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*Additional file 1 of the article:*

**Stochastic processes shape microeukaryotic community assembly in a subtropical river across wet and dry seasons**

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**Running title:** Neutral assembly of river microeukaryotes

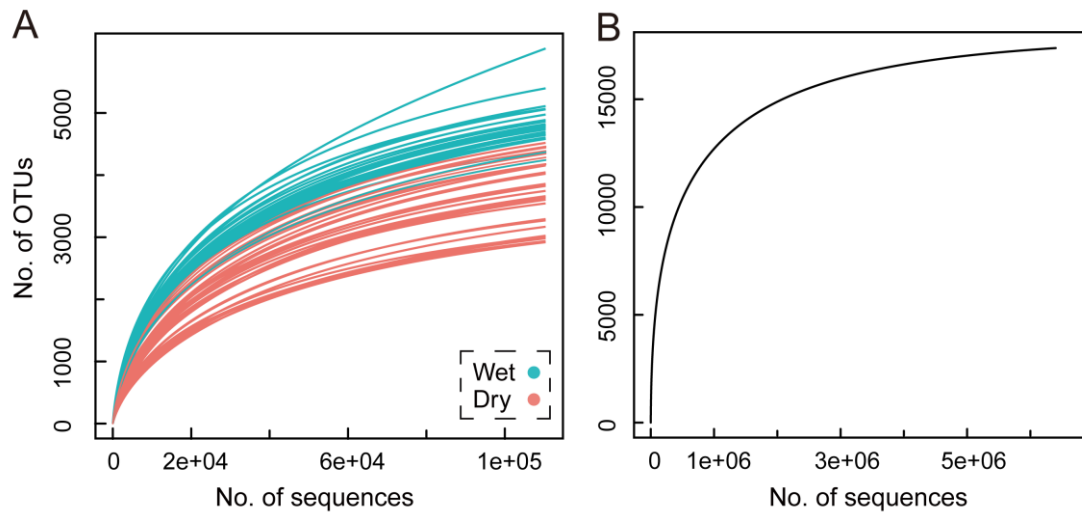
**Keywords:** Biogeography / Plankton / Microeukaryotic community / Subtropical river / Environmental factors / Neutral community model / Community assembly

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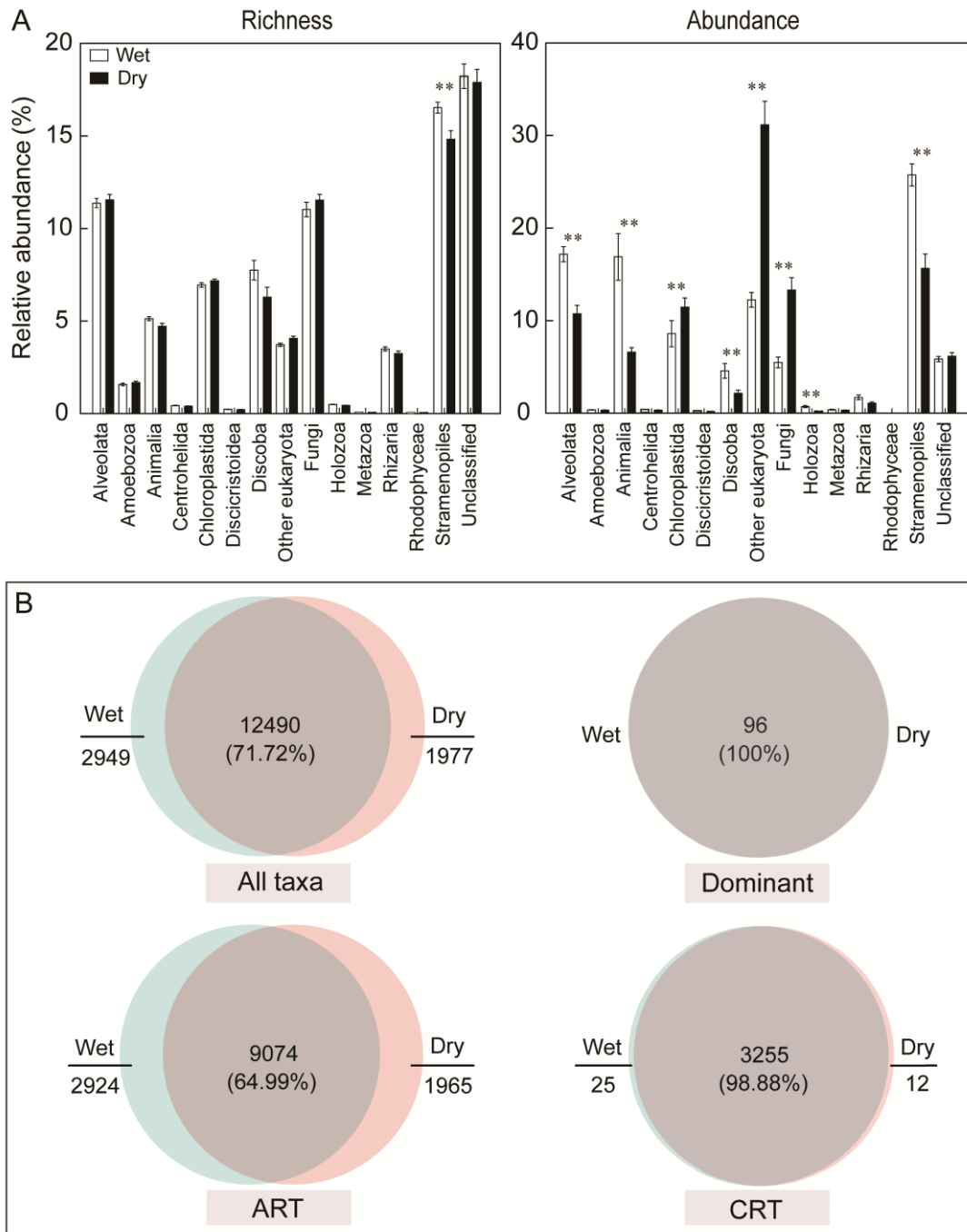
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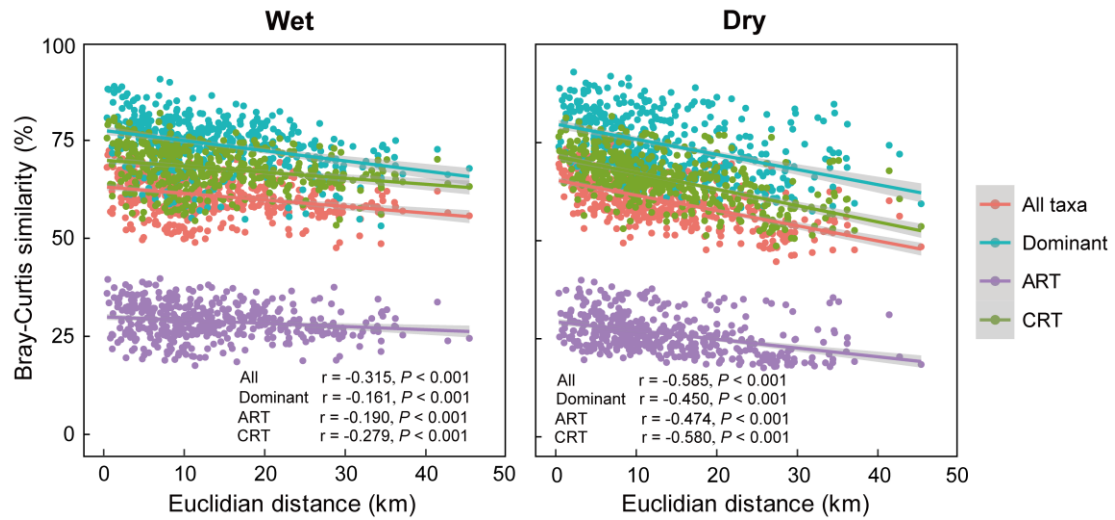
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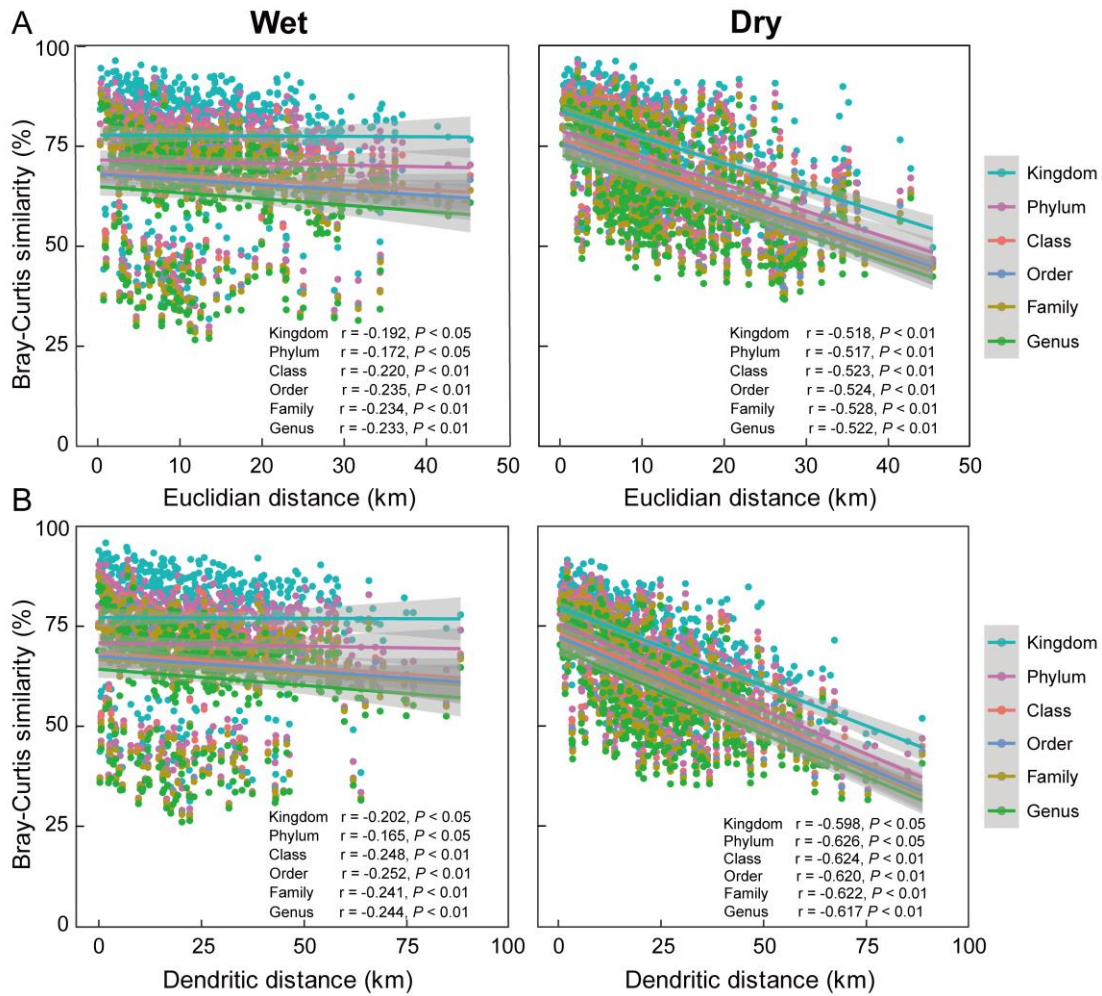
**Fig. S1** Rarefaction curves of similarity-based operational taxonomic units (OTUs) at 97% sequence similarity level. (A) The individual samples; (B) the combined set of 60 samples.



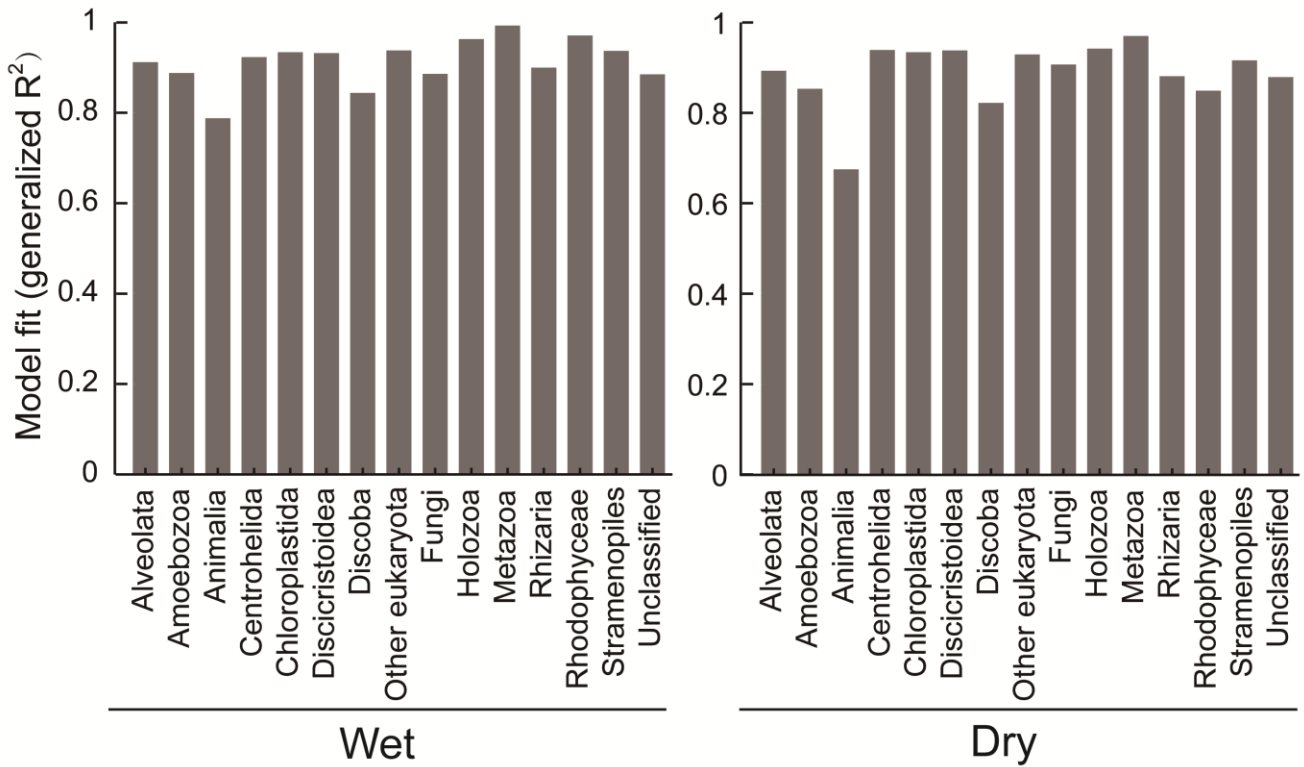
**Fig. S2** Comparison of microeukaryotic community between wet and dry seasons at supergroup and OTU levels. **(A)** Relative abundance of richness (OTU numbers) and abundance (sequence numbers) of wet season microeukaryotic taxa compared with dry season microeukaryotic taxa. The other eukaryota represents incertae sedis eukaryota. Unclassified eukaryotes (sequence similarity  $\geq 80\%$ ). Values are means  $\pm$  s.e. ( $n = 30$ ); \*\*,  $P < 0.01$  (Student's  $t$  test). **(B)** Venn diagrams showing the number and percentage of OTUs that are unique and shared between the microeukaryotic taxa between wet and dry seasons. Dominant represents taxa including AAT, CAT and CRAT. AAT: always abundant taxa; CAT: conditionally abundant taxa; CRAT: conditionally rare and abundant taxa; ART: always rare taxa; CRT: conditionally rare taxa.



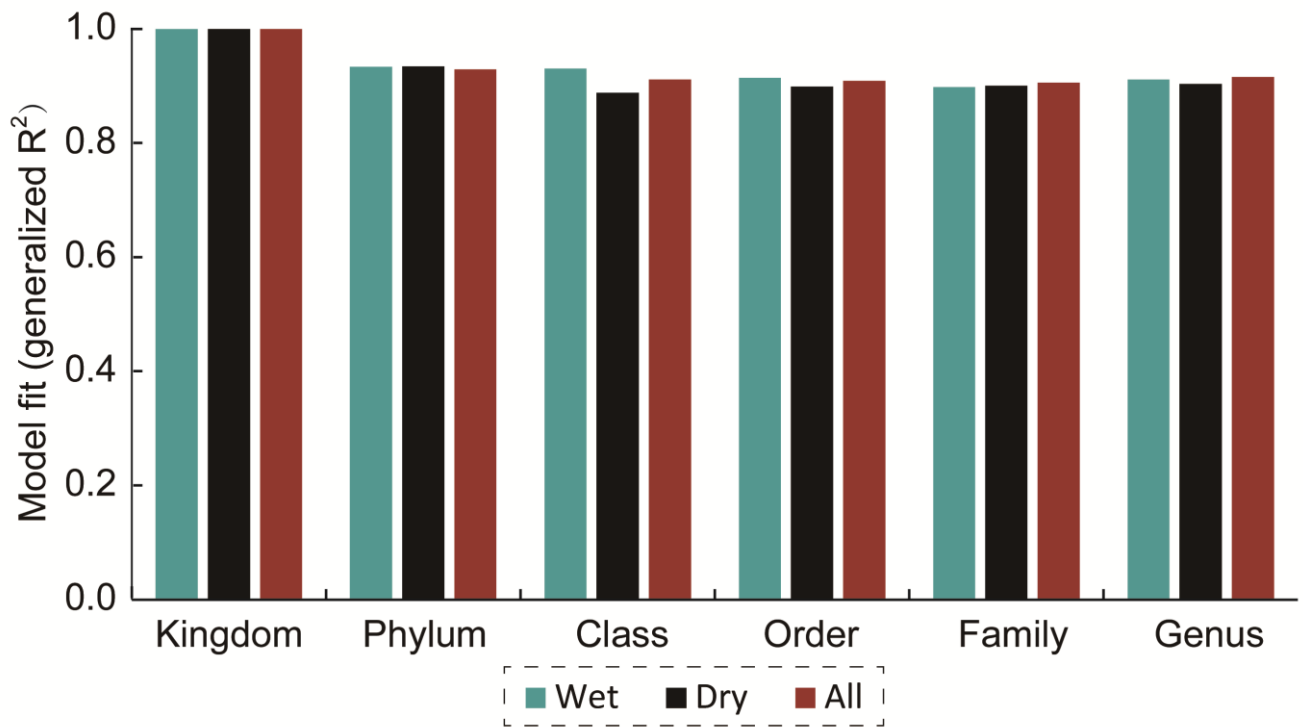
**Fig. S3** Distance-decay patterns based on Bray-Curtis similarity of microeukaryotic community composition and direct site-to-site (Euclidian) distance in wet and dry seasons, respectively (n = 435). Dominant represents taxa including AAT, CAT and CRAT. AAT: always abundant taxa; CAT: conditionally abundant taxa; CRAT: conditionally rare and abundant taxa; ART: always rare taxa; CRT: conditionally rare taxa.



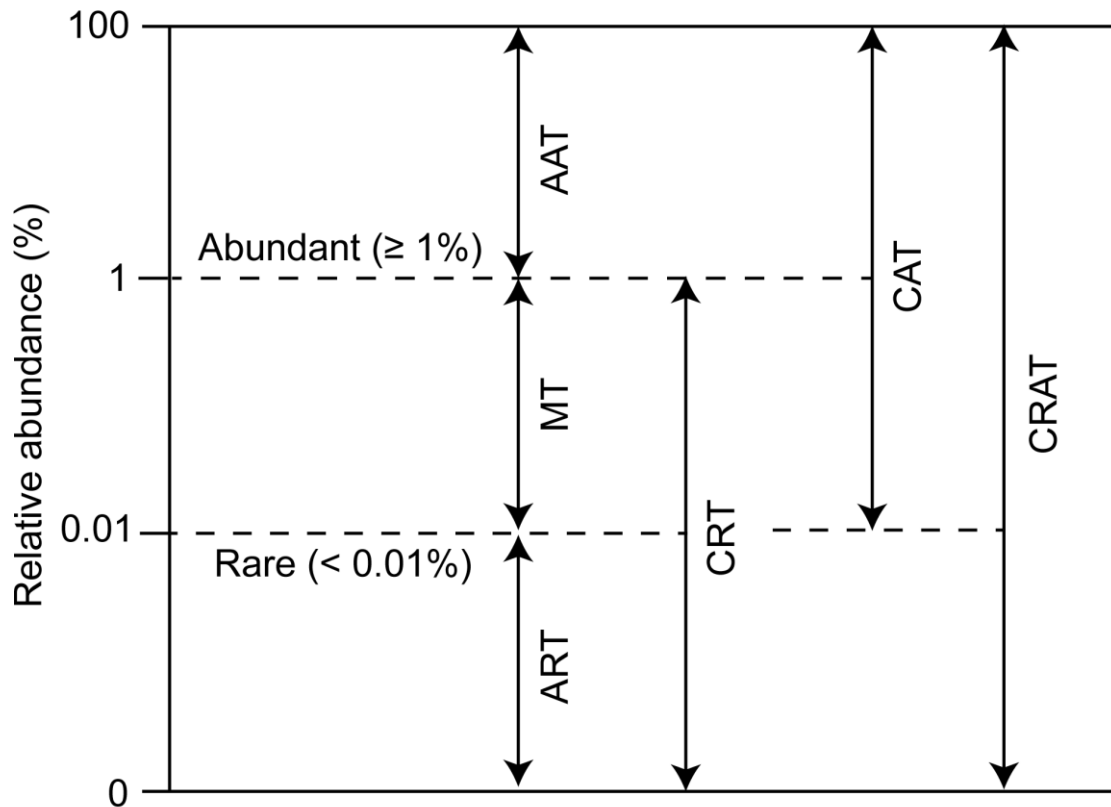
**Fig. S4** Distance-decay patterns based on Bray-Curtis similarity of microeukaryotic community composition and spatial distance at different taxonomic resolutions in wet and dry seasons, respectively ( $n = 435$ ). The spatial distance analyses are conducted based on two distinct methods: (A) direct site-to-site (Euclidian) distance; (B) cumulative dendritic distance. Taxonomy-based compositional variation is calculated based on the database annotation from genus to kingdom resolutions.



**Fig. S5** Fit of the neutral community model (NCM) for different microeukaryotic supergroups at OTU level (97% similarity) in wet and dry seasons, respectively. The other eukaryota represents incertae sedis eukaryota.

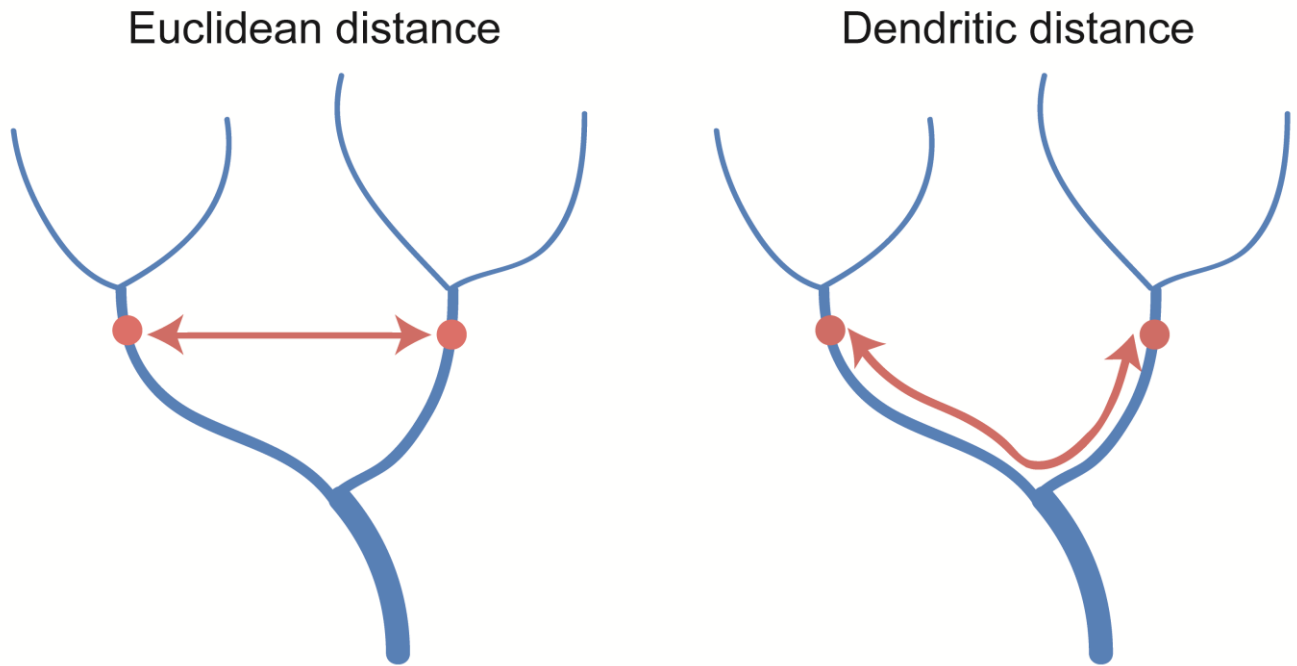


**Fig. S6** Neutral community model fit of microeukaryotes evaluated from genus to kingdom taxonomic resolutions in wet, dry and both seasons, respectively. All: both wet and dry seasons.



**Fig. S7** Definition of abundant and rare taxa of microeukaryotic metacommunity in this study. Always abundant taxa (AAT) were defined as the OTUs with a relative abundance always  $\geq 1\%$  in all samples. Conditionally abundant taxa (CAT) were defined as the OTUs with a relative abundance greater than  $0.01\%$  in all samples and  $\geq 1\%$  in some samples but never rare ( $< 0.01\%$ ). Conditionally rare and abundant taxa (CRAT) were defined as the OTUs with a relative abundance varying from rare ( $< 0.01\%$ ) to abundant ( $\geq 1\%$ ). Moderate taxa (MT) were defined as the OTUs with relative abundance between  $0.01\%$  and  $1\%$  in all samples. Conditionally rare taxa (CRT) were defined as the OTUs with a relative abundance  $< 0.01\%$  in some samples but never  $\geq 1\%$  in all samples. Always rare taxa (ART) were defined as the OTUs with a relative abundance always  $< 0.01\%$  in all samples.





**Fig. S8** The two different types of spatial distances employed in the river microeukaryotic metacommunity study. The Euclidian distance represents the straight line distance between two sampling sites; the dendritic distance is a measure of the watercourse (cumulative length of the river network) of two sampling sites.