Authors would like to recognize the thoughtful comments provided by the Reviewer which led to several important changes in our approach. We clarified the goals of this study, we focused on tower infrastructure currently measuring CH_4, and we better explained how we are measuring representativeness.

Reviewer 2

This study by Malone et. al. presents an representativeness analysis of current Eddy Covariance (EC) CH4 observation sites to understand gaps in data collection and develop guidance for new research infrastructure to reduce the uncertainties in US CH4 budget. It applies a multidimensional cluster analysis based approach to develop and assess CH4 observing network for US.

Study outlines well the limitations and uncertainties associates with current EC CH4 network in US and takes on an important research to better understand its representation. However, there are number of limitations in the data and methodoloy applied in the study, presented results does not support the conclusions and overall it does not provide much improvements over limitations in current literature that manuscript describes in introduction.

In response to Reviewer 2, we made important clarifications in the methods used and changed the way we discuss representativeness. We provide details below.

Comments on methods:

Method section is brief, lack necessary description and is at time diffcult to understand and follow.

- While cluster analysis method in itself is sound, its unclear if and how the choice of land cover and climate layers chosen to represent primary environmental conditions represent ecosystem scale CH4 fluxes. And if and how they represent the conditions for aquatic sites?

We used a combination of climate data and dominant land cover types to guide the scientific community on how we can develop a distributed observing network for the US and provide a template for the development of similar networks in other regions. We focus here on EC flux towers because they are essential for a bottom-up framework that bridges the gap between point-based chamber measurements and airborne platforms and are therefore a useful basis for identifying gaps in the current network of CH_4 observations. To understand the landscape representativeness across geographic clusters, we measured dissimilarity based on climate and land cover type, as these two factors together are characteristic of regional resource availability and disturbance regimes. It is important to note that a tower is representative of the ecosystem type and the region where it is stationed (Desai, 2010; Jung et al., 2011; Xiao et al., 2012; Chu et al., 2021); however, the landscape representativeness analysis done here uses a coarser classification of ecosystem types that are more emblematic of regional disturbance regimes, resource availability, and factors that influence how ecosystems function, not the specific

ecosystem type where the tower is situated. Chu et al., 2021 examined the land-cover composition and vegetation characteristics of 214 AmeriFlux tower site footprints. They found that most sites do not represent the dominant land-cover type of the ecosystems they exists within and when paired with common model-data integration approaches this mis-match introduces biases on the order of 4%–20% for EVI and 6%–20% for the dominant land cover percentage (Chu et al. 2021), making it essential to consider landscape characteristics in the design and evaluation of network infrastructure. Tower representativeness at the landscape scale is indicative of the capacity to upscale information by climate and the dominant ecosystems of locations within a landscape. We also calculate regional representativeness by the towers' vegetation type to understand the sampling intensity of each vegetation type within a cluster, which is also an essential component of scaling CH_4 fluxes (Knox et al., 2019). In this analysis we used the reported International Geosphere-Biosphere Programme (IGBP) vegetation type that is listed for each tower in the Ameriflux data base, where we also checked to ensure towers were currently active and providing data to the network.

- Authors highlight on Line 75-79 the limitations of existing land use products to identify CH4 source/sink, wetland classifications not suitable to scale and predict CH4 flux rates and processes. BUT they choose to use existing NLCD reclassified to 8 classes and reduced 1km resolution, thus effectively reducing the fidelity of the landcover data. Did do however improve the representation of irrigated vs non-irrigated crop ecotypes, and wetland classes. However, no quantitative analysis has been presented to demonstrate improvements their landcover scheme provide over the existing landcover.

Thank you for this comment. We moved the information on the limitation of current land cover products from the introduction to the discussion. We did this because having it in the introduction combined with the changes we made in the product gave the impression that the changes we made improved on the current product in a way that would reduce uncertainties. In fact that is not the case, the same uncertainties exist. The product we developed only allowed us to distinguish a few wetland and aquatic classes from each other.

- Line 198-200 states "The land cover and climate layers were chosen to represent the primary environmental conditions that are often indicative of a combination of resource availability and disturbance regimes." What resource availability refers to in this particular context? Also, which layer, if any, captures the disturbance regimes and what type of disturbances?

Land cover composition is a response to climate and disturbance regimes. Climatic factors influence resource availability (light, water, temperature) and although it varies geographically, disturbance is tightly linked to land cover types and cover classes have characteristic disturbances that influence the composition of classes within a landscape (Hermosilla et al. 2018). Studies have shown that either changes in climate or disturbance can lead to shifts in landscape composition (Sharp and Angelini 2019; Wang et al. 2020). For example, changes in the plant functional types across Arctic–Boreal ecosystems have been linked to wildfires and

climate-driven expansion of woody shrubs (Wang et al. 2020). The interaction of climate and disturbance both influence landscape structure and develop spatial patterns of many ecosystem processes on the landscape (Turner 2010).

- Section 2.3 Defining the state space of the US

  - Multidimensional scaling (MDS) was performed to condense ecotype, climate and location variables to two dimension. But unlike climate and location, ecotype is a categorical variable and how was a categorical value handled in the MDS scheme. Why were they condensed down to two dimension, aside from R/MASS implementation's default?

Climate, ecotype, and location (latitude/longitude) were used in a multivariate distance analysis to define the state space of the US (all 50 states & Puerto Rico) at the landscape scale and to divide the US into clusters. The purpose of this analysis is to identify the interrelatedness of all ecological components—biotic, abiotic, terrestrial, and aquatic within a dynamic landscape (Ippoliti et al., 2019). We included location (latitude/longitude) to incorporate the interaction between climate, ecotypes, and most importantly, seasonality. We first developed a dissimilarity matrix by calculating Gower dissimilarity (Gower, 1971; Huang, 1997; Podani, 1999; Ahmad and Dey, 2007; Harikumar and Pv, 2015) using the function distmix() from the package *kmed*. We used Gower dissimilarity because it can handle mixed data types. For each variable type in the data set, the dissimilarity metric that works well for that type is used and scaled to fall between 0 and 1. Then, a linear combination using user-specified weights (most simply an average) is calculated to create the final dissimilarity matrix. This approach measures the dissimilarity for each location within the U.S using ecotype, climate, and location information (ecotype, five climate variables, and location) and creating a dissimilarity matrix (20,000 x 20,000) that indicates dissimilarity for a location to every other location in the US.

Once we created a dissimilarity matrix, we used multidimensional scaling (MDS) to generate a two-dimensional ordination showing landscape dissimilarity with the *MASS* package in R (Venables WNRipley, 2002). The MDS makes it possible to evaluate dissimilarity in two dimensions, which is essential to our goal to evaluate representativeness. We used the Kruskal method of non-metric scaling with the IsoMDS function in the *MASS* package (Venables and Ripley, 2002). IsoMDS works best when applied to metric variables (Torgerson, 1958). Torgerson (1958) initially developed this method, which assumes that the data obey distance axioms. It uses eigendecomposition of the dissimilarity to identify major components and axes, and represents any point as a linear combination of dimensions. This is very similar to PCA or factor analysis, but it uses the dissimilarity matrix rather than a correlation matrix as input. Furthermore, the included dimensions are the most important dimensions produced, like PCA which is able to identify all of the dimensions that exist in the original data up to N−1, but will retain only the most important ones.

Knowing that regional patterns in climate and land cover will be important for scaling CH_4 to the regional and national scale, we divided the US into clusters to evaluate representativeness. This cluster analysis also allows us to summarize our results within a geographical context, an approach that has been used to delineate spatial sampling domains, to assess the spatial

representativeness of networks, and to suggest arrangements of study sites (Sulkava et al. 2011; Kumar et al. 2016). We used a cluster analysis to determine the optimal number of clusters using the library *cluster* and the function pam in R (Reynolds et al. 2006; Schubert and Rousseeuw 2019; Schubert and Rousseeuw 2021). This approach uses the k-medoids algorithm, which partitions data set into k groups or clusters and is a robust alternative to k-means clustering (Kaufman and Rousseeuw 2009). Each cluster is represented by one of the data points in the cluster named the cluster medoid. The medioid has the lowest average dissimilarity between it and all other objects in the cluster. The medoid can be considered a representative example of the members of that cluster. The k-medoid algorithm is less sensitive to noise and outliers, compared to k-means, because it uses medoids as cluster centers. The k-medoids algorithm requires the user to specify k, the number of clusters to be generated. A useful approach to determine the optimal number of clusters is the **silhouette** method. We fit an increasing number of clusters from 2 to 20 to construct a silhouette plot and choose the number of clusters that maximized the average silhouette width. Once we determined the number of clusters and the medoid of the cluster, we calculated the dissimilarity between every location within the cluster to the medoid to create a measure of how different each location was from the medoid condition of each cluster. We utilized the pointDistance function in the *raster* package, which provided a unit-less relative measure of dissimilarity that was determined by measuring the difference between the first and second dimensions produced by the isoMDS of each point in a cluster to the dimensions of the medioid. This analysis was repeated 10 times to ensure that the 20,000 pixel subsample would produce similar results in the dimensions and clustering. For simplicity, we show the results of the first analysis.

- ○ However, MDS was conducted only on a subset of 20,000 1km pixels subsampled across the US. What was the purpose and motivation for subsampling? And why 20,000? That sounds like a very small fraction of points across US at 1km resolution, essentially restricting the entire analysis to a very small small and perhaps biased sample of data (even if the 20,000 samples were evenly distributed across ecotypes). This is a severe limitation of the presented study.

To measure dissimilarity, we first randomly sampled (n = 20,000 1-km pixels) the US, maintaining the distribution of ecotypes and climate to define dissimilarity between observations. Although there were more than 8 million sampling points available for the U.S, there are limits to the number of samples that can be analyzed by the functions used for the MDS analysis. This analysis was repeated 10 times to ensure that the 20,000 pixel subsample would produce similar results in the dimensions and clustering. For simplicity, we show the results of the first analysis.

To extrapolate the cluster and dissimilarity layers across the entire US beyond the 20,000-pixel subsample, we fit a Random Forest model with the package *randomForest* (Liaw and Wiener, 2002) to model the first and second dimensions using the ecotype and climate layers as predictors. We then created a Random Forest model of the cluster layer using the first and second dimension as the explanatory variables. All models were then projected spatially to produce a spatially explicit cluster layer and a dissimilarity layer beyond the 20,000 sample points that were used in the MDS analysis. This allowed us to measure the importance of the original data on the first and second dimensions defined by the MDS and how the MDS leads to cluster and dissimilarity patterns. This step was essential to producing a spatially explicit cluster

and dissimilarity layers for the entire US, since the MDS analysis limits the number of observations that can be analyzed. We added more detail to the text and the results of the random forest model and the importance of the original data in explaining clustering and the first and second MDS dimensions.

      ○ Lines 218-220 states "We measured the correlation between the ecotypes, climate layers, and locations (latitude/longitude) using the envfit function in the library vegan in R (Oksanen, 2016)." What was the purpose of these correlations? And again how do you calculated correlation against categorical ecotype variable? How meaningful is it to calculated the correlation of climate or ecotype to location lat/lon? These choice of methods need some clarification beyond reference to R packages.

This was originally included to explain the main determinants of the MDS and clustering. We removed it from the analysis. The results are redundant with the inclusion of the random forest variable importance plots, which will be included in the supplement.

      ○ Lines 219-223 "This was followed by a cluster analysis to determine the optimal number of clusters using the library cluster in R, which partitions data around medoids (PAM algorithm), using the Gower dissimilarity matrix (Gower, 1971; Huang, 1997; Podani, 1999; Ahmad and Dey, 2007; Harikumar and Pv, 2015)." Its unclear if clustering was done on orignal set of ecotype, climate and location variables or two MDS dimensions? If original variables, I would repeat the need to clarify how the categorical variable was handled? I believe Gower dissimilarity matrix would consider the pairwise ecotype similarity so forest vs irrigated crops will have the same dissimilarity as irrigated vs non-irrigated crops. Is that a correction interpretation, and if so was that intended. Does that approach really help effectively use the ecotypes in this analysis, I believe not. More discussion of methods and their implication on results are needed.

We provide more details in the methods and summarize it here. Knowing that regional patterns in climate and land cover will be important for scaling CH_4 to the regional and national scale, after creating a dissimilarity matrix that was then scaled to two dimensions, we divided the US into clusters to evaluate representativeness using the first and second dimension from the MDS. This cluster analysis allowed us to summarize our results within a geographical context, an approach that has been used to delineate spatial sampling domains, to assess the spatial representativeness of networks, and to suggest arrangements of study sites (Sulkava et al. 2011; Kumar et al. 2016). We used a cluster analysis to determine the optimal number of clusters using the library *cluster* and the function pam in R (Reynolds et al. 2006; Schubert and Rousseeuw 2019; Schubert and Rousseeuw 2021). This approach uses the k-medoids algorithm, which partitions data set

into k groups or clusters and is a robust alternative to k-means clustering (Kaufman and Rousseeuw 2009). Each cluster is represented by one of the data points in the cluster named the cluster medoid. The medioid has the lowest average dissimilarity between it and all other objects in the cluster. The medoid can be considered a representative example of the members of that cluster. The k-medoid algorithm is less sensitive to noise and outliers, compared to k-means, because it uses medoids as cluster centers. The k-medoids algorithm requires the user to specify k, the number of clusters to be generated. A useful approach to determine the optimal number of clusters is the **silhouette** method. We fit an increasing number of clusters from 2 to 20 to construct a silhouette plot and choose the number of clusters that maximized the average silhouette width. Once we determined the number of clusters and the medoid of the cluster, we calculated the dissimilarity between every location within the cluster to the medoid to create a measure of how different each location was from the medoid condition of each cluster. We utilized the pointDistance function in the *raster* package, which provided a unit-less relative measure of dissimilarity that was determined by measuring the difference between the first and second dimensions produced by the isoMDS of each point in a cluster to the dimensions of the medioid.

- ○ Lines 222-224 states "We fit an increasing number of clusters from 2 to 20 to construct a silhouette plot and choose the number of clusters that maximizes the average silhouette width to determine an optimal number of clusters." However, the discussion section jumps to discuss k=10 clusters, but what about 2-9, 11-20? Why 10, why not some other number between 2-20?

We will added more detail to the results to show that the **silhouette** plots were used to determine the optimal number of clusters.

- ○ Lines 236-238 "To extrapolate the cluster and distance layers across the entire US beyond the 20,000-pixel subsample, we fit a Random Forest model with the package randomForest (Liaw and Wiener, 2002) to model the first and second MDS dimension using the ecotype and climate layers as predictors." I am struggling to understand what this statement means. A Random Model model is being fit to model first and second MDS dimension using ecotype and climate layers as predictors. BUT weren't MDS dimensions calculated using ecotype and climate layers in the first place. Is this Random Forest model a replacement for R MASS package. Why, this step makes no sense, unless I am missing something or this statement is somehow mis-written.

- ○ Lines 239-240 "We then created a Random Forest model of the cluster layer using the first and second dimension as the explanatory variables." Why

would you not just cluster the first and second MDs dimension, instead of creating a Random Forest model to identify the cluster layer. This seems like unnecessarily convoluted approach which really makes no sense and is addding methodological complexiy and model uncertainties.

To measure dissimilarity, we first randomly sampled (n = 20,000 1-km pixels) the US, maintaining the distribution of ecotypes and climate to define dissimilarity between observations. Although there were more than 8 million sampling points available for the U.S, there are limits to the number of samples that can be analyzed by the functions used for the MDS analysis. This analysis was repeated 10 times to ensure that the 20,000 pixel subsample would produce similar results in the dimensions and clustering. For simplicity, we show the results of the first analysis.

To extrapolate the cluster and dissimilarity layers across the entire US beyond the 20,000-pixel subsample, we fit a Random Forest model with the package *randomForest* (Liaw and Wiener, 2002) to model the first and second dimensions using the ecotype and climate layers as predictors. We then created a Random Forest model of the cluster layer using the first and second dimension as the explanatory variables. All models were then projected spatially to produce a spatially explicit cluster layer and a dissimilarity layer beyond the 20,000 sample points that were used in the MDS analysis. This allowed us to measure the importance of the original data on the first and second dimensions defined by the MDS and how the MDS leads to cluster and dissimilarity patterns. This step was essential to producing a spatially explicit cluster and dissimilarity layers for the entire US, since the MDS analysis limits the number of observations that can be analyzed. We added more detail to the text and the results of the random forest model and the importance of the original data in explaining clustering and the first and second MDS dimensions.

Comments on results and discussion:

Results and discussion section is more about stating the results and is really lacking in discussion of results, why they were calculated and what they mean for the science question central to the study?
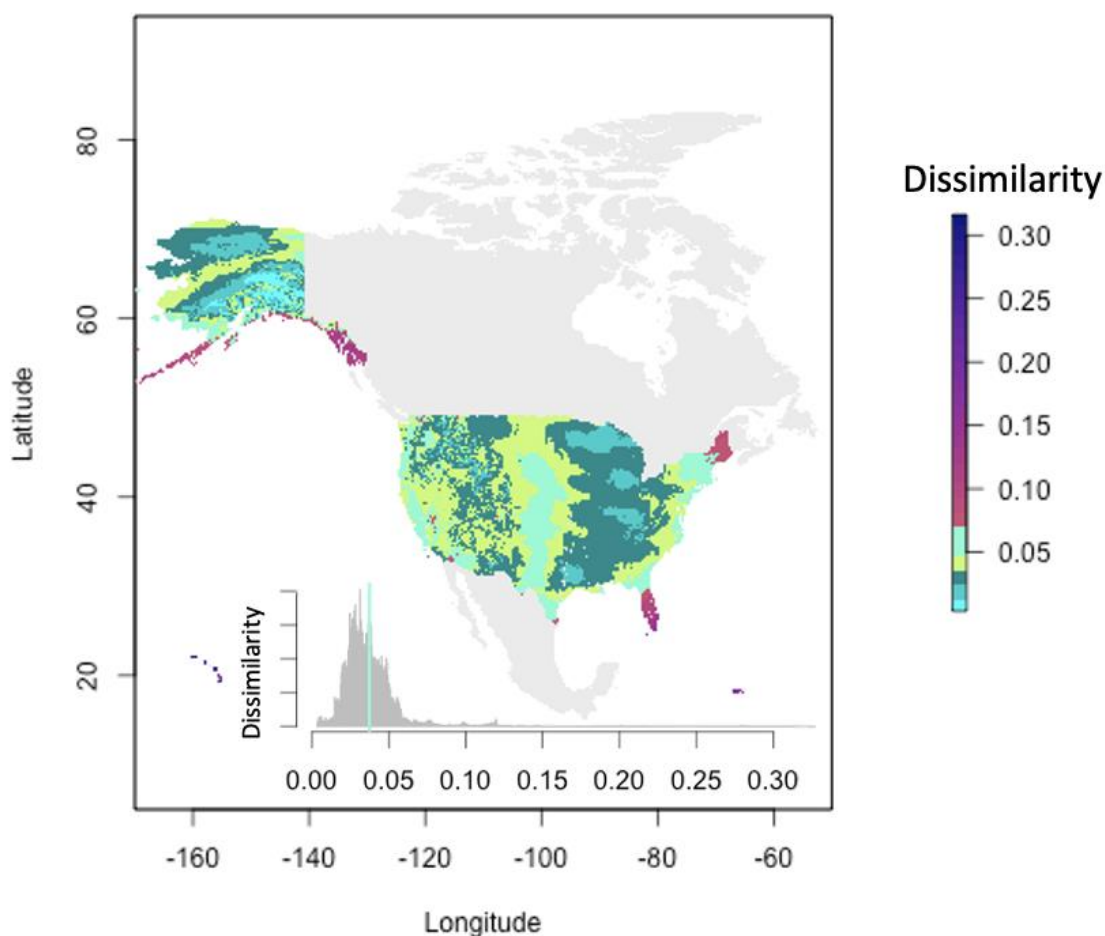
- Lines 260-263 "Latitude ($R^2 = 0.95$; $p < 0.001$), mean annual temperature ($R^2 = 0.84$; $p < 0.001$), maximum temperature ($R^2 = 0.83$; $p < 0.001$), vapor pressure deficit ($R^2 = 0.83$; $p < 0.001$), minimum temperature ($R^2 = 0.82$; $p < 0.001$), longitude ($R^2 = 0.63$; $p < 0.001$) had strong effects on clustering, whereas precipitation ($R^2 = 0.10$; $p < 0.001$), and ecotype ($R^2 = 0.03$; $p < 0.001$) showed low correlations." First, I am still not clear what these correlations are? Simply the fact that ecotype and precipitation has very low correlations for clustering is the huge red flag that these clusters are not appropriate for quantifying the representation of CH4 measurement sites. In the introduction section, authors have made strong arguments about importance of landcover, wetlands and agricultural use classifications. By their own measure, clusters that are insensitive to these landcover type are not appropriate for estimating CH4 fluxes. Purpose of study of

to identify cluster that represent CH4 and other GHG flues, and not to identify site that represent the clusters well. I believe the variable and clustering approach applied are not able to capture the heterogeneities on conditions that drive CO2 and CH4 fluxes, especially in wetlands, croplands and near aquatic sites.

These correlations were the average, not for clustering but for the first and second dimensions. We removed these results and replaced them with the variable importance from the random forest. It is important to note that the analysis done here will not capture the heterogeneity of the conditions that drive CH_4 fluxes at the ecosystem scale. It is designed to evaluate the sampling intensity of research sites at the landscape scale. In the design of a network, this course resolution influences the capacity to scale ecosystem level results to the landscape, region, and to the national level, which is required for the development of budgets and emission strategies.

- Lines 270-272 "We found the size of the cluster is not correlated to the number of towers when all towers are included in the analysis but was slightly negatively correlated with the number of EC towers that include CH 4 measurements (Figure 2)." I am not sure such correlations are meaningful at all. What is the purpose of correlations (postive or negative)? **This was removed from the analysis. It was originally included to show the poor relationship between cluster size and the frequency of towers. We agree with the review, this figure is unnecessary and is no longer relevant, since we are no longer including all towers.**
- Mediod locations of 10 clusters would be the theoretically optimal locations for locating an EC site. It would help to see a map of where these 10 locations and are perhaps a discussion of how well they appear to capture the local methane source/sinks on the ground. 10 is a small enough number to present a short and meaninful discussion to show the effectiveness of cluster medioid method.

Figure 2. Cluster dissimilarity for the US. Inset: the distributions of dissimilarity across all clusters shown in a histogram, in which the line denotes the mean dissimilarity across all clusters.

Figure 2 shows patterns in dissimilarity across the US with cyan locations having the lowest dissimilarity. We will add additional maps to the supplemental to highlight areas with the lowest dissimilarity. We also agree that it would be informative to show how towers in the medoid capture the local methane source/sinks on the ground. Unfortunately, towers are not currently distributed across cluster/medoid or IGBP to facilitate an evaluation of source sink potential. This highlights the limitations of existing measurement infrastructure which requires strategic augmentation to provide the most valuable information toward reducing uncertainties in future large-scale budget estimations. This analysis complements previous studies based on climatic or vegetation characteristics (Hargrove et al. 2003; Yang et al. 2008; Villarreal et al. 2018), and identifies regions within the US where gaps are limiting the development of upscaling techniques. To accurately understand the impact of climate and land cover change on biogenic CH_4 emissions, we need a long-term, calibrated, and strategic continental-scale CH_4 observatory network. Current gaps in existing measurement infrastructure limit our ability to capture the

spatial and temporal variations of biogenic CH_4 fluxes and therefore limit our ability to predict future CH_4 emissions. Maps of potential CH_4 emissions require land cover classification targeted at land cover types like wetlands that are important sources of CH_4 to the atmosphere. Aquatic ecosystems like streams and lakes as well as coastal ecosystems are significant and variable sources of CH_4 not well studied on a long-term basis. Through our analysis using climate, land cover, and location variables, we have identified priority areas to enhance research infrastructure to provide a more complete understanding of the CH_4 flux potential of ecosystem types in the US. For EC tower locations, dissimilarity coverage was lacking for clusters Na, W, and Nb, and currently clusters Na, W, Eb, and Nb are substantially under sampled. All aquatic sites are under sampled within each cluster. An enhanced network would allow for us to monitor both the response of CH_4 fluxes to climate and land use change as well as the impact of future policy interventions and mitigation strategies.

Few suggestions:

- Please consider including additional variables such as soil moisture, some measure of inundation, soil organic carbon to better capture the CH4 sources/sinks.

While measures of soil moisture, inundation, and soil organic carbon are important drivers of ecosystem CH_4 production and consumption, at the scale we are working on climatic conditions are more appropriate, as to not suggest we are able to represent those layers in a meaningful way at a 1 km resolution. The landscape representativeness analysis done here uses a coarser classification of ecosystem types that are more emblematic of regional disturbance regimes, resource availability, and factors that influence how ecosystems function, not the specific ecosystem type where the tower is situated. Chu et al., 2021 examined the land-cover composition and vegetation characteristics of 214 AmeriFlux tower site footprints. They found that most sites do not represent the dominant land-cover type of the ecosystems they exists within and when paired with common model-data integration approaches this mis-match introduces biases on the order of 4%–20% for EVI and 6%–20% for the dominant land cover percentage (Chu et al. 2021), making it essential to consider landscape characteristics in the design and evaluation of network infrastructure. Tower representativeness at the landscape scale is indicative of the capacity to upscale information by climate and the dominant ecosystems of locations within a landscape. We also calculate regional representativeness by the towers' vegetation type to understand the sampling intensity of each vegetation type within a cluster, which is also an essential component of scaling CH_4 fluxes (Knox et al., 2019).

Simplify the methodology and cluster the entire US and not a small 20,000 subsample to make the best use of information and variability captured in the data. Clustering + MDS + RF is unnecessarily complicated and perhaps hurt and not help the analysis.

To measure dissimilarity, we first randomly sampled (n = 20,000 1-km pixels) the US, maintaining the distribution of ecotypes and climate to define dissimilarity between observations. Although there were more than 8 million sampling points available for the U.S, there are limits to the number of samples that can be analyzed by the functions used for the MDS analysis. This

analysis was repeated 10 times to ensure that the 20,000 pixel subsample would produce similar results in the dimensions and clustering. For simplicity, we show the results of the first analysis.

To extrapolate the cluster and dissimilarity layers across the entire US beyond the 20,000-pixel subsample, we fit a Random Forest model with the package *randomForest* (Liaw and Wiener, 2002) to model the first and second dimensions using the ecotype and climate layers as predictors. We then created a Random Forest model of the cluster layer using the first and second dimension as the explanatory variables. All models were then projected spatially to produce a spatially explicit cluster layer and a dissimilarity layer beyond the 20,000 sample points that were used in the MDS analysis. This allowed us to measure the importance of the original data on the first and second dimensions defined by the MDS and how the MDS leads to cluster and dissimilarity patterns. This step was essential to producing a spatially explicit cluster and dissimilarity layers for the entire US, since the MDS analysis limits the number of observations that can be analyzed. We added more detail to the text and the results of the random forest model and the importance of the original data in explaining clustering and the first and second MDS dimensions.

- It would be of more value to consider the operational vs non-operational status of the EC sites in the analysis, so the results can inform actionable decisions.

Thank you for this comment. We made changes to the towers used in this analysis. Although we have information on the location of existing EC tower infrastructure that is a part of AmeriFlux (N=223), NEON (N=47), and known, independent PI-managed sites (n=141). We focus this analysis on the towers measuring CH_4 (n=100) and we distinguish between towers providing data to Ameriflux (yes =49, no = 51) and tower activity (active = 70; inactive = 30). We understand that additional towers exist within the U.S, but because these towers are not reporting or providing data to the flux community, we cannot include them in this analysis.

Table 4. The R $_{cluster}$ for CH_4 towers that are active and providing data to Ameriflux, the R $_{cluster}$ for all active CH_4 towers and the R $_{cluster}$ for all active towers in addition to NEON towers.

Cluster	CH_4 Towers (Data Providing)	CH_4 Towers (All)	NEON Towers
Na	3.0	34.9	35.5
NW	-	0.1	26.3
NEb	19.8	60.6	65.9
Ea	0.01	63.1	89.4
Eb	88.1	88.1	88.1
SW	2.0	3.3	17.3
W	0.01	0.01	38.8
NEa	79.3	79.3	79.3
Nb	21.3	21.3	21.3
SE	-	23.6	50.8

There were important gains in TR $_{cluster}$ when considering all CH_4 towers regardless of if they were providing data to Ameriflux (Table 4 and Figure 4). The clusters with substantial gains in representativeness (> 10%) include Na, NEb, Ea, and the SE. The TR $_{cluster}$ of the NW, Ea, SW, W, and the SE would be enhanced by more than 10% with the addition of CH_4 instrumentation at NEON sites.