***Analytics***

All analyses were performed in R version 4.2.3 (R Core Team, 2023) and all figures and data wrangling used the *tidyverse* ecosystem of packages (Wickham et al. 2019). All analyses involving species counts were restricted to records with confirmed identification. That is, all records identified to morphospecies, or genus only were excluded when examining species counts. To determine richness saturation in our sampling, we derived species accumulation curves from permutation resampling of the subsites within years for 1) all sites with net and trap collected records, 2) all sites with trap records, 3) trap records from Port of Seattle, 4) trap records from Boeing Paine Field, and 5) trap records from Seattle City Light using the R package, *vegan* version 2.6-6.1 (Oksanen et al. 2024). Preliminary analyses showed a lack of saturation (curves did not reach asymptote), therefore, we elected to estimate minimum richness following Chao et al. (2009).

To compare bee community composition across collection techniques we visualized the proportional abundance and count of unique species within each genus across all years for 1) trap and net collected records from all sites, 2) trap records from all sites, and 3) net records from all sites. Similarly, we compared community composition across the three sites using trap records across all years. Further, to quantitatively describe the differences in species composition across sites, we modeled a matrix of species abundance and subsite/year combinations as a function of the three sites using a permutation MANOVA with *vegan*::*adonis2* (Oksanen et al. 2024). Site location across community composition space was visualized by plotting the first two axes of a three-dimensional NMDS ordination (stress = 0.10) with *vegan*::*metaMDS* (Faith et al. 1987). Finally, we used a random forest model (Breiman 2001) to define the species most representative of the compositional differences in sites following similar methods in Anderson et al. (2024). Briefly, we constructed a classification model with site as the response variable and the matrix of species abundance across subsites and years as the predictor variables. We then selected the top 10th percentile of species based on variable importance score using *randomForest*::*varImp* (Liaw & Wiener 2002).

To assess the seasonal biology of bee communities at the genus and species level, we used kernel density estimation and the *ggridges* package (Wilke 2024). First, we aggregated genus and species counts over weekly intervals summed across years and sites. For genus-level density estimation, we used biased cross validation to select the smoothing parameter individually for each genus (Scott 1992). Importantly, genus-level comparisons likely include multiple species with potentially non-overlapping phenologies, therefore, this nonparametric smoother avoids making assumptions about the underlying distribution and allows for multimodality. For species-level density estimation, we used Silverman’s smoothing method which assumes a Gaussian distribution.

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