



# Linking herbivore monitoring with interpolation to map regional risk of pest species

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## Abstract

Long-term monitoring networks that generate data on pest abundance are the foundation of integrated pest management. Monitoring can estimate local risk from pests and identify when pests first arrive in particular fields. However, while data on pest abundance are collected for the purpose of making management decisions in individual fields, it is often unclear how such data can be used to make landscape scale predictions of risk from pests. We addressed this by using inverse-distance weighted interpolation models to generate predictions of abundance for multiple potato crop pests from long-term monitoring data. Specifically, we collected 30,999 abundance datapoints of four pests for 4 to 11 years and used interpolation to predict abundance of each pest across a 40,250 km<sup>2</sup> area; these predictions were compared to observed pest data to validate our approach. We show predicted pest abundance was strongly and positively correlated with observed abundance for each of the four pests studied, with Spearman rank correlations from 0.5 to 0.8. Moreover, our interpolation approach was robust to variation in the type of monitoring data used, although interpolation parameters that produced the best fit to observed data differed slightly across species and ranged from 1 to 2. This suggests that variation in the biological traits of pests can affect interpolation models, and that models should be tailored to individual species. Overall, our study shows that interpolation is a powerful tool to integrate pest monitoring data into predictive maps that can guide management for crop pests across broad spatial scales.

**Keywords** Geographical information systems · Integrated pest management · Landscape ecology · Potato · Predictive modeling

## Key message

- Pest monitoring is integral to pest management. While monitoring provides data on pest abundance in individual fields, these data are rarely used to make regional predictions of pest abundance
- We linked long-term monitoring data and interpolation models to assess if pest data from individual fields could predict regional variation in pest abundance

- We found the interpolation models effectively predict observed pest abundance, suggesting an effective approach for regional pest management

## Introduction

One of the foundational principles of integrated pest management (IPM) is that to make effective management decisions, producers should rely on pest monitoring. Monitoring networks inform growers about the abundance of pests, allowing for management decisions to be made based on known action thresholds. Across broad landscapes, pest monitoring also provides insight into the movement of pests, allowing producers to better anticipate when pests will arrive in their fields (Rosenheim and Gratton 2017). Yet, while pest monitoring is conducted in most agroecosystems, the ability to generate predictions of pest risk across regions is a nascent field (Rosenheim and Gratton 2017). To address this,

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scientists are increasingly using ecoinformatics approaches, whereby large-scale datasets collected across broad spatial and temporal scales are incorporated into ecological and statistical models to make inferences about pests (Bekker et al. 2007; Kelling et al. 2009; Michener and Jones 2012; Rosenheim and Gratton 2017).

In agricultural systems, many of the most common large datasets that are suitable for eco-informatics approaches assess pest abundance across regions. By trapping pests at regular intervals across space, the size and distribution of pest populations over time can be estimated. However, logistical challenges associated with pest monitoring across broad scales include the fact that sampling locations are often non-uniform and can depend on the landscape, cooperation with landowners, and the manpower available to check traps. This can limit the ability to use landscape-level data to make broad inferences about pest abundance. Interpolation has emerged as one tool to address this problem, as interpolation techniques can be used to make inferences about pest abundances across broad regions based on point counts in individual fields (Li and Heap 2011). By projecting pest populations, interpolation allows monitoring data collected from multiple locations to provide insight across broad production regions (Liebhold et al. 1993).

While interpolation approaches could promote sustainable pest management, interpolation assumes that nearby samples provide information about unsampled locations (Fleischer et al. 1999). This means that pest abundances at sites that are close geographically should tend to be similar, with similarities in abundance inversely related to distance. Yet, this assumption may not hold if there is variation in landscape composition, on-farm diversity and management, or pest life history across sites (Hardin et al. 1995; Costamagna et al. 2012; Rosenheim and Gratton 2017; Walter et al. 2020). Thus, for any particular system, interpolation models should be validated to determine if they provide robust predictions of particular pests. In such cases where interpolation models can be developed and validated, they may be used within decision support systems to provide real-time information on pest populations (Jones et al. 2010).

In potato agroecosystems of Washington State, we have conducted sampling of four major insect pests of economic importance for 4 to 11 years: (i) potato tuberworm (*Phthorimaea operculella* Zeller; PTW), (ii) beet leafhopper (*Circulifer tenellus* Baker; BLH), (iii) green peach aphid (*Myzus persicae* Sulzer; GPA), and (iv) potato psyllid (*Bactericera cockerelli* Šulc; PP). Since 2014, the monitoring data have been provided to growers with maps showing interpolated densities. Similar approaches have been used for Colorado potato beetle, western corn rootworm, and brown marmorated stinkbug in other systems (Weisz et al. 1995; Beckler 2004; Venugopal et al. 2015). However, few studies have validated interpolation approaches for pests, which

is problematic because interpolation could be affected by non-normal pest distributions (Zuur et al. 2010; Park et al. 2012) or due to pest management practices on farms (which strongly affect pest densities but are hard to quantify). Our study addresses this with an extensive exploration of the use of interpolation for pest management in an agroecosystem with a complex of major pests.

## Methods

### Pest monitoring network

Data on abundance of each pest were collected as part of a monitoring network that spanned the potato-growing region in Washington State, USA (Fig. 1) and covered 175 km E-W and 230 km N-S. Data on abundance of PTW and BLH were collected from 2007 to 2017, GPA was collected from 2009 to 2017, and PP was collected from 2014 to 2017 (Table S1). For each pest, abundance was measured weekly from each site (Fig. 1), beginning at plant emergence (April/May) and concluding at the vine kill stage (September/October) (Table S1).

Adult male PTW were monitored with 1 pheromone trap per site, with lures placed inside corrugated plastic delta traps with sticky liners (Trécé, Adair, OK); liners were changed weekly. Each trap was hung from a PVC pipe stand 30 cm above the soil. BLH were monitored using 2 yellow sticky cards per site (13 × 8 cm), mounted on small stakes 10 cm above the soil; these traps were placed along field edges outside of the range of irrigation. GPA were monitored by placing a small bucket (5 L, 20 cm diameter) under potato plants that were shaken to dislodge insects, with 15 plants per field. While this method targets the wingless colonizing aphids, winged migratory aphids are also counted when found. PP was monitored with four yellow sticky cards, with traps placed inside fields within 10 m of the edge and hung just above the plant canopy; trap height was adjusted as plants grew.

### Interpolation methods

Interpolation is a process where data on a response variable from individual sites are used to predict landscape-scale variation in the response (Li and Heap 2011). Interpolation functions, including inverse distance weighting, assume that predictions can be made by assuming spatial autocorrelation in the response (Li and Heap 2011). In other words, if a particular site has a high abundance of an insect, other nearby sites should have similar abundance, and sites farther away will be less similar. For example, inverse distance weighting estimates a response across a region from observations

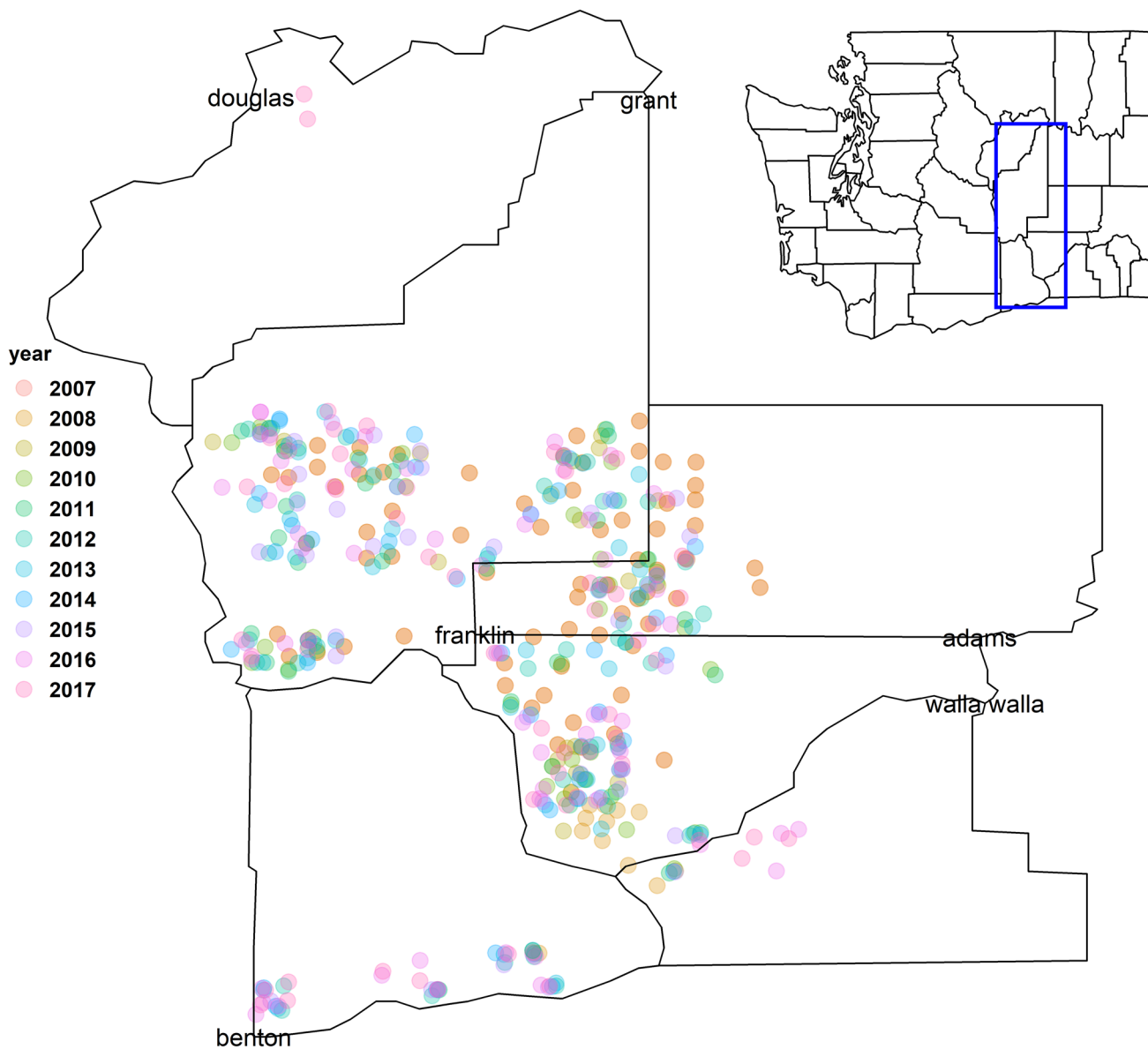


Fig. 1 A map of all sampling sites overall years where sampling occurred

at sampled sites, and the distance to the predicted site, as follows:

$$y_j = \frac{\sum_{i=1}^n \left( \frac{y_i}{d_{ij}^p} \right)}{\sum_{i=1}^n \left( \frac{1}{d_{ij}^p} \right)} \quad (1)$$

where  $y_j$  is the interpolated value of response variable at predicted site  $j$  based on the observed pest abundances from the monitoring network (sites  $i = 1$  to  $n$ ), the distance between sites  $i$  and  $j$  ( $d_{ij}$ ), and the power parameter  $p$ . In this model, the power parameter determines the strength of the spatial autocorrelation; if  $p = 1$  all sites are weighted using only

the inverse of their distance, but if  $p > 1$ , the weight of each point in the observed network has an exponentially decreasing effect on predicted abundances with increasing distance from the site. The location of sites in our monitoring network was measured to 4 decimal places which correlates with a distance of around 11 m, such that 11 m was the cell size for interpolations.

We used inverse distance weighting as our interpolation metric because it is more robust to zero-inflated data than kriging. Kriging also requires parameters derived from a fitted variogram (Gräler et al., 2016; R Core Team 2020), which could not be accomplished in weeks with low insect presence (fewer than ten sites). In contrast, the inverse distance-weighted (IDW) approach can generate results for any

week where three or more sites had insects present. With this method, our interpolations can generate predictions even when pest presence is low. While the accuracy of results with only three observation points is likely to be low, we chose this approach to maximize site inclusion and increase the probability of detecting outbreaks. A week with low pest presence but high pest abundance may overpredict abundance for the remaining sites, but those high abundances may signal the beginning of an outbreak or large migration event.

### Analysis of robustness of inverse distance weighting approach

In a series of sensitivity analyses, we assessed the robustness of our interpolation approach to (i) variation in the weight parameters, (ii) number of sites used in the interpolation (neighbor parameter), and (iii) several data transformations. These analyses were designed to test the robustness of our interpolation approach to our data treatments. Moreover, by varying weight parameters and the number of sites used in the interpolation, we were able to assess whether interpolation methods that provided the best fit differed across pest species.

*Variation in weighting by distance* The inverse distance weighting method requires three primary inputs: (i) observed pest abundances at sampled sites, (ii) the distance between sampled sites and predicted locations, and (iii) the power parameter. As the power parameter,  $p$ , increases, sites that are further away from the sampled point receive less weight (i.e., spatial autocorrelation occurs at a more local rather than regional scale). We tested five values of  $p$  for each insect tested: (i) 1, (ii) 1.5, (iii) 2, (iv) 2.5, and (v) 3. The lowest value (1) only assigns the inverse of distance as spatial autocorrelation, whereas a value of 2 represents the standard value in IDW calculations (Shepard 1968). With regards to biological traits of each pest, as the distance an organism can travel increases, the distance over which spatial autocorrelation occurs should also increase, and a lower value of  $p$  should fit better (Taylor 1984; Liebhold et al. 1993; Vinatier and Tixier 2011). We thus hypothesized that pests that move over larger distances (GPA, BLH, PP) would be best predicted with a low power parameter, while insects that move locally (PTW) would be best modeled with a high value.

*Neighbor parameter* The other parameter we varied within interpolation models was the neighbor parameter ( $N$ ), which is the number of observed sites to use in interpolations.  $N$  can vary from 1 (predictions are based only on the closest site) to the total number of sites sampled (which varied for each pest across years). Variation in this parameter might be important because a lower neighbor parameter assumes that sites that are farther away do not

affect predictions and thus might decrease the impacts of outliers far from predicted sites. We tested four values for the neighbor parameter: (i)  $N_{max}$  (total number of sampled sites for each pest in each year), (ii) 10, (iii) 5, and (iv) 3. We hypothesized that insects with greater dispersal ability would experience dispersal from distant sites and be more accurately interpolated by using all sampled sites, but insects with less dispersal capacity would only be influenced by dispersal from nearby sites and would be better predicted using a neighbor parameter that is spatially constrained.

*Data transformations* Insect count data are rarely normally distributed, rather often fitting a Poisson or negative binomial distribution. This is because count data often have many sites with low pest abundance and only a few sites of high pest abundance. Without transforming data, sites with relatively high abundance may cause overprediction in interpolation models. Normalizing the count data with a natural log transformation is one method to reduce the impact of outliers within count datasets, and this was one data transformation tested (using a  $\ln + 1$  transformation to deal with sites with values of pest abundance that were 0). A second data transformation commonly used in landscape models is to use only sites where pests are present (i.e., abundance > 0) to make predictions. Such a data transformation eliminates sites that have 0 pest abundance and focuses on making predictions only with sites that have positive pest abundance.

Overall, we tested four models, each of which had a different data transformation. The standard model used raw abundance data (base, all data) and included all sites whether they had a 0 or non-0 pest abundance. The second model ( $\ln$ , all data) used all sites but performed a  $\ln + 1$  transformation on pest abundances at each site. The third model used only sites that had non-0 pest abundance with no transformation (base, presence only). The final model used only sites that had non-0 pest abundance and conducted a  $\ln$  transformation ( $\ln$ , presence only).

### Model validation

With any parameter set for each pest, we predicted abundances based on the interpolation models for each week in each year. We used leave-one-out cross-validation to test effectiveness of the models using the *gstat* package in R (Gräler et al. 2016). This validation method is the most adaptable for datasets where the sample size varies over time and reduces the influence of outliers. Cross-validation avoids this problem by using the “leave-one-out” cross-validation (LOOCV) approach. This approach runs many validations with varying partitions for data used to test and train the model and then averages the results. By using an  $n$ -fold, the test partition is one data point in each model run, and the train partition is  $n - 1$  (all of the data except the test point). This process is repeated until each site has served as a test

point. We ran a total of 320 models (4 insects  $\times$  4 data transformations  $\times$  4 neighbor parameters  $\times$  5 power parameters).

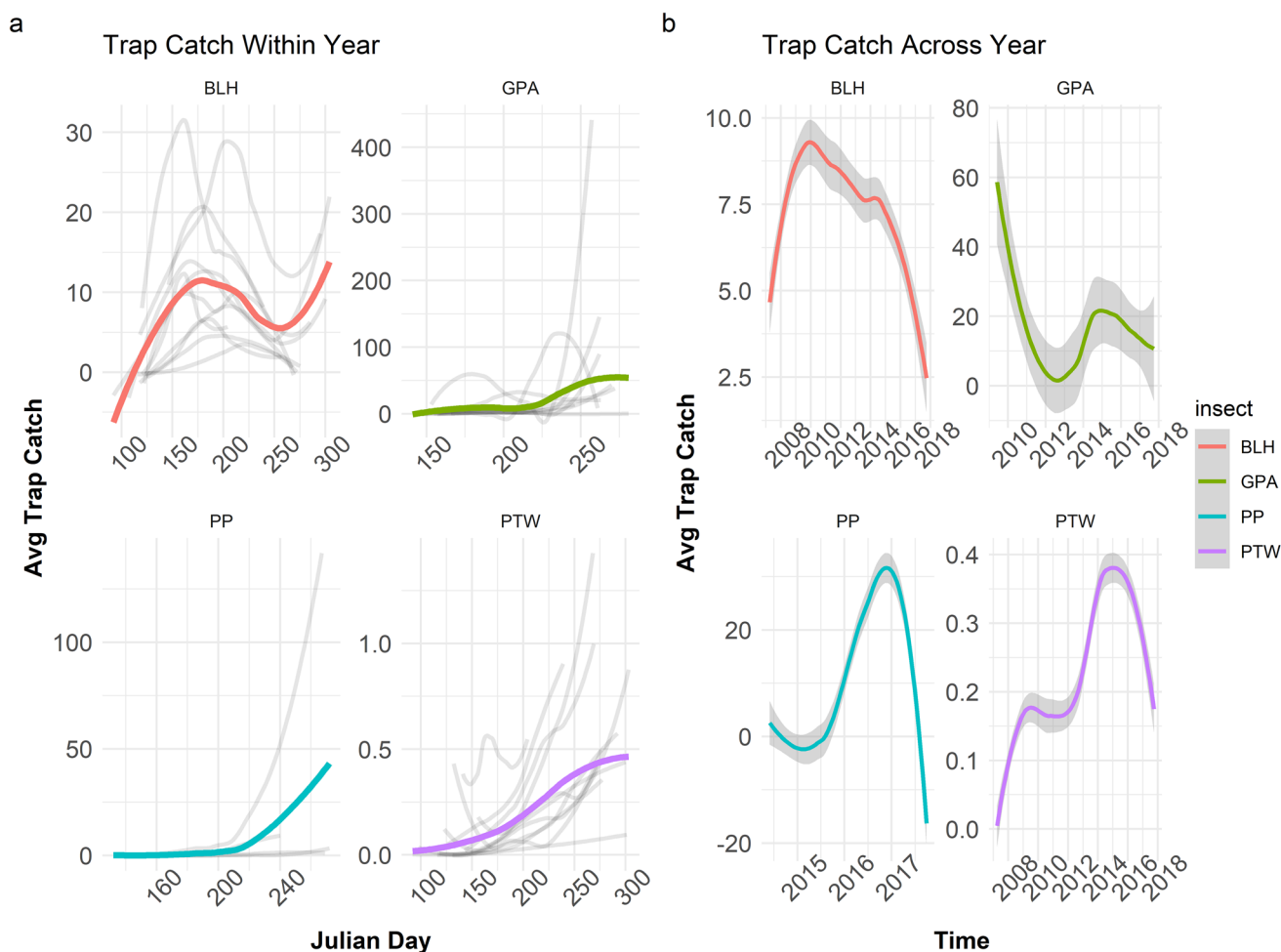
We used Spearman rank correlation between observed and predicted values from the leave-one-out cross-validation to assess the accuracy of interpolation models for each combination of predictors for each insect pest (Gauthier 2001). We also applied the 'estimated marginal means' method to generate pairwise comparisons of the variance explained by the power and neighborhood parameters using the emmeans package (Lenth et al. 2019). This technique is used to describe the effect of factors in the fitting of a model across a regular grid or surface. For each insect, we applied a linear regression model to the ln-transformed data with the residual as the response variable and generated pairwise comparisons within each set of parameters. Finally, to understand the distance at which spatial-autocorrelation occurs, we used the ncf package in R (Bjornstand and Cai 2020) to plot correlograms from

May 1 to September 30, encompassing a typical growing season. We repeated these analyses for years where all pests were sampled.

## Results

### Monitoring data

The monitoring network collected a total of 80,290 GPA, 23,233 PP, 2251 PTW, and 82,694 BLH across the total temporal extent. For each insect, the average trap catch by Julian day for each year (Fig. 2a), and the average trap catch over the entire sampling period (averaged across years) (Fig. 2b) show that abundances were variable both within and across seasons. However, PP and GPA had much greater between-year variation compared to BLH and PTW.



**Fig. 2** Fig. 2a shows the average trap catch within each year sampled for each pest. The colored lines represent the total average trap catch per week (7 Julian days) across all years, while the gray lines show

the average trap catch for each year. Figure 2b shows the total average trap catch across all years sampled for each pest. The confidence interval is represented by the gray shading



## Effects of data transformations on interpolation models

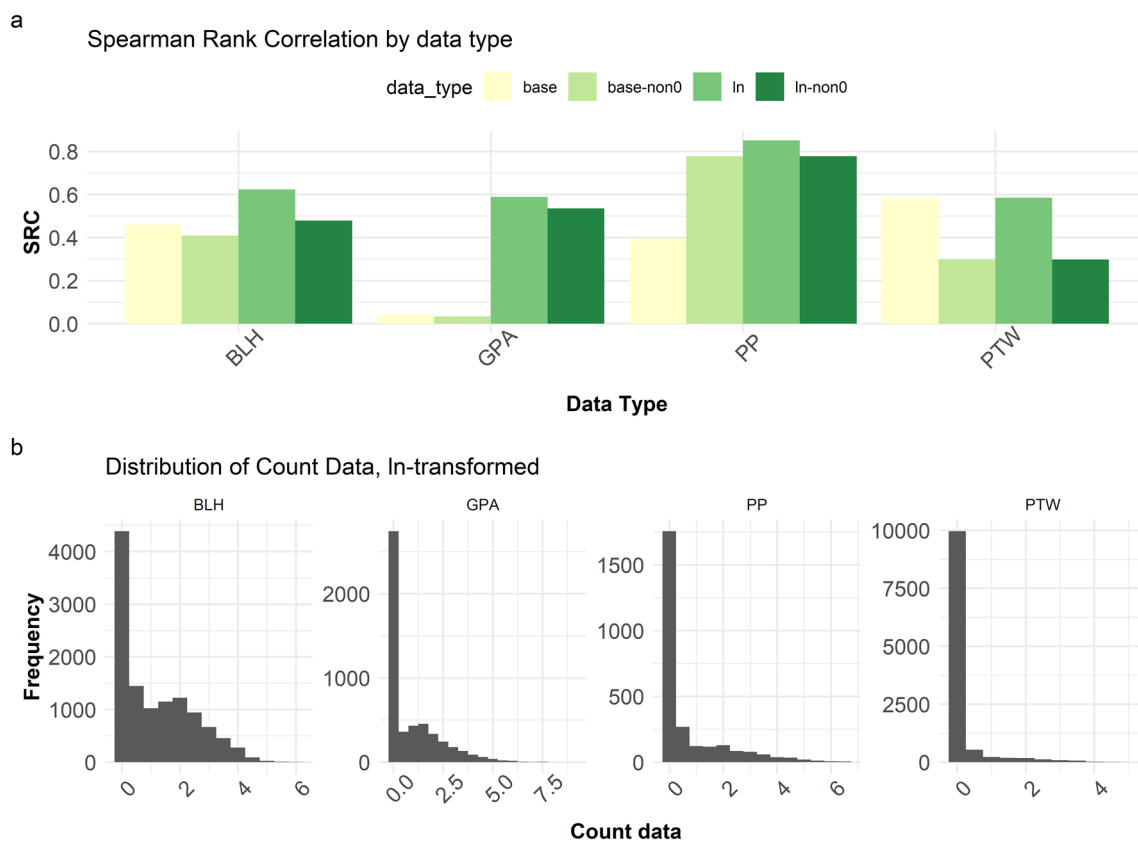
We found significant positive correlations between observed and predicted abundance with no data transformation for three pests: BLH ( $r_s=0.46$ ;  $P<0.001$ ), PTW ( $r_s=0.58$ ;  $P<0.001$ ), PP ( $r_s=0.39$ ;  $P<0.001$ ) (Fig. 3a). However, the models had a correlation coefficient close to 0 for GPA ( $r_s=0.04$ ), showing a poor fit to the observed data (Fig. 3a). We predict that the poor fit to the GPA data may be due to a single outbreak year, where high counts of wingless aphids in certain fields may have acted as “outliers” that inflated predictions at other sites. However, using a presence-only model did not improve correlations for pests except for PP ( $r_s=0.77$ ,  $P<0.001$ ), while BLH ( $r_s=0.41$ ,  $P<0.001$ ) and PTW ( $r_s=0.30$ ,  $P<0.001$ ) have a reduction, and the fit of the GPA interpolation model was largely unaffected ( $r_s=0.03$ ,  $P=0.009$ ) (Fig. 3a).

Our first two analyses suggested that the data were not normally distributed and that eliminating the absence data did not improve the accuracy of the interpolation. This

suggests that outliers caused over-inflated predictions. We addressed this by using a log transformation on the data, which increased correlation coefficients for each pest, and GPA in particular: BLH ( $r_s=0.62$ ,  $P<0.001$ ), GPA ( $r_s=0.59$ ,  $P<0.001$ ), PTW ( $r_s=0.58$ ,  $P<0.001$ ), and PP ( $r_s=0.85$ ,  $P<0.001$ ) (Fig. 3a). However, a combination of log transformation and presence-only data did not improve the fit. We thus used the log transformation with all data (presence/absence) as our “standard” model in the sections to follow for subsequent analyses.

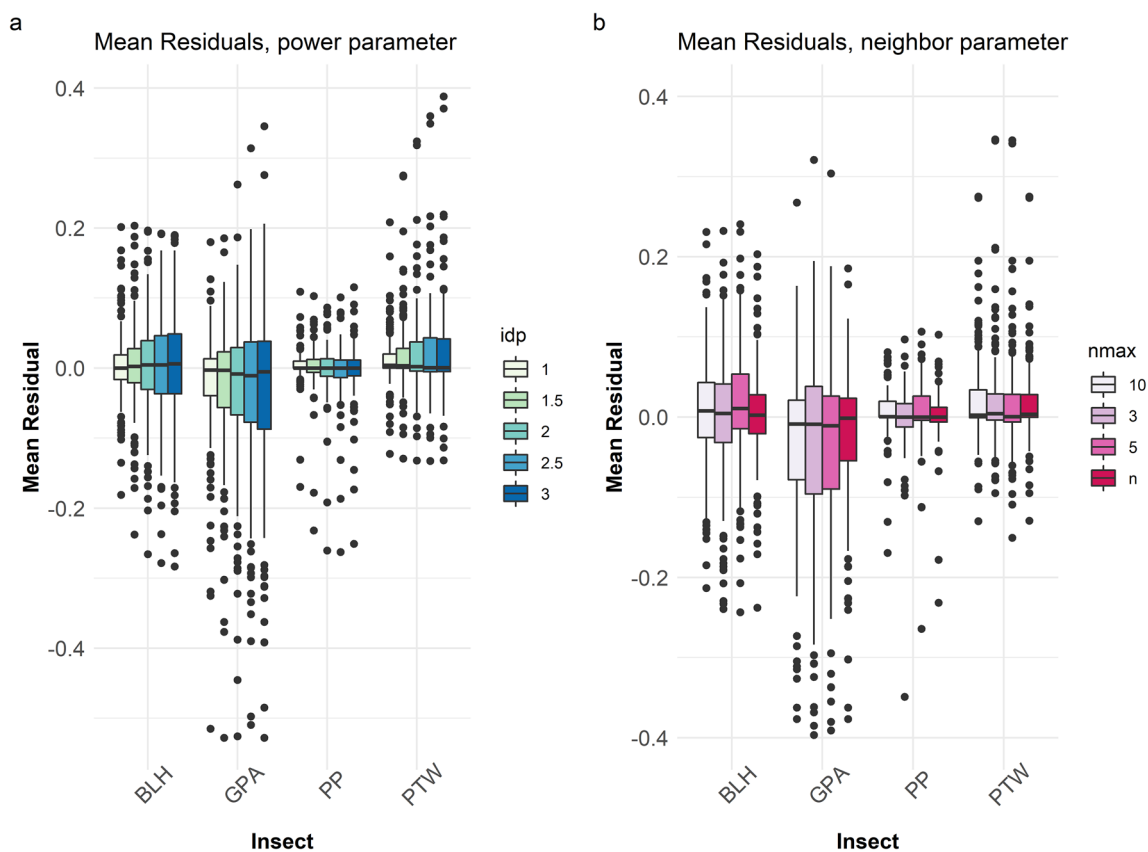
## Effect of parameters on interpolation models

For each pest, our interpolation models were robust to the power (Fig. 4a, Table S2) and neighbor (Fig. 4b, Table S3) parameters, though increasing the parameter also increased the range of predicted residuals and their outliers. However, because there were equivalent levels of positive and negative residuals, this leads to minimal differences in average residuals across power parameters. We found no statistical difference in fit of interpolation models based on either



**Fig. 3** Panel a shows the difference between observed trap catch and interpolated trap catch values across all years using Spearman rank correlation. The rank correlation is run for each combination of insect and data transformation (type), but only using interpolated data with the default interpolation parameters (power parameter of 1.5, neighbor

parameter of  $n$ ). Panel b is a histogram of ln-transformed trap catch abundance for each pest across all years. This demonstrates that all the data are not normally distributed and are closest to a Poisson distribution



**Fig. 4** Panel a is a boxplot of the mean residuals (observed – predicted) for each combination of insect and power parameter with a default neighbor parameter of  $n$ . Panel b is a boxplot of the mean residuals for each combination of insect and neighbor parameter with

a default power parameter of 1.5. Both only use the  $\ln$ -transformed data. Each dot represents an outlier, and the whiskers on each boxplot represent the standard error

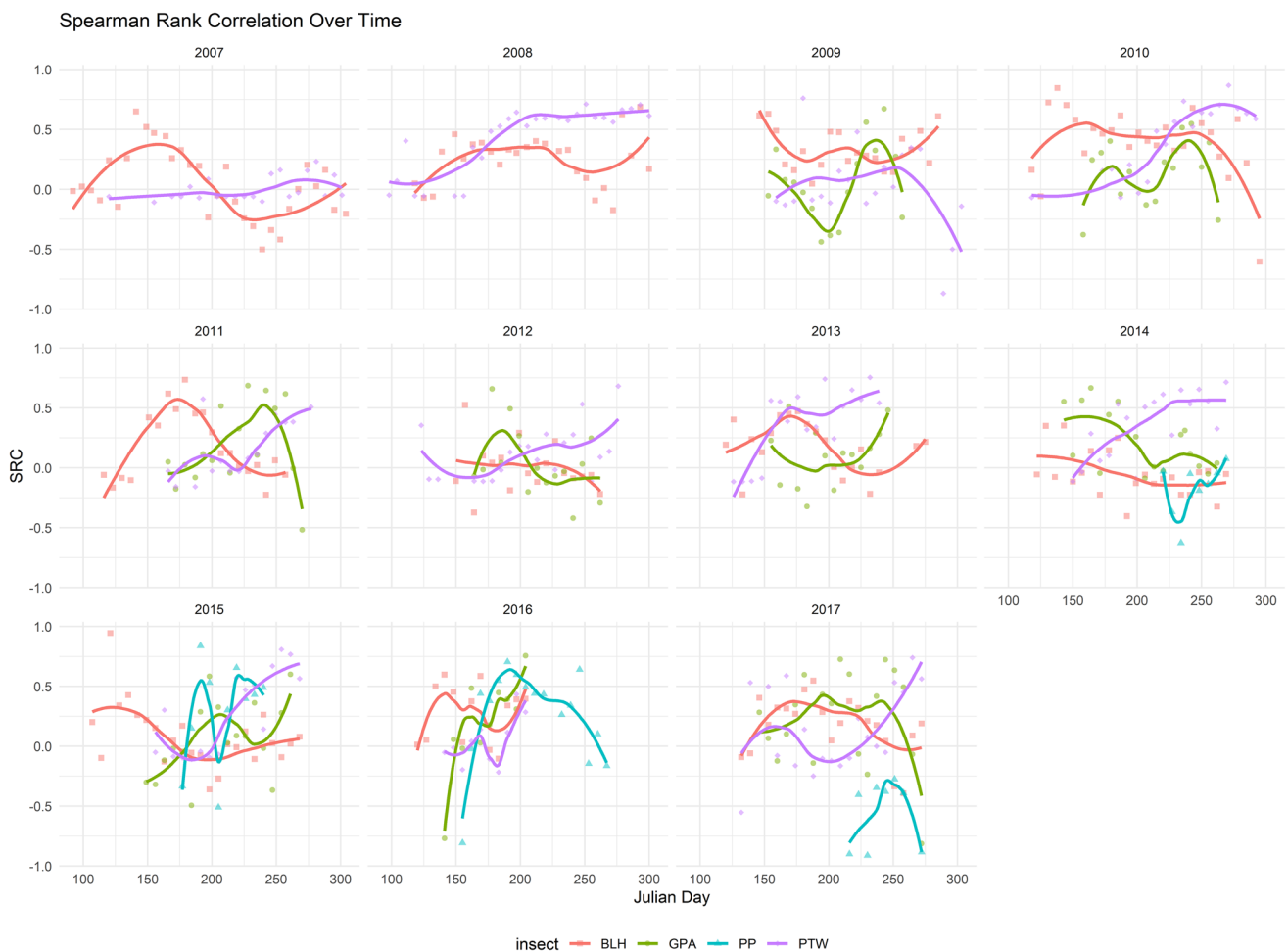
parameter (Tables S2, S3). However, within each pest, there were minor differences in which power parameter generated the highest  $R^2$  value between predicted and observed values (Fig. S1). Based on our analysis of spatial autocorrelation, we found that the range of positive spatial autocorrelation for BLH is  $12.85 \pm 8.84$  km, GPA is  $29.65 \pm 14.24$  km, PTW is  $39.16 \pm 11.92$  km, and PP is  $23.15 \pm 12.81$  km (Fig. S2–S5, Table S4). To test how the model performed across a growing season, we calculated the Spearman rank correlation for each insect across each week of sampling in each year and plotted it by Julian day (Fig. 5).

## Discussion

Our study shows that linking long-term pest monitoring data with interpolation models generates predicted pest abundances that are strongly positively correlated across large regions, as the Spearman rank correlations ranged from 0.50 to 0.80 for each insect (Fig. 3a), demonstrating a monotonic relationship between predicted and observed abundance for

insects that are also reflected in the average  $R^2$  values that range from 0.30 to 0.70 (Supp. Figure 1). These high positive correlations are striking given that potatoes are intensively managed, with often calendar-based applications of insecticides (Schreiber et al. 2018). Such insecticide sprays and other management tactics could strongly affect local pest densities. However, without access to management data or unmanaged sentinel plots, we are unable to make inferences about the effects of management on pest abundance. Thus, climatic factors which can cause autocorrelation across large distances (Koenig 2002), which we observed for each pest studied, are likely the primary drivers of regional population dynamics. Indeed, we found that pest abundances were spatially autocorrelated at up to 40 km, which suggests a strong effect of climatic drivers (Liebhold et al. 2004; Wagner and Fortin 2005; Illan et al. 2020). However, land-use patterns may also play a role in auto-correlation, as landscape homogeneity could affect the insect populations (Bianchi et al. 2006).

Interpolation models can provide growers with effective predictions of pest abundances using data from a regional



**Fig. 5** The weekly Spearman rank correlation for each pest in each year sampled, using the interpolation parameters (power parameter of 1.5, neighbor parameter of  $n$ ). Each week is equivalent to seven Julian days

sampling network. However, when looking at correlations between observed and predicted insect abundance within seasons, we did not see linear patterns. Rather, there were humps and sigmoidal curves that reflected variable model performance within seasons (Fig. 5). Although we were unable to compare statistically the performance at any given week given small sample size, visual inspection of graphs shows peak model performance typically occurred in the middle of the growing season. This is perhaps not surprising given that each pest in our monitoring network is polyphagous and can overwinter and reproduce on weedy hosts outside of potato fields and migrate into fields early in the season (Cook 1967; Van Emden et al. 1969; Cameron et al. 2002; Butler and Trumble 2012). This also means concentration of non-crop host plants may affect both the timing and abundance of pest entry into field. Sampling these non-crop hosts would be logistically difficult due to the sheer number of potential host species and their random distribution across a landscape. Moreover, if traps deployed in each field

fail to effectively estimate the population dynamics of initial dispersing individuals, models may underestimate populations until they build up in fields. Similar problems with models may occur at end of season because potato fields are harvested at variable times, driving dispersal of pests out of fields asynchronously across the region (Love and Stark 2003; Schreiber et al. 2018). Overall, these results suggest interpolation will be most effective in the middle of the growing season when potatoes throughout the region are rapidly growing and have formed a canopy. However, producers should continue to sample insect populations, especially early and late in seasons, to test for congruence with the model.

We also observed differences in the fit of models between pests that may be explained by pest life history. For example, power parameters determine how sites are weighted by distance, and insects that disperse over greater distances are modeled most effectively with a lower power parameter (Lu and Wong 2008). This system has both



hemimetabolous (BLH, GPA, PP) and holometabolous (PTW) pests, and the hemimetabolous pests mature faster given that they only have one immature nymphal stage compared to the holometabolous pests that have larval and pupal stages. The green peach aphid has a mean generation time of 11 to 12 d (Hong et al. 2019) compared to 20 to 40 d for potato tuberworm (Sporleder et al. 2004). There is also a difference in the amount of time each insect is mobile. PTW adults only live for 7 to 14 d (Sporleder et al. 2004), GPA lives for more than 20 days (MacGillivray and Anderson 1958), and PP and BLH have adult lifespans of more than 40 days (Munyanza and Upton 2005; Xiang-Bing and Tong-Xian 2009). These differences may then affect the range of individual insects over their lifespan. A mark-recapture study of PTW shows few forage beyond 250 m (Cameron et al. 2002), while potato psyllid regularly moves more than 100 m over 3 d (Cameron et al. 2013). Despite these differences, however, which we predicted would lead PTW to have a higher distance parameter, we found no significant difference in mean residuals within each pest based on power parameter (Fig. 4a). This suggests that despite variation in pest life history, interpolations were robust.

We also hypothesized that the largest neighbor parameter would produce the most precise results but found that sample density does not have a significant effect on the interpolation results (Fig. 4b, Table S3). While sample density varied across years, from 25–80 sites, sites are  $7.29 \pm 0.36$  km from each other on average. High sampling density can affect interpolations using different spatial interpolation methods (Hartkamp et al. 1999), but a meta-analysis of papers comparing interpolation methods found that sampling density did not improve outcomes (Li and Heap 2011). While the maximum range of spatial auto-correlation varies by year and by pest (Table S4), it still demonstrates that these four pests are spatially auto-correlated far beyond the range of their short-term dispersal. The high connectivity of potato fields in the sampling region (Illan et al. 2020) in addition to the relatively small sampling range (in terms of climatic variability) may explain the insensitivity of the results to the neighbor parameter.

Overall, our results suggest that interpolation methods currently used in decision support for potato growers in Washington produces a high degree of accuracy for all pests. We show that models produced predictions that were both biologically precise and strongly correlated with observed abundance. We hypothesize that the residual errors may be small enough to give growers a window to spray before crucial pest population thresholds are reached, but there is a continued need to test the efficacy of these models in the field. The interpolation models shown here also complement phenology models (D'Auria et al., 2016; Cohen et al. 2020) that can aid growers in timing pesticide sprays.

We suggest that the robustness of our interpolation models is likely due to a combination of our robust monitoring network, with 40+ sites used to estimate densities for each pest. Moreover, each insect sampled seemed to exhibit synchrony across sites due to climatic drivers, especially once they establish in the field. Furthermore, the lack of significant difference between neighbor parameters and Moran analysis suggests that the scale of auto-correlation may be higher than the average distance between sampling points due to the similarity of the local weather patterns. Thus, future sampling protocols may be able to decrease the number of sites, and therefore sampling effort, without any significant decrease in interpolation accuracy. Future research could attempt to incorporate other factors that affect pest damage, such as the ability of species like aphids and leafhoppers to transmit viruses and phytoplasma. More broadly, this interpolation is a powerful tool for precision agriculture that will contribute to future decision support tools and increase the long-term sustainability of agriculture.

## Author contributions

C.W collected the data; A.C and V.P analyzed data; A.C, D.C, J.I, and V.P prepared the manuscript. All authors read and approved the manuscript.

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**Data availability** The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

## Declarations

**Conflicts of interest** The authors of this article have no conflicts of interest related to the contents of this article.

**Ethical approval** No approval of research ethics committees was required to accomplish the goals of this study because sampling was conducted with unregulated invertebrate species.

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