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# USING PLANT FUNCTIONAL TRAITS IN PALEOECOLOGY: CALIBRATIONS FOR ARID CENTRAL ASIA.

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## INTRODUCTION

The necessity of accurate past climate reconstructions for climate modeling is a key issue in (paleo)ecology, especially drylands strongly affected by climate change. The Arid Central Asia deserts may spread in the next decades due to aridification. Several methods already exist to convert the pollen signal in quantitative climate (transfer functions) and biome (biomization) reconstructions. However, these methods are impeded by numerous biases, which could be overcome by the current breakthrough in the understanding of plant ecophysiology.

## OBJECTIVES

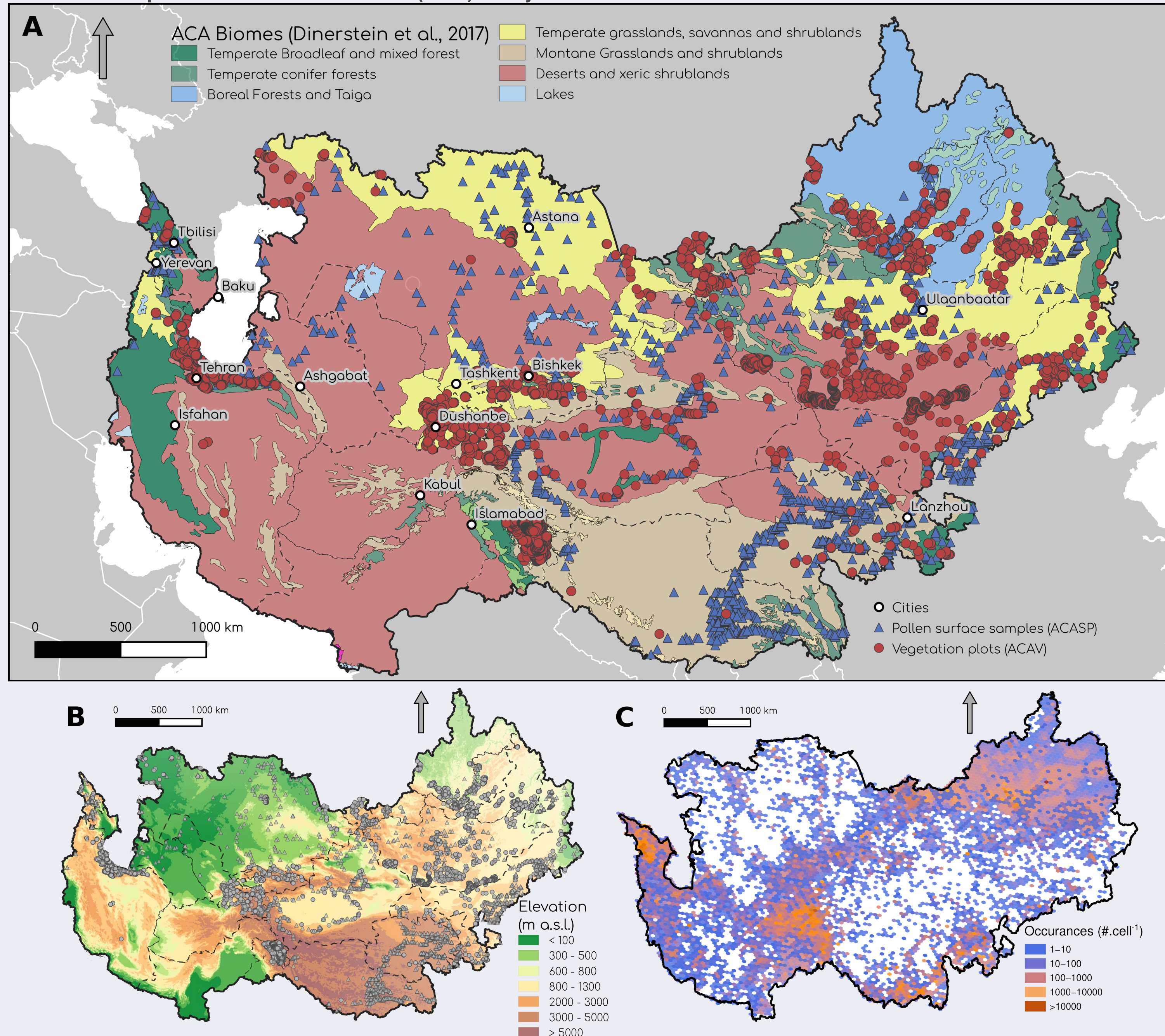
We tested the performance of combining approaches from paleoecology and plant functional ecology to validate the use of pollen samples to infer the phenotypic space of past vegetation, i.e. to test if the functional space of assemblages pollen and vegetation-based are comparable:

- ▶ What is the best scheme (coarse or fine) to assign trait values to pollen-types?
- ▶ Are the phenotypic spaces consistent between plant traits and pollen-based aggregated traits?
- ▶ Are the functional spaces pollen and vegetation-based comparable at the level of communities?

## STUDY AREA

- ▶ Arid Central Asian (ACA) deserts, steppes and their ecotones.
- ▶ Central asia (Uzbekistan, Turkmenistan, Tajikistan as well as a part of the Kirghistan, Kazakhstan and Afghanistan); Caucasus (Armenia, Georgia, Azerbaijan) and Iran; China and Russia.

FIGURE 1: Map of the Arid Central Asian (ACA) study area.



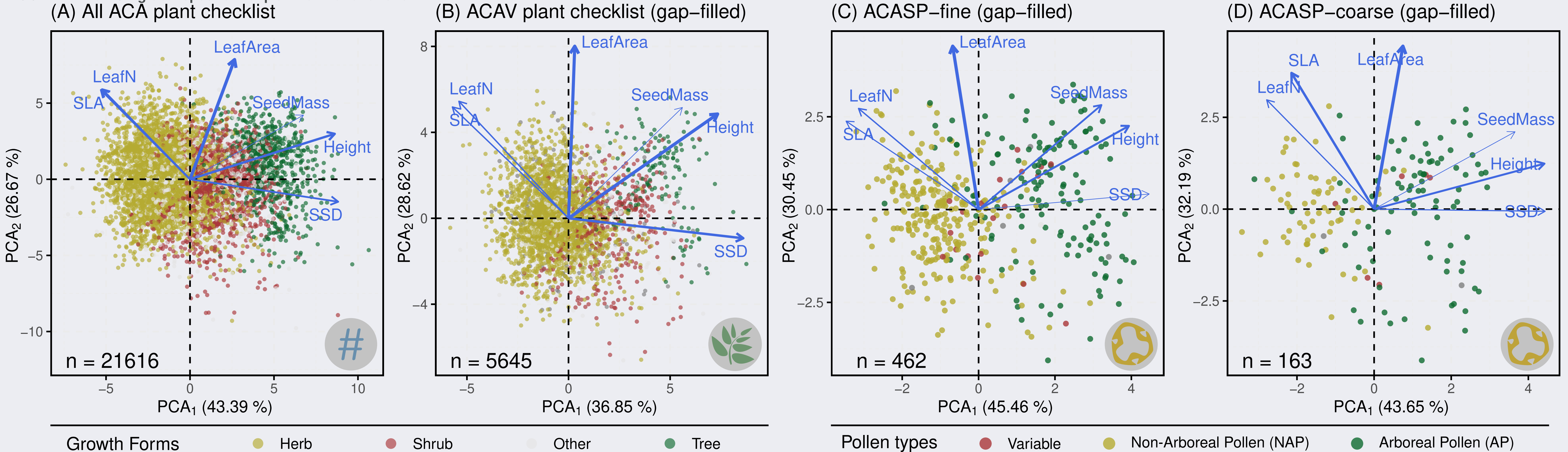
A: map of the Arid Central Asian (ACA) biomes (Dinerstein et al., 2017) with pollen surface samples (ACASP, blue triangles) and vegetation plots (ACAV, red dots); Elevation from ASTER data (B; <https://terra.nasa.gov/about/terra-instruments/aster>, last access: January 2018); C: number of plant species occurrences per hexagonal cell used to compile the ACA taxa checklist (logarithm bitmap).

## MATERIAL AND METHODS

The methodology applied in this study are graphically summarized in Fig. 2:

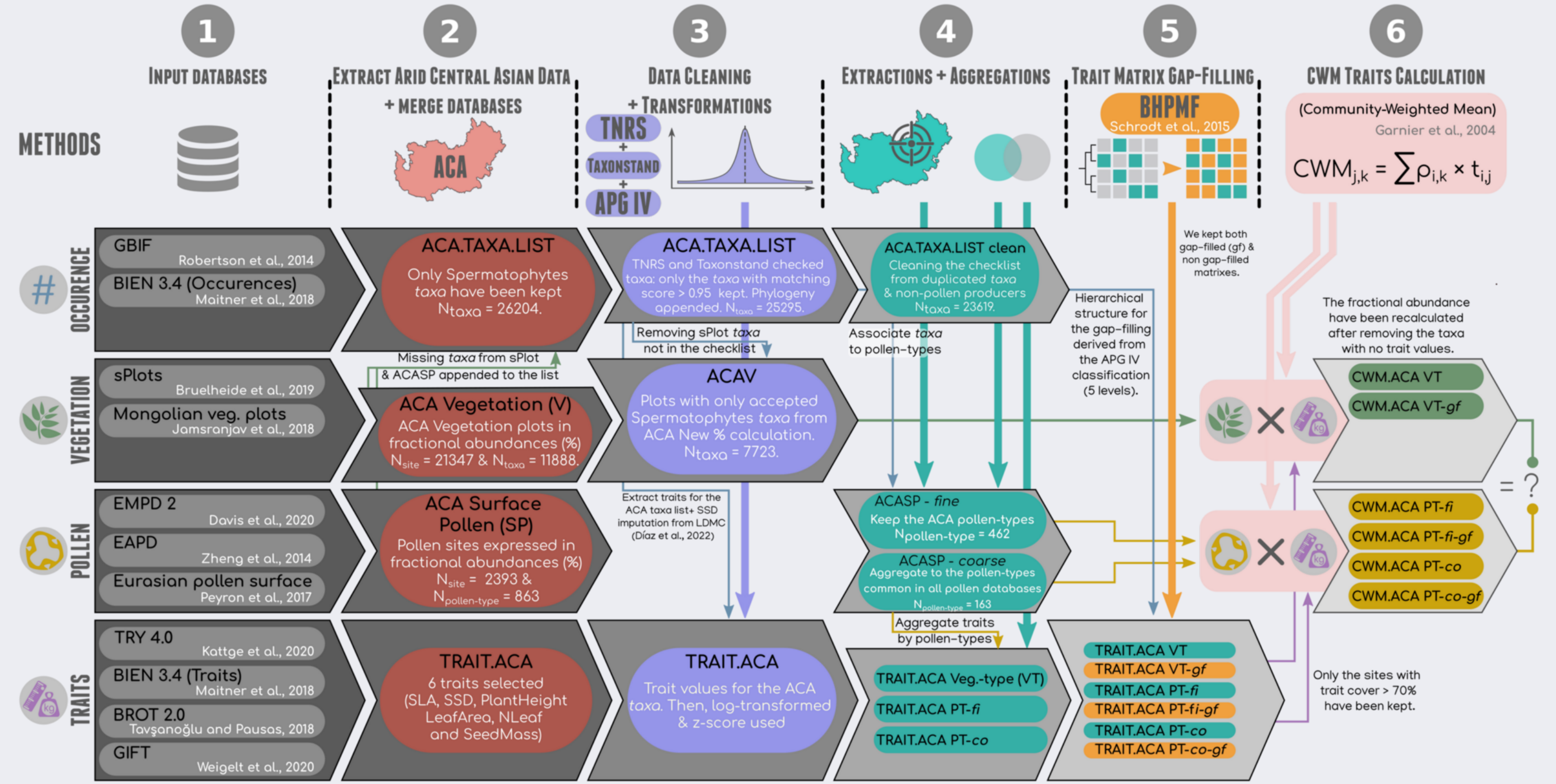
- ▶ (1) compilation of several surface pollen samples datasets, vegetation plots (sPlot) traits datasets (TRY and GIFT; Kattge et al., 2020; Weigelt et al., 2020) and biome maps;
- ▶ (2) plant functional trait selection: leaf area, plant height, Stem Specific Density (SSD), seed mass, nitrogen content per unit leaf mass ( $N_{\text{Leaf}}$ ) and Specific Leaf Area (SLA);
- ▶ (3) aggregation of trait values following *fine* or *coarse* pollen identification level;
- ▶ (4) calculation the CWM vegetation-based (ACAV) and surface pollen-based (ACASP);
- ▶ (5) comparison of the result for vegetation and pollen surface samples.

FIGURE 4: The ACA global spectrum of plant form and function.



PCA of the global spectrum of plant form based on six core traits and tested on (A) ACA's total plant checklist; (B) plants from the vegetation plot dataset (ACAV); (C) traits aggregated by pollen-types fine (ACASP-fi) and finally (D) traits aggregated by pollen-types coarse (ACASP-co). Dot colors (panels A and B) highlight growth form and the pollen types (panels C and D): Arboreal Pollen (AP), Non-Arboreal Pollen (NAP) and variable (production from herbs and trees). The thickness of the arrows indicates relative contribution to explaining the variance.

FIGURE 2: Pollen and vegetation-based trait aggregation workflow.

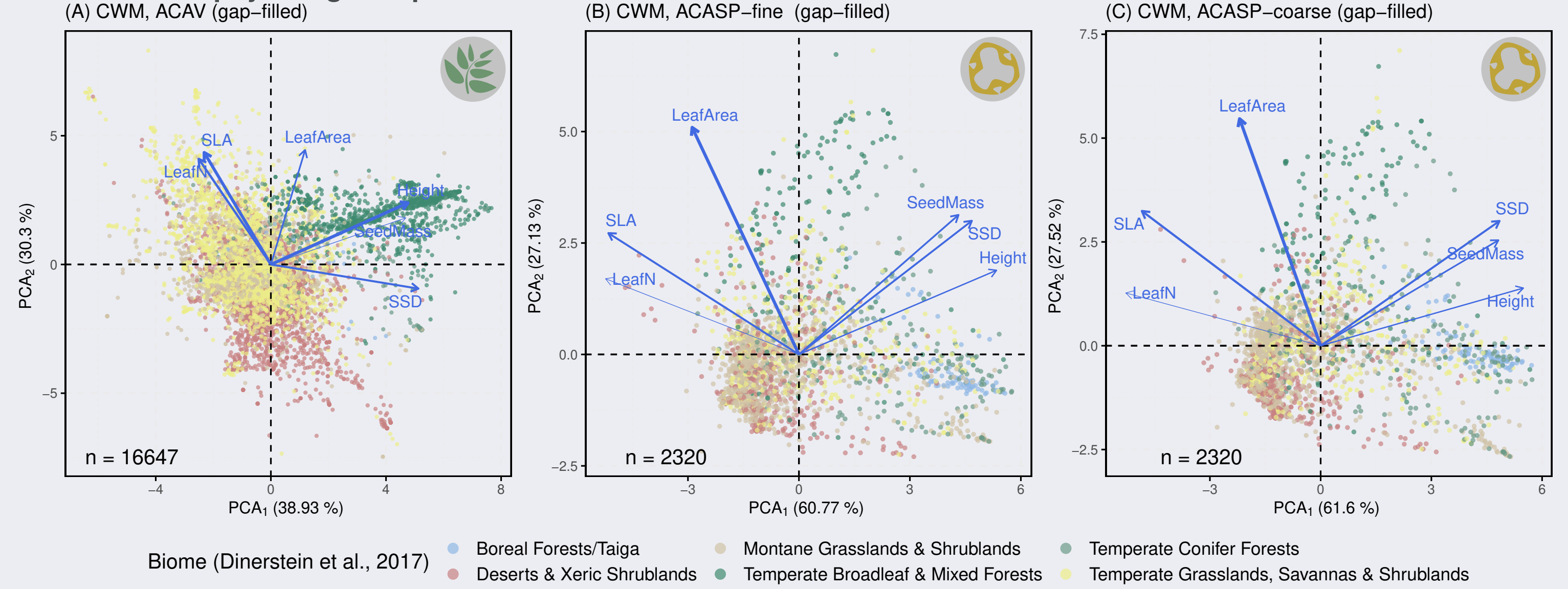


Workflow followed in this study: from the first methodological step (input methods and databases - leftward grey boxes) to the final correlation results. Each row of boxes represents a methodological step carried out in this study.

## RESULT & DISCUSSION

- ▶ The functional spaces produced in Fig. 4.A and B are very consistent with the global plant spectrum presented in Diaz et al. (2016). The same is observable for pollen.
- ▶ The aggregation scheme (ACASP-fi, highest level of pollen identification and ACASP-co common pollen-types) for pollen-based traits presents weak evidence of difference (Fig. 4).
- ▶ The worldwide organization of the functional space observed for communities (Bruehlheide et al. 2018) is conserved in ACA for both vegetation and pollen-based CWM-traits (Fig. 3).
- ▶ The selection of aggregation scheme has a minimal impact on CWM-trait values.

FIGURE 3: Ecophysiological spectrum for ACA based on the CWM-traits.



Principal Component Analysis of the variance of the 6 main traits applied on CWM-trait values calculated on ACA vegetation plots (A) and ACA surface pollen samples with ACASP-fi (B) and ACASP-co (C) aggregation scheme. The number of sites (vegetation plots or pollen surface samples) is indicated on the lower left corner of each panel. The thickness of the arrows varies with the relative contribution of each CWM-trait in the PCA1 and PCA2.

## CONCLUSION

Since past pollen studies are increasingly guided by climate and biome reconstructions, the use of plant functional trait appears as a relevant solution to combine specie abundances and ecophysiological characteristics (Birks 2020). We conclude that:

- ▶ Surface pollen samples respect trait values, leaf economic spectrum (Wright et al. 2004) and whole plant form and function spectrum (Díaz et al. 2016). Thus, trait values can be apply in paleo-pollen sequences when combined with pollen samples.
- ▶ The values of community traits (CWM-traits) applied on the pollen samples show the same correlation and co-variation between them as those already shown in vegetation based CWM-traits (Bruehlheide et al. 2018).
- ▶ Finally, the scheme of trait aggregation (pollen identification levels) appears to not impacts CWM-trait values in ACA. The schemes presented here, ACASP-fine and ACASP-coarse produce the equivalent results.

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