, Neel R., et al. "Multidrug-resistant and extensively drug-resistant tuberculosis: a threat to global control of tuberculosis." *The Lancet* 375.9728 (2010): 1830-1843. 4. Arcilla, Maris S., et al. "Dissemination of the mcr-1 colistin resistance gene." *The Lancet infectious diseases* 16.2 (2016): 147-149. 5. Berendonk, Thomas U., et al. "Tackling antibiotic resistance: the environmental framework." *Nature Reviews Microbiology* 13.5 (2015): 310.
	(c) Expected results:
	Profiling of AGRs from metagenomic data Predicting antibiotic resistance genes from metagenomic DNA sequences. These might lead to development of novel bioinformatic tools for ARGs predication from complex metagenomic data.
	(d) Relevance of the project to national development:
	At this moment there are little bit facilities with low-end computational power for analyzing big data, which is time consuming and inefficient. With the development of bioinformatics laboratory within our institutions will open the facilities for the interested students to practically involved in bioinformatics research for our country. Bangladesh is a developing country and like other developing countries, it is deprived of various research facilities. Due to the lack of proper funding, profound research is difficult to carry out in Bangladesh and people suffer from various type of disease like cancer, diabetes, malnutrition etc. We need to understand more about preventing diseases in the first place and particularly those of high risk because the major reason of high death rate from diseases is the lack of proper knowledge of antibiotic resistance and its treatment. My research plan is to understand the processes underlying the development of antibiotic resistance, with enormous implications for prevention and therapy of the disease mechanisms. My work will have a broader implementation in the public health sector to reduce the number of disease cases and patient's treatment outcome and improve the quality of life of patients. My overall goal is to achieve sustainable development goals in healthcare for Bangladesh by 2030.