Mike Zubkov presented work on the Atlantic Meridional Transect (AMT, NERC UK funded consortium) that extends from the British Isles to the Falkland Islands. Zubkov and colleagues have been using flow cytometric methods to sort cells, followed by PCR, sequencing and subsequent phylogenetic probe construction to return to the environment and identify the organism of interest to couple their identity with biogeochemical processes. They have been using tracers followed by cell-sorting to estimate the rates of amino acid uptake at ambient concentrations – this allows evaluation of microbial population growth in situ. Questions being asked include: Do *Prochlorococcus* populations in the surface waters rely on organic nutrients (such as amino acids) more than those at depth? On the contrary they found that *Prochlorococcus* living in the deeper waters was consuming 50% the amount of methionine tracer given compared to 25% of the methionine given to those *Prochlorococcus* living in the surface waters. Deep cells are taking up more of the methionine than average prokaryotic cells in these waters. This approach allows us to learn about the physiology of these cells in situ. They also found higher *Prochlorococcus* cell activity in temperate waters than inside the Gyres. In a different study they examined the mesoscale spatial variability in picoplankton in the Celtic Sea and found that cell concentrations of *Synechococcus* and heterotrophic bacteria vary up to 50-fold over distances as short as 12km. Advection of such spatial variability through a time-series site would therefore constitute a major source of 'error'. Consequently, attempts to model and to investigate the ecology of globally important microorganisms in situ must take into account and quantify the hitherto ignored local spatial variability as a matter of necessity.