MathSoft

S+SpatialStats
Version 1.5 Supplement

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Data Analysis Products Division
MathSoft, Inc.
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WELCOME TO S+SPATIALSTATS 1.5

Congratulations on acquiring Version 1.5 of the S+SPATIALSTATS module of S-PLUS. This new version features a Graphical User Interface to the functions already introduced in S+SPATIALSTATS 1.0, plus exciting new functionality.

New features in version 1.5 include:

- Block Kriging
- Variogram Fitting
- Summary and plot methods for spatial neighbor objects
- Simulation of Nonhomogenous Poisson Point Patterns
- New data set: `Glasgow.SMR`
- Numerous Bug fixes: `find.neighbor`, `quad.tree`, `sids` dataset names

The Graphical User Interface, that is, the menus and dialogs in S+SPATIALSTATS 1.5, has been designed with your convenience in mind. It also delivers the accuracy and high-quality you expect from our product.

Use this supplemental guide to:

- Get started using the dialogs in the Graphical User Interface of S+SPATIALSTATS 1.5 to facilitate your spatial data analyses.
- Learn to use other menus, dialogs, and graphical interface features in the general S-PLUS environment to perform analysis of spatial data.

INTRODUCTION 1

This guide describes how to use the S+SPATIALSTATS 1.5 Graphical User Interface (GUI). It is a companion to the S+SPATIALSTATS User's Manual. That manual provides extensive detail regarding the various techniques available for spatial data analysis, as well as information on how to perform such analyses using S-PLUS commands.

In this guide you will also find descriptions of the features in S+SPATIALSTATS that are new to version 1.5, specifically how to fit variograms, perform block kriging, simulate non-homogeneous Poisson processes, and how to create summaries and plots of spatial neighbor objects. You will also learn to use the new GUI to access the analytical tools available in previous versions and receive guidance on conducting an analysis of spatial data using the full functionality of the S-PLUS for Windows interface.

This supplemental guide has been organized according to the new menus and dialogs in the GUI of version 1.5, which are in turn organized according to the types of spatial data that can be analyzed using S+SPATIALSTATS: Geostatistical, Lattice, and Point Pattern Data.

This chapter provides an introduction to these three types of spatial data. The S+SPATIALSTATS User's Manual contains detailed discussions of each type including mathematical descriptions and assumptions of the diverse methodologies used for their analysis and consequent statistical inference.

SPATIAL DATA

Spatial data consist of measurements or observations taken at specific locations or within specific regions. In addition to values for various attributes of interest, spatial data sets also include the locations or relative positions of the data values. Locations may be *point* or *areal* referenced. For example, point referenced data are observations recorded at specific fixed locations and might be referenced by latitude and longitude. Areal referenced data are observations specific to a region; for example, the number of burglaries occurring in census tracts, where each census tract is a region. In both cases, spatial locations may be regular or irregular: point locations may fall on a regularly spaced grid, or may be irregular with varying distances between points; areal locations can comprise equally sized contiguous blocks that might occur in an agriculture field study, or may be of variable size and shape such as the city limits within a county. Spatial data may be continuous, such as the measurements of ore content from a core sample, or discrete, such as the number of measles cases reported by county. Further, the locations may come from a spatial continuum such as the point locations within a mining field, or a discrete set, such as the counties within a state.

S+SPATIALSTATS provides tools for analyzing three specific classes of spatial data: geostatistical data, lattice data, and spatial point patterns.

Geostatistical Data

Geostatistical data, also termed *random field data*, are measurements taken at fixed locations. The locations are generally spatially continuous. Examples of continuous geostatistical data include mineral concentrations measured at test sites within a mine, rainfall recorded at weather stations, concentrations of pollutants at monitoring stations, and soil permeabilities at sampling locations within a watershed. An example of discrete geostatistical data is count data, such as the number of scallops at a series of fixed sampling sites along the coast.

Lattice Data

Lattice data are observations associated with spatial regions, where the regions can be regularly or irregularly spaced. The spatial regions can be any spatial collection, and are not limited to a grid. Generally, neighborhood information for the spatial regions is available. An example of regular lattice data is information obtained by remote

sensing from satellites. The earth's surface is divided into a series of small rectangles (pixels) and the data are received as a regular lattice in R^2. An example of irregular lattice data is cancer rates corresponding to each county in a state.

Mathematically, a lattice is defined by a set of vertices and edges. The sites form the vertices, which are then connected to neighboring sites by edges. Since lattice data are defined for spatial regions, a method of referencing sites must be determined; sites are often referenced by the centroids of the regions. A lattice is composed of an index set of sites with an associated set of neighbors.

Spatial Point Patterns

Point pattern data arise when locations themselves are the variable of interest. Spatial point patterns consist of a finite number of locations observed in a spatial region. Identification of spatial randomness, clustering, or regularity is often the first analysis performed when looking at point patterns. Examples of point pattern data include locations of a species of tree in a forested region and locations of earthquake epicenters.

A *marked* spatial point pattern includes values of additional related variables at each location. The additional variables are often called mark variables and may be used to further refine the analysis of point patterns. The Lansing Woods data set, introduced in the S+SPATIALSTATS User's manual, contains a marked spatial point pattern; in addition to the locations, the tree species were also recorded.

GETTING STARTED 2

This chapter describes how to get started with the S+SPATIALSTATS graphical user interface:

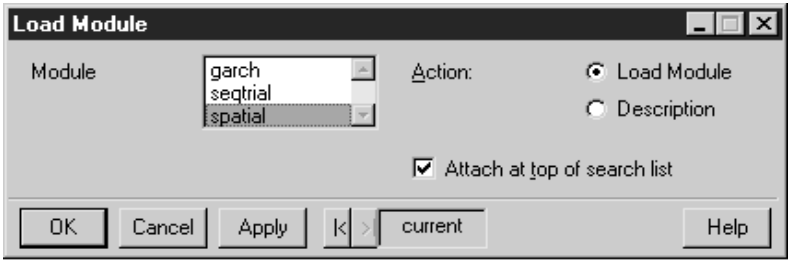
1. Load the module.
2. Examine the **Spatial** menu.
3. Find help on S+SPATIALSTATS.

LOADING THE MODULE

The first step in using S+SPATIALSTATS 1.5 is to load the module. Loading the module will make the spatial analysis functions available, create the Spatial menu, and load the S+SPATIALSTATS 1.5 dialogs.

To load the module:

Choose **File ▶ Load Module** from the main menu. The dialog below appears:

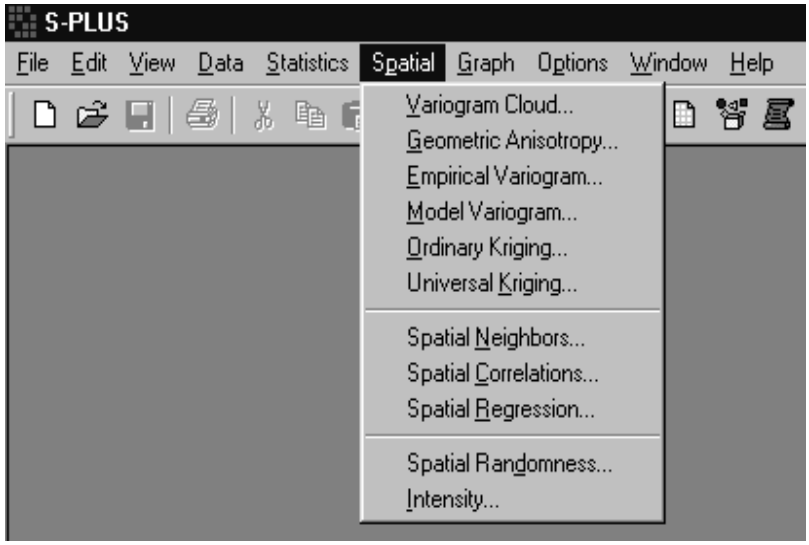


To load the S+SPATIALSTATS 1.5 module, select `spatial` as the **Module** and press **OK**.

A new menu selection, **Spatial**, will appear on the main S-PLUS menu bar. Select this menu item to access the dialogs to analyze your spatial data.

THE SPATIAL MENU

The **Spatial** menu provides access to the S+SPATIALSTATS 1.5 dialogs. To launch a dialog, simply select the desired menu item.



The menu is separated in three sections according to the type of spatial data that the corresponding methodology applies to. The first six items correspond to the analysis of geostatistical data, the next three to data observed on a lattice, and the final two apply primarily to spatial point pattern data.

GETTING HELP

Help is available in a variety of ways:

- Use the **Help ► S+SPATIALSTATS Help** menu item to open the S+SPATIALSTATS help file.
- The **Help** button on a dialog will display help for that dialog.
- The command line function `help` will provide help on a specified function.
- This supplement is also available online in a PDF file viewable using Adobe Acrobat. Use the **Help ► Online Manuals** menu item to access it.

GEOSTATISTICAL DATA 3

Geostatistical data, also termed random field data, consist of measurements taken at fixed locations. Variogram estimation and kriging are commonly used with geostatistical data. These methods were originally introduced as geostatistical methods for use in mining applications. In recent years, these methods have been applied to many disciplines including meteorology, forestry, agriculture, cartography, climatology, and fisheries.

This section describes the following dialogs:

- Variogram Cloud
- Geometric Anisotropy
- Empirical Variogram
- Model Variogram
- Ordinary Kriging
- Universal Kriging

EXPLORATORY DATA ANALYSIS

In this section, we will give specific examples of EDA for *geostatistical data*–data collected on a continuous spatial surface (see chapter 1 of the S+SPATIALSTATS User's Manual for a more precise definition). The `coal.ash` data frame is used in an example of EDA for data collected on an equally spaced grid of locations.

The `coal.ash` data will then be used to illustrate the use of the S+SPATIALSTATS 1.5 dialogs to analyze geostatistical spatial data.

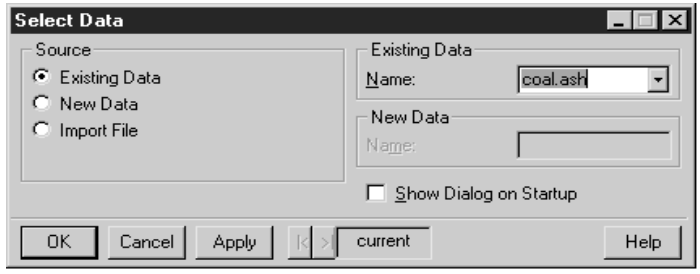
Example: The Coal Ash Data

The `coal.ash` data come from the Pittsburgh coal seam on the Robena Mine Property in Greene County, Pennsylvania (Cressie, 1993)[1].

The data frame contains 208 coal ash core samples collected on a grid given by **x** and **y** planar coordinates.

To plot the grid locations:

1. Open a view of the data on a Data Window. You can do this by selecting **Data ▶ Select Data** from the main menu and then entering `coal.ash` as the Name of the existing data set desired. The resulting dialog follows:



   You could also use the command line directive:

```
> guiOpenView(Name=coal.ash, classname="data.frame")
```

2. Proceed by selecting the first 2 columns of the data frame in the window.

---

1. Cressie, Noel A. C. (1993). *Statistics for Spatial Data*, Revised Edition. John Wiley and Sons, New York.

3. From the **Plots2D** palette, choose a scatter plot by pressing the first button on the top left-hand side corner.
4. A plot of the sampling locations appears. Notice the gridded pattern that these observations follow.

To superpose information about the percent coal ash at each sampling location we can overlay a contour map of coal ash, or make the symbols at each sampling point vary in some way according to that variable, `coal`.

For illustration purposes, we will demonstrate both in this section. The S+SPATIALSTATS User's Manual contains detailed plots that show the distribution of coal ash percentages over the sampled area, potential outliers, and trend analysis. We will refer to those results whenever necessary.

To vary symbols according to a third variable:

1. Select the Graph Sheet with the points, and click on the points themselves until a green knob appears at the bottom of the bulk of the data.
2. Right-click and select **Data to Plot** from the middle of the context menu that appears.
3. Select `coal` as the **z Column** from the drop-down list available and
4. Click the **Vary Symbols** tab.
5. Select **z Column** on the **Vary Size By** field, and change the Minimum and Maximum Heights to 0.05 and 0.20, respectively so as not to overwhelm the plot with symbols that are too large. You may also want to change the **Symbol Style** (on the **Symbol** tab) to a solid circle for better visualization of the significance of their size.

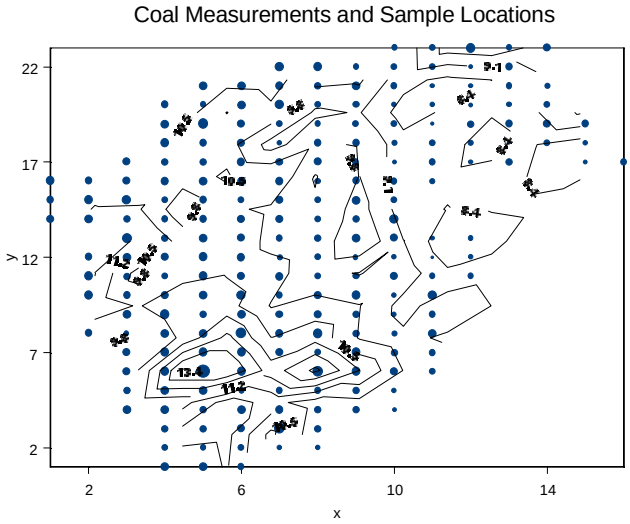
To explore how the different values of coal percentage vary over the sampling region, you may use the **Label Point** tool from the **Graph Tools** palette and move through the points clicking on them. Point 50 seems to be an outlier as exposed in the User's Manual.

To superimpose contours of coal ash percentage in the samples:

1. Select the 3 columns on the open data window: `x`, `y`, and `coal` in that order.

2. Then select the graph region in the plot above and Shift-click the **Contours** button on the **Plots2D** palette. Contour lines varying with percentage of coal will be added to the plot of the sampling locations. These contours are calculated internally in S-PLUS using Akima's fitting method (Akima, 1978)[1]. See the help file for the S-PLUS `interp` for more detail.

A few cosmetic changes can be made to the resulting plot. For example, use the **Gridding/Hist** tab of the Contour Plot properties dialog to clear the **Extrapolation** option and the **Labels** tab to add labels to the contours (set **Label Frequency** to 1) and perhaps change the font to make them more prominent. In the figure below, the number of contours was also increased and a title inserted.



The outlier, **17.6,** is quite apparent and it is driving the shape of the resulting contours.

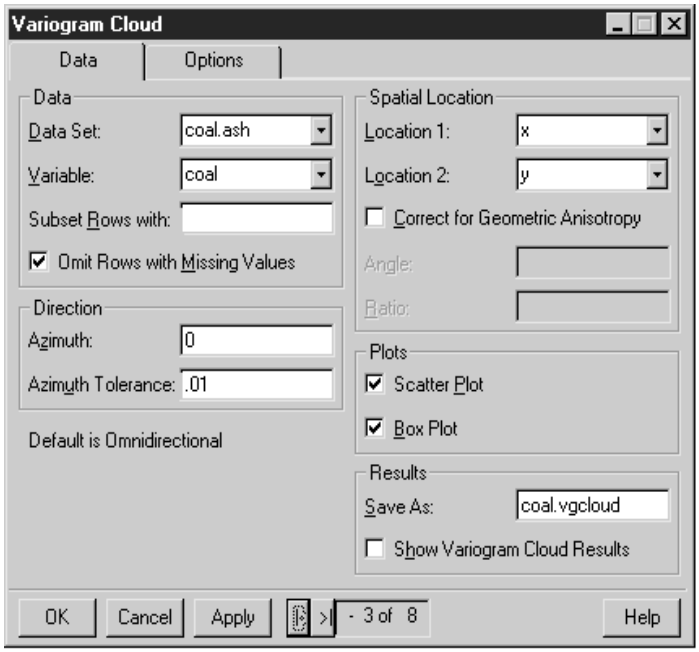
1. Akima, H. (1978). A Method of Bivariate Interpolation and Smooth Surface Fitting for Irregularly Distributed Data Points. *ACM Transactions on Mathematical Software,* **4**, 148-164.

VARIOGRAM CLOUD

The variogram cloud is a diagnostic tool that can be used to look for potential outliers or trends, and to assess variability with increasing distance. Anomalies and non-homogeneous areas can be detected by looking at short distances that yield high dissimilarities.

To plot a variogram cloud:

Choose **Spatial ▶ Variogram Cloud** from the main menu. The dialog below appears:



Example:

Use the `coal.ash` data in the S+SPATIALSTATS data sets. From the analysis in the User's Manual, we know that these data exhibit a strong East-West trend. The variogram values in the East-West direction are likely influenced by the trend (the stationarity

assumption is violated in the presence of trend). We will restrict the variogram cloud computations to points in a North-South direction by manipulating the azimuth and its tolerance, as follows.

1. Launch the **Variogram Cloud** dialog.
2. Enter `coal.ash` as the **Data Set** to be analyzed.
3. Select `coal` as the **Variable** to be analyzed and select `x`, and `y`, as **Location 1** and **Location2**, respectively.
4. Change the **Azimuth Tolerance** from the omnidirectional value of 90 degrees to a narrow .01.
5. Save the resulting object as `coal.vgcloud`.
6. Press **OK**.

A two-page Graph sheet appears containing a box plot and a scatter plot of the variogram cloud. The variogram cloud shows a scatter of high value points for the full range of distance values.

There is a method in S+SPATIALSTATS that can be used to identify points in a variogram cloud; to invoke this method enter the following command in the Commands Window while the Variogram Cloud is the current active plot (this is required):

```
> identify(coal.vgcloud)
```

Identifying the high values in the variogram cloud shows that they all are paired with observation 50, which was determined to be an outlier indeed. We will remove observation 50 from further variogram modeling.

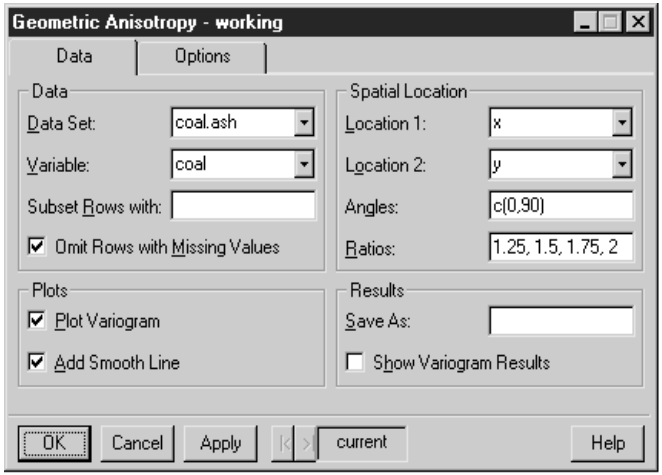
The variogram cloud provides a diagnostic tool to look for potential outliers or trends and to assess variability with increasing distance. It provides the distribution of the variance between *all* pairs of points at *all* possible distances and, as a consequence, it may yield extremely dense point clouds that may be difficult to interpret. To reach a point when we can model the variability in the data, a smoother version of the variogram is available through the **Empirical Variogram** dialog.

GEOMETRIC ANISOTROPY

Anisotropy is present when the spatial autocorrelation of a process changes with direction. Unlike a variogram from an isotropic process, the variogram from an anisotropic process is not purely a function of distance, but is a function of both distance and direction. The anisotropy plot is useful for exploring whether the process the data comes from is isotropic or whether the shape of the variogram changes with direction.

To create an anisotropy plot:

Choose **Spatial ▶ Geometric Anisotropy** from the main menu. The dialog below appears:



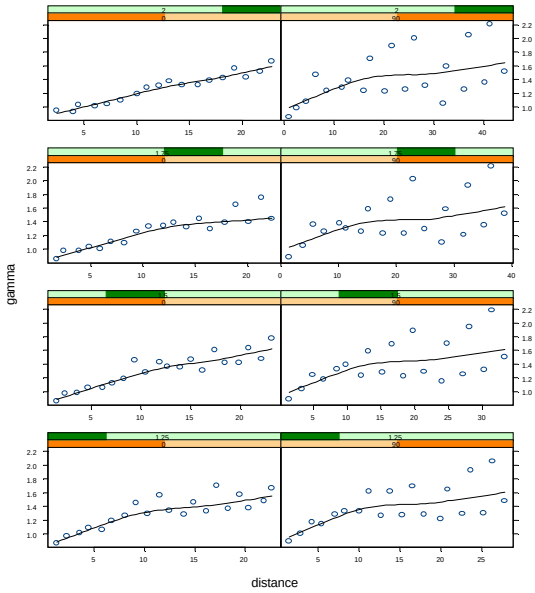
Example:

Use the coal data once again:

1. Enter `coal.ash` as the **Data Set** of interest.
2. Select `coal` in the **Variable** field, and `x` and `y`, respectively as **Location 1** and **Location 2**.
3. Enter -50 in the **Subset Rows with** field to remove observation **50**.
4. Enter **c(0,90)** as the **Angles** of anisotropy to explore, that is, the East-West and North-South directions.

5. Press **OK**.

A multipanel plot appears in a Graph sheet, with several directional variograms for all combinations of four ratio values for each of the 2 directions entered. The plot follows



There are no apparent changes for differing ratio values (between rows) but the variograms on the left do look different from those on the right.

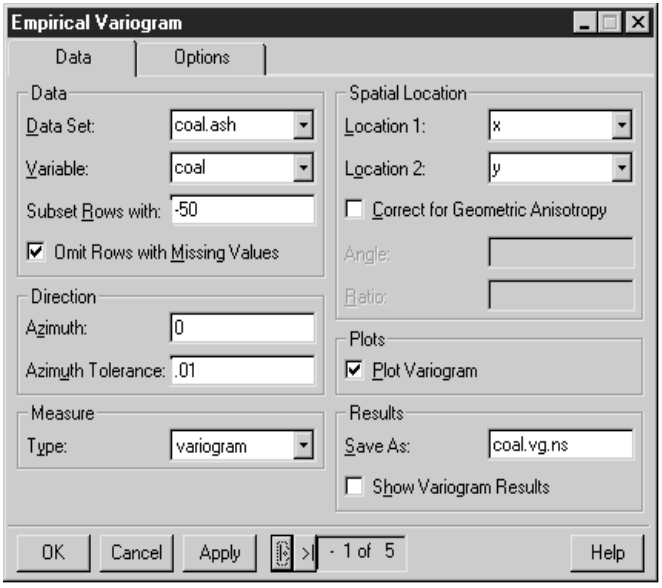
The **Geometric Anisotropy** dialog also provides an **Options** tab where the user can specify parameters to control the estimation of the variogram values for each combination of angle and ratio values. See the dialog's help file for detailed information or section 4.1.4 of the S+SPATIALSTATS User's Manual.

EMPIRICAL VARIOGRAM

The empirical variogram provides a description of how the data are related (correlated) with distance. The distances are binned and the corresponding variogram values averaged for each bin thereby producing a smoother version of the variogram which leads to easier modeling. You can control the degree of smoothing by adjusting the size of the "bins" or "lags", the number of points in each bin, and the *distance of reliability* (half the maximum distance over the field of data by default) for the variogram. Several directional variograms can be returned and as usual, a correction for Geometric Anisotropy can be made to the data before processing.

To plot an empirical variogram:

Choose **Spatial ▶ Empirical Variogram** from the main menu. The dialog below appears:



Example:

Continue analyzing the `coal.ash` data in S+SPATIALSTATS.

1. Launch the **Empirical Variogram** dialog.

2. Select `coal` in the **Variable** field, and `x` and `y`, respectively as **Location 1** and **Location 2**.
3. Enter -50 in the **Subset Rows with** field to remove observation **50**.
4. Change the **Azimuth Tolerance** to .01.
5. Save the result as `coal.vg.ns`.
6. Press **OK**.

A plot of the empirical variogram appears in a Graph sheet.

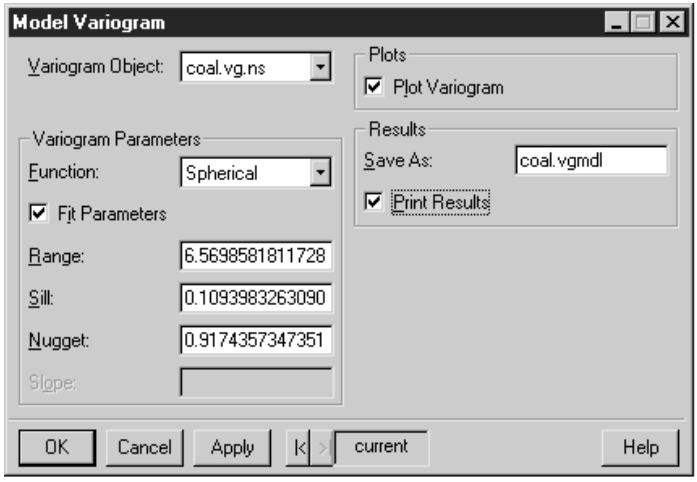
Note that restricting our computation to only points in a North-South direction is not the same as Correcting for Geometric Anisotropy. When using the variogram values for those pairs that are related in a North-South direction *only*, we are assessing one way the variance-covariance of the process changes without making any corrections to it. We are trying to understand variability only in the N-S direction. This makes some sense in applications that relate to physical data where gradients are quite possible. Later on, we apply our knowledge about this directional variation to the fitting of a kriging surface to the data using Universal Kriging techniques.

MODEL VARIOGRAM

In order to perform kriging, it is necessary to specify a theoretical variogram function for the process. The **Model Variogram** dialog is useful for examining the goodness-of-fit of various theoretical variograms to the observed empirical variogram. Typically this dialog will be used repeatedly to determine an appropriate variogram function and parameter values.

To fit a theoretical variogram:

Choose **Spatial ► Model Variogram** from the main menu. The dialog below appears:



Example:

Use the `coal.ash` data in S+SPATIALSTATS. Note that for the purposes of this example we will fit a theoretical variogram to the North-South empirical variogram we estimated above. In practice, we want to first remove trend and explore the data further as is done in the User's Manual.

1. Launch the **Model Variogram** dialog.
2. Select the name of a fitted empirical variogram object from the drop-down list in the **Variogram Object** field. Enter the object saved after using the Empirical Variogram dialog, `coal.vg.ns`.

3. Select a function to fit to the variogram, say a **Spherical**.
4. At this point you may check **Fit Parameters** and have the variogram parameters fitted automatically using the S+SPATIALSTATS function `variogram.fit`, or enter your own. Check the **Fit Parameters** check box.
5. The parameters values are filled in automatically. Enter a name in the **Save As** field to save the resulting variogram model. Enter **coal.vgmdl.**
6. Press **Apply**.

You could also fit the variogram by trying different values of the parameters and looking at the Objective Function. When doing this, make sure that the **Fit Parameters** box is not checked.

1. The empirical variogram plot suggests that a **Nugget** of around 0.7 and a **Sill** of around 1.1 are appropriate. Enter these parameter values.
2. Now try various values of **Range** by entering them one at a time and pressing **Apply** after each input. Look at the resulting plot each time along with the objective value printed on the plot to assess how well the specified theoretical variogram matches the empirical variogram.
3. A **Range** of 6 gives a local minima in the objective value. After we have selected this **Range**, we may wish to try other values of **Sill** and **Nugget** to further reduce the objective value.
4. Trying various values suggests that an empirical variance function with range of 6.5, sill of 1.9, and nugget of 1.1 matches the empirical variogram pretty well. Enter these values and press **Apply**.
5. Press **OK** or **Cancel** to dismiss the dialog.

Try fitting the variogram without removing observation 50 and see how much influence this value has on the final variogram model. You will need to fit an empirical variogram first and then proceed to the **Model Variogram** dialog.

The results, saved in the object named as stated in the **Save As** field, can be given to one of the kriging dialogs to fit a kriging surface to the spatial process of interest.

ORDINARY AND UNIVERSAL KRIGING

Kriging is a linear interpolation method that allows predictions of unknown values of a random field from observations at known locations. Kriging incorporates a model of the covariance of the random function when calculating predictions of the unknown values.

S+SPATIALSTATS provides two **Kriging** dialogs to support both ordinary and universal kriging.

Ordinary kriging uses a random function model of spatial correlation to calculate a weighted linear combination of available samples, for prediction of a nearby unsampled location. Weights are chosen to ensure that the average error for the model is zero and that the modeled error variance is minimized.

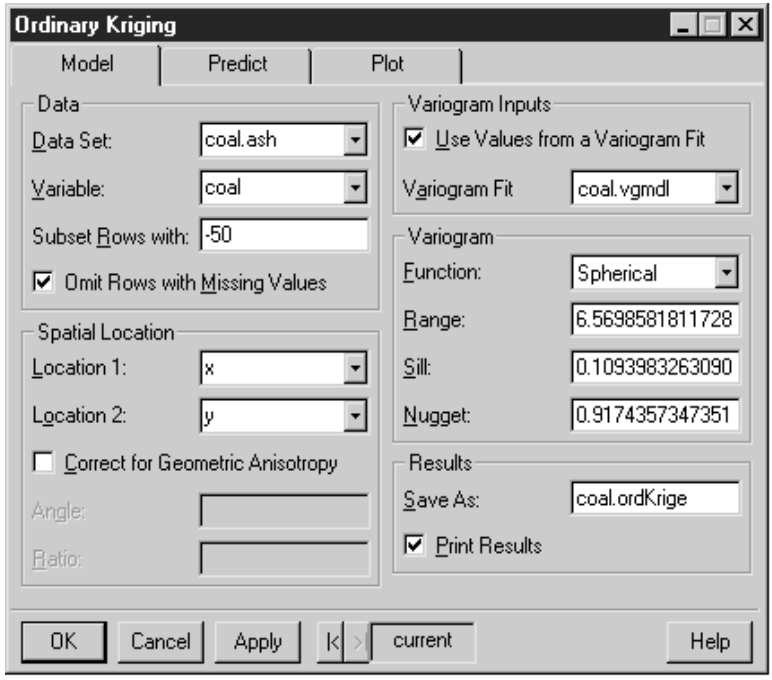
Universal kriging is an adaptation of ordinary kriging that accommodates trend. The trend is modeled as a polynomial function of spatial location. Universal kriging can be used to both produce local estimates in the presence of trend, and to estimate the underlying trend itself. Universal kriging with a constant mean is equivalent to ordinary kriging.

The **Ordinary** and **Universal Kriging** dialogs provide several options for prediction. **Block Kriging** predictions (the average over a rectangular area) are possible using the dialogs as well as **Point** predictions either on a grid or at new sampling points.

Several different plots can be requested to help visualize both the predictions and their standard errors.

To perform ordinary kriging:

Choose **Spatial ▶ Ordinary Kriging** from the main menu. The dialog below appears:



Example:

Let us krige the coal data.

1. Launch the **Ordinary Kriging** dialog.
2. Enter `coal.ash` as the Data Set of interest.
3. Select `coal` in the **Variable** field, and `x` and `y`, respectively as **Location 1** and **Location 2**.
4. Enter -50 in the **Subset Rows with** field to remove observation **50**.
5. Check the **Use Values from a Variogram Fit** box.

6. Select `coal.vgmdl` from the drop-down list in the **Variogram Fit** field. This is the `variogram.fit` object that we obtained using the **Model Variogram** dialog. The fields for the **Variogram** parameters automatically fill.
7. Save to an object named `coal.ordKrige`.
8. Move to the **Plot** tab. Specify **Surface** Plots for both the predictions and their standard errors.
9. Press **OK**.

You see a summary of the fitted object, `coal.ordKrige`, in a Report window, and the plot on different pages of a Graph sheet.

The exploratory plots of the data presented in the S+SPATIALSTATS User's Manual indicated the presence of a strong gradient in these data. This gradient might be apparent if we plot the observations against location.

To plot the coal observations against location:

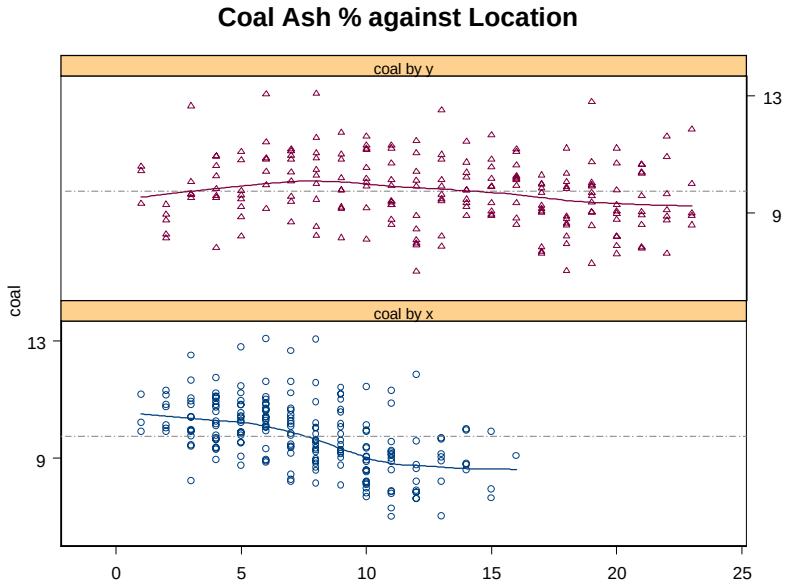
1. Create a new data set by removing observation 50 from the `coal.ash` data frame by entering these commands in the Commands Window:

```
> coal.no50 <- coal.ash[-50,]    # Remove 50th row
```

2. Choose **Data ▶ Select Data** from the main menu and open the `coal.no50` data frame.
3. Select columns `x` and `coal`.
4. From the **Plots2D** palette, choose a scatter plot with a `loess` fit through it by pressing the corresponding button (a scatter plot with an **L** on it).
5. Click on the graphsheet and choose **Insert ▶ Annotation ▶ Reference Line ▶ Horizontal** and add a horizontal dashed line at the mean of the observations, that is set **Position** at 9.740725, to the plot of the observations against `x`.
6. Go back to the Data Window and select `y` and `coal` this time.
7. Click on the graphsheet with the observations vs. `x` plot and SHIFT-click on the scatter plot with a `loess` fit on the **Plots2D** palette. The plot of `coal` against `y` will be superimposed on the other plot.

8. Separate the plots by clicking on the plot region (not on a data point) and selecting **Multipanel** from the resulting menu.
9. Select **By Plot** as the **Panel Type** and set the **Layout** to be a 1 column by 2 rows plot arrangement.

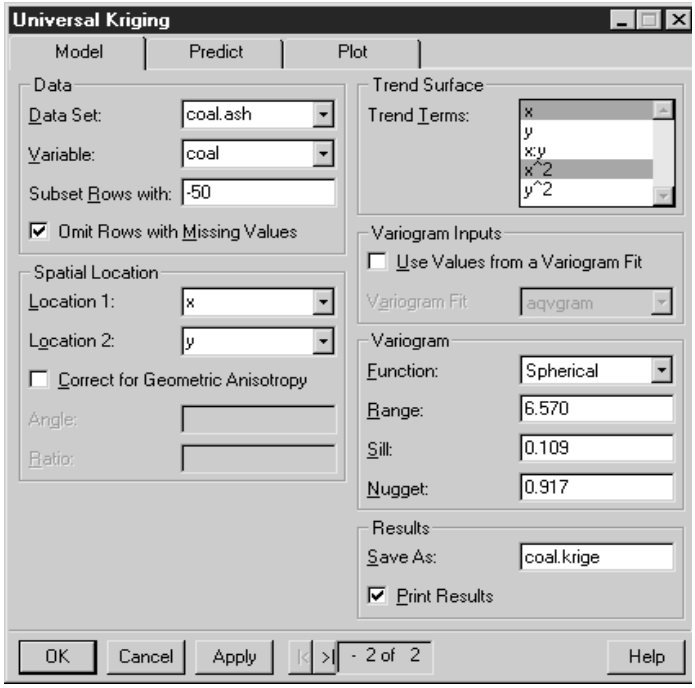
After inserting a title, you see the figure below:



The trend is apparent from the bottom plot. We will try to model this trend as a second order polynomial in x as part of a Universal Kriging fit in the following section.

To perform universal kriging:

Choose **Spatial ▶ Universal Kriging** from the main menu. The dialog below appears:



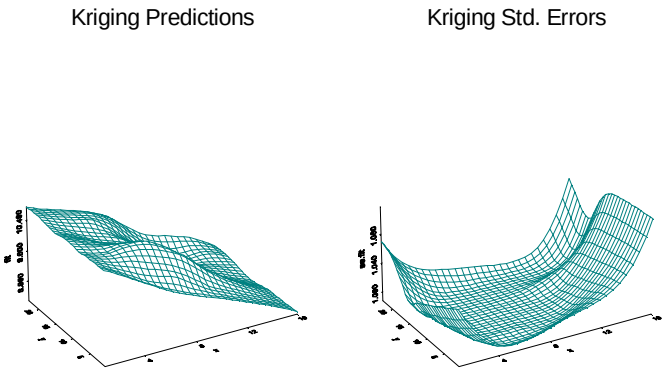
As an example, krige the coal data.

1. Launch the **Universal Kriging** dialog.
2. Enter `coal.ash` as the Data Set of interest.
3. Select `coal` in the **Variable** field, and `x` and `y`, respectively as **Location 1** and **Location 2**.
4. Enter -50 in the **Subset Rows with** field to remove observation **50**.
5. Select **x** and **x^2** as trend terms.
6. Select a **Spherical** Variogram Function with **Range** of 6.570, **Sill** of 0.109, and **Nugget** of 0.917, the values fitted using the **Empirical Variogram** dialog.

7. Save to an object named `coal.krige`.
8. Move to the **Predict** tab and check the boxes specifying that the **Predictions** and **Standard Errors** should be saved. Enter `coal.kgpred` in the **Save In** field**.**
9. Leave the **Locations Type** set to its default value of **Grid**. The predicted values will be on a grid.
10. Move to the **Plot** tab. Specify **Surface** Plots for both the predictions and their standard errors.
11. Press **OK**.

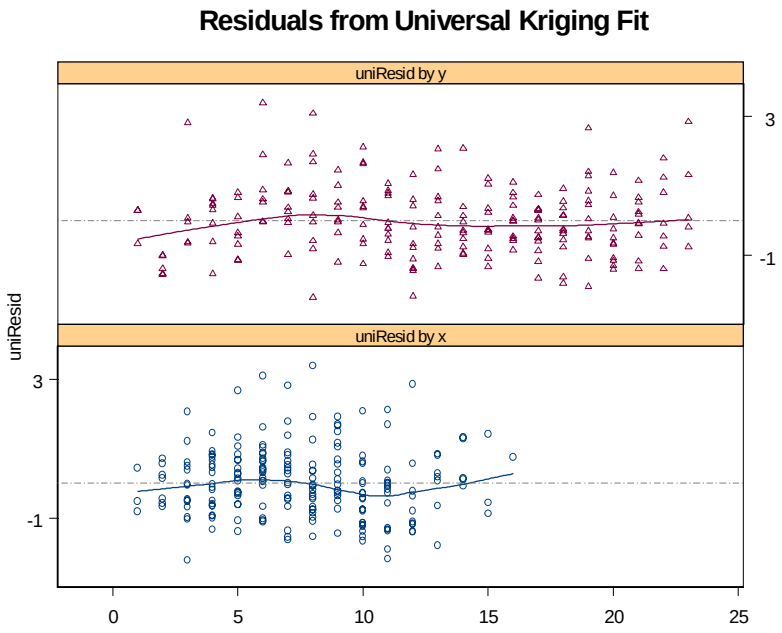
You see a summary of the fitted object, `coal.krige`, in a Report window, and the plot on different pages of a Graph sheet, and a Data window with the predictions.

A plot of both the predictions and their standard errors follows:



Compare this with Figure 4.25 of the S+SPATIALSTATS User's Manual. Other plots can be generated by having the prediction object `coal.kgpred` open. Select 3 columns `x`, `y`, and `fit`, and try different displays but pushing buttons on the **Plots2D** and **Plots3D** palettes. You may want to rotate different graphs to look at the predictions from several different angles.

Plotting the residuals from this fit produces a tighter fit about the 0 reference lines though there are still a few high values.



Block Kriging

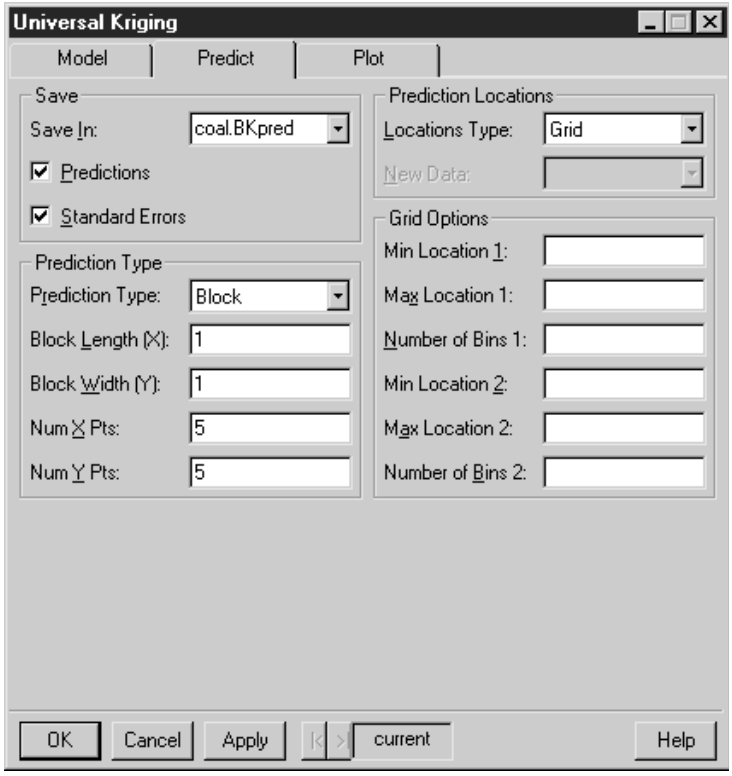
Block kriging is the general term used for the prediction of the average value of a random field over a segment, surface, or volume. The term *Point kriging* refers to prediction of the field at a point.

In S+SPATIALSTATS, block kriging is computed by the `predict` method for objects of call `"krige"`, `predict.krige`, and is implemented on the **Predict** tab of both **Kriging** dialogs.

Block kriging is restricted to prediction of the average value over a rectangular area. The integral over the block rectangular is approximated by the average of the point predictions within the block. You may control the number of points to be considered in the average as well as the block size.

To perform block kriging on the coal data:

1. Choose **Spatial ▶ Universal Kriging** from the main menu.
2. Use the rollback button at the bottom of the dialog to recover the settings used in performing Universal Kriging on the coal data.
3. Move to the **Predict** tab. The dialog below appears:



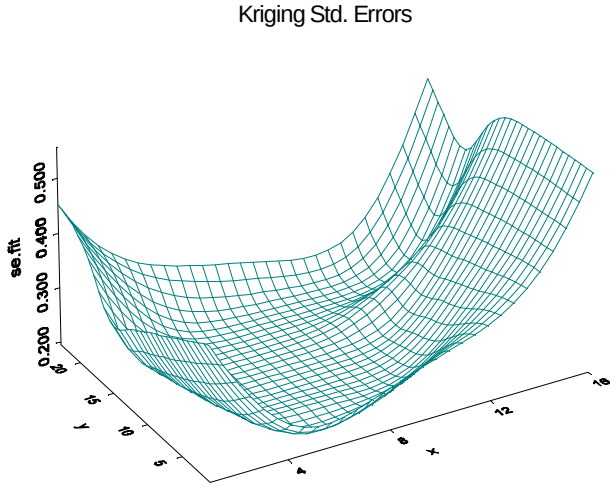
4. Enter `coal.BKpred` as the name of the object to save the predictions in.
5. Check both **Predictions** and **Standard Errors** to be saved.
6. Choose **Block** as the **Prediction Type**.
7. Specify a 1 x 1 block by entering 1 as the **Block Length(X)** and the same as the **Block Width (Y)** (or leaving the default values in).

8. Specify 5 as the number of points in the X direction to be averaged for each block.
9. Specify also 5 points in the Y direction.
10. Click **OK**.

The predictions are calculated with the supplied prediction locations in the center of the block. The block prediction will be the average of point predictions at 25 locations within each block.

The predicted values are very similar to those obtain with the default Point kriging when performing Universal Kriging. That is to be expected.

The standard errors are much smaller for the block kriging since the predictions are averages.



LATTICE DATA 4

Lattice data are observations from a random process observed over a countable collection of spatial regions, and supplemented by a neighborhood structure. The observation locations can be regular (equally spaced grid) or irregular, and data at a particular location typically represent the entire region. The data observed at each site may be continuous or discrete.

Before modeling the spatial component of lattice data in S+SPATIALSTATS, we assume stationarity and multivariate normality of the small-scale variation in the data, that is, of the error term. This means that trend must be removed, and transformations may be required to stabilize the variance and/or to approximate normality.

The primary tools available for examining lattice data are **Spatial Correlations** and **Spatial Regression**. These dialogs require a data set containing the observations at each location, and a spatial neighbor object describing the spatial relationship between the observations. The **Spatial Neighbors** dialog creates a spatial neighbor object.

This section describes the following dialogs:

- Spatial Neighbors
- Spatial Correlations
- Spatial Regression

EXPLORATORY ANALYSIS

The sample data frame `sids` contains spatial data collected on a *lattice*. The collection points are counties in the state of North Carolina, and the data are the rates of death from Sudden Infant Death Syndrome (SIDS) for the years 1974-1978 (Cressie, 1993)[1]. The components of the SIDS data frame are:

```
> names(sids)
[1] "id"          "easting"     "northing"    "sid"
[5] "births"      "nwbirths"    "group"
[8] "sid.ft"      "nwbirths.ft"
>
```

Data for the years 1979-1984 are also available in `sids2`. See the `sids` help file for explanations of the individual variables.

To form a spatial lattice, you must have data locations and *neighborhood* information. The locations for the SIDS data are stored in `easting` and `northing`. Neighborhood information is typically stored in a neighbor matrix, where two regions *i* and *j* are neighbors if the *ij*-th element of the neighbor matrix is non-zero. In S+SPATIALSTATS, neighbor information is stored in an object of class "`spatial.neighbor`", a sparse matrix representation of the neighbor matrix. The S-PLUS object `sids.neighbor` already contains the neighbor information for the SIDS data.

To summarize a spatial neighbor:

We can summarize the neighborhood information calling the summary method for a spatial neighbor as follows:

```
> summary(sids.neighbor)
Matrix was NOT defined as symmetric
Number of Regions: 100
Average Number of Connections: 4.020408
Average Weight: 0.1306507
Least Number of Connections: 1 for Regions with Indices:
[1] 10 16 67
Maximum Number of Connections: 8 for Regions with Indices:
```

1. Cressie, Noel A. C. (1993). *Statistics for Spatial Data*, Revised Edition. John Wiley and Sons, New York.

```
[1] 21
Missing Row Indices:
[1] 28 48
Missing Column Indices:
[1] 28 48
Indices of Regions with No Connections (islands):
[1] 28 48
>
```

The resulting summary describes the neighborhood as being defined for 100 regions with varying neighbor weights. Each county has about 4 neighbors on the average with one county having 8 neighbors and 2 having none. The latter are known as "islands" in S+SPATIALSTATS. We can use the row names of the data frame to determine which neighbors are special.

```
> row.names(sids)[21]
[1] "Chowan"
> row.names(sids)[c(28,48)]
[1] "Dare" "Hyde"
>
```

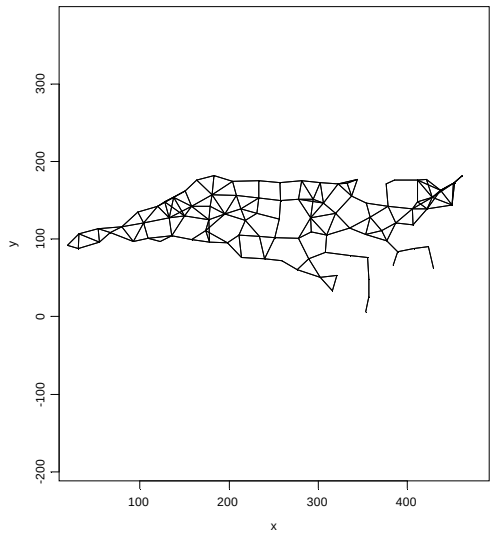
Chowan has the most neighbors while Dare and Hyde counties are isolated.

To plot a spatial neighbor object:

A neighbor object can be plotted from the Command line in version 1.5 of S+SPATIALSTATS by issuing a command such as

```
> plot(sids.neighbor, xc=sids$easting, yc=sids$northing,
+ scaled=T)
```

The following figure is produced:



We see, roughly, the shape of the state of North Carolina, as the county seats are joined by line segments to indicate their neighbor relationship.

SPATIAL NEIGHBORS

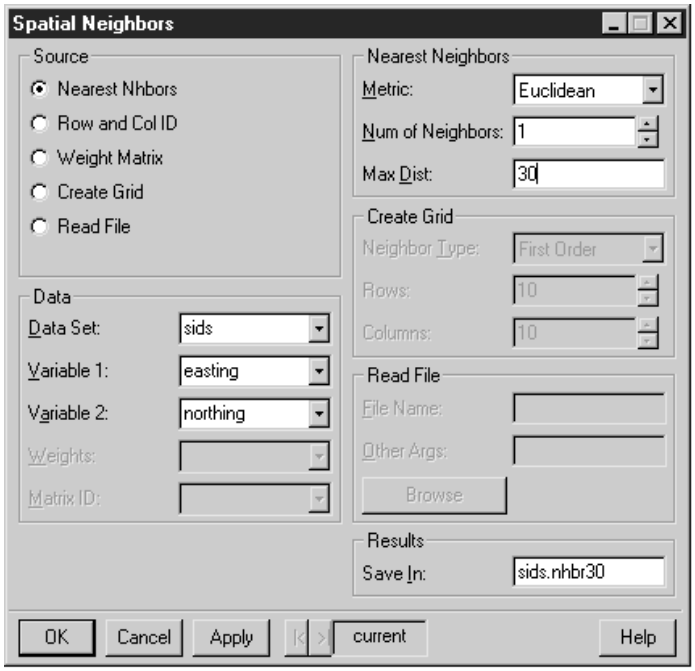
Lattice modeling is the spatial analogue to time series modeling. A time series is modeled by predicting the outcome for each time based on its dependence on the preceding observation or set of observations. A spatial process is modeled by predicting the outcome for each region based partially on its dependence on nearby or neighboring regions. Choosing a neighborhood structure is the first step in the analysis of lattice data. The result determines the covariance structure used for the spatial component of a more general linear regression model.

Neighbors may be defined as regions which border each other, or as regions within a certain distance of each other. The neighbor relationship is not necessarily symmetric. For example, the underlying process may flow in only one direction, or a region that is very large might exhibit influence on, but not be influenced by, a smaller region. Since the neighborhood structure is the basic structure for the covariance model for lattice data, the careful definition of spatial neighbors is a crucial analysis step.

The **Spatial Neighbors** dialog provides a variety of ways to create a spatial neighbor object.

To create a spatial neighbor object:

Choose **Spatial ▶ Spatial Neighbors** from the main menu. The dialog below appears:



Example:

Model the spatial neighborhood structure for the `sids` dataset in S+SPATIALSTATS.

1. Launch **Spatial Neighbors** dialog.
2. Select **Nearest Nhbrs** as the source of neighborhood information. This implies that the neighbors will be defined by distances between point locations and so the location variables will need to be provided.
3. Enter `sids` as the **Data Set** of interest.
4. Select `easting` and `northing` as **Variables 1** and **2** respectively.
5. Specify **Max Dist** of 30, keeping Euclidean as the metric and 1 as the number of neighbors to consider.
6. Enter `sids.nhbr30` in the **Save In** field.

7. Press **OK**.

A Data Window opens containing the spatial neighbor object. We can use this object to compute spatial correlations and perform spatial regression.

Several sources are considered when using the **Spatial Neighbors** dialog depending on how the neighborhood information is stored in S-PLUS or on an ascii file to be read in. These are:

- **Nearest Nhbrs,** to be used when you have point locations.
- **Row and Col ID,** to enter data that is already paired up by neighbors with row and column identifiers for each neighbor pair.
- **Weight Matrix,** if the square matrix containing the neighbor weights is available for input.
- **Create Grid,** to generate regular lattices.
- **Read File,** to browse an ASCII file of varying record length and a set of neighbors per row.

Click the **Help** button on the dialog for more specifics on each of these options and the corresponding S+SPATIALSTATS function.

After using this dialog for your data, make sure that the results are saved and then explore their structure with both the `summary` and `plot` methods illustrated above for objects of class `"spatial.neighbor"`.

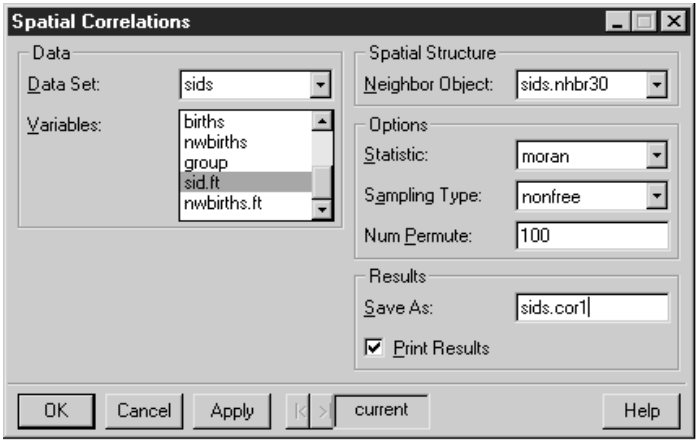
SPATIAL CORRELATIONS

If a process is spatially autocorrelated, there may be a need for spatial modeling. A test for spatial autocorrelation can be performed as an exploratory technique to decide whether spatial modeling should be used. The null hypothesis is of no correlation, and the alternative hypothesis is specifically defined by a weighted neighbor matrix. The result is therefore sensitive to the choice of neighbors and weights, so it may be desirable to run the autocorrelation under several different scenarios. The calculation of spatial autocorrelation assumes constant mean and variance. If the process contains trend or non-constant variance, the results should be used with caution.

The **Spatial Correlations** dialog computes spatial autocorrelation and related estimates of variation.

To compute spatial correlations:

Choose **Spatial ▶ Spatial Correlations** from the main menu. The dialog below appears:



Example:

Calculate Spatial Correlations for the `sids` data. If you haven't already used the data to create the spatial neighbor object `sids.nhbr30`, follow the steps in the previous section before proceeding.

The occurrence of SIDS is not likely to have constant variance, since counties with low birth rates will have more variance. The `sid.ft` column contains rates standardized using the Freeman-Tukey square root transformation. We will look at the spatial correlation of the transformed variable.

1. Launch the **Spatial Correlations** dialog.
2. Select `sids` as the **Data Set**.
3. Select `sids.ft` from the **Variables** list. Notice that multiple selections are allowed.
4. Select `sids.nhbr30` as the **Neighbor Object**.
5. Specify **Statistic** of `moran`, **Sampling Type** of `free`, and **Num Permute** of `100`.
6. Press **OK**.

A summary of the spatial correlation is displayed in a Report window. The small Normal p-value and permutation p-value suggest that spatial autocorrelation is present for this variable.

```
        *** Spatial Correlations **

        Spatial Correlation Estimat

Statistic = "moran" Sampling = "fre

Correlation =  0.259
Variance    =  0.00478
Std. Error  =  0.0691

Normal statistic =  3.89
Normal p-value (2-sided) =  9.927e

Null Hypothesis:  No spatial autocorrelati

Summary of the permutation-correlations
    Min.  1st Qu.   Median     Mean 3rd Qu.   Ma
 -0.1432 -0.08002 -0.01972 -0.01936 0.03252 0.15

permutation p-value =
```

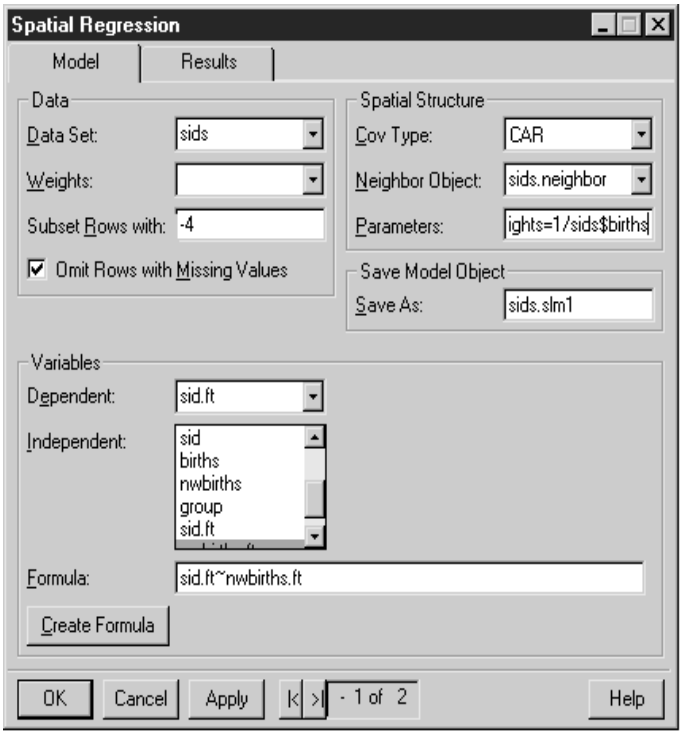
SPATIAL REGRESSION

To model spatial lattices, we look at two levels of variation–large-scale change in the mean due to spatial location or other explanatory variables, and small-scale variation due to interactions with neighbors. The change in mean is modeled as a linear model, taking into account an autoregressive or moving average covariance model reflecting the interactions with neighbors.

The **Spatial Regression** dialog fits a linear model with spatial dependence using generalized least squares regression.

To fit a spatial regression model:

Choose **Spatial ► Spatial Regression** from the main menu. The dialog below appears:



Example:

Fit a Spatial Regression model to the `sids` data frame. See the S+SPATIALSTATS User's Manual for a detailed explanation on the choice of regression variables and Covariance Model. This example is equivalent to the example run on page 131 of the Manual.

1. Launch the **Spatial Regression** dialog.
2. Enter `sids` as the **Data Set** to be modeled.
3. Select the `sid.ft` and `nwbirths.ft` columns as **Dependent** and **Independent** variables, respectively.
4. Enter -4 in the **Subset Rows with** field to remove observation **4** as it was identified as an outlier in section 3.3 of the User's Manual**.**
5. Set the **Cov Type** to `CAR`.
6. Enter `sids.neighbor` as the **Neighbor Object**.
7. To enter spatial weights, consult the help file for the S+SPATIALSTATS function `slm` and enter the argument `weights=1/sids$births` in the **Parameters** text box.
8. Enter `sids.slm1` in the **Save As** field.
9. Press **OK**.

A summary of the spatial regression is displayed in a Report window. It includes the actual call to the S+SPATIALSTATS function `slm`, the coefficients of the regression, their variance-covariance matrix, and other parameters of the spatial relationships and covariance matrix structure. In particular, the coefficients for this model indicate a highly significant effect of non-white births on rates of SIDS in North Carolina.

```
Coefficients
             Value Std. Error t value Pr(>|t
(Intercept) 1.6456 0.2385     6.8990  0.00
nwbirths.ft 0.0345 0.0066     5.2068  0.00
```

Diagnostic plots on the residuals should follow this analysis to assess the adequacy of the model fitted. You can save the residuals by indicating so in the **Results** tab of the **Spatial Regression** dialog. Alternatively, you may extract them from the fitted model using the residuals method as follows:

```
> sids.slm1.resid <- residuals(sids.slm1)
> summary(sids.slm1.resid)
 Min. 1st Qu. Median Mean 3rd Qu. Max.
 -106  -18.79   7.01 3.61   26.27 77.8
> qqnorm(sids.slm1.resid)
```

For example, the sequence of commands above would yield a quantile-quantile normal plot of the residuals to assess the normality assumption.

SPATIAL POINT PATTERNS 5

A mapped spatial point pattern is a collection of points located within a bounded region of space. The points can denote locations of naturally occurring phenomena such as earthquakes or plants, or social events such as the locations of small towns or the occurrences of a particular disease.

The data locations or points might be randomly located, tending to cluster in groups, or follow a regular and predictable pattern. A typical data analysis of a point pattern focuses on the question of whether the point locations are *completely spatially random* (CSR) or whether we should make an attempt to model an apparent lack of spatial randomness.

Formal checks for CSR and modeling techniques for spatial point patterns are described in chapter 6 of the S+SPATIALSTATS User's Manual. In this section, we describe ways to use the GUI of S-PLUS and S+SPATIALSTATS to visualize spatial point patterns and to assess the hypothesis of CSR.

A data set containing the mapped locations of maple and hickory trees in a 19.6 acre square plot in Lansing Woods, Clinton County, Michigan, will be used for the examples in this section (Diggle, 1983)[1]. The data have been scaled so that they reside on the unit square, although this is not necessary for their analysis. See the User's Manual for a more complete description of the data set.

This section describes the following dialogs:

- Spatial Randomness
- Intensity

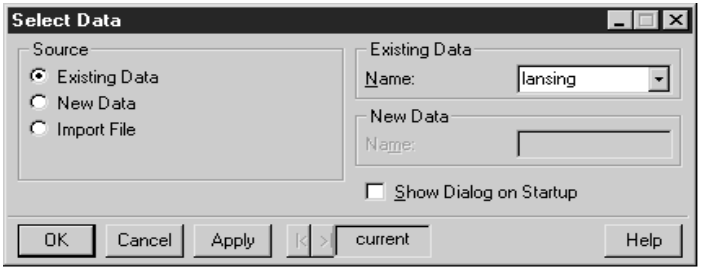
1. Diggle, Peter J. (1983). *Statistical Analysis of Spatial Point Patterns.* Academic Press Inc., New York.

EXPLORATORY ANALYSIS

The exploratory analysis of a spatial point pattern begins with a map of the observations.

To view a spatial point pattern:

1. First open a view of the data on a Data Window. You can do this by selecting **Data ▶ Select Data** from the main menu and then entering `lansing` as the Name of the existing data set desired. The resulting dialog follows:



   You could also use the command line directive:

```
> guiOpenView(Name=lansing, classname="data.frame")
```

2. Proceed by selecting all 3 columns of the data frame in the window, starting with the first column, column `x`.
3. From the **Plots2D** palette, choose a scatter plot by pressing the first button on the top left-hand side corner. A scatter plot of the tree locations appears. In this scatter plot the points will be plotted with a different symbol for each species.

You may change the symbol color and shape independently for each species to suit your taste and help you differentiate the 2 species better.

4. Position the cursor on a data point and right-click.
5. Select **Symbol** from the middle of the resulting context menu.
6. Change the symbol's **Style** and **Color** as preferred, pressing **Apply** to assess each change.
7. Press OK, when satisfied.
8. Repeat steps 4-7 for the other symbol.

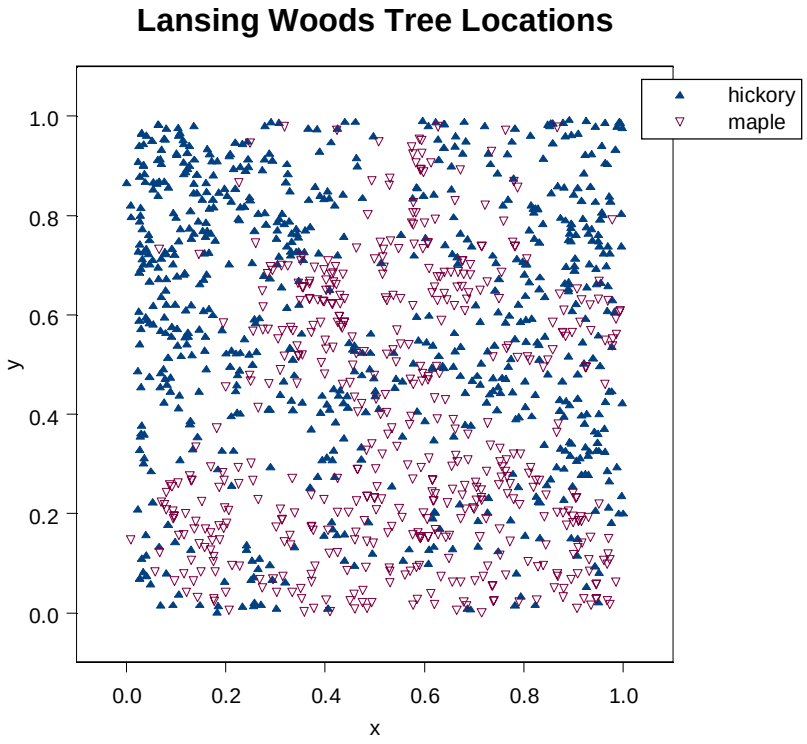
9. Chose **Insert ▶ Legend** from the main menu and insert a legend. Move the legend by dragging it and position as desired on or outside the plot.
10. Chose **Insert ▶ Titles ▶ Main** from the main menu and insert a title on top of the plot.

When plotting spatial data such as these, it is preferable to have both axis scaled the same way for geometric accuracy, that is, a scale that conforms to the actual observation locations.

To scale the axis:

1. Right-click on the plot region of the scatter plot (not on a data point).
2. Select **Position/Size** from the middle of the resulting context menu.
3. Change the **Aspect Ratio** from **Auto** to `1` **(**or set to **Proportional Units)**.
4. Click **OK**.

Insert a title and a legend by choosing **Insert** from the main menu. The resulting plot would look as the one below, perhaps with different symbols depending on your choice:



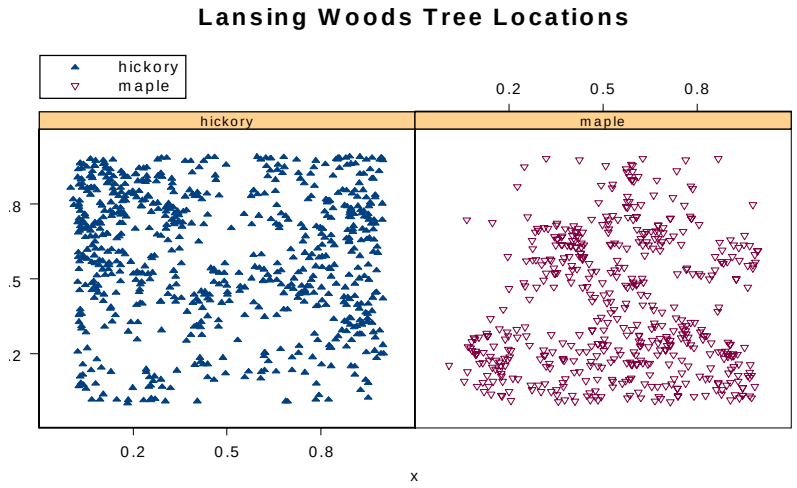
No spatial pattern is immediately obvious as the Lansing Woods data is very dense when the 2 species are taken together. The data is an example of a bivariate point pattern. We can plot the species separately and see if any patterns come to light.

To separate the plot into 2 panels by species:

1. Right-click on the scatter plot region again.
2. This time, select **Multipanel** from the middle of the resulting context menu.
3. From the **Panel Type** drop-down, select **By Plot**. Set **# of Columns** to 2 in the **Layout** group on the same page.

4. Click **OK**.

The figure below appears. Reposition the legend to uncover the axes..



These plots show that there may be interaction between the two tree species. It may be that the presence of one species inhibits the presence of the other.

SPATIAL RANDOMNESS

Typical assumptions of interest for point pattern data are:

1. The intensity of the point pattern does not vary over the boundary region.
2. There are no interactions among the points–points neither inhibit nor encourage each other.

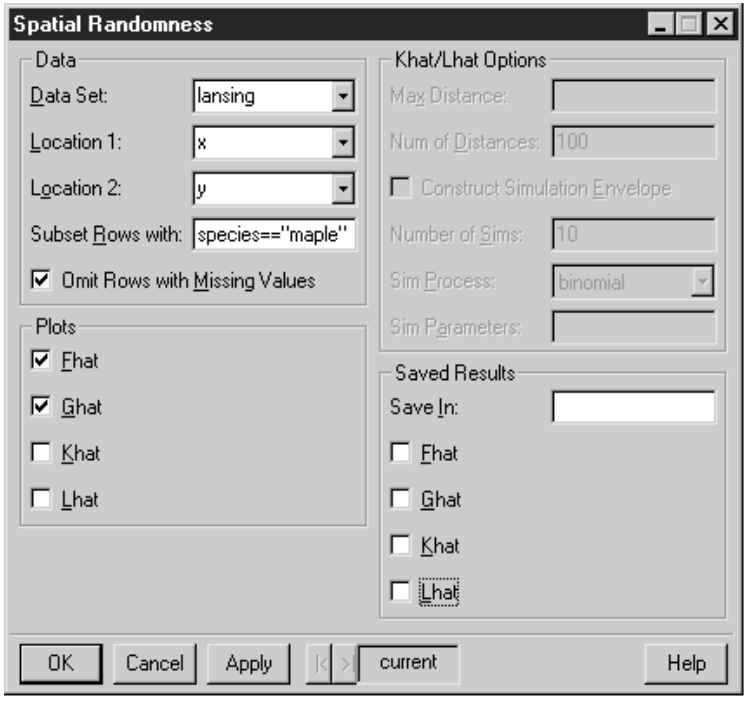
A spatial point pattern with these properties is said to be *Completely Spatially Random*. See Chapter 6 of the S+SPATIALSTATS user's Manual for a more rigorous definition and further examples.

The Fhat and Ghat statistics are useful for assessing the first assumption (constant intensity). The Khat and Lhat statistics are useful for assessing the second assumption (second-order intensity which does not depend on absolute location).

The **Spatial Randomness** dialog provides plots and saved values for Fhat, Ghat, Khat, and Lhat.

To calculate measures of spatial randomness:

Choose **Spatial ▶ Spatial Randomness** from the main menu. The dialog below appears:



Example:

Explore the Spatial Randomness of the `lansing` data frame in S+SPATIALSTATS:

1. Launch **Spatial Randomness** dialog.
2. Enter `lansing` as the **Data Set** of interest.
3. Select `x` and `y` as the **Location 1** and **2** variables, respectively.
4. Type `species=="maple"` in the **Subset Rows with** field. This will subset those rows of the data frame that correspond to the maples only. (Note that another approach would be to choose **Data ▶ Subset** from the main menu, to create a data set of just the maples.)
5. Check **Fhat** and **Ghat** plots.
6. Press **OK**.

A Graph sheet opens displaying the Fhat and Ghat plots for the maples. These are plots of the Empirical Distribution Function (EDF) of the *origin-to-point* (Fhat) and the *point-to-point* (Ghat) nearest neighbor distances for the maples in the Lansing Woods.

Values of Ghat are computed for every neighbor distance in the point process by default. The grid of *origins* in the Fhat calculation is determined by the square root of the total number of points in the given point process. For more specifics on the calculations, consult the individual S+SPATIALSTATS help files for Fhat and Ghat.

Visual judgement of Ghat is based on the fact that if there is clustering in the data, we would expect to see an excess of short distance neighbors, while if there is regularity in the data, then there would be an excess of long distance neighbors.

The interpretation of the Fhat plot is opposite that of the Ghat plot. An excess of high distance values is interpreted as clustering. As before, we could compare this statistic to simulations from a CSR process for a visual interpretation.

When edge effects need to be considered, we can assess the hypothesis of CSR using Monte Carlo techniques. For example, we can simulate the EDF of nearest neighbor distances from several realizations of a CSR process on *A*, the region containing the original point pattern. The average of the simulations provides a reference line, and the maximum and minimum provide a simulation envelope.

The **Spatial Randomness** dialog provides the ability to draw simulation envelopes for both the Khat and Lhat statistics.

To compute a simulation envelope for an estimate of Lhat:

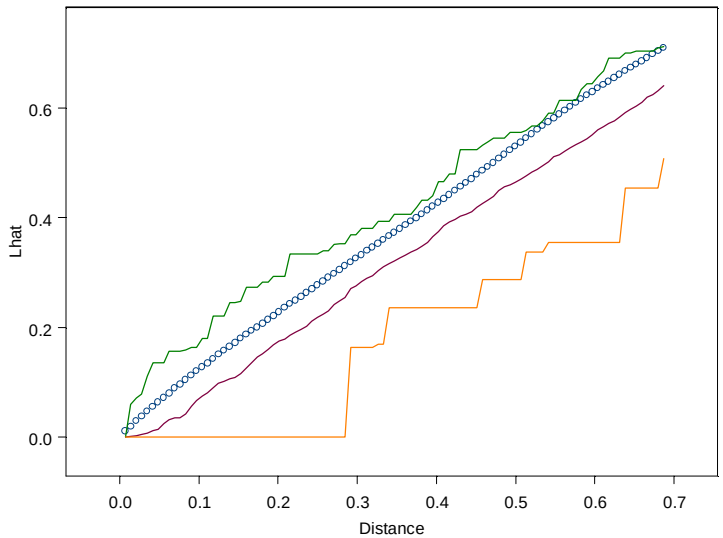
1. Launch **Spatial Randomness** dialog.
2. Enter `lansing` as the **Data Set** of interest (or press the Roll Back button and skip to step 5).
3. Select `x` and `y` as the **Location 1** and **2** variables, respectively.
4. Type `species=="maple"` in the **Subset Rows with** field. This will subset those rows of the data frame that correspond to the maples only.
5. Check **Lhat** plot. The **Khat/Lhat Options** group is enabled.

6. Check **Construct Simulation Envelope** and specify 50 simulations to estimate the envelope.
7. Select `"poisson"` as the process to simulate.
8. Set the lambda parameter of the Poisson to 10 by entering `lambda=10` in the **Sim. Parameters** field.
9. Press OK.

Warning:

The number of simulations does not need to be large, and in fact if a large number of simulations is requested, S-PLUS may take a long time to complete the simulations.

The picture below appears:



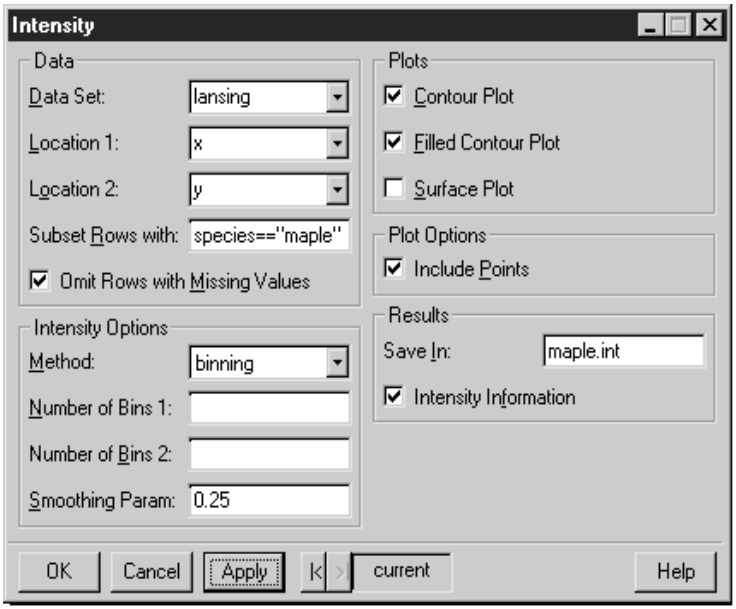
The second-order properties of spatial point processes describe how the interaction or spatial dependence between points varies through space. These properties are usually described by the second-order intensity of the spatial point pattern. An alternative description of the second order properties is defined by the *K-function* defined in section 6.3.2 of the S+SPATIALSTATS User's Manual.

INTENSITY

The intensity of a point pattern is the mean number of points per unit area. Intensity plots display a smooth estimate of intensity for a spatial point pattern. The intensity estimate may be saved and displayed in a Data window for further exploration using the point-and-click graphics.

To calculate intensity:

Choose **Spatial ▶ Intensity** from the main menu. The dialog below appears:



Example:

Calculate and plot the intensity for the `lansing` data in S+SPATIALSTATS

1. Launch **Intensity** dialog.
2. Enter `lansing` as the **Data Set** of interest.
3. Select `x` and `y` as the **Location 1** and **2** variables, respectively.

4. Type `species=="maple"` in the **Subset Rows with** field. This will subset those rows of the data frame that correspond to the maples only.
5. Select `"binning"` as the **Method**.
6. Specify `0.25` as the **Smoothing Parameter.**
7. Check the **Contour Plot**, and **Filled Contour Plot** boxes.
8. Check **Include Points**.
9. Type `maple.int` into the **Save In** field.
10. Click **OK.**

A graph sheet appears with the intensity plots, and a Data window with the intensity estimates.

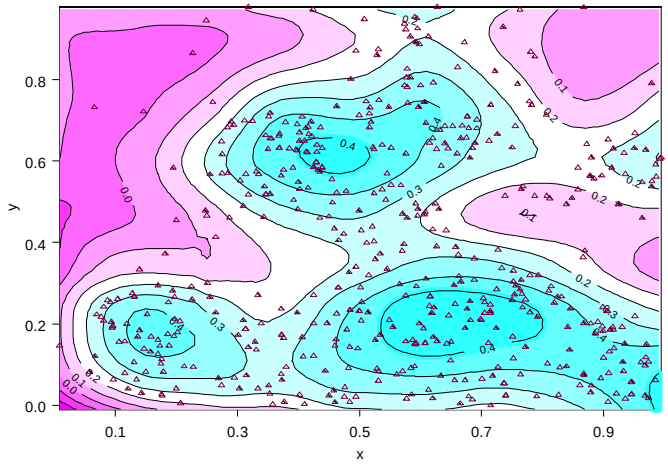
Having the estimates of intensity of the maple process on a Data Window helps you to continue with other visualization of the data. For example:

11. Select all three columns in the `maple.int` Data window.
12. Open the **Plots3D** palette. Press the **32 Color Surface** button to create a filled surface plot of intensity.

You may also rotate the resulting plot and get different views of its peaks and valleys in doing so.

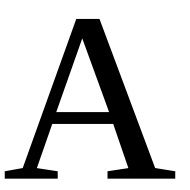
Three methods are available to estimate the intensity of a spatial point pattern using the **Intensity** dialog in S+SPATIALSTATS: *binning*, *kernel*, and *gauss2d*. These three methods estimate the intensity locally over the total region *A*, and return a data frame containing smoothed intensity estimates which may vary over *A*, as well as interpolated **x** and **y** values to facilitate plotting. Several S-PLUS 3D plot types can then be used to visualize this variation and to assess the hypothesis of a constant intensity throughout the sampling area.

The *binning* method uses a two-dimensional histogram to form rectangular bins. The counts in these bins are smoothed using a loess smoothing algorithm. Using the binning method for the maple data as explained in the sequence above yielded the following plot:



All of the intensity estimation and other visualization techniques used in this section show that the intensity of the maple trees in the Lansing Woods appears to vary more than would be expected by random fluctuations. This might be due to the deficit of maple trees in the north corners of the plot, which might be explained by interaction with hickory trees.

APPENDIX A: DATA AND FUNCTION REFERENCE



The functions and data sets described in this appendix are included with S+SPATIALSTATS. The information in this appendix is also found in the online help. For more information on accessing the online help, see Chapter 2, Getting Started.

anisotropy.plot Explore Corrections For Geometric Anisotropy **anisotropy.plot**

DESCRIPTION

Computes corrections for geometric anisotropy for two dimensional spatial data and plots variograms based on the corrections.

USAGE

```
anisotropy.plot(formula=formula(data), data=sys.parent(),
                subset, na.action, lag=<<see below>>,
                nlag=20, tol.lag=lag/2, maxdist=<<see below>>,
                angle=c(0, 45, 90, 135),
                ratio=seq(1.25, 2, length = 4),
                minpairs=6, method="classical",
                smooth=T, plot.it=T, panel=panel.xyplot, ...)
```

REQUIRED ARGUMENTS

`formula` formula defining the response and the predictors. In general, its form is:

```
z ~ x + y
```

The `z` variable is a numeric response. Variables `x` and `y` are the locations. All variables in the formula must be vectors of equal length with no missing values (`NA`s). The formula may also contain expressions for the variables, for example, `sqrt(count)`, `log(age+1)` or `I(2*x)`. (The `I()` is required since the `*` operator has a special meaning on the right side of a formula.)

OPTIONAL ARGUMENTS

`data` an optional data frame in which to find the objects mentioned in `formula`.

`subset` expression saying which subset of the rows of the data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included.

`na.action` a function to filter missing data. This is applied to the `model.frame` after any `subset` argument has been used. The default (with `na.fail`) is to create an error if any missing values are found. A possible alternative is `na.omit`, which deletes observations that contain one or more missing values.

`lag` a numeric value, the width of the lags. If missing, `lag` is set to `maxdist / nlag`.

`nlag` an integer, the maximum number of lags to calculate.

`tol.lag` a numeric value, the distance tolerance.

`maxdist` the maximum distance to include in the returned output. The default is half the maximum distance in the transformed data.

`angle` a vector of direction angles (in degrees, clockwise from North) to consider as directions of anisotropy.

`ratio` a vector of ratios of anisotropy. These should all be greater than 1.

`minpairs` the minimum number of pairs of points (minimum value for `np`) that must be used in calculating a variogram value. If `np` is less than `minpairs`, that value is dropped from the variogram.

`method` a character string to select the method for estimating the variogram. The possible values are `"classical"` for Matheron's (1963) estimate and `"robust"` for Cressie and Hawkins (1980) robust estimator. Only the first character of the string needs to be given.

`smooth` a logical flag, if `TRUE`, a loess smooth line is drawn for each variogram panel. If `panel` is supplied then this value is ignored.

`panel` a panel function to be used in plotting the variograms. If `plot.it=FALSE`, this value is ignored.

`plot.it` a logical flag, if `TRUE`, a plot of all the variogram is drawn.

`...` additional arguments to be passed down to the panel function for plotting.

VALUE

a data frame with columns:

`distance` the average distance for pairs in the lag.

`gamma` the variogram estimate.

`np` the number of pairs in each lag.

`angle` a factor denoting the angle for the geometric anisotropy.

`ratio` a factor with levels denoting the ratio for the geometric anisotropy.

SIDE EFFECTS

If `plot.it=TRUE` (the default) the variogram for each combination of `angle` and `ratio` is plotted. The plot is drawn using `xyplot`.

DETAILS

For each combination of `angle` and `ratio` the locations are corrected for geometric anisotropy. The correction consists of multipling each location pair (`x[i],y[i]`) by the symmetric 2 x 2 matrix `A` where `A[1,1]=cos(angle)^2+ratio*sin(angle)^2`, `A[1,2]=(1- ratio) * sin(angle) * cos(angle)` and `A[2,2]=sin(angle)^2+ratio*cos(angle)^2`. See Journel and Huijbregts (1978, pp 179-181). The variogram is then estimated using these corrected locations.

REFERENCES

Cressie, N. and Hawkins, D. M. (1980). Robust estimation of the variogram. *Mathematical Geology* **12**, 115-125.

Journel, A. G. and Huijbregts, Ch. J. (1978). *Mining Geostatistics.* Academic Press, New York.

Matheron, G. (1963). Principles of geostatistics. *Economic Geology* **58**, 1246-1266.

SEE ALSO

`loc`, `variogram`, `xyplot`.

EXAMPLES

```
anisotropy.plot(log(tcatch+1) ~ long + lat, data=scallops, lag=.075)
```

`check.islands` Detect Isolated Spatial Regions `check.islands`

DESCRIPTION

Given an object of class `"spatial.neighbor"` detects spatial units that have no neighbors (islands).

USAGE

```
check.islands(x, remap=F)
```

REQUIRED ARGUMENTS

`x` an object of class `"spatial.neighbor"`.

OPTIONAL ARGUMENTS

`remap` logical flag: if there is an island, should we recode the indexing of the spatial contiguity matrix to eliminate the rows and columns with all zeroes? That is, should we renumber components `row.id` and `col.id` of the spatial neighbor object?

VALUE

if `remap=FALSE` the list of existing islands is returned. Otherwise, an object of class `"spatial.neighbor"` with remapped `row.id` and `col.id`.

SIDE EFFECTS

the attribute `"nregion"` of the output may differ from that of `x` when `remap=T`.

SEE ALSO

`spatial.neighbor`, `spatial.subset`, `spatial.weights`

EXAMPLES

```
sids.nhbr2 <- check.islands(sids.neighbor,remap=T)
```

`find.neighbor` Find the Nearest Neighbors of a Point `find.neighbor`

DESCRIPTION

Find the k nearest neighbors of a vector `x` in a matrix of data contained in an object of class `"quad.tree"`.

USAGE

```
find.neighbor(x, quadtree=quad.tree(x), k=1, metric="euclidean",
              max.dist=NULL, drop.self=F)
```

REQUIRED ARGUMENTS

`x` a vector (or matrix) containing the multidimensional point(s) at which the nearest neighbors are desired. The vector must have the same number of elements as the number of columns in the numeric matrix used to construct `quadtree`. If a matrix is used, the matrix must have the same number of columns as the numeric matrix used to construct `quadtree`, and nearest neighbors are found for each row in the matrix.

OPTIONAL ARGUMENTS

`quadtree` an object of class `"quad.tree"` containing the sorted matrix of data for which a nearest neighbor search is desired. Defaults to `quad.tree(x)` if `x` is a matrix but it is required when `x` is a vector.

`k` the number of nearest neighbors to be found. If the data `x` is the same data that was used to construct the `"quad.tree"` object, then `k = 1` results in each element having itself as its own nearest neighbor.

`metric` a character string giving the metric to be used when finding "nearest" neighbors. Partial matching is allowed. Possible values are: `"euclidean"`, `"city block"`, and `"maximum absolute value"` for the l_2, l_1, and l_∞ norm, respectively. For two vectors x and y, these are defined as:

$$l_1 = \sum_i |x_i - y_i|,$$

$$l_2 = \sqrt{\sum_i (x_i - y_i)^{2)}},$$

$$l_\infty = \max_i |x_i - y_i|$$

`max.dist` if `max.dist` is given, argument `k` is ignored, and all of the neighbors within distance `max.dist` of each row in `x` are found.

`drop.self` a logical value, if `TRUE` then rows with `distances` equal to `0` and `index1 == index2` (self neighbors) are dropped from the returned object. This definition retains coincident points as neighbors although their distance apart is zero. If `quadtree` is not supplied, `k=1`, and `drop.self=T`, a warning is printed (since this results in nothing being returned) and the value of `k` is set to `2`.

VALUE

a matrix with three named columns:

`index1` if `x` is a matrix, the row in `x` for this nearest neighbor. If `x` is not a matrix, the value 1.
`index2` the row in the matrix from which the quad tree was formed for this nearest neighbor. If the quad tree was formed from a matrix `y`, then x[index1[i],] and y[index2[i],] are neighbors.
`distances` the corresponding nearest neighbor distances.

DETAILS

An efficient recursive algorithm is used to find all nearest neighbors. First the quad tree is traversed to find the leaf with medians nearest the point for which neighbors are desired. Then all observations in the leaf are searched to find nearest neighbors. Finally, if necessary, adjoining leaves are searched for nearest neighbors.

REFERENCES

Friedman, J., Bentley, J. L., and Finkel, R. A. (1977). An algorithm for finding best matches in logarithmic expected time. *ACM Transactions on Mathematical Software* **3**, 209-226.

SEE ALSO

`quad.tree`.

EXAMPLES

```
x <- cbind(sids$easting, sids$northing)
sids.nhbr <- find.neighbor(x, max.dist = 30)

# Find the nearest neighbors for the Lansing hickories
hickory <- lansing[lansing[,3] == "hickory", 1:2]
hickory.nhbr1 <- find.neighbor(hickory, k=2, drop.self=T)

# Now find the closest maple for each hickory
maple <- lansing[lansing[,3] == "maple", 1:2]
hmn <- find.neighbor(hickory, quad.tree(maple))
# and plot the tree locations with lines joing the neighbors
par(pty='s')
plot(maple[,1], maple[,2], pch=16)
points(hickory[,1], hickory[,2], pch=1, col=2)
segments(hickory[hmn[,1],1], hickory[hmn[,1],2],
     maple[hmn[,2],1], maple[hmn[,2],2])
```

`Glasgow.neighbor` Neighbors for Glasgow Mortality Rate Data `Glasgow.neighbor`

SUMMARY

An object of class `"spatial.neighbor"` containing the neighbor specification among the 87 community medicine areas in Glasgow, Scotland. The standardized mortality rate (SMR) values for this data are contained in `Glasgow.SMR`.

DATA DESCRIPTION

Four hundred and fifty neighbor relationships are specified. The neighbor relationships are not symmetric. See `spatial.neighbor.object` for a description of the data within an object of class `"spatial.neighbor"`.

SOURCE

The data are presented and analyzed in Haining (1990).

REFERENCES

Haining, R. (1990). *Spatial Data Analysis in the Social and Environmental Sciences.* Cambridge University Press. Cambridge.

SEE ALSO

`Glasgow.SMR`.

`Glasgow.SMR` Standardized Mortality Rates for Glasgow **`Glasgow.SMR`**

SUMMARY

The `Glasgow.SMR` data frame contains standardized mortality rates for 87 community medicine areas in Glasgow, Scotland for 1980-1982.

DATA DESCRIPTION

This data frame contains the following columns:

`AllDeaths`	the standardized mortality rate (SMR) for all deaths.
`Accidents`	the SMR for death by accidents.
`Cancer`	the SMR for deaths due to cancer.
`Respiratory`	the SMR for deaths due to respiratory disease accidents.
`Heart`	the SMR for deaths due to ischaemic heart disease.
`Cerebrovascular`	the SMR for deaths due to cerebrovascular disease.
`Population`	the population (in 1000's).
`Easting`	the x coordinate of the community medicine area (CMA) relative to an arbitrary origin, where the x-axis is parallel to the latitude.
`Northing`	the y coordinate of the CMA relative to an arbitrary origin, where the y-axis is parallel to the longitude.

DETAILS

The standardized mortality rate for a community medicine area is the observed deaths due to that cause divided by the expected number of deaths given the age and sex combination in that area multiplied by 100.

SOURCE

The data are presented and analyzed in Haining (1990).

REFERENCES

Haining, R. (1990). *Spatial Data Analysis in the Social and Environmental Sciences.* Cambridge University Press. Cambridge.

SEE ALSO

`Glasgow.neighbor`.

Kenv Compute Simulations of `Khat` **Kenv**

DESCRIPTION

Computes `Khat` (`Lhat`) for simulations of point processes. Returns upper and lower bounds, as well as the average of all simulated values.

USAGE

```
Kenv(object, nsims=100, maxdist=<<see below>>, ndist=100,
     process="binomial", boundary=bbox(object), add=T, ...)
Lenv(object, nsims=100, maxdist=<<see below>>, ndist=100,
     process="binomial", boundary=bbox(object), add=T, ...)
```

REQUIRED ARGUMENTS

`object` an object of class `"spp"` representing a spatial point pattern, or a data frame or matrix with first two columns containing locations of a point pattern.

OPTIONAL ARGUMENTS

`nsims` integer. Number of desired simulations.

`maxdist` numeric value indicating the maximum distance at which `Khat` (or `Lhat`) should be estimated. Defaults to half the length of a diagonal of the sample's bounding box.

`ndist` desired number of default distances at which to compute `Khat` (or `Lhat`). Default is `100`.

`process` a character string with one of five possible processes for the spatial arrangement of the resulting pattern. This must be one of `"binomial"`, `"poisson"`, `"cluster"`, `"Strauss"`, or `"SSI"`. See the help file for `make.pattern` for information on parameters for each process.

`add` logical flag: should the envelope be added to an already existing plot of `Khat` (or `Lhat` for `Lenv`)? Defaults to `TRUE`.

`...` other parameters as needed by the requested process.

VALUE

invisibly returns a list with 4 numeric vectors each representing:

`dist` the distances at which all values were computed.

`lower` the minimum of all resulting `Khat` (or `Lhat` for `Lenv`) for the simulations.

`upper` the maximum of all resulting `Khat` (or `Lhat` for `Lenv`) for the simulations.

`average` the average of all resulting `Khat` (or `Lhat` for `Lenv`) for the simulations.

SIDE EFFECTS

if `add=TRUE` an envelope is added to an existing plot of `Khat`.

SEE ALSO

`Khat`, `Lhat`, `make.pattern`.

EXAMPLES

```
Khat(bramble)
Kenv(bramble,nsims=50)
Lhat(lansing)
Lenv(lansing,nsims=50)
```

Khat Ripley's K Function for a Spatial Point Pattern Object **Khat**

DESCRIPTION

Calculates `K(t)`, Ripley's K function for a spatial point pattern.

USAGE

```
Khat(object, maxdist=<<see below>>, ndist=100, boundary=bbox(object),
     plot.it=T)
```

REQUIRED ARGUMENTS

`object` an object of class `"spp"` representing a spatial point pattern, or a data frame or matrix with first two columns containing locations of a point pattern.

OPTIONAL ARGUMENTS

`maxdist` numeric value indicating the maximum distance at which `Khat` should be estimated. Defaults to half the length of a diagonal of the sample's bounding box.

`ndist` desired number of default distances at which to compute `Khat`. Default is `100`. The distances for which `Khat` will be estimated are calculated as `seq(0,maxdist,ndist)`, both `maxdist` and `ndist` will change if not reasonable for the given `object`.

`boundary` points defining the boundary polygon for the spatial point pattern. This version accepts only rectangles, for which `boundary` should be given as a list with named components `"x"` and `"y"` denoting the corners of the rectangular region. For example, for the unit square the boundary could be given as `bbox(x=c(0,1),y=c(0,1))`, the bounding box of two diagonally opposed points. Defaults to a rectangle covering the range of points.

`plot.it` logical flag: should the resulting `K`-estimates be plotted? Default is `TRUE`.

VALUE

a list containing components :

`values` a two column matrix. The first column, named `dist`, contains the distances at which `Khat` was computed, and the second column, named `Khat`, contains the values of `K(dist)`.

`ndist` number of distances returned. This could be smaller than its input value if the extent of the distances is too large.

`mindist` minimum distance between any pair of points.

`maxdev` maximum deviation from `K(t)=t`. See DETAILS.

SIDE EFFECTS

if `plot.it=TRUE`, a plot of the value of `K(t)` against distance will be produced on the current graphics device.

DETAILS

`Khat` computes Ripley's (1976) estimate of K(t) for a spatial point pattern:

$$K(t) = \lambda^{-1} E[\textit{number of events} \leq \textit{distance } t \textit{ of an arbitrary event}].$$

where λ is the intensity of the spatial point pattern.

The theoretical K-function for a Poisson (completely spatially random) process is $K(t) = \pi t^2$, so $L(t) = \sqrt{K(t)/\pi}$ is equal to `t`, the distances. The default plots `K(t)` versus `t`. See function `Lhat` for estimation of `L(t)`.

REFERENCES

Ripley, Brian D. (1976). The second-order analysis of stationary point processes. *Journal of Applied*

Probability, **13**,255-266.

SEE ALSO

`Kenv`, `Lhat`.

EXAMPLES

```
lansing.spp <- as.spp(lansing)
lansing.khat <- Khat(lansing.spp)
Khat(wheat)
abline(0,1)
```

`krige` Ordinary and Universal Kriging `krige`

DESCRIPTION

Performs ordinary or universal kriging for two dimensional spatial data. The function `predict.krige` can then be called to compute interpolation surfaces and prediction errors.

USAGE

```
krige(formula, data=sys.parent(), subset, na.action=na.fail,
      covfun, nc=10000, ...)
```

REQUIRED ARGUMENTS

`formula` a formula describing the kriging variable and the spatial location variables and optionally a polynomial trend surface. Its simplest form is:

```
z ~ loc(x,y)
```

where `z` is the kriging variable and `x` and `y` are the spatial locations, that is, `z[i]` is observed at the location (`x[i],y[i]`). The right hand side must contain a call to the function `loc`. A polynomial trend surface is of the form:

```
z ~ loc(x,y) + x + y + x^2 + y^2
```

The polynomial must be in the same variables as the first two arguments used in the `loc` function. A constant term is always fit. All terms on the right hand side must be entered with a `+` sign. The `loc` call can include arguments `angle` and `ratio` to correct for geometric anisotropy; see the `loc` help file. Note that an evaluated `loc` object cannot be used in `formula`.

`covfun` a function that returns the distanced based covariance between two points. The first argument to the function must be the distance. Additional parameters will be passed through the `...`.

OPTIONAL ARGUMENTS

`data` an optional data frame in which to find the objects mentioned in `formula`.

`subset` expression saying which subset of the rows of the data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included.

`na.action` a function to filter missing data. This is applied to the data in `formula` after any `subset` argument has been used. The default (with `na.fail`) is to create an error if any missing values are found. A possible alternative is `na.omit`, which deletes observations that contain one or more missing values.

`nc` the number of points to use internally by the algorithm in approximating the distance-based covariance function. Note: this argument has nothing to do with the number of observed points used in computing the kriging. All observed points are used in computing kriging predictions.

`...` additional named arguments can be passed to `covfun`.

VALUE

an object of class `"krige"` with components:

`x` the first spatial location vector i.e. the first argument in `loc` function call in `formula`.

`y` the second spatial location vector i.e. the second argument in `loc` function call in `formula`.

`coefficients` the vector of coefficients for the trend surface. These are for the polynomial based on the scaled spatial location vectors (see the DETAILS section).

`residuals` the vector of residuals from the trend surface.

`call` an image of the call that produced the object.

Other components are included that are used by `predict.krige` for computing interpolations.

DETAILS

The kriging system is solved using generalized least squares (see Ripley, 1981). The polynomial terms are scaled to (-1, 1) internally to avoid numeric problems; the `coefficients` component returned is for these scaled terms.

This implementation of kriging does not handle multiple observations at a point.

Methods for objects of class `"krige"` include `predict` and `print`.

REFERENCES

Cressie, Noel A. C. (1993). *Statistics for Spatial Data*, Revised Edition. Wiley, New York.

Ripley, Brian D. (1981). *Spatial Statistics.* Wiley, New York

SEE ALSO

`exp.cov`, `loc`, `predict.krige`.

EXAMPLES

```
# krige the Coal Ash data with a quadratic trend in the x direction
#   using a spherical covariance function:
kcoal <- krige(coal ~ loc(x, y) + x + x^2, data = coal.ash,
        covfun = spher.cov, range = 4.31, sill = 0.14, nugget = 0.89)
# predictions over default 30 x 30 grid
pcoal <- predict(kcoal)
# plot prediction surface
wireframe(fit ~ x * y, data = pcoal,
        screen = list(z = 300, x = -60, y = 0), drape = T)
```

Lhat — Ripley's K Function for a Spatial Point Pattern Object — Lhat

DESCRIPTION

Calculates `L(t)=sqrt(K(t)/pi)`, where `K(t)` is Ripley's K function for a spatial point pattern and `L(t)` is linear for a completely random point process.

USAGE

```
Lhat(object, maxdist=<<see below>>, ndist=100, boundary=bbox(object),
     plot.it=T)
```

REQUIRED ARGUMENTS

`object` an object of class `"spp"` representing a spatial point pattern, or a data frame or matrix with first two columns containing locations of a point pattern.

OPTIONAL ARGUMENTS

`maxdist` numeric value indicating the maximum distance at which `Lhat` should be estimated. Defaults to half the length of a diagonal of the sample's bounding box.

`ndist` desired number of default distances at which to compute `Lhat`. Default is `100`. The distances for which `Lhat` will be estimated are calculated as `seq(0,maxdist,ndist)`, both `maxdist` and `ndist` will change if not reasonable for the given `object`.

`boundary` points defining the boundary polygon for the spatial point pattern. This version accepts only rectangles, for which `boundary` should be given as a list with named components `"x"` and `"y"` denoting the corners of the rectangular region. For example, for the unit square the boundary could be given as `bbox(x=c(0,1),y=c(0,1))`, the bounding box of two diagonally opposed points. Defaults to a rectangle covering the range of points.

`plot.it` logical flag: should the resulting `K`-estimates be plotted? Default is `TRUE`.

VALUE

a list containing components :

`values` a two column matrix. The first column, called `dist`, contains the distances at which `Lhat` was computed, and the second column, called `Lhat`, contains the values of `L(dist)`.

`ndist` number of distances returned. This could be smaller than its input value if the extent of the distances is too large.

`mindist` minimum distance between any pair of points.

`maxdev` maximum deviation from `L(t)=t`. See DETAILS.

SIDE EFFECTS

if `plot.it=TRUE`, a plot of the value of `L(t)` against distance will be produced on the current graphics device.

DETAILS

`Khat` computes Ripley's (1976) estimate of K(t) for a spatial point pattern:

$$K(t) = \lambda^{-1} E[\textit{number of events} \leq \textit{distance } t \textit{ of an arbitrary event}].$$

where λ is the intensity of the spatial point pattern.

The theoretical K-function for a Poisson (completely spatially random) process is $K(t) = \pi t^2$, so $L(t) = \sqrt{K(t)/\pi}$ is equal to `t`, the distances. The default plots `L(t)` versus `t` which should approximate a straight line for a homogeneous process with no spatial dependence. See function `Khat` for estimation of `K(t)`.

REFERENCES

Ripley, Brian D. (1976). The second-order analysis of stationary point processes. *Journal of Applied Probability* **13**,255-266.

SEE ALSO

`Lenv`, `Khat`.

EXAMPLES

```
lansing.spp <- as.spp(lansing)
lansing.khat <- Lhat(lansing.spp)

Lhat(wheat)
abline(0,1)
```

make.pattern Generate a Spatial Point Process **make.pattern**

DESCRIPTION

Generates points in two-dimensional space given their desired spatial distribution.

USAGE

```
make.pattern(n, process="binomial", object, boundary=bbox(x=c(0,1),
             y=c(0,1)), lambda, maxlambda, radius, cpar)
```

REQUIRED ARGUMENTS

`n` integer denoting the desired number of points in the resulting object.

OPTIONAL ARGUMENTS

`process` a character string with one of five possible processes for the spatial arrangement of the resulting pattern. This must be one of `"binomial"`, `"poisson"`, `"cluster"`, `"Strauss"`, or `"SSI"`. See the DETAILS section for each definition. Defaults to `"binomial"` for a completely spatially random process conditioned to `n` points within `boundary`. Partial matching is allowed.

`object` a spatial point pattern object. An object of class `"spp"`. When this is given, the resulting pattern has the same `n` and its `boundary` is that same as the bounding box of `object`.

`boundary` points defining the boundary polygon for the spatial point pattern. This version accepts only rectangles, for which `boundary` should be given as a list with named components `"x"` and `"y"` denoting the corners of the rectangular region. For example, for the unit square the boundary could be given as `bbox(x=c(0,1),y=c(0,1))`, the bounding box of two diagonally opposed points. Defaults to `bbox(object)` if `object` is given or to the unit square otherwise.

`lambda` the intensity when `process="poisson"`. If `lambda` is a numerical value then `make.pattern` simulates a two dimensional homogeneous Poisson process with that constant intensity. `lambda` can also be a function with two arguments that defines the intensity over the region. `n`, if given, will be ignored if this argument is provided.

`maxlambda` if `lambda` is a function then this should be the maximum value of the function over the region. If this is not supplied, a nonlinear optimization will be run (using `nlminb`) to find the maximum. Supplying this value will speed up the simulation and avoid any possible problems with the nonlinear optimization. `maxlambda` is used only if `lambda` is a function.

`radius` the inhibition distance. This is needed for process `"Strauss"`, `"SSI"` and `"cluster"`. Options `"Strauss"` and `"SSI"` will NOT generate points closer than `radius`. For this reason, this parameter needs to be reasonably small. The exception is when `process="cluster"` in which case it should contain the desired size of the clusters. See DETAILS section for more information.

`cpar` the inhibition parameter needed when `process="Strauss"`. This parameter is also required if `process="cluster"`. In that case, it represents the intensity of the "parent" Poisson process which will determine the random placement of clusters and their number. See the DETAILS section for more information.

VALUE

an object of class `"spp"` whose `n` points are distributed according to `process`. If `process="poisson"` results on a process with zero points, the returned value will be a classless matrix with zero rows and a warning will be issued.

DETAILS

The `"binomial"` process option generates a spatially random pattern of `n` points within the given `boundary`. This is in essence a homogeneous Poisson process conditional on the given number of points `n`.

The `"poisson"` process option generates a Poisson process with intensity `lambda`. This argument is required for this option. If `lambda` is a function the Poisson process is generated by a rejection sampling algorithm (Diggle, 1983): a homogeneous Poisson process with intensity `maxlambda` is generated over the region and then points are retained with probability `lambda(x, y)/maxlambda`.

The `"SSI"` process generates a random pattern where no two points are within the inhibition distance determined by its parameter `radius`. This process is equivalent to sequentially laying down discs of radius `radius` which will not overlap.

The `"Strauss"` process accepts each randomly generated point with probability `cpar^s` where `s` is the number of existing points within radius `radius` of the potential new point. The parameter `cpar` must be in [0,1] for this process, where `cpar=0` corresponds to complete inhibition at distances up to `radius`.

The user should exercise caution when determining the value of `radius`, for if it is too big in relation to the area defined by `boundary`, the algorithm will run out of possible area to place the subsequent disc and the generation of the desired process may be impossible or very slow.

The option `"cluster"` generates a Poisson cluster process. This is defined by generating a "parent" Poisson process with intensity `cpar` and a "daughter" process of clusters with radii determined by the value of `radius`.

WARNING

If `radius` is too large, it may be impossible or nearly impossible to generate the number of requested points. The call may "hang" in some extreme cases.

REFERENCES

Diggle, Peter J. (1983). *Statistical Analysis of Spatial Point Patterns.* Academic Press, London.

Ripley, Brian D. (1981). *Spatial Statistics.* John Wiley & Sons, New York.

Ripley, Brian D. (1976). The second-order analysis of stationary point processes. *Journal of Applied Probability* **13**,255-266.

SEE ALSO

`runif`, `rnorm`, `rpois`, `rbinom`.

EXAMPLES

```
# A completely random process in the unit square
rand <- make.pattern(100)

plot(make.pattern(100, process="Strauss", rad=0.1, c=0.5))

plot(make.pattern(500, proc="cluster", rad=20, c=10,
       boundary=list(x=c(0,200), y=c(0,200))))

# A nonhomogeneous Poisson pattern with a linear trend in x
#  over a 10 x 10 square
lxy <- function(x, y) 1.5*x
xy <- make.pattern(proc="poisson", boundary=bbox(x=c(0,10),
       y=c(0,10)), lambda=lxy)
plot(xy)
```

`model.variogram` Display a Variogram Object and Theoretical Model **`model.variogram`**

DESCRIPTION

Plots an empirical variogram object and displays the fit of a theoretical variogram model on that plot. Optionally allows interactive parameter updates to the theoretical model and displays the new fit.

USAGE

```
model.variogram(object, fun, ..., ask=T, objective.fun=<<see below>>,
                plot.it=T)
```

REQUIRED ARGUMENTS

`object` an object that inherits from class `"variogram"` (this includes classes `"covariogram"` and `"correlogram"`). The `azimuth` column should have only one level.

`fun` a theoretical variogram function (or covariogram or correlogram function, depending on the class of `"object"`). Its first argument should be distance. Its remaining arguments are considered parameters that can be changed to update the fit of `fun` to `object`.

OPTIONAL ARGUMENTS

`...` additional arguments to `fun` that do not have default values must be specified here by full name.

`ask` a logical value, if `TRUE`, a command line menu is displayed allowing the user to change the values of the parameters to `fun`. After changing a value the plot is updated. If `FALSE`, the data in `object` is plotted, the value of `fun` evaluated at `object$distance` is added to the graph, and the function returns.

`objective.fun` a function with three arguments, `y`, `yf`, and `n` that gives a measure of the fit of `yf` to `y` with weights `n`. It is used as a measure of fit of `fun` to the data in `object`. The default is the sum of squared residuals, `sum((y-yf)^2)`.

`plot.it` a logical value, if `TRUE`, a plot of the variogram and its fitted model is displayed.

VALUE

invisibly returns a named list of the final parameters used. This list has the last value of the objective function as an attribute.

DETAILS

This function can be used to fit a variogram or covariogram model "by eye". The value of `objective.fun` is displayed on the plot.

A weighted least squares objective function for variograms (Cressie, 1993, p. 97) is:

```
objective.fun <- function(y,yh,n) sum(n*(y/yh-1)^2)
```

REFERENCES

Cressie, Noel. (1993). *Statistics For Spatial Data*, Revised Edition. Wiley, New York.

SEE ALSO

`correlogram`, `plot.variogram`, `variogram`.

EXAMPLES

```
vg.iron <- variogram(residuals ~ loc(easting, northing), data=iron.ore)
model.variogram(vg.iron, spher.vgram, range=8.7, sill=3.5, nugget=4.8)
```

plot.spatial.neighbor Plot a spatial.neighbor Object **plot.spatial.neighbor**

DESCRIPTION

Plot an object of class "spatial.neighbor" with lines connecting points that are neighbors.

USAGE

```
plot.spatial.neighbor(x, xcoord, ycoord, line.col=1, line.type=1,
                      line.width=1, matrix.id=1, add=F, arrows=F,
                      size.arrow=0.1, scaled=T, ...)
```

REQUIRED ARGUMENTS

`x` an object of class "spatial.neighbor".

`xcoord` a numeric vector containing the x-coordinates of the data whose neighbor relations are defined in `x`.

`ycoord` a numeric vector containing the y-coordinates of the data whose neighbor relations are defined in `x`. Must be the same length as `xcoord`.

OPTIONAL ARGUMENTS

`line.col` a numeric value indicating the color to draw the lines connecting the points that are neighbors. See the `col` parameter in the `par` help file.

`line.type` a numeric value indicating the line type to use for the lines connecting the points that are neighbors. See the `lty` parameter in the `par` help file.

`line.width` a numeric value indicating the line width to use for the lines connecting the points that are neighbors. See the `lwd` parameter in the `par` help file.

`matrix.id` a positive integer indicating which spatial neighbor matrix is to be plotted. Only one spatial neighbor matrix can be plotted per call to the function but objects of class "spatial.neightbor" can contain more than one matrix.

`add` a logical value, if `TRUE` no initial plot is drawn, only the lines joining the neighbors are added to the current plot.

`arrows` a logical value, if `TRUE`, arrows are drawn from each point to its neighbor, if `FALSE`, segments are drawn from each point to its neighbor. Plotting with arrows can be useful when there are one way neighbor relations in `x` i.e. point B is a neighbor of point A but point A is not a neighbor of point B. If `x` is a symmetric spatial neighbor object, (`attr(x,symmetric)` is `TRUE`) then all neighbor relations are bi-directional and setting `arrows=TRUE` just results in a messy graph.

`size.arrows` the size of the arrowhead width in inches. See the `arrows` help file for details.

`scaled` a logical value, if `TRUE` then `scaled.plot` is used to set up the plot coordinates instead of `plot`. This produces an equally scaled plot which is often useful when `xcoord` and `ycoord` are geographic locations.

Graphical parameters may also be supplied as arguments to this function (see `par`).

SIDE EFFECTS

a plot is produced on the current graphics device or lines are added to the current plot (if `add=T`).

DETAILS

The coordinate system for the plot is drawn based on the values in `xcoord`, `ycoord`. The graphical parameters specified in `...` are used to draw this initial graph. If `scaled=TRUE` the `scale.ratio` parameter to `scaled.plot` can also be passed in the `...` arguments. The lines are added through a call to `segments` or `arrows`. The graphical parameters `line.col`, `line.type` and `line.width` are used in the call to `segments` or `arrows`.

This function is a method for the generic function `plot` for class `spatial.neighbor` . It can be invoked by calling `plot` for an object of the appropriate class, or directly by calling `plot.spa-`

tial.neighbor regardless of the class of the object.

BUGS

With S-PLUS 5.1, if you are calling this function as a plot method (i.e. plot) you must specify the xcoord and ycoord arguments by name (not by position) otherwise the wrong method will be called.

SEE ALSO

spatial.neighbor, spatial.neighbor.object, plot, scaled.plot, par, segments.

EXAMPLES

```
# Plot the sids.neighbor object using the easting and northing
#   values from sids as the coordinates
plot(sids.neighbor, xc=sids$easting, yc=sids$northing, scaled=T)

# Create a second order spatial neighbor object on a 10 x 10 grid
ng10 <- neighbor.grid(10, 10, neighbor.type="second.order")
sn10 <- spatial.neighbor(ng10)
# Generate a 10 x 10 set of coordinates
xy <- expand.grid(x=1:10, y=1:10)
# Plot the spatial neighbor object
plot(sn10, xc=xy$x, yc=xy$y)

# Create and plot spatial neighbor object for the bramble canes
#   nearest neighbors
nb <- find.neighbor(bramble, k=2, drop.self=T)
sn <- spatial.neighbor(nb)
plot(sn, xc=bramble$x, yc=bramble$y)
```

plot.vgram.fit — Plot Results from variogram.fit — plot.vgram.fit

DESCRIPTION

Plot a vgram.fit object, ustually the result from a call to variogram.fit.

USAGE

```
plot.vgram.fit(x, line.col=1, line.type=1, line.width=1, add=T,
               npoints=100, ...)
```

REQUIRED ARGUMENTS

x an object of class "vgram.fit".

OPTIONAL ARGUMENTS

line.col a numeric value indicating the color for the variogram fit line. See the col parameter in the par help file.

line.type a numeric value indicating the line type for the variogram fit line. See the lty parameter in the par help file.

line.width a numeric value indicating the line width for the variogram fit line. See the lwd parameter in the par help file.

add a logical value, if TRUE no initial plot is drawn, only the variogram fitted line is added to the current plot.

npoints a numeric value, the number of to evalute the variogram function at.

Graphical parameters may also be supplied as arguments to this function (see `par`).

SIDE EFFECTS

a plot is produced on the current graphics device or lines are added to the current plot (if `add=T`).

DETAILS

The function specified by `x$funName` must exist. It is evaluated at `npoints` between `0` and `x$distRange[2]`.

This function is a method for the generic function `plot` for class `vgram.fit` . It can be invoked by calling `plot` for an object of the appropriate class, or directly by calling `plot.vgram.fit` regardless of the class of the object.

SEE ALSO

`variogram.fit`, `variogram`.

EXAMPLES

```
vg.iron <- variogram(residuals ~ loc(easting, northing), data=iron.ore)
vfit.iron <- variogram.fit(vg.iron, param=c(range=8.7, sill=3.5,
          nugget=4.8), fun=spher.vgram)
plot(vg.iron)
plot(vfit.iron, add=T)
```

`points.in.poly` Find Points Inside a Given Polygon `points.in.poly`

DESCRIPTION

Determine whether points are inside a polygon.

USAGE

```
points.in.poly(x, y, polygon)
```

REQUIRED ARGUMENTS

`x`	the X-coordinates of the points
`y`	the Y-coordinates of the points. Must be the same length as `x`.
`polygon`	a list with named components "x" and "y".

VALUE

a logical vector the same length as `x`. If `TRUE` then the corresponding point is inside the given polygon and so on.

BUG

if a ray from a point to an edge intersects a horizontal edge, i.e. is collinear with it, the C program will return `TRUE` even if such point is not in the polygon.

SEE ALSO

`poly.grid`, `poly.area`.

EXAMPLES

```
# 100 points on a unit square
x <- runif(100); y <- runif(100)
# A square polygon in the center:
pcenter <- list(x=c(.25,.25,.75,.75), y=c(.25,.75,.75,.25))
```

```
pin <- points.in.poly(x, y, pcenter)
# Plot the unit square and the center square:
plot(x, y, type='n'); polygon(pcenter, density=0, col=2)
# Plot only the points in the center square:
points(x[pin], y[pin], col=3)
```

poly.grid Generate a Grid Inside a Given Polygonal Boundary **poly.grid**

DESCRIPTION

Generates a grid of points and then clips them to lie within a given boundary.

USAGE

```
poly.grid(boundary, nx, ny, size)
```

REQUIRED ARGUMENTS

`boundary` a list with components named `"x"` and `"y"` or a matrix with 2 columns representing the vertices of a convex polygon. Endpoint need not be repeated.

`nx` integer representing the number of cells in the horizontal direction.

`ny` integer representing the number of cells in the vertical direction.

OPTIONAL ARGUMENTS

`size` numeric vector containing the size of each cell. If it has length one then the cells will be squared with the same side sizes. If it has length two then the cells will have width `size[1]` and height `size[2]`.

VALUE

a two-column matrix containing the coordinates of the resulting grid.

DETAILS

A rectangular `nx` by `ny` grid is overlaid on the polygon defined by `boundary` and then those points that fall outside are dropped. If `size` is given then the values `nx` and `ny` are redundant and if given will be ignored.

SEE ALSO

`points.in.poly`

EXAMPLES

```
plot(as.spp(bramble))
bramble.chull <- bramble[chull(bramble),]
polygon(bramble.chull, den=0)
points(poly.grid(bramble.chull, size=c(.1,.1)), col=2)
```

predict.krige Point and Block Kriging Prediction **predict.krige**

DESCRIPTION

Computes point or block kriging predictions and standard errors at locations in `newdata` using an object returned by `krige`.

USAGE

```
predict.krige(object, newdata, se.fit=T, grid=<<see below>>,
              blocksize=c(1, 1), nxy=c(1, 1))
```

REQUIRED ARGUMENTS

`object` an object of class `"krige"` as returned by the function `krige`.

OPTIONAL ARGUMENTS

`newdata` a data frame or list containing the spatial locations for the predictions. The names must match the names of the locations used in the call to `krige` (see `attr(object,"call")`).

`se.fit` a logical value, if `TRUE`, the standard errors of the predictions are returned. Currently the standard errors are always computed internally. This `se.fit` only determines if the returned data frame includes the `se` column.

`grid` a list containing two vectors, the names of the vectors must match the names of the locations used in the call to `krige`. The vectors are each of length 3 and specify the minimum, maximum and number of locations in that spatial coordinate, respectively. A grid is then computing using `expand.grid`. The default value is to use the range of the original location data for the minimum and maximum, and 30 points. This argument is ignored if `newdata` is supplied.

`blocksize` for block kriging, a numeric vector of length 2 specifying the size of the block in x (first value) and y (second value) direction. The locations specified by `newdata` or `grid` are at the center of the blocks.

`nxy` for block kriging, a numeric vector of length 2 specifying the number of discretization points inside the block. If both values are set to `1` (the default) then point kriging predictions are computed.

VALUE

a data frame where the first two columns are the locations of the prediction along with:

`fit` the predicted values.

`se.fit` the standard error of the prediction. Only included if `se.fit = TRUE`.

DETAILS

This function is a method for the generic function `predict` for class `krige` . It can be invoked by calling `predict` for an object of the appropriate class, or directly by calling `predict.krige` regardless of the class of the object.

REFERENCES

Ripley, Brian D. (1981). *Spatial Statistics.* Wiley, New York.

SEE ALSO

`krige`, `loc`.

EXAMPLES

```
# krige the Coal Ash data
kcoal <- krige(coal ~ loc(x, y) + x + x^2, data = coal.ash,
        covfun = spher.cov, range = 4.31, sill = 0.14, nugget = 0.89)
# predictions over default 30 x 30 grid
pcoal <- predict(kcoal)
```

```
# plot prediction surface
wireframe(fit ~ x * y, data = pcoal,
        screen = list(z = 300, x = -60, y = 0), drape = T)
# block kriging predictions with block of size 2 x 2 at 4 locations
predict(kcoal, data.frame(x=c(4,5,9,11), y=c(7,13,9,18)),
       blocksize=c(2,2), nxy=c(5,5))
```

spatial.neighbor Create a "spatial.neighbor" Object **spatial.neighbor**

DESCRIPTION

Function used to create an object of class "spatial.neighbor" given its component parts.

USAGE

```
spatial.neighbor(row.id, col.id, weights=rep(1, length(row.id)),
                 neighbor.matrix, nregion=max(c(row.id,col.id)),
                 symmetric=F, matrix.id=<<see below>>)
```

REQUIRED ARGUMENTS

`row.id` an integer vector containing the row indices of the non-zero elements of the neighbor weight matrix. The `i`-th element of `row.id` and the `i`-th element of `col.id` specify two regions which are spatial neighbors. Two regions are spatial neighbors if observations from the two regions have a non-zero spatial weight and vice-versa. `row.id` can also be a two column matrix containing the row indices (the first column) and the column indices (the second column). This argument is ignored if `neighbor.matrix` is given.

`col.id` integer vector (of the same length as `row.id`) with the column indices of the non-zero elements of the neighbor weight matrix. This is ignored if `neighbor.matrix` is given or if `row.id` is a matrix.

It is important to note that even if a pair of regions `c(row.id[i],col.id[i])` are spatial neighbors, the permuted pair `c(col.id[i],row.id[i])` does not have to define spatial neighbors (corresponding contiguity matrix element can be zero). For example, consider two regions on a river, and suppose that a region corresponding to `row.id[i]` is downstream from the region in `col.id[i]` and neighbors. By this definition, "downstream of" the transpose pairing need not satisfy a neighbor relationship. See argument `symmetric` below.

`neighbor.matrix` a matrix of neighbor weights (where all weights are often `1`) from which the object of class "`spatial.neighbor`" is to be constructed. This must be a square matrix such that if element `[i,j]` is non-zero, then spatial regions `i` and `j` are considered neighbors, and its value is used as a weight in measures of correlation or in further model-fitting. This is also known as the contiguity matrix.

OPTIONAL ARGUMENTS

`weights` numeric vector of the same length as `row.id` and `col.id`. `weights[i]` gives a weight for the corresponding neighbor pair relationship, given in `c(row.id[i],col.id[i])`. If `weights` is not specified (and argument `neighbor.matrix` is not used), then the spatial weights are all set equal to `1`. Each spatial weight defines the strength of the association between two neighbors. This argument is ignored if `neighbor.matrix` is given as each of the matrix elements are then considered to be neighbor weights.

`nregion` integer stating the total number of regions or spatial units. If not given, this value is computed from the number of unique elements in `row.id` and `col.id` as the maximum of all the regions given therein `max(c(row.id,col.id))`.

`symmetric` logical flag: should the neighbor matrix be considered symmetric?. If `TRUE`, the spatial weights matrix is computed by assuming that if the i-th neighbor pair `c(row.id[i],col.id[i])` has neighbor weight given by `w=weights[i]` then so does the matrix element `c(col.id[i],row.id[i])`. Only half of the weights need be specified in this case. If `TRUE`, routine `spatial.condense` is called to re-

move redundant values. When `neighbor.matrix` is given, its symmetry is determined within the function, otherwise, it defaults to `FALSE`.

`matrix.id` integer vector of length equal to the total number of spatial neighbors. This can be used to differentiate various types of neighbors. For example, spatial regression models may differentiate between north-south neighbors as compared to east-west neighbors. The values of vector `matrix.id` should then indicate the neighbor types. If missing, a single neighbor type is assumed (with one neighbor matrix).

VALUE

an object of class `"spatial.neighbor"`. This object inherits from class `"data.frame"` and describes the relationship among spatial regions using a sparse representation of the Weight or Contiguity matrix (or matrices). It has columns `row.id`, `col.id`, `weights` and `matrix` (determined by `matrix.id`).

DETAILS

Objects of class `"spatial.neighbor"` are required by the spatial regression, spatial correlation, and other functions in S+SPATIALSTATS. Two methods for constructing a spatial neighbor object are available. A matrix of weights (where all weights are often `1`) can be given as input, and the `"spatial.neighbor"` object is constructed from its non-negative elements. In this case argument `neighbor.matrix` must be a square matrix such that if element `c(i,j)` of the matrix is non-zero, then spatial regions `i` and `j` are neighbors, with weight given by the value of the element (usually a `1`).

Another method for constructing an object of class `"spatial.neighbor"` is by directly specifying the row and column numbers (and the weight value) of the non-zero elements of the contiguity matrix which is usually a sparse matrix. A sparse representation is usually preferred in practice. In this case, `row.id[i]` gives the row of the `i`-th non-negative element of the neighbor matrix, and the corresponding element `col.id[i]` gives its column index. Thus, each pair `c(row.id[i],col.id[i])` represents a pair of neighboring spatial units. The strength of their association can then be given by `weights[i]`.

Notice that `row.id` and `col.id` contain INDICES of the contiguity matrix and NOT the region identifiers which could be character strings or some such. These are used to expand the full contiguity matrix, so we should have representation for all indices `1` through `nregion`, though it is possible to have islands in between. Use the function `check.islands` to check for these islands, and remap their indexing if that is desirable.

It is possible to specify two or more types of neighbor relationships. For example, the user may want to model a spatial relationship depending upon the angle of the line connecting neighbor centers i.e. considering directional relationships. For this example, let Type-1 neighbors be north-south neighbors, and let Type-2 neighbors be east-west neighbors; neighbors along a diagonal could be modeled with weights proportional to `.707` (the sine of 45 degrees), for instance.

Consider the elements of `row.id`, `col.id`, and `weights` corresponding to a distinct value, `k`, of the vector `matrix.id`. The spatial neighbor matrix can be expressed as a matrix `A[k]` such that `A[k][row.id,col.id]=weights`, and all other elements are zero. Consider a parameter vector `rho` of length `g`, many spatial covariance matrices used in spatial regression models can be expressed as a weighted linear combination of the contiguity matrices `A[k]`, `rho[k]*A[k]`, for values of `k` varying in `1:g`.

SEE ALSO

`check.islands`, `plot.spatial.neighbor`, `summary.spatial.neighbor`.

EXAMPLES

```
row.index <- c(1,1,2,2,3)
col.index <- c(2,3,1,3,4)
```

```
# Assume we have no information about the strength of the spatial
# association.  All weights are 1.
nghb <- spatial.neighbor(row.id=row.index, col.id=col.index)
summary(nghb)
# Another way to create the same spatial.neighbor object:
nmat <- matrix(c(0, 1, 1, 0,
                 1, 0, 1, 0,
                 0, 0, 0, 1,
                 0, 0, 0, 0), ncol=4, byrow=T)
nghb2 <- spatial.neighbor(neighbor.matrix=nmat)
```

`spatial.neighbor.object` Class `"spatial.neighbor"` `spatial.neighbor.object`

DESCRIPTION

Class of objects used to define neighbor relationships for spatial data on a regular or irregular lattice.

GENERATION

This class of objects is constructed using the function `spatial.neighbor`. Alternatively, the functions `read.neighbor`, or `neighbor.grid` may be used. In general, the user must construct these objects whenever estimates of spatial correlation and spatial regression are desired.

An object of class `"spatial.neighbor"` contains all the information required to determine which spatial units on a region of interest are neighbors, as well as the strength of their relationship.

METHODS

The class `"spatial.neighbor"` has associated methods, `print.spatial.neighbor`, `plot.spatial.neighbor`, and `summary.spatial.neighbor`.

INHERITANCE

Class `"spatial.neighbor"` inherits from class `"data.frame"`.

STRUCTURE

The `"spatial.neighbor"` object is in essence a data frame with additional attributes. Each row of the data frame denotes a pair of neighboring spatial units. The data frame contains the following columns:

- `row.id` the row index in the neighbor matrix that corresponds to a region or spatial unit. This implies a numbering of regions from `1` to the total number of regions.
- `col.id` the column index in the neighbor matrix that corresponds to the neighbor of the region defined by the corresponding element of `row.id`.
- `weights` a numeric value giving the relative strength of the neighbor relationship. The larger the value, the stronger the relationship.
- `matrix` if multiple types of neighbor matrices are possible, this column contains the type of the neighbor this weight represents - it gives a numeric identifier for each spatial neighbor [contiguity] matrix.

SPECIAL ATTRIBUTES

- `nregion` the number of total regions in the study. The row and column identifiers given in `row.id` and `col.id` might not include ALL the spatial units in the area of interest. This happens when units are isolated, i.e. have no neighboring regions. In this case, `nregion` must be used to determine the total number of rows and columns in the contiguity matrix.

`symmetric` logical flag. It provides an indication of whether the contiguity matrix is symmetric (`TRUE`) or not (`FALSE`). If `TRUE`, only the weights for the upper (or lower) triangle of the contiguity matrix need to be specified in the object. Use the function `spatial.weights` to expand the full symmetric weights matrix.

DETAILS

An object of class `"spatial.neighbor"` is a sparse matrix representation of a square matrix (or a number of square matrices).

The function `plot.spatial.neighbor` will show a graphical view of the spatial.neighbor object and `summary.spatial.neighbor` will compute summary statistics on the object.

The functions `spatial.multiply`, and `spatial.cg.solve` can be used to form products of the form `rho[i]*N[i]*x` and `(rho[i]*N[i])^(-1)*x`, for neighbor weight matrices `N[i]`, vector of constants or parameters, `rho[i]`, and arbitrary vectors `x`, should that be needed to form a neighbor or contiguity matrix as a weighted linear combination of others.

SEE ALSO

`spatial.neighbor plot.spatial.neighbor`, `summary.spatial.neighbor`, `read.neighbor`, `neighbor.grid`, `spatial.multiply`, `spatial.cg.solve`, `spatial.weights`.

`spatial.solve` — Solve `Sb=x` — `spatial.solve`

DESCRIPTION

Solves `Sb=x` for `b`, where `S` is a sparse matrix obtained from an object of class `"spatial.neighbor"`.

USAGE

```
spatial.solve(neighbor, x, transpose=F, rho=0, product=F,
              weights=NULL, region.id=NULL, absThreshold=0,
              relThreshold=0, diagPivoting=0, shareMemory=F)
```

REQUIRED ARGUMENTS

`neighbor` an object of class `"spatial.neighbor"` containing the sparse matrix representation of the spatial neighbor matrix (or matrices, see function `spatial.neighbor`).

`x` the right hand side for which a solution is desired. Alternatively, `x` can be a matrix. In this case, a solution is obtained for each column in `x`.

OPTIONAL ARGUMENTS

`transpose` with the default arguments, `S` is taken as `I` minus the sum over `i` of `rho[i] * A[i]`. Here `I` is an identity matrix, `rho[i]` is a scalar, and `A[i]` is the `i`-th weight matrix in `neighbor`. If `transpose` is `TRUE`, then the transpose of this matrix is used for `A`.

`rho` a scalar (or vector) of constants used in defining the matrix `S` (see argument `transpose`).

`product` let `B=I` minus the sum of `rho[i]*A[i]` as described in argument `transpose`. When `product` is `FALSE`, `S=B`. When `product` is `TRUE`, `S` is `t(B)%*%B`.

`weights` if provided, the inverse weights are included along the diagonal matrix `W` and incorporated into the model for `S` as follows: Let `R` be `I` minus the sum of `rho[i]*A[i]`. Then

product	transpose	S
F	F	`R %*% W`
F	T	`t(R) %*% W`
T	F	`t(R) %*% W %*% R`

```
                T   |   T    | R %*% W %*% t(R)
```

`region.id` a vector with length equal to the number of regions in the spatial lattice. If variables `row.id` and `col.id` of argument `neighbor` are not integer valued variables with sequential values from 1 to the number or regions in the lattice, then argument `region.id` must be specified and is used to obtain a sequential coding of the lattice regions.

`absThreshold` the pivot threshold (between zero and 1). Values near 1 result in complete pivoting, while values near zero result in a strict Markowitz solution. In general, you should choose a value as close to zero as roundoff error will permit. A value of 0.001 has been recommended by Kundert (1988) in some cases.

`relThreshold` the absolute magnitude an element must have to be considered as a pivot candidate, except as a last resort. This should be set to a small fraction of the smallest (absolute) diagonal element.

`diagPivoting` if `TRUE`, pivot selection should be confined to the diagonal if possible.

`shareMemory` if `TRUE`, the in-memory representation of the sparse matrix will be shared by other routines. If memory is shared, it needs to be released later. One way to release the memory is to call `.C("destroy_sparse_matrix")` after the in-memory representation of the matrix is no long needed. Most users should use the default value, `FALSE`.

VALUE

a matrix (or vector), `b`, solving the linear system `Sb=x`.

DETAILS

This routine uses the sparse matrix code of Kenneth Kundert and Alberto Sangiovanni-Vincentelli (1988). The University of California, Berkeley, holds the copyright for these routines.

REFERENCES

Kundert, Kenneth S. and Sangiovanni-Vincentelli, Alberto (1988). A Sparse Linear Equation Solver. Department of EE and CS, University of California, Berkeley.

SEE ALSO

`spatial.cg.solve`, `spatial.multiply`, `spatial.neighbor`, `spatial.neighbor.object`.

EXAMPLES

```
x <- 1:4
row.id <- c(1,1,2,2,3)
col.id <- c(1,3,1,3,4)
alpha <- 0.3
neighbor <- spatial.neighbor(row.id=row.id, col.id=col.id, symmetric=T)
a <- solve(diag(attr(neighbor, "nregion"))-alpha*
       spatial.weights(neighbor), x)
b <- spatial.solve(neighbor, x, rho=alpha)$result
print(max(abs(a-b)) < 1e-14)
```

`summary.spatial.neighbor` Summary Method `summary.spatial.neighbor`

DESCRIPTION

Returns a summary list for objects of class `"spatial.neighbor"`.

USAGE

```
summary.spatial.neighbor(object)
```

REQUIRED ARGUMENTS

`object` an object that inherits from class `"spatial.neighbor"`.

VALUE

an object of class `"summary.spatial.neighbor"` which is a list of lists, one list for each unique value of `matrix` in `object`. The sublists each contain the components that summarize the particular spatial neighbor matrix:

`nregion` an integer indicating the number of regions `object` covers. This is the same as `attr(object,"nregion")`

`symmetric` a logical value, if `TRUE` the `object` is assumed to be symmetric. This is the same as `attr(object,"symmetric")`

`minConnected` a named vector of the least connected regions. The names are the row indices that have the smallest number of connections for the i-th matrix in `object`. The values (all the same) are the minimum number of neighbors.

`maxConnected` a named vector of the most connected regions. The names are the row indices that have the largest number of connections for the i-th matrix in `object`. The values (all the same) are the maximum number of neighbors.

`aveNumLinks` a single value giving the mean number of neighbors each region has.

`aveWeight` a single value giving the mean weight value for this matrix.

`rowMissing` a vector of indices that are not present in `object$row.id` for the i-th matrix. This will be printed as `"none"` by the print method if there are no missing row indices and it is not printed at all if `object` is a symmetric spatial neighbor matrix since all missing row indices will be islands (see below).

`colMissing` a vector of indices that are not present in `object$col.id` for the i-th matrix. This will be printed as `"none"` by the print method if there are no missing column indices and it is not printed at all if `object` is a symmetric spatial neighbor matrix since all missing column indices will be islands (see below).

`islands` the indices for regions that have no neighbors. These indices do not appear in either the `object$col.id` or `object$row.id` for the i-th matrix. This will be printed as `"none"` by the print method if there are no islands.

DETAILS

This function is a method for the generic function `summary` for class `spatial.neighbor` . It can be invoked by calling `summary` for an object of the appropriate class, or directly by calling `summary.spatial.neighbor` regardless of the class of the object.

SEE ALSO

`spatial.neighbor`, `check.islands`.

EXAMPLES

```
summary(sids.neighbor)

# Create two symmetric spatial neighbor matrices with one island
#   in the second matrix:
ri <- c(1,1,2,3,4,5,1,1,2,5,5)
ci <- c(2,3,3,4,5,6,2,3,3,3,6)
mat <- c(1,1,1,1,1,1,2,2,2,2,2)
sn <- spatial.neighbor(ri, ci, symm=T, matrix=mat)
summary(sn)
```

`triangulate` Delaunay's Triangulation **`triangulate`**

DESCRIPTION

Calculate Delaunay's triangulation for points with given coordinates `x` and `y`.

USAGE

```
triangulate(x, y, plot.it=T, shrink=0.1)
```

REQUIRED ARGUMENTS

`x` a list with components `"x"` and `"y"`, a 2-column matrix, or a vector containing the horizontal coordinates of the vertices that form the polygon of interest.

OPTIONAL ARGUMENTS

`y` if `x` is a vector of X-coordinates then `y` must contain the corresponding vertical or Y-coordinates.

`plot.it` logical flag: should the resulting triangulation be plotted? Default is `TRUE`.

`shrink` fraction by which the triangles will be shrunken for better discrimination of the individual triangles in the plot, no edges overlap if `shrink > 0`.

VALUE

invisibly returns a list with 2 components:

`ipt` a matrix with 3 rows, for each column the 3 row-values can be used to index `x` and `y` and extract corresponding triangle vertices. This provides an ordering of the triangles as well.

`ipl` another integer matrix with 3 rows. These are the point numbers of the end points of the border line segments and their corresponding triangle number.

SIDE EFFECTS

if `plot.it = TRUE` a colorful representation of the triangulation is produced.

DETAILS

A Delaunay triangulation of a point set is a triangulation whose vertices are the point set, with the property that no point in the point set falls in the interior of the circumcircle (circle that passes through all three vertices) of any triangle in the triangulation.

EXAMPLES

```
triangulate(scallops[,c("lat","long")])
```

`variogram.cloud` Calculate Variogram Cloud **`variogram.cloud`**

DESCRIPTION

Calculates all pairwise differences in a random field data set.

USAGE

```
variogram.cloud(formula, data=<<see below>>, subset=<<see below>>,
                na.action=<<see below>>, azimuth=0, tol.azimuth=90,
                maxdist=<<see below>>, bandwidth=1e+307,
                FUN=function(zi, zj) (zi - zj)^2/2))
```

REQUIRED ARGUMENTS

`formula` formula defining the response and the predictors. In general, its form is:

```
z ~ x + y
```

The `z` variable is a numeric response. Variables `x` and `y` are the locations. All variables in the formula must be vectors of equal length with no missing values (`NA`s). The formula may also contain expressions for the variables, e.g. `sqrt(count)` or `log(age+1)`. The right hand side may also be a call to the `loc` function e.g. `loc(x,y)`. The `loc` function can be used to correct for geometric anisotropy, see the `loc` help file.

OPTIONAL ARGUMENTS

`data` an optional data frame in which to find the objects mentioned in `formula`.

`subset` expression saying which subset of the rows of the data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included.

`na.action` a function to filter missing data. This is applied to the `model.frame` after any `subset` argument has been used. The default (with `na.fail`) is to create an error if any missing values are found. A possible alternative is `na.omit`, which deletes observations that contain one or more missing values.

`azimuth` the clockwise direction angle in degrees from North-South. Only pairs of points in this direction plus or minus `tol.azimuth` will be included in the output.

`tol.azimuth` the tolerance angle, in degrees. `tol.azimuth` greater than or equal to 90 implies the of use all directions.

`maxdist` the maximum distance to consider. The default is half the maximum observed distance.

`bandwidth` the maximum perpendicular distance to consider.

`FUN` a function of two variables that is to be computed. The default function is the contribution to the classical empirical variogram for the pair `z[i]`, `z[j]`.

VALUE

an object of class `"vgram.cloud"` that inherits from `"data.frame"`. The columns are:

`distance` the distance between the two points.

`gamma` the value of `FUN` for the `z[iindex]`, `z[jindex]`.

`iindex` the index into the original data for the first value of the pair.

`jindex` the index into the original data for the second value of the pair.

The return object has an attribute `call` with an image of the call that produced the object.

DETAILS

Methods for class `"vgram.cloud"` include `boxplot`, `plot` and `identify`.

If all directions and distances are included the return object will have n*(n-1)/2 rows where n is the number of observations. This can get very large, even for relatively small n. The argument `maxdist` can be used to limit the size. Typically values beyond half the maximum distance in the data are not used in estimating the variogram function.

REFERENCES

Cressie, Noel. (1993). *Statistics For Spatial Data*, Revised Edition. Wiley, New York.

SEE ALSO

`boxplot.vgram.cloud`, `identify.vgram.cloud`, `plot.vgram.cloud`, `variogram`.

EXAMPLES

```
v1 <- variogram.cloud(coal ~ x + y, data=coal.ash)
plot(v1)
```

```
boxplot(v1)
```

variogram.fit — Fit a Variogram Model — variogram.fit

DESCRIPTION

Fits a theoretical variogram model to an empirical variogram object using a local minimizer for smooth non-linear functions subject to bounded parameters.

USAGE

```
variogram.fit(vobj, param, fun=spher.vgram, lower=rep(0, n.param),
              upper=Inf)
```

REQUIRED ARGUMENTS

`vobj` an object that inherits from class `"variogram"` representing an empirical variogram. Usually, the result of the `variogram` function.

OPTIONAL ARGUMENTS

`param` a named vector with initial values for the parameters to fit. Usually, these are the `"nugget"`, `"sill"`, and `"range"` or a subset of these. If missing, the function will try to determine the parameter names and initial values based on the arguments to the function specified in `fun`.

`fun` a theoretical variogram function The first argument should be distance. The remaining arguments are considered parameters that can be changed to update the fit of fun to object.

`lower` either a single numeric value or a vector of length equal to the number of parameters giving lower bounds for the parameter values. If it is a single value then all parameters have that as their lower bound. See the help page for `nlminb` for more information.

`upper` either a single numeric value or a vector of length equal to the number of parameters giving upper bounds for the parameter values. If it is a single value then all parameters have that as their upper bound. See the help page for `nlminb` for more information.

VALUE

an object of class `"vgram.fit"` with components:

`parameters` a named vector with the fitted values for the parameters.

`objective` the final value of the objective function.

`funName` the `fun` argument as a character string.

`distRange` a numeric vector containing the minimum and maximum distance values from `vobj`.

DETAILS

If fun is one of `exp.vgram`, `gauss.vgram`, `linear.vgram`, `power.vgram` or `spher.vgram` and `param` is not supplied the function sets special initial starting values for `param`. Otherwise, if `param` is not supplied it is set to a vector of ones.

The weighted least squares objective function used in the fitting process (Cressie, 1993, p. 97) is:

```
objective.fun <- function(y,yh,n) sum(n*(y/yh-1)^2)
```

The `nlminb` function is used for the optimization.

REFERENCES

Cressie, Noel. (1993). *Statistics For Spatial Data*, Revised Edition. Wiley, New York.

SEE ALSO

`variogram`, `plot.vgram.fit`, `model.variogram`, `nlminb`.

EXAMPLES

```
vg.iron <- variogram(residuals ~ loc(easting, northing), data=iron.ore)
vfit.iron <- variogram.fit(vg.iron, param=c(range=8.7, sill=3.5,
          nugget=4.8), fun=spher.vgram)
plot(vg.iron)
plot(vfit.iron, add=T)
```