Electronic Appendix

Prey field characterisation

To investigate the complexity of the prey field we determined spatial distribution patterns of different prey-biomass classes within the field by calculating the biomass-frequency distribution and comparing it with known statistical distributions. Six 14-d prey fields were extracted for the time period 21 May to 12 August, which corresponded to the time period showing the widest range in biomass. Pixel (biomass) values were allocated to biomass classes (bin width range, mg m\(^{-3}\): 0–850). The resulting histogram of zooplankton-biomass frequency distribution was overlaid with fitted Poisson and negative binomial distributions derived using the same pixels and bin widths to determine congruence in peak maxima between observed and fitted distributions.

Zooplankton biomass values within the prey landscape were skewed in the frequency distribution towards the lower end between 10 and 100 mg m\(^{-3}\), with a long “tail” of higher values extending from 100 to over 250 mg m\(^{-3}\) (Fig. 1). We found the biomass distribution comprised two distinct maxima that were approximated by fitted clustered (negative binomial) and random (Poisson) distributions. This indicates complexity within the landscape made up of different types of prey distributions.

[Appendix Fig. 1 Heterogeneity in prey-biomass densities distributed within the prey field for the period 21 May – 12 August. Note secondary axis for Poisson and negative Binomial distributions are both scaled within the primary axis for comparability with the prey field maxima.]

Discussion of tracking methodology

The method of reconstructing tracks we used has been employed in several recent studies with pelagic fish (e.g. Block et al. 2001; Block et al. 2005), but positional errors are greater with this technique than for locations determined directly by Argos satellites (Teo et al. 2004). This is because geolocations are fixed principally using light-level intensity for longitude and sea surface temperature (SST) for latitude, variables which depend on several factors, including weather conditions affecting light-intensity measurements aboard the tag, and the availability of cloud-free high-resolution SST satellite images on the days longitude estimates were available. The
mean error distances associated with geolocations in this study ranged from about 21 to 130 km, which is similar to the geolocation error range reported in a validation study carried out with bluefin tuna and blue sharks (Teo et al. 2004). This suggests any potential errors arising from the geolocation methodology were minimised within the error ranges possible using this indirect tracking technique. Nevertheless, the greater uncertainties inherent in position-fixing using light-level geolocation means that basking shark track reconstructions represent best estimates of movement paths within a quantified error envelope. Importantly, the estimation of relative prey encounter success from routing tracks through the prey field was not dependent on geolocation errors, because prey-field minimum resolution (~50 km) was matched to the geolocation mean error field (~75 km). Moreover, prey biomass values were determined at each grid node (each 0.5° apart) using a ‘search’ radius of 2.7°, so that each node represented the average copepod biomass value within an area larger than the geolocation error footprint. This indicates the prey encounter estimates were robust to variations in geolocation accuracy. Indeed, having tracks with much lower associated error (e.g. Argos class 1, < 1 km) would mean the prey field would require a similar resolution to improve the accuracy of estimated prey encounter rates. Such a prey field would not be possible to produce over the large spatial scales our prey field encompassed, because unfeasible numbers of additional samples would be required (we estimate at least an order of magnitude more; ~1 million samples). Thus, our coupling of reconstructed movements with a novel prey field at comparable resolution represents a first step towards dynamic integration of predator foraging patterns with prey distributions.

References

