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Supplement of

A climate network perspective on the intertropical convergence zone

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To further validate the results described in our main paper and the robustness of the employed methodological framework, we have conducted several tests, the results of which will be further detailed in the following.

S1 Jackknife test

To demonstrate the qualitative stability of the results of our cluster analysis framework based on the zonal mean network characteristics, we first conduct a jackknife test. For this purpose, we split the full 30-year data into two parts containing 15 years each. Thereby, we create two samples that we can individually analyze with our approach. Employing the clustering framework based on the global network connectivity pattern as described in the main manuscript, we obtain two dendrograms (shown in Fig. S1), which we compare with the one based on the full time series (Fig. 3, left panel) in the main text.

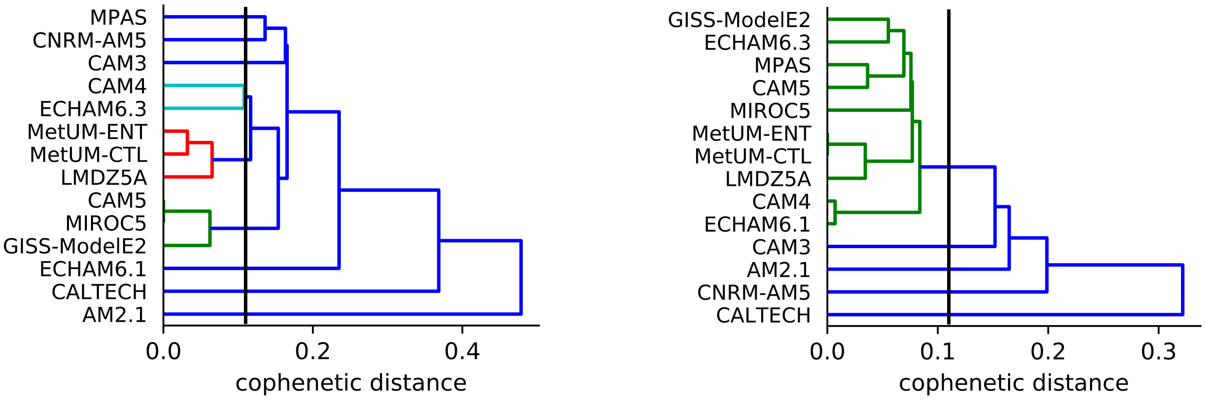

Fig. S1: Dendrograms in full analogy with Fig. 3 (left panel) of the main text, but based on the first (left) and second (right) 15 years of the model simulations, respectively. The horizontal lines indicate the cophenetic distance at which we have cut the dendrogram for the full data set to obtain the clusters described in the main text.

Comparing the left panel of Fig. S1 with Fig. 3 (left panel), we observe a tendency towards larger cophenetic distances between the models at which they become grouped into respective clusters. We hypothesize that this could be related to residues from the spin-up process, along with a generally larger statistical variability originating from a smaller sample size. Therefore, the dendrogram looks slightly different as compared to the results for the full data, while we can still observe the main features of the full data analysis. Specifically, the sub-cluster containing the models MetUM-ENT, MetUM-CTL, LMDZ5A, CAM4 and ECHAM6.3 nearly completely matches the original cluster 1 (only ECHAM6.1 exhibits larger cophenetic distances and therefore joins the CALTECH and AM2.1 models in the outlier group). Additionally, we find the six cluster 2 models of Fig. 3 now being split into distinct sub-clusters.

Comparing the dendrogram obtained from the second 15 years (shown in Fig. S1, right panel) with the full data analysis, we again recognize several similarities. First of all, we essentially recover the some sub-clusters which make up clusters 1 and 2 in the full 30-year model runs, except for CAM3 and CNRM-AM5, both which are classified as two additional outliers (CALTECH and AM2.1 are again categorized as single model clusters).

We conclude that the main features (i.e., several sub-clusters and outliers) can already be identified when using only half of the simulation data, highlighting the qualitative stability of the reported group structure among the analyzed models.

S2 Robustness of zonal mean network characteristics

To further support our findings reported in the main text, we design an additional bootstrapping test. For this purpose, from the full 30-year simulation period, we randomly select 20 one-year blocks which we subsequently concatenate and treat as a new data set. Repeating this for several independent realizations (here 20) enables us to compute the mean over the results obtained for the bootstrapped data sets. For each of the models, we subsequently compare the zonal mean network measures of the full data analysis with their mean pattern for the different bootstrapped data sets. Since this is being performed for all 14 models and two network measures individually, we provide here only a typical example of the zonal mean degree of the MIROC5 model for illustrative purposes (Fig. S2).

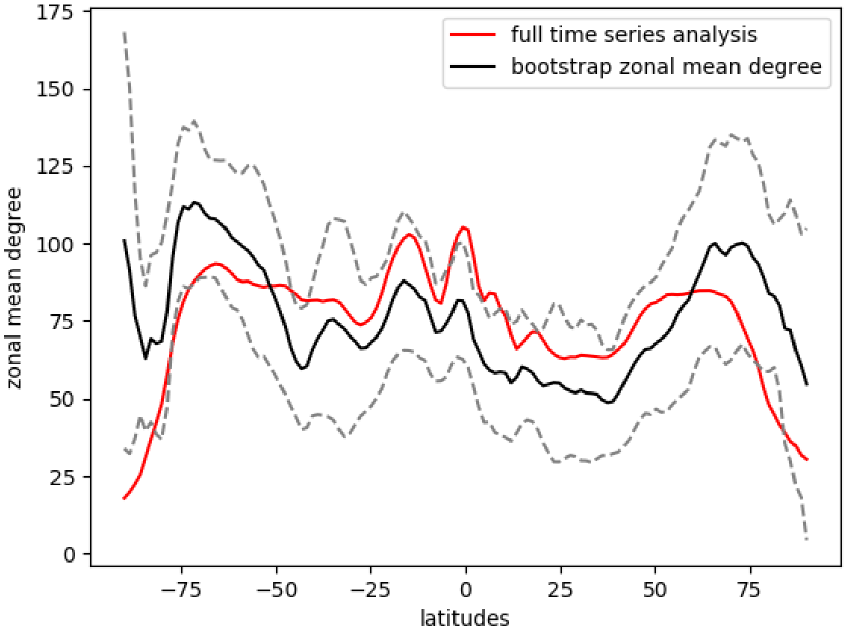

Fig. S2: Zonal mean degree of the full 30-year simulation (red) and average over the 20 independent 20-year subsamples (black) for the MIROC5 model. Dashed lines indicate the standard deviation of the zonal mean degree values.

Figure S2 clearly illustrates that the main features found in the full data (double peak around ITCZ position, additional maxima in the extratropics) are retained if we randomly select, shuffle and recombine annual blocks of data. Similar observations can also be made for the other models. We, therefore, conclude that the patterns of zonal mean network properties exhibit characteristic and distinct qualitative patterns involving general trends along with local maxima and minima, which reflect the specific dynamics of each particular model.

S3 Hierarchical cluster analysis

As already discussed in the main text, we consider the single linkage approach as the best suited method for our hierarchical cluster analysis. To illustrate that the results are, however, similar for other methodological variants, we also studied hierarchical cluster formation when employing the alternative *average* and *complete* linkage schemes. As for the single linkage method, the corresponding analysis results in one new dendrogram for each linkage option. The corresponding results for average and complete linkage approaches are shown in Figs. S3 and S4, respectively.

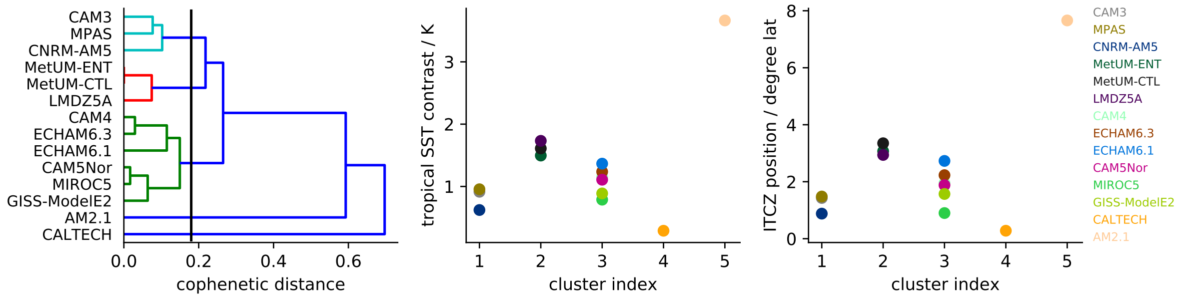

Fig. S3: Model clustering of the AquaControl global networks (left) along with the tropical SST contrast (middle) and ITCZ position (right) for the four identified hierarchical clusters when employing the average linkage method. The left panel shows the dendrogram obtained from the clustering of the zonal-mean network measures. The vertical line indicates the level of cophenetic distance at which we split the models into four clusters.

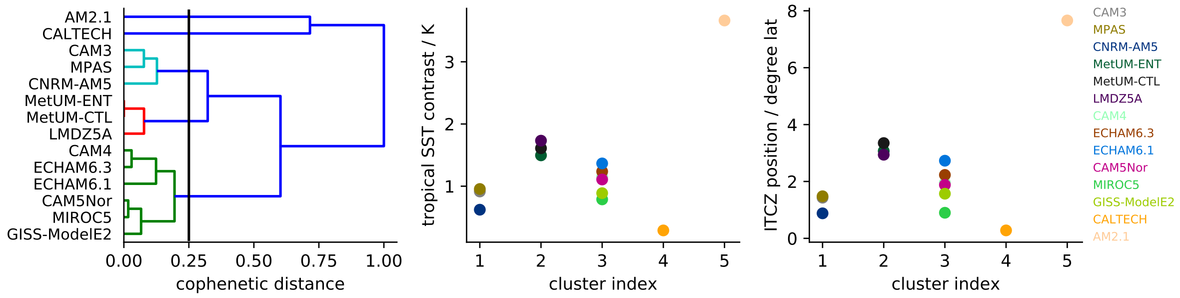

Fig. S4: Same as for Fig. S3, but utilizing the complete linkage approach.

Regarding the average linkage method, when comparing the respective dendrograms in the left panels of Fig. S3 and Fig. 3 of the main text, we find that AM2.1 and CALTECH are consistently identified as outliers and, therefore, categorized into single model clusters. At an initial visual inspection, the rest of the cluster structure seems to appear rather dissimilar under single and average linkage clustering, respectively. However, the low number of models enables us to analyze in more detail the stepwise mergers of the models. This analysis of the dendrograms reveals that certain groups of models appear as core elements of clusters in both clustering approaches. In particular, we observe four sub-groups, each of which comprises 3 models, i.e., Group 1: CAM3, MPAS, CNRM-AM5; Group 2: MetUM-CTL, MetUM-ENT, LMDZ5A; Group 3: CAM4, ECHAM6.1, ECHAM6.3; Group 4: CAM5Nor MIROC5, GISS-MODELE2. All groups (except for

ECHAM6.1 in Group 2) can be also found in the dendrogram in Fig. 3 (left panel). As already mentioned in the main text, we hypothesize that the strong overall similarity among the models leads to the emphasis of some minor dissimilarities between certain pairs by other linkage methods than single linkage (where only the largest similarity – i.e., the shortest cophenetic distance – among pairs of models is considered) and, thus, a different group structure.

Interestingly, utilizing the complete linkage approach leads to a rather similar dendrogram as for the average linkage method. As before, all the subgroups are well visible in the dendrogram. As a result of the different clustering methods, the indicated level of cophenetic distance at which we identify the clusters is increasing from single linkage (0.11) to complete linkage (0.25), which is indicated by the vertical lines (note the differently scaled horizontal axes in Fig. 3 of the main text and Figs. S3 and S4). Furthermore, the separation between the clusters is not as clear as when using the single linkage method. Yet, there are still noticeable differences between the different clusters of models identified in Figs. S3 and S4, respectively. However, not only the specific cluster-core structures described above are retained across all three dendrograms obtained with the different linkage options, but there are also clearly visible differences between the respective time-mean ITCZ positions and tropical SST gradients among the individual clusters as identified by each method. We therefore conclude that our framework is robust enough to draw the general conclusions about inter-model similarities and differences as discussed in our main text.