

# My PhD thesis

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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**

# Bibliography

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- Béjà O., Suzuki M. T., Heidelberg J. F., Nelson W. C., Preston C. M., Hamada T., Eisen J. A., Fraser C. M., and DeLong E. F. Unsuspected diversity among marine aerobic anoxygenic phototrophs. *Nature*, 415(6872):630–633, February 2002.
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Ye Y. and Doak T. G. A Parsimony Approach to Biological Pathway Reconstruction/Inference for Genomes and Metagenomes. *PLoS Computational Biology*, 5(8):e1000465, August 2009.

## 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**

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## **Chapter 3**

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



## **Chapter 4**

## **Conclusions**