Methods

Sea Surface Temperature (SST) data were collected as surface temperature from CMIP5 climate ensembles for both RCP4.5 wm-2 and RCP8.5 wm-2 (ESM2M or ESM2G? where did this trend data come from "trend\_yearmean\_ensemble\_tos\_RCP85.nc”? It was while we were looking at the downscaled data from Ruben but I can’t find a directory to a site for info - Feb 6th – 21st email string) at a spatial resolution of 1x1 degree as well as at a downscaled <5km scale. The 1x1 degree data ranged from 90oN to 90oS whereas the downscaled data ranged from 45oN to 45oS. These data were saved as raster files and imported into R Studio (R Core Team 2015) using the R package ‘*raster’* (Hijmans & van Etten, 2014).

The downscaling procedure for CMIP5 data was done by R. van Hooidonk more downscaling info? I’m not sure where to find a summary of his methods in downscaling. Because the geographic restriction of the downscaled data, it was used to validate the use of 1x1 degree resolution data for the analysis. This was done by comparing extracted values at the MPA coordinates between the two datasets within the overlapping geographic extent and testing for bias along a latitudinal gradient.

The future climate scenarios RCP4.5 and RCP8.5 were collected as both the mean and maximum rate of change between current temperatures (2006) and predicted 2100 temperatures.

Coordinates and information for Marine protected areas (MPAs) around the world were gathered from?. Climatic data were extracted from the raster cell closest to the centroid of the spatial polygon for each MPA, and the distance between the raster value and centroid was measured. A downscaled SST raster from Bio-ORACLE (tyberghein et al. 2012) was used as a land mask for the CMIP5 ensemble data to filter out unwanted MPA coordinates. To prevent the analysis from including both freshwater MPA’s, such as ones in the great lakes, and MPA’s with incorrectly labelled coordinates, extracted cells greater than 50 km away from the MPA centroid were removed from the analysis.

The extracted temperature data were then stratified into four groups, 1) polar, ranging from 66.5° to 90° latitude (n=166); 2) temperate, ranging from 40° to 66.5° latitude (n=2738); 3) subtropical, ranging from 23.5° to 40° latitude (n=2738); and tropical ranging from -23.5oS to 23.5oN across the equator (n=2458). All analyses were also run as a global composition of MPA’s (n=8236) as well as the small subset of no-take reserves (n=309). These groups were analyzed for both RCP 8.5 and RCP 4.5 climate scenarios. The rate of change in SST at the sites of MPA’s was compared to the background rate of change. This comparison was done at each of the four geographic strata and globally.

R Core Team (2015). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Robert J. Hijmans (2015). raster: Geographic Data Analysis and Modeling. R package version 2.4-20. http://CRAN.R-project.org/package=raster

Tyberghein L, Verbruggen H, Pauly K, Troupin C, Mineur F, De Clerck O (2012) Bio-ORACLE: a global environmental dataset for marine species distribution modelling. Global Ecology and Biogeography, 21, 272–281.

If you are running short on references the raster package citation can typically be removed with the removal of using the R package ‘*raster’* (Hijmans & van Etten, 2014) without being innacurate. You can possibly remove the CRAN citation and referencing that you did work in R as well, but maybe in sups if you include your code.

Also a comment on “The exception is Polar MPAs, for which the rate is far lower than the forecasted background rate of polar oceans.” – this is probably fine because you don’t actually run a statistical test, but you may get comments about autocorrelation in these comparisons. I think a good rebuttal or a reason not to include autocorrelation is that one of highlights of this experiment is that many MPS’s are autocorrelated because of the biases that go into choosing their locations and we don’t want to ignore that bias.

Another comment on using all cells in the region, I think it should be annotated “N=44012” instead of “n=44012” because it is the complete population of cells, not just a sample.