

Microbial Ecology and Biogeography  
OF THE  
Southern Ocean

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# Acknowledgements





# Abstract



# Chapter 1

## Introduction

### 1.1 Some test text to preview layout *etc.*

The Roseobacter clade is an abundant and ecologically significant group of marine bacteria, found at high (> 15%) abundance in most marine surface environments (Ano (2005) and references therein). Unlike some other major proteobacterial groups which are strongly associated with a particular ecological niche (e.g. the SAR11 clade), roseobacters have diverse metabolic abilities, with members capable (for example) of aerobic anoxygenic phototrophy (Biebl, 2005; Béjà *et al.*, 2002), degradation of dimethylsulfoniopropionate (DMSP) by at least two pathways (Moran *et al.*, 2007; ?), carbon monoxide oxidation (King, 2003) and heterotrophic utilisation of a broad range of substrates (reviewed in (Brinkhoff *et al.*, 2008)). Roseobacters are found in the planktonic fraction as well as in commensal association with phytoplankton and metazoans (reviewed in Ano (2005)).

### 1.2 Microbial ecology of the Southern Ocean

### 1.3 Oceanography of the Southern Ocean

#### 1.3.1 Water masses and fronts

#### 1.3.2 Effect of climate change

### 1.4 Role of the Polar Front in biogeography

### 1.5 Project questions and hypotheses



## **Chapter 2**

# **The Polar Front as a major biogeographic boundary in the Southern Ocean**

### **2.1 Summary**

### **2.2 Introduction**

Here are some citations just to test chapter-specific bibliographies: (Lauro *et al.*, 2010; Ye and Doak, 2009; Weber and Deutsch, 2010).

## **2.3 Methods**

### **2.3.1 Sampling**

### **2.3.2 Metagenomic sequencing**

### **2.3.3 Phylogenetic analysis of metagenomic data**

### **2.3.4 Functional analysis of metagenomic data**

## **2.4 Results**

### **2.4.1 Metagenomic sequencing**

### **2.4.2 Phylogenetic analysis of metagenomic data**

### **2.4.3 Functional analysis of metagenomic data**

## **2.5 Discussion**

## **2.6 Conclusions**

## **Chapter 3**

# **Meso-scale biogeographic drivers of planktonic diversity**





## **Chapter 4**

# **Conclusions**



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