

PROJECT GROUP FOUR (4)



BIOGEOCHEMICAL RESPONSES TO SEASONAL AND DECADAL CHANGES IN ATLANTIC OCEAN

PRESENTED BY

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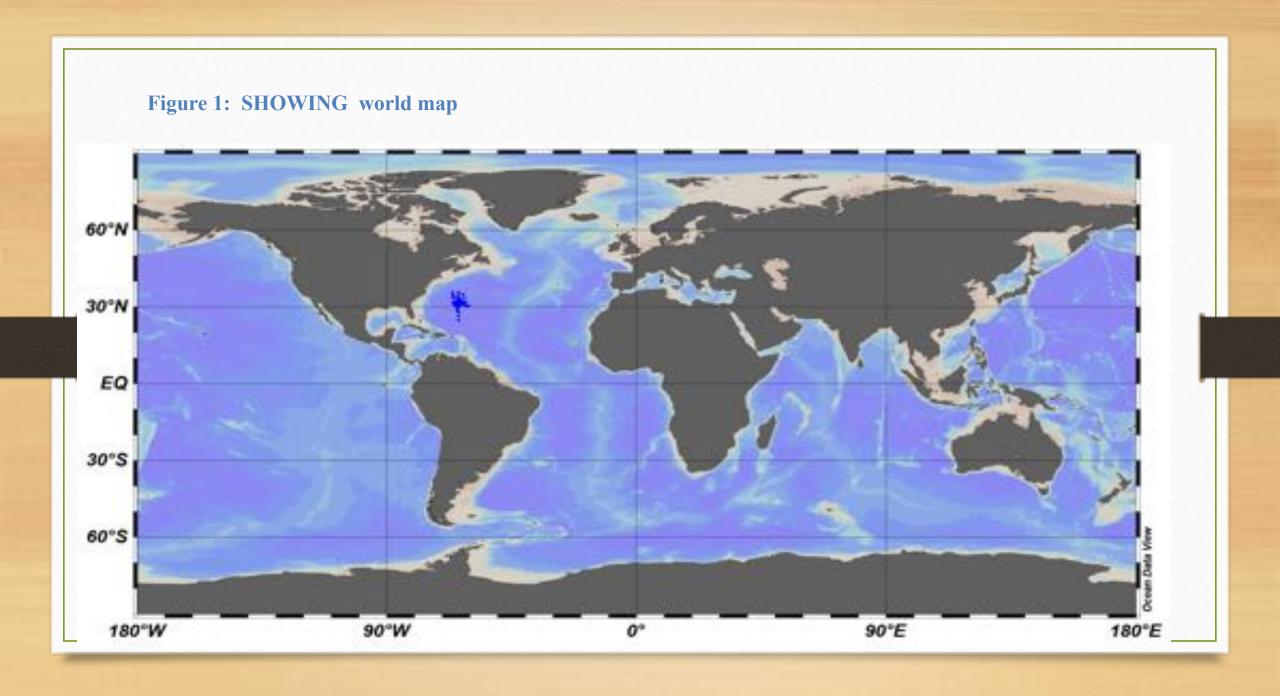
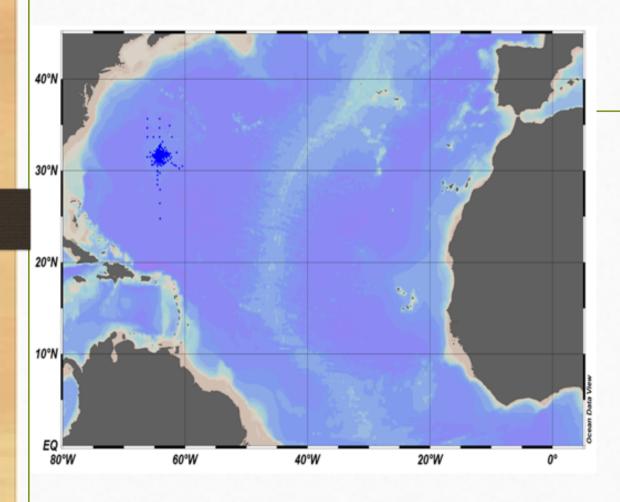
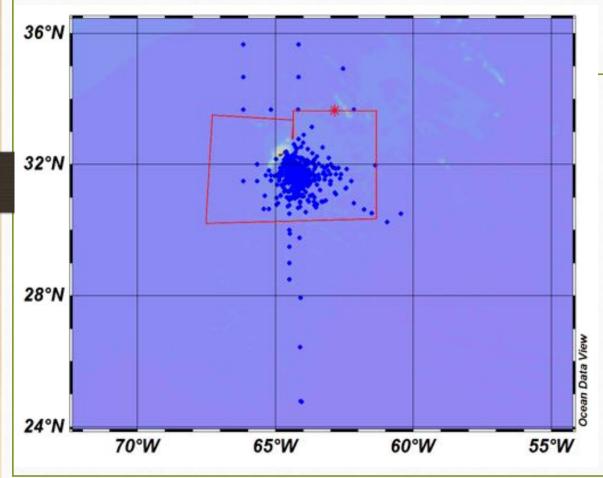


FIGURE 2: SHOWING ATLANTIC OCEAN



- Atlantic Ocean is the 2nd largest
- 106,400,000Km2
- Covers about 20% of the earth surface

CO-ORDINATES OF THE DATA POINTS: BERMUDA ATLANTIC TIME-SERIES STUDY (BATS)



- Longitude: -64.097
- Latitude: 31.971
- Duration:

The data span through 1988 to 2017

AIM AND OBJECTIVES

• Aim:

• To determine the concentration and seasonal variations in biogeochemical parameter in the coastal waters of Atlantic oceans.

Specific objectives:

- To determine variations in temperature, salinity, phosphates, nitrates and nitrites and bacteria abundance in the Atlantic oceans.
- To determine the level of dissolved inorganic nutrients in the selected points.

METHODOLOGY AND DATA ANALYSIS

- Temperature (°C), Dissolved oxygen, Electrical Conductivity, and Salinity
- CTD_S (PSS-78) was measured using Sea-Bird CTD Instrument.
- Nutrients were determined using Colorimetric Methods.
- Bacterial abundance was counted using DAPI Stain on 0.2µm filter.
- Python and Ocean Data View (ODV) software were used for the statistical data analysis

PARAMETERS OF INTEREST

Temperature °C

• Salinity PSS

• Depth m

• Time hh mm

• Decade year

Dissolved inorganic carbon CO₂ μmol/kg

• TOC µmol/kg

• TN µmol/kg

• PO₄ μmol/kg

• NO_3^{2-} µmol/kg

• $NO_2^ \mu mol/kg$

• Bacterial enumeration cells x 10⁸/kg

HYPOTHESIS

Evaporation

1. Temp — Salinity

2. Temp Bacterial abundance

NULL HYPOTHESIS:

- ✓ There is no correlation between seasonal changes in temperature and salinity at p = 0.05 significant level.
- \checkmark There is no correlation between seasonal changes in temperature and bacterial abundance at p = 0.05 significant level.
- ✓ Data were analyzed using Ocean Data View and Python 3.7.0 version tools

Libraries

```
In [1]: import numpy as np
import pandas as pd
import seaborn as sb
import matplotlib.pyplot as plt
import scipy
from scipy.stats.stats import pearsonr
```

Data Selection and Reduction

```
data yymmdd - data.loc[data.yymmdd !- -999, :]
In [3]: 1
        data decy - data yymndd.loc[data yymndd.decy !- -999.:]
        data_time = data_decy.loc[data_yymmdd.time != -999,:]
        data_depth - data_time.loc[data_time.Depth !- - 999,:]
        data temp = data depth.loc[data depth.Temp != -999.:]
        data CTD = data temp.loc[data temp.CTD S != -999,:]
        data Sali - data temp.loc[data temp.Sali !- 999.:]
        data all - data Sali.loc[data Sali.Sigth !- .000.:]
        data sil: - data sil.loc[data sil.021 !- 999,:]
        data all2 - data all1.loc[data all1.OsFixT !- -999,:]
        data all3 - data all2.loc[data all2.Amoms !- -999,:]
        data all4 - data all3.loc[data all3.co2 !- 999.:]
        dets alls - dets alls, locidate alls, alk !- -999.: ]
        data elle = data ells.loc[data ells.mo31 != -909,:]
        data al17 - data al16.locidata al16.M021 !- -999.:1
        data all8 - data all7.loc[data all7.PO41 !- -999,:]
        data all9 - data all8.loc[data all8.Sit !- -999,:]
        data alli0 - data all0.loc[data all0.POC !- -999.:]
        data_all11 - data_all10.loc[data_all10.PON |+ -999,:]
        data alli2 - data alli1.loc(data alli1.Toc !- -000,: ]
        data allin + data allin.loc(data allin.Th !+ -999,:)
        data alli4 + data alli3.locidata alli3.Bact !- - 000,: ]
        data all15 - data all14.loc[data all14.TDP !- -999,:]
        data all16 - data all15.loc[data all15.POP 1+ -999,:]
        data alli7 - data alli6.loc[data alli6.580 !- 000.7]
        print (data all15)
```

Data Selection and Reduction Cont'

```
In [17]: final_data = data_all15.loc[:,('Depth','Temp','Sal1','Alk','NO31','NO21','PO41','Bact','TDP')]
print(final_data)
```

	Depth	Temp	Sal1	Alk	N031	NO21	P041	Bact	TDP
1020700413	301.3	18.133	36.574	2387.9	3.43	0.010	0.14	1.0	203
1020700414	401.8	17.921	36.546	2385.6	3.97	0.009	0.19	0.9	247
1020801003	398.2	17.791	36.510	2386.5	4.99	0.008	0.20	0.5	248

Correlation Matrix

```
In [21]: data_all18 = final_data.loc[final_data.Depth < 201,:]
    corr = data_all18.corr()
    corr</pre>
```

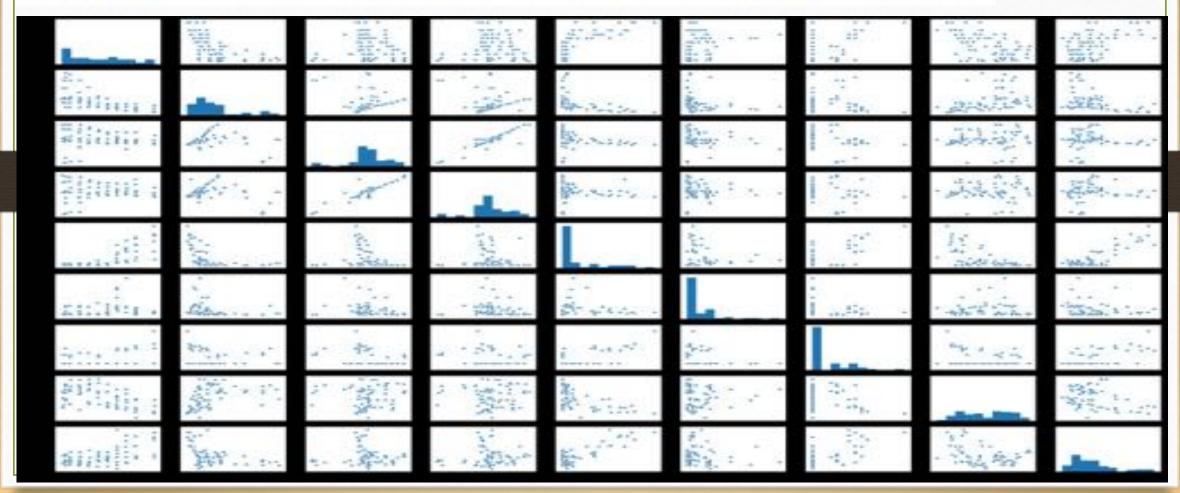
Ont[51]:

	Depth	Temp	Salt	Alk	NO31	NO21	PO41	Bact	TOP
Depth	1 000000	-0.652437	-0.051401	0.012246	0.742928	0.250639	0.334225	-0.592564	0.580173
Тетр	-0.652437	1 0000000	-0.316513	-0.312314	-0.474860	-0.312110	-0.022668	0.410575	-0.405448
Salt	-0:061401	-0.316513	1.000000	0.945417	-0.192274	-0.121042	-0.301158	0.008757	-0.074497
	0.012246								
N031	0.742928	-0.474959	-0.192274	-0.113298	1,000000	0.024901	9.683175	-0.611802	0.829935
N021	0.250639	-0.312110	-0.121042	-0.066036	0.024901	1.000000	-9.177357	-0.034716	-0.097591
P041	0.334225	-0.022668	-0.301168	-0.211415	0.683175	-0.177357	1.000000	-0.298572	0.573776
Bact	0.592564	0.410575	0.008757	-0.013356	-0.611802	-0.034716	-0.290172	1.000000	-0.368343
	0:500373								

Scatter Plot matrix

In [23]: sb.pairplot(data_all18)

Out[23]: <seaborn.axisgrid.PairGrid at 0xfc294d3ba8>



Correlation and P-value

```
In [24]: mgd - data all18['8act']
        hp - data allis[ Temp']
        pearsonr_coefficient, p_value = pearsonr(mgd, hp)
        print (pearsonr coefficient, p value)
        In [27]: mgd - data allim TDP
        hp - data all18[ NO31 ]
        pearsonr_coefficient, p_value - pearsonr(mgd, hp)
        print (pearsonr coefficient, p value)
        0.8299349143984127 1.8735195281922717e-20
In [28]: mgd = data_all18["PO41"]
        hp = data_all18['NO31']
        pearsonr coefficient, p value - pearsonr(mpd, hp)
        print (pearsonr coefficient, p value)
        0.6831754499416509 7.634146070908527e-12
In [29]:
        mgd - data_all18['Temp']
        hp - data allis[ Sali ]
        pearsonr coefficient, p value - pearsonr(mgd, hp)
        print (pearsonr coefficient, p value)
```

FIELD OBSERVATIONS

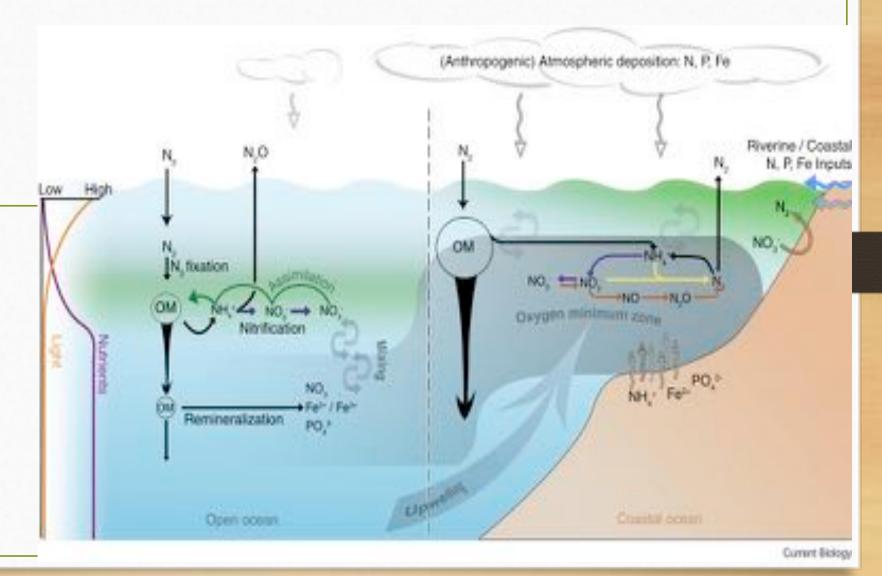
- In this research work our emphasis were on
 - 1. Total Dissolved Phosphorus (TDP)
 - 2. Nitrite
 - 3. Nitrate
 - 4. Bacterial and production
 - 5. Salinity
 - 6. Temperature
- Firstly, we look at nutrient variation along Atlantic Ocean with time using Ocean Data View
- secondly, based on the data gathered in the ocean both in the surface and deep ocean (i.e Between 0 up to 200 m).

FIG 3: SCHEMATIC SHOWING NITROGEN CYCLE PROCESSES

Schematic showing nitrogen cycle processes occurring in the open ocean (left) and the coastal ocean, with an oxygen minimum zone (right).

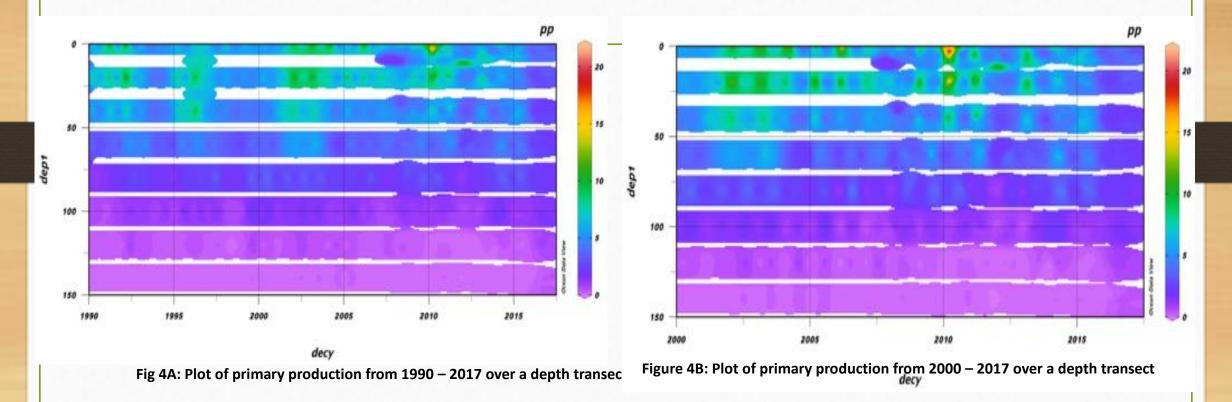
Depth profiles (far left) show typical distributions of light and nutrients (nitrate and phosphate) in the open ocean that can lead to the formation of a deep chlorophyll a maximum (green shading).

The processes depicted in the open ocean also occur in the coastal ocean; in the presence of an OMZ, denitrification and anammox lead to nitrogen loss.



PRIMARY PRODUCTION RATES

According to the studies carried out by Janet et el., 2012, there is a significant correlation between temperature in open ocean waters and Primary production rates.



PRINCIPAL FACTORS REGULATING BACTERIAL GROWTH AND ABUNDANCES

- The principal factors regulating bacterial growth and abundances are temperature, substrate supply, predation and mortality due to viruses (Li & Dickie 1987, White et al. 1991, Fuhrman 1992 and Kirchman et al. 1995)
- Surprisingly, the qualitative and quantitative relationships among these factors are poorly understood as show in this second plot of bacteria.
- In low to middle latitudes, bacterial activities are normally at a minimum when water temperatures are low (Findlay et al. 1991, Shiah & Ducklow 1995 etc.

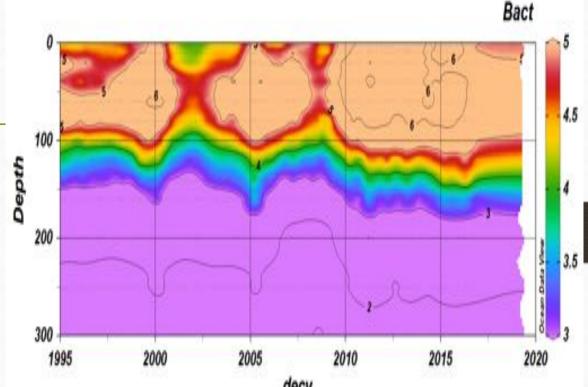
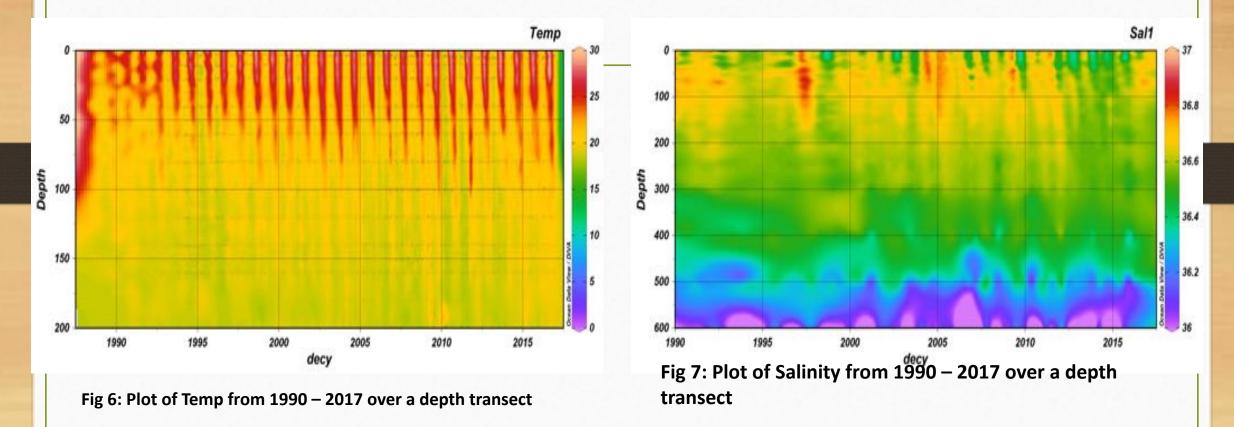
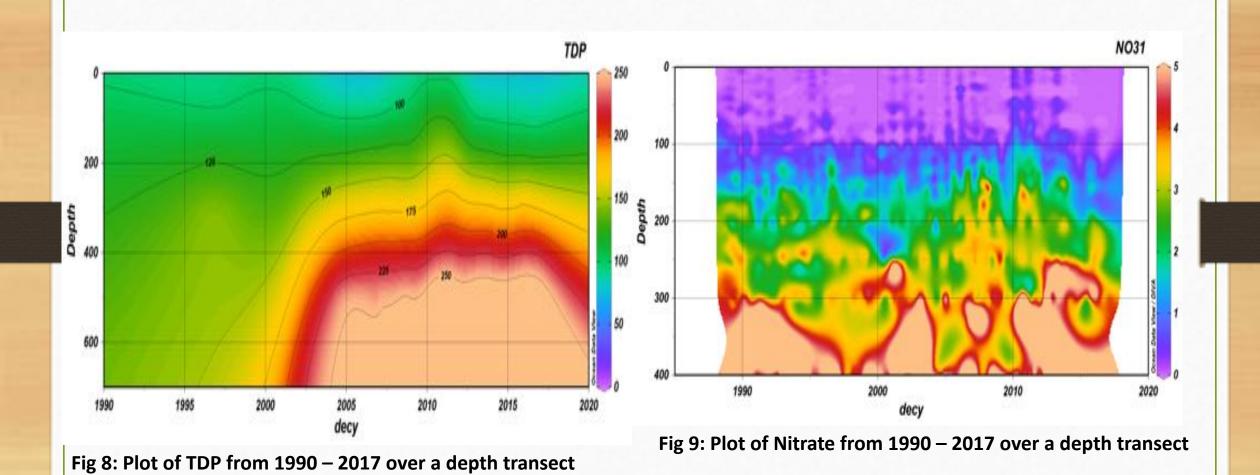


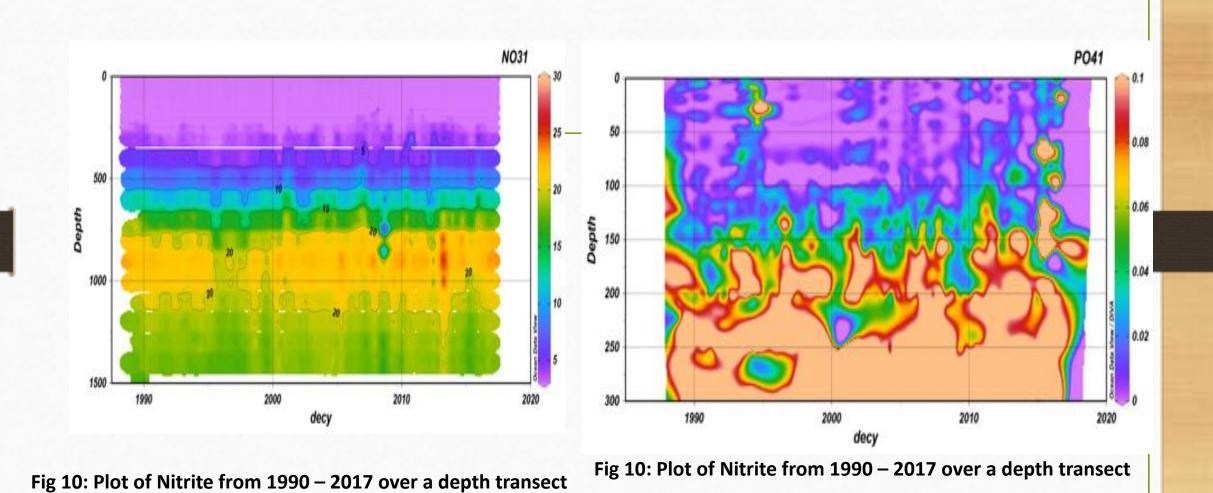
Fig 5: Plot of Bacterial from 1990 – 2017 over a depth transect

TEMPERATURE AND SALINITY

The salinity of the ocean is a function of several factors; one major factor is Temperature.







CONCLUSION AND RECOMMENDATIONS

There is significant correlation between temperature and bacterial production rates.

Temperature increases with time which confirms effect of global warming in the ocean.



