

# Spatial Interpolation

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**Methods for extending information on  
spatial data fields**

**John Lewis**

# Spatial Interpolation

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- Data Integration
  - merging spatially incompatible data sets
    - » household survey data with census tract data
- Predicting Values for Locations with no Observations
  - use **information on (spatial) pattern** at one set of locations/scale to predict values at different locations/scale
- Interpolation and Extrapolation
  - extrapolation: **outside range** observed values

# The type of Spatial Interpolation depends on:

- **what type of surface model you want to produce**
- **what data are available**
  - **point, line or area**
  - **continuous or discrete**

# Interpolation techniques are classified as:

- ***Global*** - surface model considers all the points
  - ***Local*** - uses only values in a prescribed “nearby” neighborhood
- 
- ***Exact*** - retains the original values of the sample on the resulting surface
  - ***Inexact*** - assigns new values to known data points
- 
- ***Deterministic*** – provides no indication of the extent of possible error
  - ***Stochastic*** – methods provide probabilistic estimate

# Interpolating Spatial Objects

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## ➤ Point to Point

- from observed points to unobserved points
  - » e.g. monitoring stations to house locations

## ➤ Point to Area

- from observed points to areal units
  - » e.g. from monitoring stations to census tracts

## ➤ Area to Area

- from one set of observed areas to a different (overlapping) set of areas = areal interpolation
  - » e.g. from counties to water management zones

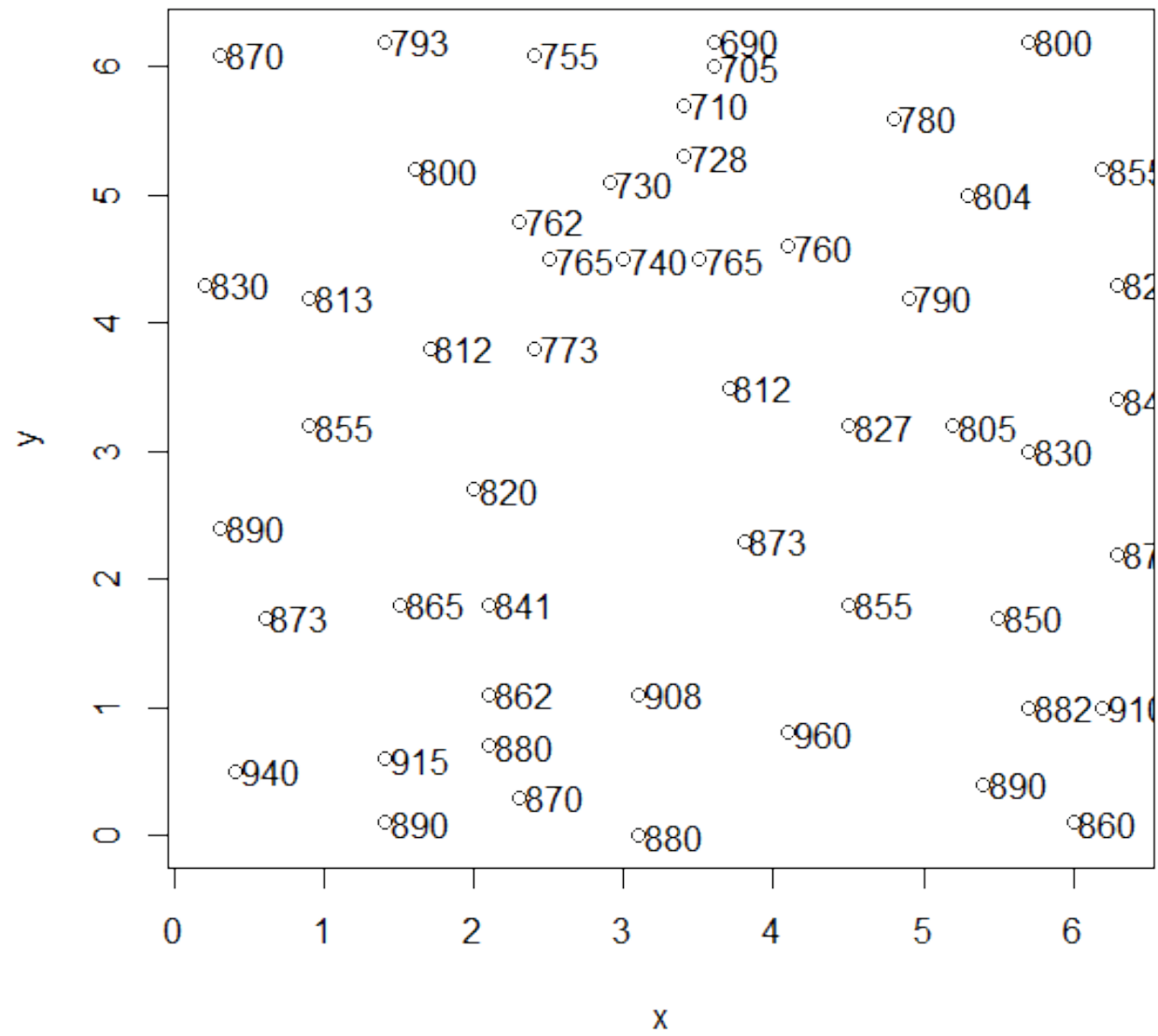
# General list of techniques (points)

- ***trend surface*** - a global interpolator which calculates a best overall surface fit
- ***IDW*** - inverse distance weighting
- ***loess*** – local weighted smoothing regression (weighted quadratic least squares regression)
- ***spline*** - mathematical piecewise curve fitting
- ***Kriging*** - using geostatistical techniques

# Other procedures

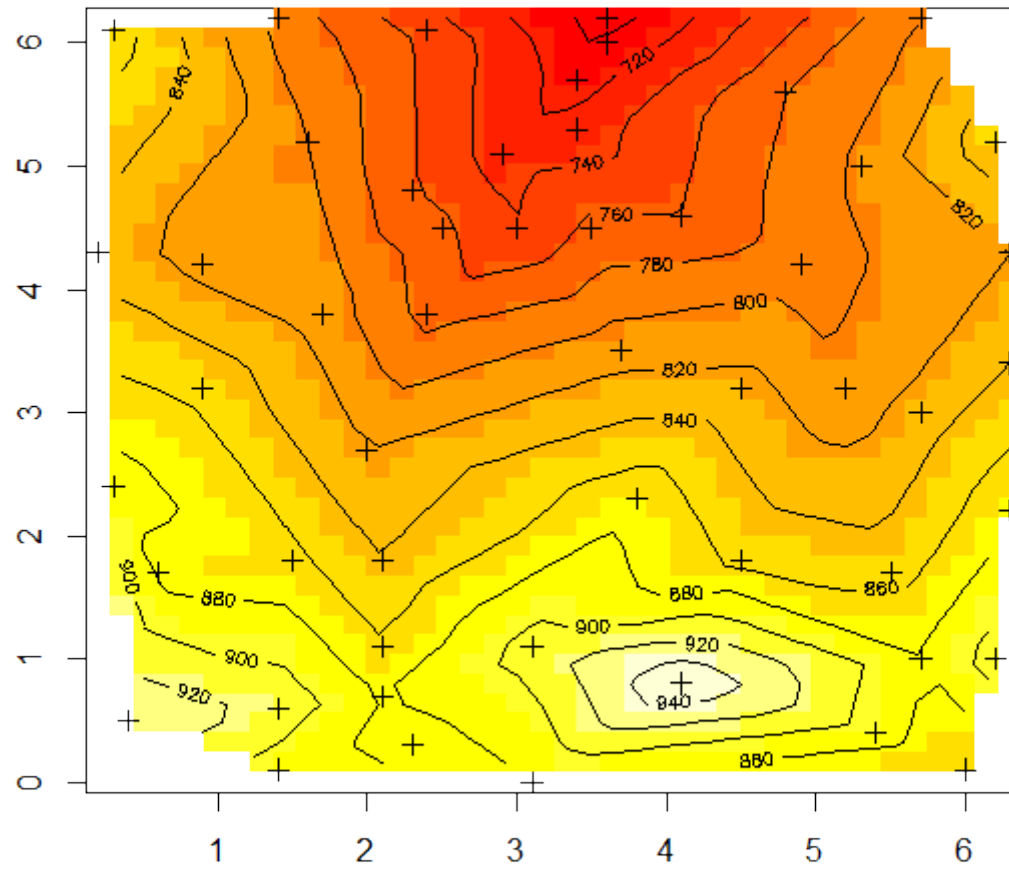
- ***Thiessen or Voronoi tessellation*** - area divided into regions around the sample data points where every pixel or area in the region is assigned to the data point which is the closest
- ***TIN*** - sample data points become vertices of a set of triangular facets covering the study area

topo example data

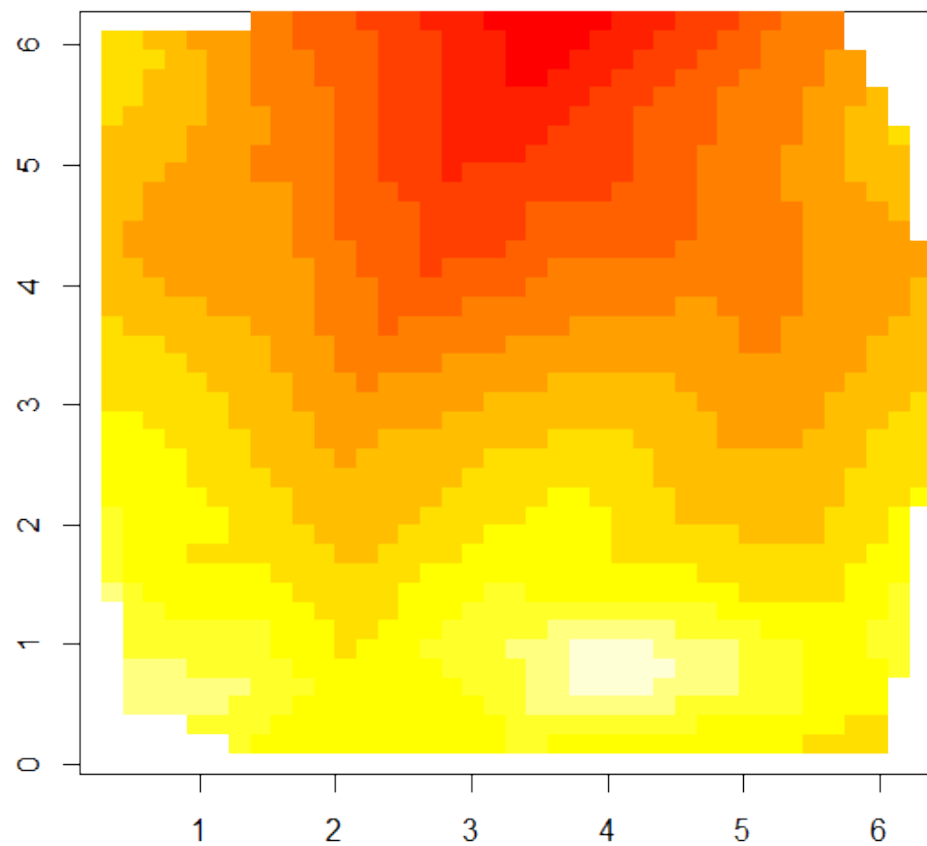




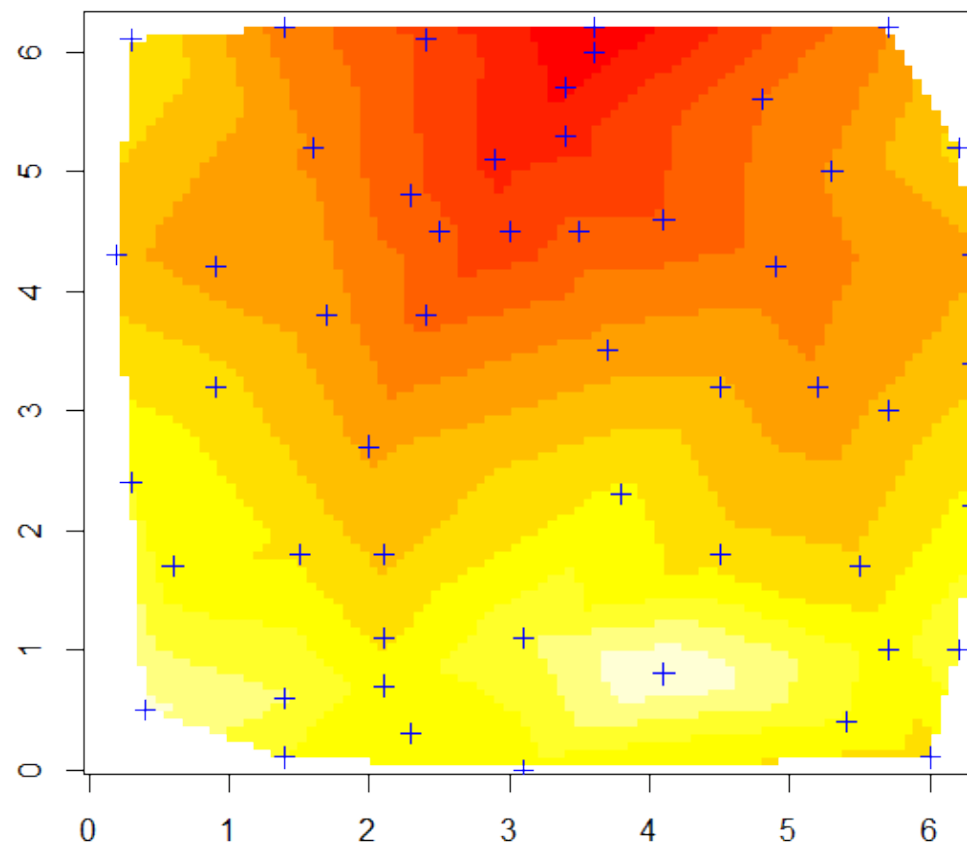
topo example data(linear interpol default (40x40))



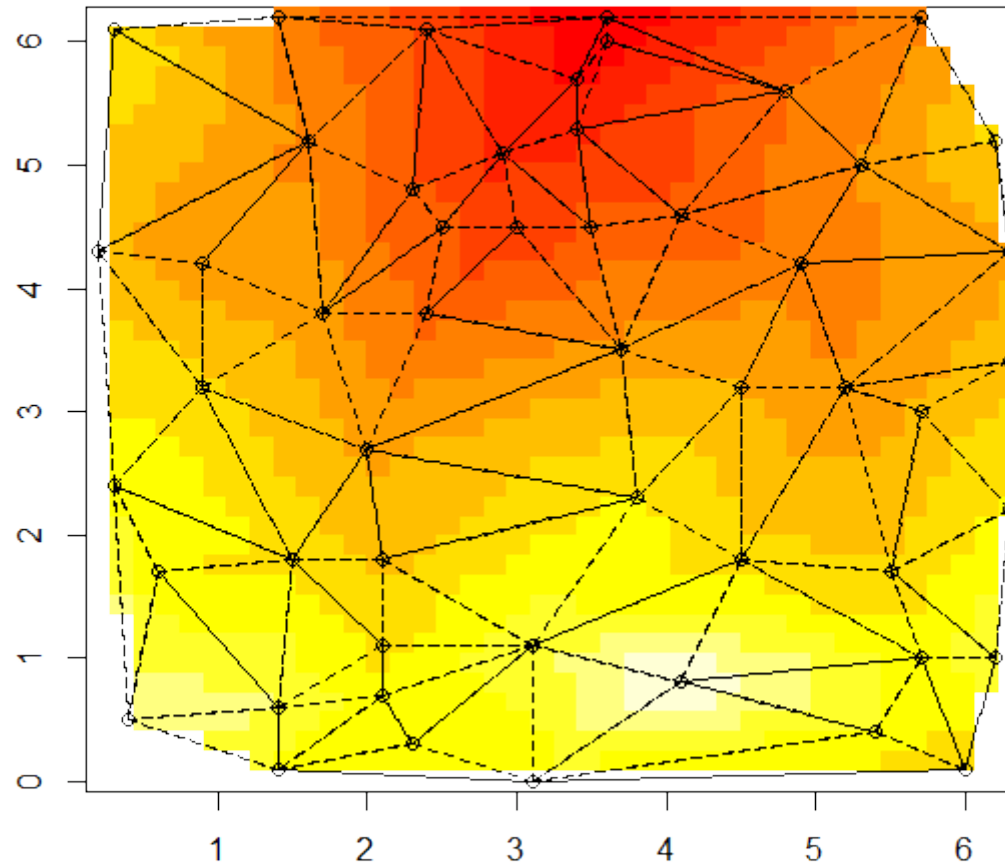
**topo example data(linear interpol default (40x40))**



**topo smooth interp (on finer grid 100x100)**

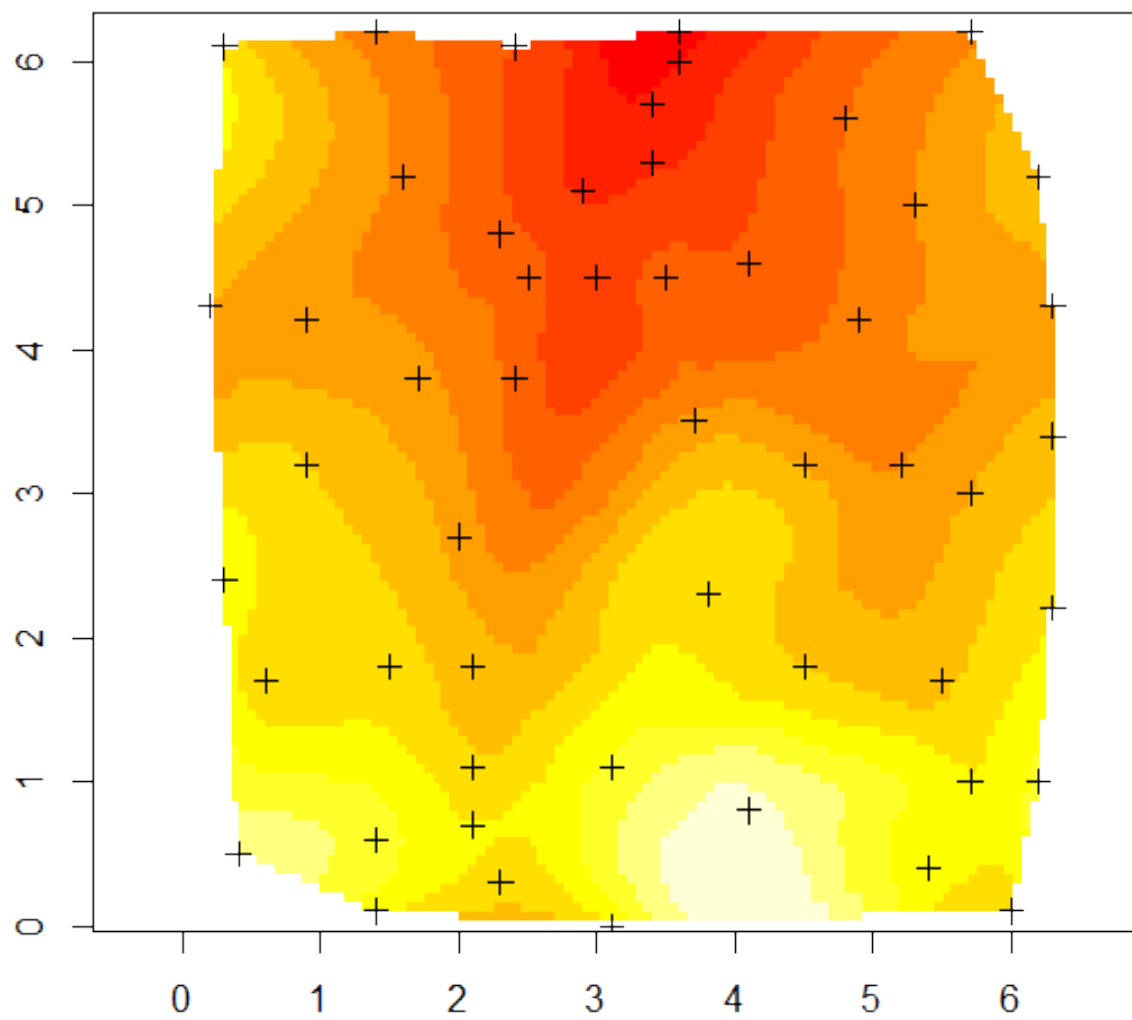


topo example data(topo-linear interpol default (40x40))



Minimum angle triangles, bounded by data points, are used in the linear interpolation algorithm

topo smooth interp(\* bicubic100x100)



## Polynomial trend surfaces

- A global predictor which models a **regional trend**
- The value of a variable at each point depends only on its **coördinates** and parameters of a fitted surface
- This is modelled with a smooth function of position,  $z = f(x, y) = f(E, N)$  for grid coördinates; this is called the **trend surface**
- Simple form (plane, 1<sup>st</sup> order):

$$z = \beta_0 + \beta_x E + \beta_y N$$

- Higher-order surfaces may also be fitted (beware of fitting the noise!)

## General trend surfaces

- General form: a surface of order  $p$ :

$$f((x,y)) = \sum_{r+s \leq p} \beta_{r,s} x^r y^s$$

- Order should be suggested by the process
  - \* One-way trend: 1<sup>st</sup> order (plane)
  - \* Dome or depression: 2<sup>nd</sup> order
  - \* Folded structure: Higher orders, depending on number of inflection points

Properties: stochastic, inexact, global

(from David Rossiter)

## Trend surface interpolation

Polynomials in  $x, y$  (or  $x, y, z$ ):

$$Z(x, y) = \beta_0 + \beta_1x + \beta_2y + e(x, y)$$

$$Z(x, y) = \beta_0 + \beta_1x + \beta_2y + \beta_3x^2 + \beta_4y^2 + \beta_5xy + e(x, y)$$

coefficient vector  $\beta$  is globally constant:

- allows testing, etc.
- testing assumes... independence

## Fitting trend surfaces

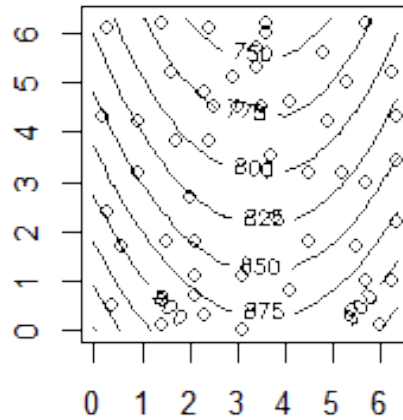
- The trend surface is predicted by **linear regression** with **coördinates as the predictor variables** and the response variable to be predicted, using data from all sample points.
- All samples participate equally in the prediction
- We can measure the **goodness of fit** of the trend surface to the sample by the residual sum of squares
- The same **cautions** as in feature-space regression analysis!
- **Ordinary Least Squares** (OLS) is often used but is not really correct, since it ignores possible **correlation among closely-spaced samples**; better is **Generalised Least Squares** (GLS)

(from David Rossiter)

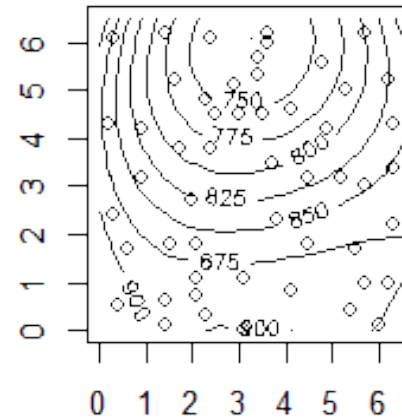


# Trend Surface – Topo

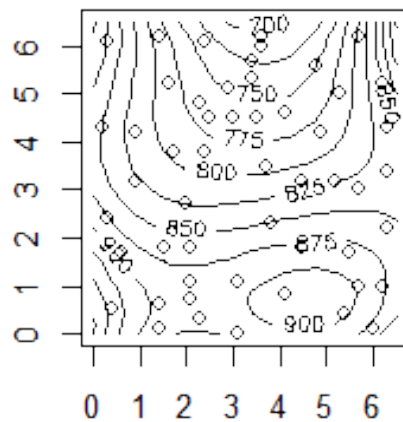
**Degree=2**



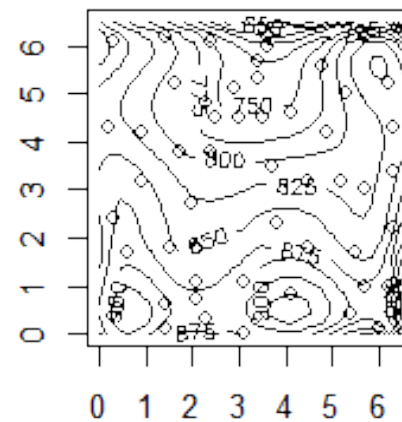
**Degree=3**



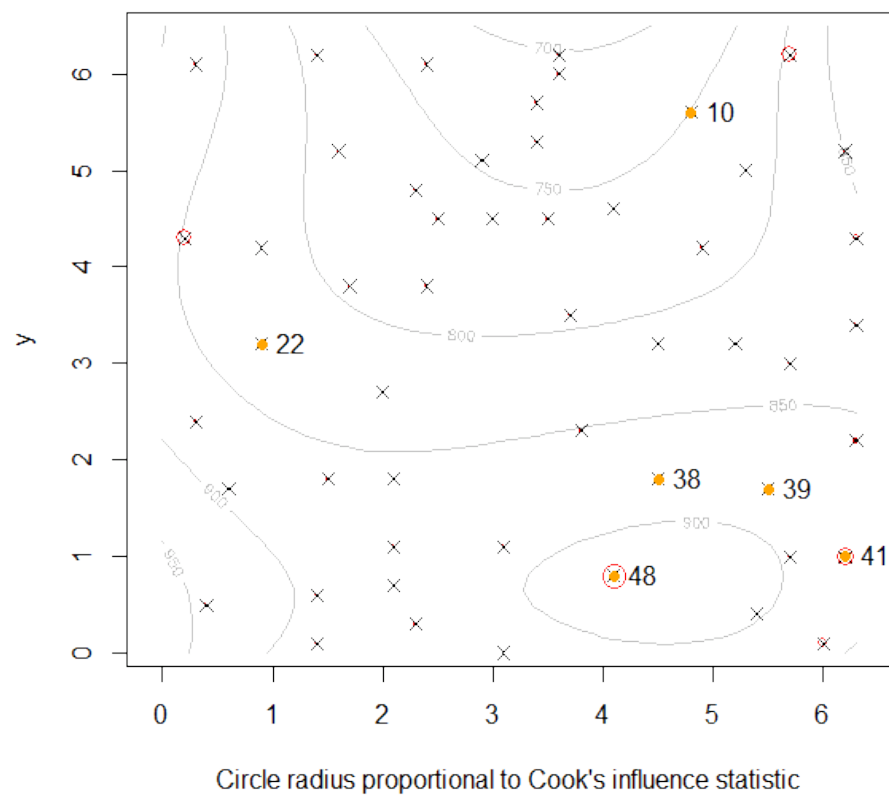
**Degree=4**



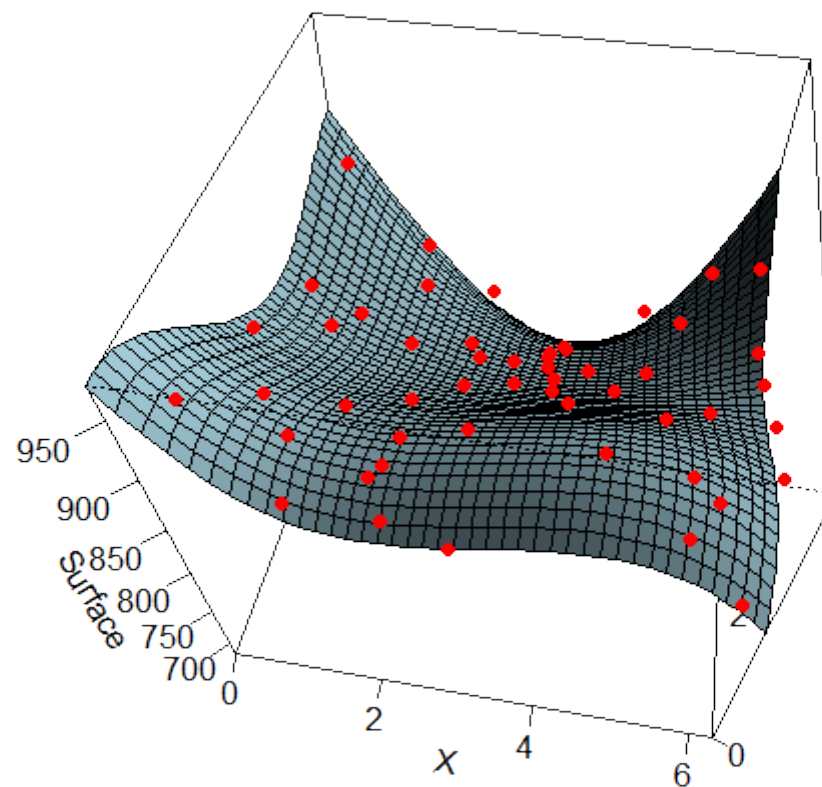
**Degree=6**



topo - trend surface - degree=4



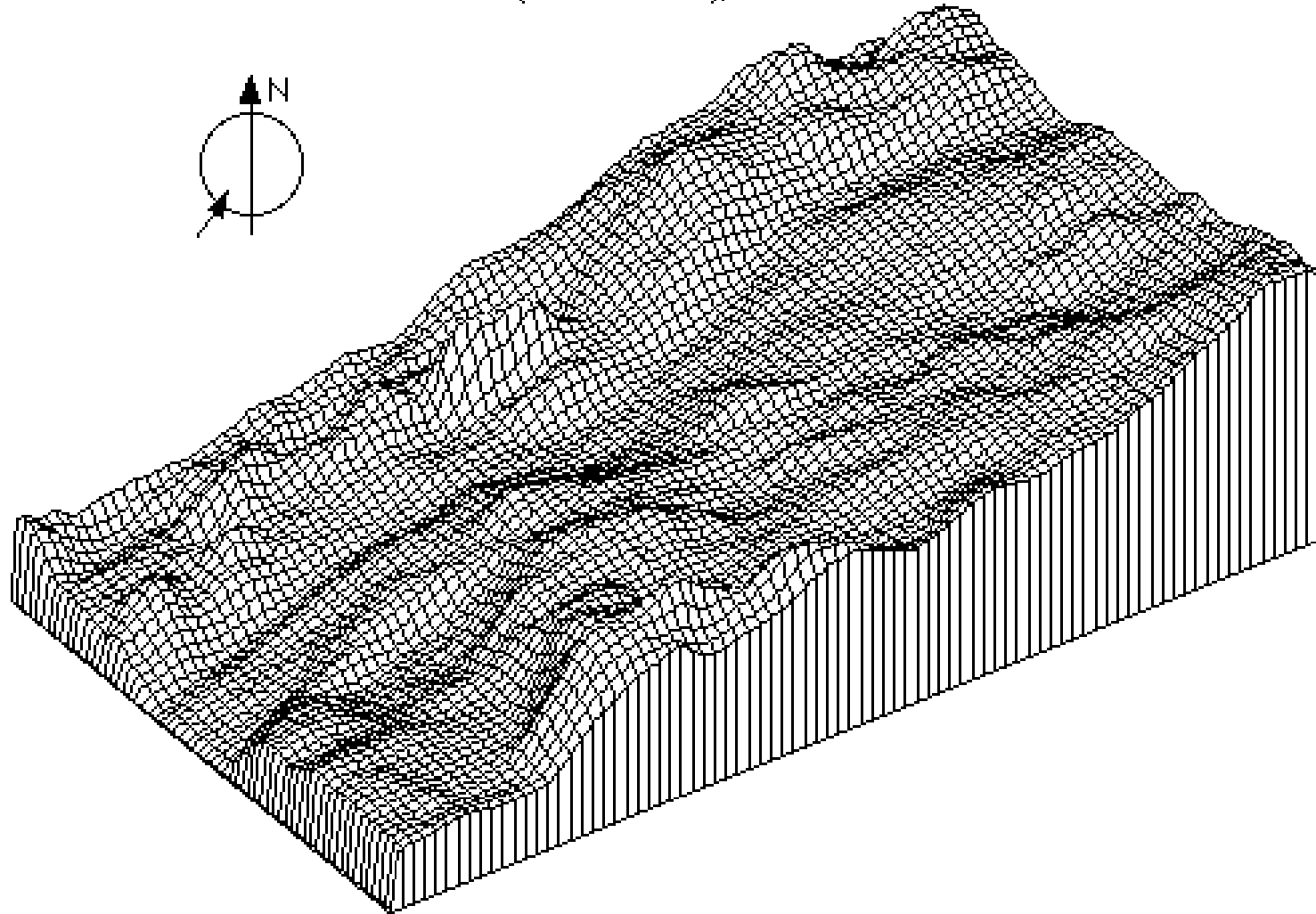
TOPO Trend Surface degree=4



# Trend surface examples

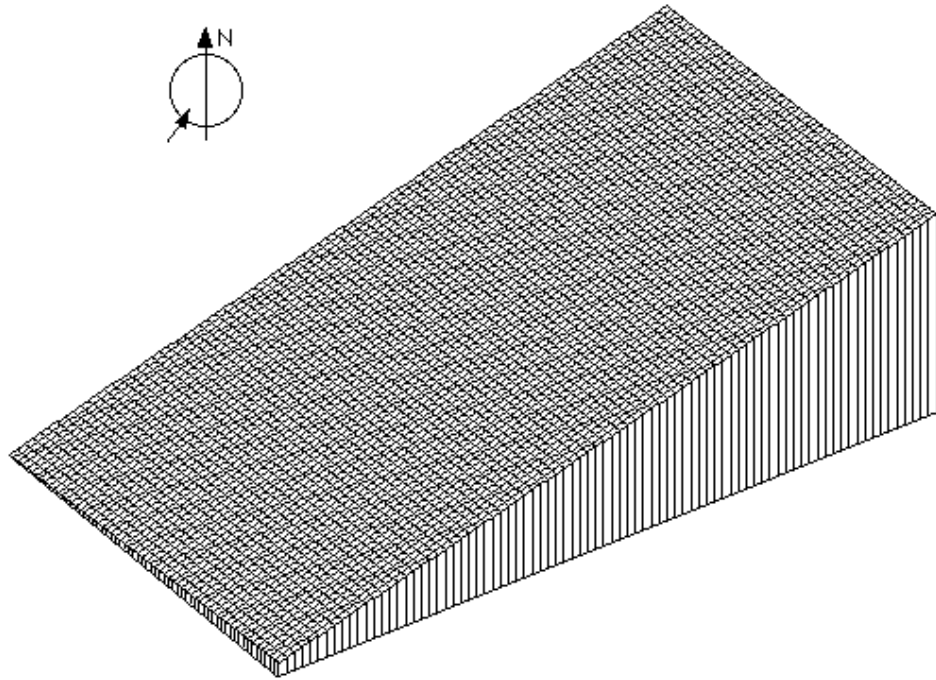
## Bouguer gravity, northwest Kansas

Azimuth  $-35^\circ$  ( $0^\circ$  is South), elevation  $35^\circ$



### Bouguer gravity, first-order trend, northwest Kansas

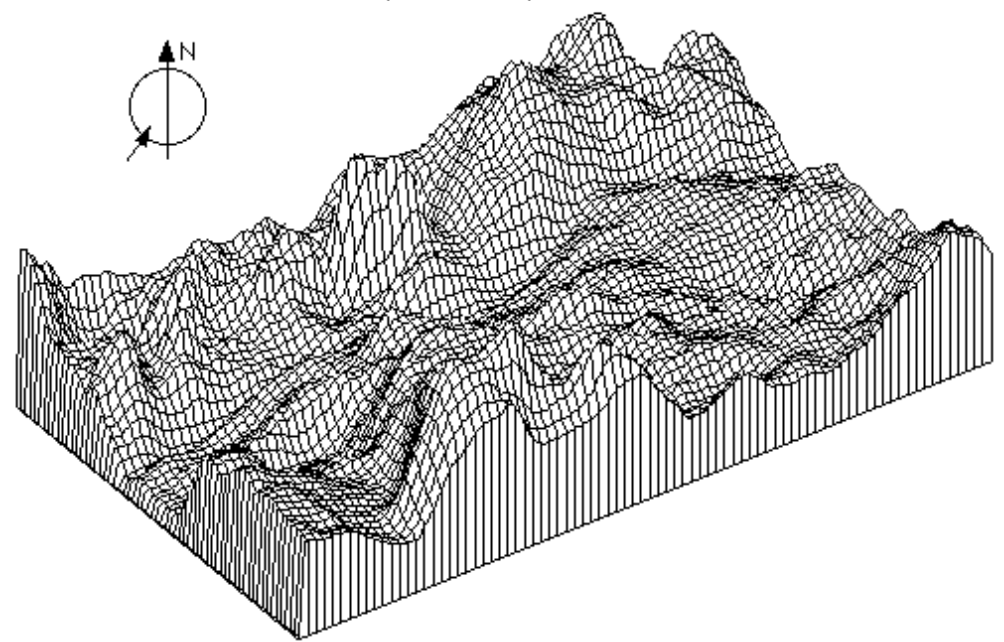
Azimuth -35° (0° is South), elevation 35°



The first-order polynomial of the gravity data set shows the strong east-to-west gradient.

### Bouguer gravity, first-order residual, northwest Kansas

Azimuth -35° (0° is South), elevation 35°



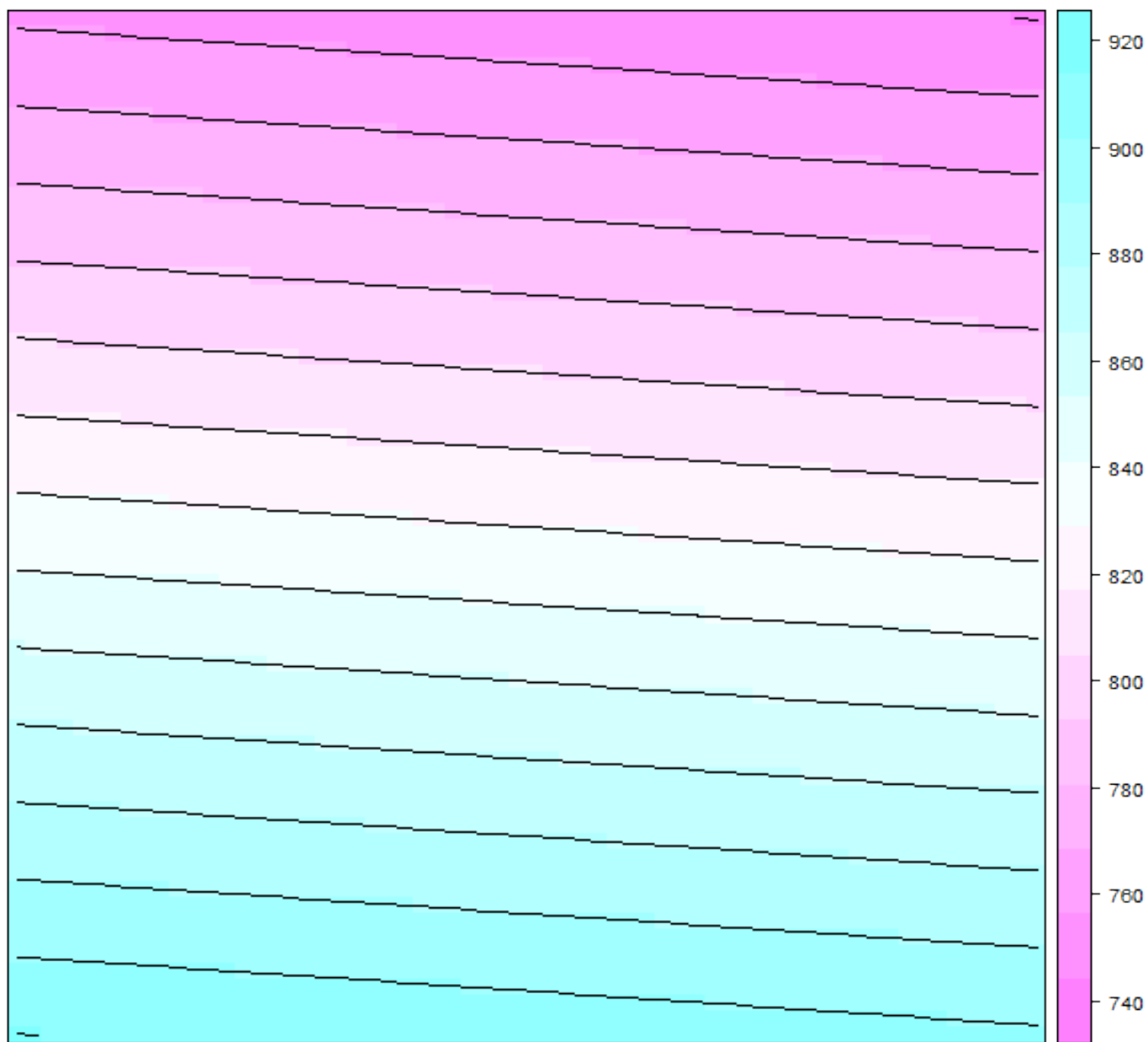
Once the background gradient is removed, the local anomalies are displayed more clearly.

# Trend surface in gstat

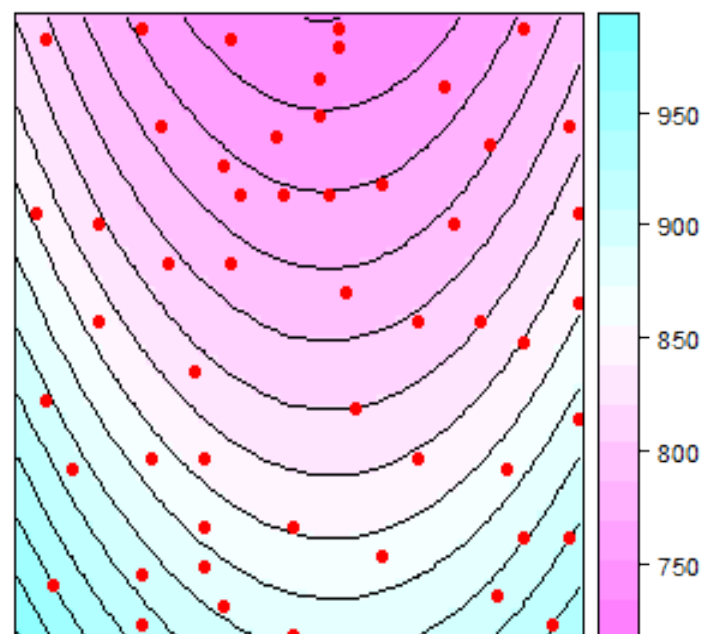
*gstat* treats this as a special case of universal kriging with no spatial dependence (i.e. NULL model) ## just to degree=2: this example

```
data(topo)
coordinates(topo) <- ~ x+y
x=seq(0,6.3, by=0.1);y=seq(0,6.3, by=0.1)
topo.grid <- expand.grid(x=x,y=y)
gridded(topo.grid) <- ~x+y
# 1st-order trend surface
x <- gstat(formula=topo$z ~ 1, data=topo, degree=1)
kt <- predict(x, newdata=topo.grid)
spplot(kt[1], contour=TRUE,main="topo trend surface (1)-gstat")
# 2nd order trend surface
x <- gstat(formula=topo$z ~ 1, data=topo, degree=2)
kt2 <- predict(x, newdata=topo.grid)
p1 <- spplot( kt2[1], contour=TRUE, main="topo trend surface (2)-
  gstat",sp.layout=list(list("sp.points", topo@coords, pch=19,
    col=2)))
# prediction error from OLS regression
p2 <- spplot(kt2[2], contour=TRUE,sp.layout=list(list("sp.points",
  topo@coords, pch=19, col=2)),main="prediction error from OLS
  regression")
print(p1, position = c(0,.5,1,1),more=T)
print(p2, position = c(0,0,1,.5))
```

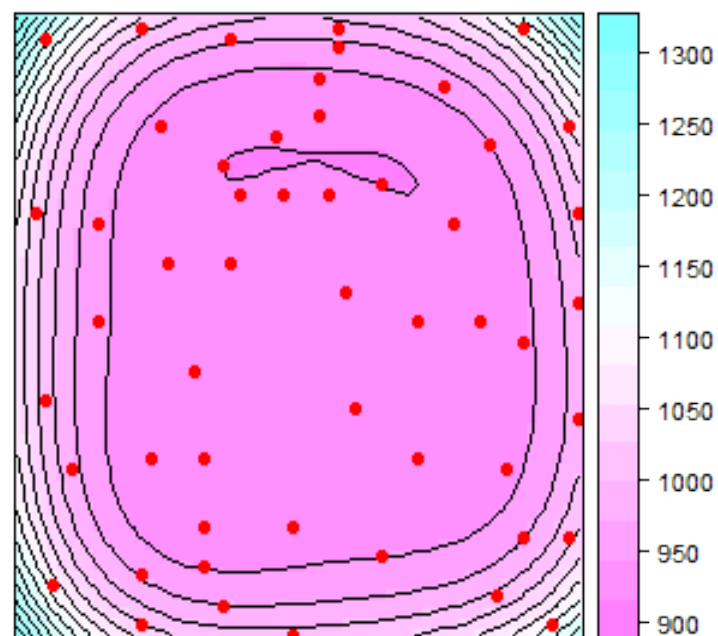
topo trend surface (1)-gstat



**topo trend surface (2)-gstat**



**prediction error from OLS regression**



## Some Problems with Trend Surfaces

1. Extreme simplicity in form of a polynomial surface as compared to most natural surfaces.
2. Unfortunate tendency to accelerate without limit to higher or lower values in areas where there are no control points, such as along the edges of maps.
3. Computational/statistical difficulties may be encountered if a very high degree polynomial trend surface is fitted.
4. Has problems with outliers



# Tessellations

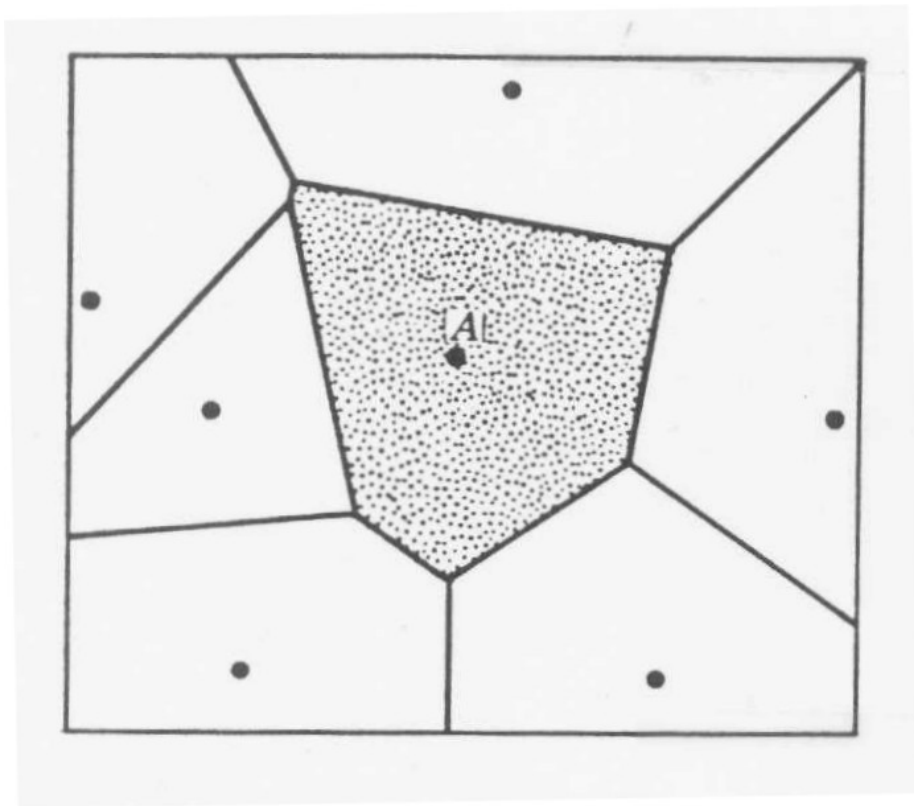
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## ➤ Thiessen Polygons

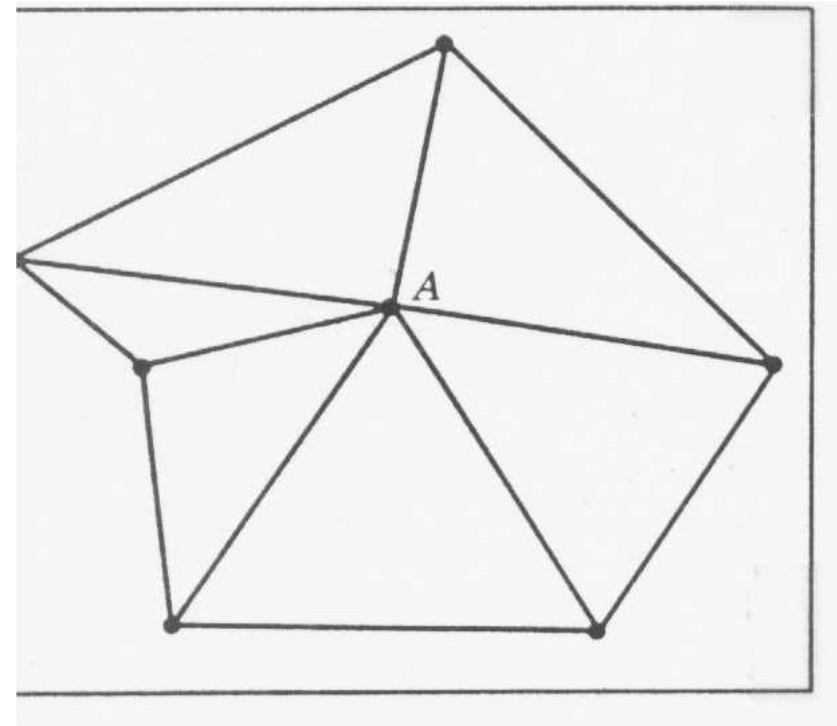
- collection of all points in a plane that are closer to the central point than to any other point
- notion of minimum transport cost **market area**
- all points in the polygon are assigned the **same value as the central point**

## ➤ Properties

- **local, exact, deterministic**
- interpolated values underestimate heterogeneity

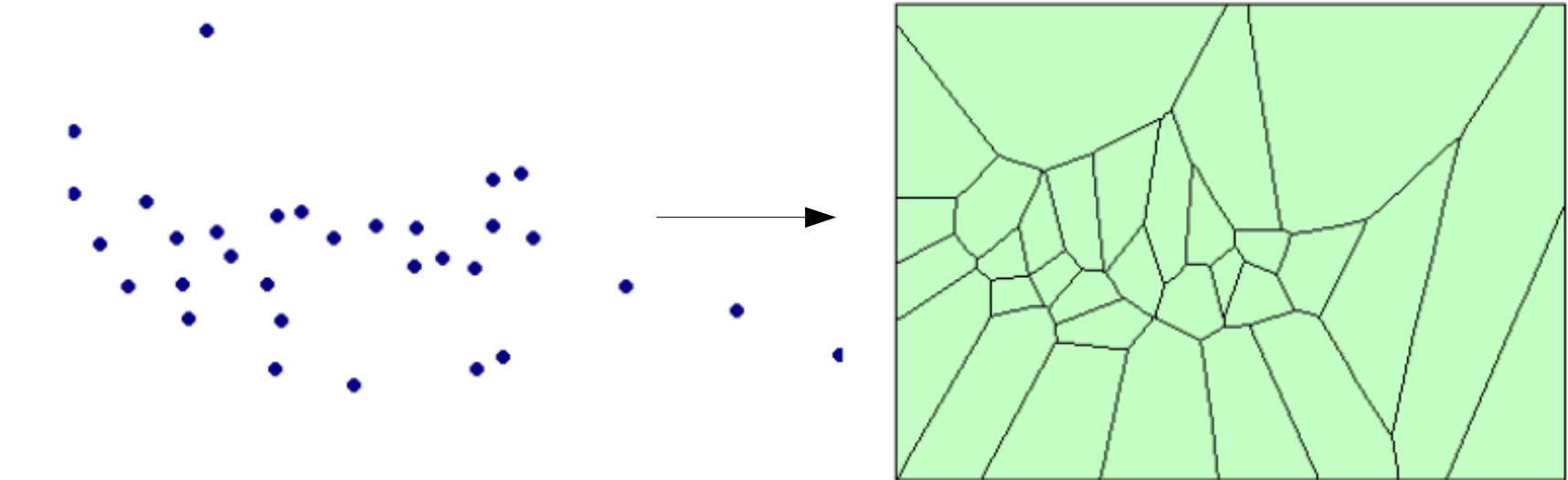


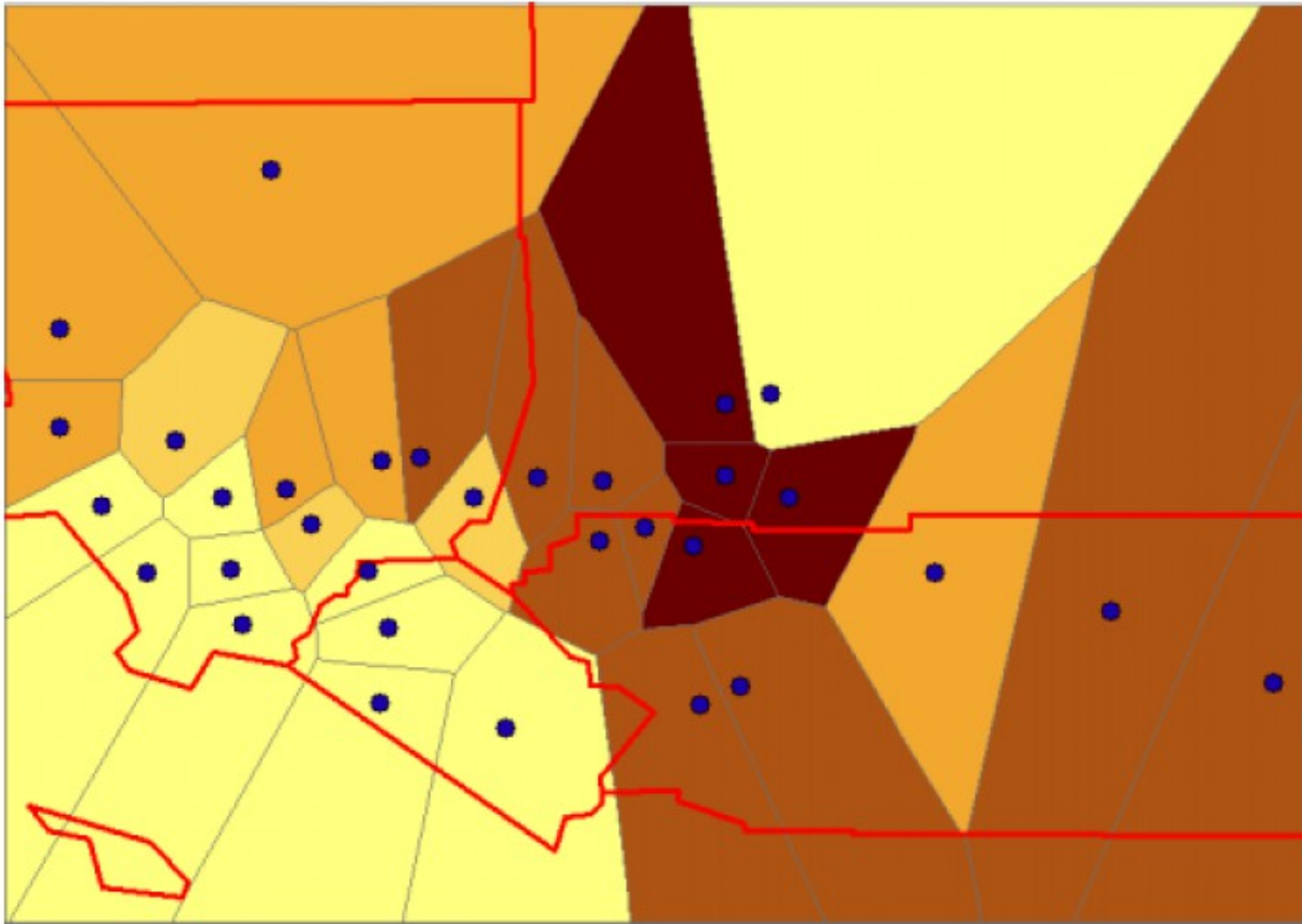
**FIGURE 5.45** Thiessen polygon (shaded) around point A. All locations within polygon are closer to A than to any other point.



**FIGURE 5.46** Delaunay triangle network around point A. All connected points are Thiessen neighbors of A.

from points to polygons: Thiessen polygons for LA basin





Thiessen Polygon Interpolation - LA Basin Ozone

# Inverse distance weighted interpolation (IDW)

This is one of the simplest and most readily available methods. It is based on an assumption that the value at an unsampled point can be approximated as a weighted average of values at points within a certain cut-off distance, or from a given number  $m$  of the closest points (typically 10 to 30). Weights are usually inversely proportional to a power of distance

The method often does not reproduce the local shape implied by data and produces local extrema at the data points

# Inverse Distance Weighting

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## ➤ Tobler's Law

- in space, everything is related to everything else, but closer locations more so
- use distance decay

## ➤ IDW

- $z_x = \sum_i \lambda_i z_i$  with  $\sum_i \lambda_i = 1$  or  $z_x = \sum_i w_i z_i / \sum_i w_i$
- $w_i$  = weight
  - » inverse distance function:  $1/d_{ix}^2$

## ➤ Properties

- local, exact, deterministic
- interpolated values are always within range

# Inverse Distance Weighting

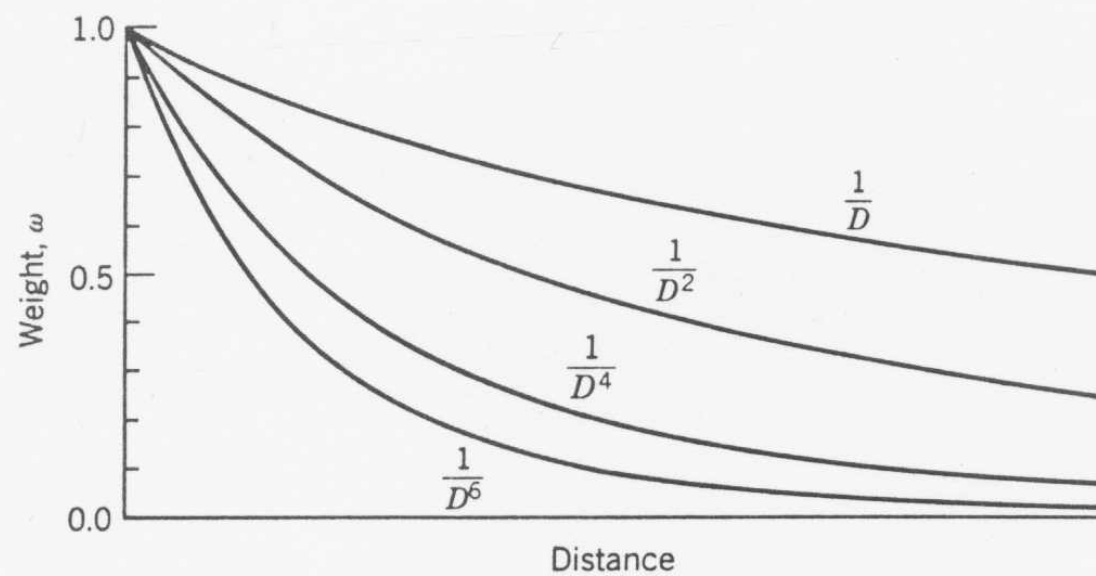
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Substitute ( $d_i$ )

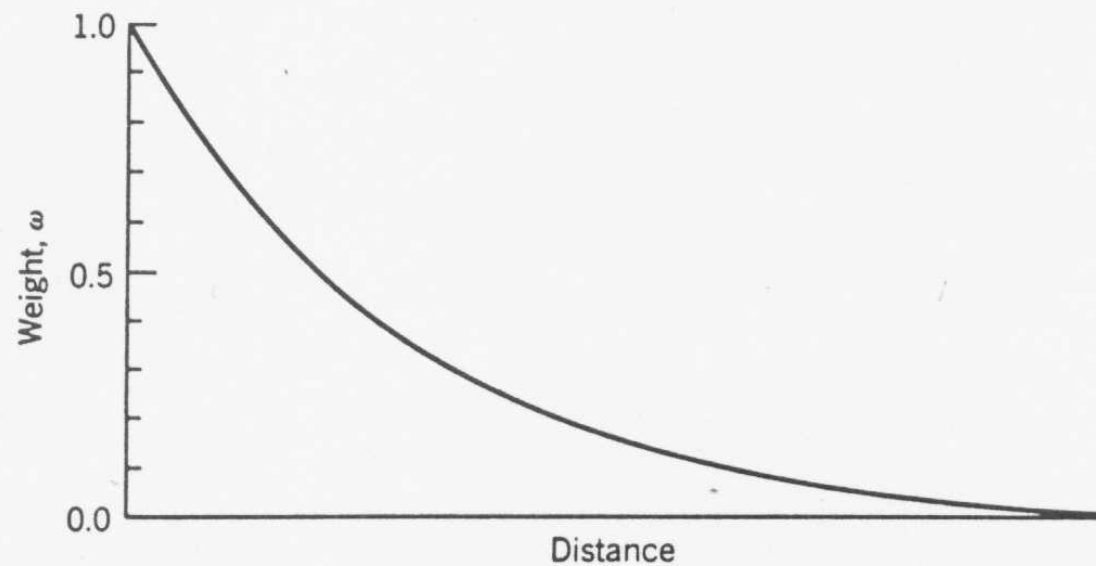
**estimated**  $Z_p \approx \frac{\sum_{i=1}^n (Z_i / d_i)}{\sum_{i=1}^n (1 / d_i)}$  **actual values**

where

$$d_i = \{(x_i - x_p)^2 + (y_i - y_p)^2\}^{0.5}$$



(a)



(b)

**FIGURE 5.56** Distance weighting functions used in contouring programs. (a) Inverse distance-powered functions. (b) Scaled inverse distance-squared function.



# Defining sample subsets

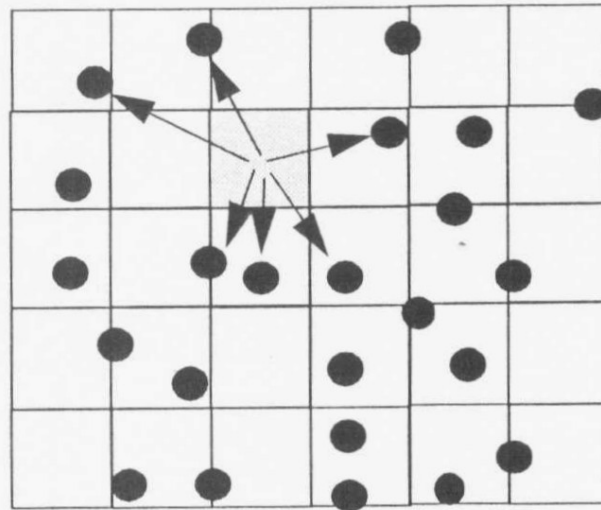
- Which samples are considered during interpolation?

Nearest number of neighbors

Samples within a radius

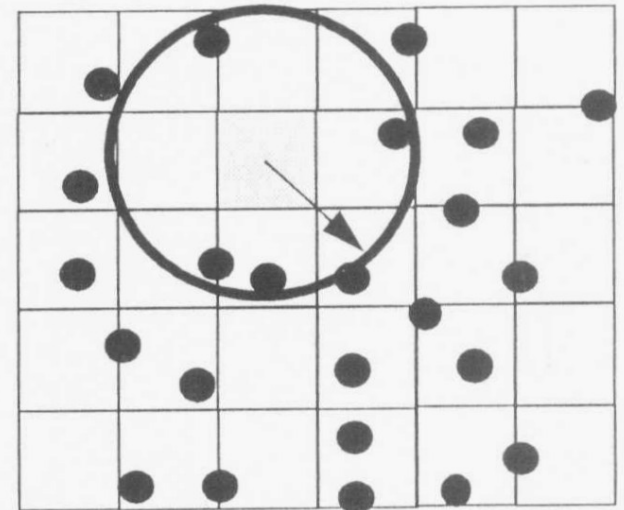
- Only select points are used

Nearest neighbors



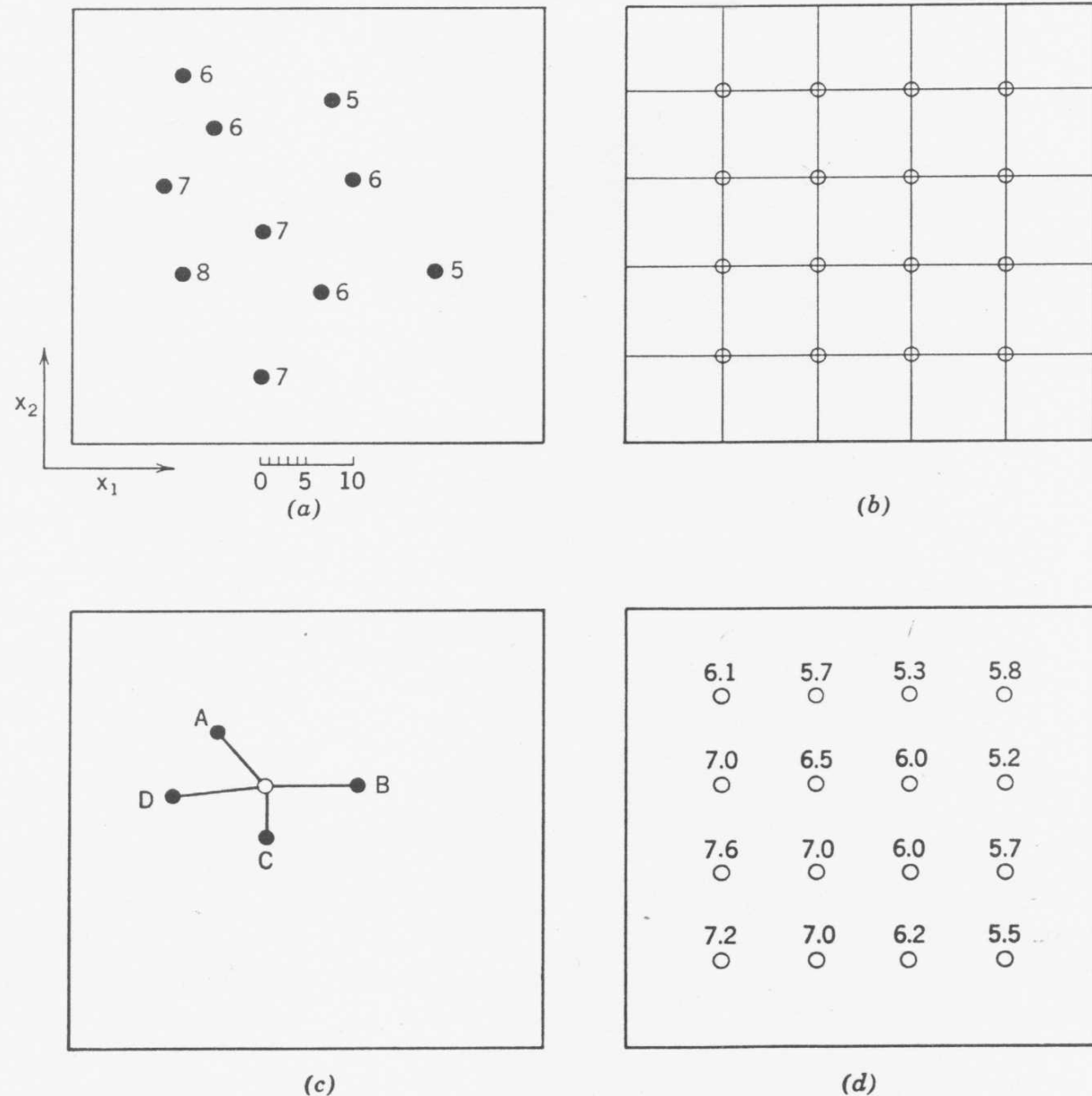
Number of nearest neighbors = 6

Fixed radius

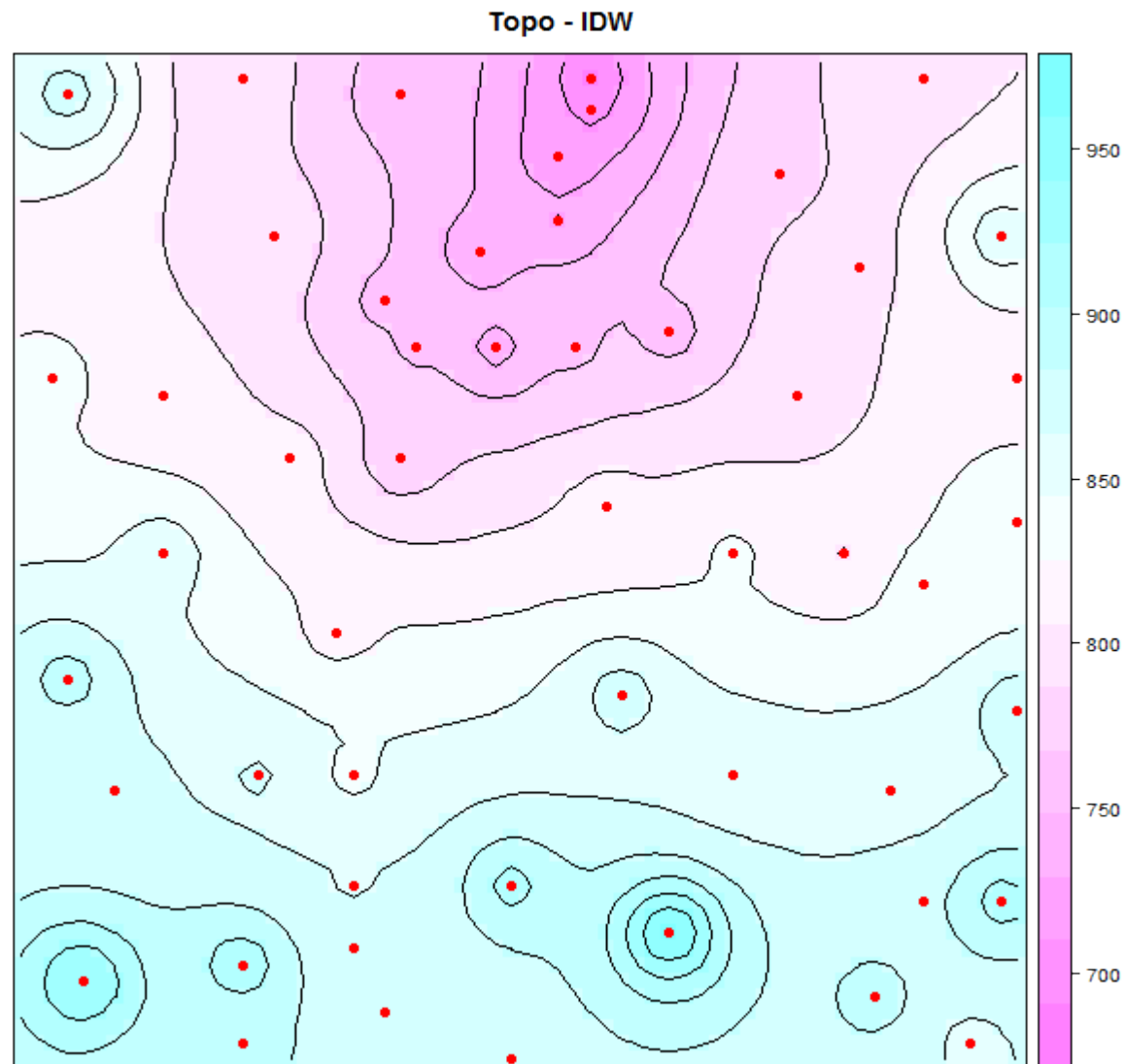


Radius = 1280  
Samples = 4

# A PROBLEM



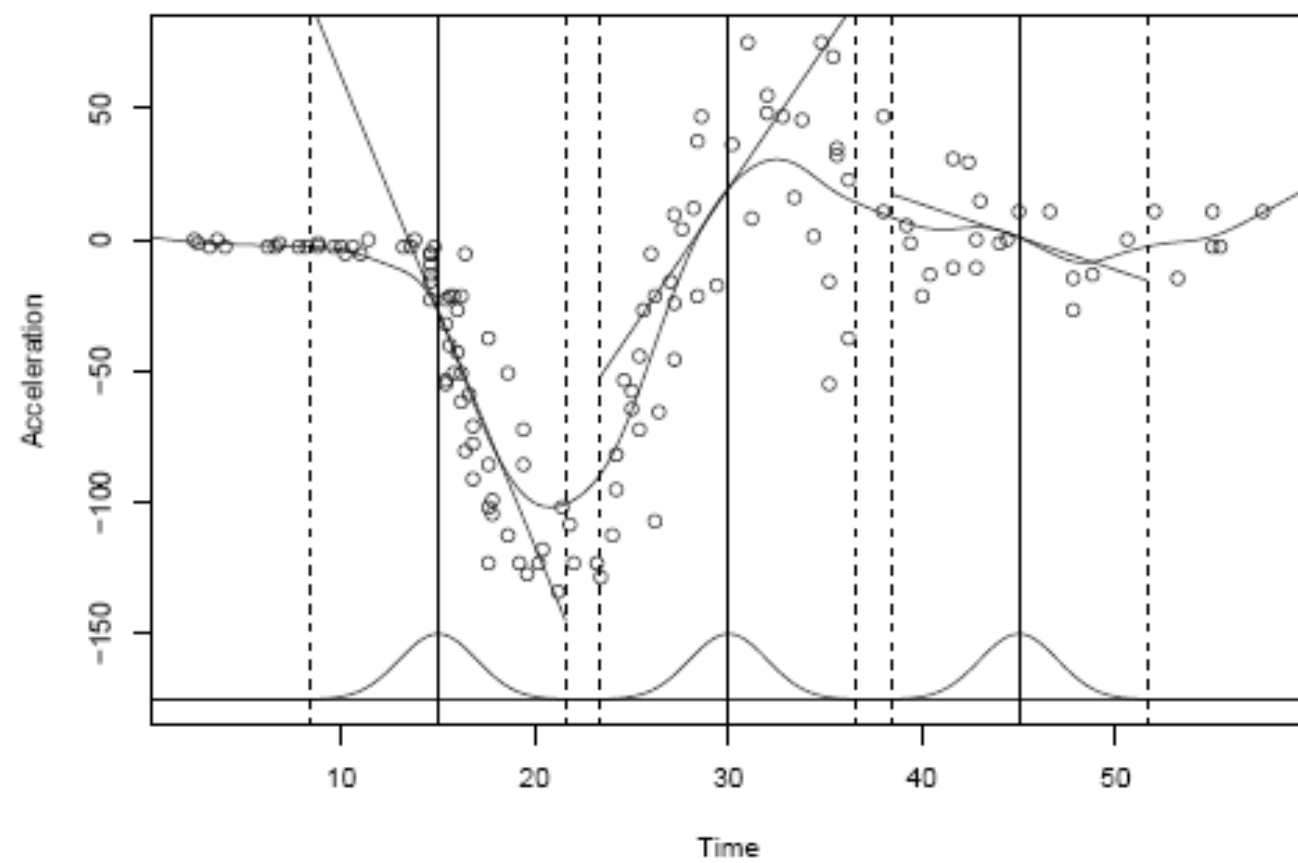
**FIGURE 5.53** Steps in computation of grid value for contouring. (a) Original set of irregularly spaced control points on a map. Numbers are "elevations." (b) Regularly spaced grid network, with nodes whose values are to be calculated. (c) Location of four nearest control points to one grid node. These four nearest values will be used to calculate grid value. (d) Completed grid with estimated elevations at every node.



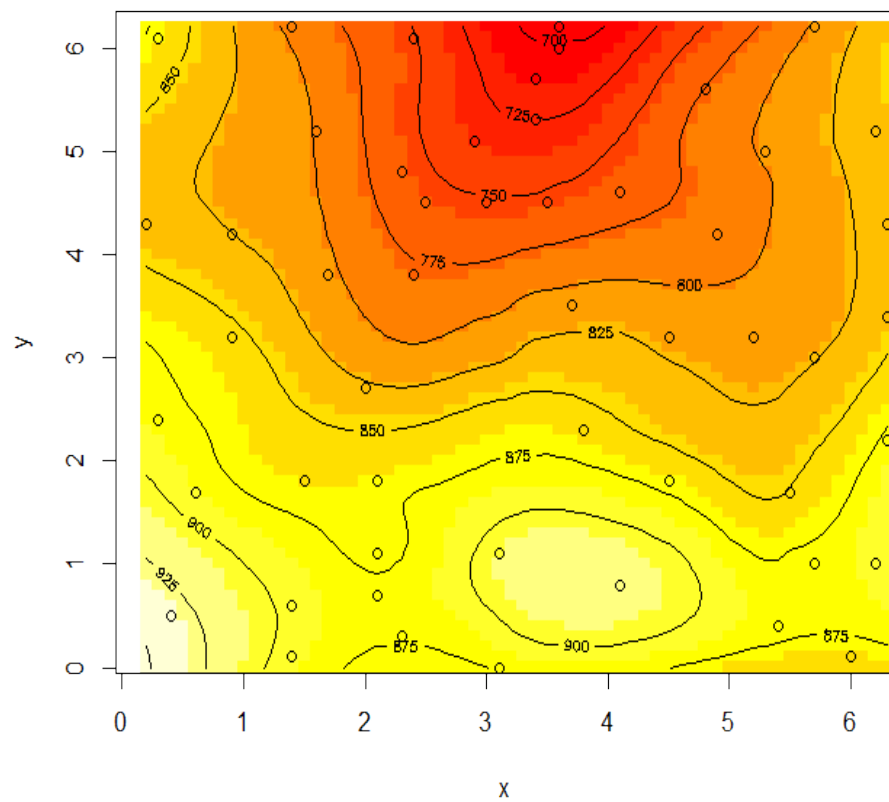
```
#IDW
kid <- krige(topo$z ~ 1, topo, topo.grid, NULL)
spplot(kid["var1.pred"], main = "TopIDW", contour=TRUE,
       sp.layout=list(list("sp.points", topo@coords, pch=19,
                           col=2)))
```

# Local Polynomial Regression Fitting (LOESS)

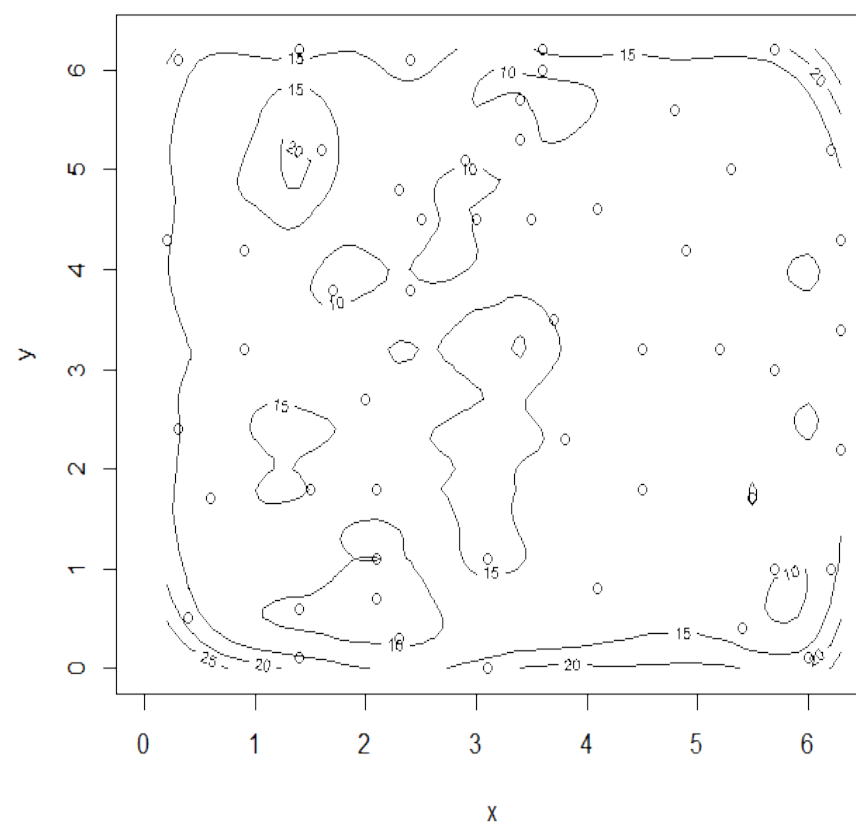
- Fitting is done *locally*. The fit is made using points in a neighbourhood of  $x$ , weighted by their distance from  $x$ .
- The size of the neighbourhood is controlled by  $\alpha$  (set by span parameter and controls the degree of smoothing).
- The neighbourhood points ( $\alpha < 1$ ) have tricubic weighting (proportional to  $(1 - (\text{dist}/\text{maxdist})^3)^3$ ).
- For  $\alpha > 1$ , all points are used, with the 'maximum distance' assumed to be  $\alpha^{(1/p)}$  times the actual maximum distance for  $p$  explanatory variables.



topo Loess degree = 2



loess -topo standard error degree=2



# Spline Regression

Spline regressions are regression line segments that are joined together at special join points known as spline knots. By definition, there are no abrupt breaks in a spline line. However, at their knots, splines may suddenly change direction (i.e., slope), or, for curved lines, there may be a more subtle, but just as sudden, change in the rate at which the slope is changing. Splines are used instead of quadratic, cubic, or higher-order polynomial regression curves because splines are more flexible and are less prone to multi-collinearity, which is the bane of polynomial regression.

“You can add a spline to whatever model, so your dependent variable, can be continuous, bounded, discrete, categorical, or whatever else you can or cannot think of. A spline is added because you think that the effect of a variable is non-linear, so it makes only sense when the explanatory variable is continuous.” (Lawrence C. Marsh)

## B-splines

uses a piecewise polynomial to provide a series of patches resulting in a surface that has continuous first and second derivatives ensures continuity in:

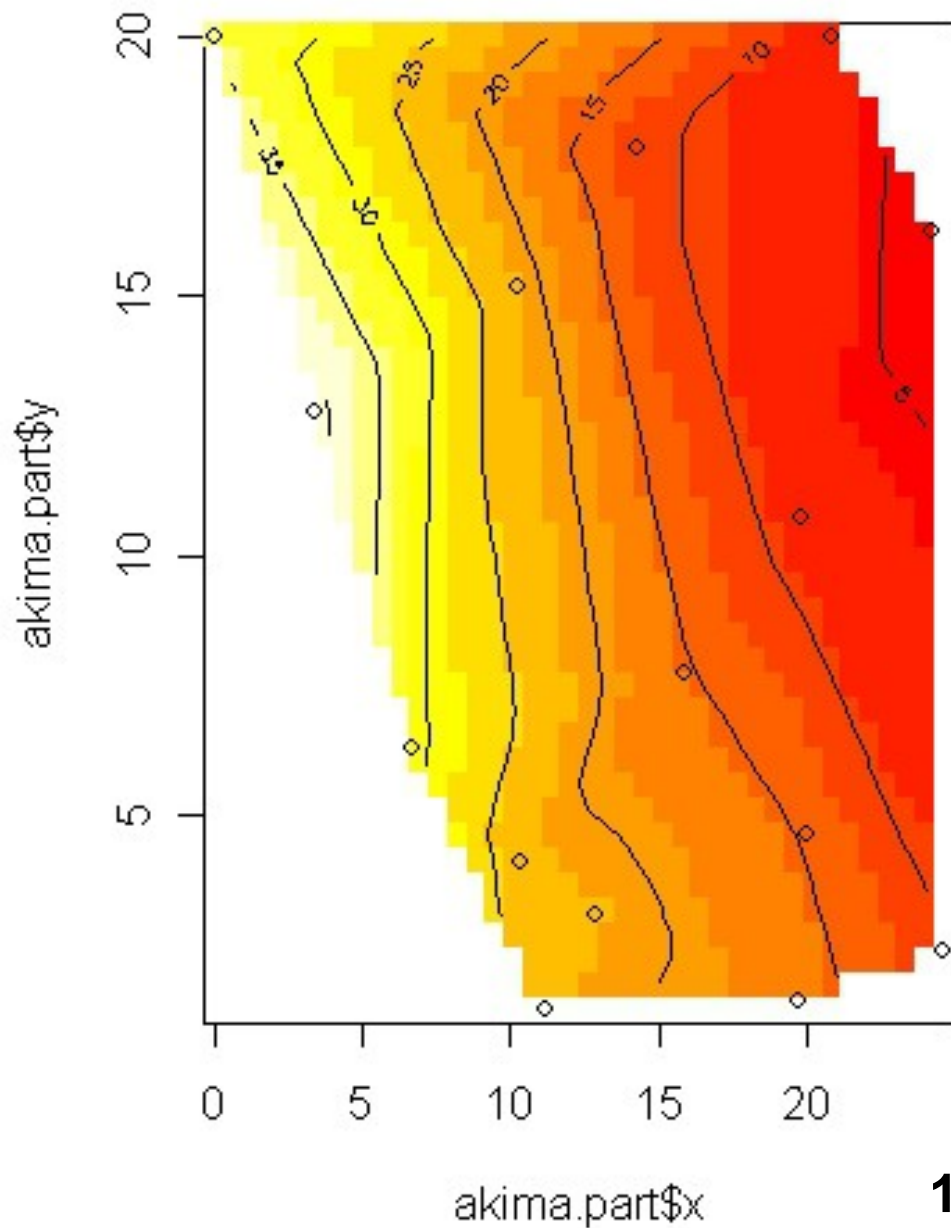
- elevation (zero-order continuity) - surface has no cliffs

- slope (first-order continuity) - slopes do not change abruptly, there are no kinks in contours

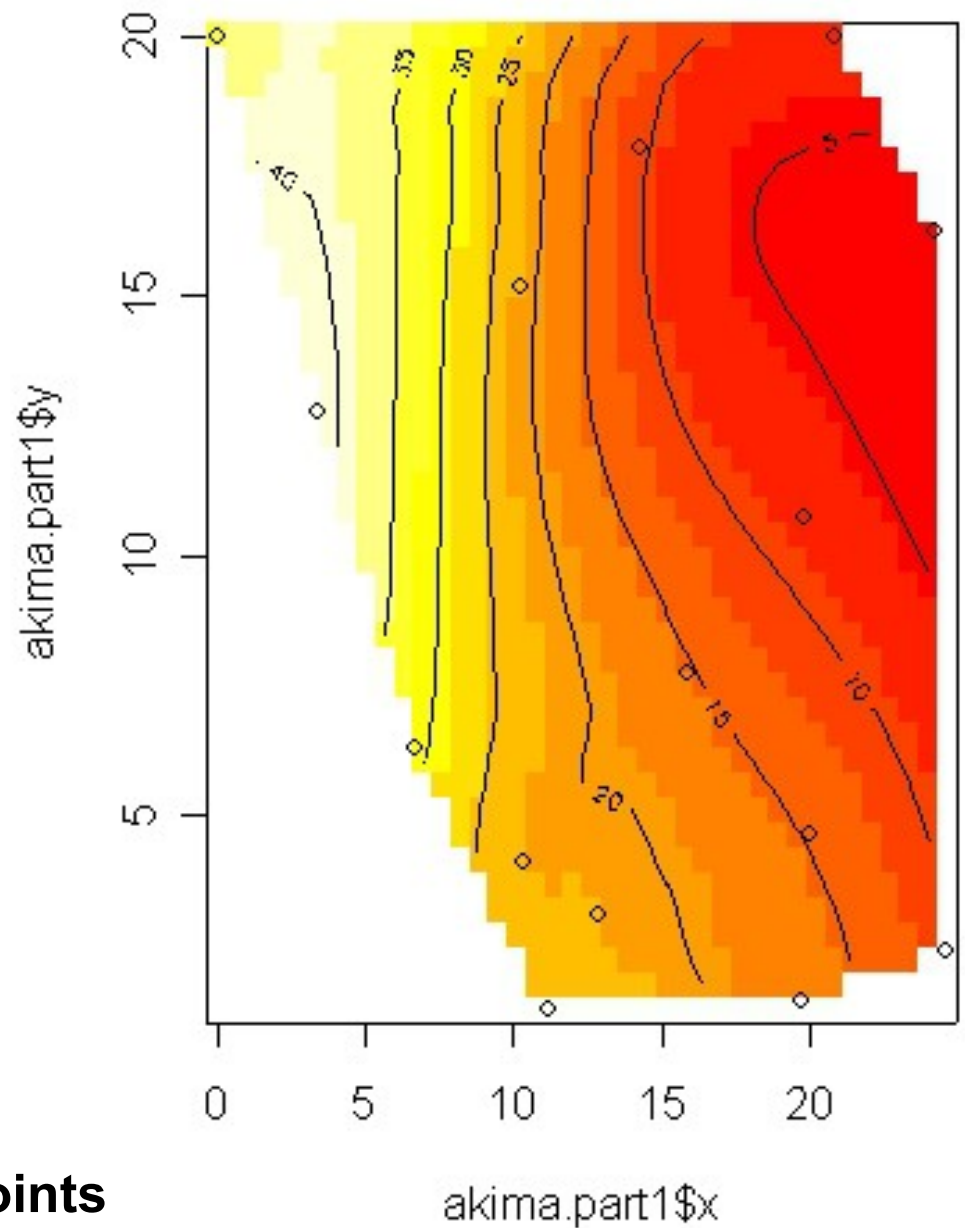
- curvature (second order continuity) - minimum curvature is achieved produces a continuous surface with minimum curvature

## SPLINE

### Akima - Linear Interpolation



### Bicubic Spline Interpolation

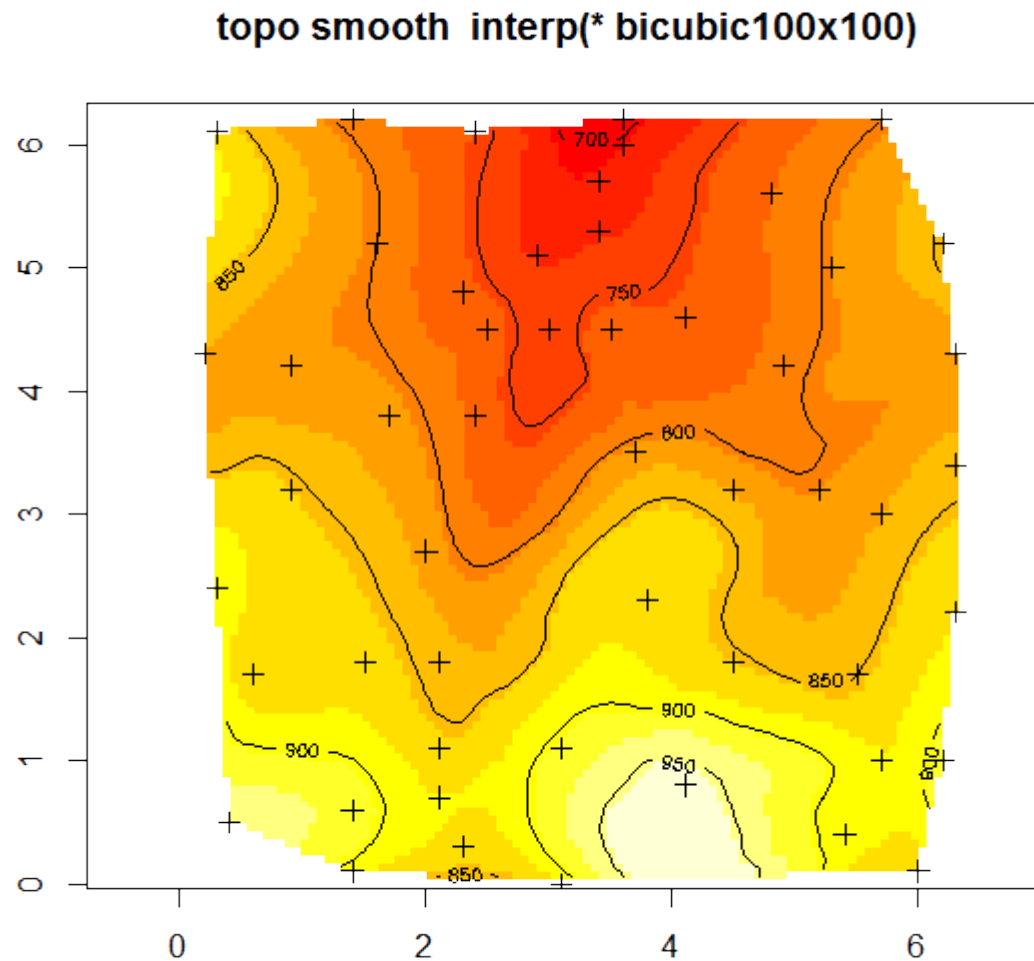


**15 points**



# Bicubic spline

- interpolation of a bivariate function,  $z(x,y)$ , is made on a rectangular grid in the  $x$ - $y$  plane.
- the interpolating function is a piecewise function composed of a set of bicubic (bivariate third-degree) polynomials, each applicable to a rectangle of the input grid in the  $x$ - $y$  plane. Each polynomial is determined locally - with the piecewise segments joined at *knots* and with various degrees of smoothness.



```
akima.spl <- with(topo, interp(x,y,z, xo=seq(0,6.3,  
  length=100), yo=seq(0,6.3, length=100),linear=FALSE))  
image(akima.spl,asp=1,main = "topo smooth  interp(*  
  bicubic100x100)")  
contour(akima.spl,add=TRUE)  
points(topo,pch=3)
```

# Thin Plate Spline

The thin plate spline is a two-dimensional variation of the cubic spline. It is the fundamental solution to the biharmonic equation, and has the kernel form

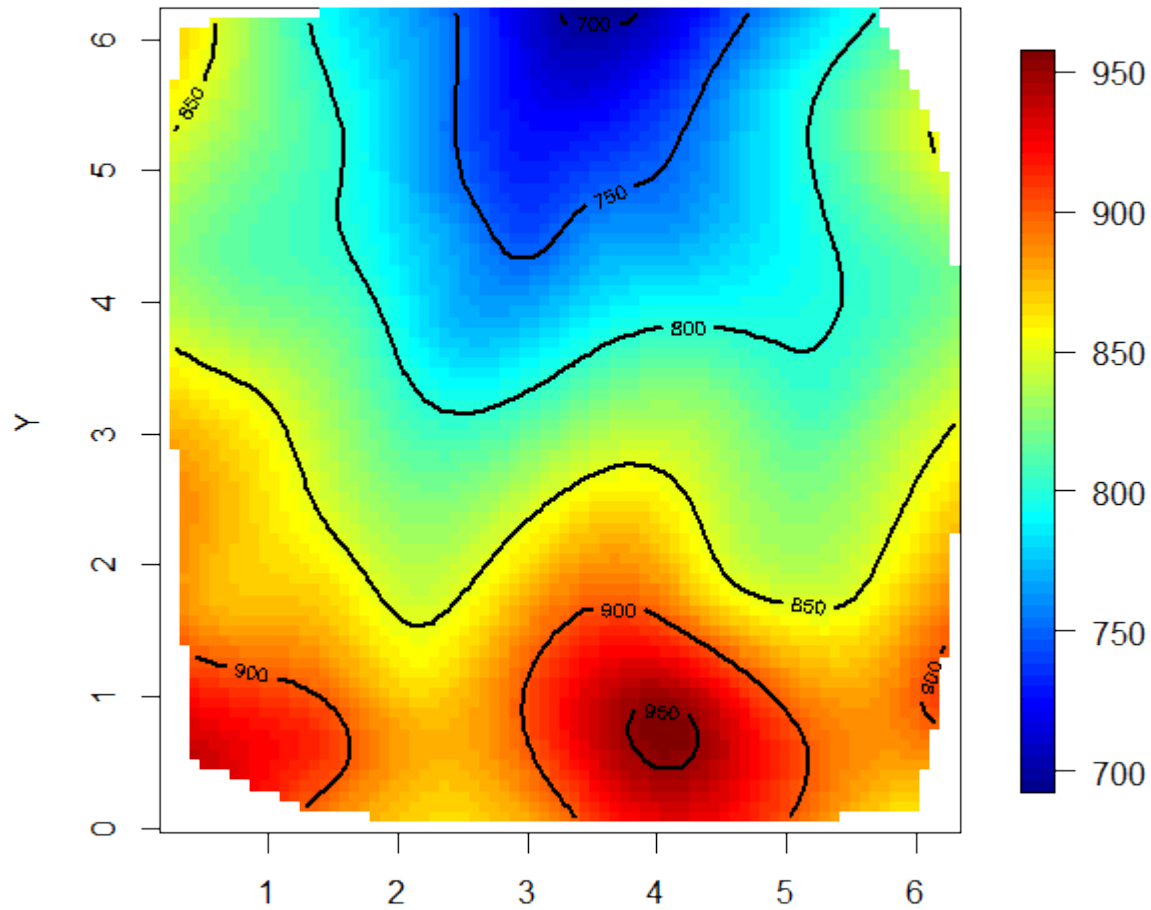
$$U(r) = r^2 \ln r.$$

Given a set of data points, a weighted combination of thin plate splines centered about each data point gives the interpolation function that passes through the points exactly while minimizing the so-called "bending energy" or tension. Bending energy is defined here as the integral over domain of the squares of the second derivatives:

$$I[f(x, y)] = \iint_{\mathbb{R}^2} (f_{xx}^2 + 2 f_{xy}^2 + f_{yy}^2) dx dy.$$

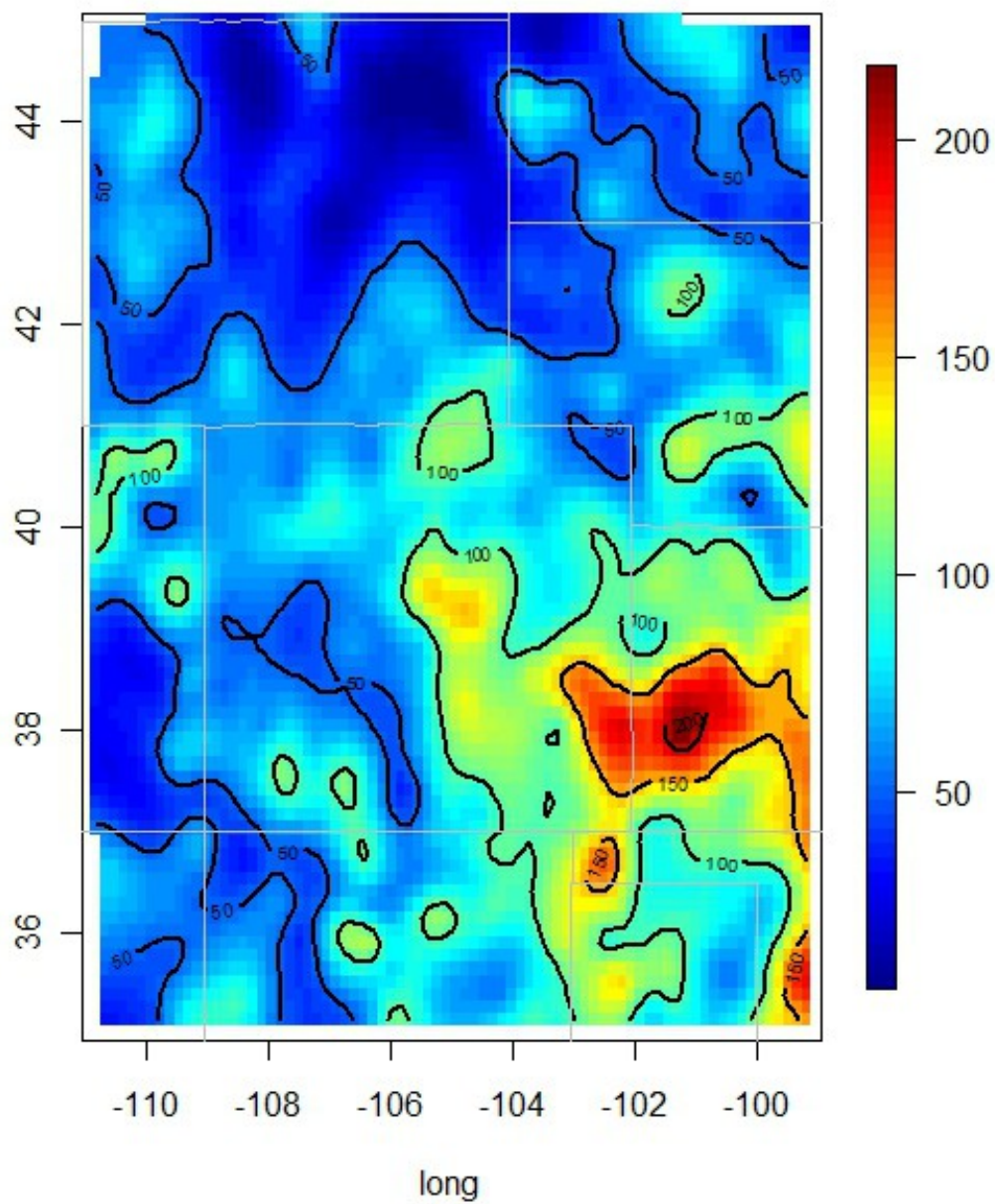
Regularization may be used to relax the requirement that the interpolated point pass through the data points exactly.

Thin plate splin from fields(Topo)

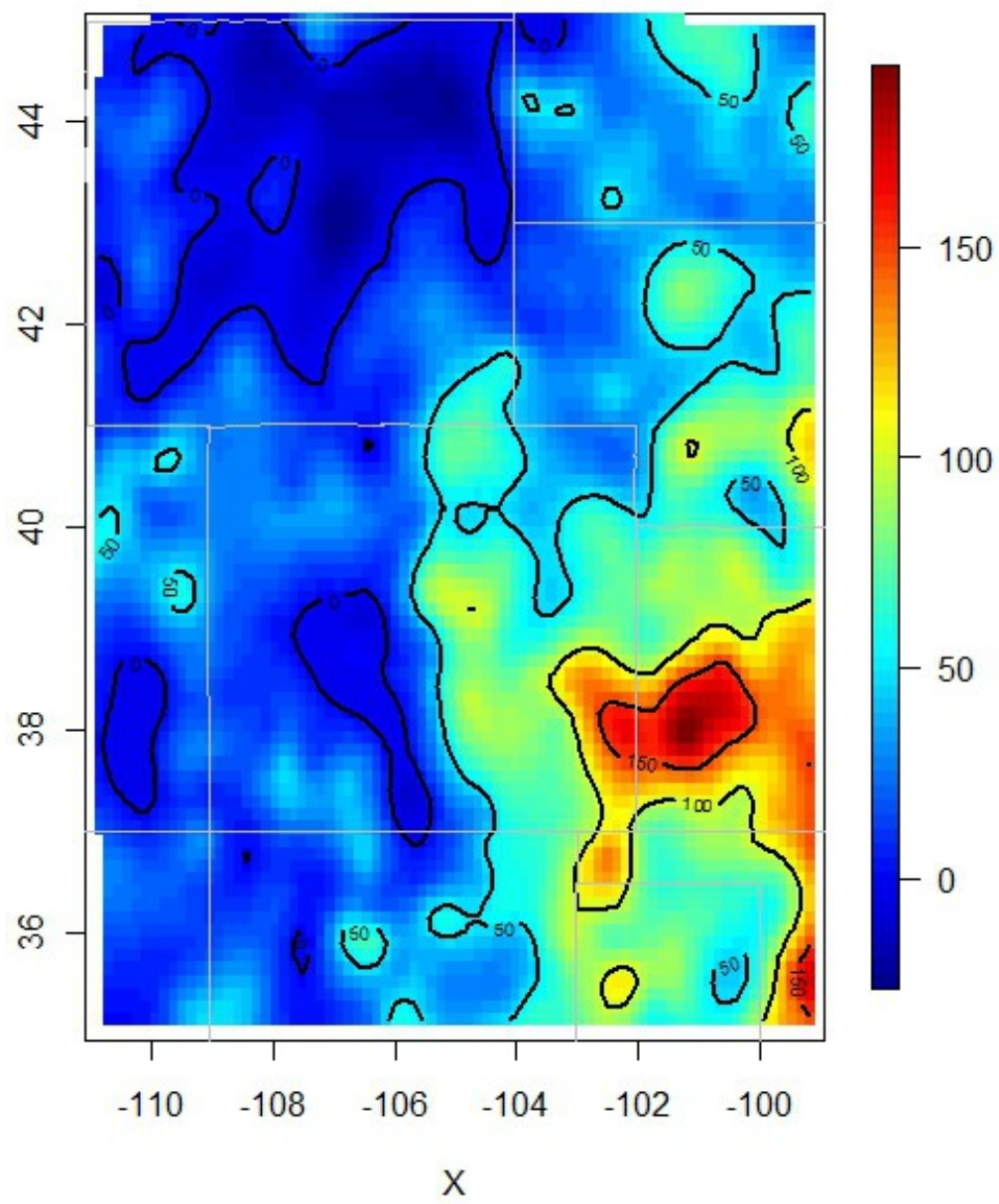


```
#Tps from "fields" for topo x
data(topo)
setting up data for Tps
x <- topo$x; y <- topo$y; z <- topo$z
tp <- cbind (x,y); tpo <- list(x=tp,y=z)
tout <- Tps(tpo$x,tpo$y) #thin plate spline function
surface(tout)
title("Thin plate spline from fields(Topo)")
```

**Precip**

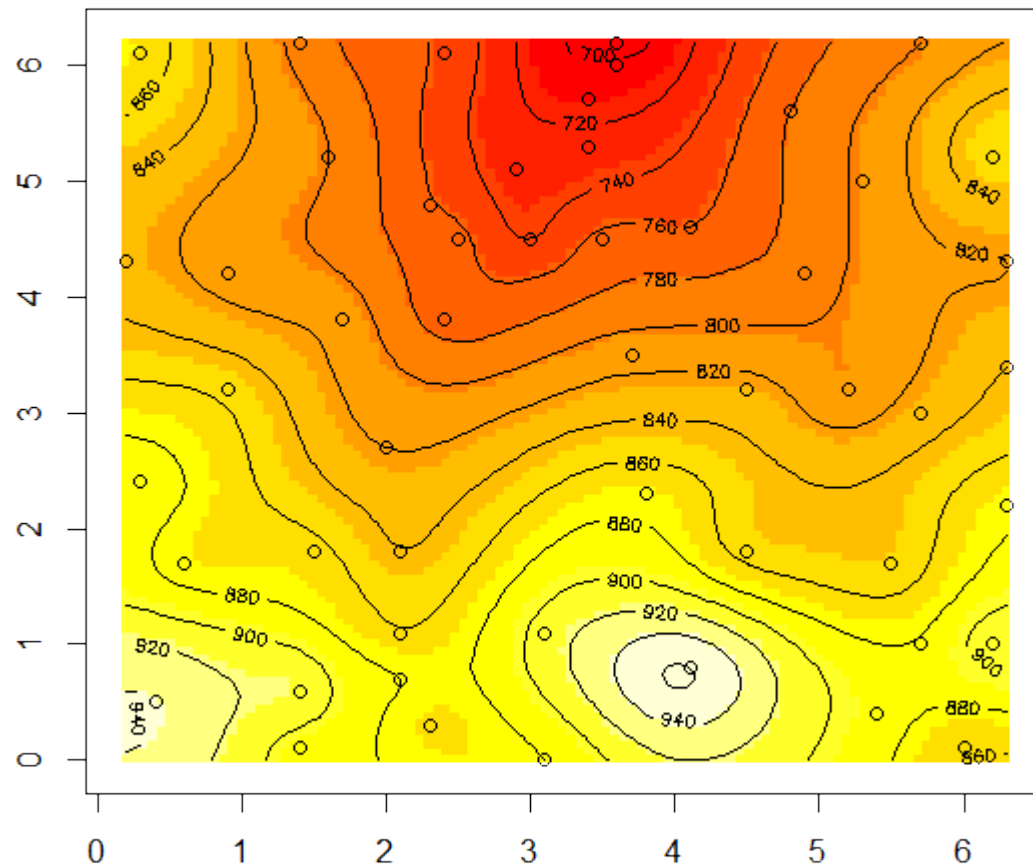


**Precip with Elev**

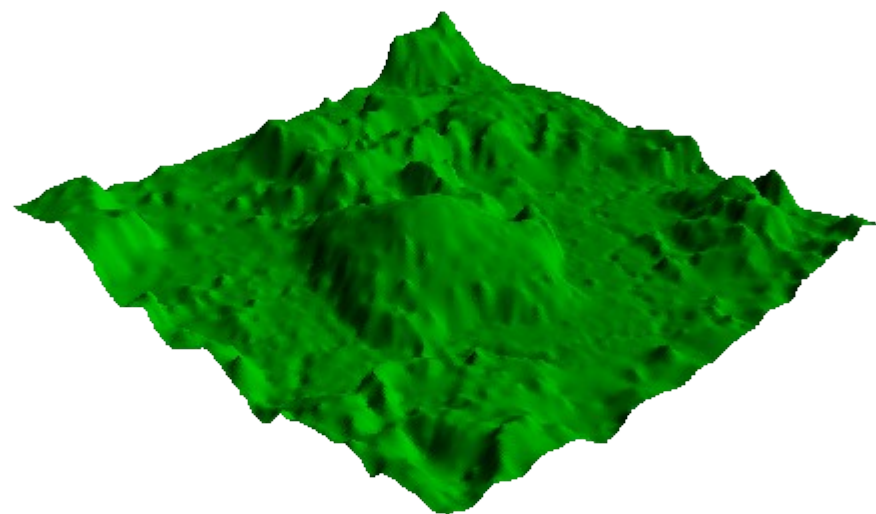
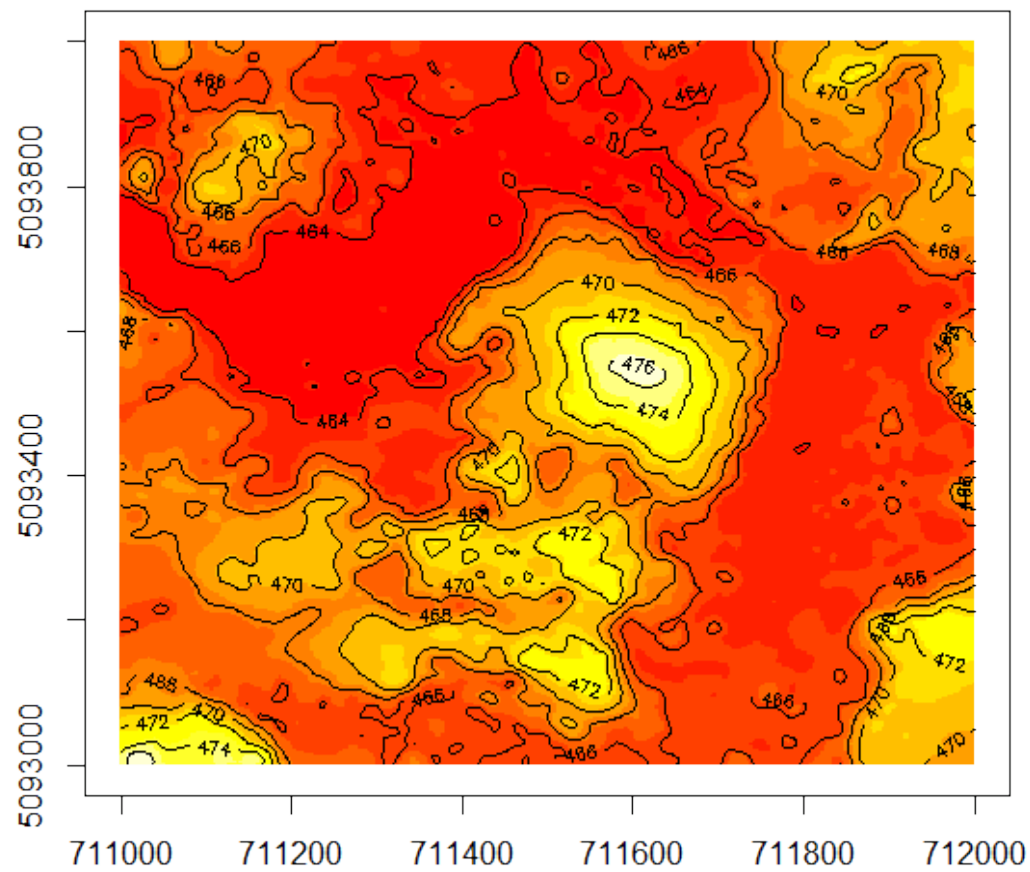


# Mult-level B-splines

MBA - topo 100x100



**MBA - LIDAR forest data**



# Surface approximation from bivariate scattered data using multilevel B-splines

```
require(MBA)
data(LIDAR)# 10123 points taken over forest area
mba.int <- mba.surf(LIDAR, 300, 300, extend=TRUE)
  $xyz.est
##Image plot
image(mba.int, xaxs="r", yaxs="r",main="MBA - LIDAR
  forest data")
contour(mba.int,add=TRUE)
##Perspective plot
persp(mba.int, theta = 135, phi = 30, col = "green3",
  scale = FALSE, ltheta = -120, shade = 0.75, expand
  = 10, border = NA, box = FALSE)
```



# Spline Interpolation

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- **Fits a minimum-curvature surface through input points**
- **Like a rubber sheet that is bent around the sample points**
- **Best for gently varying surfaces such as elevation**
- **Estimates can result in spurious ridges and valleys**

# Spatial Prediction-Kriging

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## ➤ Model of Spatial Variability – theory of regionalized variable

- $Z(x) = \mu(x) + k(x) + \varepsilon$

- $\mu(x)$  is a deterministic function describing the ‘structural’ component of  $Z$
- $k(x)$  denotes the stochastic, locally varying but spatially dependent residuals from  $\mu(x)$ -the regionalized variable
- $\varepsilon$  is a spatially independent Gaussian noise term with zero mean and variance  $\sigma^2$

# Kriging

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➤ Kriging is a “collection of generalized linear regression techniques for minimizing an estimation variance defined from a prior model of covariance” (Olea, 1991)

$$\hat{Z}(s_o) = \sum_{i=1}^n \lambda_i Z(s_i) \quad \text{with}$$

$$\sum_{i=1}^n \lambda_i = 1$$

# Kriging

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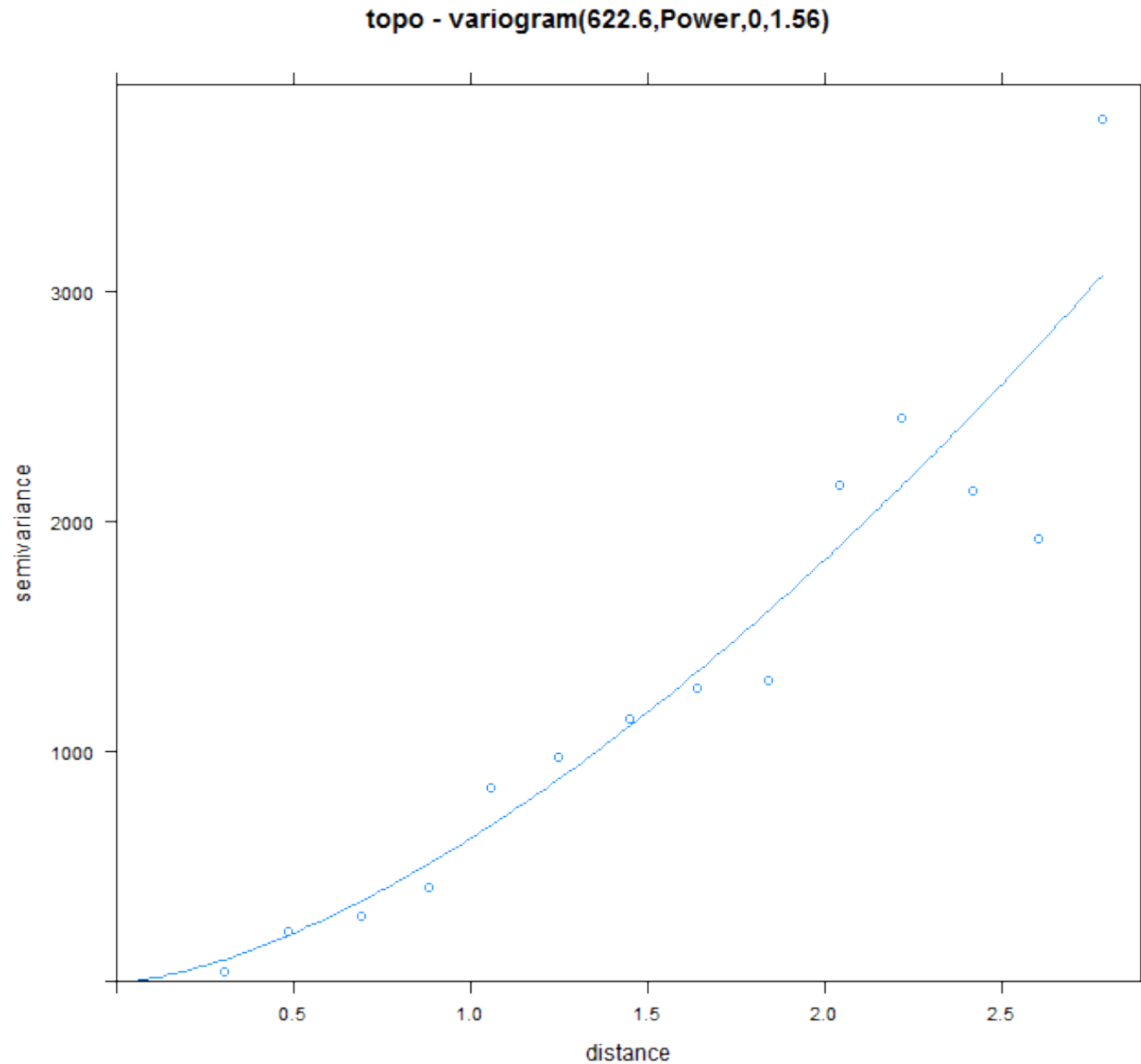
## ➤ Principle

- obtain the **best unbiased linear** predictor
- takes into account the covariance structure as a function of distance

## ➤ Best Predictor

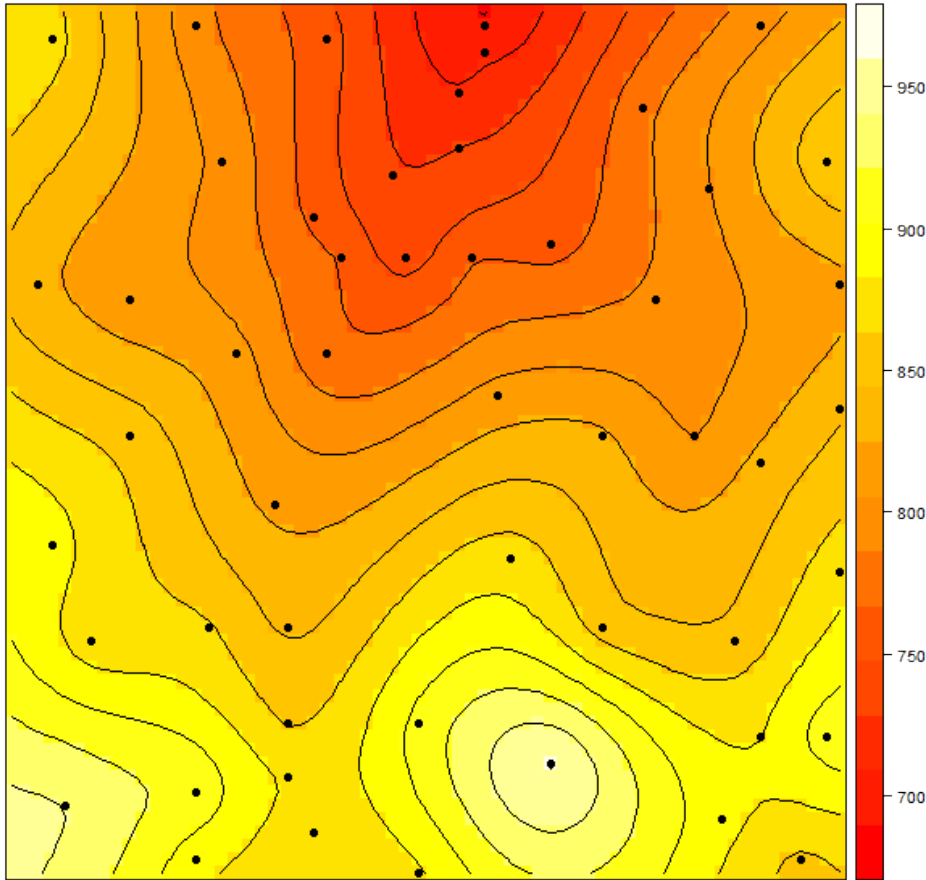
- unbiased:  $E[z^p - z] = 0$  or **no systematic error**
- **minimum** variance of  $z^p$  for any other combination of the observed values
- predict for a **new locations (s)** based on the covariance

# Estimating the variogram as a measure of spatial covariance

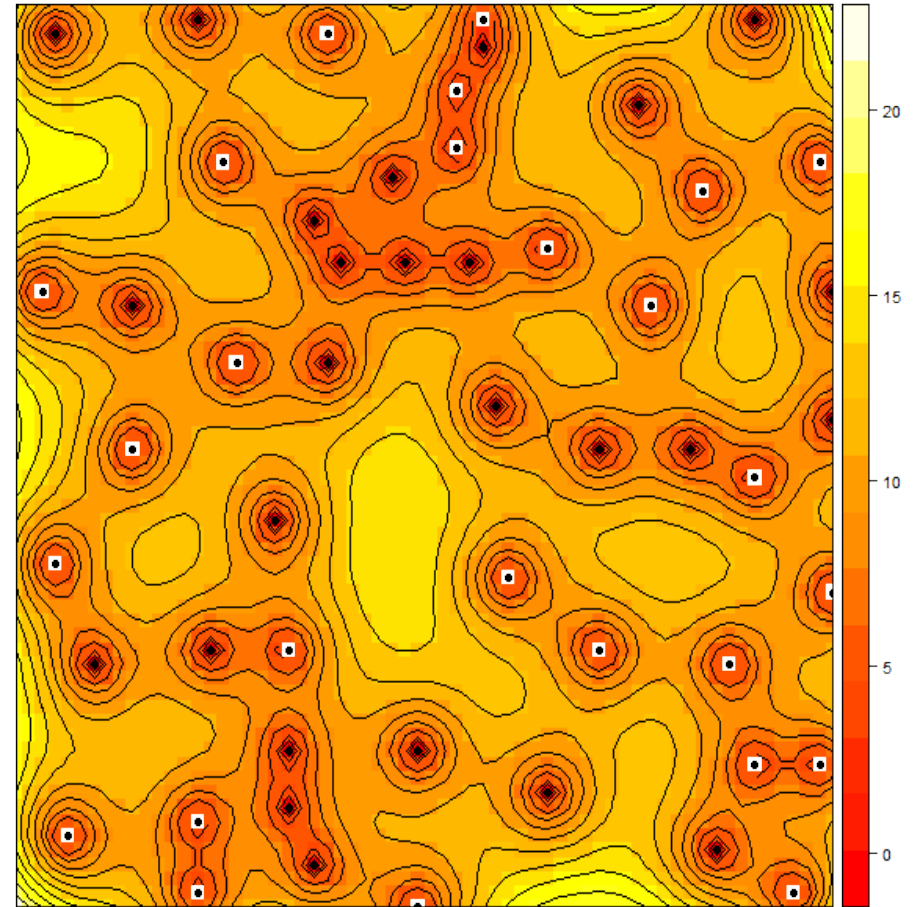


# Kriging TOPO

universal kriging predictions



Topo-universal kriging se



# Is Kriging Better??

---

- it provides the no. of points needed to compute the local average
- provides the size, orientation and shape of neighborhood from which the points are drawn
- indicates if there are better ways to estimate the interpolation weights
- its strengths are in the statistical quality of its predictions (e.g. unbiasedness) and in the ability to indicate some measure of the spatial distribution of uncertainty.
- It has been less successful for applications where local geometry and smoothness are the key issues and other methods prove to be competitive or even better

# Spatial Simulation

- A stochastic technique of *conditional* simulation is used to generate alternative, equally probable realizations of a surface, reproducing both data and the estimated covariance.
- From such a set of statistical samples one can estimate a spatially-dependent picture of the uncertainty which is inherent in the data.

**Simulation** is not an instant picture of reality but only a version of it among a myriad of other possibilities. There are two questions that are paramount when doing simulations:

- 1) How confident can I be of the results?
- 2) How many simulations should we generate?



# Why spatial simulation?

- Recall: the **theory of regionalized variables** assumes that the values we observe come from some **random process**; in the simplest case, with one **expected value** (first-order stationarity) with a **spatially-correlated error** that is the same over the whole area (second-order stationarity).
- So we'd like to see “**alternative realities**”; that is, spatial patterns that, by this theory, *could have* occurred in some “parallel universe” (i.e. another **realization** of the **spatial process**).
- In addition, **kriging maps are unrealistically smooth**, especially in areas with low sampling density.
  - \* Even if there is a high nugget effect in the variogram, this variability is *not* reflected in adjacent prediction points, since they are estimated from almost the same data.

Goovaerts: “Smooth interpolated maps should not be used for applications sensitive to the presence of **extreme values and their patterns of continuity**.” (p. 370)

Example: ground water travel time depends on sequences of large or small values (“critical paths”), not just on individual values.

(from David Rossiter)

## Local uncertainty vs. spatial uncertainty

- Recall: kriging prediction also provides a **prediction error**; this is the BLUP and its error **for each prediction location separately**.
- So, at each prediction location we obtain a probability distribution of the prediction, a measure of its **uncertainty**. This is fine for evaluating each prediction individually.
- But, it is *not* valid to evaluate the set of predictions! Errors are *by definition* spatially-correlated (as shown by the fitted variogram model), so we can't simulate the error in a field by simulating the error in each point separately.
- **Spatial uncertainty** is a representation of the error over the **entire field of prediction locations** at the same time.

(from David Rossiter)

# Types of Simulation Procedures

---

- **Simple Monte Carlo** method – simulate values for each point which has a unique and an equiprobable value. Since each cell is independent-the results are a stationary noise surface.

$$z(x) = \Pr(Z)$$

where  $Z$  is a spatially independent, normally distributed probability distribution function with mean  $\mu$  and variance  $\sigma^2$

**Unconditional Simulation** – use the variogram to impart spatial information but the actual data points are not used. With the variogram parameters and Monte Carlo procedures the most likely outcome per cell are computed.

$$z(x) = \Pr(Z), \gamma(h)$$

## Conditional simulation

This simulates the field, while **respecting the sample**.

The simulated maps look more like the best (kriging) prediction, but usually much more spatially-variable (depending on the magnitude of the nugget).

These can be used as inputs into **spatially-explicit models**, e.g. hydrology.

## What is preserved in conditional simulation?

1. Mean over field
2. Covariance structure
3. Observed data (points are predicted exactly)

## Conditional simulation

Idea: generate a large set of fields (realizations) that

- honour the data (are conditioned to the data)
- on average, reflect the kriging prediction and variance
- each have a spatial variability, equal to that of the data (in contrast to the kriging prediction map, which is much smoother than the data)
- when to use it? When  $Z$  is input to a non-linear model, e.g. some transport or flow model.

(from Edzer Pebesma)

# Steps in Simulation Modelling

---

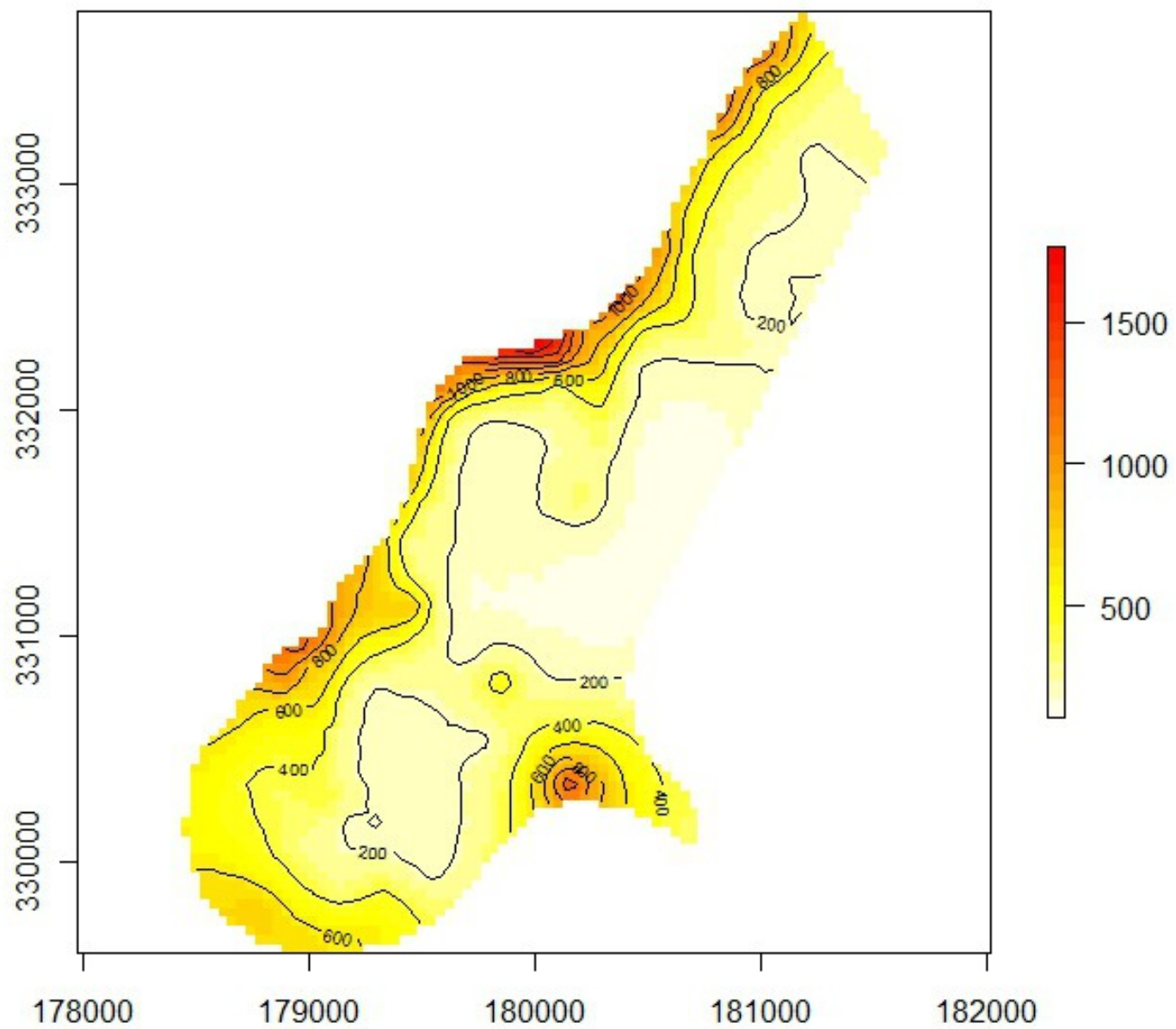
1. Set up the usual equations for simple/ordinary kriging with an overall mean.
2. Select an unsampled data point at random. Compute kriging prediction and standard error using data from the data set in the locality of the point.
3. Draw a random value from the probability distribution defined by the prediction and standard error. Add this to the list of data points.

# **Steps in Simulation (continued)**

---

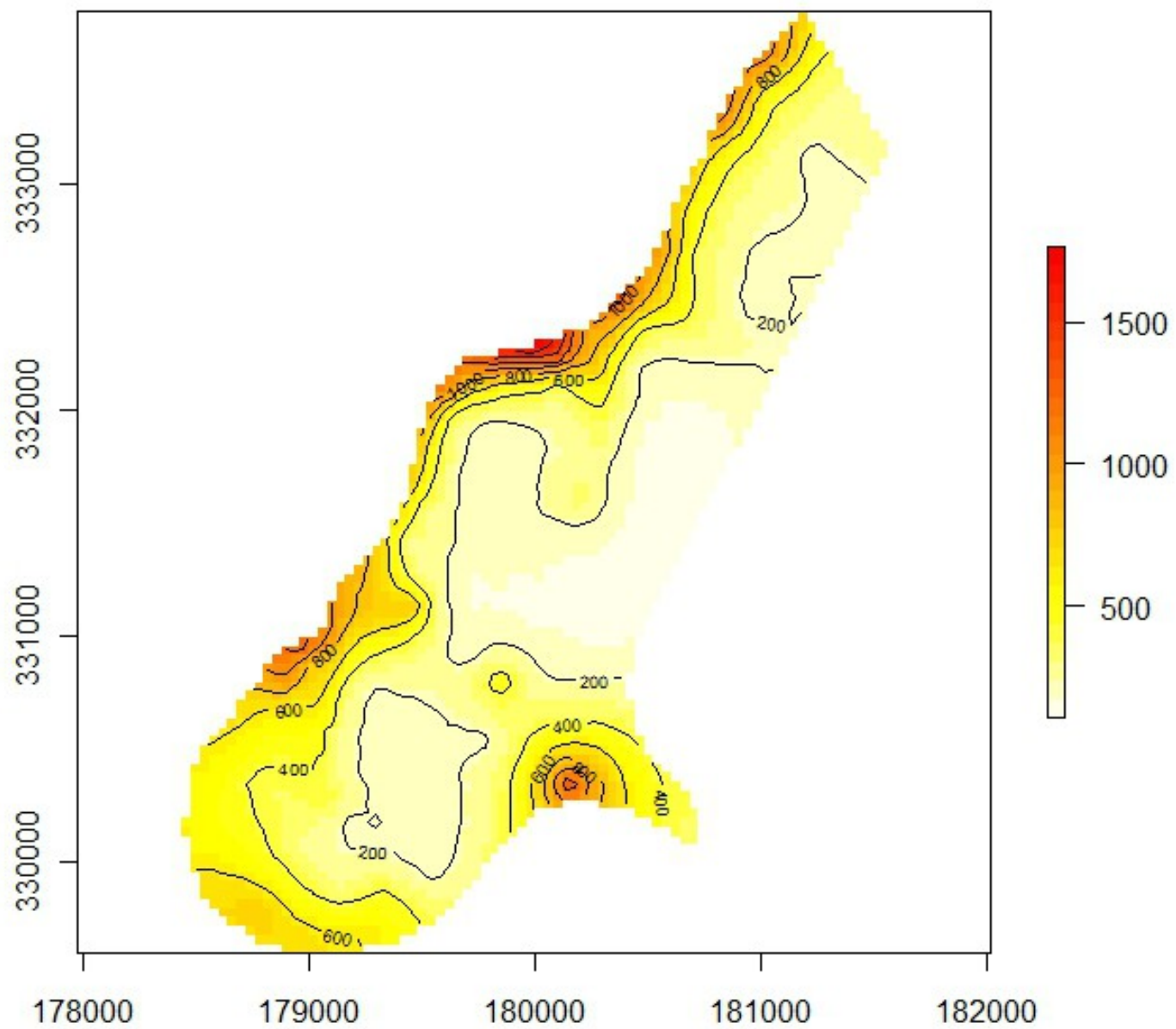
- 4. Repeat steps 2-3 until all cells/points have been visited and the simulation of one realization is completed.**
- 5. Repeat steps 1-4 until “sufficient” realizations have been created.**
- 6. Compute surfaces for the mean values and standard deviation from all the realizations.**

Krige prediction (Zn)

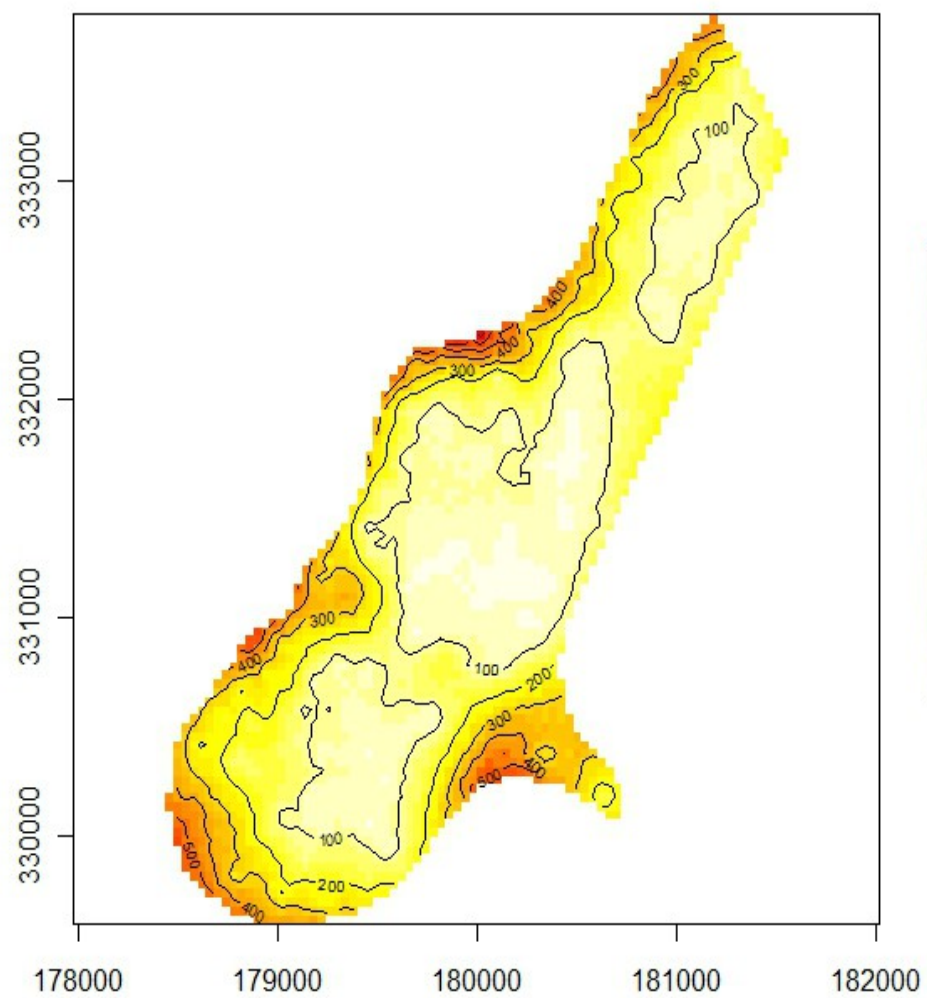




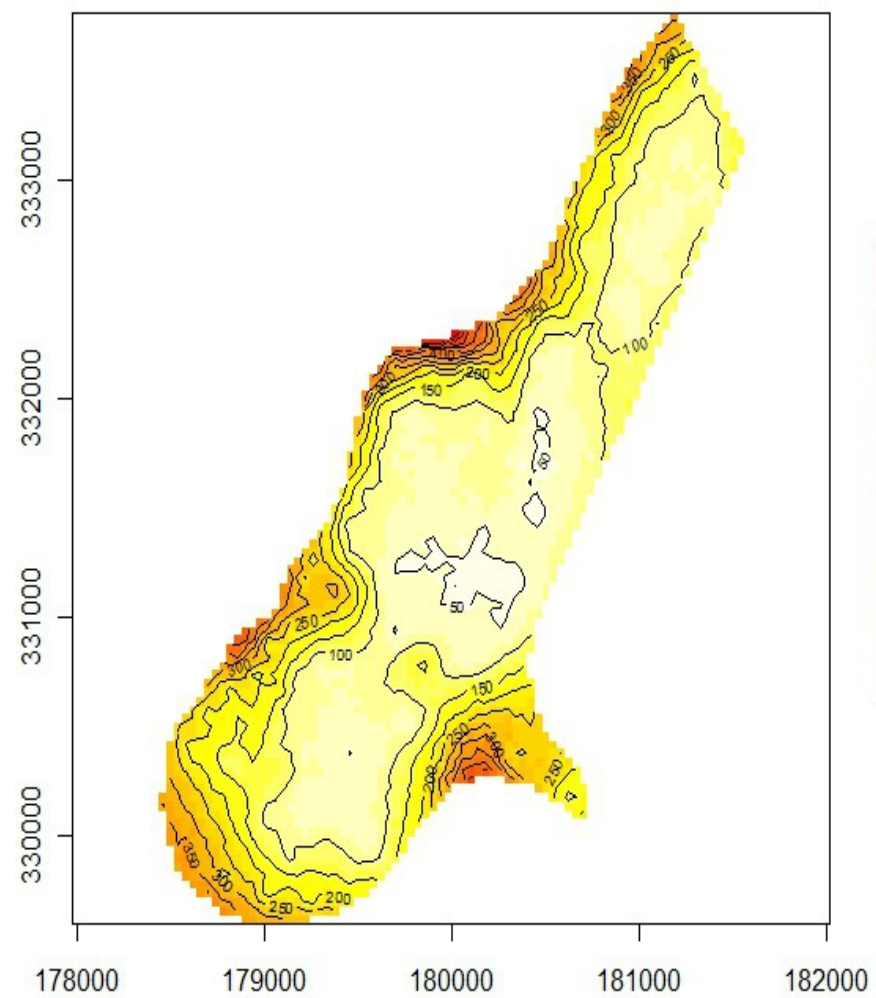
Krige prediction (Zn)



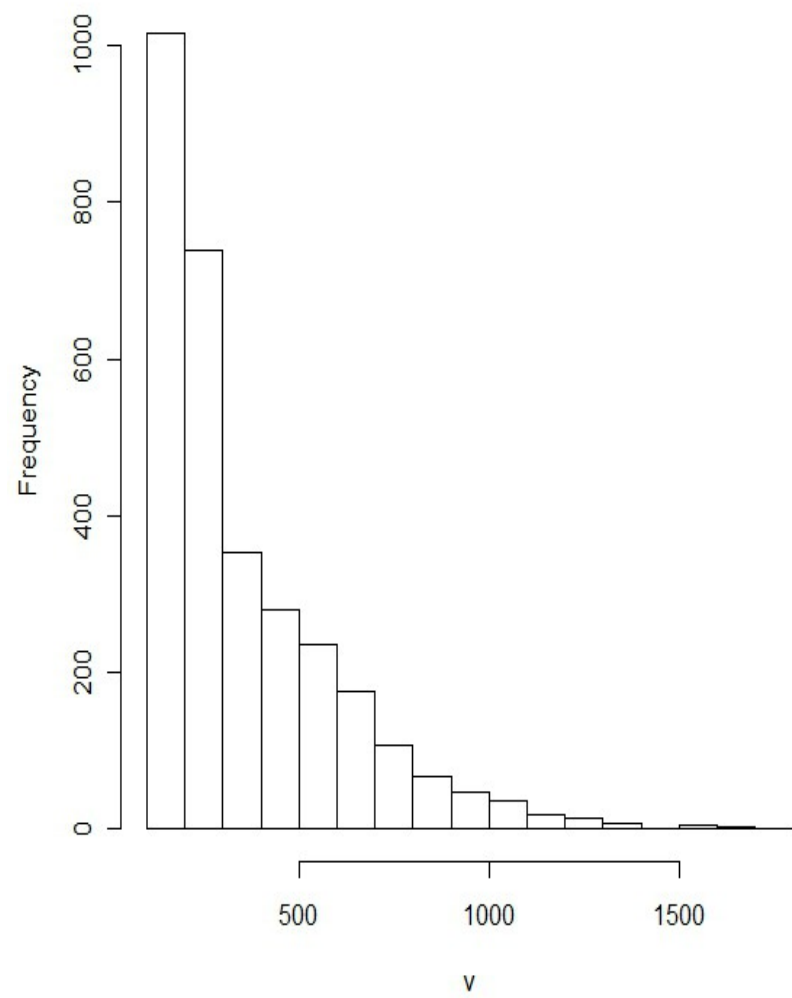
**simulation-median (Zn) n=1000**



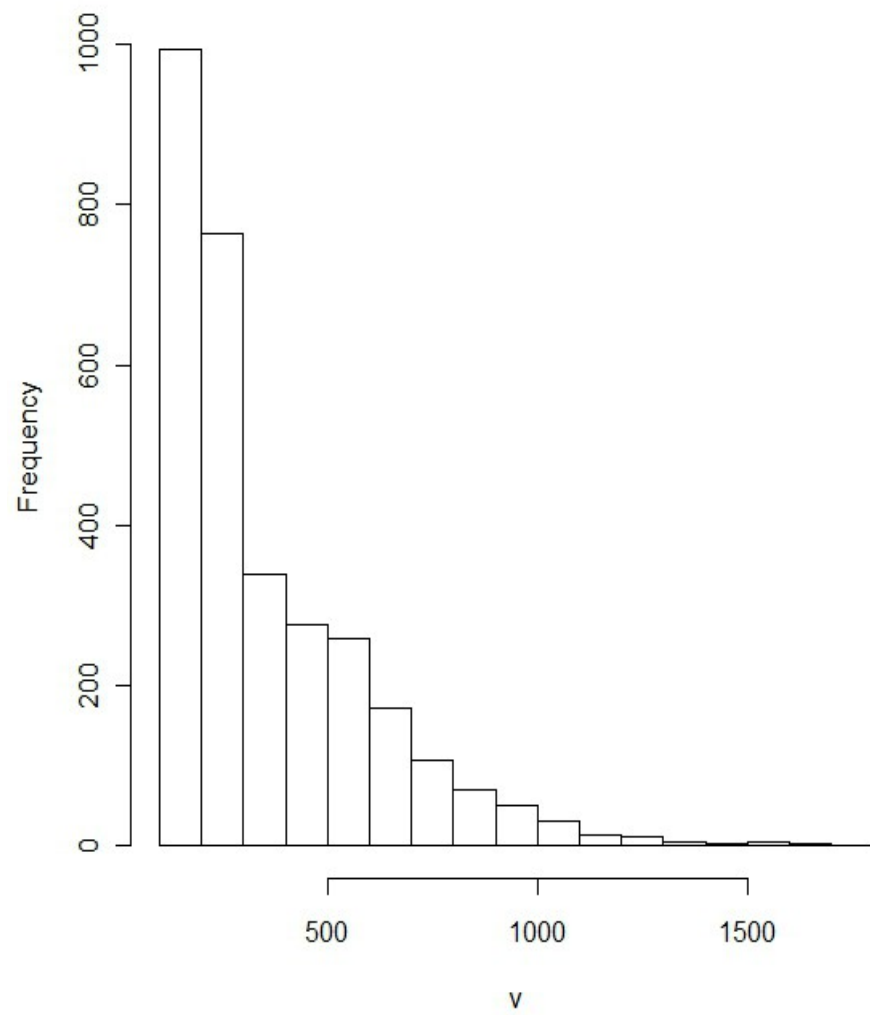
**simulation-mad (Zn) n=1000**



**Observed Krige Prediction**



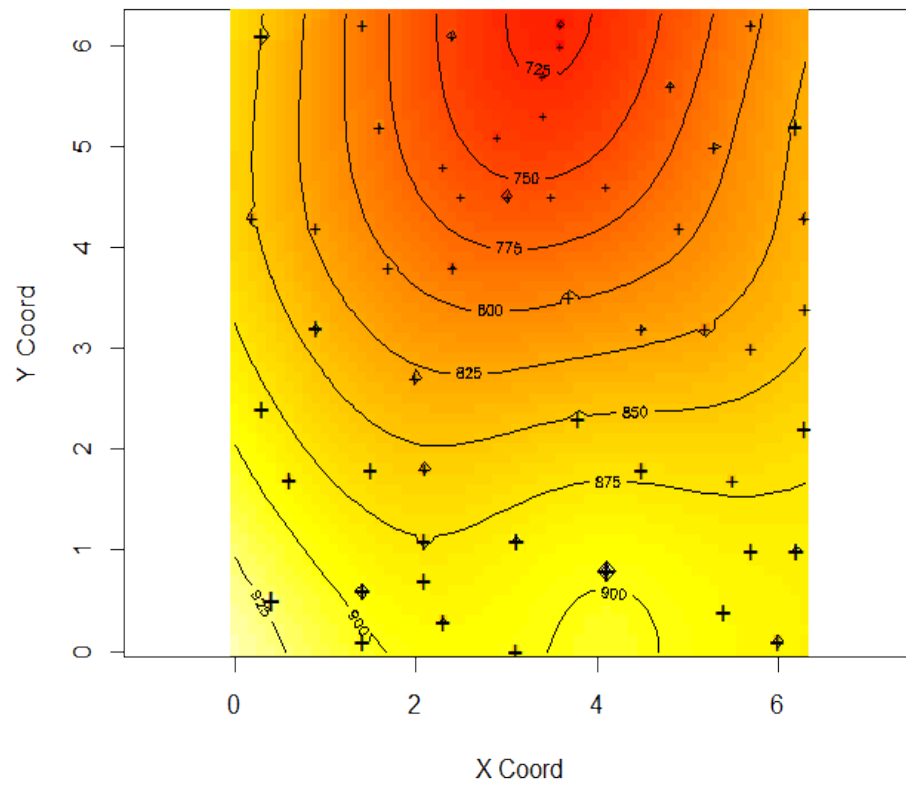
**simulation-median (Zn)**



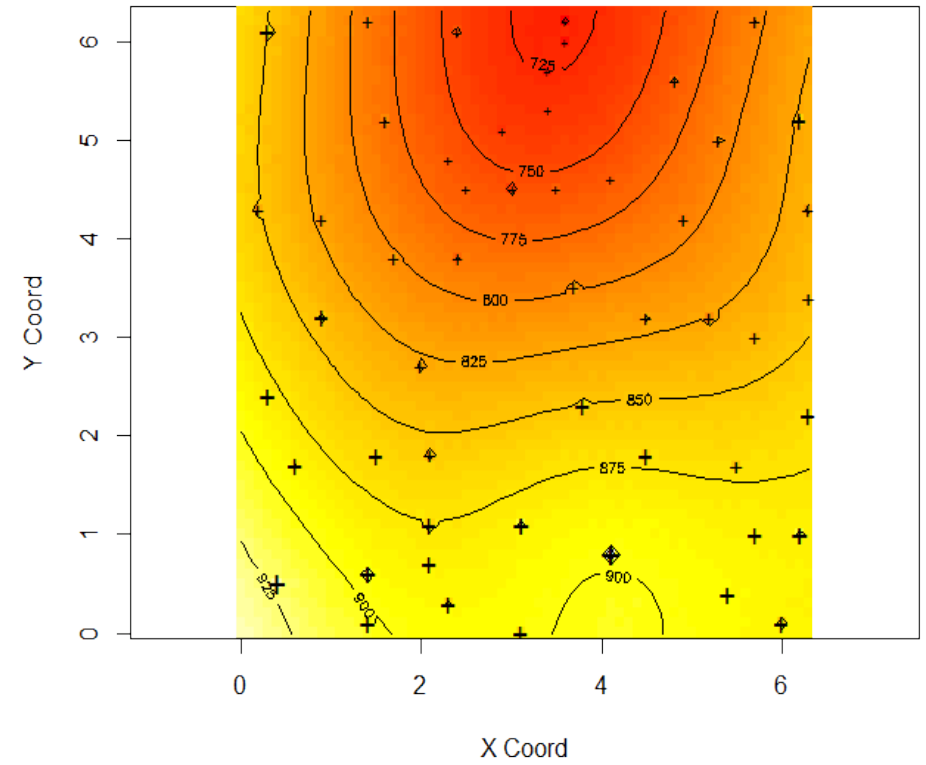
# Conditional Simulation in gstat with use of raster

```
require(raster)
set.seed(234)
.
.
v = variogram(log(zinc)~1, meuse)
v.m = fit.variogram(v, vgm(1, "Sph", 900, 1))
tsr <- 1000
sim = krige(log(zinc)~1, meuse, meuse.grid, v.m, nsim = tsr,
            nmax = 20)
s <- brick(sim)
rs2 <- calc(s, fun=function(x){exp(x)}) #backtransform log data
b1 <- stackApply(rs2, indices=c(rep(1,tsr)),
                fun=median, progress="window")
plot(b1,col=rev(heat.colors(25)),main="simulation-median (Zn)
      n=1000")
contour(b1, add=TRUE)
hist(b1,main=("simulation-median (Zn)"))
b2 <- stackApply(rs2, indices=c(rep(1,tsr)),
                fun=mad, progress="window")
plot(b2,col=rev(heat.colors(25)),main="simulation-mad (Zn)
      n=1000")
contour(b2, add=TRUE)
```

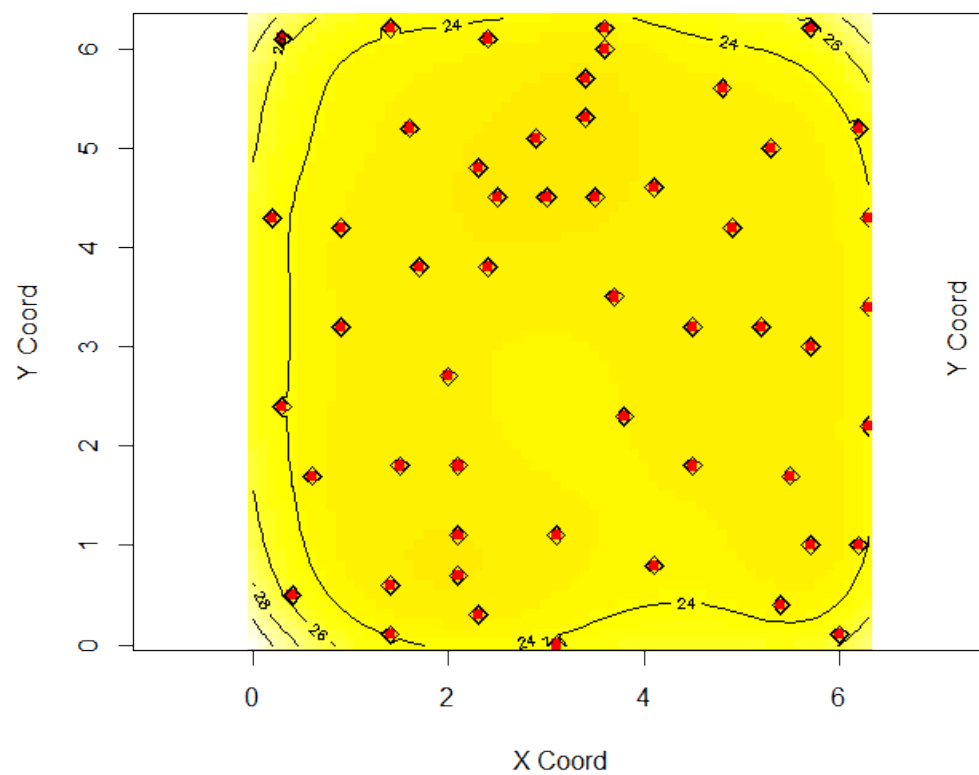
Topo -elevation - Predicted



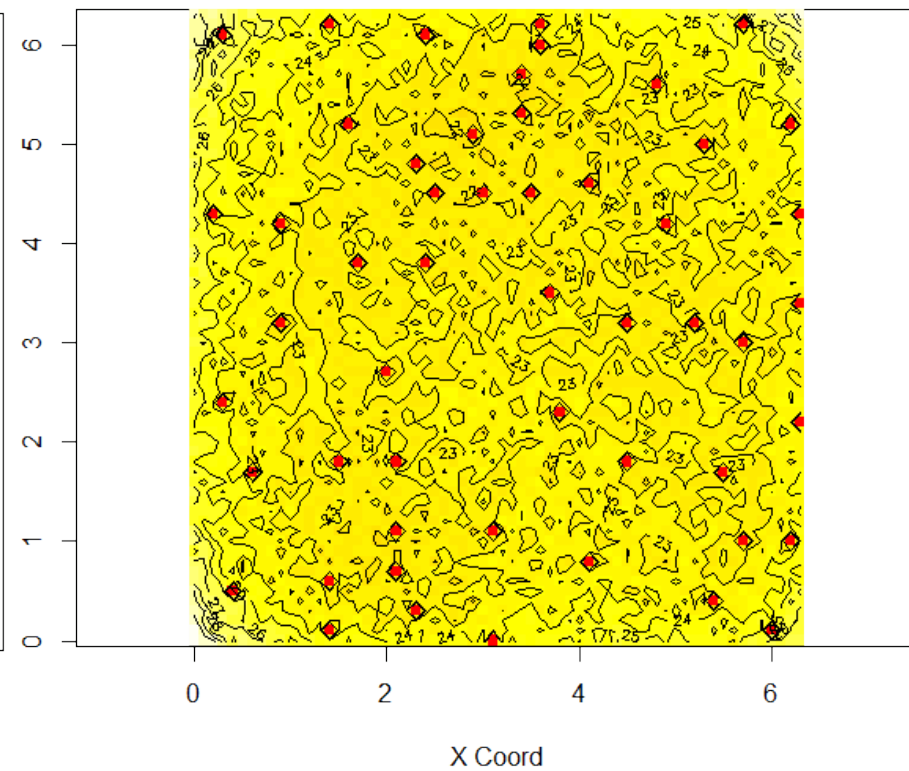
Topo-elevation - meanSimulations



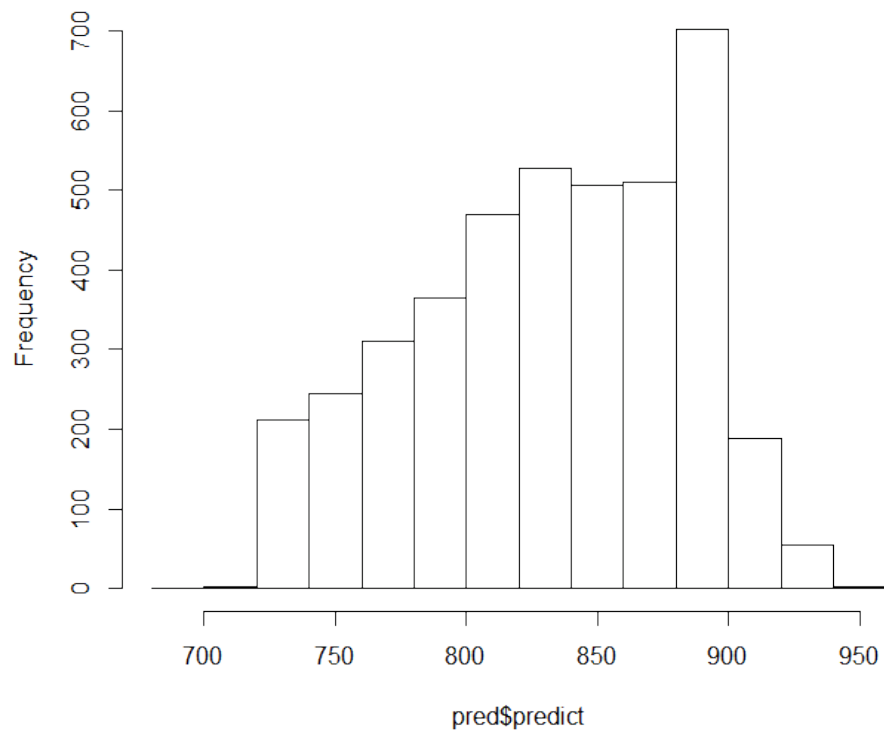
**Topo-elevation - Standard Error**



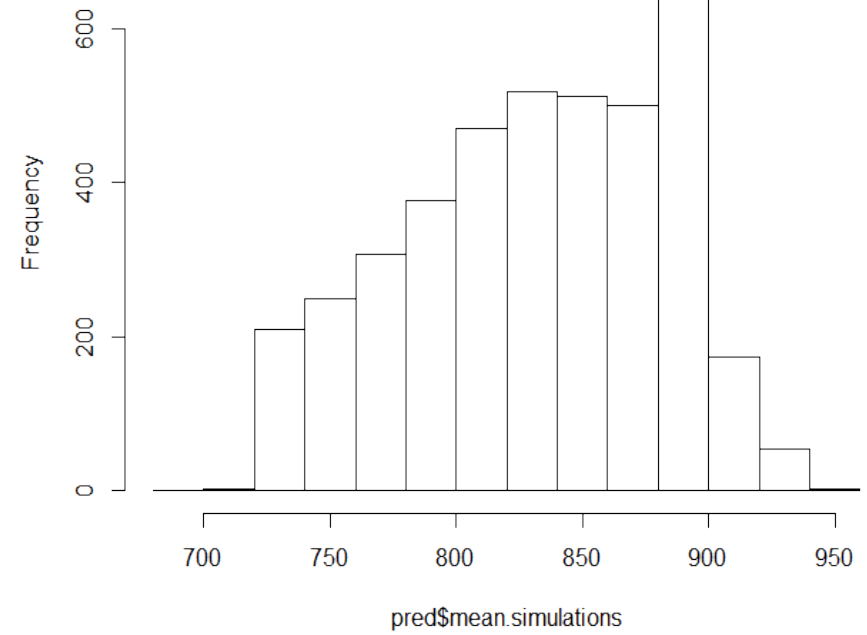
**Topo-elevation - Simulated Standard Error**



**Histogram of pred\$predict**



**Histogram of pred\$mean.simulations**



# Model Verification

---

- Regression diagnostics
- Cross Validation
- AIC



# AIC

---

**Akaike (1973, 1974) introduced a criterion for model adequacy, first for time-series models and then more generally. He relates how his secretary suggested he call it 'An Information Criterion',**

**AIC.**

# AIC

---

**AIC has a very appealing simplicity:**

$$AIC = -2 \log(\text{maximized likelihood}) + 2p$$

**where  $p$  is the number of estimated parameters.**

**Choose the model with the smallest AIC (and perhaps retain all models within 2 of the minimum).**

# Cross-validation

---

## Leave-one-out CV

**The idea is that given a dataset of  $N$  points, we use our model-building procedure on each subset of size  $N-1$ , and predict the point we left out. Then the set of predictions can be summarized by some measure of prediction accuracy. Idea goes back at least as far as Mosteller & Wallace (1963).**

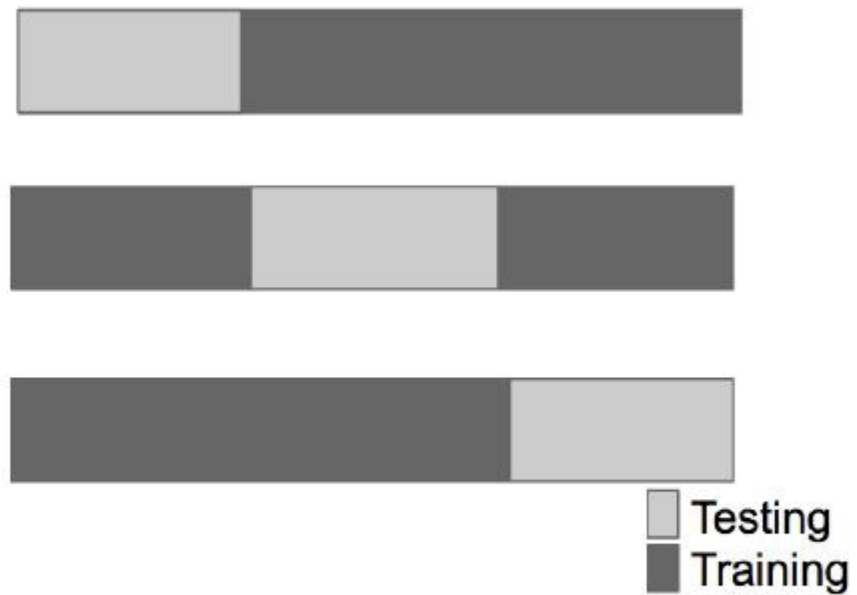
# Leave one out



## V-fold cross-validation

- **Divide the data into  $V$  sets, and amalgamate  $V - 1$  of them, build a model and predict the result for the remaining set. Do this  $V$  times leaving a different set out each time.**
- **How big should  $V$  be? We want the model-building problem to be realistic, so want to leave out a small proportion. We don't want too much work. So usually  $V$  is 3–10.**

# K-fold



<file:///Users/jtleek/Dropbox/Public/courseraPublic/week6/002crossValidation/index.html#1>

## Cross validation statistics

Ideally

- the correlation between  $Z(s_i)$  and  $\hat{Z}_{[i]}(s_i)$  should be close to 1
- the variability of  $\hat{Z}_{[i]}(s_i)$  should be close to that of  $Z(s_i)$  (but will always be smaller: the *smoothing effect*)
- residuals should have zero mean, and small variance (small range, etc.)
- z-scores should contain no outliers (values outside, say  $[-3, 3]$ )
- z-scores should have unit standard deviation (only this “validates” the prediction error standard deviation).

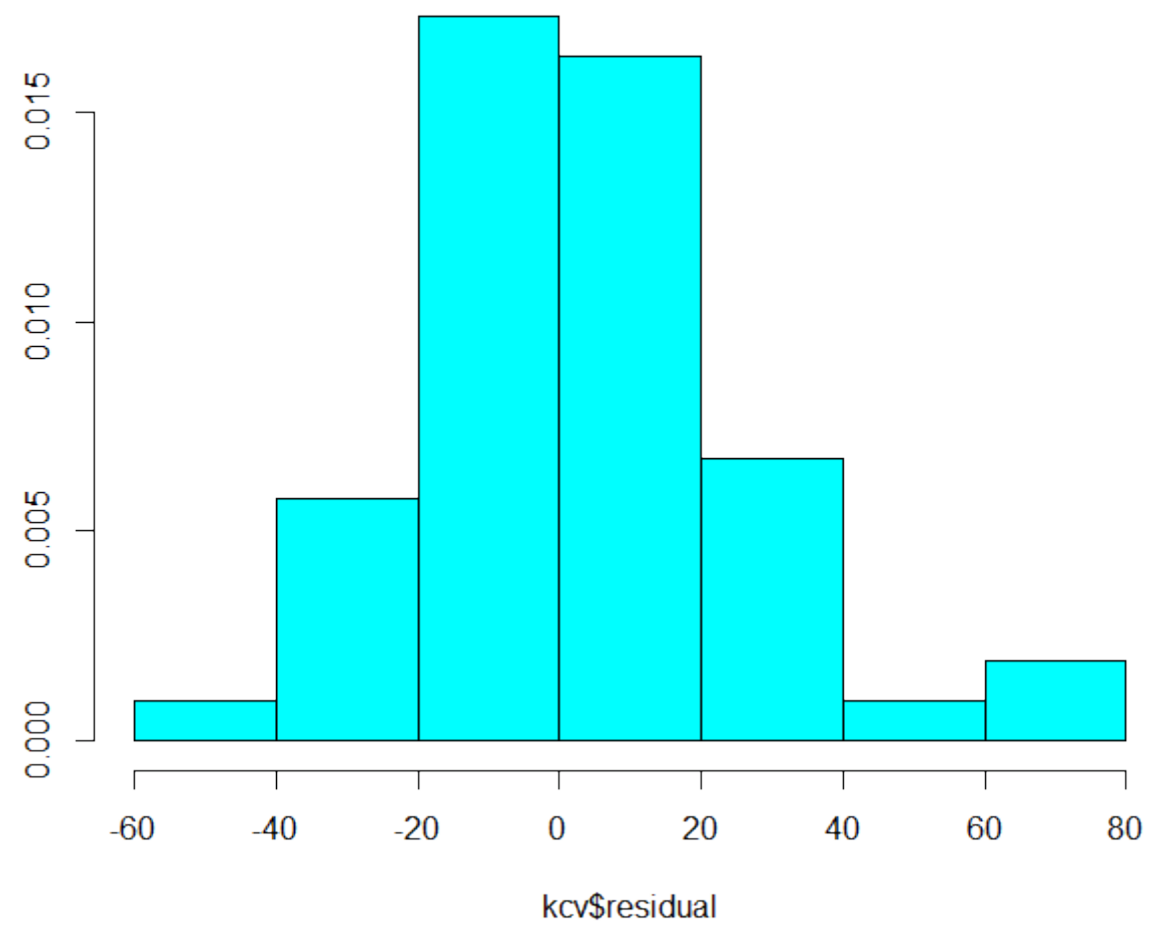
(from Edzer Pebesma)

- calculate the residual  $Z(s_i) - \hat{Z}_{[i]}(s_i)$  and the normalized residuals, or z-score,

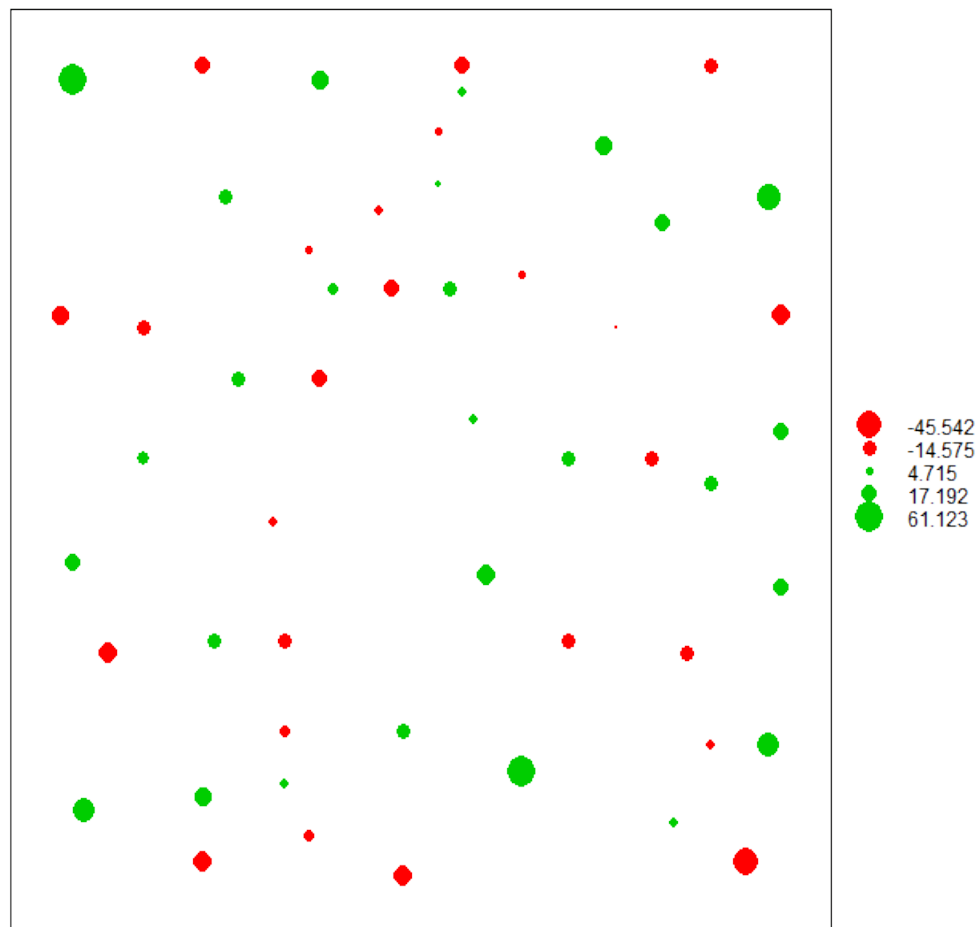
$$\frac{Z(s_i) - \hat{Z}_{[i]}(s_i)}{\sigma(s_i)}$$



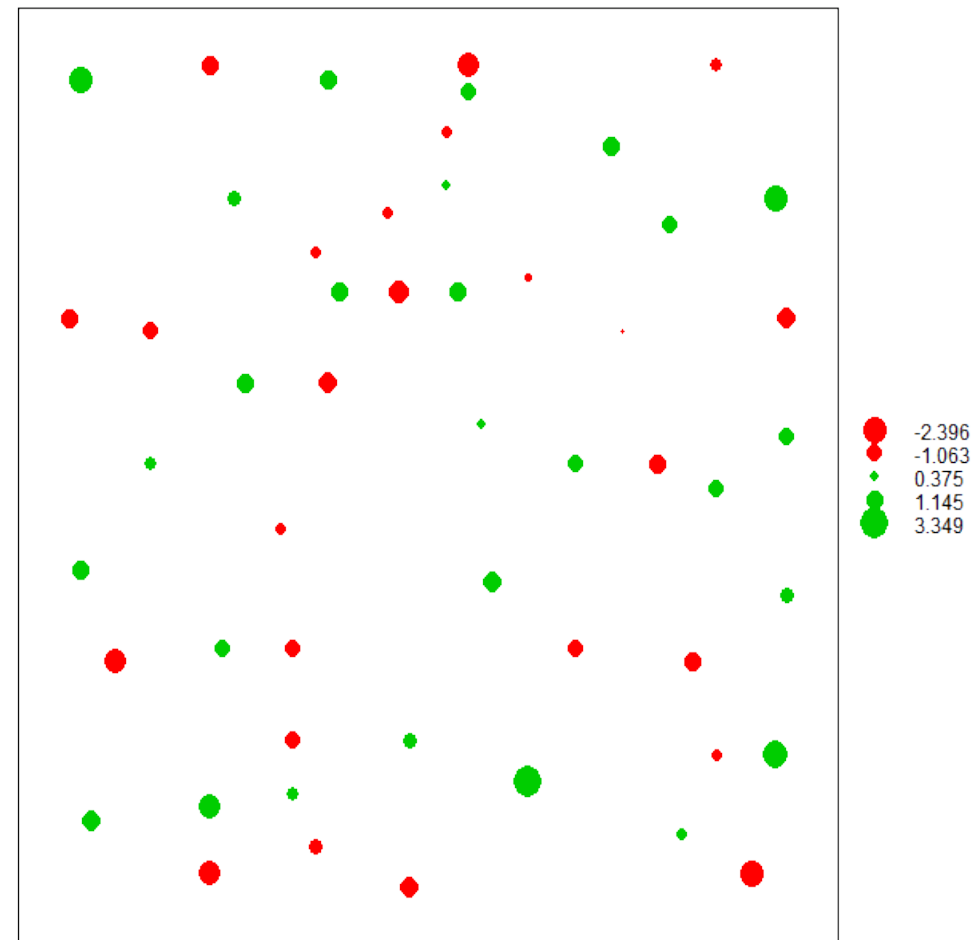
**Topo residuals for standard cv run**



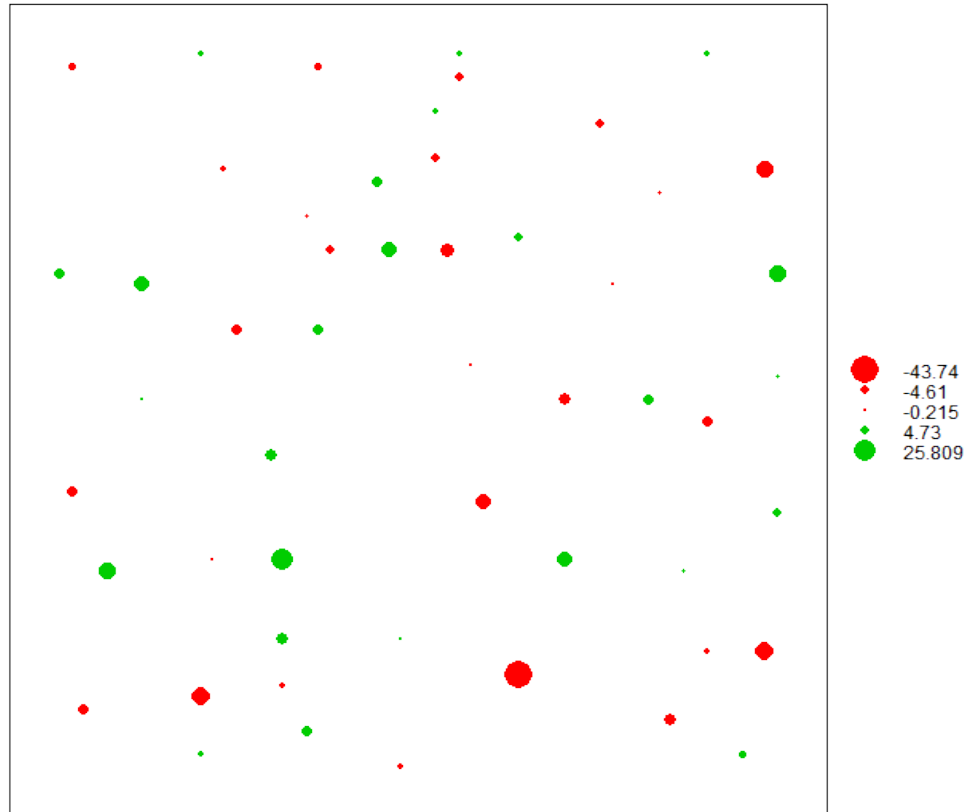
cv.residuals-krig topo



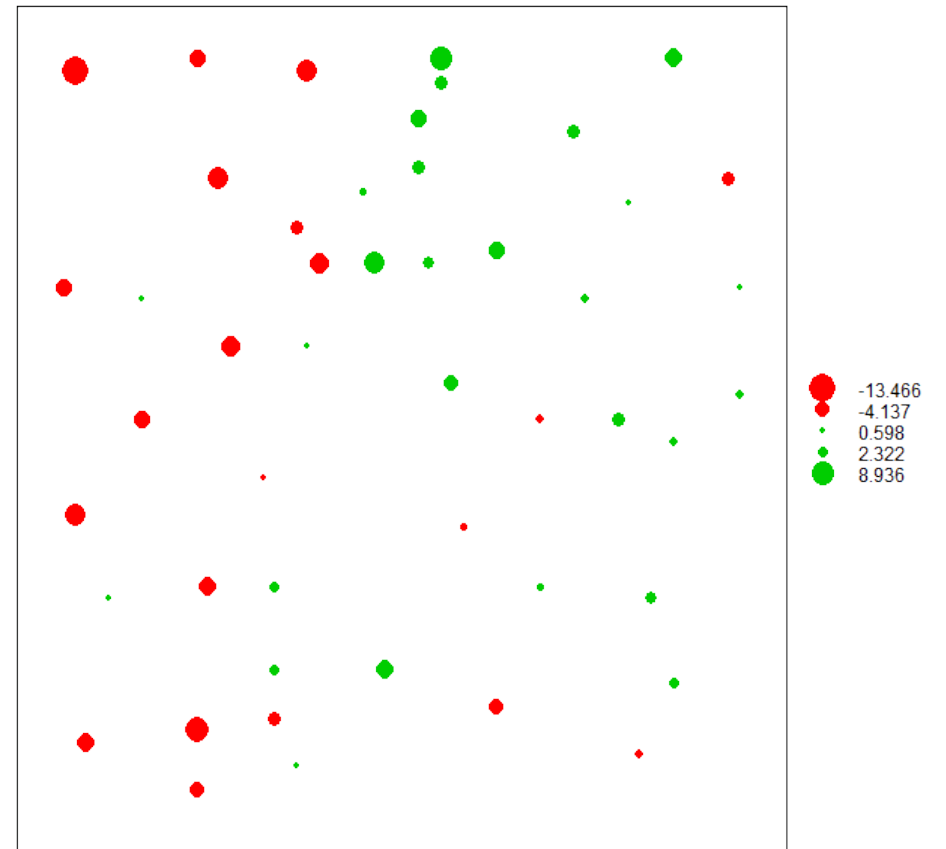
cv.zscores-krig topo



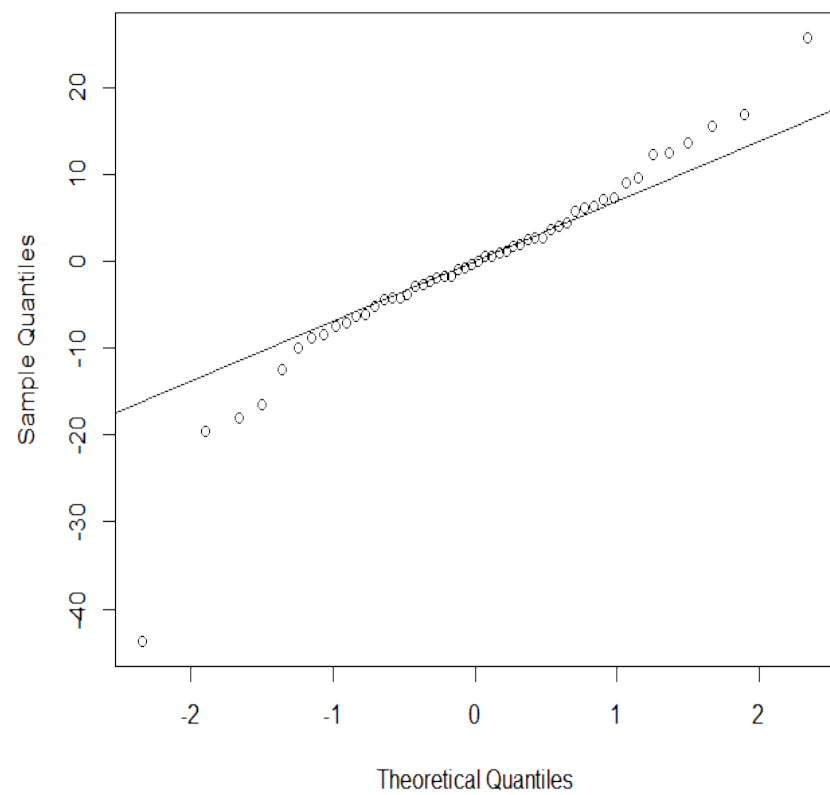
cv.residuals-loess topo



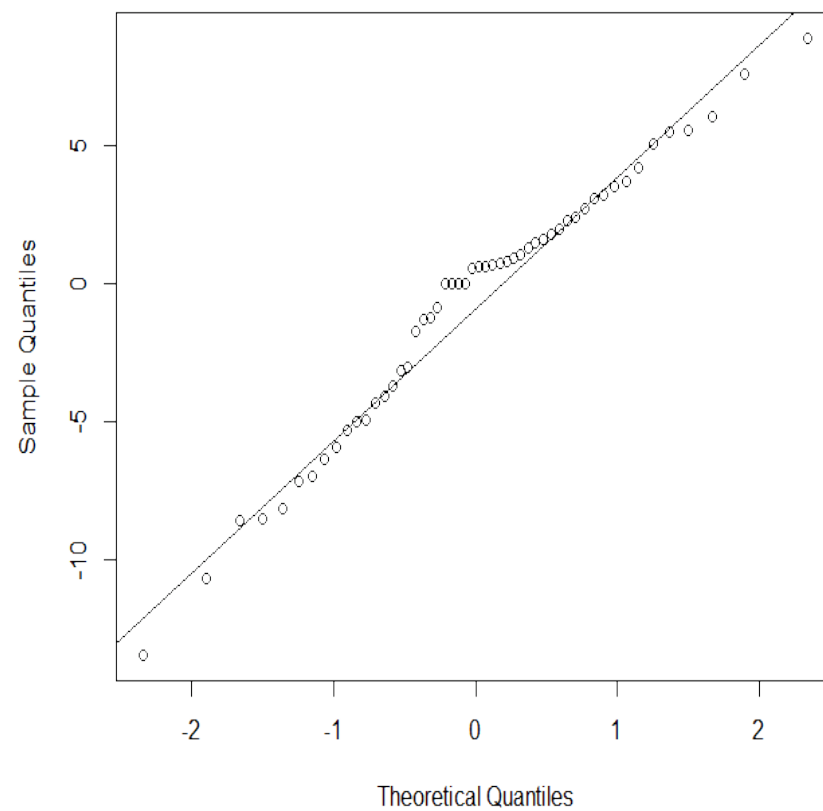
cv.residuals-tps topo



**Residuals - Loess Topo**



**Residuals - Tps Topo**



# Cross Validation Statistics for TOPO

# mean error, ideally 0:

```
> (mpe <- mean(kcv$residual))
```

```
[1] 3.214332
```

```
> mpe/mean(topo$z) #standardize to the data mean
```

```
[1] 0.003886376
```

> # MSPE, ideally small

```
> mean(kcv$residual^2)
```

```
[1] 507.5754
```

> # Mean square normalized error, ideally close to 1

```
> mean(kcv$zscore^2)
```

```
[1] 1.876445
```

> #RMSE

```
> (rmse <- sqrt(mean(kcv$residual^2)))
```

```
[1] 22.52944
```

```
> rmse/sd(topo$z)
```

```
[1] 0.3633912
```

```
> rmse/IQR(topo$z)
```

```
[1] 0.2635022
```

> # amount of variation ( $R^2$ ) explained by the models:

```
> 1-var(kcv$residual, na.rm=T)/var(topo$z)
```

```
[1] 0.8680982
```

> # correlation predicted and residual, ideally 0

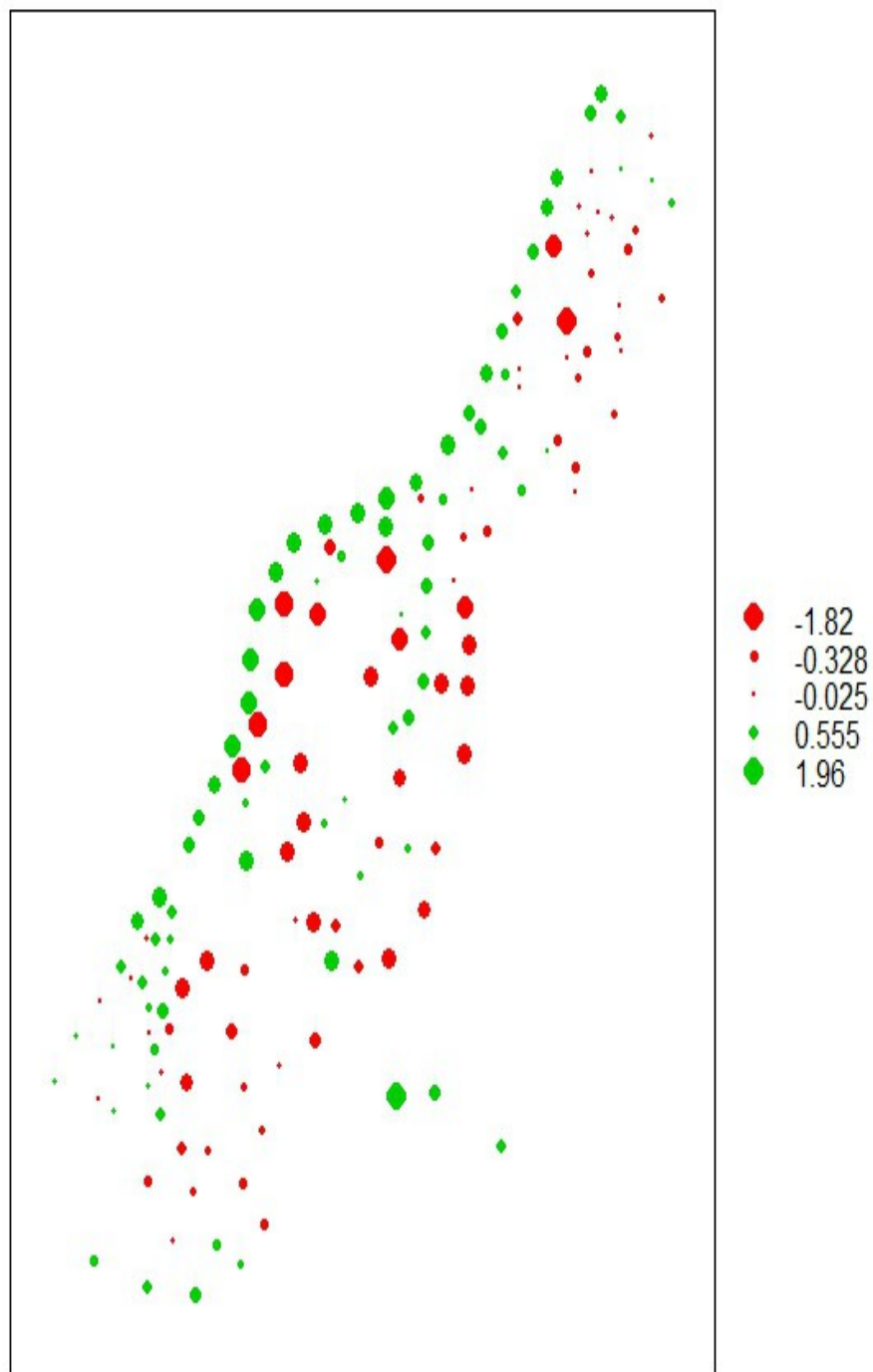
```
> cor(kcv$observed - kcv$residual, kcv$residual)
```

```
[1] -0.06767013
```

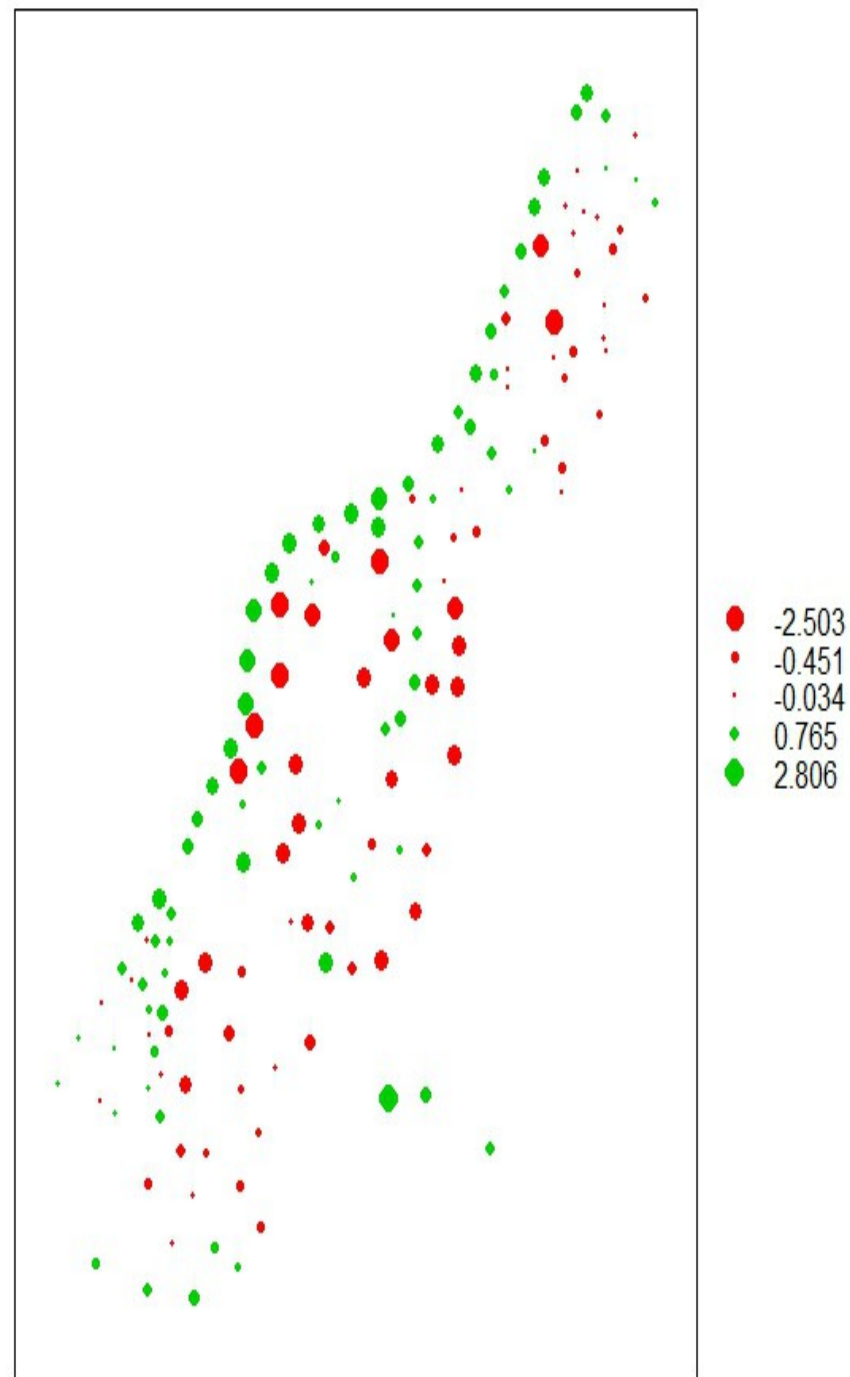
# Comparison of TOPO model statistics

	<u>loess</u>	<u>Tps</u>	<u>UK.cv</u> <u>nfold=10</u>
<b>ME</b>	<b>-0.48</b>	<b>-0.69</b>	<b>1.16</b>
<b>RMSE</b>	<b>10.52</b>	<b>4.80</b>	<b>22.0</b>
<b>RMSE/sd</b>	<b>0.17</b>	<b>0.08</b>	<b>0.87</b>
<b>R<sup>2</sup></b>	<b>0.97</b>	<b>0.99</b>	<b>0.87</b>

log(cadmium): 5-fold Residuals Cross Validation-Z-Scores



log(cadmium): 5-fold Residuals Cross Validation-Residuals



### ### 5-fold Cross Validation

#####

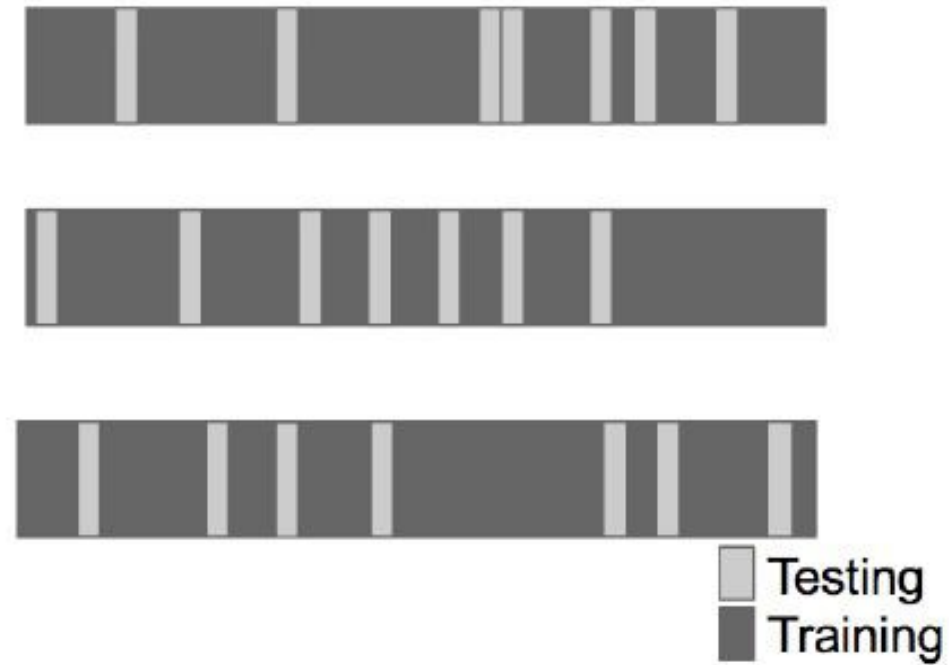
```
v.fit <- vgm(.5, "Exp", 790, 1.7)
coordinates(meuse) <- ~x+y
cv155 <- krige.cv(log(cadmium)~1, meuse, v.fit,
  nfold=5)
```

#####

```
bubble(cv155, "residual", main = "log(cadmium): 5-fold
  Residuals Cross Validation-Residuals",maxsize = 1.5)
bubble(cv155, "zscore", main = "log(cadmium): 5-fold
  Residuals Cross Validation-Z-Scores",maxsize = 1.5)
```



# Random subsampling

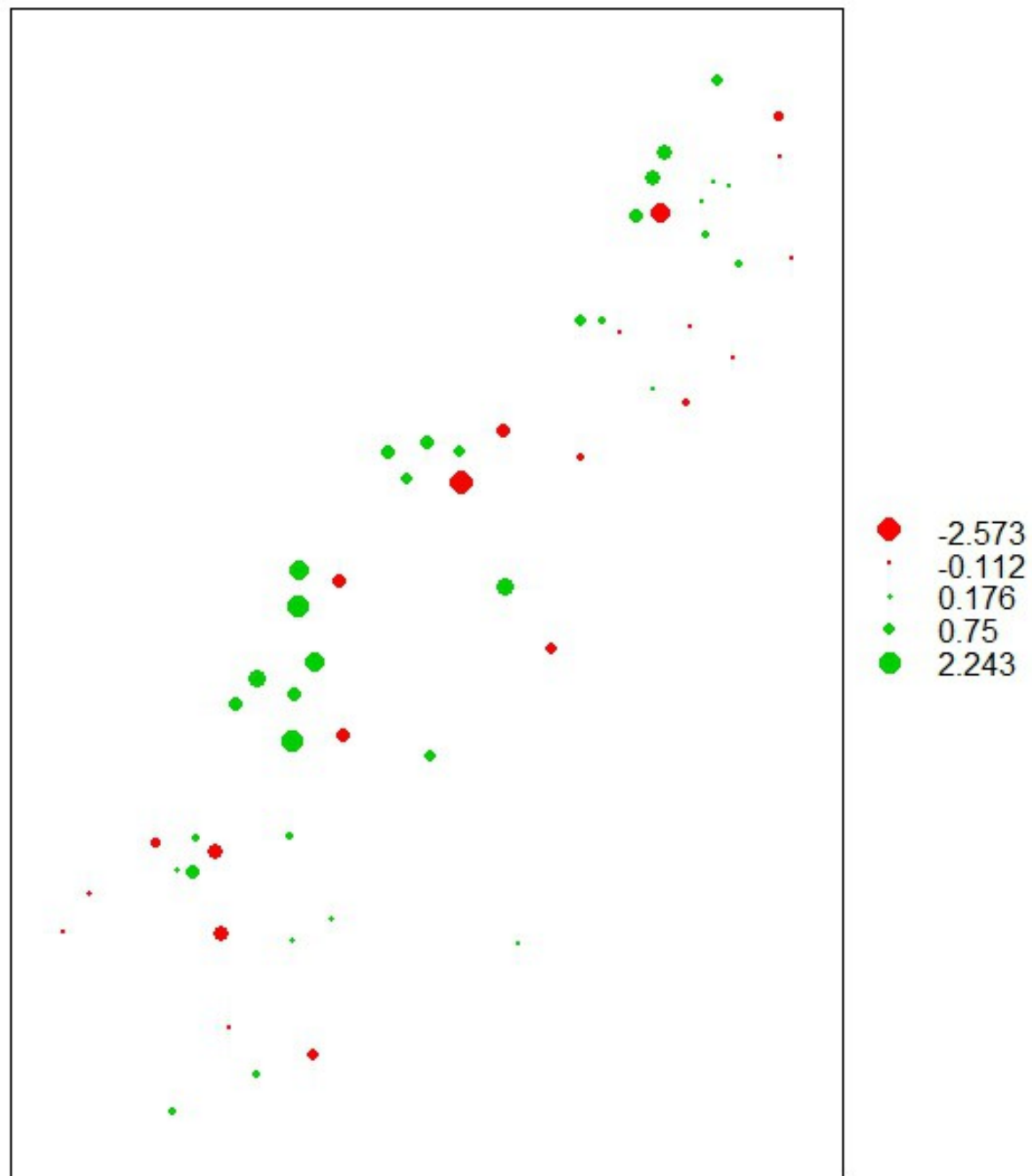


## # Validating Kriging Model by subsampling

```
set.seed(1357531)
#####
sel100 <- sample(1:155, 100)
m.model <- meuse[sel100,]
m.valid <- meuse[-sel100,]
coordinates(m.model) <- ~ x+y
coordinates(m.valid) <- ~ x+y
v100.fit <- fit.variogram(variogram(log(cadmium)~1,
  m.model), vgm(.5, "Exp", 800, 1.7))
m.valid.pr <- krige(log(cadmium)~1, m.model, m.valid,
  v100.fit) # predict at #m.valid sites

resid.kr <- log(m.valid$cadmium) - m.valid.pr$var1.pred
# residuals
summary(resid.kr)
resid.mean <- log(m.valid$cadmium) -
mean(log(m.valid$cadmium))
R2 <- 1 - sum(resid.kr^2)/sum(resid.mean^2)
R^2 = 0.34
```

Residuals on 55 sample validation data-Cadmium

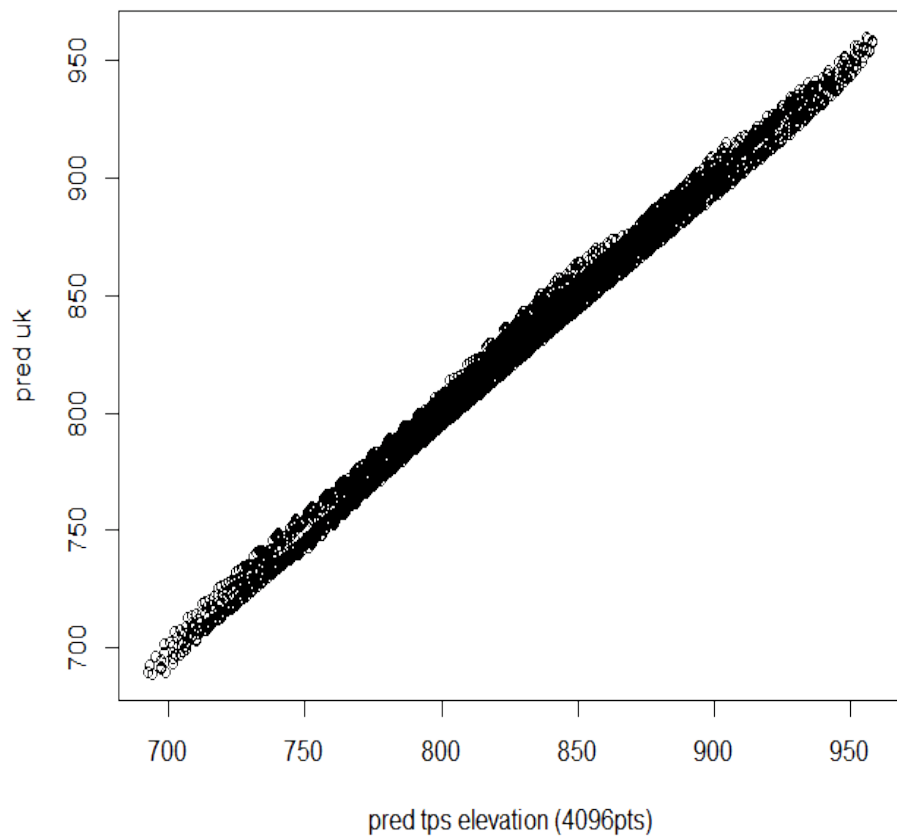


# CROSS VALIDATION

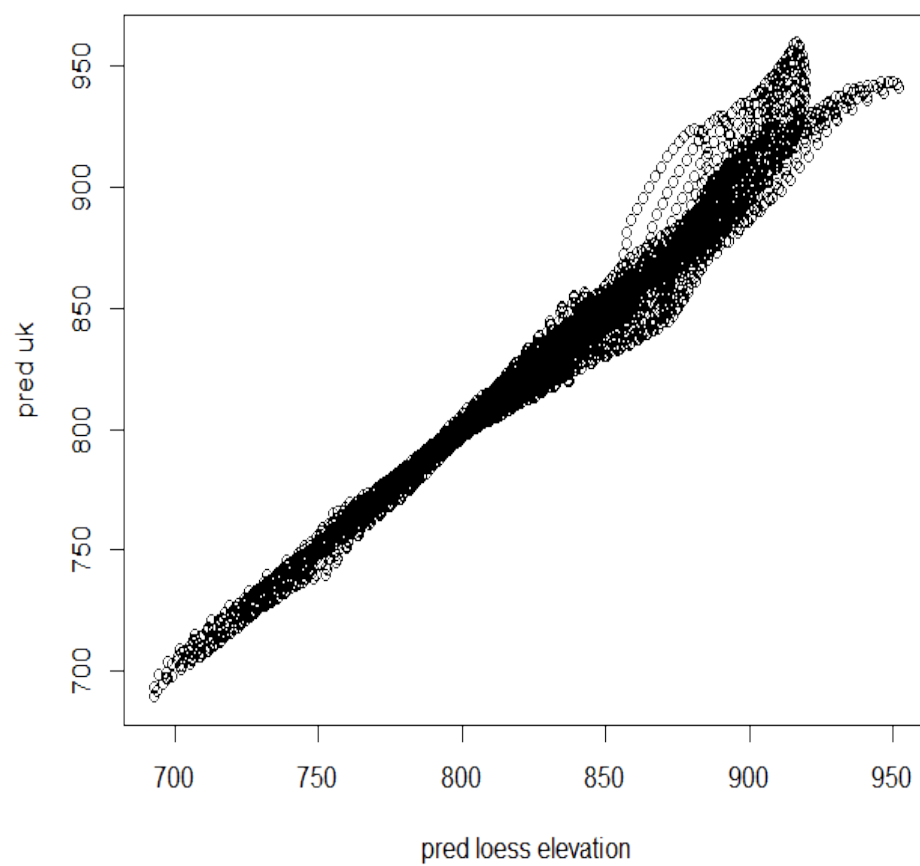
---

- When in prediction mode (i.e., kriging), cross validating the model is **one way** to diagnose problems occurring with the model's fit.
- The **purpose** of checking the modeled variogram with cross validation is to **expose** obvious mistakes, and to view where the model has possible trouble predicting.
- It does **not prove** the model is **right**; it only shows where the model **fails**. Likewise, it is not recommended to confirm the correctness of different model types, e.g. spherical versus power models.

Model prediction tps vs UKrig Topo



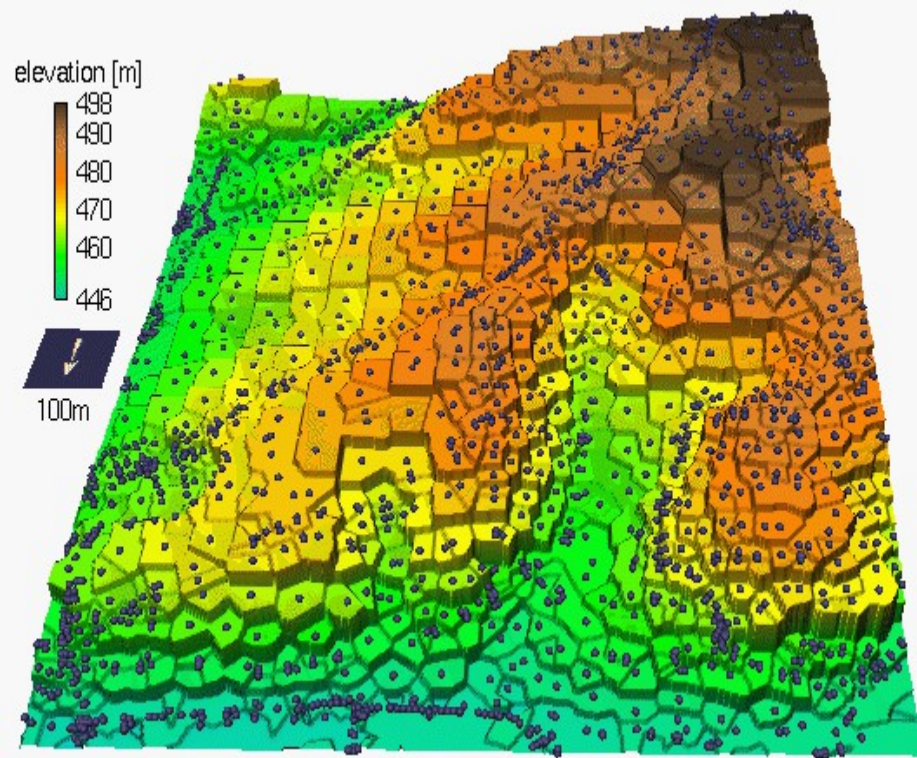
Model prediction loess vs UKrig Topo



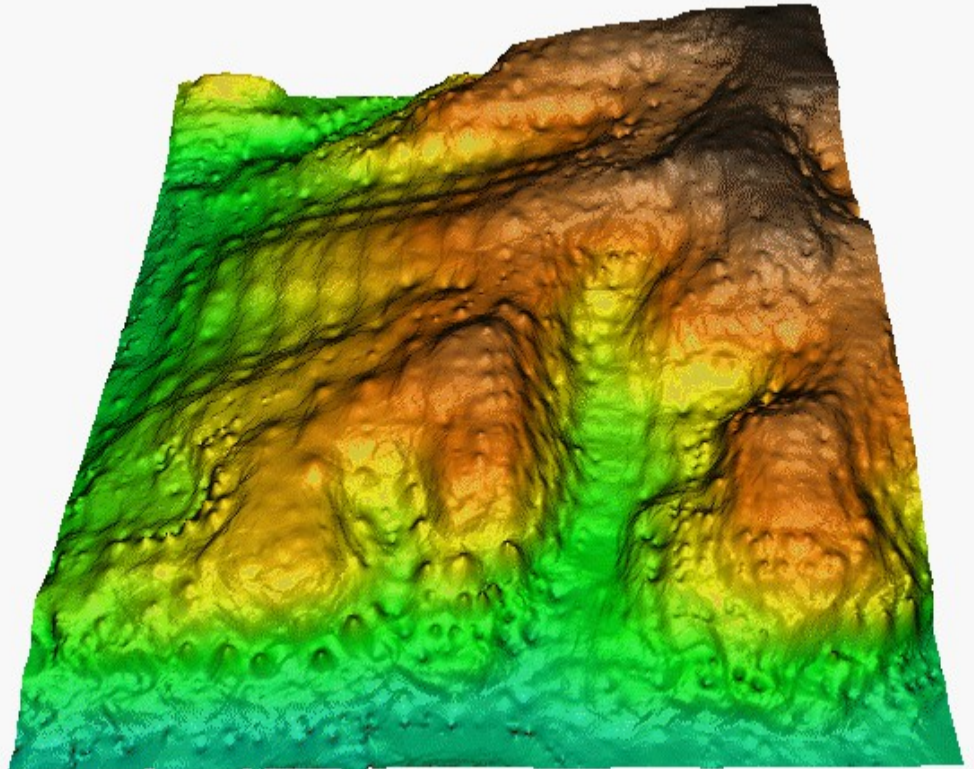
## Which approach is “best”?

- No theoretical answer
- Depends on how well the approach models the ‘**true**’ **spatial structure**, and this is unknown (but we may have prior evidence)
- Should correspond with what we know about the **process** that created the spatial structure

## Voronoi Tessellation



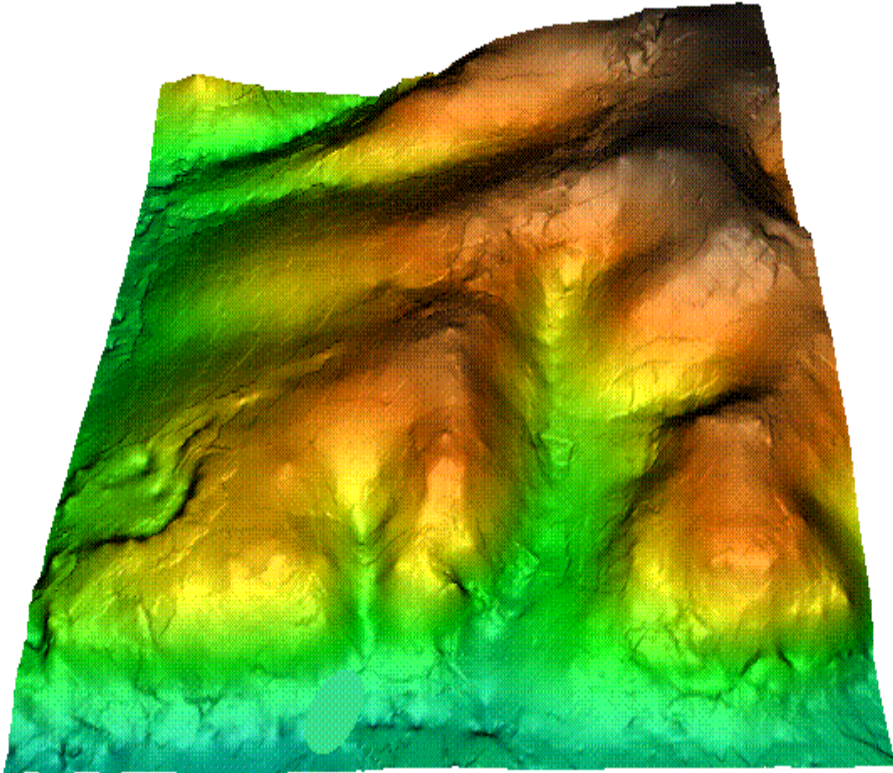
## IDW



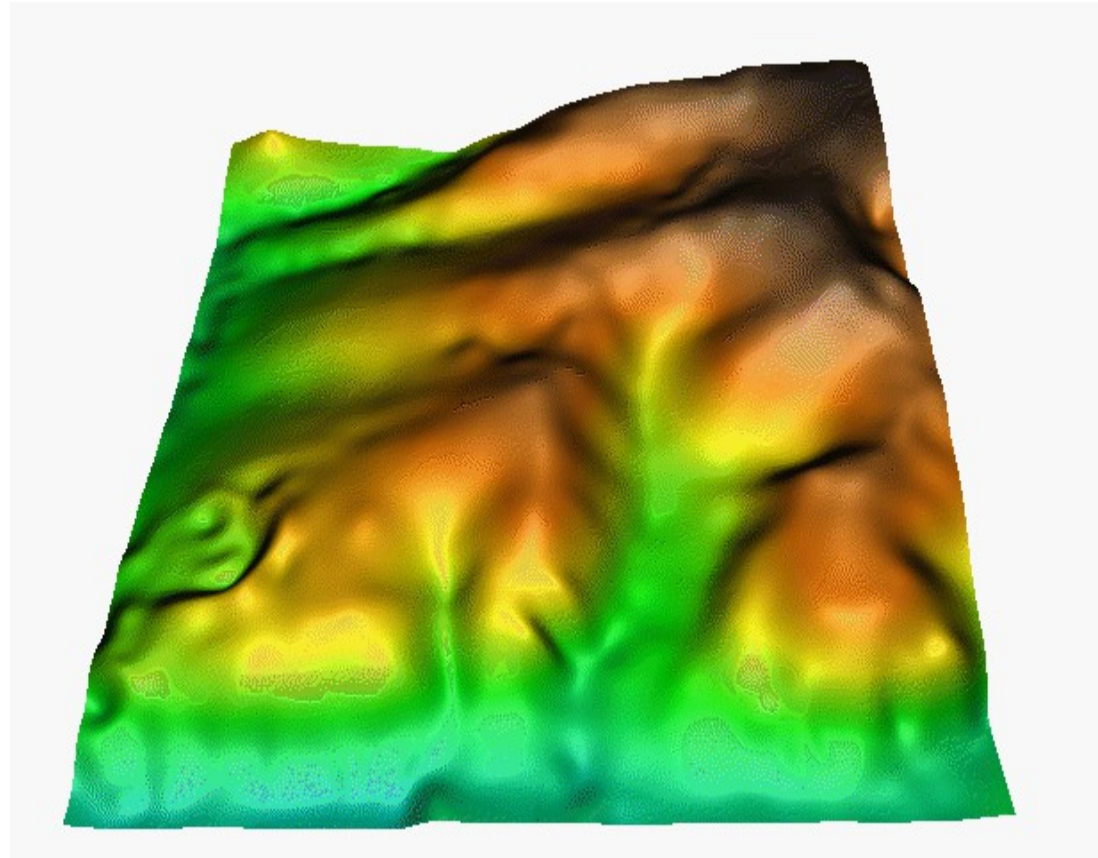
Helena Mitasova: <http://skagit.meas.ncsu.edu/~helena/gmslab/interp/>



Kriging



Thin plate spline



Helena Mitasova: <http://skagit.meas.ncsu.edu/~helena/gmslab/interp/>



## Approaches to prediction: Global (Regional) Predictors

- Value of the variable depends on **relative geographic position** within a spatial field
  - \* Example: thickness of a layer of volcanic ash over a buried soil
  - \* Example: amount of quartz gravels in a soil derived from conglomerate residuum
  - \* Groundwater depth below a reference level
- Since there is only one process (global), **all** sample points are used to compute the prediction
- (Sometimes the sample points are limited to a region, e.g. in moving trend surfaces or splines)

(from David Rossiter)

## Which predictor is “best”? (continued)

- What do we know about the process being modelled?
- Check against an independent **validation** dataset
  - \* **Mean squared error** (“precision”) of **prediction** vs. **actual** (residuals)
  - \* **Bias** (“accuracy”) of predicted vs. actual mean
- With large datasets, model with one part and hold out the rest for validation
- **Cross-validation** for small datasets with a modelled structure

# Choosing a Surface Interpolation Model

---

- **Characteristics of the input sample data**
- **Precision of the sample point measurements**
- **Frequency and distribution of sample points relative to the scale of variation**
- **Surface shape and level of local variability**
- **The context in which the surface model will be used**

## Interpolate a surface.

Different methods provided by R.

- #a) Trend surface fitting polynomial regression surface by least squares (surf.ls, trmat) {spatial package} & (krige) {gstat}
- #b) Trend surface fitting by generalized least squares (surf.gls, trmat) {spatial package} & {gstat}
- #c) Local polynomial regression fitting with error prediction (loess, predict.loess) {stats}
- #d) Bilinear or Bicubic spline interpolation (interp) {akima package}
- #e) Multi-level B splines (mba.surf) {MBA package}
- #f) Thin plate spline (Tps) {fields package}
- #e) Kriging with
  - ##variogram calculation (Variogram) {gstat} & (variog) {geoR}
  - ##kriging calculation (krige) {gstat} ; (krige.conv) {geoR} ; (Krig) {fields package}
  - ##Bayes kriging (krige.bayes) {geoR}
- #f) other packages:
  - ##variogram calculation (Variogram) {nlme package}
  - ##covariance estimation with correlogram (correlogram, variogram) {MASS package}
- #g) and many others:
  - ## {constrainedKriging} {GEOmap} {geospt} {intamap} {LatticeKrig} {ModelMap} {ramps}
  - {RandomFields} {sgeostat} {spatstat} {spBayes} {SpatialExtremes}
- # Automatic interpolation package {automap package}
- # Areal interpolation for GIS data {AIGIS package}

Which method to use, you ask? Why not just explore the **gstat** or **geoR** package or for that matter any of the other packages doing spatial interpolation?

C:\geostat\_quebec\spatInter\_G13\Demoauto.mappackage&spatial interpolation.htm