

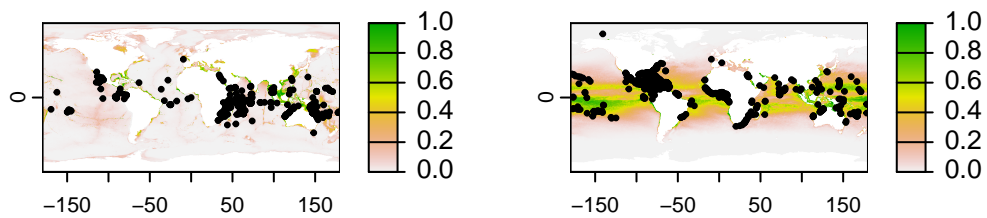
# SDMs MHS

## Example of application

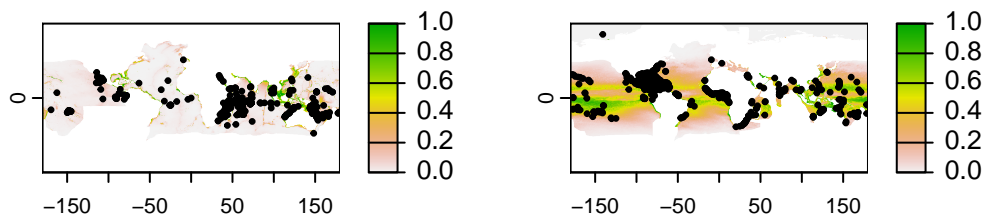
Considering only two species to see if its worthwhile:

1. *Carcharhinus albimarginatus*
2. *Aetobatus narinari*

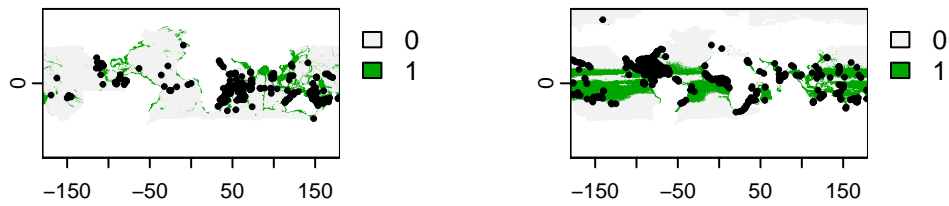
Load maps and points:



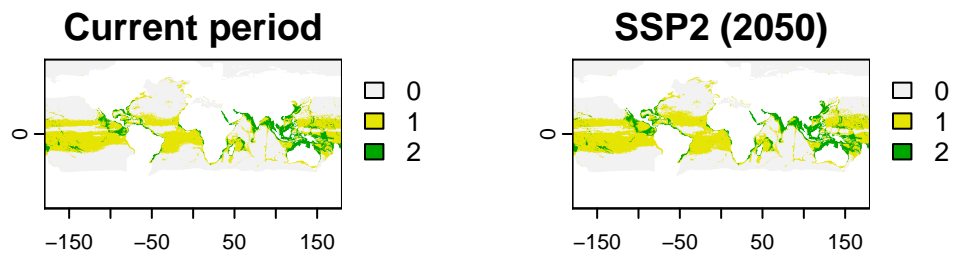
Apply masks to isolate to “native” areas:



Convert to binary format (maybe we can do without it also - in fact, it may be a better choice, but interpretation is a little bit more tricky):



Sum results to get a “richness” indicator:



Once we aggregate multiple species, we can assess how much richness will change in the WHSs.