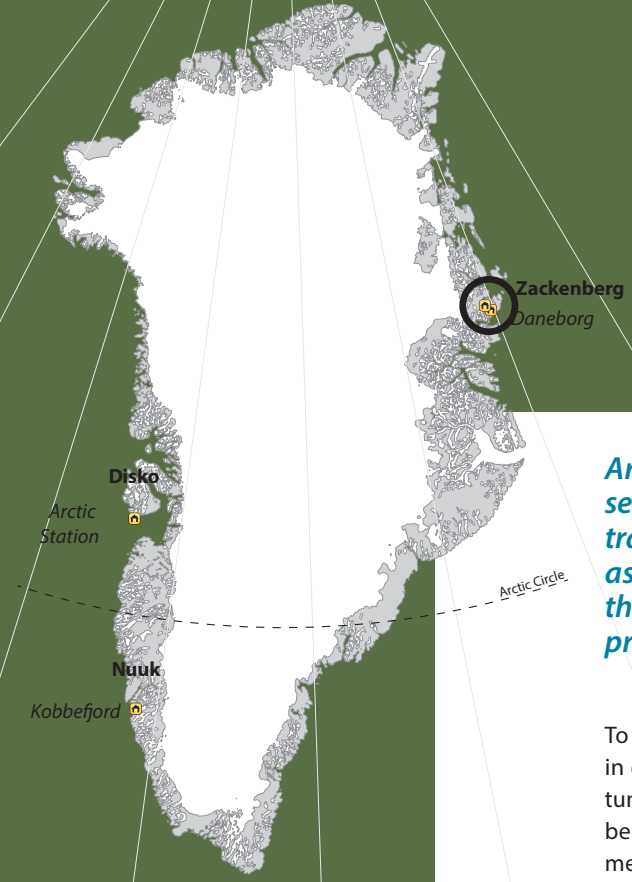
# RELIABLE ESTIMATES
# BIOMASS MATTER FOR




***Arthropods are a fundamental component of terrestrial ecosystems, serving as key prey for many predators and playing vital roles in energy transfer. Understanding their abundance and availability is crucial for assessing ecosystem processes, but how abundance is measured – as the number of individuals or as their biomass – affects ecological interpretations.***

To understand the role that arthropods play in ecosystems, such as the arctic terrestrial tundra, their variation in abundance needs to be monitored. Arthropod abundance can be measured in different units, for example the number of individuals or their biomass. The choice between either may depend on the context of the study or be based on practical reasons. For example, biomass is a more ecologically meaningful metric when considering energy fluxes, while individual counts may be more relevant in population studies. Many studies rely on arthropod counts because measuring individual biomass is labour-intensive. However, we show that using numbers instead of biomass can lead to significantly different conclusions, particularly in studies of trophic interactions and phenological mismatches.

To improve biomass estimation, we developed length-biomass regressions for 27 Arctic arthropod families from two High Arctic sites: Zackenberg (northeast Greenland) and Knipovich Bay (Siberian Russia). Our results show that biomass estimates vary substantially depending on which regression equations are used (Fig. 1). For example, applying previously published and often used order-level regressions to arthropods at Zackenberg led to biomass overestimations of 69.7% to 130% compared to site-specific regressions (Fig. 1). This underlines the importance of using locally derived relationships for accurate biomass estimates.

*Sticky trap with many flies. Photo: Jeroen Reneerkens.*

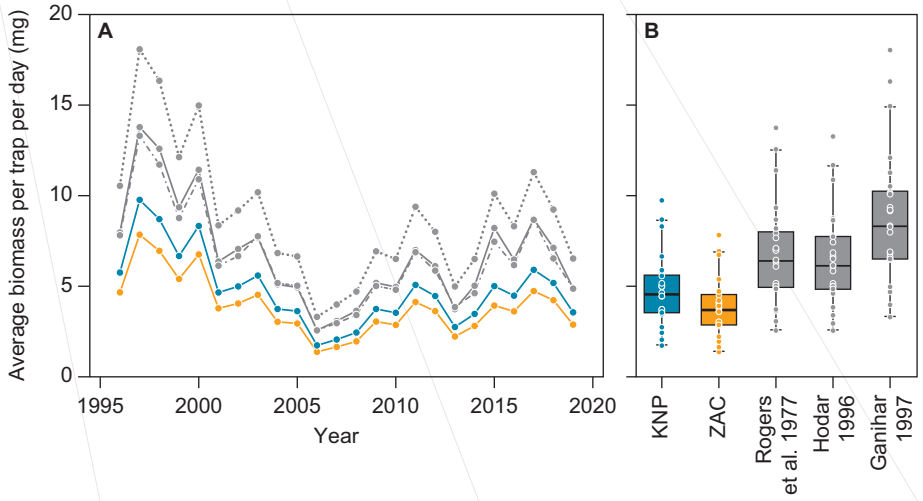



*Figure 1. Estimates of average biomass per pitfall trap per day at Zackenberg (1996 –2019), calculated based on regressions from five different sources. Data depicted in blue are calculated using family-level length-biomass regressions for Knipovich (KNP) and data in orange using family-level regressions for Zackenberg (ZAC). Data depicted in grey are calculated using order-level regressions extracted from literature, where the solid grey line is based on regressions from Rogers et al. (1977; Ann. Entomol. Soc. Am. 70: 51–53), the dashed grey lines on regressions from Hódar (1997; Misc. Zool. 20: 1–10) and the dotted grey line on regressions from Ganihar (1997; J. Biosci. 22: 219–224). Boxplots summarize the spread in the data, where horizontal white bars indicate the median, the box depicts the interquartile range and whiskers represent 1.5 times the interquartile range from the upper/lower quartile.*

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**Data source:**

BioBasis Zackenberg

Data can be accessed on GEM database, https://data.g-e-m.dk

# OF ARTHROPOD
## ECOLOGICAL STUDIES

GEM
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We also examined how the choice of metric – biomass or numbers – affects our understanding of the temporal overlap between arthropods and their predators. Using data from an Arctic-breeding shorebird, Sanderling (*Calidris alba*), we found that the median peak of arthropod biomass occurred, on average, 6.9 days later than the median peak in arthropod numbers, with some years showing discrepancies of up to 21 days (Fig. 2). This can be explained by a later emergence of larger arthropod specimens as compared to smaller specimens. Over a 23-year period, Sanderling hatch dates became less synchronized with the peak in arthropod numbers but remained more in synchrony with peak biomass.

Our findings emphasize that biomass-based estimates are essential for accurately assessing ecological interactions, particularly in studies of predator-prey interactions. We recommend that length-biomass regressions be developed for specific study regions to ensure reliable biomass estimates and that biomass, rather than numbers, are used when examining phenological mismatches between arthropods and their predators.

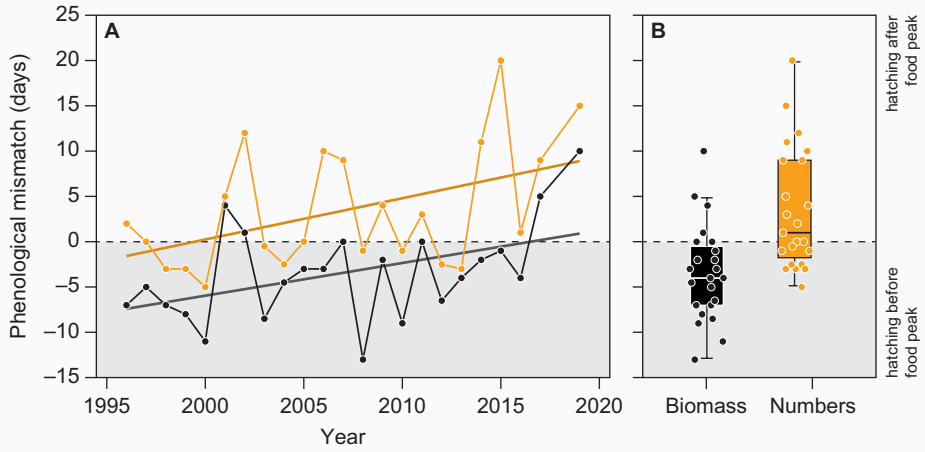


*Figure 2. Mismatch between Sanderling median hatch dates and the date when 50% of cumulative arthropod abundance (orange) or cumulative arthropod biomass (black) was sampled in pitfalls in Zackenberg (1996–2019, excluding 2018). Positive values indicate that the median hatch date occurred after the 50% date in arthropod abundance or biomass. Fitted linear models are shown as solid straight lines. Boxplots summarize the spread in the data, where horizontal white bars indicate the median, the box depicts the interquartile range and whiskers represent 1.5 times the interquartile range from the upper/lower quartile. For visual clarity we applied a horizontal jitter to the raw data depicted in the boxplots.*

## References


Versluijs, T.S.L., Zhemchuzhnikov, M.K., Kutcherov, D., Roslin, T., Martin Schmidt, N., van Gils, J.A. & Reneerkens, J. 2023. Site-specific length-biomass relationships of arctic arthropod families are critical for accurate ecological inferences. - PeerJ 11: e15943.

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Photo: Misha Zhemchuzhnikov.

Photo: Tom Versluijs.