

Interactive comment on “Adult life strategy affects distribution patterns in abyssal isopods – implications for conservation in Pacific nodule areas” by Saskia Brix et al.

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Dear referees, thank you very much for the constructive comments on our manuscript. Especially the direct implementation in the pdf made it highly valuable to work with. AllsSpecific comments from the annotated pdf were implemented in the word doc manuscript version and will be visible via the track changes version. We did consider all comments from the annotated pdf.

Please also note the supplement to this comment:
<https://bg.copernicus.org/preprints/bg-2019-358/bg-2019-358-AC2-supplement.pdf>

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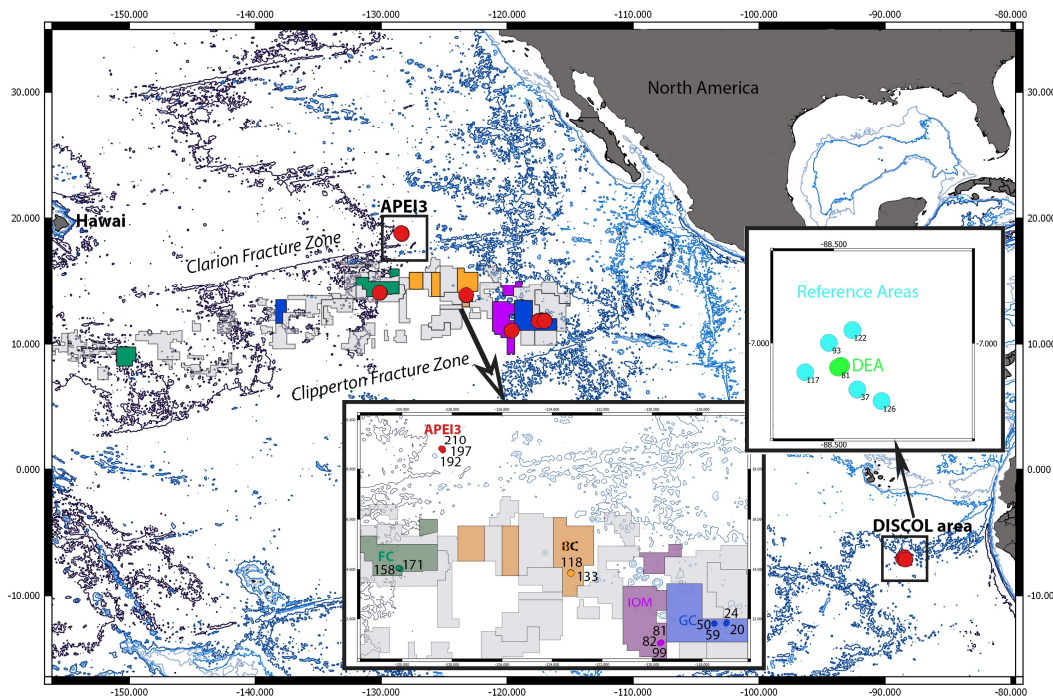


Fig. 1. Map of the locations of the EBS sampling sites (red dots) within the manganese nodule contractor and the DISCOL Experimental Area (DEA) areas in the north- and south-eastern Pacific. The colourcode in

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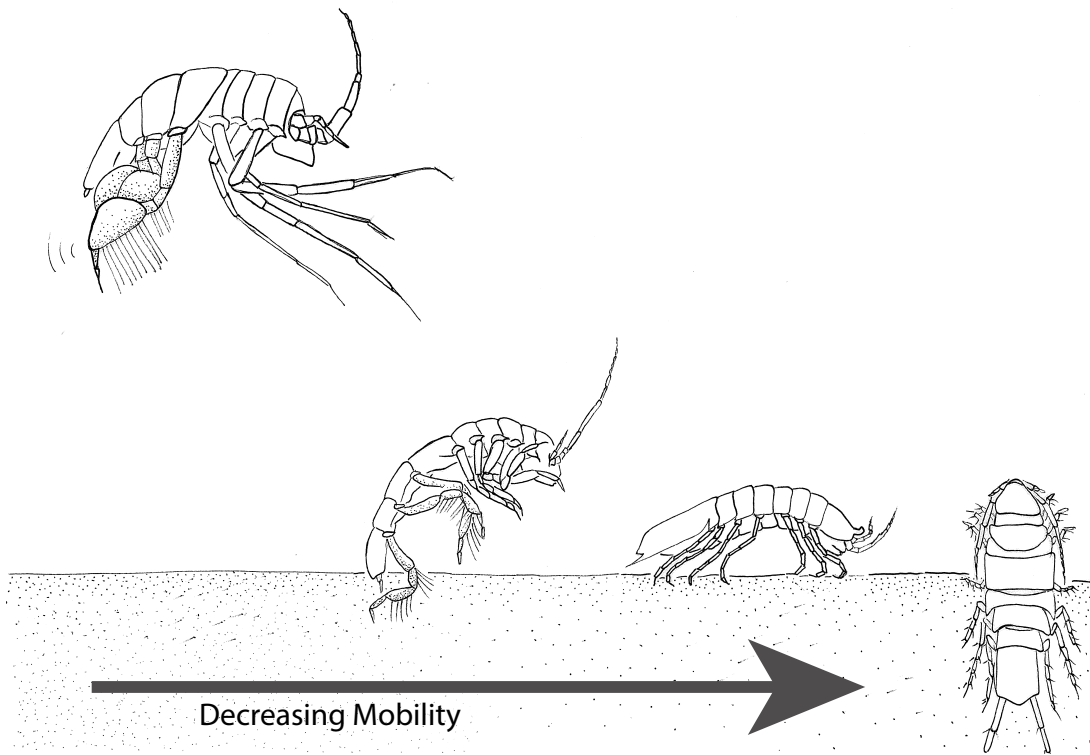


Fig. 2. Illustration of the locomotion of the four isopod families. From right to left: Munnopsidae – swimming, Desmosomatidae – walking/swimming, Haploneiscidae – walking, Macrostylidae – burrowing.

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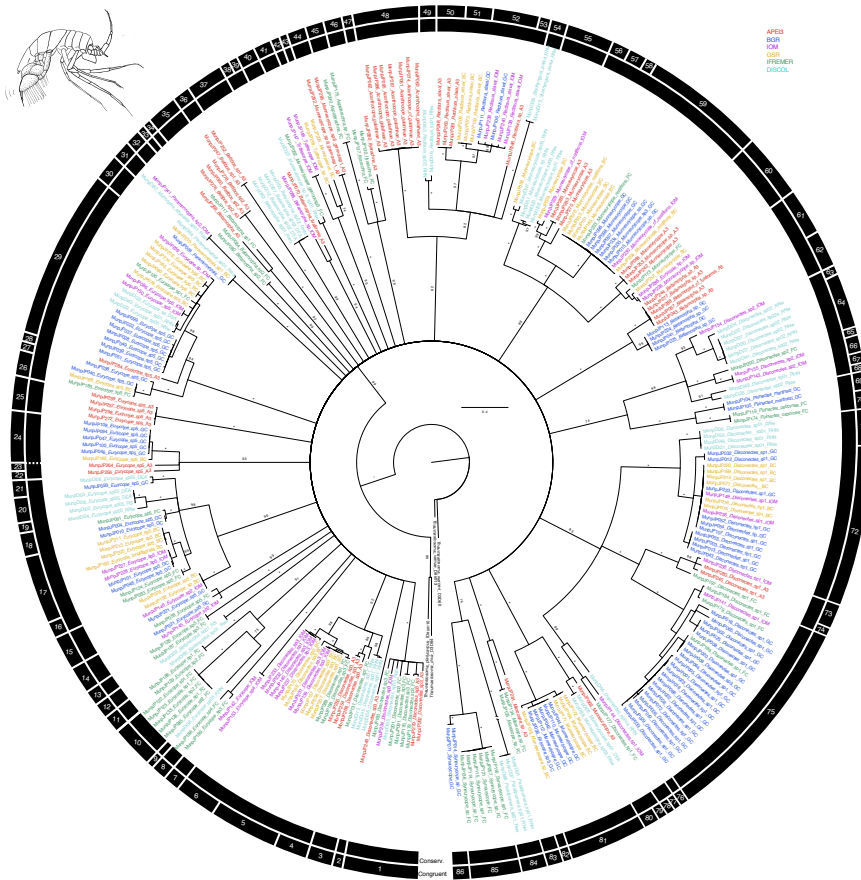


Fig. 3. Phylogenetic tree of all munnopsid samples based on 16S and COI sequences for 294 specimens. Colours indicate collection location, with black indicating outgroups. All unsupported branches were colla

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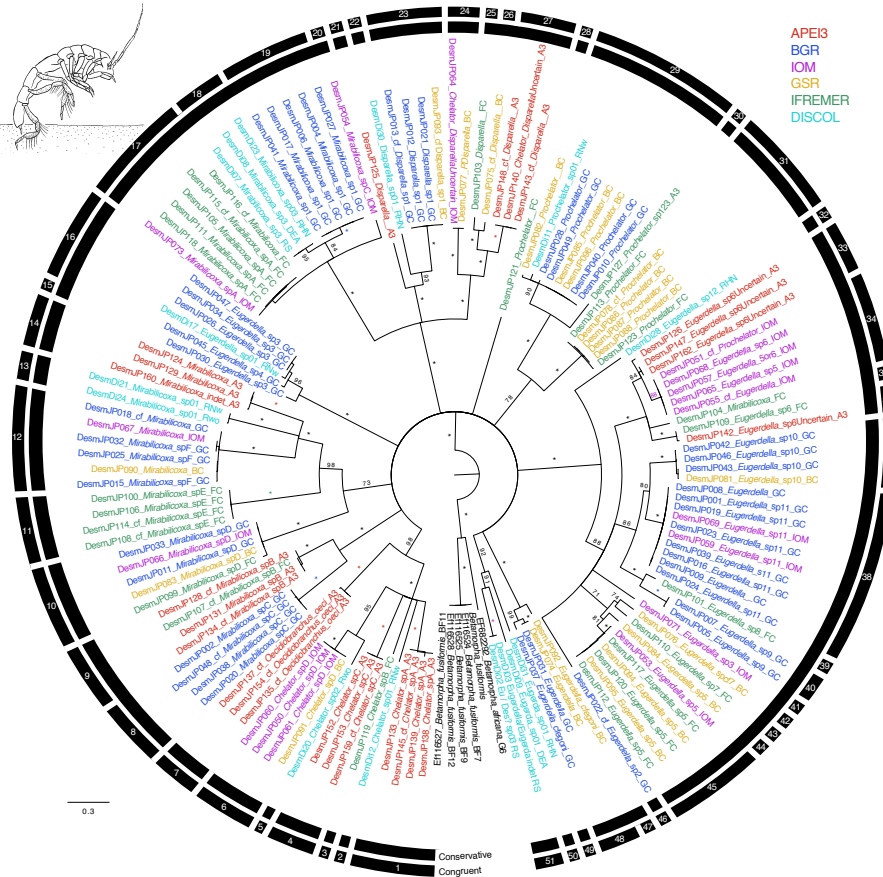


Fig. 4. Phylogenetic tree of all desmosomatid samples based on 16S and COI sequences for 143 specimens. Colors indicate collection location, with black indicating outgroups. All unsupported branches were co

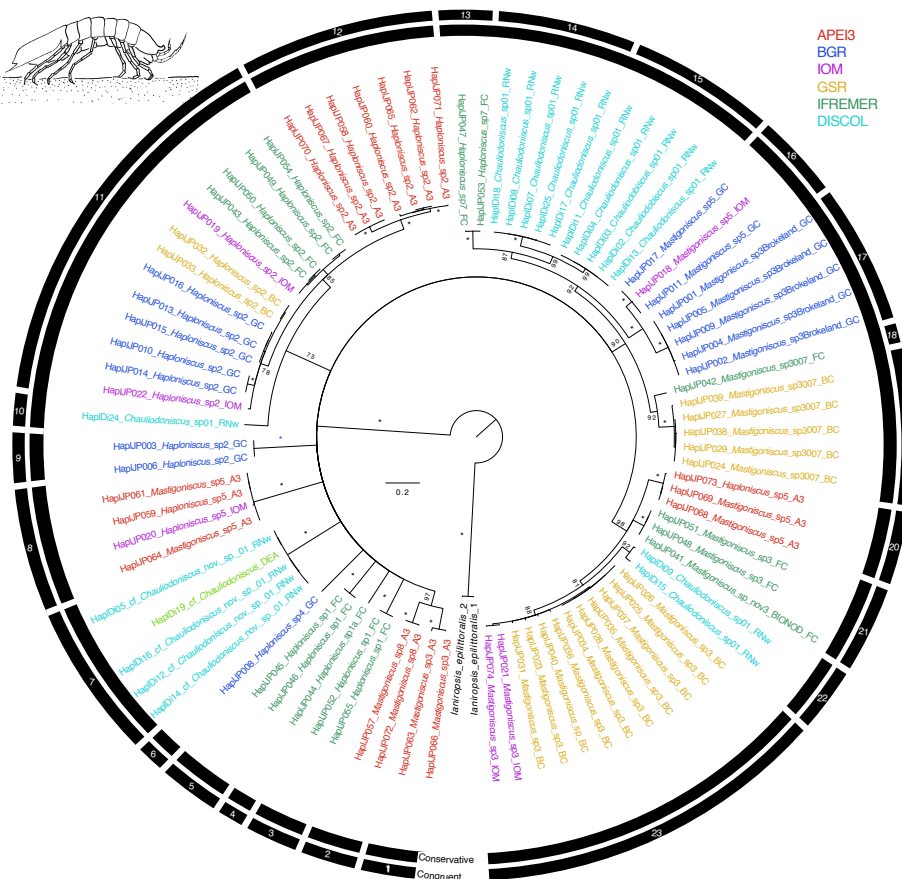
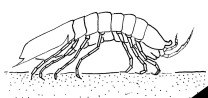
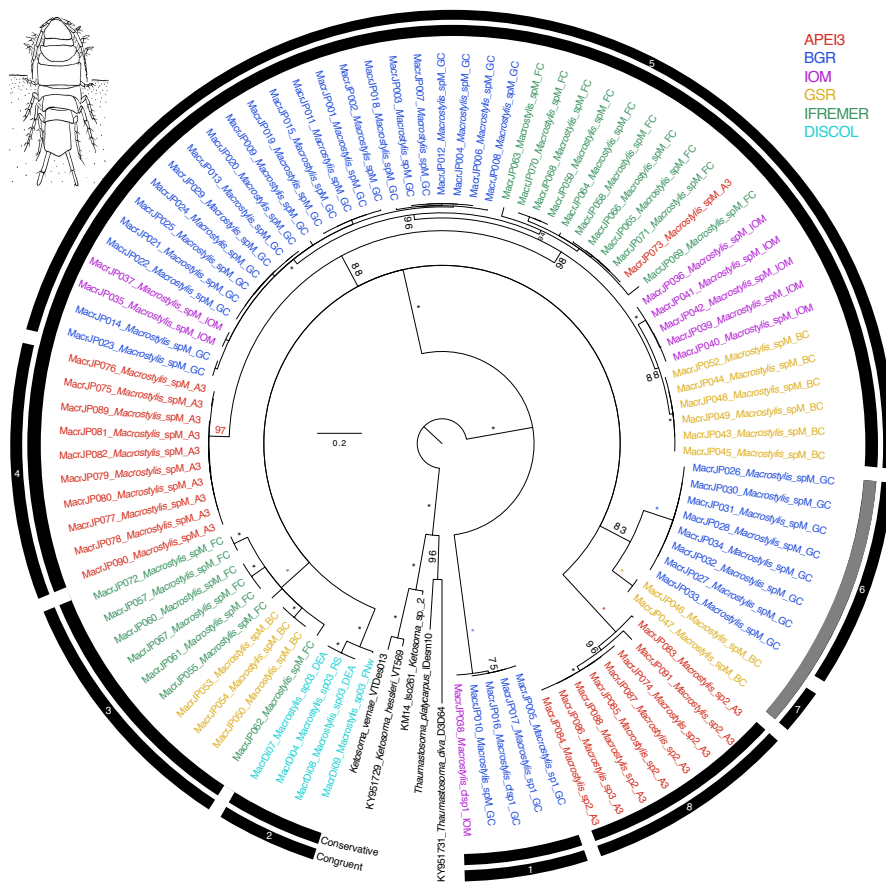
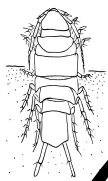


Fig. 5. Phylogenetic tree of all haploniscid samples based on 16S and COI sequences for 88 specimens. Colors indicate collection location, with black indicating outgroups. All unsupported branches were coll

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Fig. 6. Phylogenetic tree of all macrostyloid samples based on 16S and COI sequences for 94 specimens. Colors indicate collection location, with black indicating outgroups. All unsupported branches were coll

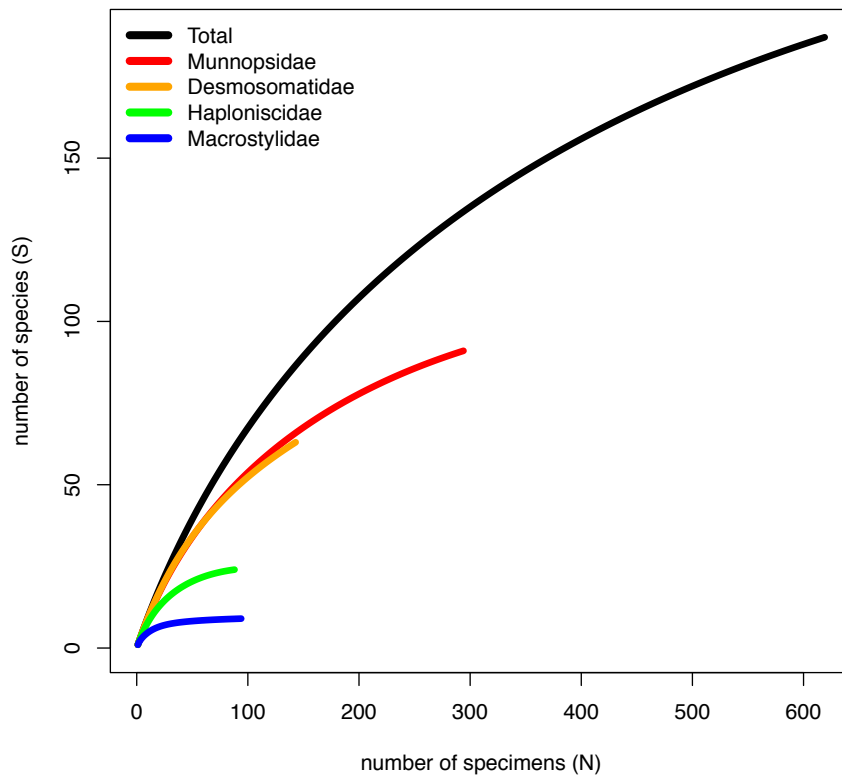


Fig. 7. Rarefaction analysis by isopod family, considering all areas together.

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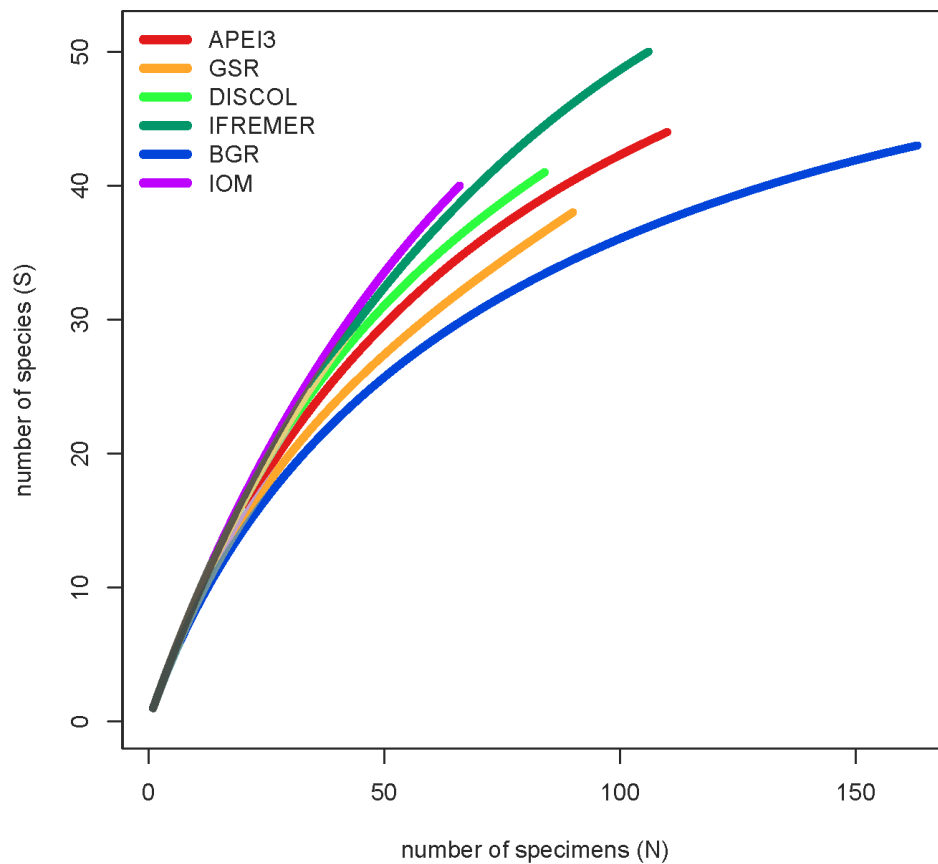


Fig. 8. Rarefaction analysis by area, considering all families together.

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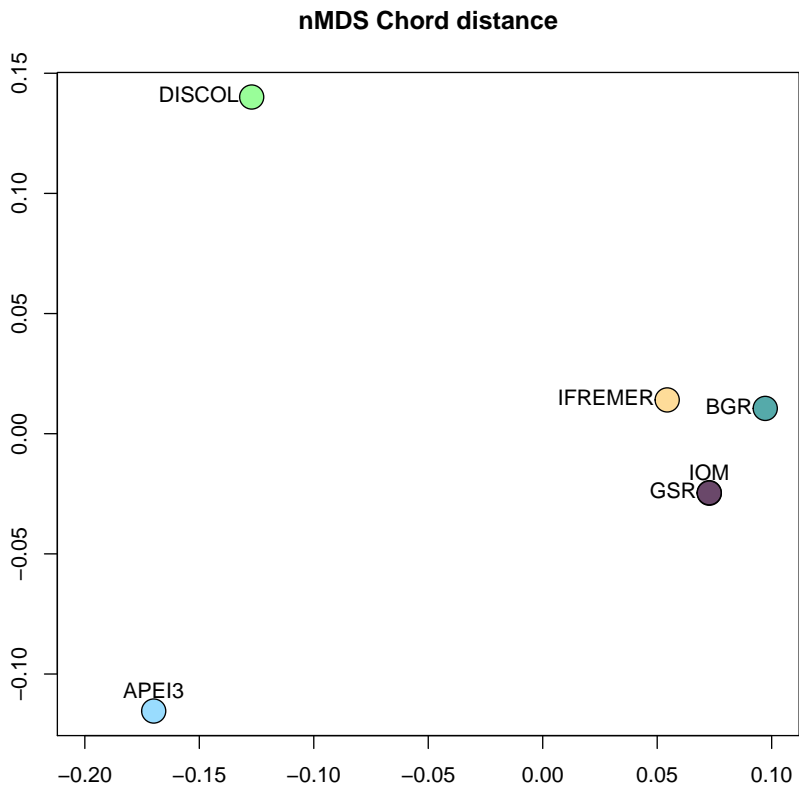


Fig. 9. nMDS ordination plot of Chord-distance between areas.

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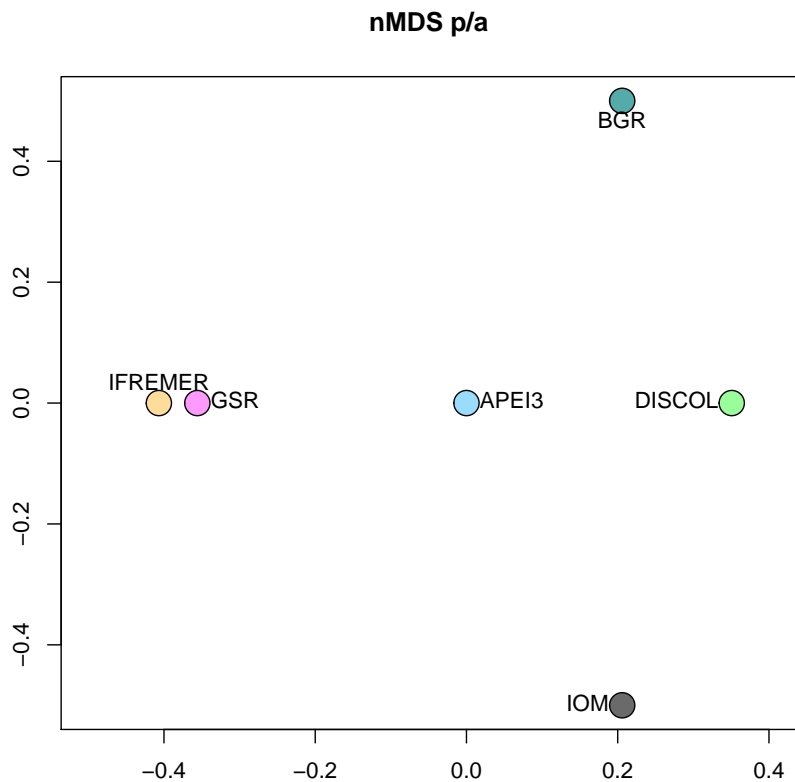


Fig. 10. nMDS ordination plot of Euclidean-distance between areas of presence-absence transformed data.

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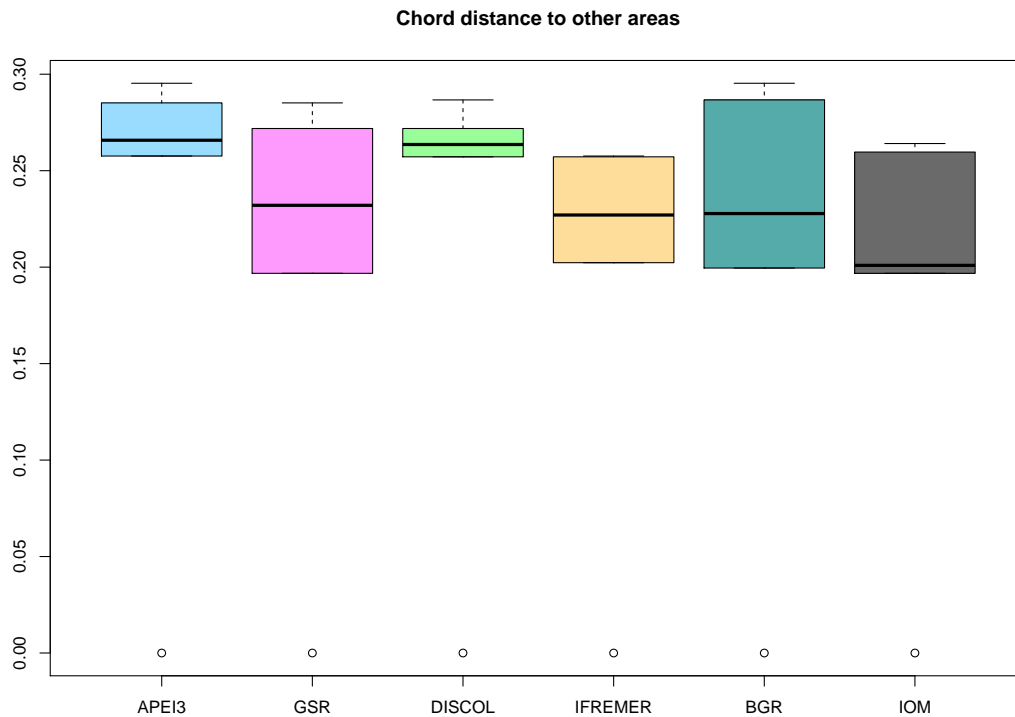


Fig. 11. Box and whiskers plot showing the median and range of the Chord distance of every area to other areas

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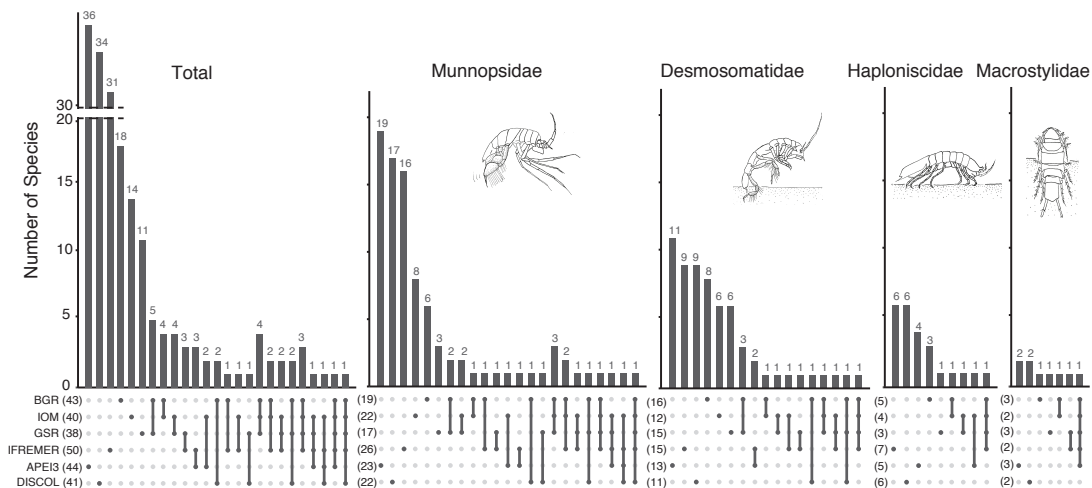


Fig. 12. Upset plot showing the number of species shared between sampling sites. The lower panel shows the sets of combination of sites. Sites sharing species are indicated by dots joined by a vertical line. T