Intro:

- Make a Venn diagram with the different kinds of traits and where they overlap, giving examples, in the introduction.

* I have added Figure 1.2 (line 218).

- More distinction between responses to climate and climate sensitivity in the introduction.

* I have amended the paragraph from line 258 to line 274.

Functional trait correction in box 1 of chapter 2.

* I have corrected the text box on page 39.

Chapter 4:

- Scale issues: for species with large range size particularly, a resolution of 5 km2 will result in commission errors (assuming the species is present in that 5x5 area when it is not) and increase their climatic niche if cells have high or low environmental conditions. This is due to how range maps are draw https://pubmed.ncbi.nlm.nih.gov/16972877/. For small species using a lower resolution also lead to commission errors as you shows in the supplementary figure. During the viva we discussed the idea of using different resolutions for different range sizes. As you already calculated the climate variables for 5, 10 and 50 km2 resolutions the easiest solution would be to create two range size categories and use each resolution for each class. We realise this may not be straightforward (where to put the cut-off points), so alternatively you could see if results are qualitatively different when changing the resolution. Manuela is happy to discuss this a bit more if useful.

* I have run the models again using different resolutions for the estimation of climate-change sensitivity, depending on the range area of the species. The methods are explained lines 1558-1570.
* The results are congruent with the main results (lines 1667-1669 and Supporting Figures S4.21, S4.22, S4.23).

- Non-breeding area issue: removing the climatic conditions of the non-breeding area can likely affect how the climatic niche is described, and species that spend several months during the non-breeding season in an area likely can withstand those conditions. Also currently you are taking annual values for the breeding range, but the species will not be affected by these, they migrate in response to climatic changes. Properly including those species would require obtaining climate data for each area (breeding and non-breeding) within the relevant time window when individuals are there. The required information on seasonality and climatic data may not be available, so alternatively, we discuss removing species with distinct breeding and non-breeding ranges. This will bias your sample, but as currently presented the climatic niches of those species are not correctly characterized.

* I have run the models for mammals and birds again after excluding species identified as migratory, using lists of migratory species for mammals and birds (methods lines 1552-1557).
* The results were congruent with those from the main models (results lines 1664-1666; Supporting Figures S4.18, S4.19, S4.20).

*Check how to cite/acknowledge list of migratory species from BirdLife*

- Optional for PhD thesis, but strongly advised for manuscript submission: turn open-ended questions into directional, supported hypotheses in the intro, and make sure that these are explicitly linked in the rest of the document.

* Keeping this piece of advice for the article manuscript.

Chapter 5:

- Phylogenetic imputation and circularity: using body mass (+taxonomy) to estimate RMR and then calculating the residuals of RMR ~body mass, creates circularity, for imputed species the residuals will only represent how that taxonomic group differs from the predicted, which is not very informative and not how you are interpreting the values. Instead, we recommend results are presented only for species with empirical RMR estimates.

* I have changed the data used in this analysis so that I only use known RMR values (Methods: paragraph 5.2.6 starting line 1964; Results: Figure 5.4, paragraph 5.3.2).

- You may with to consider using taxonomic slopes when calculating the residuals RMR~body mass\*taxonomy, this way you would avoid having entire groups showing as high (or low) residuals because the entire group has a different relationship between body size and RMR

* I have recalculated the residuals with random slopes (Methods lines 1966-1969 & Figure 5.2(b)), only for the subset of species with known RMR values.

*Residuals(log(RMR ~ log(body mass) + (1 + log(body mass)|Class/Order)).*

**Discussion:**

**- Higher integration, context dependency, implications, strengths and weaknesses, future directions.**

* **I have re-reorganised the General discussion throughout.**