Matters Arising: Response to Crossley et al. 2020

Title

Comment on Crossley et al. (2020): Meta-analyses of insect temporal trends must account for the complex sampling histories inherent to many long-term monitoring efforts

Response to:

Crossley *et al.* 2020. No net insect abundance and diversity declines across US Long Term Ecological Research sites. *Nature Ecology & Evolution* (2020) doi:10.1038/s41559-020-1269-4.

Authors

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Abstract

In an article recently published in Nature Ecology & Evolution (Crossley et al. 2020 “No net insect abundance and diversity declines across US Long Term Ecological Research sites”), sampling effort within Long-Term Ecological Research (LTER) datasets was assumed to be consistent across years. Given the complex history of many long-term datasets at LTER sites, this assumption often does not hold and we believe this assumption led errors in Crossley et al.’s analysis. Here we first use the Konza Prairie grasshopper dataset as an example of how changes in sampling locations and effort can cause errors when data are assumed to be collected with invariant sampling. Second, we describe similar and additional errors in Crossley et al.’s data use from 7 of the 13 LTER sites included Crossley et al. (2020)’s analysis.

Matters Arising

Crossley et al. (2020)[1] conducted a meta-analysis to examine patterns of change in insect abundance and diversity across US Long-Term Ecological Research (LTER) sites, concluding “a lack of overall increase or decline”. This is notable if true, given mixed conclusions in the literature regarding the nature and ubiquity of insect declines across regions and taxonomic groups[2–5]. The data analyzed, downloaded from and collected by US LTER sites, represent unique time series of arthropod abundances. While such long-term datasets often provide much needed insights, capturing both steady changes and responses to sudden unpredictable events, they are also rarely uniform in sampling effort across their full duration as a result of the changing goals and abilities of a research site to collect data. We suggest that Crossley et al.’s results rely upon a key, but flawed, assumption, that sampling was collected “in a consistent way over time within each dataset”. We highlight how this incorrect assumption contributed to errors in their key finding for the Konza Prairie (KNZ) grasshopper dataset (CGR02), and we describe other errors in Crossley et al.’s data use, listing only errors from datasets of which either we ourselves are the PIs or we have been able to confirm with the corresponding LTER PIs and information managers.

The KNZ CGR02 dataset documents grasshopper species abundances on 15 KNZ watersheds, and spans 1982-present (up to 2015 included in Crossley et al. 2020). Crossley et al. analyze time series of individual species from each dataset (increasing the number of “Time trends” in their Table 1). At the same time, regardless of variant sampling effort, they regularly sum all individuals within LTER datasets to yield a single value of abundance for a given species and year. This is the case for KNZ grasshoppers, and most other included LTER datasets (number of “Sites” in their Table 1). Importantly, sampling effort at KNZ and other LTER sites was not constant. At KNZ, the number of watersheds in which grasshoppers were collected, and the number of samples per watershed, both varied over time (Fig. 1). The number of watersheds sampled per year has varied from 6-14. Most notably, 6 bison-grazed watersheds were added to KNZ sampling in 2002. Changes in watersheds sampled over time are documented in the online metadata (https://portal.edirepository.org/nis/metadataviewer?packageid=knb-lter-knz.29.12).

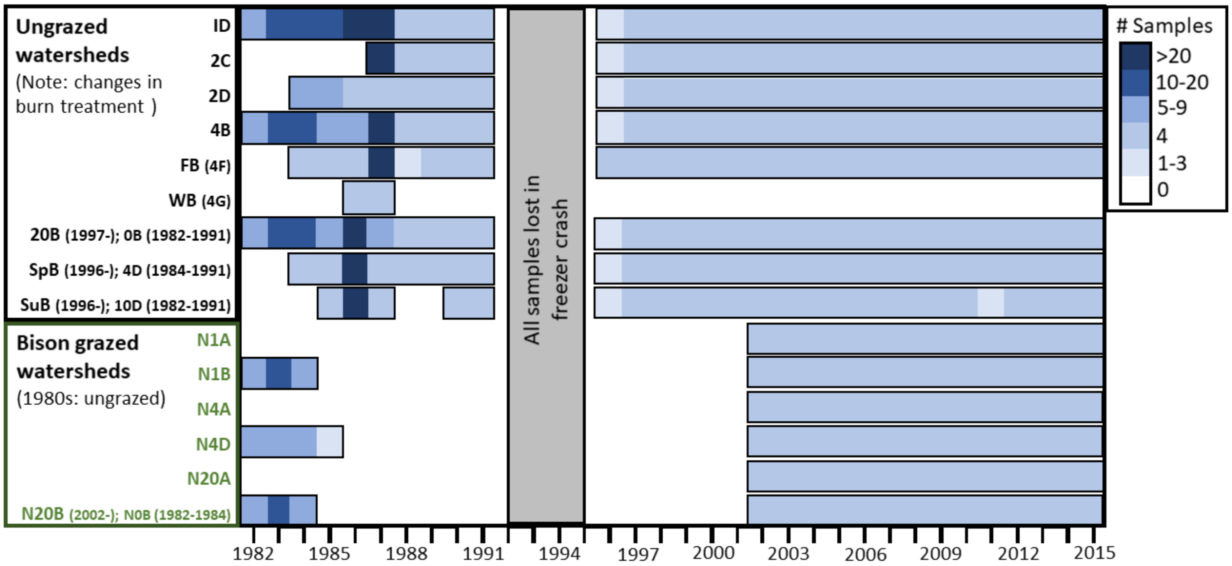

Figure 1. The complex history of sampling of the KNZ grasshopper dataset. The KNZ grasshopper dataset (CGR01) exhibits high variance both in number of watersheds sampled per year (number of bars per year) and number of samples collected within each watershed each year (depicted in color). Other complexities include the tragic loss of three years (1992-1995) of sampling due to a freezer crash, changes in sampling month, changes in watershed burn frequencies, and the reintroduction of bison to six of the later sampled watersheds in the 1990s.

Accounting for KNZ's complex sampling history matters. Bison-grazed watersheds support higher grasshopper abundances and species richness[6,7]. In a recent analysis using the CGR02 dataset, to account for this change in sampling effort, data were combined only from watersheds collected in the same years (e.g. by splitting samples from grazed watersheds into a separate time series) and abundances within each watershed and year were divided by the number of samples. Analysis of the data structured in this way showed a 2% annual decline in grasshopper abundance, with only one common species increasing[8]. Crossley et al., in contrast, report no such decline in grasshoppers, and instead report most grasshopper species increased in abundance from 1982-2015. The authors of Crossley et al. (2020) note the discrepancy with both this study[8] and another meta-analysis[3] and suggest it is "driven by falling numbers of just two once-dominant species… whereas many other formerly rare species have become more abundant and both evenness and species richness have increased". However, we believe the discrepancy arises because Crossley et al. did not account for variable sampling effort, including KNZ's incorporation of additional, more diverse grazed habitats midway in the time series, leading to the perception of increased grasshopper abundances over the full time series record.

We have thus far been able to confirm issues with data used from 7 of the 13 LTER sites included in Crossley et al. (2020). Very similar data misuse (i.e. where raw annual abundances were summed irrespective of changes in sampling effort and location) was observed for data from six additional LTER sites (Cedar Creek, Central Arizona-Phoenix, Harvard Forest, Hubbard Brook, North Temperate Lakes, and Sevilleta). Other notable inaccuracies include: the inappropriate use of experimental datasets with confounding treatment effects from Cedar Creek, Harvard Forest, and North Temperate Lakes; the inclusion of taxa from the KNZ grasshopper dataset for the full time series (1982-2015) which were only recorded in the dataset starting in

2013, not accounting for multi-year population cycles in time series known to have these dynamics such as Hubbard Brook Lepidoptera and KNZ grasshoppers[8,9], and non-inclusion a of dataset in the final analysis stated to be included (in Crossley et al. (2020)'s Table 1) from North Temperate Lakes due to the replacement of all abundance values with zeros. We provide details about these and other errors in the Supplementary Information.

Given these mistakes, we urge skepticism regarding Crossley et al. (2020)'s general conclusion of no net decline in insect abundances at US LTER sites in recent decades. Although their goal is laudable, we believe that no conclusion can be reached at this point regarding general trends in US insect populations, in part due to flaws in their analyses. Failure to take into account sampling effort in long-term datasets at best will increase measurement error and bias toward a null result (as was the case with Crossley et al's overall conclusion). At worst, when a site's sampling effort increases or decreases among years, it can generate even more erroneous conclusions regarding population change. Recently, a study reporting widespread collapse of rainforest insect populations at the LTER site Luquillo necessitated a similar correction[5]. We echo those authors, when they suggest that scientists can avoid such fixable errors by reading corresponding metadata and contacting in advance (or even including as authors) the data providers. Like the ecology they document, it is important to take into account that long-term monitoring efforts by LTERs and similar institutions are themselves complex and full of history.

Author Contributions

E.A.R.W., A.J., and M.K. jointly conceived the idea for the paper. E.A.R.W. wrote the first draft. A.M.E., D.L., S.R., N.R., and E.S. identified further errors in the Crossley et al. online data. All authors significantly contributed to revisions.

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Competing Interests

The authors declare no competing interests.

Data Availability

KNZ grasshopper abundance data are available from the Long-Term Ecological Research Data Portal (https://doi.org/10.6073/pasta/7b2259dcb0e499447e0e11dfb562dc2f). Links to additionally described LTER datasets are provided in the Supplementary Information.

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Supplementary Information for Matters Arising:
Meta-analyses of insect temporal trends must account for the complex sampling histories inherent to many long-term monitoring efforts

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Description of data use errors in Crossley et al. (2020)[1]

The most common error we have noted in Crossley et al. (2020)'s use of Long-Term Ecological Research Network (LTER) data was to use raw annual sums of individuals for entire LTER datasets, which, combined with variation in sampling effort and location, produced unreliable results. It is evident that Crossley et al. (2020)'s analysis did not account for sampling variation because **1)** they state that they considered all included datasets to have invariant sampling effort, **2)** complex datasets were considered one time series in their analyses, and **3)** for many datasets it is evident that no averaging occurred because the sum of all species abundances in their online data (https://datadryad.org/stash/dataset/doi:10.5061/dryad.cc2fqz645) totals the same number as the total individuals collected within entire LTER datasets.

The errors noted here are all examples of issues that can arise from the use of publicly available online datasets, without reading metadata or first communicating with the Principal Investigators (PIs) whose research created the datasets. The National Science Foundation funded LTER Network has specific data access and user policies (https://lternet.edu/data-access-policy/). While the LTER network strives to make research data publicly available, LTER also urges users of LTER datasets to contact the PIs of datasets with questions about methodology, and encourages data users to collaborate with the data authors. None of the authors of datasets described here are aware of being contacted by the authors of Crossley et al. (2020). We ask readers to read metadata and communicate (or even collaborate) with the PIs of publically available datasets that you intend to use for meta-analysis publications. Following these guidelines improves our ability to conduct good solid science.

We note that Crossley et al. did consider quantifying sampling effort as they include a column in their online data called "n.obs". However, the corresponding author of Crossley et al. (2020), Michael Crossley, informed us that n.obs was never used in their analyses. We further note that even if abundances had been divided by n.obs, this may not appropriately account for changes in sampling effort/location because: **1)** based on Crossley et al. (2020)'s code, n.obs does not always capture sample observations correctly (e.g. watershed is not included in the calculation of n.obs for the Konza grasshopper dataset and n.obs is incorrectly listed as "1" for all rows of Crossley et al.'s online data for both Central Arizona-Phoenix pitfall datasets, the Cedar Creek grasshopper dataset, the Hubbard Brook White Mountains Region caterpillar dataset, the Sevilleta grasshopper dataset, and the Sevilleta pitfall dataset), and **2)** as we have shown for the Konza grasshopper dataset, that if changes in sampling location correspond to the gain/loss of habitats that support different species and abundances, it is not appropriate to divide abundances by the number of sampling locations. In this case, combining sampling locations into one time series is only appropriate if the same sampling locations are sampled for the same duration of time.

Here we describe where the assumption of invariant sampling error occurred in Crossley et al. (2020)’s use of LTER datasets and provide the raw numbers of individuals from each dataset to more transparently allow others to check our work. We additionally provide information on other documented errors. We include information only where either we ourselves are the PIs of these datasets or we have been able to confirm errors with PIs and information managers from corresponding LTERs. LTER sites are listed in alphabetical order and include Cedar Creek, Central Arizona-Phoenix, Harvard Forest, Hubbard Brook, Konza Prairie, North Temperate Lakes, and Sevilleta.

Cedar Creek

1) **Grasshopper dataset (ghe014)**
   https://www.cedarcreek.umn.edu/research/data/dataset?ghe014,
   - **A)** No correction was made for variation in sampling effort and changes in sampling locations which are documented in the metadata (https://www.cedarcreek.umn.edu/research/data/methods?e014). The sum of all individuals in the Crossley et al. (2020) online data time series (52,116 individuals) is the same as the total individuals collected from the entire ghe014 dataset. The "n.obs" (number of observations) in Crossley et al. (2020)'s online data is set to "1" for all rows.
   - **B)** This dataset is not correctly linked in Supplementary Table 1 and incorrectly described.

2) **Arthropod "Sweep1" dataset (arce153)**
   https://www.cedarcreek.umn.edu/research/data/dataset?arce153
   - **A)** This dataset is not appropriate to answer questions about general insect trends, since it is an experiment including nitrogen addition treatments and herbivore exclosures.
   - **B)** This dataset is not correctly linked in Crossley et al. (2020)'s Supplementary Table 1.

3) **Arthropod "Sweep2" dataset (aage120)**
   https://www.cedarcreek.umn.edu/research/data/dataset?aage120
   - **A)** Either no or an inappropriate correction was made for variation in sampling effort and changes in sampling locations which are documented in the metadata (https://www.cedarcreek.umn.edu/research/data/methods?e120). No correction was made if "n.obs", Crossley et al. (2020)'s calculation of the number of observations, was not used in analyses as asserted by corresponding author Michael Crossley; an inappropriate correction was applied if n.obs was included in the analyses. The sum of all individuals in the Crossley et al. (2020) online data time series (151,227 individuals) is the same as the total individuals collected from the entire dataset (after subtracting the 44,027 unidentified "undet undet" individuals). The calculation of n.obs in Crossley et al. (2020)'s R code does not include plot number, only month and year of observation.
   - **B)** This dataset is not appropriate to answer questions about general insect trends, since it is an experiment with treatments having different levels of plant diversity.
   - **C)** This dataset is not correctly linked and incorrectly described in Crossley et al. (2020)'s Supplementary Table 1.

Central Arizona-Phoenix

1) **Arthropod sweep dataset (knb-lter-cap.652.2)**
   https://doi.org/10.6073/pasta/0669ee6a71b24abb1ae3827f4ee77f6d
   No correction was made for variation in sampling locations which are documented in the metadata (https://data.sustainability.asu.edu/cap-portal/metadataviewer?packageid=knb-lter-cap.652.2). The sum of all individuals in the Crossley et al. (2020) online data time series (34,316) is a similar number to the total individuals (34,323) in the entire dataset. There is 1 individual listed as unidentified but we cannot account for the discrepancy of the 6 remaining individuals. The calculation of n.obs in Crossley et al. (2020)'s R code does not include subsite, only sample date.

2) **Ground arthropod pitfall central Arizona-Phoenix dataset (knb-lter-cap.41.16)**
   https://data.sustainability.asu.edu/cap-portal/mapbrowse?packageid=knb-lter-cap.41.16
   It is likely that no correction was made for variation in sampling effort and changes in sampling locations which are documented in the metadata (https://data.sustainability.asu.edu/cap-portal/metadataviewer?packageid=knb-lter-cap.41.16). While we cannot account for the discrepancy between the number of individuals in the full pitfall dataset (2,563,183 individuals) and the number in the Crossley et al. (2020) online data time series (2,529,604 individuals, 98% of those in the full dataset), considering the high variability in subsite number and location per year in this dataset we remain concerned that sampling effort and location were not accounted for. The "n.obs" (number of observations) in Crossley et al. (2020)'s online data is set to "1" for all rows.

3) **Ground arthropod pitfall McDowell dataset (knb-lter-cap.643.2)**
   https://sustainability.asu.edu/caplter/data/view/knb-lter-cap.643.2/
   No correction was made for variation in sampling effort and changes in sampling locations which are documented in the metadata (https://data.sustainability.asu.edu/cap-portal/metadataviewer?packageid=knb-lter-cap.643.2). The sum of all individuals in the Crossley et al. (2020) online data time series (22,360 individuals) is the same as the total individuals collected from the entire dataset from (after subtracting the 1 unidentified "Unknown" individual). The "n.obs" (number of observations) in Crossley et al. (2020)'s online data is set to "1" for all rows.

Harvard Forest

1) **Harvard Forest Hemlock Removal Experiment Ant dataset (knb-lter-hfr.118.30) https://doi.org/10.6073/pasta/7a6b956fb0960d7fe8bb048b1fe26956**

   A) Sampling effort differed among years for the Harvard Forest Hemlock Removal Experiment (HF-HeRE) dataset analyzed by Crossley et al. (2020). These ants were collected within a long-term experiment in which there were four plot types: two controls (intact hemlock and intact mixed hardwood) and two canopy manipulations (hemlocks girdled and logged).

   B) In the Crossley et al. (2020) analysis this dataset is coded with Locales: "ants.pitfall", "ants.bait", "ants.hand", and "ants.litter" that represent pitfall trapping, bait sampling with cookies and tuna fish, hand collections, and sieved litter samples of ants from 2003-2015. Sampling effort differed among years for these different sampling methods coded as "Locales" in the Crossley et al. (2020) analysis. All four sampling methods (i.e., "Locales" equal to "ants.pitfall", "ants.bait", "ants.litter", and "ants.hand" were sampled in June, July, and August from 2003-2005, in July and August in 2006, and in July only from 2007-2008. From 2009-2015, only pitfall traps were set within the HF-HeRE. The number of pitfall traps set from 2003-2012 was 25 traps total (situated in a 10 m × 10 m array). In 2012, a deer and moose exclosure was set up within the experimental plots of the HF-HeRE and an additional 10 m × 10 m array of 25 pitfall traps was set up within the exclosure (i.e., pitfall trap sampling effort doubled from 2012-2015 relative to the number of pitfall traps from 2003-2011. We note that Crossley et al. (2020) do account for the different sampling methods and that the baits, litter, and hand samples were only collected from 2003-2008, but other differences in sampling effort were not accounted for. The "n.obs" (number of observations) in Crossley et al. (2020)'s online data is set to one for all rows in the dataset, so it does not account for differences in numbers of samples per year.

   C) For the Harvard Forest ant data, Crossley et al. (2020) treat the number of ants collected by pitfall, bait, and litter samples as raw abundances, which may overestimate abundance of ants if they happen to occur nearby colonies with actively foraging workers[2].

2) **Nantucket ant dataset (knb-lter-hfr.147.21) https://doi.org/10.6073/pasta/3493424abf9fc36eac7b62b732e4ea55 (hf147-09-nantucket-sites-2004-09.csv)**

   This dataset contains ants sampled with pitfall traps in two bogs and surrounding forests in 2000 combined with ants sampled from upland habitats from 2004–2009 by a variety of methods and at different intensities and sites. It also includes "velvet ants", a group of ant-mimicking wasps, which were identified only to family (Mutillidae). These data were collected to assess relationships of ant diversity with habitat and management regime[3] and cannot be used to analyze temporal trends within a site. Either no or an inappropriate correction was made for this variation in sampling effort and changes in sampling locations, all of which are documented in the metadata (https://portal.lternet.edu/nis/metadataviewer?packageid=knb-lter-hfr.147.21). No correction was made if "n.obs", Crossley et al. (2020)'s calculation of the number of observations, was not used in analyses as asserted by corresponding author Michael

Crossley; an inappropriate correction was applied if n.obs was included in the analyses. The sum of all individuals in the Crossley et al. (2020) online data time series (32,146 individuals) is the same as the total individuals collected from the entire dataset (after subtracting the 9 individuals with year listed as “NA” and 2 individuals with species code listed as “NA”). The calculation of n.obs in Crossley et al. (2020)’s R code does not include subsite (“site”) or collection method, only community type (habitat description), month, and year of observation.

3) **Tick dataset (knb-lter-hfr.299.3)**
https://doi.10.6073/pasta/ b29a97941c11ddf45540ea30066fde35

A) These data are collected with student time sheets for payroll to raise awareness of tick bites for students in the Harvard Forest Summer Research Program in Ecology. The tick survey is voluntary, has variable response rates each year depending on the group of students, and generally shows a decline in collection intensity during the summer as students increasingly fail to report weekly data. The summer of 2019 also had a much lower response rate because the program switched to using digital, rather than paper, time sheets. The calculation of n.obs (for this dataset coded as “n.y1”) in Crossley et al. (2020)’s R code is the sum of hours reported by the tick survey, which is the number of hours worked during the day when the student found a tick on their body. This number does not represent the response rate of the survey, which would need to be accounted for to address differences in samples per year.

B) For the tick data, Crossley et al. (2020) analyze 30 separate time series based on the locations of collection, but it is not clear how those locations were delineated. Many of the “location.names” from this dataset have overlap as they are filled in with text by students in the survey form. For instance, the “location.names” of “Harvard Forest” in the survey overlaps with many possible locations listed by students (e.g., “greenhouse”, “Prospect Hill”, “Shaler Hall”). Thus, it is not appropriate to analyze these data as separate time series as they refer, in some instances, to the same general location.

4) **Carnivorous plant prey dataset (knb-lter-hfr.111.16)**
https://doi.org/10.6073/pasta/cb95637eda0f96c3fdbd1a97e632c7b7

These data were from a global review of arthropod prey spectra of carnivorous plants[4]. None of the data were collected at Harvard Forest (and most were collected on other continents), and for each carnivorous plant species, “year” indicates the year the data were published and no time-series (repeat collection) was observed or implied by the data or discussed in the review. Although these data were not included in the final analysis of Crossley et al. (2020), rows for these data are listed in Crossley et al. (2020)’s online data (https://datadryad.org/stash/dataset/doi:10.5061/dryad.cc2fqz645; External_Database_S1_PerSpecies_Abundance_LTER_annotated.csv) and all abundance values are listed as zero. The rows corresponding to this dataset (lines 28497 – 36898: 8401 records) were inaccurately included in Crossley et al. (2020)’s count of 82,777 observations (the number of rows in their online data: External_Database_S1_PerSpecies_Abundance_LTER_annotated.csv).

5) We also note more generally that for the Harvard Forest datasets that the environmental data are all for the Harvard Forest site in Petersham in central Massachusetts, but the Nantucket dataset should report different environmental data as it was collected from an island off eastern Massachusetts that has very different climate from central Massachusetts. Furthermore, the locations in the tick dataset, which are each given a different time series should also have location specific environmental data as locations of data collections were variable (e.g., most in western MA at Harvard Forest, but some in Connecticut; Cambridge, MA; etc.).

Hubbard Brook

1) **Lepidoptera datasets (knb-lter-hbr.82.8) https://doi.org/10.6073/pasta/5d2a8c67c5a3278032b2b14d66c09a7f**
   - **A)** Sampling effort differed among plots and years for one of the two Hubbard Brook datasets analyzed by Crossley et al. (2020). These data, coded as Locale: “Lepidoptera1”, represent visual counts of caterpillars on one plot, 1986-2018. Consistent sampling effort occurred throughout this time series; however, sampling effort differed among both plots and years for the dataset coded as Locale “Lepidoptera2”. This second dataset spans 1986-1995 and represents three different plots in the White Mountains Region that are located outside of the Hubbard Brook valley. The sum of all individuals in the Crossley et al. (2020) online data time series (4,030 individuals) is the same as the total individuals collected from the entire White Mountains Region caterpillar dataset. The “n.obs” (number of observations) in Crossley et al. (2020)’s online data is set to “1” for all rows for the White Mountains Region dataset.
   - **B)** Crossley et al. do not acknowledge that these data include Lepidoptera identified only to the family level as noted in the online metadata (https://portal.edirepository.org/nis/mapbrowse?scope=knb-lter-hbr&identifier=82).
   - **C)** The caterpillar populations documented in these data exhibit outbreaks at long intervals (e.g., 10-13 years apart[5]), limiting the ability of linear trend analysis to detect meaningful trends with time series of shorter lengths (10-33 years for Hubbard Brook data used in Crossley et al.(2020)).
   - **D)** Only one of the two Hubbard Brook datasets analyzed is described in Crossley et al. (2020)’s Supplementary Table 1.

Konza Prairie

1) **Grasshopper dataset (CGR02)**
   https://doi.org/10.6073/pasta/7b2259dcb0e499447e0e11dfb562dc2f
   A) Either no or an inappropriate correction was made for variation in sampling effort and changes in sampling locations which are documented in the metadata (https://portal.edirepository.org/nis/metadataviewer?packageid=knb-lter-knz.29.12). No correction was made if "n.obs", Crossley et al. (2020)'s calculation of the number of observations, was not used in analyses as was asserted by corresponding author Michael Crossley; an inappropriate correction was applied if n.obs was included in the analyses. The sum of all individuals in the Crossley et al. (2020) online data time series (121,229 individuals) is the same as the total individuals collected from the entire CGR02 dataset from 1982-2015 (after subtracting the 459 unidentified "unknown" individual grasshoppers). The calculation of n.obs in Crossley et al. (2020)'s R code does not include watershed, only month, day, and the replicate code within the watershed ("a" or "b").
   B) Three taxa (Tettigoniidae, Oecanthinae, and Gryllidae) included in Crossley et. al. (2020)'s analysis for the full duration (1982-2015) were only recorded in the KNZ dataset starting in 2013.
   C) The grasshopper populations documented in these data exhibit cycles at ~5 year intervals, limiting the ability of linear trend analysis to detect meaningful trends with time series of shorter lengths[6].

2) **Gall insects (CGP01)**
   http://dx.doi.org/10.6073/pasta/b2ac9e918a66dbbb18c7a6b39dc1efab
   Either no or an inappropriate correction was made for variation in sampling locations and plant species sampled which are documented in the metadata (https://portal.edirepository.org/nis/metadataviewer?packageid=knb-lter-knz.27.11). No correction was made if "n.obs", Crossley et al. (2020)'s calculation of the number of observations, was not used in analyses as was asserted by corresponding author Michael Crossley; an inappropriate correction was applied if n.obs was included in the analyses. The sum of all individuals in the Crossley et al. (2020) online data time series (27,819 galled stems is the same as the total galled stems in the entire CGP01 dataset. The calculation of n.obs (for this dataset coded as "n.y1") in Crossley et al. (2020)'s R code does not include watershed or account for the different plant species sampled and only accounts for the number of sampled stems.

North Temperate Lakes

1) **Benthic macroinvertebrate dataset (knb-lter-ntl.11.34)**
   https://doi.org/10.6073/pasta/1bad728523ce4c39ade38fa666a59aee
   - **A)** Likely due to program R being case sensitive, the time series for Sparkling Lake which was coded both “SP” and “sp” was accidentally split into two time series with “sp” having non-zero values only in 2016-2017. However, Crossley et al. (2020) considered Locale “sp” a separate time series spanning 1981-2017.
   - **B)** No correction was made for variation in sampling effort and changes in sampling locations if “n.obs”, Crossley et al. (2020)’s calculation of the number of observations, was not used in analyses as was asserted by corresponding author Michael Crossley. While we have not been able to identify why there is a discrepancy between the number of individuals in the Crossley et al. (2020) online data time series (126,041 individuals) and those in the full dataset (140,100 individuals), if n.obs was not included in trend calculation, sampling effort changes were not accounted for as the full time series (1981-2017) was included in Crossley et al. (2020)’s analysis, even though some lakes did not have sampling in all years.

2) **Pelagic macroinvertebrate dataset (knb-lter-ntl.14.30)**
   https://doi.org/10.6073/pasta/cc25694cdde49853271df465a15007fb
   While listed in Crossley et al. (2020)’s Table 1 and Supplemental Table 1, these data do not appear to be included in Crossley et al.’s online data, nor are they referenced in Crossley et al. (2020)’s online R code.

3) **Crayfish dataset (knb-lter-ntl.3.28)**
   https://doi.org/10.6073/pasta/61619e749daf99c71a289dcadafb795c
   While included in Crossley et al.’s online time series data (“External_Database_S1_PerSpecies_Abundance_LTER_annotated”), all abundance values are listed as zero. No entries from this dataset are listed in Crossley et al.’s online trend data (“External_Database_S2_time_trends_arthropods_relaxed”), thus these data were not included in Crossley et al. (2020)’s final analysis.

4) **Crayfish dataset (knb-lter-ntl.217.9)**
   https://doi.org/10.6073/pasta/4a22c4b3707f68ba5c03cc3ed70e98b6
   - **A)** This dataset has an incorrect link listed in Crossley et al. (2020)’s Supplementary Table 1. We were able to reconstruct which dataset was used by matching total sums between North Temperate Lakes crayfish datasets and finding identical yearly sums between the Crossley et al. (2020) online data and knb-lter-ntl.217.9 for 2001-2010 (both totaling 95,066 individuals for this duration).
   - **B)** Crossley et al. (2020) online data for this dataset contains data from 2011, when none exists in the dataset.
   - **C)** This dataset is not appropriate to answer questions about general arthropod trends, since it contains data on an experiment of crayfish removal.
   - **D)** This dataset documents an invasive crayfish species, and therefore may not be appropriate for understanding general arthropod population trends.

Sevilleta

1) **Grasshopper dataset (sev-106)**
   https://doi.org/10.6073/pasta/c1d40e9d0ec610bb74d02741e9d22576
   No correction was made for changes in sampling locations (termination of the pinyon-juniper [Goat Draw] vegetation type sampling site, and the initiation of a new [Blue Grama] sampling site at SEV in 2002) which are documented in the metadata (https://portal.edirepository.org/nis/metadataviewer?packageid=knb-lter-sev.106.152976). The sum of all individuals in the Crossley et al. (2020) online data time series (36,634 individuals) is the same number as total individuals in the entire sev-106 dataset. The "n.obs" (number of observations) in Crossley et al. (2020)'s online data is set to "1" for all rows. The added Blue Grama site had considerably higher numbers of grasshoppers than the old pinyon-juniper site, and this change in sampling location likely inflated the numbers of grasshoppers in Crossley et al. (2020)'s calculation starting in 2002.

2) **Ground arthropod dataset (sev-29)**
   https://doi.org/10.6073/pasta/9e7e6dc9c9d8f72e9e0bca07a1e76ccd
   No correction was made for changes in sampling locations (termination of the pinyon-juniper [Goat Draw] vegetation type sampling site, and the initiation of a new [Blue Grama] sampling site at SEV in 2002) which are documented in the metadata (https://portal.edirepository.org/nis/metadataviewer?packageid=knb-lter-sev.29.175390). Collection of ground arthropods for this dataset also varied in number of traps per collection period/subsite. Some traps in each sample set of 3 subsample traps were often omitted from data tabulation due to individual traps being disturbed by precipitation runoff, or vertebrate animals. Summing omitted subsample traps (missing values, not zeros) would have reduced the sum counts for a line of 3 traps. While we cannot account for the discrepancy between the number of individuals in the Crossley et al. (2020) online data time series (39,926 individuals) and those in the full sev-29 dataset (52,188 individuals identified to genus level), this discrepancy appears to arise from Crossley et al. (2020)'s analysis removing species (they state 365 species/morphospecies were used in their Table 1) from the sev-29 full dataset (we count 433 species/morphospecies identified to genus). Crossley et al. did include some taxa identified to genus but not species in their analysis, so the reason for removing species/morphospecies is unclear. The "n.obs" (number of observations) in Crossley et al. (2020)'s online data is set to "1" for all rows. The added Blue Grama site had considerably higher numbers of ground arthropods than the old pinyon-juniper site, and this change in sampling location likely inflated the numbers of ground arthropods in Crossley et al. (2020)'s calculation starting in 2002.

Supplementary Information References

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