

Name of student:

Institutional Affiliations:

Name of course:

**GENETIC AND FUNCTIONAL MICROBIAL ANALYSSIS OF SOIL FROM
MELBOURNE, AUSTRALIA**

Abstract

Adequacy in the methods that can be used for the conservation of the different ecosystems in this research depends on the methods used for analysis and research. The five ecosystems that are contained therein are the LTU moat, cherry lake, Gresswell forest, sporting field, and the compost. In essence, the research was conducted through the dilution of soil colonies from the samples taken from the above locations and determining the number of colonies forming units in the output. Other analyses involved the use of a microbial electric cell, the use of CMD and AMR and the absorbance of the soil.

In the CMD and AMR, the methodology involves the separation of the 16s rRNA genes of the bacteria of each of the soil samples. This was through the biolog plate OD analysis. By defining the gene samples, it was easy to sequence and analyze using the open access clone library.

Research Analysis

Heavy metals form a group of hazards that are not well defined. These compounds cannot decompose by either chemical or biological means. Nevertheless, the most common heavy metals found in contaminated soils are chromium, cadmium, Arsenic, copper, Nickel, Mercury, copper and zinc.

Determination of the sequencing of amino acids in all the soil samples was done at an interval of 24 hours using the biology plate. This was done to profile the molecules making up the compost, sporting field, moat, cherry lake, and forest samples. As such, using the average metabolic response as well as the community metabolic diversity enabled the use of statistical analysis to calculate the analysis of variance (Gomez, et al., 2006). AMR is used as a tool for the comparison of the complete metabolism within the soil communities (wang, et al., 2009). This is on both the aerobic and facultative microorganisms contained therein (Zhang, 2008). On the other hand, the CMD is used to identify the complete amount of substrates present (Sigler, et al., 2008). These substrates will be effectively used on a metabolic perspective by each microbial community. By basing the analysis on the gene sequencing, the biology Eco plate provided a platform for the analysis of both the metabolism as well as the functional efficiency of the bacteria (Gryta, et al., 2014).

Since the CMD is used to measure the diversity in the source of carbon (Yergeau, et al., 2012). In this case, any positive value shows there is absorbance while the negative values indicate that there is no absorbance (Kaimi, et al., 2006). No absorbance is only observed in the compost sample after 24 hours. On the other hand, the AMR values determine the number of carbon sources that are usable (Fargione, et al., 2008). After 96 hours, the highest AMR values can be seen in the forest sample, sports sample, and the cherry lake samples. It may be an indication of

the ecological biodiversity in these sources which indicates a high carbon content. However, the main shortcoming of the method is that it does not indicate the patterns used in the utilization of carbon.

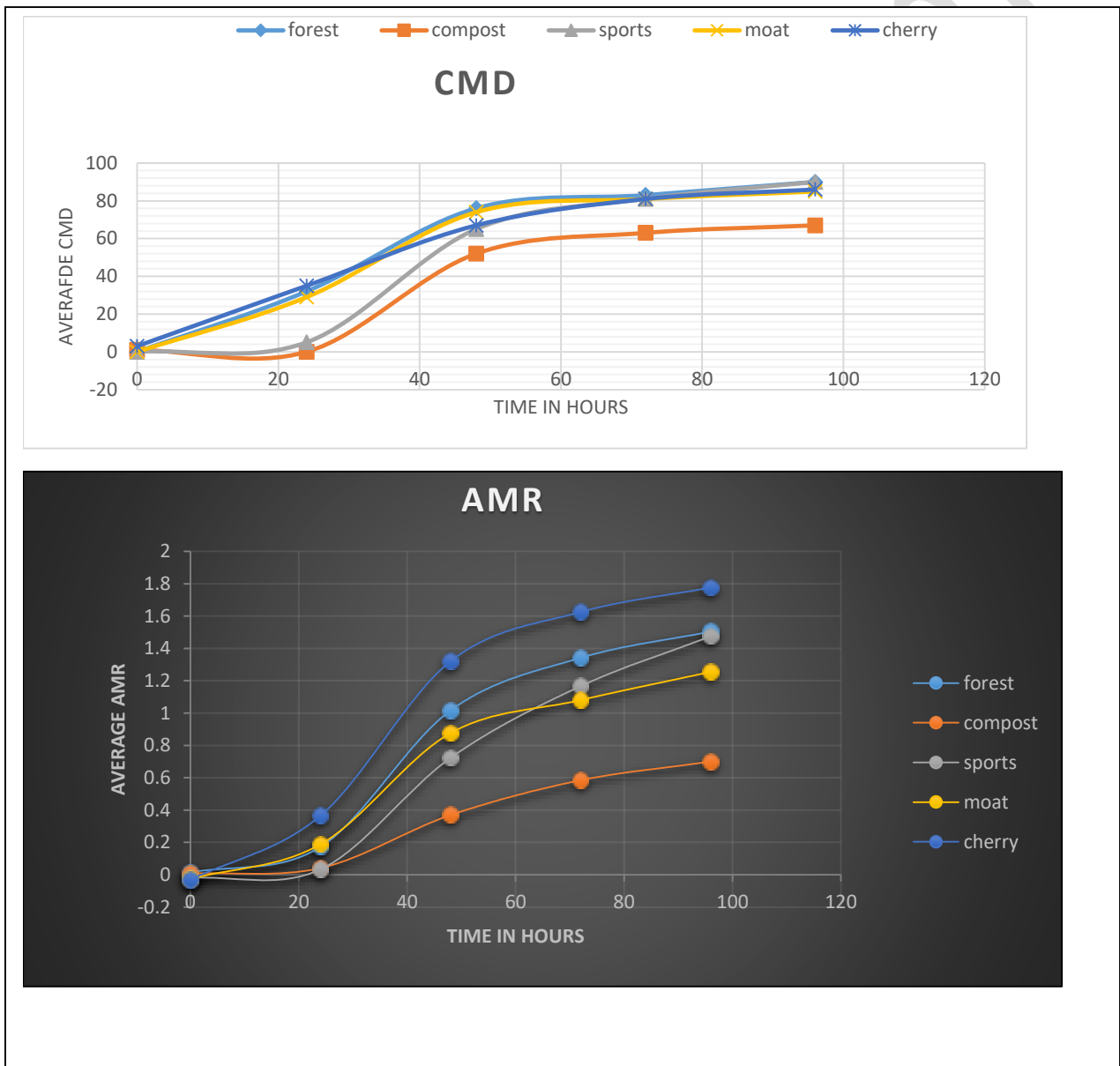


Fig 1: CMD and AMR

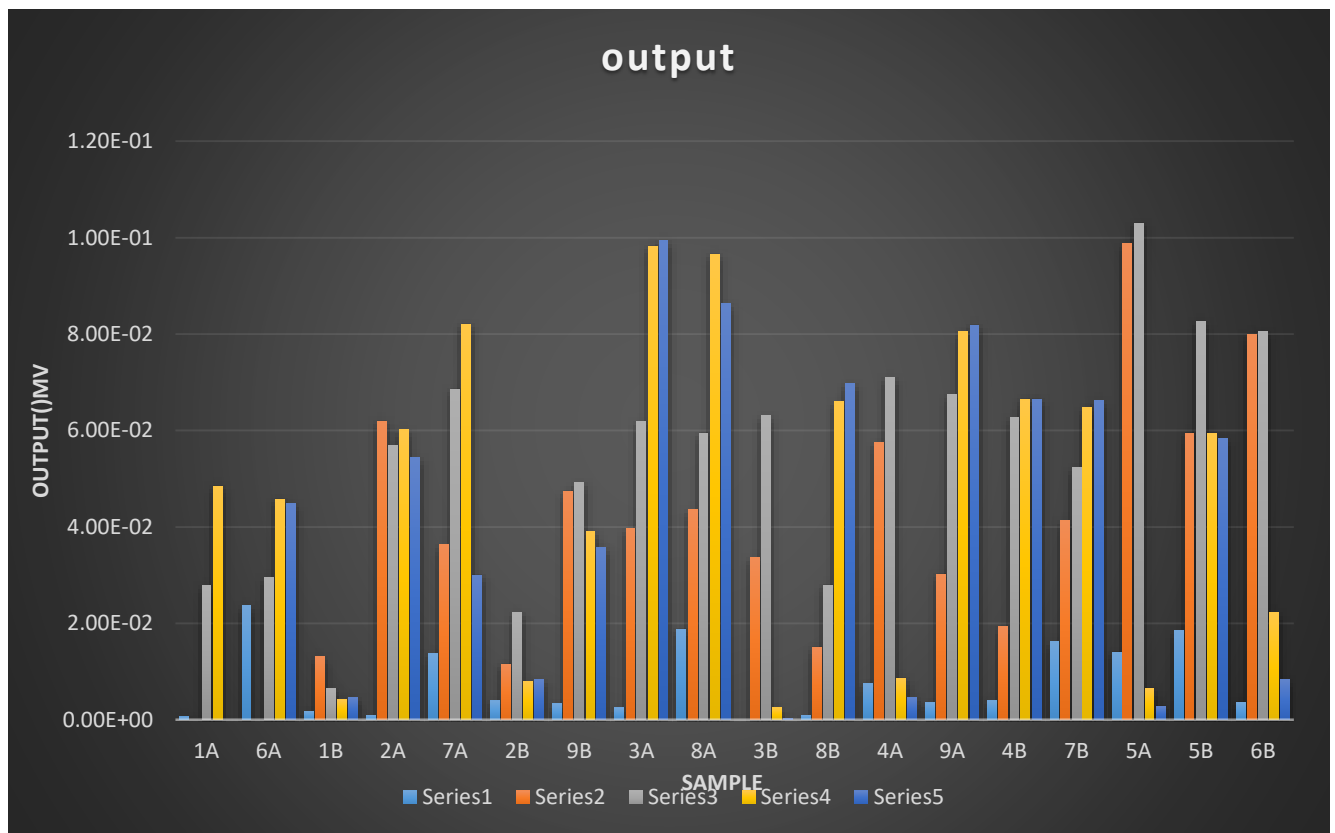
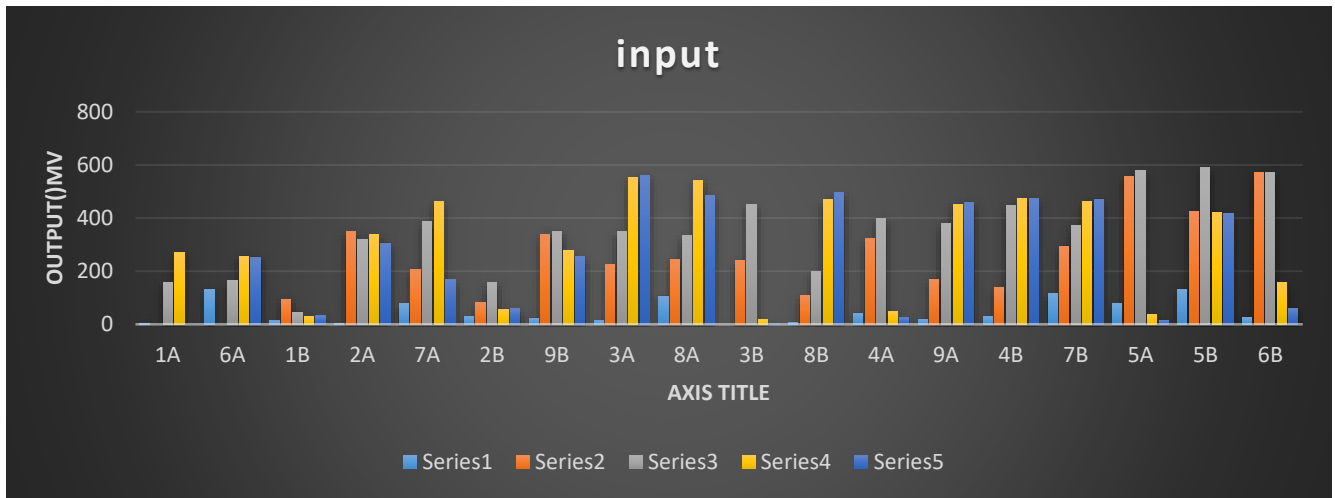
On the other hand, the ability of the soil to degrade the hydrocarbon was done by combining the soil with petroleum diesel (Liu, et al., 2006). The standard deviation was used in this analysis in 6 scenarios. The first scenario was that of a baseline solution, the second was for control and it was an autoclaved solution, the third involved peroxide, the other nitrate, the fifth was that of iron hydroxide and finally, potassium permanganate. Nevertheless, the degradation on an interval of 18 days with the first degradation being tested after 4 days

The analysis of variance was conducted as per each of the time period. It was conducted on each of the compounds of the rRNA. In essence, the highest was observed after 48 hours for the forest sample while the highest for the compost sample was after 96 hours. This was also the highest time required to observe the highest ANOVA for all the other samples. However, there was no relative dissertation between the ANOVA and the CMD and the AMR results.

The colony forming units formed in each of the soil samples was established by the use of an agar solution. This is a test used to determine the resistance of the heavy metals. Nevertheless, the incubation of the solution was done at 30 degrees. The input was measured in each of the soil samples by using a predetermined dilution.

Considering the results after 18 days of the CLPP test, the control solution indicated that the standard deviation decreases over time but this was not observed in the other solutions. All over across the other soil samples, there was an inconsistency with most standard deviations decreasing over time. However, there was an increase in the standard deviation in the compost, sports field and forest samples treated with iron oxide. On the other hand, the LTU moat mud and cherry lake solutions showed a reduction in the standard deviation over the test period

As with the test conducted for the current generation, that is the microbial fuel cell data, it can be observed that the input of the compost heap was the highest. The amount of input from this sample was 38.7mV. However, there were samples whose input was 0 mV such as the sporting field and the Graswell forest. Nevertheless, it can be assumed that there were insufficient data to draw a conclusion since the Gesswell forest also produced an input in the ranges of 155 on other testing days. On the other hand, the output of electricity was highest in the test conducted on the Cherry Lake (0.103mV). The bacteria that are contained in these high-end microbial fuel cells are responsible for the movement of electrons which improve the rate of electricity production (Liu & Logan, 2004). Nevertheless, the amount of electricity produced was a measure of the rate of respiration of the electromagnetic bacteria in each of the soil samples (Logan & Min, 2004).



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Thurs 4/ Friday 5

Fig 2: The Input and output of the microbial fuel cell as per the change in days (practical E)

The colony forming units in the final test were very high in the ranges of X1, 000 to X1000,000. This may be determined by the inhibitory effect of the metals present in these samples especially copper (Hunting, et al., 2013). An increase in the number of colony forming units presents an increased resistance. It has been known that certain metals enhance the growth of bacteria while other metals can be used by bacteria for the purpose of fission which in essence means an increase in their numbers. The highest number of colony forming units are observed in metals such as Nickel and lead, as per the same experiment.

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