

# Replication of “Titling community land to prevent deforestation: An evaluation of a best-case program in Morona-Santiago, Ecuador”

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## **Abstract<sup>1</sup>**

Buntaine, et al (2015) find that donor-financed, government-implemented land tenure legalization efforts in forested areas have a negligible effect on the rate of deforestation versus that found in areas not subject to such an intervention. The major results of their analysis was successfully replicated in this study. In the present paper, I explore how spatial autocorrelation in both the treatment and the outcome affects the treatment effect found by the original authors. This illustrates the importance of including spatial relationships into models attempting to explain causality within explicitly spatial datasets.

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<sup>1\*</sup> All analysis and data for this paper is available here

## Introduction

“Titling community land to prevent deforestation: An evaluation of a best-case program in Morona-Santiago, Ecuador” (Buntaine, Hamilton, and Millones 2015) is an evaluation of the impact of a donor-funded land titling and land management program for indigenous communities in Morona-Santiago, Ecuador. They claim that the presence of all the known contextual factors that lead to successful land legalization-led deforestation efforts makes this a best-case policy intervention. The data for the model was generated from spatial data on intervention areas and title boundaries provided by USAID and NGOs and publicly available spatial raster data such as population density (Landscan) and forest cover (Hansen, et al’s (2013) Global Forest Change (GFC) dataset). The change in GFC value in an area is used as the metric for deforestation. Areas receiving the program treatment were matched with areas that did not receive the treatment using a genetic matching algorithm. The treatment effect over the five years after is then estimated with a difference-in-difference OLS model. They find that treatment does not have a significant effect on deforestation rates.

I successfully replicated all of the paper’s major results. The authors made their raw data and code available on Harvard’s Dataverse; matched data was made available upon request to the corresponding author. All analysis, both for the original paper and this one, were done in the R statistical programming language (R Core Team 2019).

## Paper Review

Following the lead of the property right evangelist Hernando de Soto, over the past two decades governments, international institutions, and academics have looked to land titling as a solution for a range of vexing land-based problems. Reframed as market failures, challenges like deforestation are addressed by legitimizing the land tenure claims of otherwise unrecognized landholders. Recognizing their claims, the reasoning goes, means that landholders will be better able to exclude competing users while also incentivizing more sustainable forest management in order to maximize long-term benefits. However, evidence in support of this line of reasoning is mixed, since analyses often do not isolate the causal effects of land titling programs on forest loss from the factors that motivate the targeting of such programs in the first place and other predictors of forest loss.

Buntaine, et al (2015) draw on a combination of parcel-level data from a USAID-funded land titling program and a range of geospatial data sources to produce a more robust analysis of the causal effects of land titling on deforestation. The *Programa de Sostenibilidad y Unión Regional Sur* (PSUR) was a US \$27 million program implemented for 170,000 hectares of indigenous land in the heavily forested province of Morona-Santiago, Ecuador from 2002-2007. Under PSUR, communities of the Shaur indigenous people were able to codify exclusive claims over their customary lands and, hopefully, prevent the encroachment of non-indigenous colonizers. The end result of the legalization process was a Land Legalization Plan (*Plan de Manejo para Legalización*, PML). Every participating community completed a PML as part of the program. Starting in 2003, the second year of the PSUR, all communities (80% of the eventual total) also completed supplementary management plans (*Plan de Manejo Integral*, PMI) which were co-designed with USAID partner organizations and delineated a roadmap for sustainable resource management in the area.

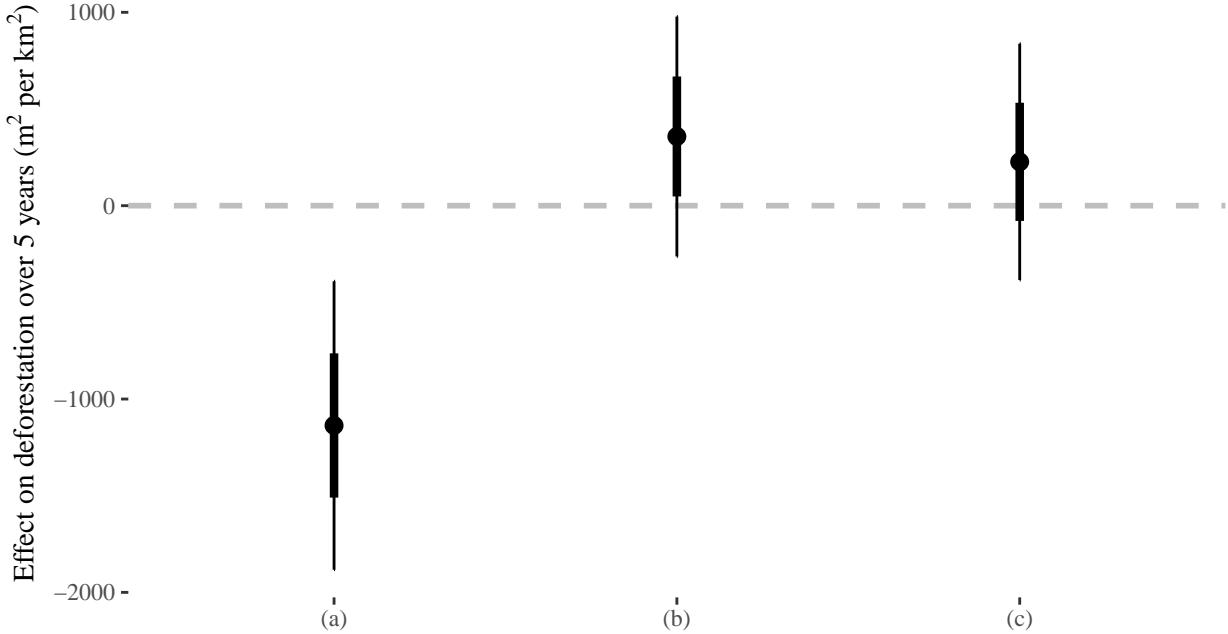
To begin their analysis, the authors divided the province into 27,984 0.87 square kilometer grid cells (this being the size of the coarsest input dataset used). The outcome measure was the amount of forest loss in each grid cell following legalization, using data from Hansen, et al’s (2013) Global Forest Cover (GFC) dataset. To isolate the treatment effect of legalization, grid cells within the PSUR areas were matched with grid cells outside with similar pre-treatment characteristics to create a set of control cells. This is done using a genetic matching algorithm with twelve covariates that have strong associations with deforestation in the literature. Three are measures of forest loss; four are distances to features or land use disturbance; three are demographic or institutional variables; and two are geophysical—elevation and slope. Two iterations of matching were done—one for plots receiving the PML-only treatment from 2002, and one for those receiving the PML + PMI intervention from 2003–2007.

$$\rho(X_i|T_i = 1) \approx \rho(X_i|T_i = 0)$$

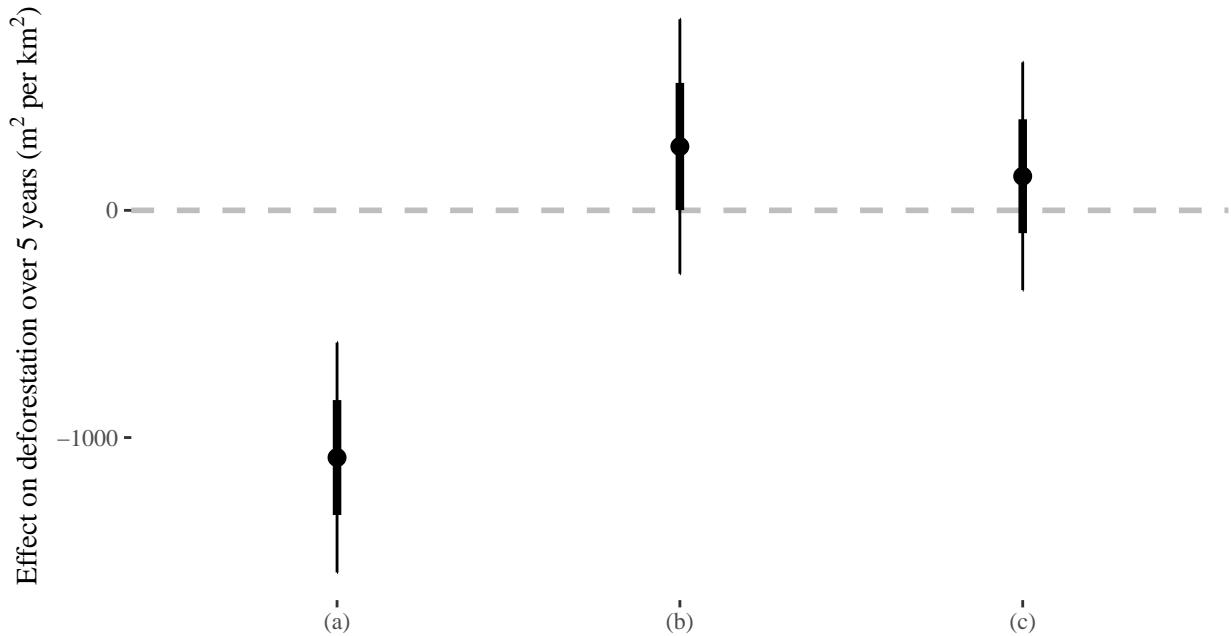
These same covariates were then used, along with the treatment variable, to estimate difference-in-differences of forest loss for the five years after intervention between treatment and control plots for PML-only and PMI treatment groups:

$$a_i(Y_i(t = x)) - Y_i(t = 0) = a(\alpha + \tau T_i + \beta X_i)$$

where  $Y_i$  is the amount of forest cover at different times,  $a_i$  is the square root of the weight for each observation,  $\alpha$  is the regression intercept,  $\tau$  is the treatment effect of the PSUR intervention, and  $\beta$  is a vector of coefficients for control variables. The treatment coefficients of their models are plotted in Figures 1 and 2.



*Figure 1: Difference in differences over five years for PSUR plots with legalization plan (PML) and title versus non-PSUR plots with no plan or title, 2002–2012. Notes: Figure shows treatment effect of tenure status for models as follows: (a) covariates, no pre-matching; (b) no covariates, pre-matching; (c) covariates, pre-matching.*

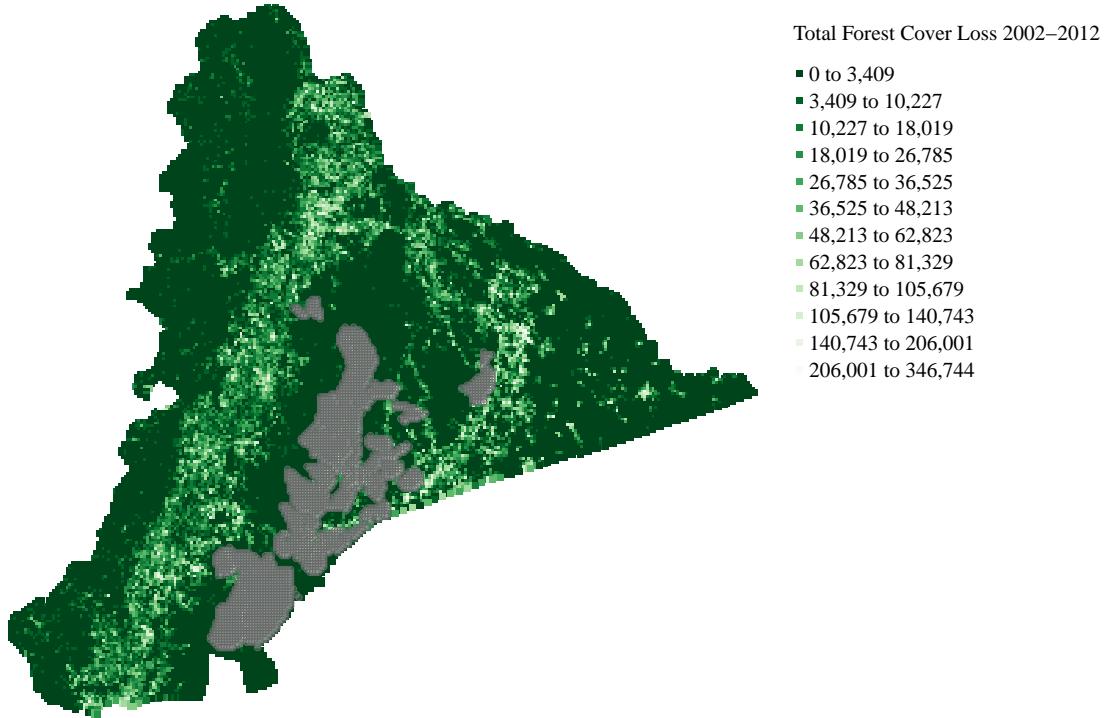


*Figure 2: Difference in differences over five years for PSUR plots with legalization plan (PML), title, and supplementary management plan (PMI) versus non-PSUR plots with no plan or title, 2002–2012. Notes: Figure shows treatment effect of tenure status for models as follows: (a) covariates, no pre-matching; (b) no covariates, pre-matching; (c) covariates, pre-matching. # # # Replication*

I was able to successfully replicate all of the major results from their paper, including coefficients for PML-only and PMI plots both before and after matching. Their tests for lagged effects over the five years after the start of the intervention were also successfully replicated. An example can be found in the first appendix to this paper.

## Extension

The authors' main conclusion—that the legalization of land tenure in Morona-Santiago had a negligible effect on deforestation rates in those areas—hinges on the claim that they have successfully isolated the treatment effect from the various factors that lead to the non-random targeting of such interventions, as well as from the background noise of ten years of change in the area. This claim is warranted by robust preprocessing of the data in order to make their causal inference. Specifically, this is done by matching PSUR-treated plots to untreated plots outside PSUR areas using genetic matching. The covariates used in the matching process draw on the broad consensus of the scholarly literature on deforestation. They include three measures of forest loss (the amount of forest cover in the cell and the pre-treatment rate of forest loss in the cell and within ~5 km of it); three demographic or institutional variables (population density within 5km, protected land status, and indigenous community presence); three distance-based variables (distance to major roads, to rivers, and to areas classified as “disturbed” by NASA’s MODIS land cover type product); and two geophysical ones(elevation and slope). Only one of these variables—neighborhood average forest loss—accounts for a strong predictor of deforestation: colocation with areas previously deforested. As Walter Tobler famously described the phenomenon of spatial autocorrelation (1970), “Everything is related to everything else, but near things are more related than distant things.” In this extension, I explore the effects of spatial autocorrelation on their conclusions and attempt to address these issues through standard spatial-analytic approaches.

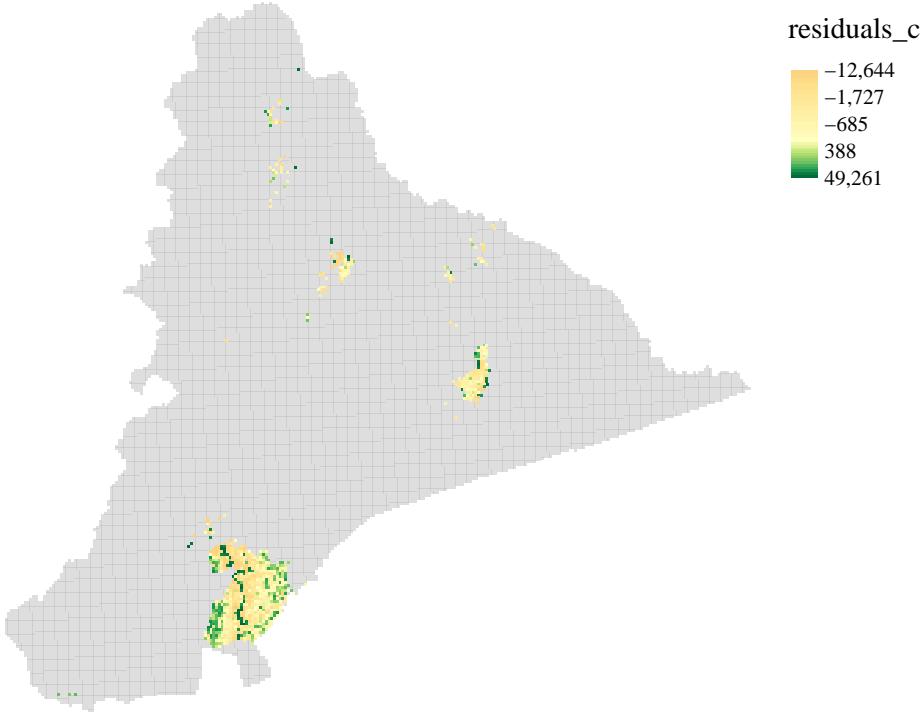


*Figure 3: Spotting spatial autocorrelation. Total deforestation in Morona-Santiago, per pixel, according to the Global Forest Cover dataset over the entire study period (2002-2012). Ghosted areas are PSUR intervention sites.*

Figure 3 shows the total forest in each observation cell in the dataset from 2002-2012. It is clear from a glance that the spatial patterning of forest loss is not random. Observations of high values cluster with other observations of high values, and vice-versa. This is unsurprising; indeed, the authors discuss the non-random spatial distribution of deforestation in the PSUR intervention areas (the ghosted areas in Figure 3), noting that clusters are located along a major roadway.

The authors use standard OLS models to estimate difference-in-differences of the outcome; as such, the independence of residuals is assumed. Spatial autocorrelation of individual variables in a model does necessarily imply the same issue in residuals since estimates may still account for it. However, when the residuals of the matched models in the paper are mapped patterns clearly emerge, as can be seen in Figure 4, which plots the residuals from the PML-only model “C” from above, i.e. using a matched dataset and all matching covariates. Interestingly, the patterning of the error terms echoes that of the forest loss trends mapped in Figure 3; for example, higher values are found along the same river valley in both maps. This echoing is found in the other key models, as well (residual maps for the other models are included in the Supporting Figures and Tables appendix below).

```
## Variable(s) "residuals_c" contains positive and negative values, so midpoint is set to 0. Set midpoint
```



*Figure 4:* Maps of residuals for PMI + PML model C from preceding section—matched datasets: PML+PMI treatment with all matching covariates included.

However, it is plausible that this visible clustering is more an artifact of the breaks used this map. Therefore, we check for spatial autocorrelation using Moran's  $I$  (Moran 1950), which is a measure of the covariance of observed values and values in the neighborhood around them. This takes the form:

$$I = \left[ \frac{n}{\sum_{i=1}^n (y_i - \bar{y})^2} \right] \left[ \frac{\sum_{i=1}^n \sum_{j=1}^n (y_i - \bar{y})(y_j - \bar{y})}{\sum_{i=1}^n \sum_{j=1}^n w_{i,j}} \right]$$

Where  $(y_i - \bar{y})$  and  $(y_j - \bar{y})$  are deviations in values for observations  $i$  and  $j$ ,  $w_{i,j}$  is the spatial weight between them, and  $\sum_{i=1}^n (y_i - \bar{y})^2$  is the aggregate of all weights in the dataset.<sup>2</sup> Values typically range from -1 to 1, and is interpreted under a null hypothesis of no spatial autocorrelation, or a value of zero. The residuals of each of the matched models were found to have small, yet significant, measures of spatial autocorrelation using Moran's  $I$ . This was confirmed by comparing them to repeated simulations in which residual values were randomly redistributed to the observations in the dataset and a Moran's  $I$  calculated for each permutation. A comparison between 999 such simulations and the actual observed Moran's  $I$  value for the residuals of one of the matched models (PML+PMI with all covariates) is shown in Figure 5.<sup>3</sup>

<sup>2</sup>The construction of the weights matrix for calculating measures of spatial autocorrelation requires three key decisions: (1) Whether to use a k-nearest neighbor-defined or a distance-defined neighborhood around each observation; (2) the scale of this neighborhood, i.e. how many neighbors or how large a radius; (3) the type of function to use in generating weights for the observations in the neighborhood. For the present analysis a 40-nearest-neighbor neighborhood was used; since cells are  $0.87 \text{ km}^2$ , this approximates the 5-km radius for average forest cover loss previously calculated by the authors. Distance- and KNN-based neighborhoods were calculated and returned similar results; the latter was used because it is more computationally efficient. Other parameters were left as package defaults.

<sup>3</sup>Throughout this section I typically visualize my extension results for one of the six most meaningful models from the original paper; similar figures for the remaining models can be found in the Supporting Figures and Tables appendix.

## Comparing Simulated Moran's I Values to Observed

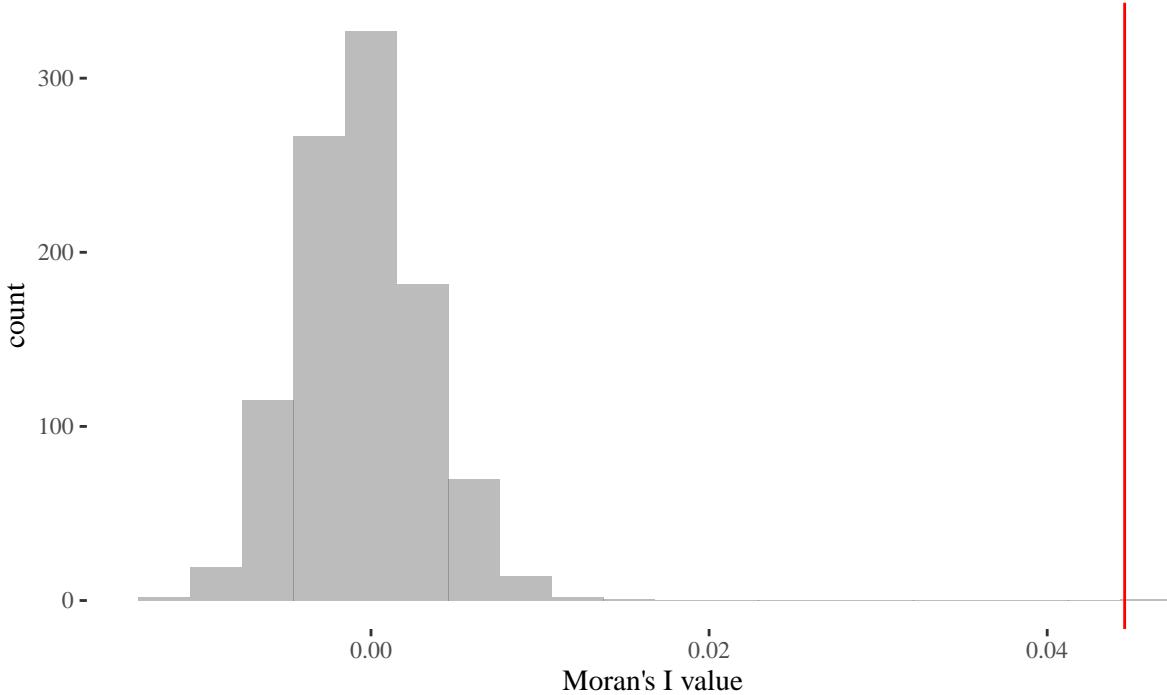
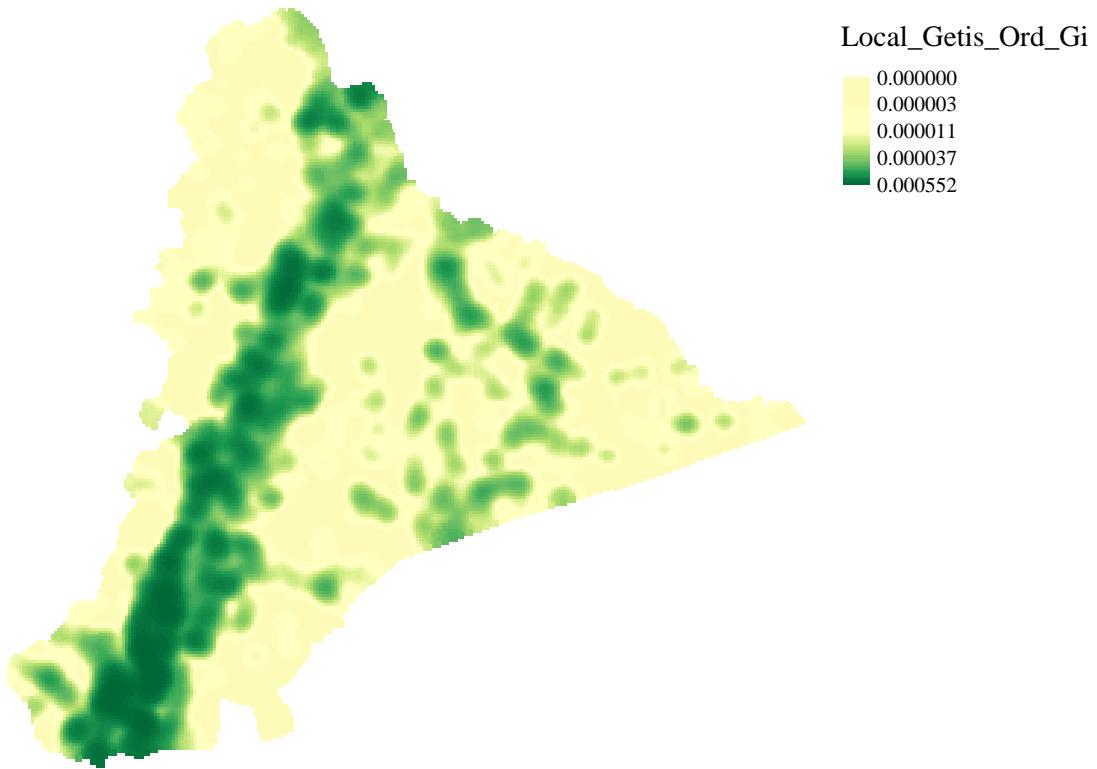


Figure 5: Comparing the spatial autocorrelation of simulated distributions of original model residuals to the observed value. The model results used are for matched PMI+PML intervention using all covariates (corresponding to that shown as Figure 6 C in the original paper).

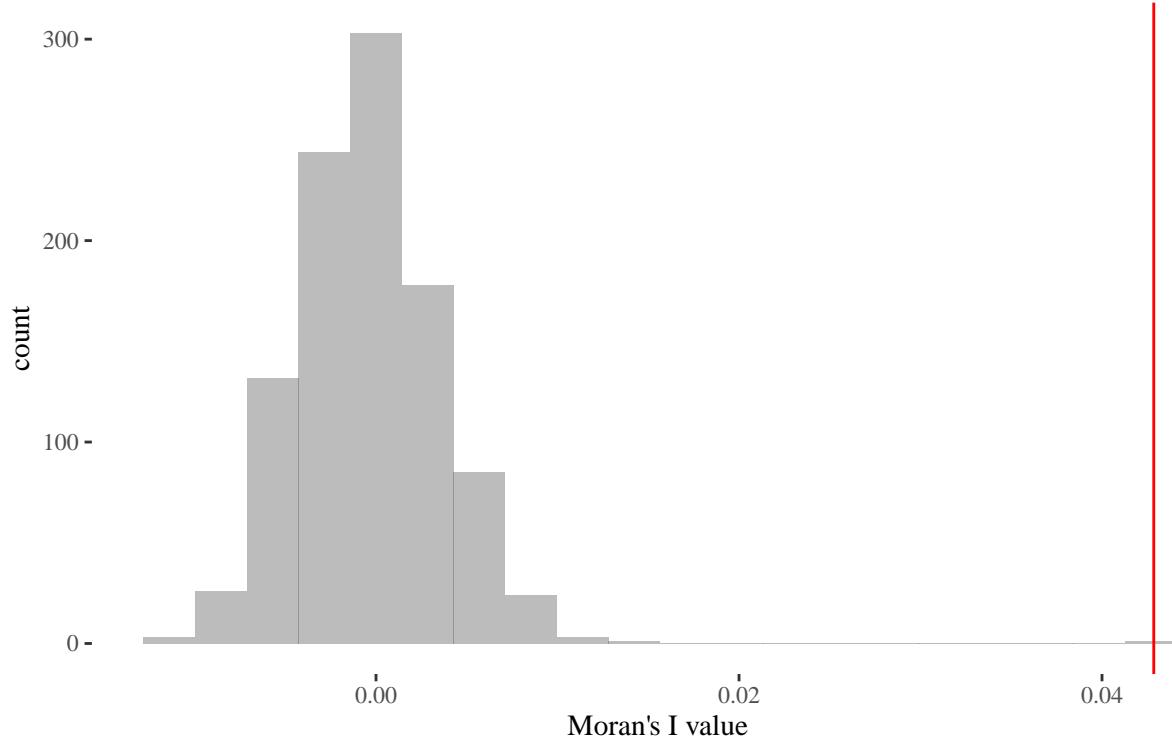
The Moran's  $I$ , however, is a global measure, that is, it returns a single value representing the spatial autocorrelation for all observations in the study space. The nature of spatial autocorrelation itself indicates that measures of it are scale dependent, subject to the modifiable areal unit problem (Fotheringham and Wong 1991). While they do not escape this latter problem entirely, local indicators of spatial autocorrelation (LISAs) produce observation-specific values representing the spatial autocorrelation in the neighborhood around each observation (Anselin 1995). As a first attempt to control for spatial autocorrelation in these models, we calculated one such LISA, the Getis-Ord  $G_i$ , for the pre-treatment response variable and added it to the list of covariates used to match treated and untreated plots. The  $G_i$  is a ratio of the weighted average of the values in neighboring locations to the sum of all values, not including the value of  $x$  at observation  $i$ :

$$G_i(d) = \frac{\sum_{j=1, i \neq j}^n w_{ij}(d)x_j}{\sum_{j=1}^n x_j}$$



*Figure 6: Getis-Ord  $G_i$  values for pre-treatment forest loss across the study area. When mapped, the  $G_i$  resembles a much-smoothed version of the raw forest loss map seen in Figure 3. Cells within the vicinity of higher rates of forest loss have higher values, and vice versa.*

However, when the same Moran's  $I$  simulation analysis is run on the residuals produced using the same model parameters from the original paper using this re-matched dataset we find hardly any change, as seen in Figure 7. Explicitly including a LISA of the pre-treatment response variable in a genetic matching process in this case has no effect on the spatial autocorrelation of the residuals in the ensuing DiD model.



*Figure 7: Comparing simulated Moran's  $I$  values to the observed value for residuals using data rematched by including  $G_i$  alongside all previously included covariates and model parameters (corresponding to that shown as Figure 6 C in the original paper).*

We also, somewhat unconventionally, check the effects of adding this LISA into the models themselves. That is, starting with the re-matched dataset, we include the previously calculated  $G_i$  of the response variable alongside the other twelve covariates included in the original DiD models from the paper. This results in minor changes in the estimated treatment effect, though it does reduce the magnitude of the changes observed by the original authors between unmatched and matched datasets (coefficient plots for multiple iterations of these models are included in the Supporting Tables and Figures appendix). The residuals of this new LISA-inclusive model display a noticeable reduction of spatial autocorrelation, though still beyond the null hypothesis of the Moran's  $I$ , seen in Figure 8.

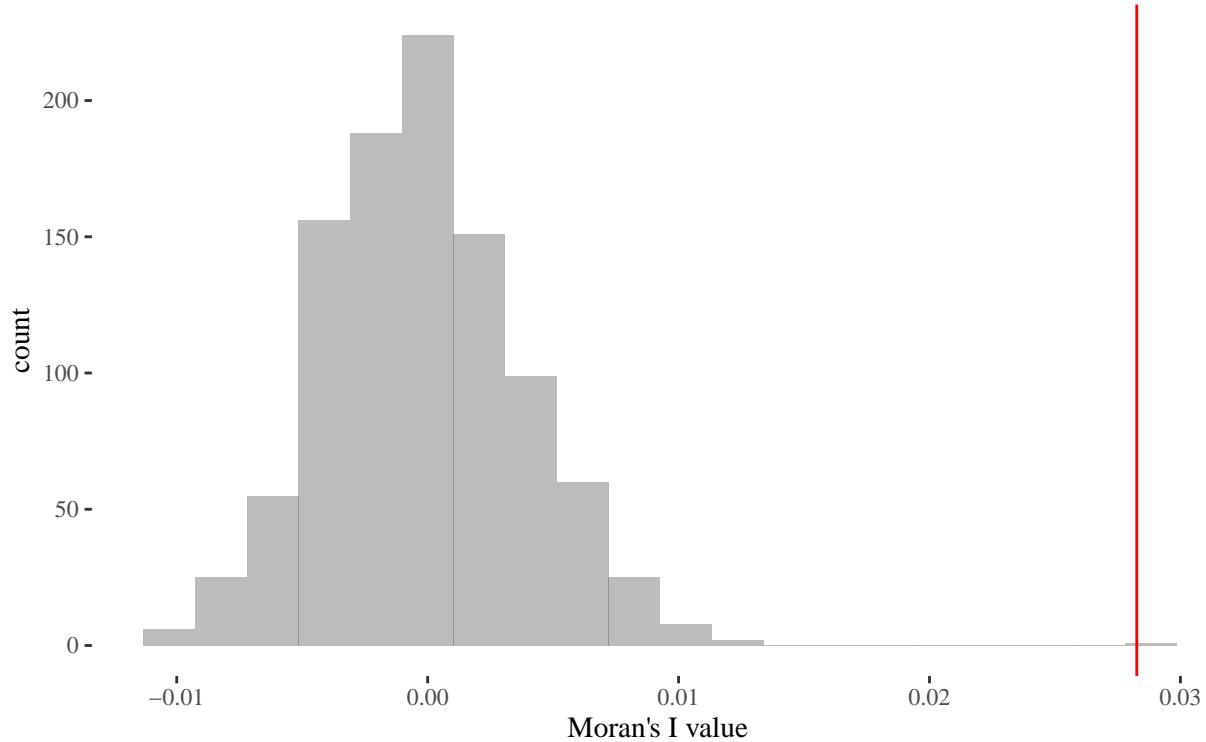


Figure 8: Comparing simulated Moran's  $I$  values to the observed value for residuals using data rematched by including  $G_i$  alongside all previously including covariates and previous model parameters (corresponding to that shown as Figure 6 C in the original paper) plus the  $G_i$  statistic.

Since this experimental search for a robust solution to the problem of spatial autocorrelation in the model results has made a limited impact, we follow a more widely-used procedure for addressing this challenge. We run two kinds of spatial regression and use Lagrange multiplier (LM) tests to determine which best accounts for spatial dependence in the original matched data. This is a version of the steps laid out in Figure 9, a flowchart from Anselin (2005).

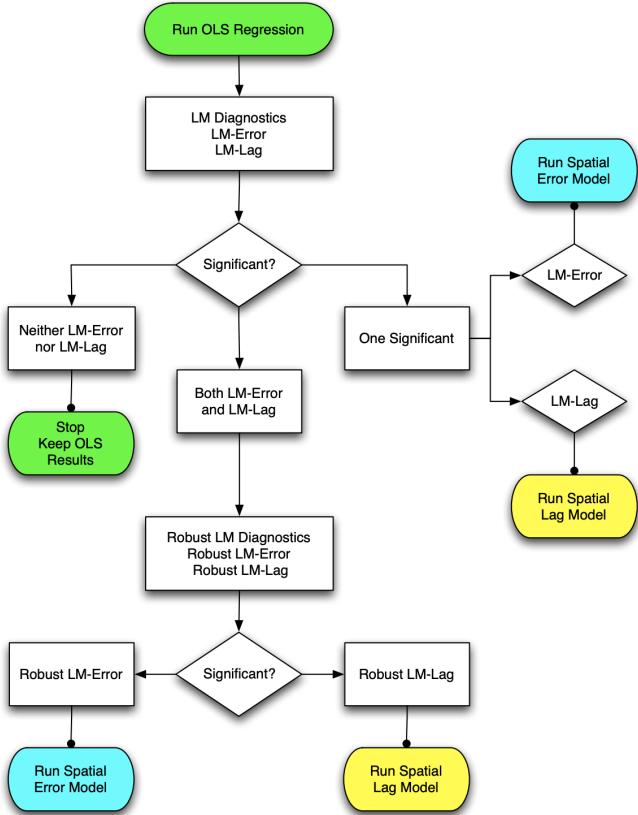


Figure 23.24: Spatial regression decision process.

*autocorrelation in OLS models from Anselin (2005) p. 199.*

Spatial regression models are a type of generalized linear model which specifically address the problem of spatial autocorrelation, in different ways, by incorporating the same kind of neighborhood-based spatial weighting system as used by Moran's  $I$  and the Getis-Ord  $G_i$ . Spatial lag, or autoregressive, models take the form:

$$Y = \beta_0 + \beta_1 X_1 + \cdots + \beta_n X_n + \rho W y + \epsilon$$

Where  $W$  is a weights matrix and  $\rho$  is a spatial lag parameter. This shows that the lag model addresses spatial dependency in the outcome variable, that is, observation  $y_i$  is dependent on lagged values of itself in its neighborhood (Anselin 1988). Spatial error models, on the other hand, directly address spatial autocorrelation in OLS residuals:

$$Y = \beta_0 + \beta_1 X_1 + \cdots + \beta_n X_n + u u = \lambda W u + \epsilon$$

The error term  $\epsilon$  is decomposed into a spatially lagged error term  $\lambda W u$  and an identically and independently distributed error term  $\epsilon$ .  $\lambda$ , like  $\rho$  in the lag model, reflects the presence or absence of spatial autocorrelation.

Following Anselin (2005), we use a battery of Lagrange multiplier tests on the original OLS models and the spatial lag and error variants of them, looking for which returns the highest calculated LM value and lowest p-value, based again on a null hypothesis of no spatial autocorrelation. Results are shown in Table 1. Of the four key models, only the PMI+PML models with covariates leans towards a preference for a spatial error model; the others all show more promise with a spatial lag model. Thus, for parsimony's sake we use a spatial lag model on all four. However, the endogenous spatial dependence in the lag model makes it challenging to directly interpret the coefficients. We do find significant coefficients  $\rho$  in each model. However, spillover effects between individual observations and their neighbors, a key feature of the model, means that

Figure 9: Flowchart for addressing spatial

autocorrelation in OLS models from Anselin (2005) p. 199.

Table 1: Langrange Multiplier Test Results

PML-only, no covariates	LMerr	151.17081900	0.00000000
*	LMlag	169.57040200	0.00000000
*	RLMerr	121.72510300	0.00000000
*	RLMlag	140.12468500	0.00000000
PML-only, covariates	LMerr	2.19624800	0.13834710
*	LMlag	4.95498200	0.02601559
*	RLMerr	-13.63206600	1.00000000
*	RLMlag	-10.87333200	1.00000000
PMI + PML, no covariates	LMerr	1581.27991000	0.00000000
*	LMlag	1617.44695200	0.00000000
*	RLMerr	144.11122300	0.00000000
*	RLMlag	180.27826500	0.00000000
PMI + PML, covariates	LMerr	132.67383700	0.00000000
*	LMlag	123.70679200	0.00000000
*	RLMerr	16.76127900	0.00004239
*	RLMlag	7.79423400	0.00524132

coefficients of covariates cannot be understood exactly as in OLS. This because these spatially-lagged  $\beta$  coefficients now assess the effects of each  $x$  on  $y$  while controlling for spatial dependence in  $y$ , i.e. the extent to which the variation in each observation  $y_i$ 's forest loss can be accounted for by the forest loss in the other observations within its neighborhood. Therefore we use the `spatialreg` package's built-in `impacts()` function, which uses the impact measures developed by LeSage and Pace (2009) to isolate the effects of each covariate on the outcome. The results can be seen below.

```

## Impact measures (lag, exact):
##          Direct Indirect      Total
## PML -250.1149 -422.6714 -672.7863

## Impact measures (lag, exact):
##          Direct     Indirect      Total
## PML     86.33198681  2.421528e+01 110.54726358
## fl.pre.5cell   0.05713378  1.602546e-02  0.07315924
## forest.pre    -0.01666817 -4.675260e-03 -0.02134343
## pop.den.5km.pre 31.93828488  8.958376e+00 40.89666099
## dist.disturb.pre -0.02035032 -5.708064e-03 -0.02605838
## A128       -0.06240130 -1.750295e-02 -0.07990425
## A129       -0.24945490 -6.996966e-02 -0.31942455
## A130        0.01152264  3.231987e-03  0.01475462
## A154      -505.79923671 -1.418717e+02 -647.67096883
## A361       -1.34881489 -3.783294e-01 -1.72714426
## A362      -84.29021732 -2.364258e+01 -107.93279774

## Impact measures (lag, exact):
##          Direct Indirect      Total
## PMI  5.560399 19.75997 25.32037

## Impact measures (lag, exact):
##          Direct     Indirect      Total
## PMI     8.946065334  7.685117390 1.663118e+01
## fl.pre.5cell   0.109318947  0.093910441 2.032294e-01
## forest.pre    -0.049147676 -0.042220311 -9.136799e-02

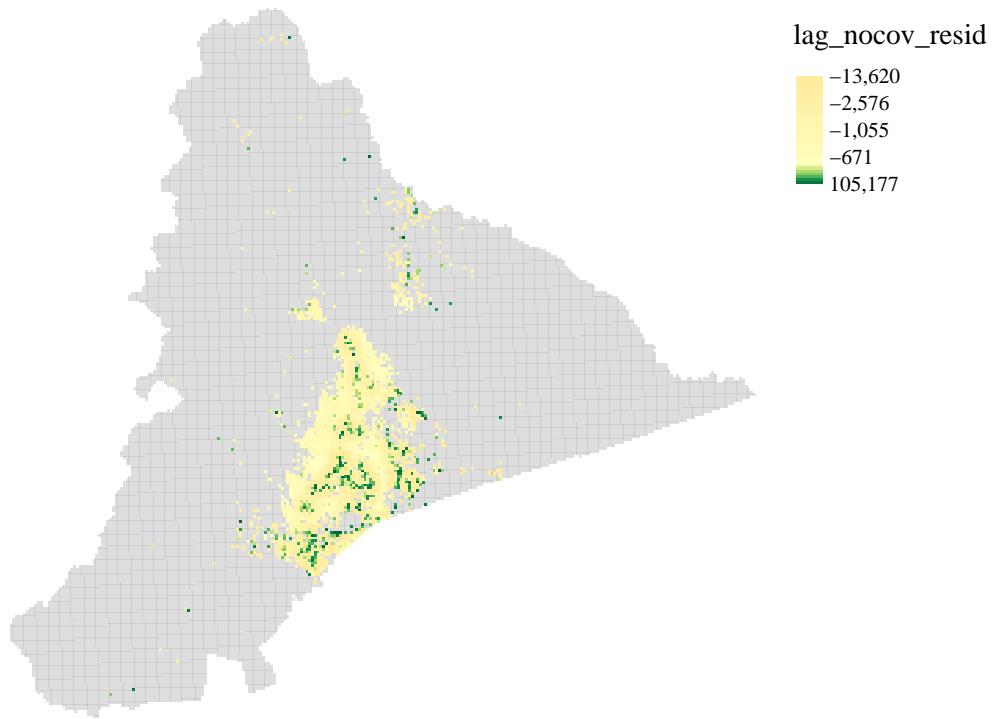
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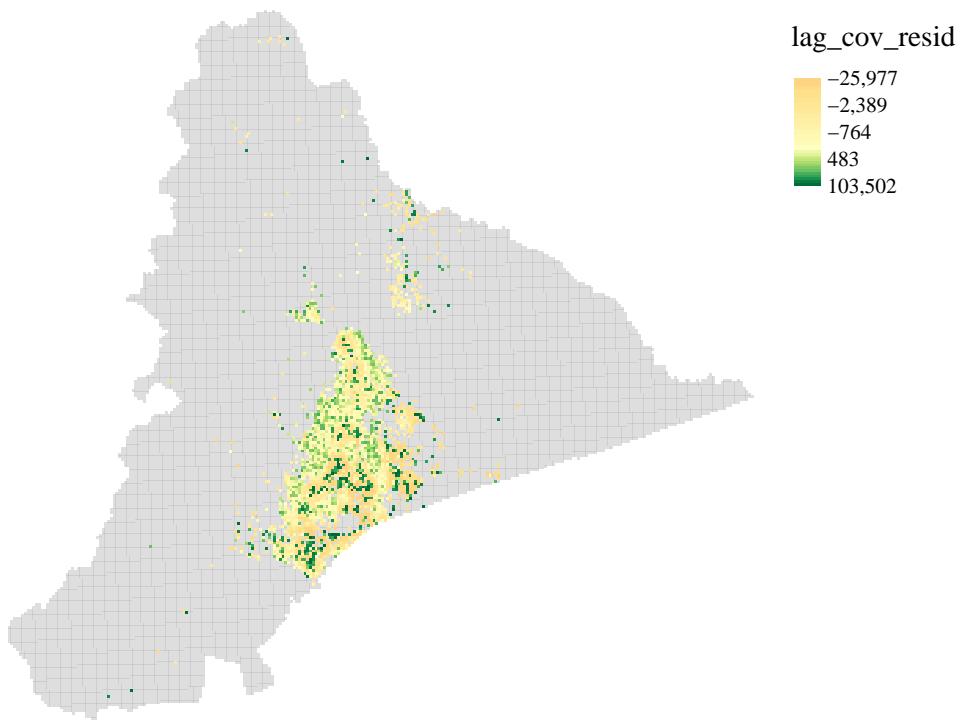
## pop.den.5km.pre  31.113963453  26.728450181  5.784241e+01
## dist.disturb.pre 0.023043083   0.019795161  4.283824e-02
## A128            -0.013878810  -0.011922591 -2.580140e-02
## A129            -0.016213362  -0.013928089 -3.014145e-02
## A130             0.003172317   0.002725179  5.897497e-03
## A154             350.510523758 301.106064048  6.516166e+02
## A347             434.414321781 373.183621407  8.075979e+02
## A361             -2.449524595  -2.104264094 -4.553789e+00
## A362             -56.937591096 -48.912237406 -1.058498e+02

```

```
## Variable(s) "lag_nocov_resid" contains positive and negative values, so midpoint is set to 0. Set midp
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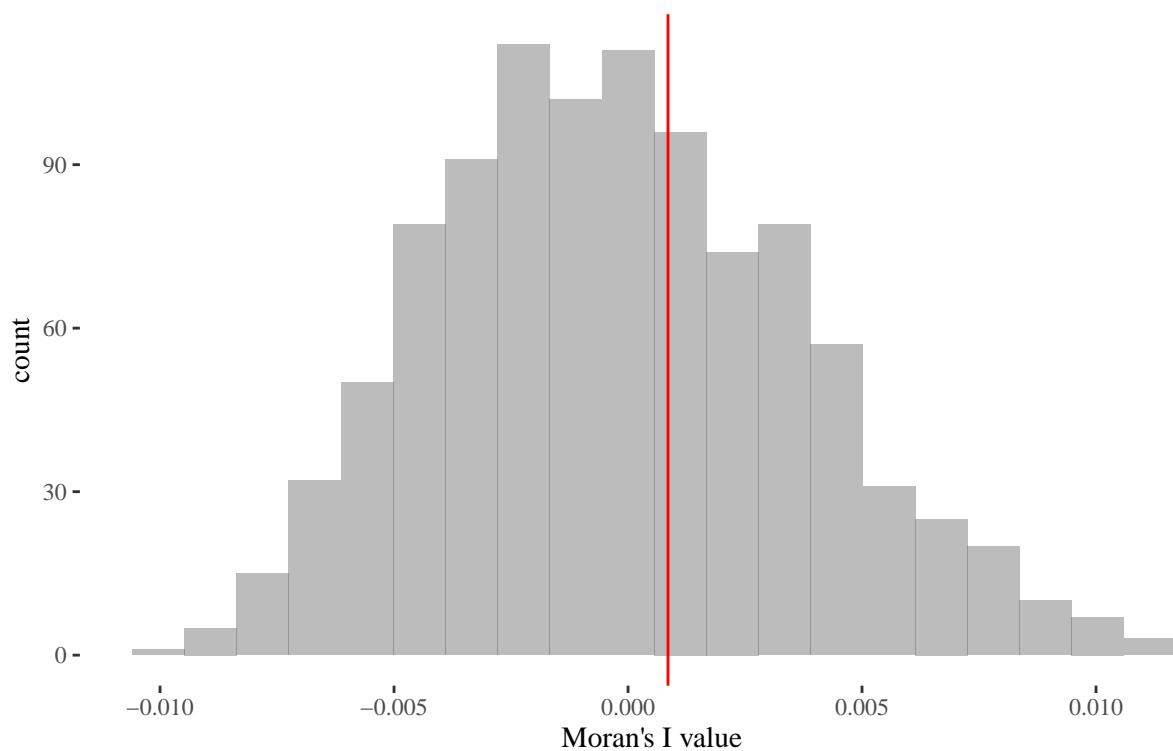
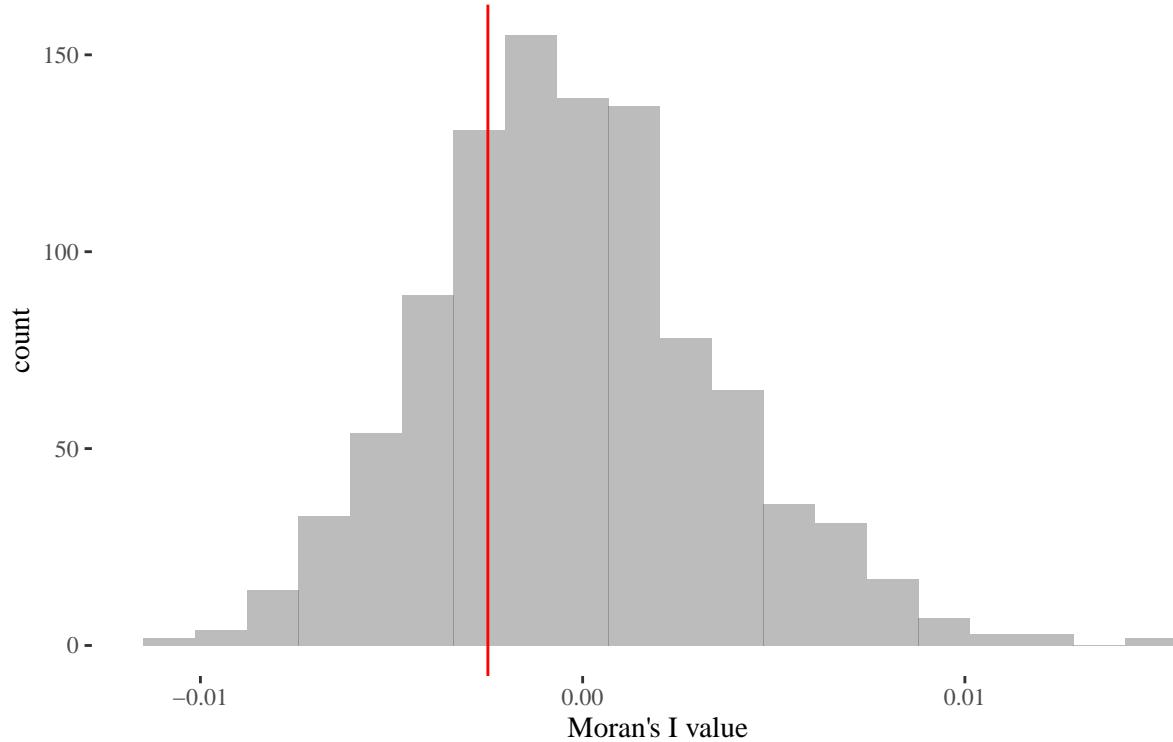


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*Figures 10 and 11: Mapping the residuals of spatially-lagged PMI + PML models. Top is without covariates, bottom is including covariates.*

When mapped (Figures 10 and 11) we see that, while not perfect, generalizing the original models to include a spatial lag term has greatly reduced the spatial autocorrelation of the original residuals (shown here are those for the two PMI + PML models). This is confirmed through Moran's  $I$  simulations, shown in Figures 12 and 13.



*Figures 12 and 13: Comparing the spatial autocorrelation of simulated distributions of the residuals from spatially-lagged versions of the original PMI + PML models to the observed ones.*

## Conclusion

In this exploratory extension of Buntaine et al. (2015), we found and attempted to account for the presence of spatial autocorrelation in the data used. Using visual inspection and a global measure of spatial autocorrelation—Moran's  $I$ —we found spatial dependency in both the response variable and the residuals of the original paper's models. Based on this, we first re-did the genetic matching at the heart of the paper's causal claims by including a local indicator of spatial autocorrelation—the Getis-Ord  $G_i$ —of the response variable as a matching covariate. We found little change in the treatment effects found in the original paper.

We then followed in Anselin's (2005) footsteps and fit spatial regression models to the original matched data, testing for the optimum with a series of Lagrange multiplier tests. The spatial lag, or spatial autoregressive, model consistently performed better on these tests. The inclusion of this model's lagged weight matrix greatly reduced, though did not eliminate entirely, the problem of residual spatial autocorrelation in all models. The impact of this on the treatment effects observed by the authors is less clear and deserves further exploration. To what degree is comparing the treatment effect, the coefficient of a treatment variable in an OLS regression, to the impact measures developed by LeSage and Pace a justifiable or robust approach? For the PML-only model with no covariates, the spatial lag impact was very different from the treatment effect from the original paper; this difference becomes unimportant after all covariates are included as the treatment effect falls to near zero. The impact measures for the PMI + PML models, on the other hand, do not change the results from the original paper dramatically.

This exploration was only an initial foray. The inclusion of spatial effects into causal models, especially those about phenomena for which spatial relations are of major importance, has the potential to improve the robustness of impact evaluations such as the one being replicated here. One area of particular interest for future exploration is the potential for integrating Bayesian approaches into the study of spatial autocorrelation and, therefore, of the means for accounting for it in regression models. The measures used in this paper—the Moran's  $I$  and Getis-Ord  $G_i$ —both define significant spatial autocorrelation as a deviation from a null hypothesis of no spatial autocorrelation at all. However, it is well known that spatial autocorrelation is the norm—indeed, by quoting Tobler above I am perpetuating a major cliche in spatial analysis and geography. If the fact that things near each other are more similar than things farther apart is a *law*, as it is usually put (somewhat cheekily), then establishing measures of spatial autocorrelation based on a null hypothesis makes little sense. How could descriptive statistics of spatial autocorrelation, and models that account for it, better integrate the prior knowledge of some kind of spatial autocorrelation? What effect would that have on the robustness of spatial analyses, especially of those making causal claims?

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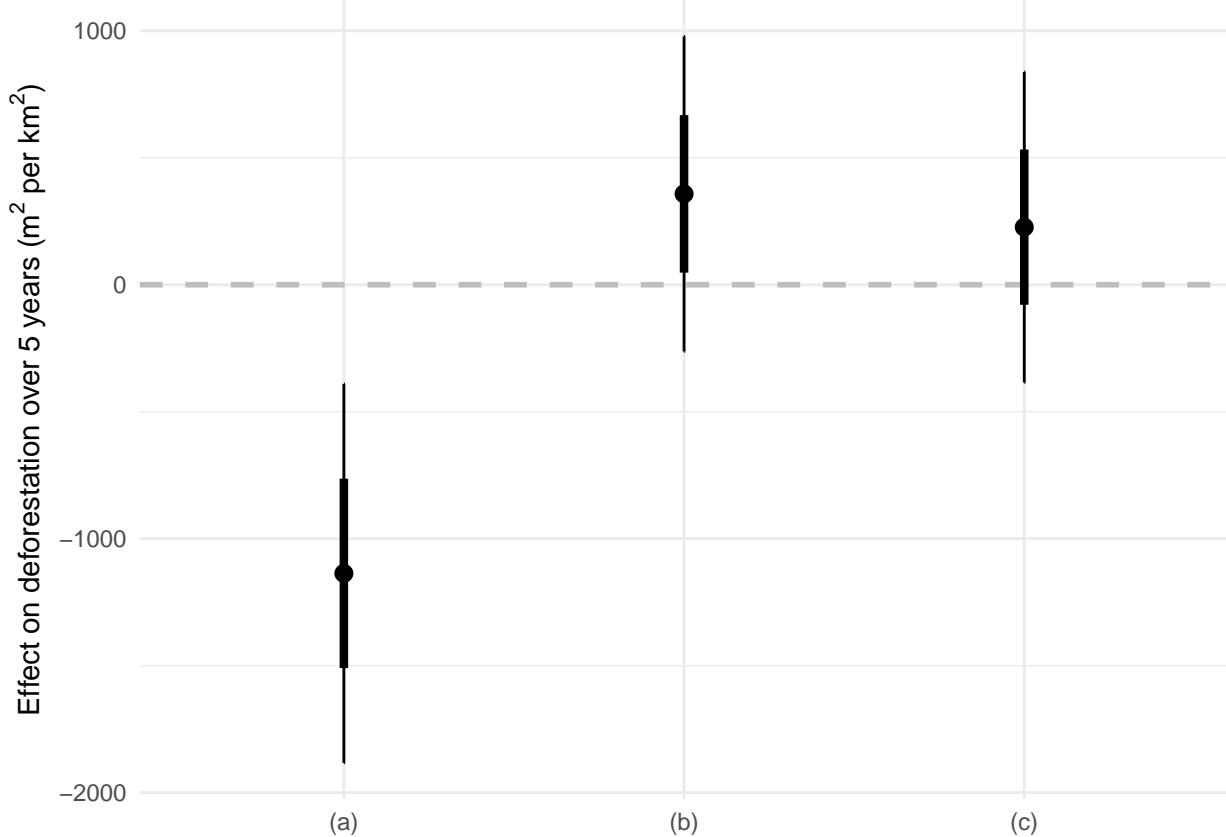
R Core Team. 2019. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. <https://www.R-project.org/>.

Tobler, W. 1970. “A Computer Movie Simulating Urban Growth in the Detroit Region.” *Economic Geography*, no. 46: 234–40.

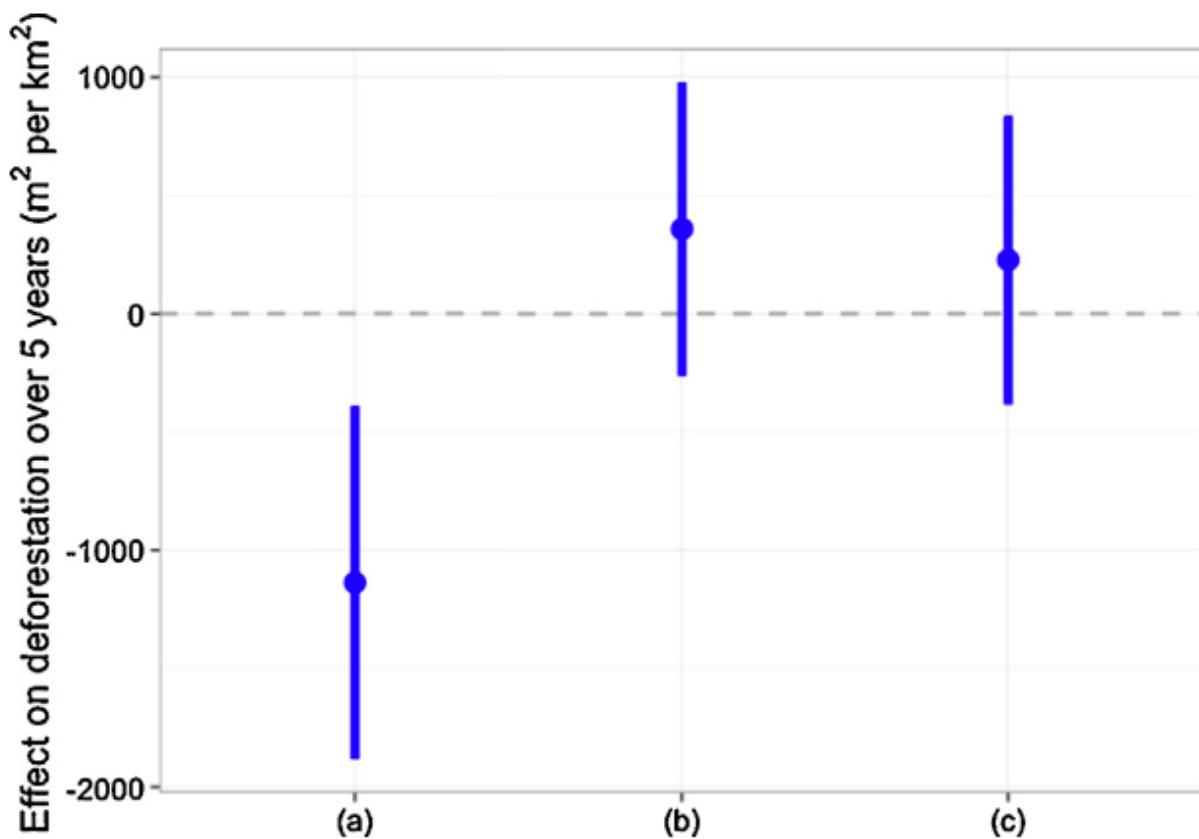
## Appendix: Replication of Key Results

Since this paper is, after matching, a straightforwardly evaluative difference-in-differences model, the key result is the treatment effect of land tenure legalization. In the paper, this is the only result presented—all of the non-treatment variables in the four main regressions were a non-representative set of observations created to isolate the effect of the treatment variable. In this appendix, I exhibit my reproduction of the first two of the four most important graphics in the paper (figures 4 & 5).

The first is figure 4 from the paper (this is the same as was produced for Milestone 5). It shows the treatment effect of legalization on the first set of treated plots, i.e. those that received only the PML legalization, without any other community development planning.

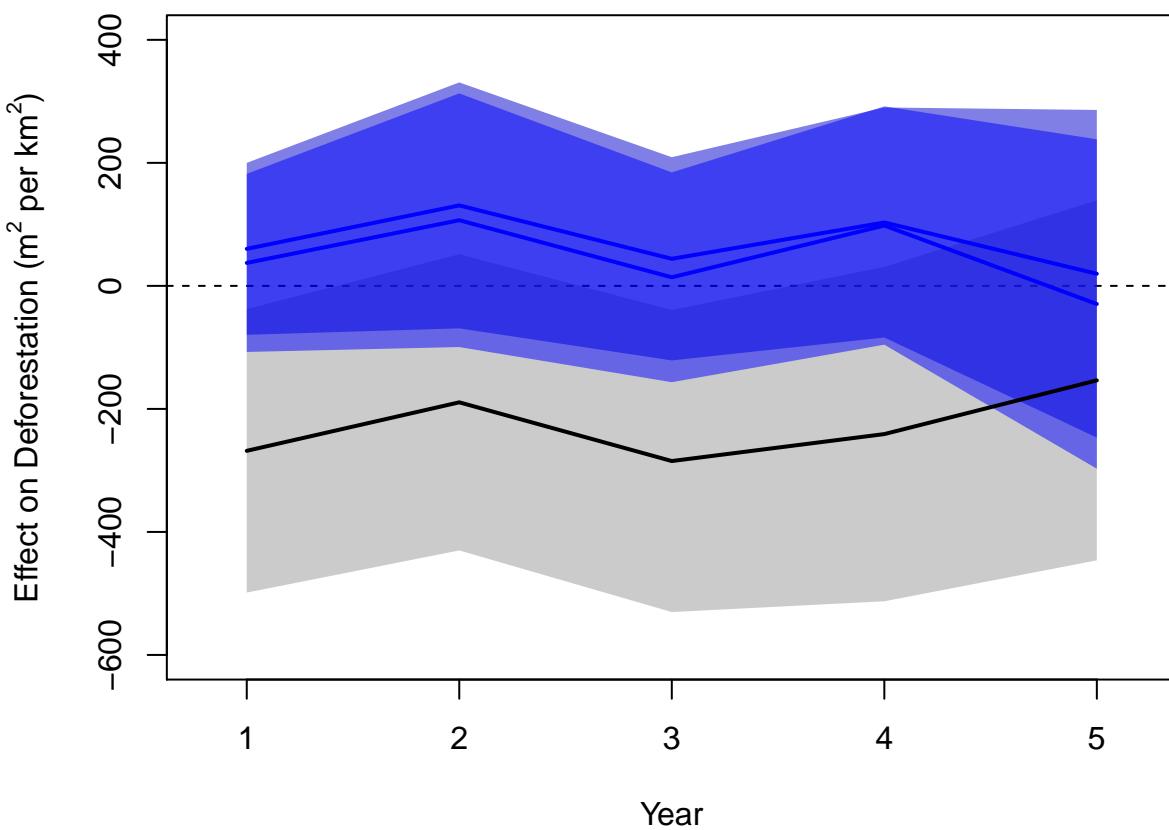


*Replicated fig 4 from original paper: Difference in differences over five years for PSUR plots with legalization plan (PML) and title versus non-PSUR plots with no plan or title, 2002–2012. Notes: Figure shows treatment effect of tenure status for models as follows: (a) covariates, no pre-matching; (b) no covariates, pre-matching; (c) covariates, pre-matching.*



**Fig. 4.** Difference in differences over five years for PSUR plots with legalization plan (PML) and title versus non-PSUR plots with no plan or title, 2002–2012. Notes: Figure shows treatment effect of tenure status for models as follows: (a) covariates, no pre-matching; (b) no covariates, pre-matching; (c) covariates, pre-matching.

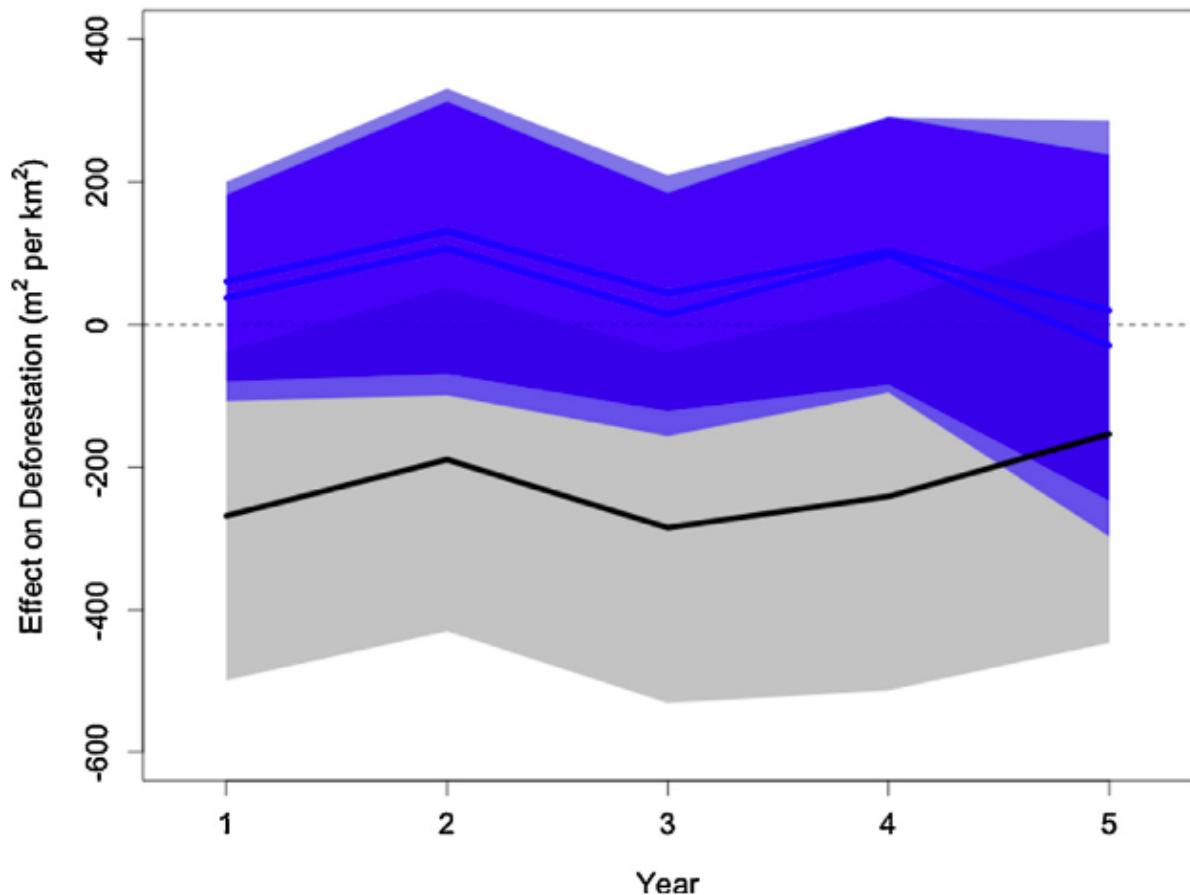
Figure 1: Original figure 4



*Replicated figure 5 from original paper: PML-only effects on an annual basis following treatment. The black line/gray error bars are regression without pre-matching; the blue lines and error bars are regression estimates with pre-matching both with (dark blue) and without (light blue) covariates. The error bars show two standard errors.*

#### Appendix: Supporting Figures and Code

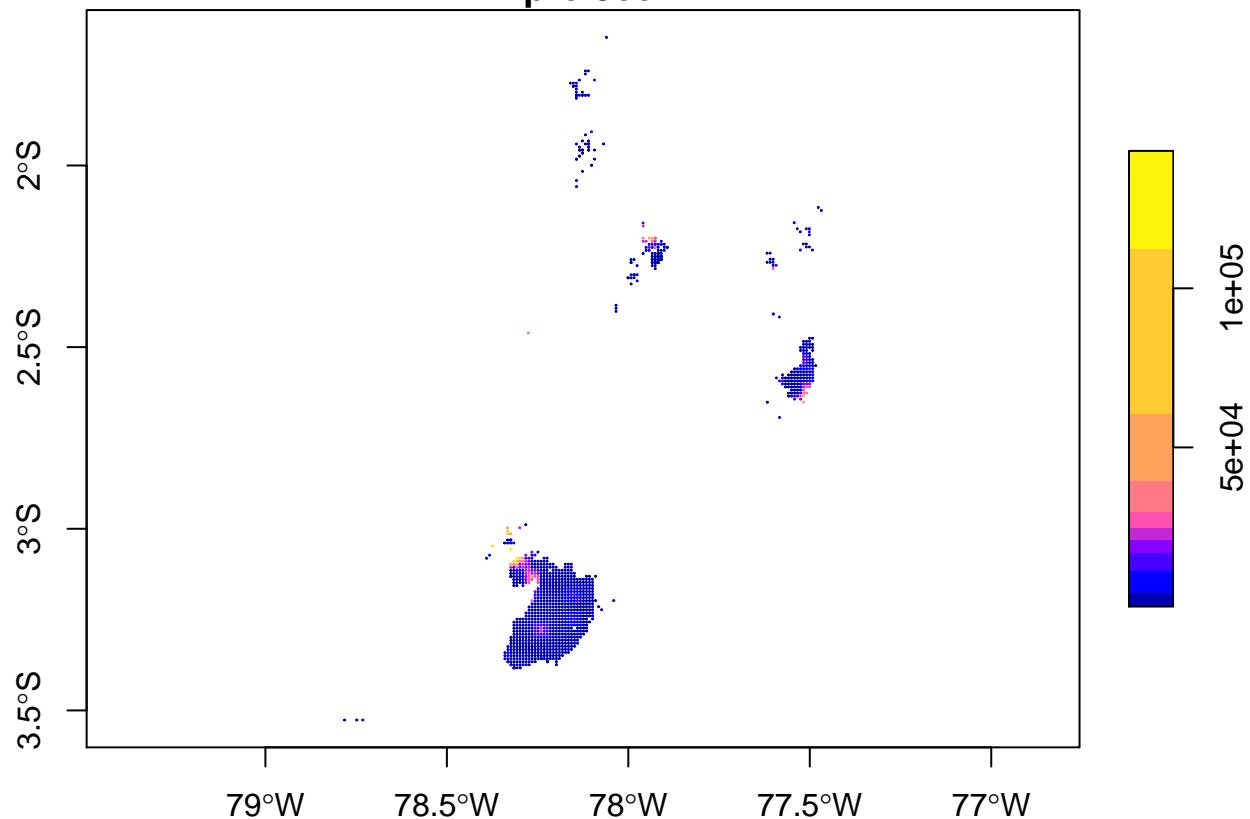
##### Supporting Figures



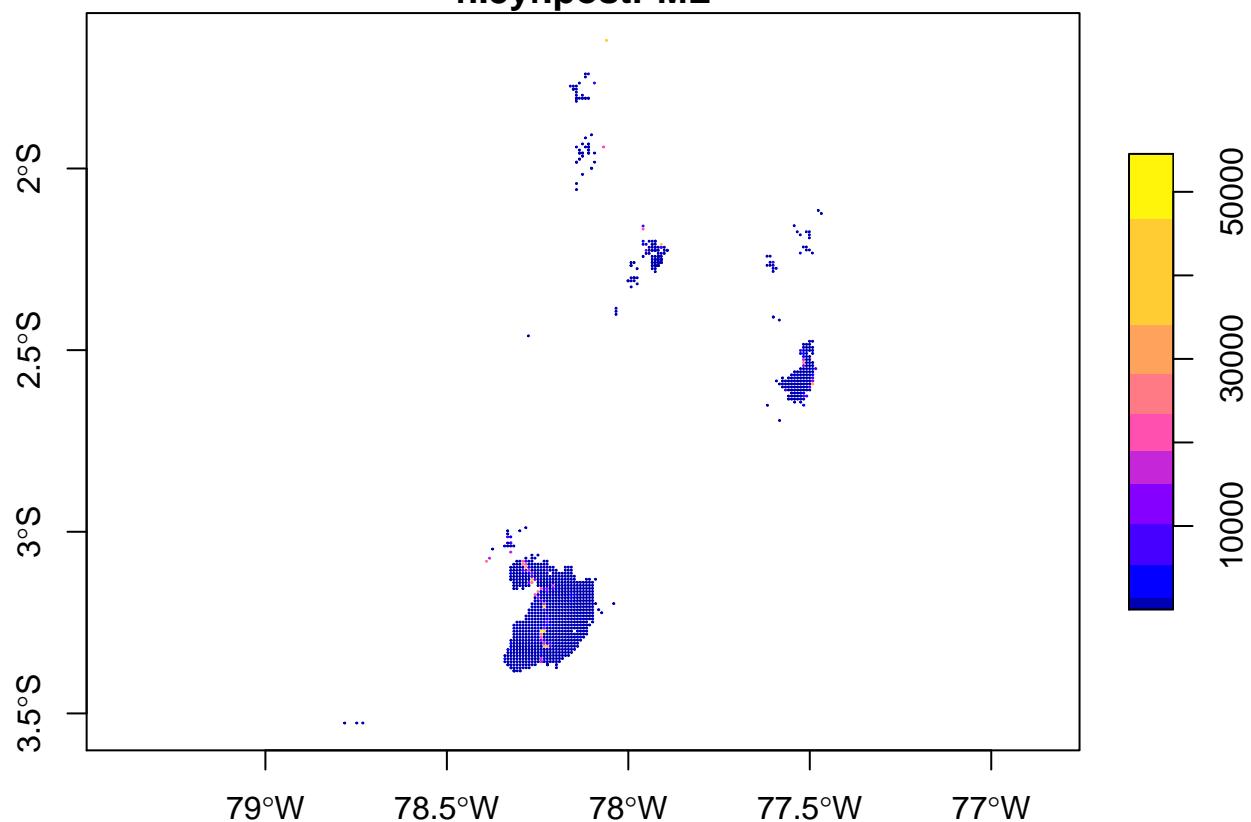
**Fig. 5.** PML-only effects on an annual basis following treatment. Notes: The black line/gray error bars are regression without pre-matching; the blue lines and error bars are regression estimates with pre-matching both with (dark blue) and without (light blue) covariates. The error bars show two standard errors. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

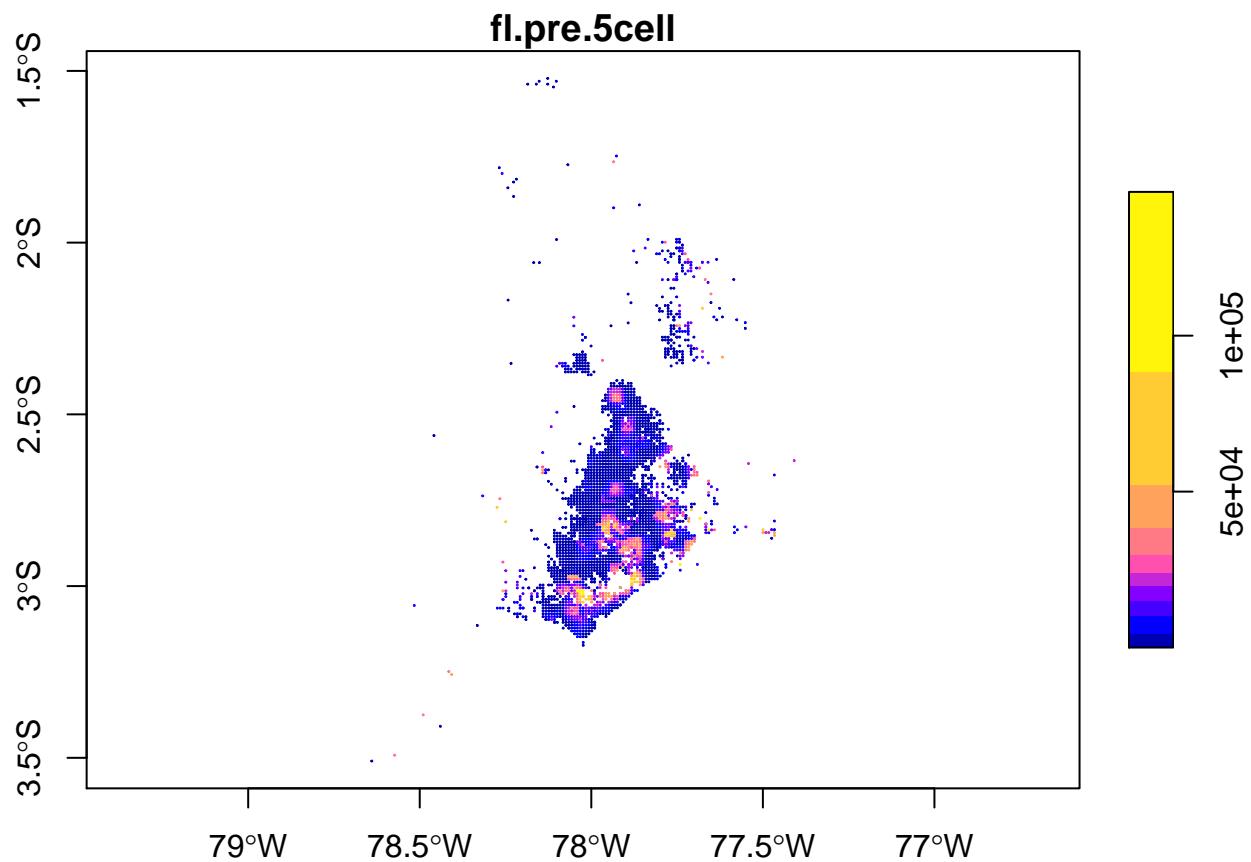
Figure 2: Original figure 4

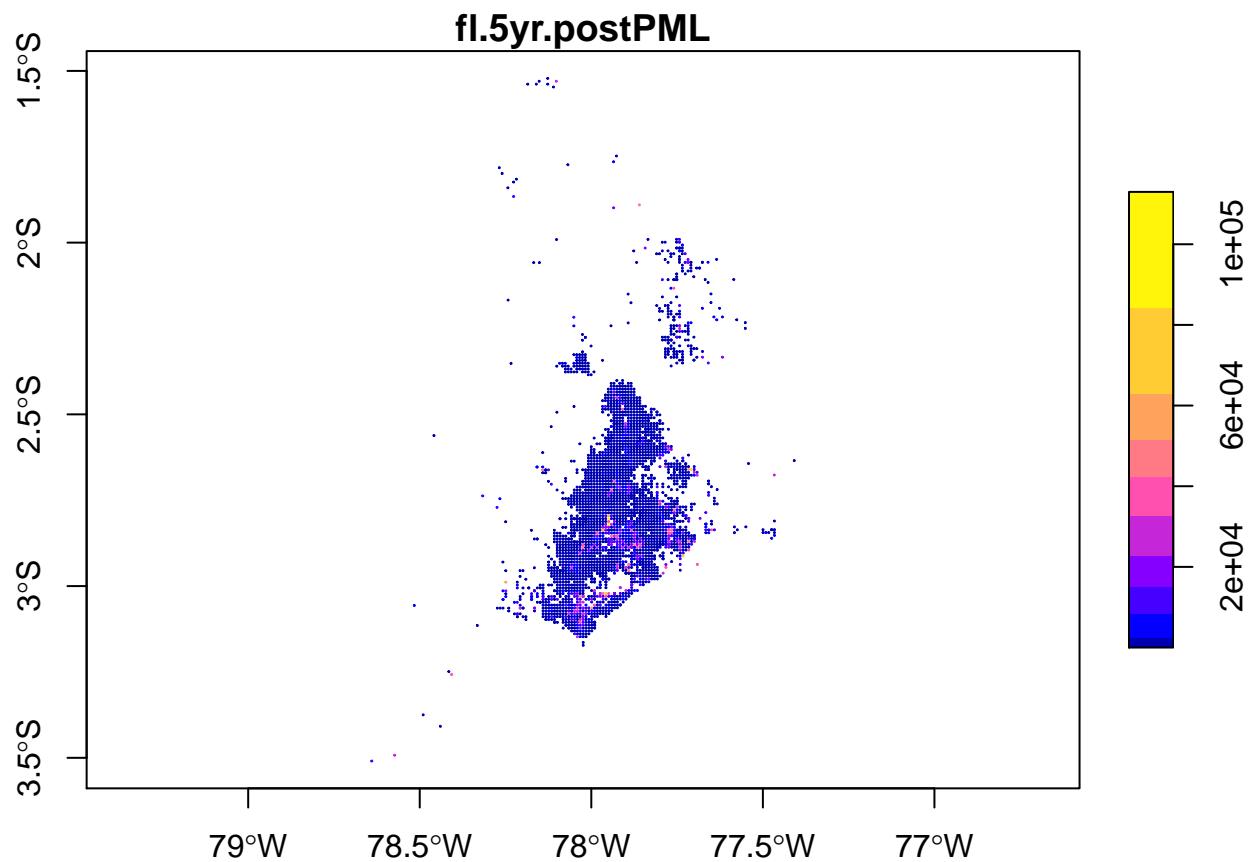
**fl.pre.5cell**

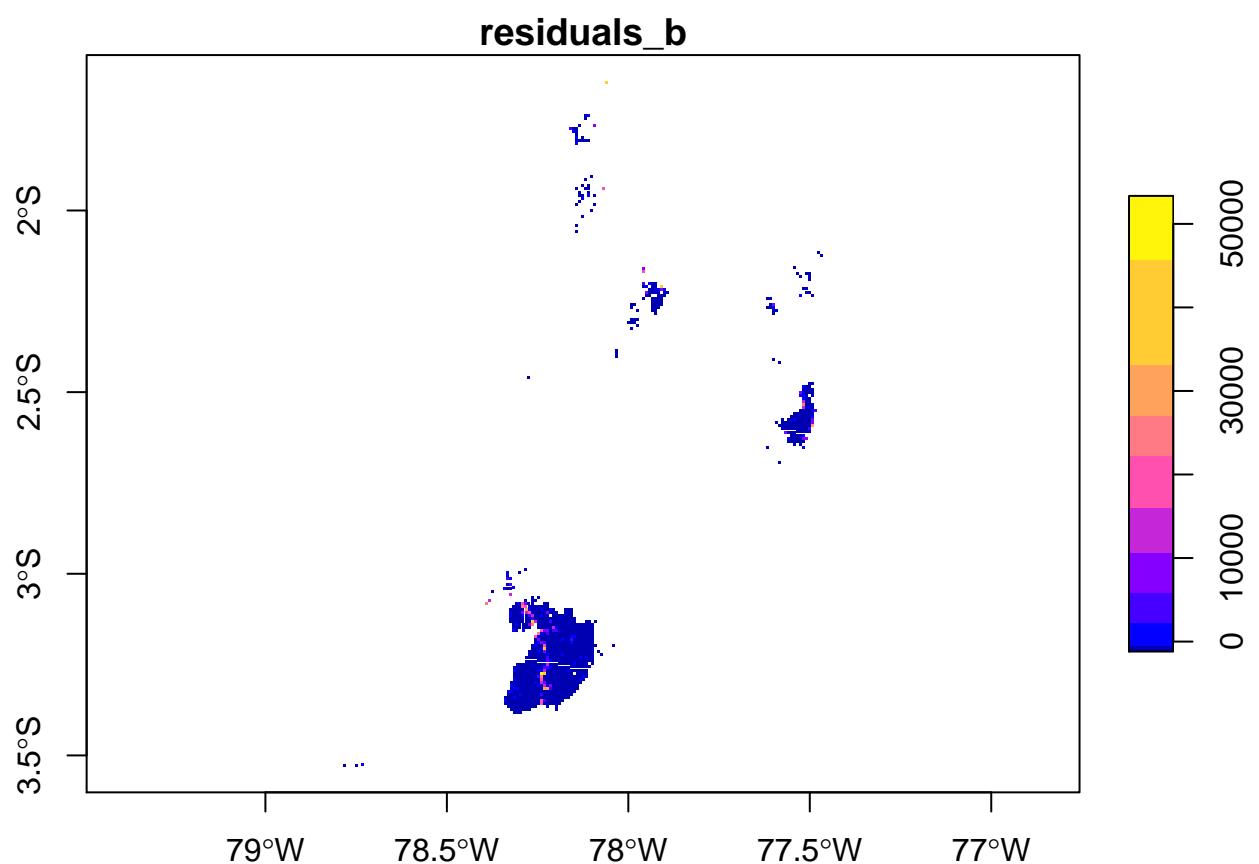


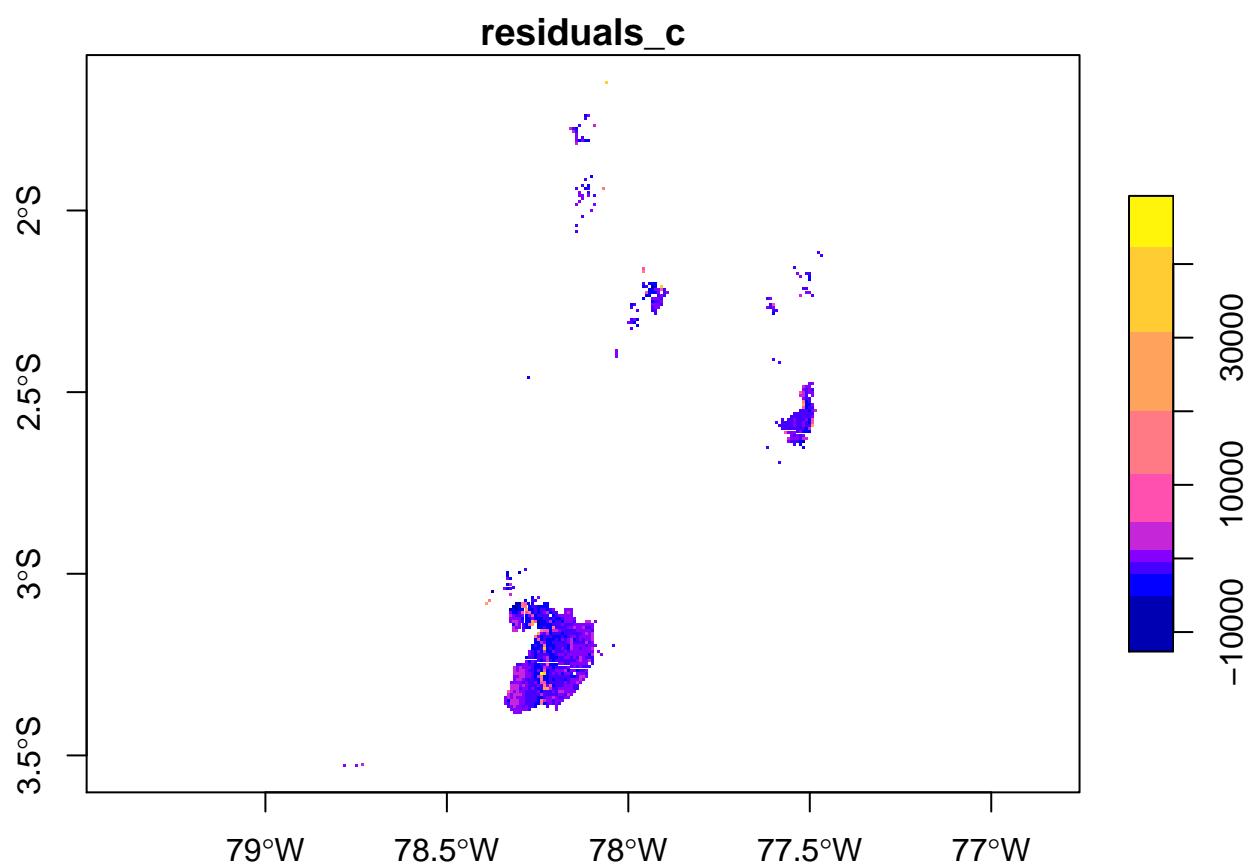
**fl.5yr.postPML**

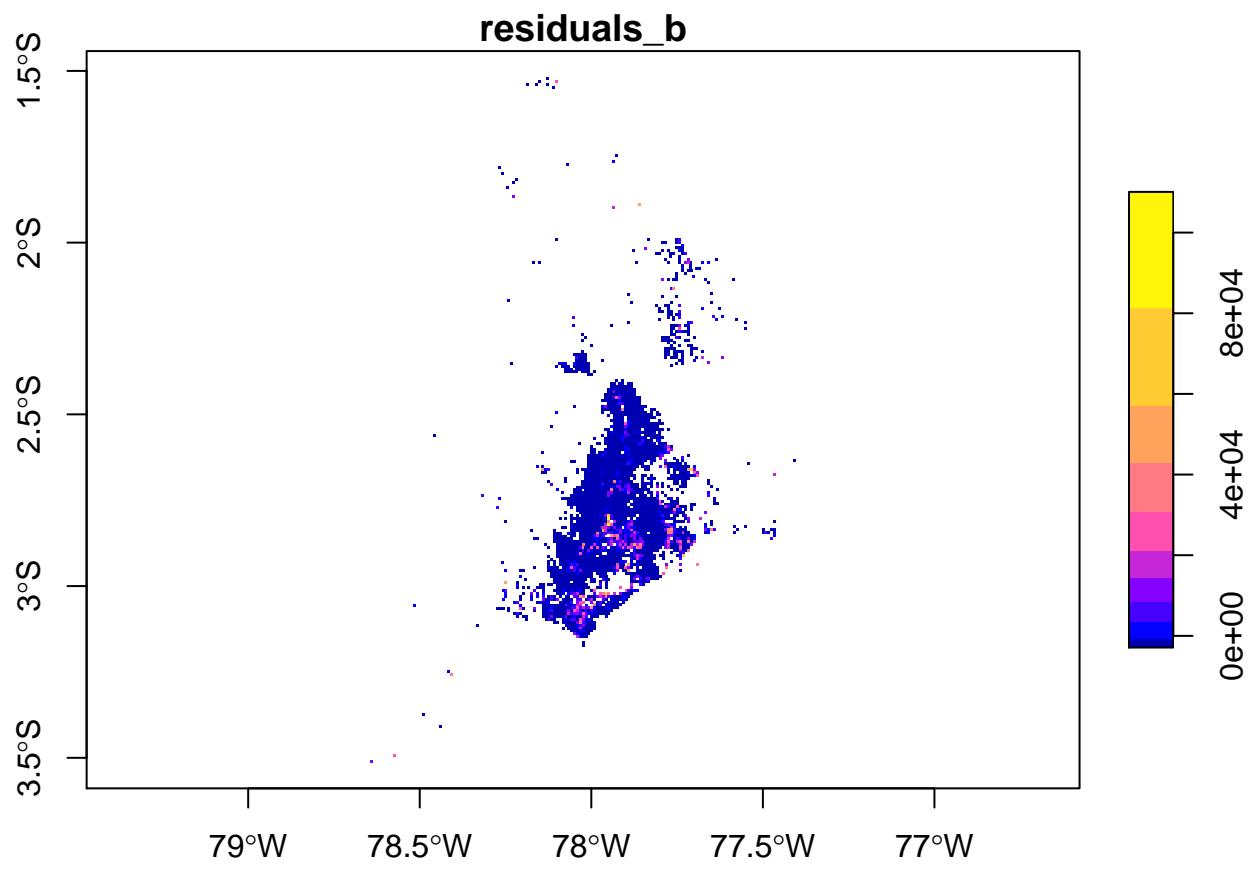




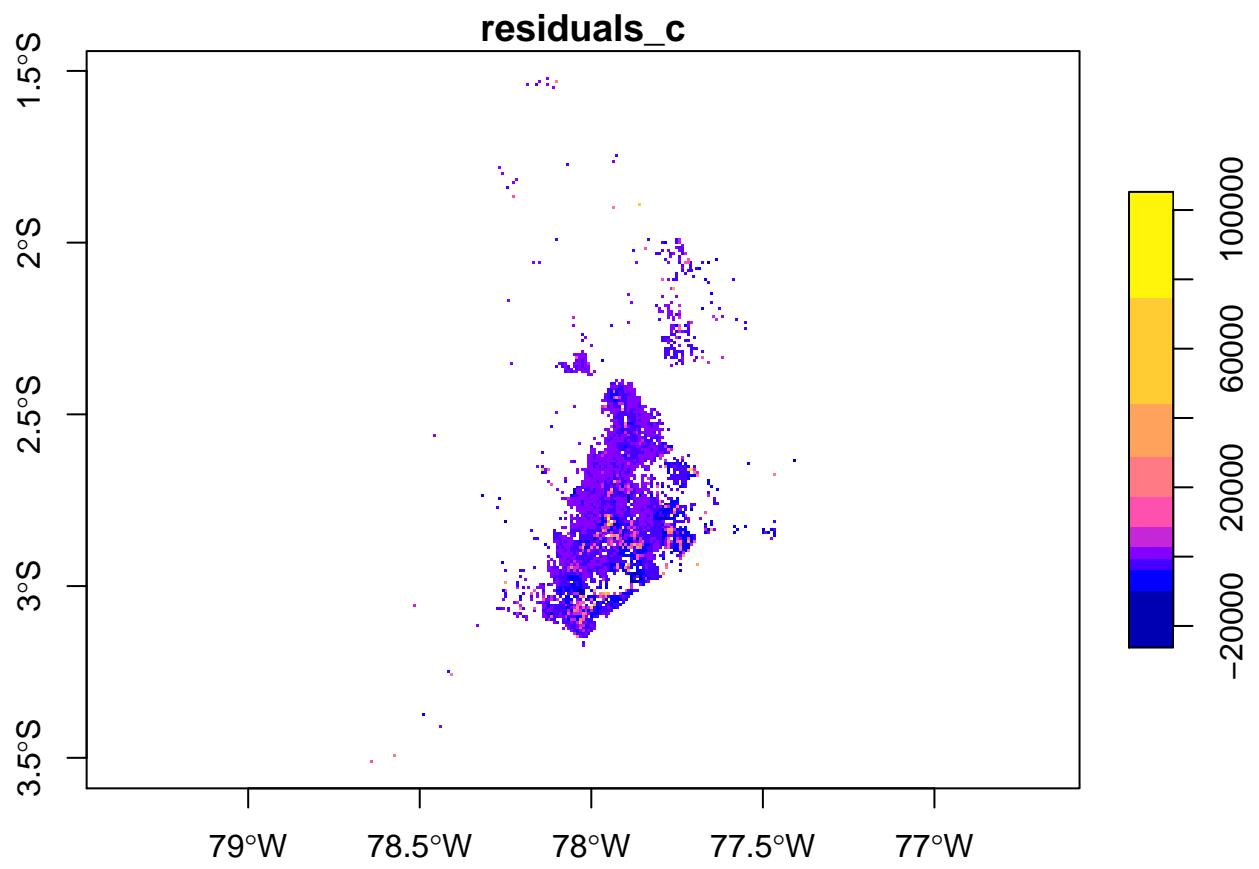




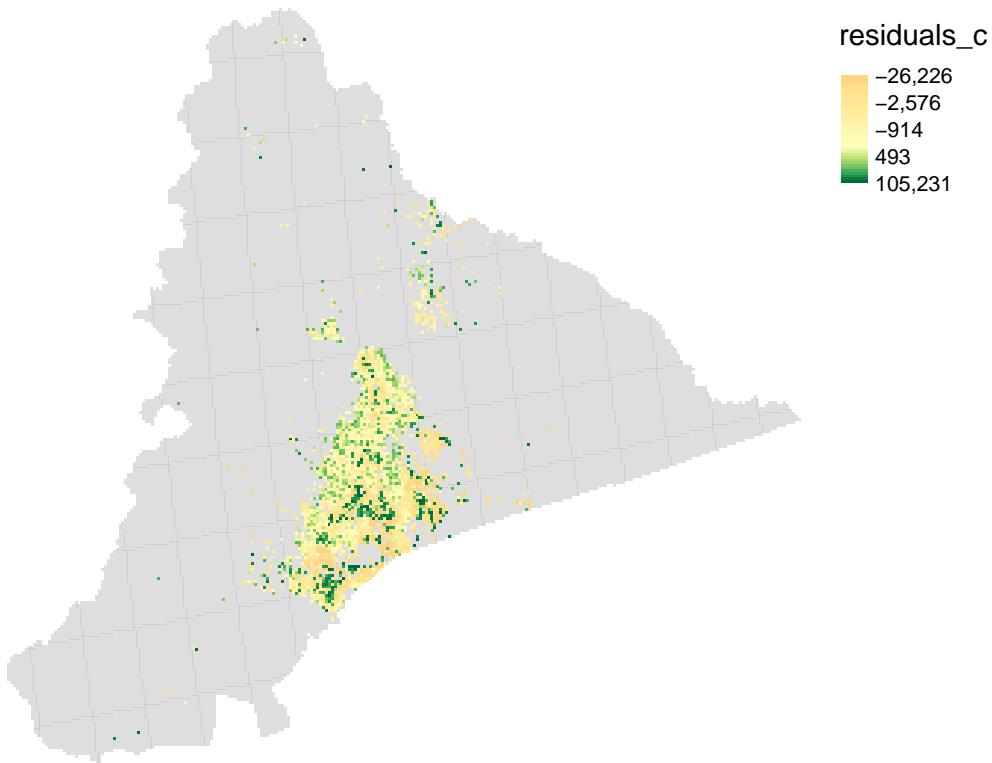




```
## Warning in classInt::classIntervals(v0, min(nbreaks, n.unq), breaks, warnSmallN
## = FALSE): N is large, and some styles will run very slowly; sampling imposed
```



```
## Variable(s) "residuals_c" contains positive and negative values, so midpoint is set to 0. Set midpoint
```



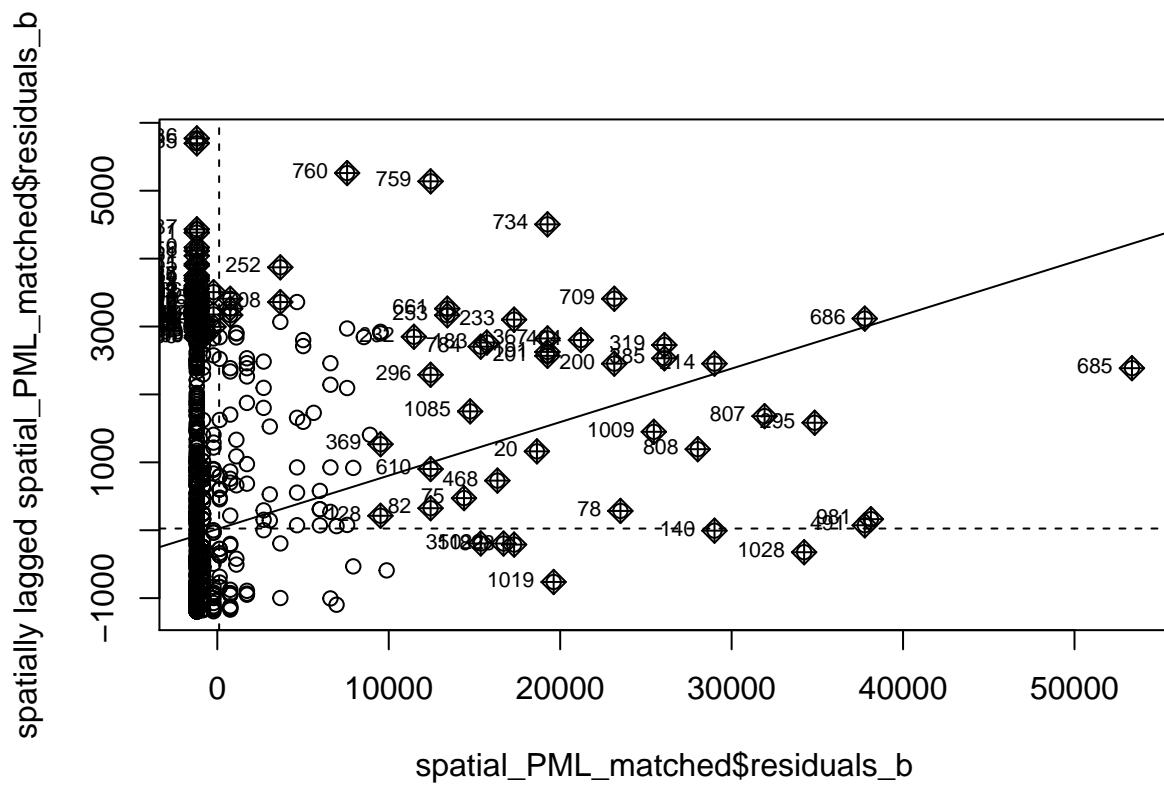
```

## Warning in knearneigh(spatial_PML_matched, k = 40, longlat = TRUE): dnearneigh:
## longlat argument overrides object

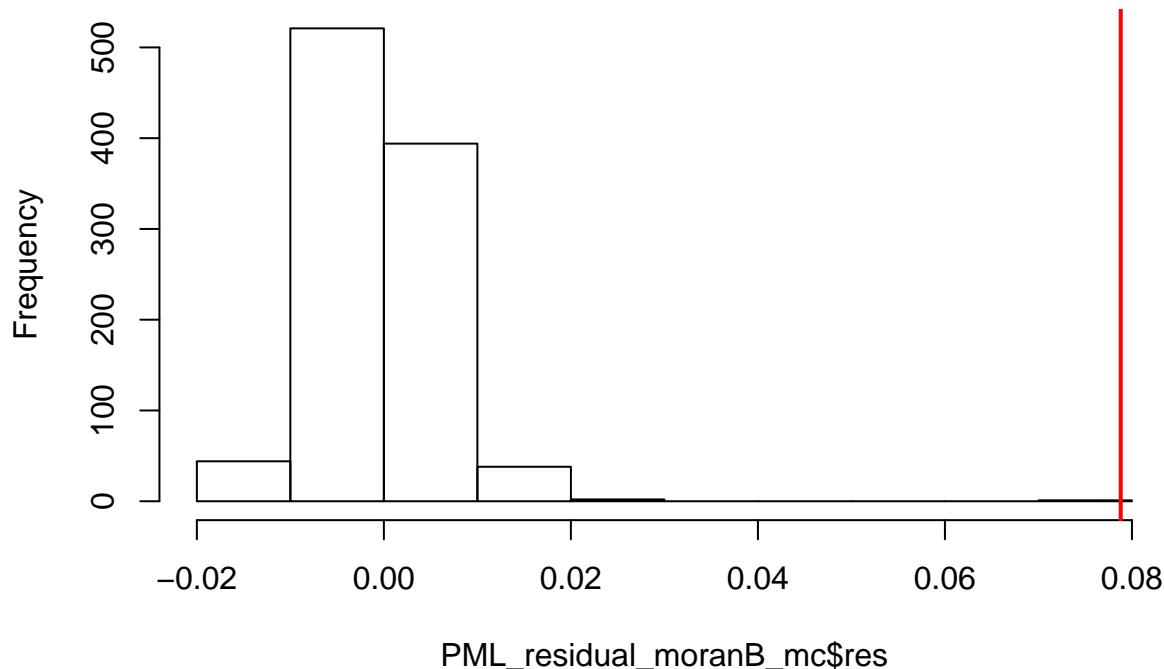
## Warning in knearneigh(spatial_PML_matched, k = 40, longlat = TRUE): knearneigh:
## identical points found

##
## Moran I test under randomisation
##
## data: spatial_PML_matched$residuals_b
## weights: kwl_pml
##
## Moran I statistic standard deviate = 12.897, p-value < 2.2e-16
## alternative hypothesis: greater
## sample estimates:
## Moran I statistic      Expectation      Variance
##    7.880003e-02   -8.896797e-04   3.818127e-05

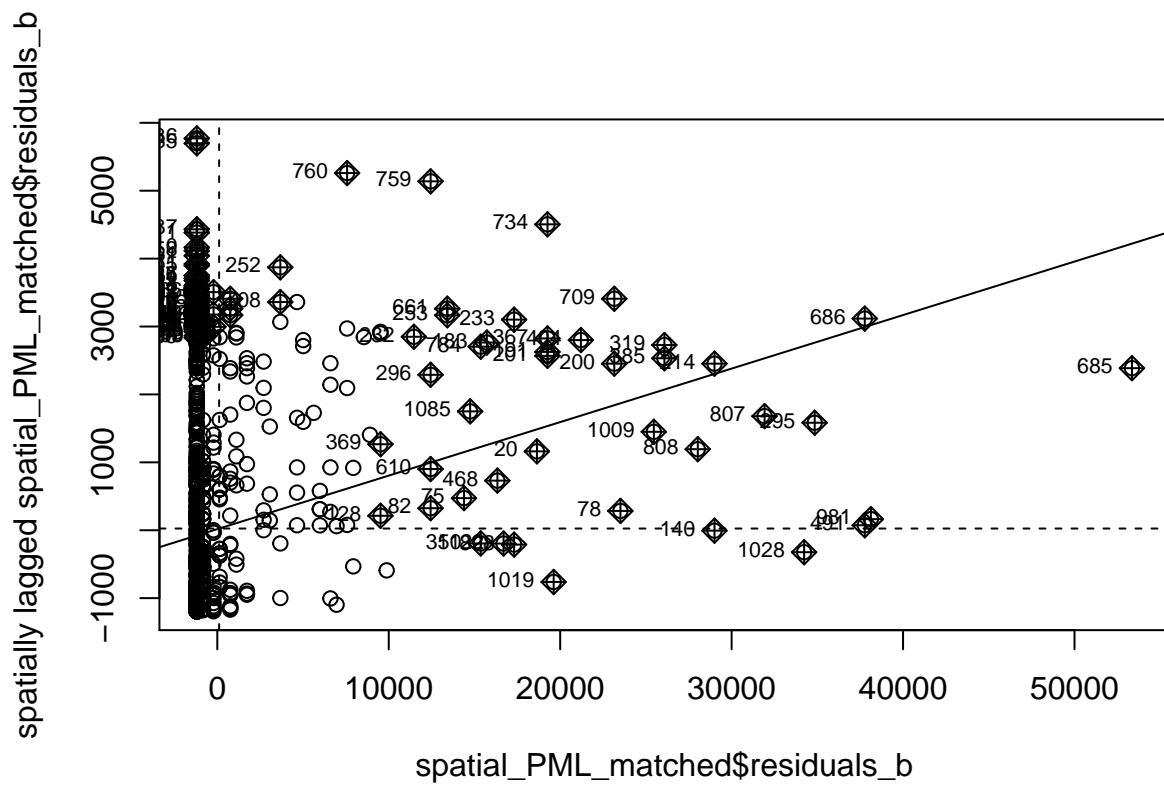
```

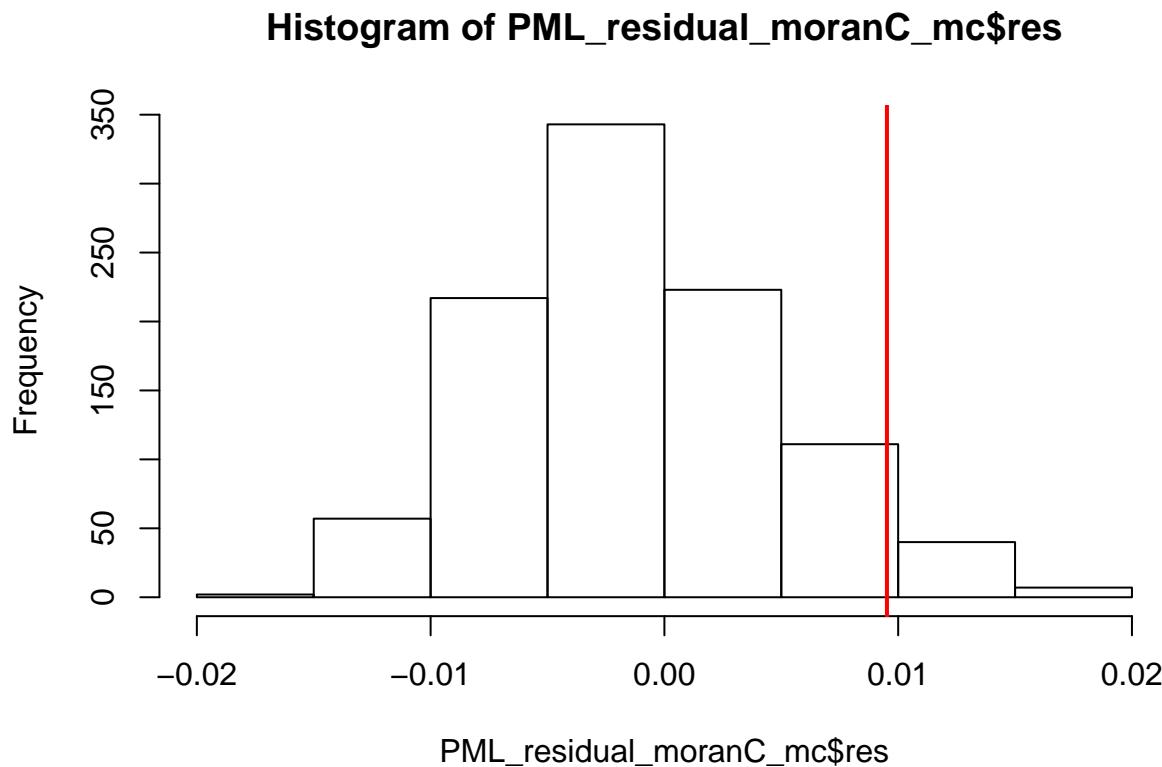


**Histogram of PML\_residual\_moranB\_mc\$res**



```
##  
## Moran I test under randomisation  
##  
## data: spatial_PML_matched$residuals_c  
## weights: kwl_pml  
##  
## Moran I statistic standard deviate = 1.6817, p-value = 0.04631  
## alternative hypothesis: greater  
## sample estimates:  
## Moran I statistic      Expectation      Variance  
##      0.0095198638     -0.0008896797    0.0000383130
```





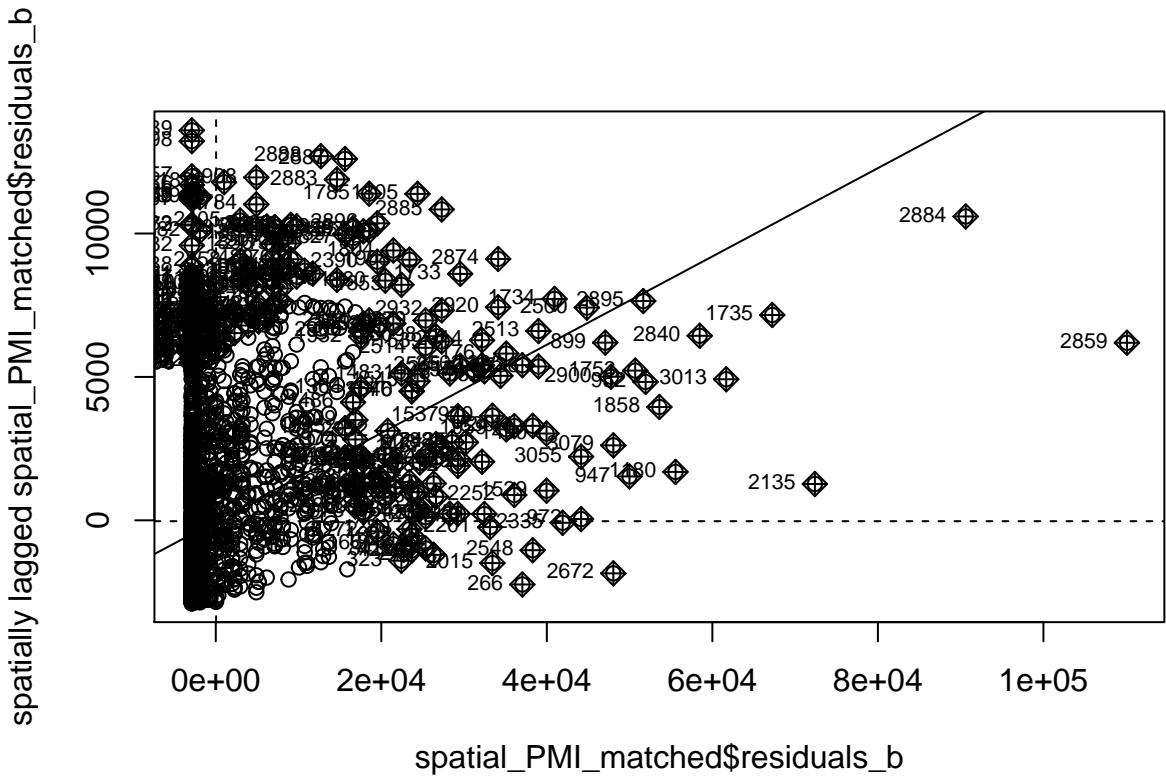
```

## Warning in knearneigh(spatial_PMI_matched, k = 40, longlat = TRUE): dnearneigh:
## longlat argument overrides object

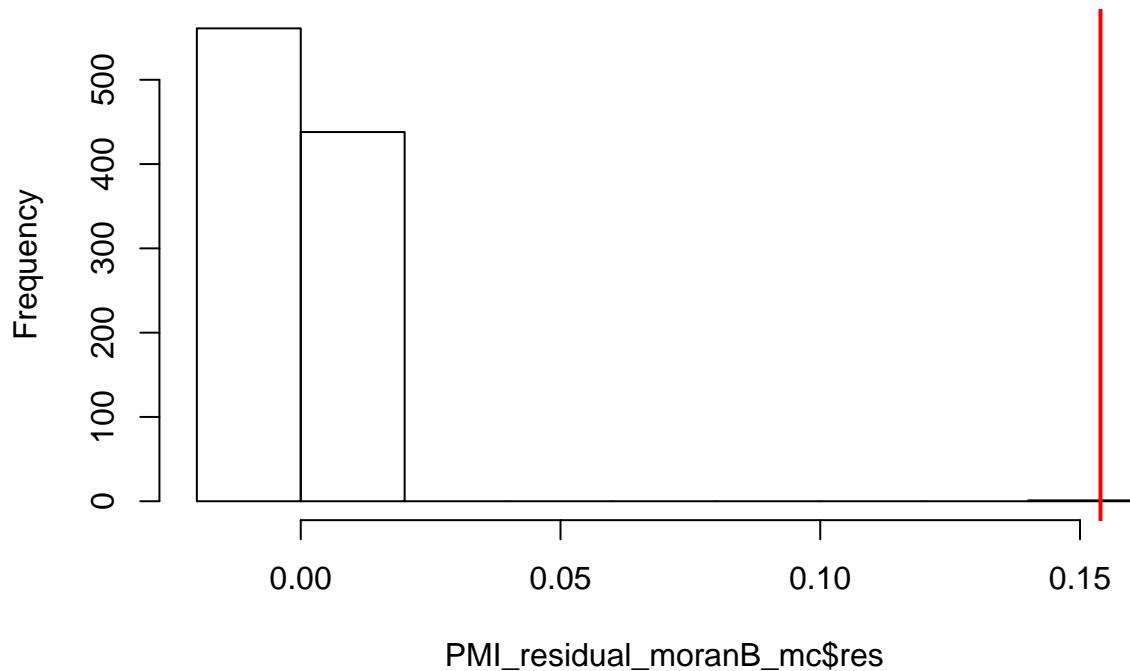
## Warning in knearneigh(spatial_PMI_matched, k = 40, longlat = TRUE): knearneigh:
## identical points found

##
## Moran I test under randomisation
##
## data: spatial_PMI_matched$residuals_b
## weights: kwl_pmi
##
## Moran I statistic standard deviate = 40.37, p-value < 2.2e-16
## alternative hypothesis: greater
## sample estimates:
## Moran I statistic      Expectation      Variance
##        1.539469e-01     -3.215434e-04    1.460313e-05

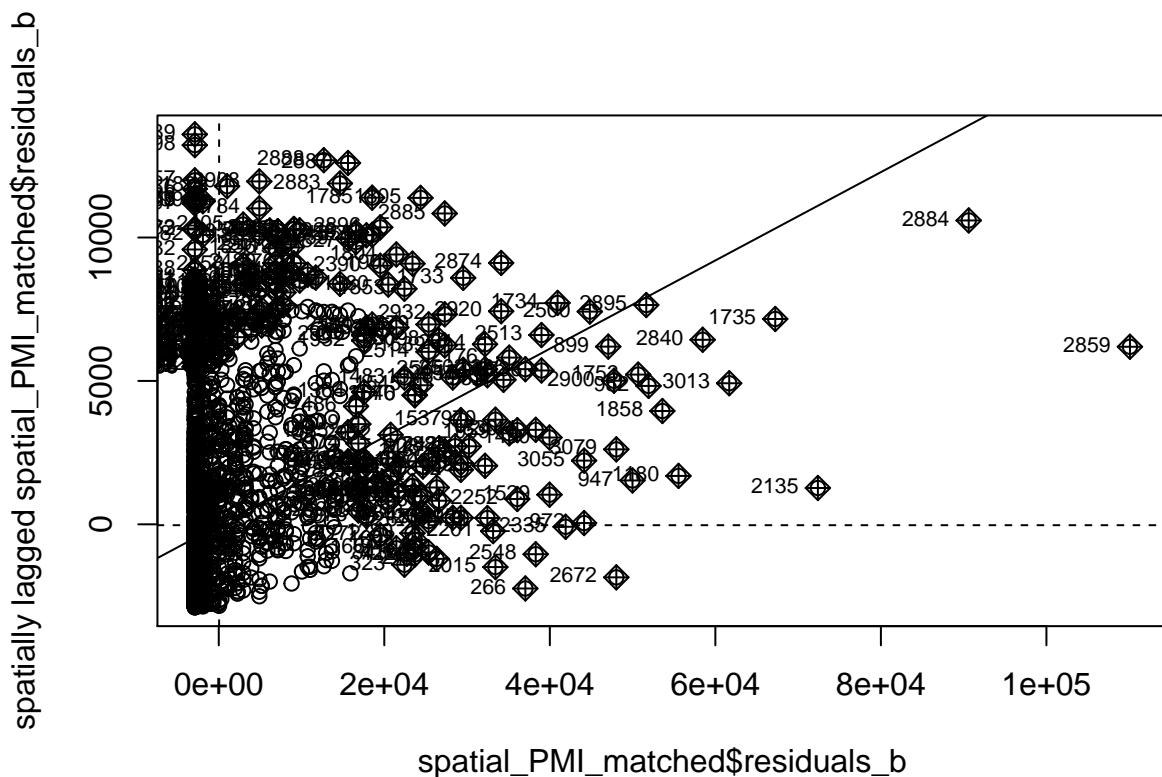
```

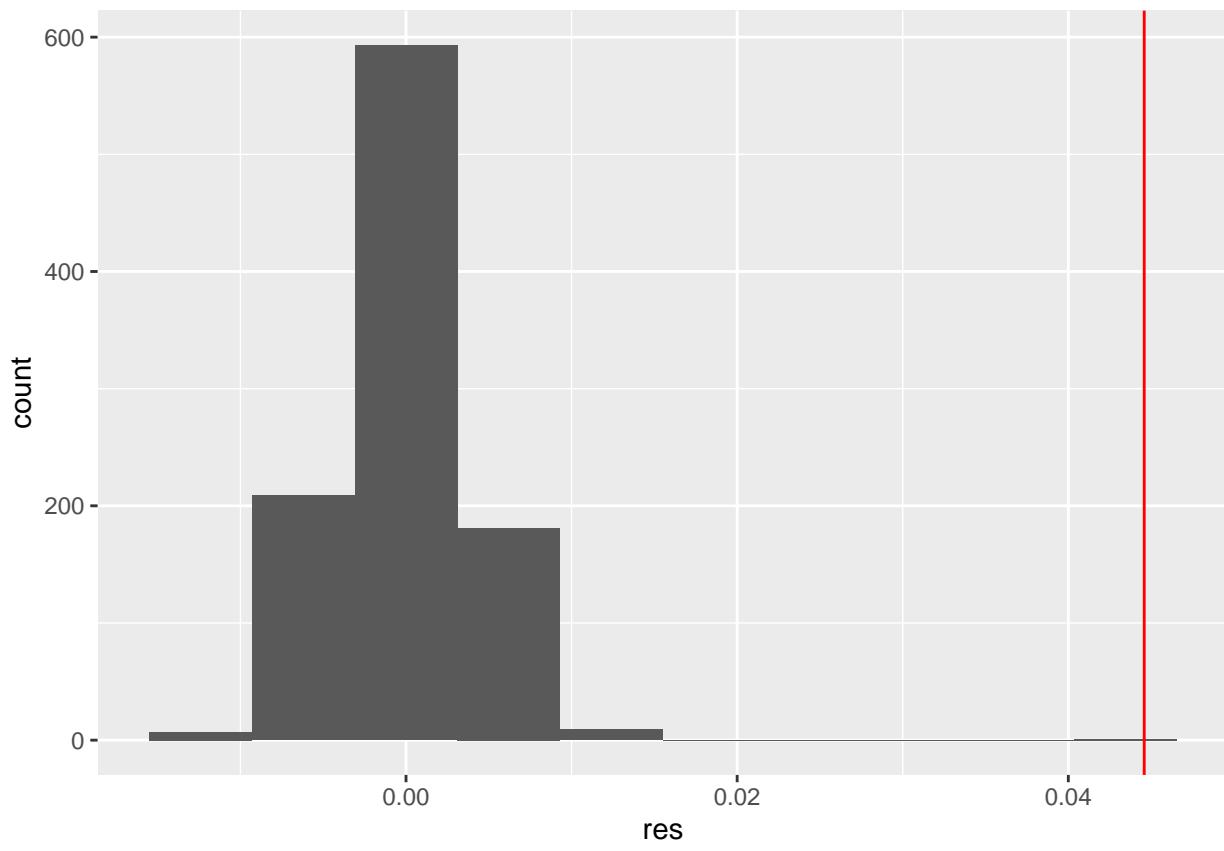


**Histogram of PMI\_residual\_moranB\_mc\$res**

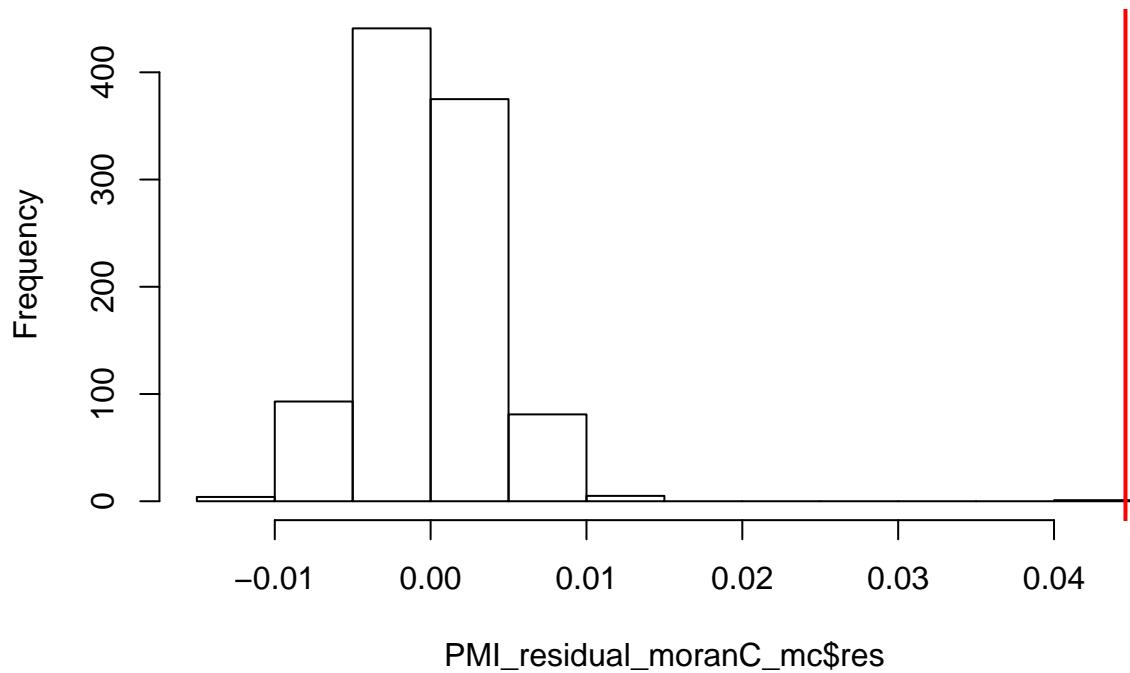


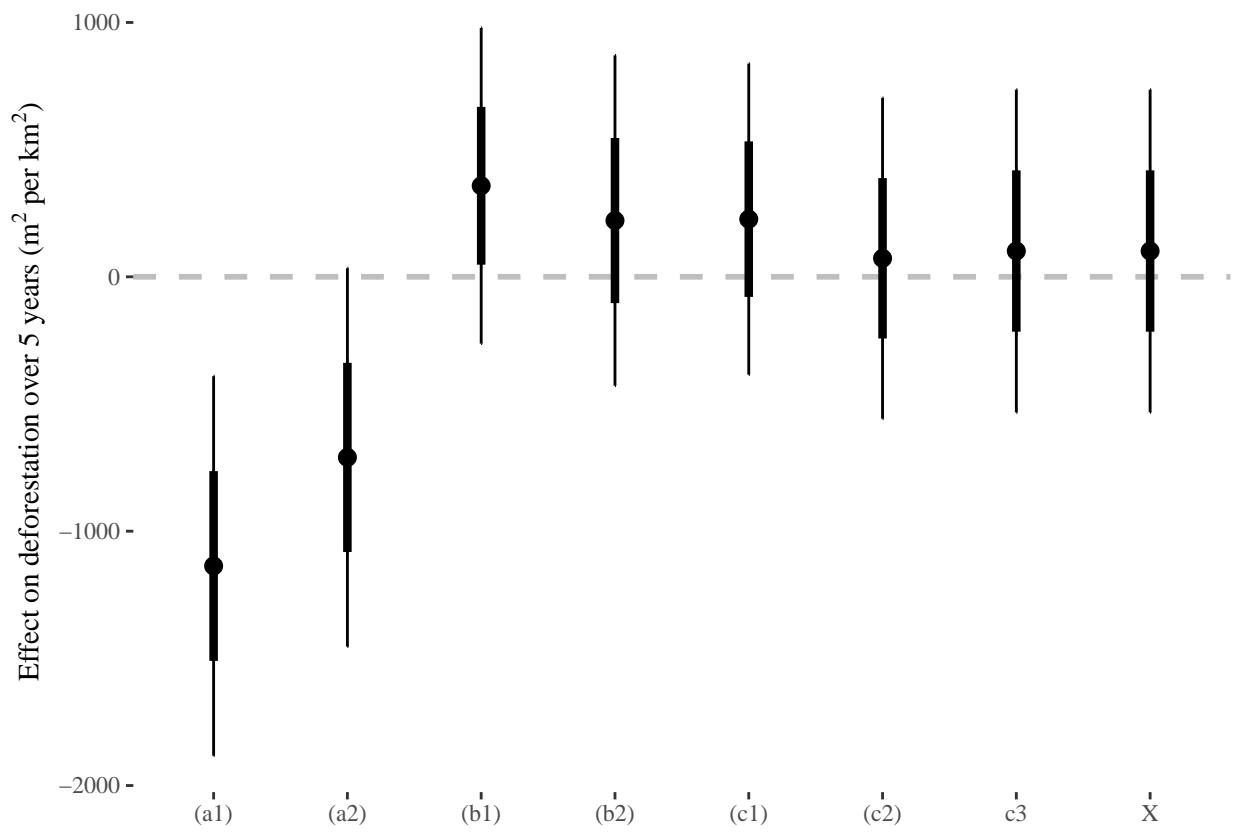
```
##  
## Moran I test under randomisation  
##  
## data: spatial_PMI_matched$residuals_c  
## weights: kwl_pmi  
##  
## Moran I statistic standard deviate = 11.755, p-value < 2.2e-16  
## alternative hypothesis: greater  
## sample estimates:  
## Moran I statistic      Expectation      Variance  
##        4.458401e-02    -3.215434e-04   1.459238e-05
```

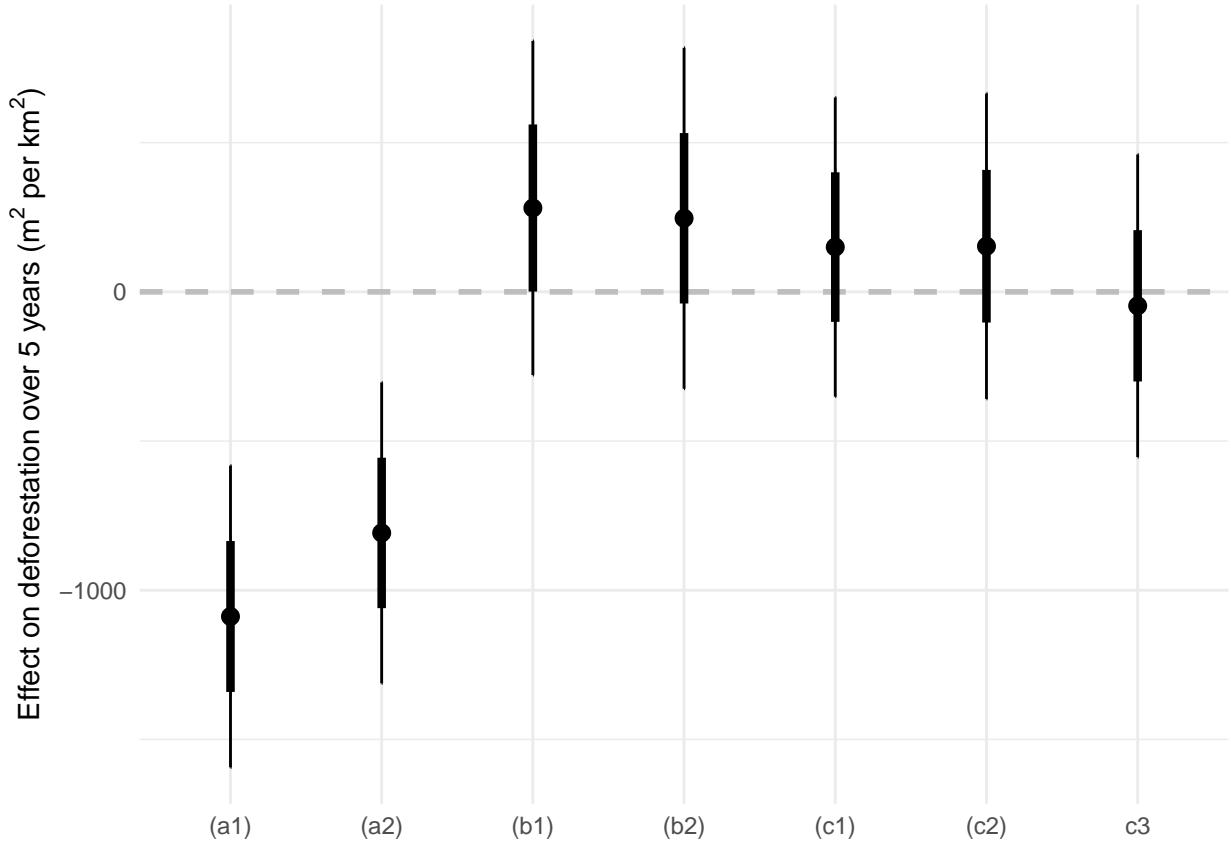




**Histogram of PMI\_residual\_moranC\_mc\$res**







## Supporting Code

```

# run an lag model for each of the original paper's post-matching models.
# (Can try with the rematched ones later if I have time)

# PML only lags
# PML only weights have only been made for spatialized or rematched
# versions so far, so need to do it again

knn_pml <- knearneigh(spatial_PML_matched,
                       k = 40, longlat = TRUE)
knn_pml <- knn2nb(knn_pml)
kwl_pml <- nb2listw(neighbours = knn_pml, style = 'W')

PML_lag_nocov <- lagsarlm(f1.5yr.postPML ~ PML, weights = "weights",
                            data = data.PMLonly.flat.matched, listw = kwl_pml)

PML_lag_cov <- lagsarlm(f1.5yr.postPML ~ PML + fl.pre.5cell +
                         forest.pre + pop.den.5km.pre + dist.disturb.pre +
                         A128 + A129 + A130 + A154 + A347 + A361 + A362, weights = weights,
                         listw = kwl_pml, data = data.PMLonly.flat.matched)

# PMI lags
PMI_lag_nocov <- lagsarlm(f1.5yr.postPML ~ PML, weights = weights,
                           data = data.PMI.flat.matched, listw = kwl_pmi)

```

```

PMI_lag_cov <- lagsarlm(f1.5yr.postPML ~ PML + f1.pre.5cell +
                         forest.pre + pop.den.5km.pre + dist.disturb.pre + A128 + A129 + A130 + A154 + A347 + A36
                         data = data.PMI.flat.matched)

impacts(PML_lag_nocov, listw=weights)
impacts(PML_lag_cov, listw=weights)
impacts(PMI_lag_nocov, listw=weights)
impacts(PMI_lag_cov, listw=weights)

# lag residuals mapping
# attach residuals

spatial_PML_matched$lag_nocov_resid <- residuals(PML_lag_nocov)
spatial_PML_matched$lag_cov_resid <- residuals(PML_lag_cov)
spatial_PMI_matched$lag_nocov_resid <- residuals(PMI_lag_nocov)
spatial_PMI_matched$lag_cov_resid <- residuals(PMI_lag_cov)

# make maps
tm_shape(spatialized_data) +
  tm_symbols(border.lwd = 0, size = 0.01,
             col = "grey", shape = 15,
             alpha = 0.5) +
  tm_layout(legend.outside = TRUE, frame = FALSE,
            fontfamily = "serif") +
  tm_shape(spatial_PML_matched) +
  tm_symbols(border.lwd = 0, size = 0.01,
             shape = 15, style = "order",
             col = "(PML_lag_nocov", palette = "RdYlGn",
             contrast = c(0, 1))

tm_shape(spatialized_data) +
  tm_symbols(border.lwd = 0, size = 0.01,
             col = "grey", shape = 15,
             alpha = 0.5) +
  tm_layout(legend.outside = TRUE, frame = FALSE,
            fontfamily = "serif") +
  tm_shape(spatial_PML_matched) +
  tm_symbols(border.lwd = 0, size = 0.01,
             shape = 15, style = "order",
             col = "(PML_lag_cov", palette = "RdYlGn",
             contrast = c(0, 1))

tm_shape(spatialized_data) +
  tm_symbols(border.lwd = 0, size = 0.01,
             col = "grey", shape = 15,
             alpha = 0.5) +
  tm_layout(legend.outside = TRUE, frame = FALSE,
            fontfamily = "serif") +
  tm_shape(spatial_PMI_matched) +
  tm_symbols(border.lwd = 0, size = 0.01,
             shape = 15, style = "order",
             col = "(PMI_lag_nocov", palette = "RdYlGn",
             contrast = c(0, 1))

```

```

tm_shape(spatialized_data) +
  tm_symbols(border.lwd = 0, size = 0.01,
             col = "grey", shape = 15,
             alpha = 0.5) +
  tm_layout(legend.outside = TRUE, frame = FALSE,
            fontfamily = "serif") +
  tm_shape(spatial_PMI_matched) +
  tm_symbols(border.lwd = 0, size = 0.01,
             shape = 15, style = "order",
             col = "(PMI_lag_cov)", palette = "RdYlGn",
             contrast = c(0, 1))

# simulations and plotting
# run sims

PML_lag_nocov_residual_moran <-
  moran.test(x = spatial_PML_matched$lag_nocov_resid,
             listw = kwl_pml)
PML_lag_nocov_residual_moran_mc <- moran.mc(spatial_PML_matched$lag_nocov_resid,
                                              kwl_pml, nsim = 999)

PML_lag_cov_residual_moran <-
  moran.test(x = spatial_PML_matched$lag_cov_resid,
             listw = kwl_pml)
PML_lag_cov_residual_moran_mc <- moran.mc(spatial_PML_matched$lag_cov_resid,
                                             kwl_pml, nsim = 999)

PMI_lag_nocov_residual_moran <-
  moran.test(x = spatial_PMI_matched$lag_nocov_resid,
             listw = kwl_pmi)
PMI_lag_nocov_residual_moran_mc <- moran.mc(spatial_PMI_matched$lag_nocov_resid,
                                               kwl_pmi, nsim = 999)

PMI_lag_cov_residual_moran <-
  moran.test(x = spatial_PML_matched$lag_cov_resid,
             listw = kwl_pmi)
PMI_lag_cov_residual_moran_mc <- moran.mc(spatial_PMI_matched$lag_cov_resid,
                                             kwl_pmi, nsim = 999)

# plot the sims and observed

x <- as.data.frame(PML_lag_nocov_residual_moran_mc$res)
x <- x %>%
  mutate(res = PML_lag_nocov_residual_moran_mc$res)
x %>%
  ggplot(aes(x = res)) +
  geom_histogram(bins = 20, alpha = 0.4, position = "identity") +
  geom_vline(
    xintercept = PML_lag_nocov_residual_moran[['estimate']][['Moran I statistic']],
    colour = "red") +
  theme_tufte() +
  labs(x = "Moran's I value")

```

```

x <- as.data.frame(PML_lag_cov_residual_moran_mc$res)
x <- x %>%
  mutate(res = PML_lag_cov_residual_moran_mc$res)
x %>%
  ggplot(aes(x = res)) +
  geom_histogram(bins = 20, alpha = 0.4, position = "identity") +
  geom_vline(
    xintercept = PML_lag_cov_residual_moran[['estimate']]['Moran I statistic'],
    colour = "red") +
  theme_tufte() +
  labs(x = "Moran's I value")

x <- as.data.frame(PMI_lag_nocov_residual_moran_mc$res)
x <- x %>%
  mutate(res = PMI_lag_nocov_residual_moran_mc$res)
x %>%
  ggplot(aes(x = res)) +
  geom_histogram(bins = 20, alpha = 0.4, position = "identity") +
  geom_vline(
    xintercept = PMI_lag_nocov_residual_moran[['estimate']]['Moran I statistic'],
    colour = "red") +
  theme_tufte() +
  labs(x = "Moran's I value")

x <- as.data.frame(PMI_lag_cov_residual_moran_mc$res)
x <- x %>%
  mutate(res = PMI_lag_cov_residual_moran_mc$res)
x %>%
  ggplot(aes(x = res)) +
  geom_histogram(bins = 20, alpha = 0.4, position = "identity") +
  geom_vline(
    xintercept = PMI_lag_cov_residual_moran[['estimate']]['Moran I statistic'],
    colour = "red") +
  theme_tufte() +
  labs(x = "Moran's I value")

# PML only error models
PML_err_nocov <- spatialreg::errorsarlm(fl.5yr.postPML ~ PML, weights = weights,
                                         data = data.PMLonly.flat.matched, listw = kwl_pml)

PML_err_cov <- errorsarlm(fl.5yr.postPML ~ PML + fl.pre.5cell +
                           forest.pre + pop.den.5km.pre + dist.disturb.pre +
                           A128 + A129 + A130 + A154 + A347 + A361 + A362,
                           weights = weights, listw = kwl_pml,
                           data = data.PMLonly.flat.matched)

# PMI lags

PMI_err_nocov <- errorsarlm(fl.5yr.postPML ~ PML, weights = weights,
                             data = data.PMI.flat.matched, listw = kwl_pmi)

PMI_err_cov <- errorsarlm(fl.5yr.postPML ~ PML + fl.pre.5cell +
                           forest.pre + pop.den.5km.pre + dist.disturb.pre +
                           A128 + A129 + A130 + A154 + A347 + A361 + A362,
                           weights = weights, listw = kwl_pmi,
                           data = data.PMI.flat.matched)

```

```

A128 + A129 + A130 + A154 + A347 + A361 + A362,
weights = weights, listw = kwl_pmi,
data = data.PMI.flat.matched)

# attach residuals

spatial_PML_matched$err_nocov_resid <- residuals(PML_err_nocov)
spatial_PML_matched$err_cov_resid <- residuals(PML_err_cov)
spatial_PMI_matched$err_nocov_resid <- residuals(PMI_err_nocov)
spatial_PMI_matched$err_cov_resid <- residuals(PMI_err_cov)

# make maps
tm_shape(spatialized_data) +
  tm_symbols(border.lwd = 0, size = 0.01,
             col = "grey", shape = 15,
             alpha = 0.5) +
  tm_layout(legend.outside = TRUE, frame = FALSE,
            fontfamily = "serif") +
  tm_shape(spatial_PML_matched) +
  tm_symbols(border.lwd = 0, size = 0.01,
             shape = 15, style = "cont",
             col = "err_nocov_resid", palette = "RdYlGn",
             contrast = c(0, 1))

tm_shape(spatialized_data) +
  tm_symbols(border.lwd = 0, size = 0.01,
             col = "grey", shape = 15,
             alpha = 0.5) +
  tm_layout(legend.outside = TRUE, frame = FALSE,
            fontfamily = "serif") +
  tm_shape(spatial_PML_matched) +
  tm_symbols(border.lwd = 0, size = 0.01,
             shape = 15, style = "order",
             col = "(PML_err_cov", palette = "RdYlGn",
             contrast = c(0, 1))

tm_shape(spatialized_data) +
  tm_symbols(border.lwd = 0, size = 0.01,
             col = "grey", shape = 15,
             alpha = 0.5) +
  tm_layout(legend.outside = TRUE, frame = FALSE,
            fontfamily = "serif") +
  tm_shape(spatial_PMI_matched) +
  tm_symbols(border.lwd = 0, size = 0.01,
             shape = 15, style = "order",
             col = "(PMI_err_nocov", palette = "RdYlGn",
             contrast = c(0, 1))

tm_shape(spatialized_data) +
  tm_symbols(border.lwd = 0, size = 0.01,
             col = "grey", shape = 15,
             alpha = 0.5) +
  tm_layout(legend.outside = TRUE, frame = FALSE,

```

```

        fontfamily = "serif") +
tm_shape(spatial_PMI_matched) +
tm_symbols(border.lwd = 0, size = 0.01,
           shape = 15, style = "order",
           col = "(PMI_err_cov", palette = "RdYlGn",
           contrast = c(0, 1))

# run sims

PML_err_nocov_residual_moran <-
  moran.test(x = spatial_PML_matched$err_nocov_resid,
             listw = kwl_pml)
PML_err_nocov_residual_moran_mc <- moran.mc(spatial_PML_matched$err_nocov_resid,
                                              kwl_pml, nsim = 999)

PML_err_cov_residual_moran <-
  moran.test(x = spatial_PML_matched$err_cov_resid,
             listw = kwl_pml)
PML_err_cov_residual_moran_mc <- moran.mc(spatial_PML_matched$err_cov_resid,
                                              kwl_pml, nsim = 999)

PMI_err_nocov_residual_moran <-
  moran.test(x = spatial_PMI_matched$err_nocov_resid,
             listw = kwl_pmi)
PMI_err_nocov_residual_moran_mc <- moran.mc(spatial_PMI_matched$err_nocov_resid,
                                              kwl_pmi, nsim = 999)

PMI_err_cov_residual_moran <-
  moran.test(x = spatial_PML_matched$err_cov_resid,
             listw = kwl_pmi)
PMI_err_cov_residual_moran_mc <- moran.mc(spatial_PMI_matched$err_cov_resid,
                                              kwl_pmi, nsim = 999)

# plot the sims and observed

x <- as.data.frame(PML_err_nocov_residual_moran_mc$res)
x <- x %>%
  mutate(res = PML_err_nocov_residual_moran_mc$res)
x %>%
  ggplot(aes(x = res)) +
  geom_histogram(bins = 20, alpha = 0.4, position = "identity") +
  geom_vline(
    xintercept = PMI_err_nocov_residual_moran[['estimate']][['Moran I statistic']],
    colour = "red") +
  theme_tufte() +
  labs(x = "Moran's I value")

x <- as.data.frame(PML_lag_cov_residual_moran_mc$res)
x <- x %>%
  mutate(res = PML_lag_cov_residual_moran_mc$res)
x %>%
  ggplot(aes(x = res)) +
  geom_histogram(bins = 20, alpha = 0.4, position = "identity") +

```

```

geom_vline(
  xintercept = PML_lag_cov_residual_moran[['estimate']]['Moran I statistic'],
  colour = "red") +
theme_tufte() +
labs(x = "Moran's I value")

x <- as.data.frame(PMI_lag_nocov_residual_moran_mc$res)
x <- x %>%
  mutate(res = PMI_lag_nocov_residual_moran_mc$res)
x %>%
  ggplot(aes(x = res)) +
  geom_histogram(bins = 20, alpha = 0.4, position = "identity") +
  geom_vline(
    xintercept = PMI_lag_nocov_residual_moran[['estimate']]['Moran I statistic'],
    colour = "red") +
  theme_tufte() +
  labs(x = "Moran's I value")

x <- as.data.frame(PMI_lag_cov_residual_moran_mc$res)
x <- x %>%
  mutate(res = PMI_lag_cov_residual_moran_mc$res)
x %>%
  ggplot(aes(x = res)) +
  geom_histogram(bins = 20, alpha = 0.4, position = "identity") +
  geom_vline(
    xintercept = PMI_lag_cov_residual_moran[['estimate']]['Moran I statistic'],
    colour = "red") +
  theme_tufte() +
  labs(x = "Moran's I value")

```

```

# run AIC

AIC(PMLmod.b, PML_err_nocov, PML_lag_nocov)
AIC(PMLmod.c, PML_err_cov, PML_lag_cov)
AIC(PMImod.b, PMI_err_nocov, PMI_lag_nocov)
AIC(PMImod.c, PMI_err_cov, PMI_lag_cov)

# run log-likelihood (ANOVA)

anova(PML_err_nocov, PML_lag_nocov)
anova(PML_err_cov, PML_lag_cov)
anova(PMI_err_nocov, PMI_lag_nocov)
anova(PMI_err_cov, PMI_lag_cov)

```

## Appendix: All code for this report