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# Exercise: Exploratory Data Analysis with GeoDa

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**Note:** This exercise is an adaptation and extension of one prepared by Dr. Diana Sinton for Cornell course PLSCS/NTRES 6200 in 2016.

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## 1 Introduction

GeoDa is an open-source program, cross-platform program designed as a simple tool for exploratory spatial data analysis (ESDA) and some spatial modelling of **spatial polygon** data, that is, maps of polygon units such as census tracts or political divisions with a set of **attributes** measured on each one.

GeoDa was first developed at Arizona State University and is now hosted at the University of Chicago<sup>1</sup>. The GeoDa program, documentation and sample data is freely available for download from the Geodata Center's GitHub<sup>2</sup>.

GeoDa allows users to experiment with visualization functionality such as linking and brushing across windows. This can be very helpful both for interpretation of and communication about these spatial patterns. It also incorporates several spatial statistical models.

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**TASK 1 :** Download and install GeoDa. •

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**TASK 2 :** Start GeoDa. •

## 2 Dataset

We will analyze a small dataset, part of the larger “New York leukemia dataset” developed by Waller and Gotway [2] and adapted by Bivand et al. [1]. This is information on the census tracts in an eight county area including Syracuse (NY) city, relating possible causes to the incidence of leukemia, in particular, exposure to the industrial chemical TCE<sup>3</sup>.

I have reduced this to just Syracuse city to reduce the size of maps and graphs.

**Note:** In the USA census tracts have 1 500–8 000 people (optimum size 4 000). They are designed to be socio-economically and demographically fairly homogeneous. Each tract has several block groups; these are made up of 20–40 individual blocks. The tract is usually large enough to compile reliable statistics.

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**TASK 3 :** Load the Syracuse leukemia incidence dataset into GeoDa, using the File | New ... menu item or the file open icon. This is a shapefile with base name Syr, so select Syr.shp •

You will see a plain map of the polygons (Fig. 1).

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<sup>1</sup> <https://spatial.uchicago.edu/geoda>

<sup>2</sup> <http://geodacenter.github.io>

<sup>3</sup> Trichloroethylene, an industrial solvent often found in groundwater

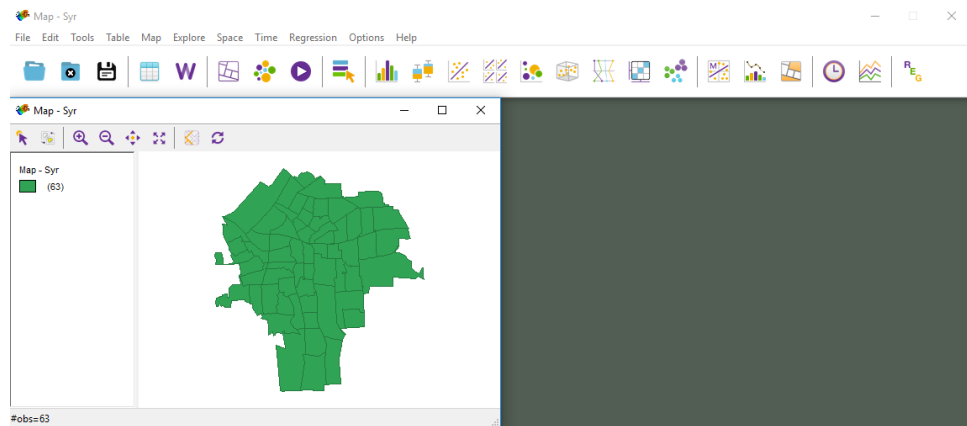


Figure 1: Base map and GeoDa tool bar

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**TASK 4 :** Open the data table by clicking the Table icon. Examine the rows and columns. •

We will work with these variables (fields):

These are all reported on the basis of 1980 census tracts. First, the **response** (dependent) variables:

**Cases :** the number of leukemia cases 1978-1982; some cases had insufficient georeference, these were added proportionally to tracts, so some “counts” are not integers.

**Z :** log-transformed rate, i.e., normalized by census tract population:  $Z_i = \log(1000[\text{Cases} + 1]/n)$ , where  $n$  is the population of the tract.

Second, possible **predictors**:

**PEXPOSURE :** potential exposure, computed as the logarithm of 100 times the inverse of the distance between a census tract centroid and the nearest TCE-producing site;

**PCTAGE65P :** percent older than 65 years; this could represent long-term exposure to any environmental factor;

**PCTOWNHOME :** percent home ownership; this could indicate lifestyle or economic level.

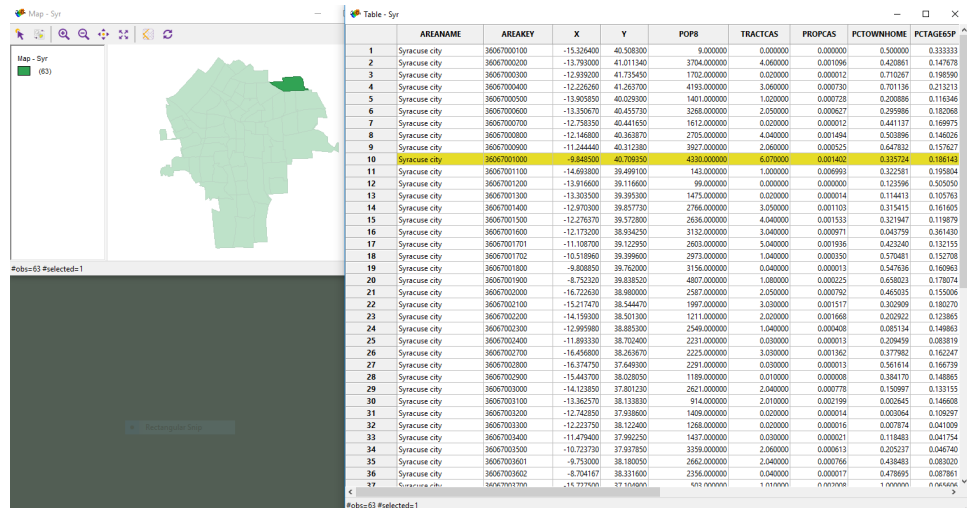
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**TASK 5 :** Rearrange the Table and the Map so that you can view both. •

The basic GIS “linking” functionality is in place; you can click on polygons in the map and their associated records in the table will highlight, and vice versa. To unselect objects, click anywhere in the white area surrounding the map or at the upper-left of the table. You can select multiple polygons (on the map) or tracts (in the attribute table) with Shift-click

for a set or Ctrl-click to add one-by-one. You can also “brush” over the map by holding down the left mouse button, to select in a window,

**Q1 :** Click on the northeasternmost census tract. What is its AREAKEY? What is its population? What percent of its homes are owned rather than rented?



## 3 Exploratory Data Analysis

### 3.1 Univariate

**TASK 6 :** Display some themed maps in the Map menu, for one or more of the variables, for example PCTSGE65P.

Compare quantile, percentile, box, and natural breaks maps. Examine how they present the same theme in different ways (Fig. 2).

**Q2 :** Look at the southeasternmost census tract in these four maps. How do they describe its proportion of older residents, compared to the entire City? Which map(s) best show(s) whether it is unusual?

**Q3 :** Which map is best for assessing spatial autocorrelation of this variable? Why? Does there appear to be autocorrelation? Across how many neighbouring census tracts?

### 3.2 Bivariate

Now we explore some feature-space plots.

**TASK 7 :** Under the Explore menu, create a Histogram of PCTAGE65P.

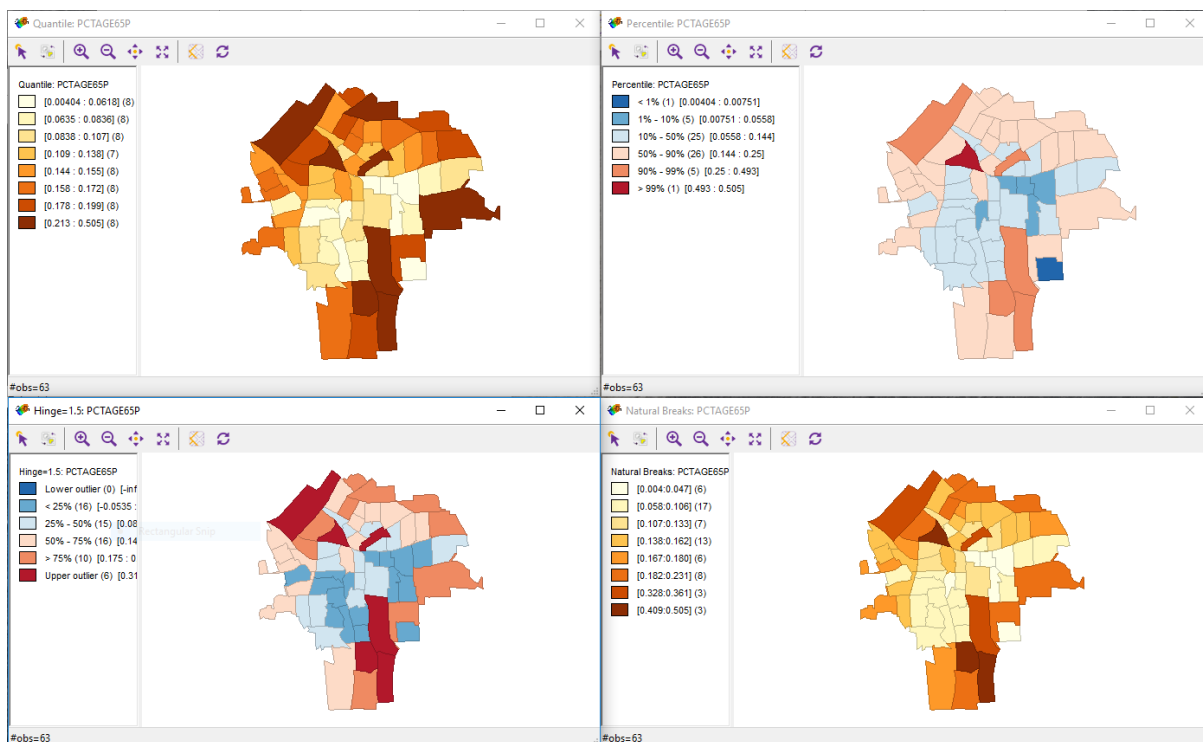


Figure 2: Thematic maps

Also create a Scatter Plot of the proportion of residents over the age of 65 PCTAGE65P (Y variable) and the proportion of homes that are owned rather than rented. PCTOWNHOME (X variable)

See Figure 3.

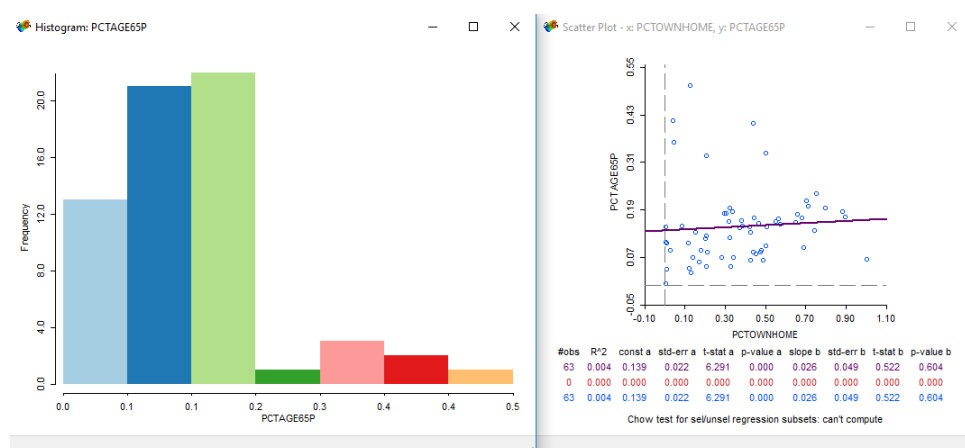


Figure 3: Histogram and scatterplot

Q4: Which tract has the highest proportion of older residents?

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**Q5 :** Describe the relation between these two attributes.

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**TASK 8 :** Find an unusual tract (not fitting the overall pattern for the city) and click on its point in the scatterplot.

See Figure 4.

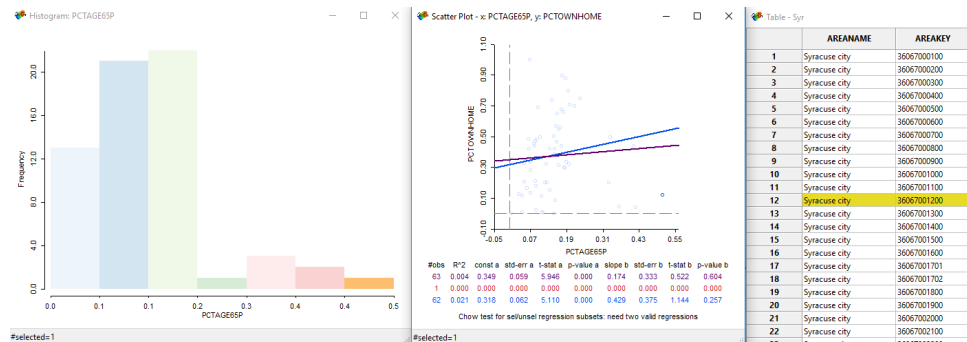


Figure 4: An unusual tract

Because all of the individual graphic elements for each of the 63 polygons are linked, any time that one or more are selected in one window or in one of the exploration plots, their linked highlighted display will activate in all other windows.

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**Q6 :** Which tract did you select? Where is it located?

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**TASK 9 :** Brush over the southern few tracts by holding down the left mouse button as you define a rectangular window.

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**Q7 :** What is the overall relation between home ownership and proportion of over-65 residents? What is this relation for the four southernmost tracts? How do you explain this?

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Another interesting plot is the Cartogram.

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**TASK 10 :** Make a cartogram (Map | Cartogram) of the proportion over 65 years old PCTAGE65P as the circle size, with the disease incidence Z as the circle colour.

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See Figure 5.

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**Q8 :** How are the circles placed in the plot? What insight does this give you into the relation between disease incidence and older residents?

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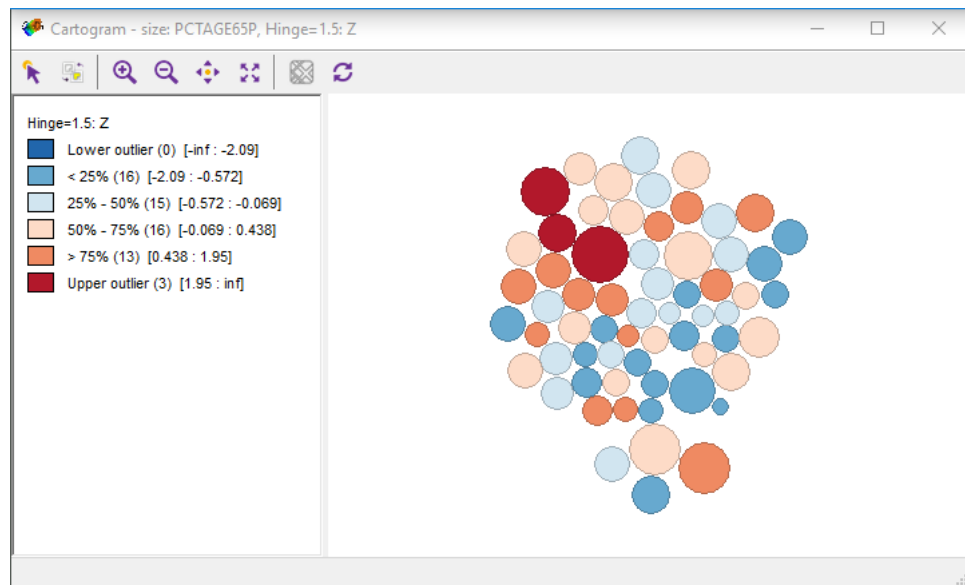


Figure 5: Cartogram of leukemia incidence vs. older residents

### 3.3 Multivariate

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**TASK 11 :** Open a scatterplot matrix (Explore | Scatter Plot Matrix) of the three PCTOWNHOME, PCTAGE65P, and PEXPOSURE, as well as the response variable Z.

See Figure 6.

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**Q9 :** Describe the feature-space distributions of the four variables. Looking at the proposed bivariate linear regressions, which have tracts with high leverage, i.e., that greatly influence the line?

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**TASK 12 :** In the matrix, select the histogram bar for the lowest proportion of home ownership, i.e., where more households rent.

Note how the linked maps highlight these tracts. See Figure 7.

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**TASK 13 :** With the scatterplot matrix displayed, select menu option Options | View | Regime Regression. This will then show the separate regression lines and statistics for the overall, selected, and non-selected census tracts.

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**Q10 :** Look at the red proposed regression lines – which bivariate correlations are substantially different from the overall correlations if we only consider these tracts?

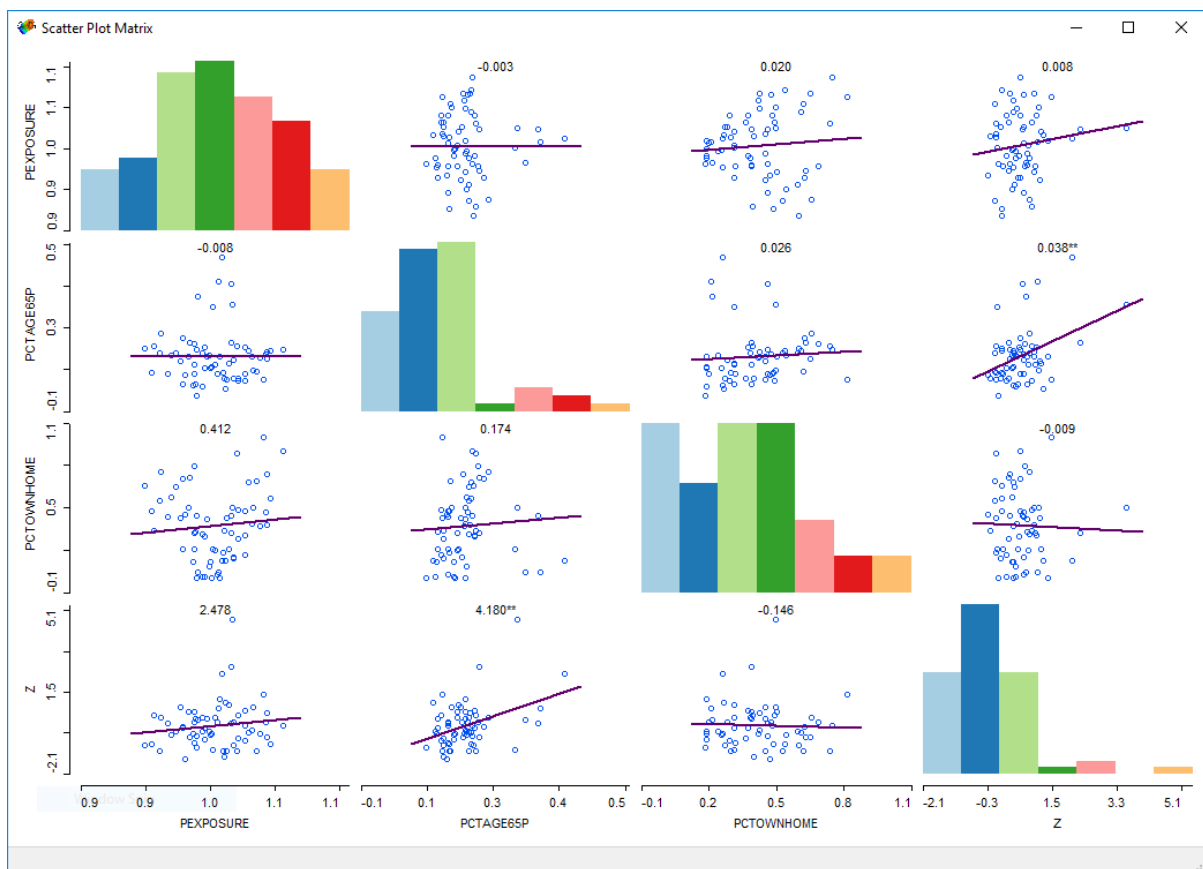


Figure 6: Scatterplot matrix

**TASK 14 :** Open a Parallel Coordinate Plot (PCP) and Include the three possible predictors PCTOWNHOME, PCTAGE65P, and PEXPOSURE, as well as the response variable Z.

**Q11 :** *What is their overall inter-relation?*

**TASK 15 :** Click on the line to the highest response.

See Figure 8.

**Q12 :** *Which tract is this? How is this response related to the three predictors?*



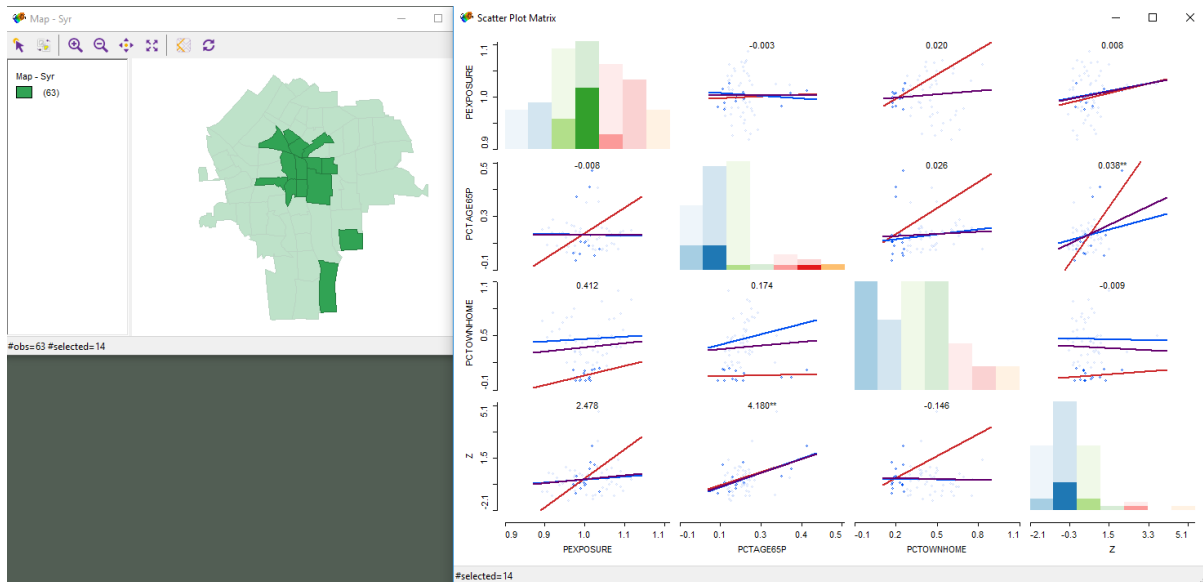


Figure 7: Scatterplot matrix with low home ownership tracts selected

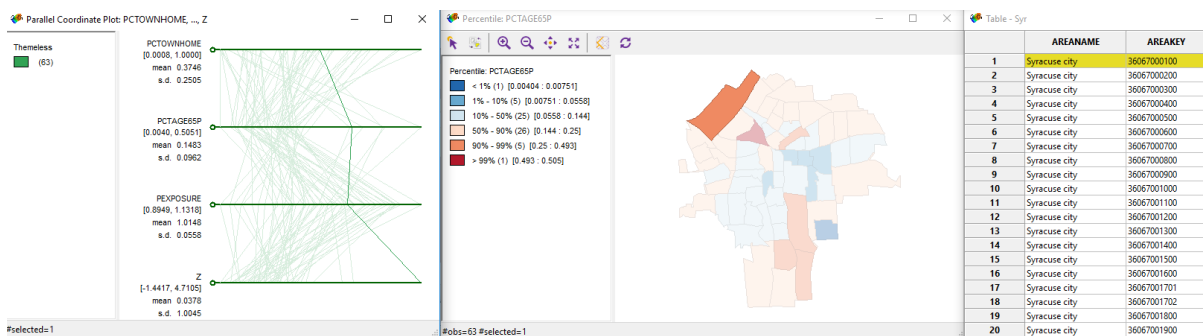


Figure 8: Parallel coordinate plot, highest response selected

## 4 Neighbors and Distances

For spatial models, we must impose some **spatial structure** on the 63 polygons, that is, how they are related in space. Then we can assess this statistically.

One way is by **distance between polygon centroids**, as in point geo-statistics; the spatial weights are based on separation, typically as inverse distance. This considers that distance is the only factor driving any spatial correlation.

However, there are other ways to build a **weights matrix** that relates neighbours; these relate to different hypotheses about how space affects the response. For example, a binary neighbours weighting considers that all first-order neighbours contribute equally to any spatial effect, i.e., it is averaged across the neighbours. With this weighting every tract is influenced equally (on average) by neighbours, and this influence is divided among the neighbours.

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**TASK 16 :** Generate two weights files: (1) Distance Weights and indicate X and Y coordinates, (2) order-1 Contiguity with Queen neighbours (i.e., tracts meeting only at a point are also considered to be neighbours). •

To generate a Weights File, choose **Tools | Weights Manager | Create**. Every shape must have its own unique ID, so check the **Add ID Variable** and use the existing AREAKEY variable. By default, the new ID variable will be named POLY\_ID, or you can choose otherwise. You can then select a type of weighting methods

For the distance weighting, the Threshold distance will automatically be calculated at the minimum distance to ensure that every polygon has at least one neighbor, but you can set any distance you desire. The distance units will be the units associated with the shapefile. For example, if we think that the phenomenon might be spatially-correlated (after accounting for the feature-space regression) to 2.4 km, set the threshold distance to 2400 m.

See Figure 9.

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**Q13 :** *What is the maximum number of neighbours considered for any tract in this distance weighting?* •

**Note:** You could also use the k-Nearest Neighbors option to specify a set number of its closest neighbors that you wish each polygon to use.

When your choices are set, Create the file and name the file with a label indicating the approach used to calculate the neighbors. For example, **Queen1.gal** would indicate a Queen directionality with 1 order of contiguity; **Dist24.gwt** would indicate a 2400 m radius inverse-distance weighting.

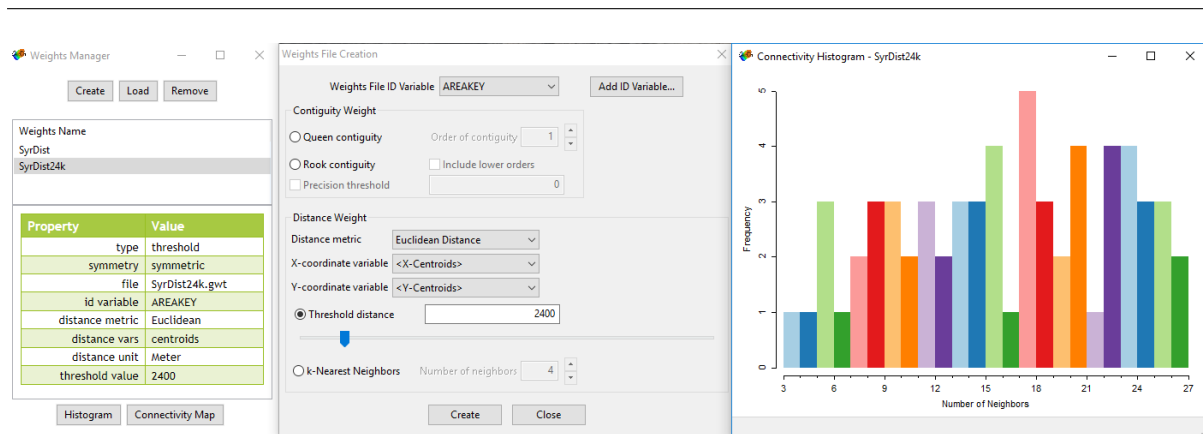


Figure 9: Creating a distance weighting

As you are deciding which method derives the most valid weights file for your question of interest, you can visually compare the results by using the **Connectivity Histogram** button in the **Weights Manager** window, each time after you select your different weights tables. See Figure 10.

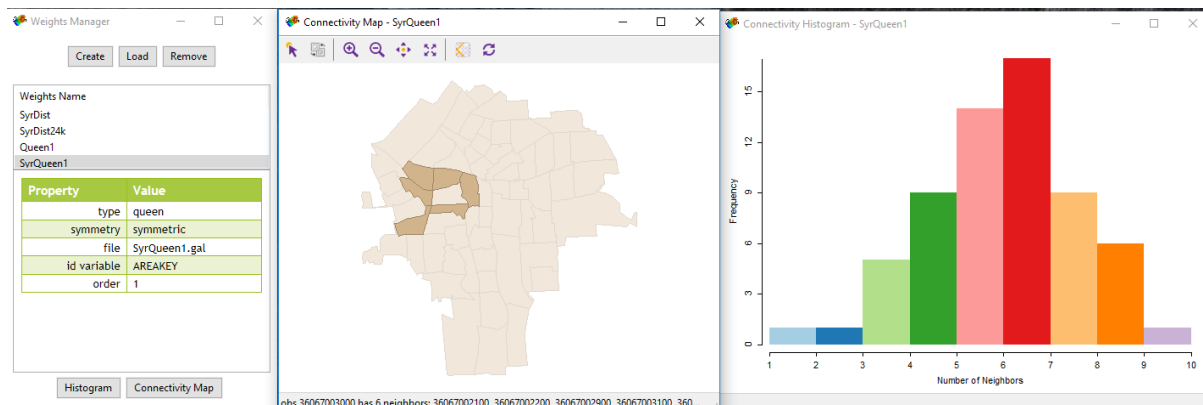


Figure 10: Connectivity map and histogram, Queen lag-1 neighbours

**Q14:** *What is the most common number of neighbours using the Queen lag-1 neighbours?*

## 5 Assessing Global Spatial Autocorrelation

Here we evaluate whether the rates of leukemia across the study area may be spatially auto-correlated, without considering any predictors.

**TASK 17:** Use Space | Univariate Moran's I, with Z as the variable, to produce a global Moran's I plot. Do this for all the weighting schemes you defined. •

See Figure 11.

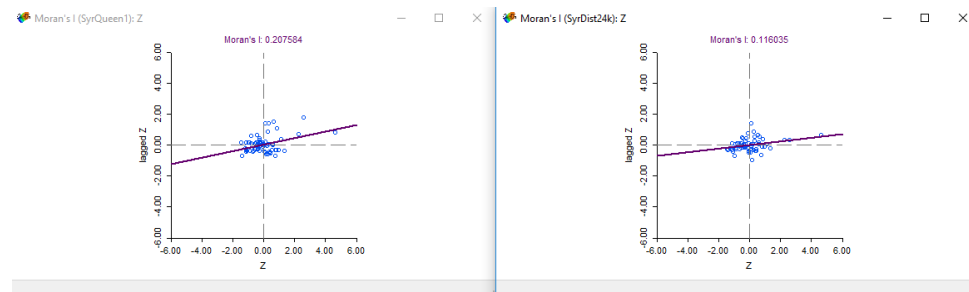


Figure 11: Global Moran's I

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**Q15 :** *Do the weighting schemes all give the same value of global Moran's I? If not, which implies stronger spatial correlation? Why?* •

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**TASK 18 :** Open two themed maps: decile (10-quantile) of Z (incidence) and PEXPOSURE (exposure).

In the Moran's I scatterplot, click on the highest positive Z (incidence) and highest weighted lag Z. •

See Figure 12.

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**Q16 :** *Where is this tract located? Does it also have a high exposure? Do its neighbours have high incidences? Do they have high exposures?* •

## 6 Assessing Local Spatial Autocorrelation

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**TASK 19 :** Examine where in the map are the hotspots of local autocorrelation. •

First, make sure that your desired Weights file is set as the default, i.e., highlighted in the Weights Manager window.

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**TASK 20 :** Use Space | Univariate Local Moran's I, with Z as the variable, to produce a local Moran's I plot. Do this for all the weighting schemes you defined. Generate two output windows: the Significance Map and the Cluster Map. •

The Significance map shows where there are leukemia values that are statistically significantly higher **or** lower than the neighboring values would

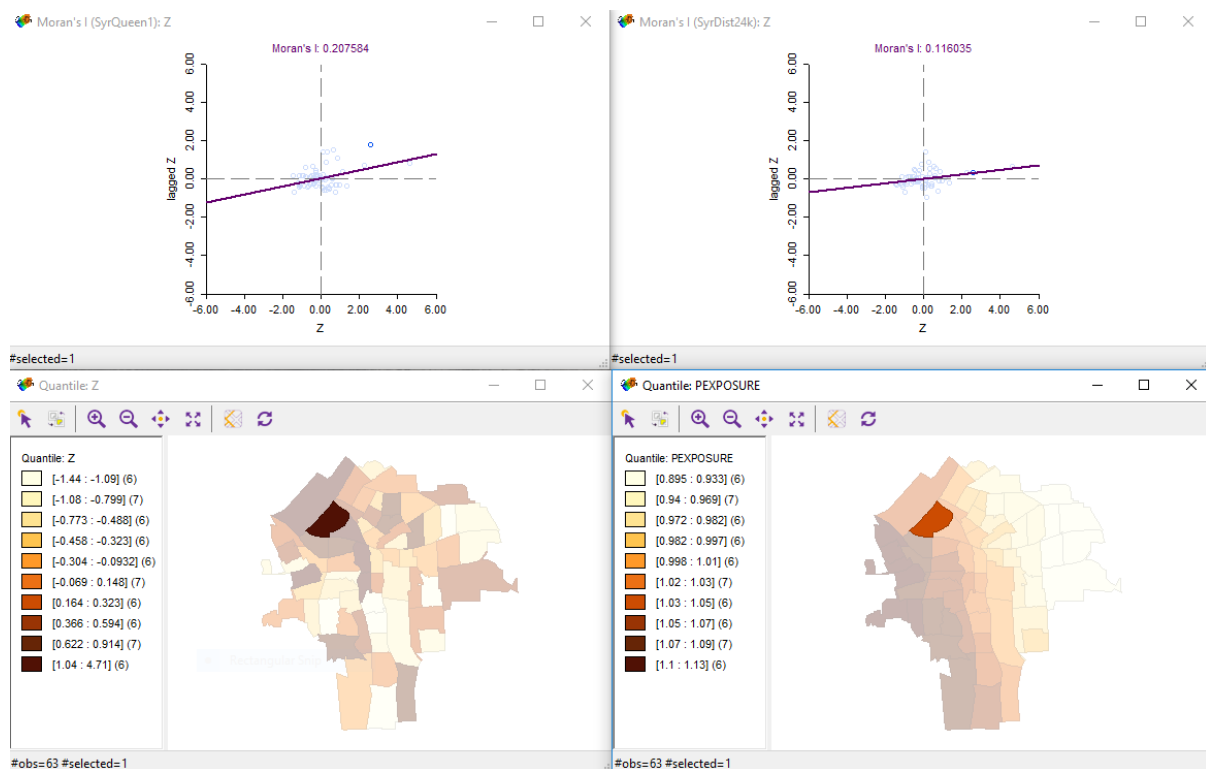


Figure 12: Global Moran's I

have predicted. With the Cluster Map, you can see where the higher-than-expected and lower-than-expected values vary.

See Figure 13.

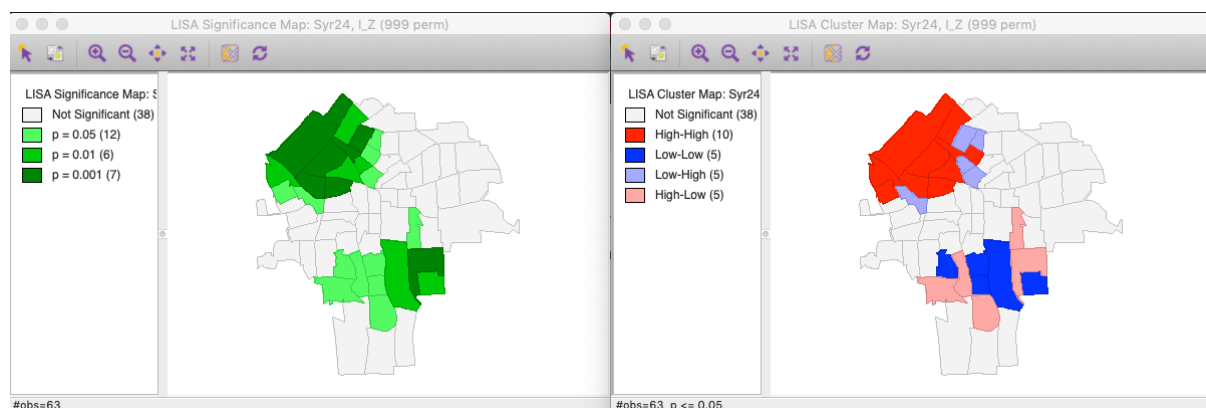


Figure 13: Local Moran's I significance and clusters

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**Q17 :** Which areas of the city are clusters of high leukemia incidence? Are there any tracts that have high incidence, but are surrounded by tracts with low incidence? •

Another way to find hot spots is with Geary's G or G\*; if you want you can experiment with these.

## 7 Spatial Regression

Here we try to find the covariates (“predictors”) correlated (which maybe cause) leukemia. Of course, we can do this non-spatially, i.e., all in attribute space, not taking spatial relations into account.

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**TASK 21 :** Compute a multivariate linear regression model of leukemia incidence (response) as predicted by the three possible causative factors (predictors). This is with the Regression menu item. Select Z as the dependent variable, and PCTOWNHOME, PCTAGE65P, and PEXPOSURE as the covariates. This is the Classic linear model, i.e., not taking spatial correlation into account. •

Non-spatial linear model:  $Y = X\beta + \varepsilon$

Figure 14 shows how to specify the regression; Figure 15 shows the results.

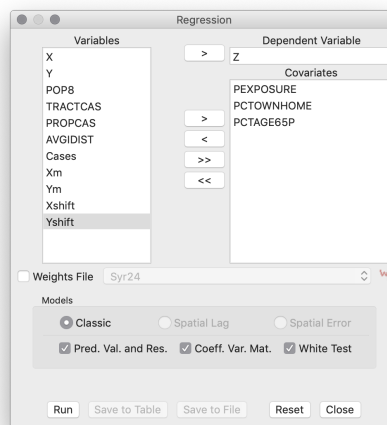


Figure 14: Specifying a “classic” linear regression

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**Q18 :** What is the adjusted  $R^2$  of this model? What are the signs of the slopes for each predictor? What is the interpretation? Which (if any) predictors are significantly different from zero? •

The model summary shows many problems with the linear model:

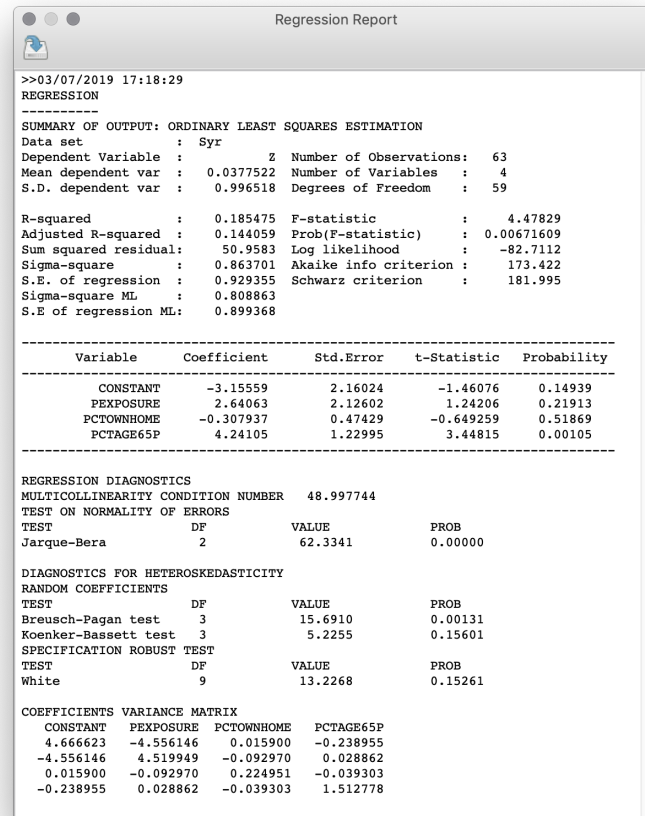


Figure 15: Multiple linear regression results

1. The **multicolilnearity** (or multiple) **condition number** represents the sensitivity of the model to small changes in the design matrix, i.e., the values of the covariables. A high value (often  $> 30$ ) indicates high colinearity in one or more predictors; here we see that is the case.
2. The Jarque-Bera test is whether the residuals have the skewness and kurtosis matching a normal distribution. Here we see a high value, quite unlikely to be normal.

However we will not fix up this model, we proceed to compare it to models which do take into account spatial correlation.

## 7.1 Spatial Error model

The first model with a spatial component we will consider is the **spatial error model**. This allows **residuals** of the linear model to be spatially-correlated, and quantifies to what extent they are included in the model.

This typically occurs when there is some spatially-correlated covariate that (1) affects the response and (2) we do not know, or maybe even

suspect – otherwise we would identify it, measure it, and include in the linear model. However, we may suspect a factor that we have not, or can not, measure, and this factor has spatial correlation.

For example, this database does not report the proportion of different ethnic groups, nor of different occupational groups (factory workers, office workers, service workers ...). These may be (1) related to leukemia (genetic susceptibility, occupational exposure), (2) spatially-correlated. If such factors influence leukemia, they will be represented in the residuals, and thus the spatial error model will be provably better than the feature space-only model.

The spatial error model is:

- formula:  $\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \lambda\mathbf{W}\mathbf{u} + \varepsilon$
- $\mathbf{W}$  is a matrix representing the spatial structure (e.g., neighbour weights)
- $\mathbf{u} = (\mathbf{Y} - \mathbf{X}\boldsymbol{\beta})$  are the spatially-correlated **residuals**
- $\lambda$  is the strength of autoregression of the errors
- $\varepsilon$  is the independent error (not autoregressive)

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**TASK 22 :** Compute a multivariate linear regression model of leukemia incidence (response) as predicted by the three possible causative factors (predictors). This time (1) select a Weights file (one you created above), and then you can specify the SAR **Spatial Error** linear model. This takes spatial correlation of the **linear model residuals** into account, considering the values of the model **residual** in each tract's neighbourhood, as defined by the weights. •

Figure 16 shows the results.

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**Q19 :** *What is the adjusted  $R^2$  of this model? Is it higher or lower than that for the feature-space only model? Is this expected? How can it be explained?* •

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**Q20 :** *What are the signs of the slopes for each predictor? What is the interpretation? Which (if any) predictors are significantly different from zero? What changes in this model compared to the feature-space multiple regression? I.e., which predictors become more or less important and/or significant?* •

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**Q21 :** *What is the strength of the autocorrelation parameter  $\lambda$ ?* •

The **likelihood ratio test** gives the probability that the SAR spatial error model is *not* better than the feature-space-only multiple regression.



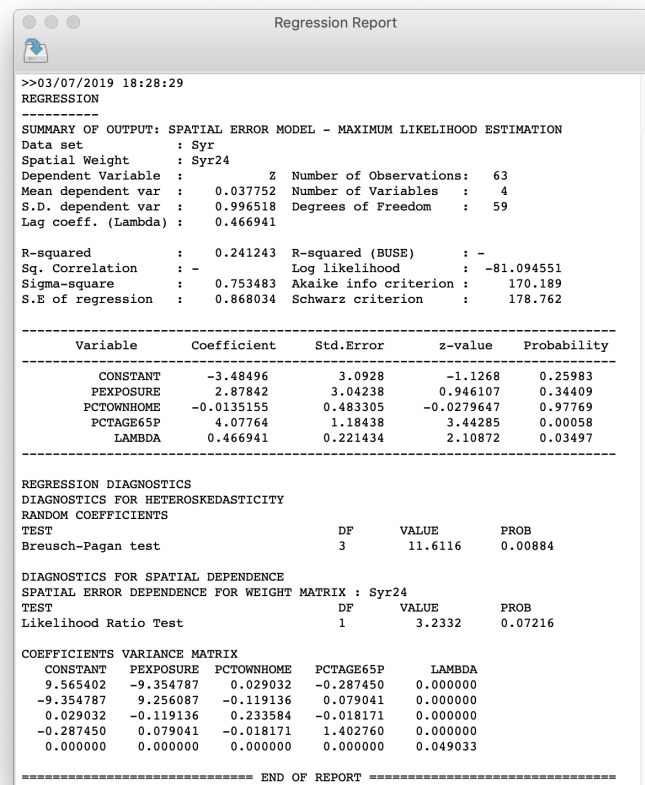


Figure 16: SAR spatial error model regression results

**Q22 :** *What is the probability that the SAR spatial error model is not better than the feature-space-only multiple regression? What does this imply about the possible causes of leukemia?* •

## 7.2 Spatial Lag model

Another possible effect of spatial autocorrelation is in the response, that is, the values of the response in a tract's neighbours directly influence the response in the tract, after taking into account the feature-space prediction. This measures “contagion”, which seems unlikely for human leukemia<sup>4</sup>, however we still evaluate this.

**TASK 23 :** Compute a multivariate linear regression model of leukemia incidence (response) as predicted by the three possible causative factors (predictors). This time (1) select a Weights file (one you created above), and then you can specify the SAR **Spatial Lag** linear model. This takes

<sup>4</sup> although quite likely for feline leukemia, if infected cats travel across tract boundaries

spatial correlation into account, considering the values of the **response** variable in each tract's neighbourhood, as defined by the weights. •

The spatial lag model is:  $Y = \rho WY + X\beta + \varepsilon$ , where  $\rho$  is the strength of autoregression of the response; this multiplies the weights matrix times the response  $WY$  on the right-hand (predictor) side of the equation.

Figure 17 shows the results.

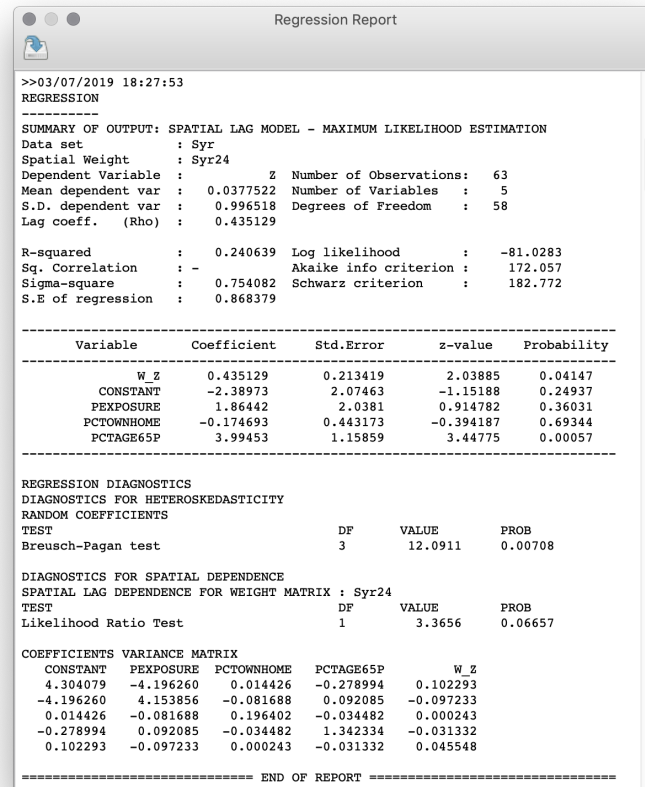


Figure 17: SAR spatial lag model regression results

**Q23 :** *Is the lag coefficient  $\rho$  significant in the regression? What is the probability that the SAR spatial lag model is not better than the feature-space-only multiple regression? What does this imply about the possible causes of leukemia?* •

## 8 Finishing with GeoDa

GeoDa provides several opportunities to save images or export newly derived data in tabular form. If while using GeoDa you have derived values and added variables to the attribute table of your shapefile, you will be prompted to Save these as you Exit. Otherwise, the program can

simply be closed.

## References

- [1] Roger S. Bivand, Edzer J. Pebesma, and V. Gómez-Rubio. *Applied Spatial Data Analysis with R*. Springer, 2nd edition, 2013. ISBN 978-1-4614-7617-7; 978-1-4614-7618-4 (e-book). URL <http://www.asdar-book.org/>.
- [2] L. A. Waller and C. A. Gotway. *Applied spatial statistics for public health data*. Wiley-Interscience, Hoboken, N.J., 2004.