Interpolation and Autocorrelation

HES 505 Fall 2022: Session 17

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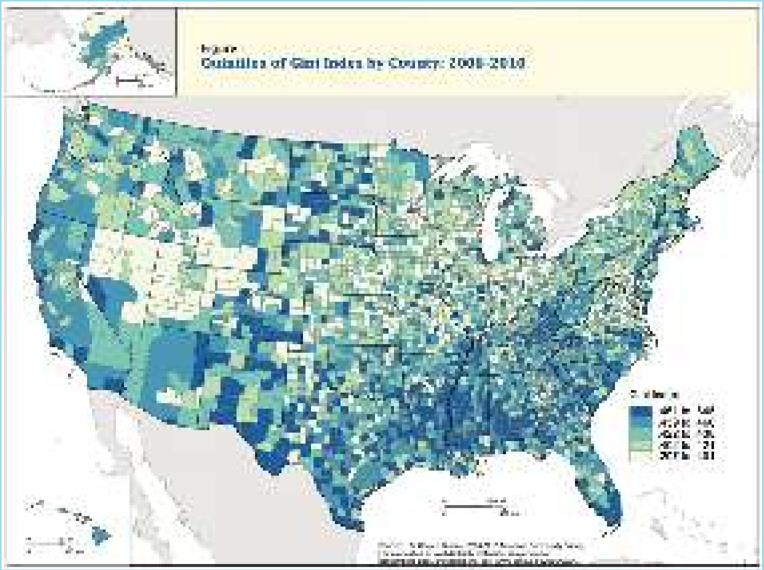
Objectives

By the end of today you should be able to:

- Distinguish deterministic and stochastic processes
- Define autocorrelation and describe its estimation
- Articulate the benefits and drawbacks of autocorrelation
- Leverage point patterns and autocorrelation to interpolate missing data

Description vs. process?

- Vizualization and the detection of patterns
- The challenge of geographic data
- Implications for analysis



Inequality in the United States: Quintiles of Gini Index by County: 2006–2010. The greater the Gini index, the more unequal a county’s income distribution is.

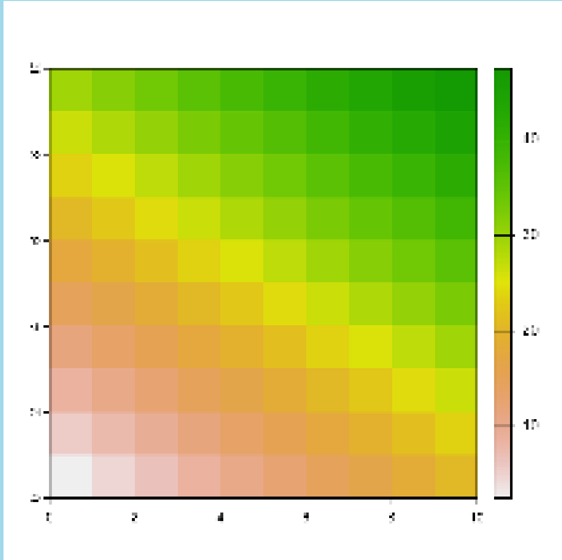
Patterns as realizations of spatial processes

- A **spatial process** is a description of how a spatial pattern might be *generated*
- **Generative models**
- An observed pattern as a *possible realization* of an hypothesized process

Deterministic vs. stochastic processes

- Deterministic processes: always produces the same outcome

$$z = 2x + 3y$$



- Results in a spatially continuous field

```r
x <- rast(nrows = 10, ncols=10, xmin = 0, xmax=10,
values(x) <- 1
z <- x
values(z) <- 2 * crds(x)[,1] + 3*crds(x)[,2]
```

Deterministic vs. stochastic processes

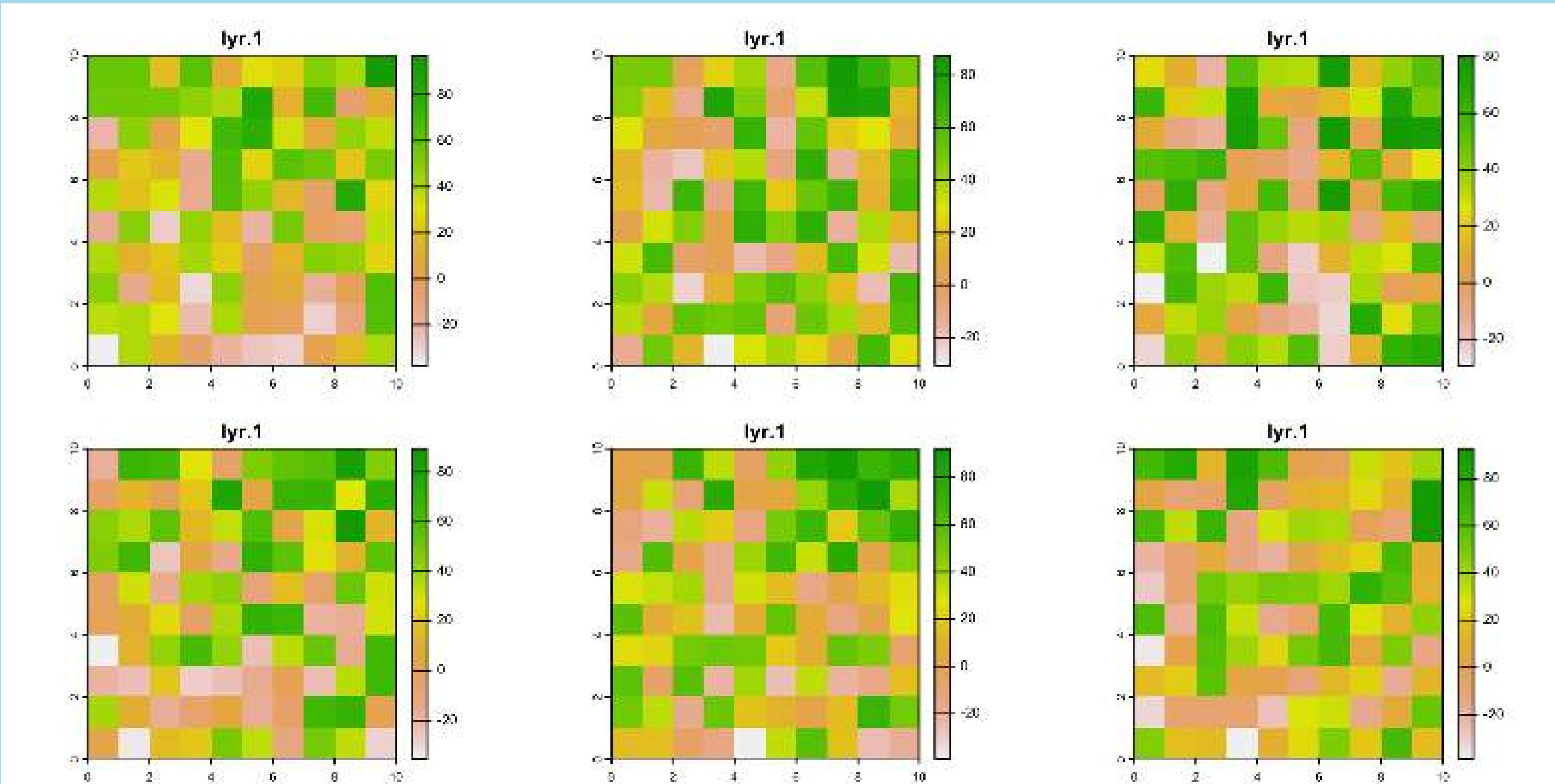
- Stochastic processes: variation makes each realization difficult to predict

$$z = 2x + 3y + d$$

- The *process* is random, not the result (!!)
- Measurement error makes deterministic processes appear stochastic

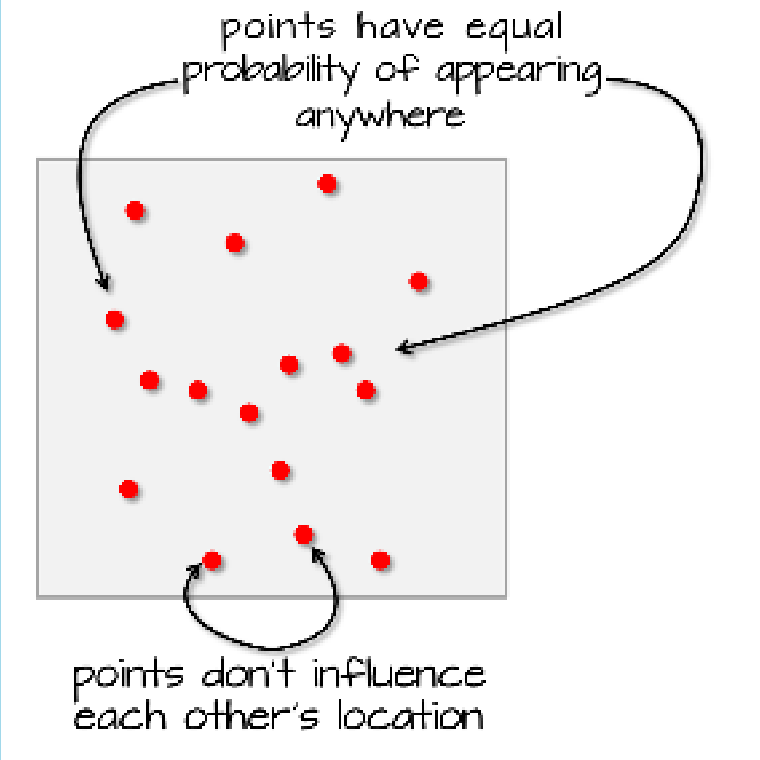
```
x <- rast(nrows = 10, ncols=10, xmin = 0,
values(x) <- 1
fun <- function(z){
a <- z
d <- runif(ncell(z), -50,50)
values(a) <- 2 * crds(x)[,1] + 3*crds(x)[,
return(a)
}

b <- replicate(n=6, fun(z=x), simplify=FAL
d <- do.call(c, b)
```

Deterministic vs. stochastic processes



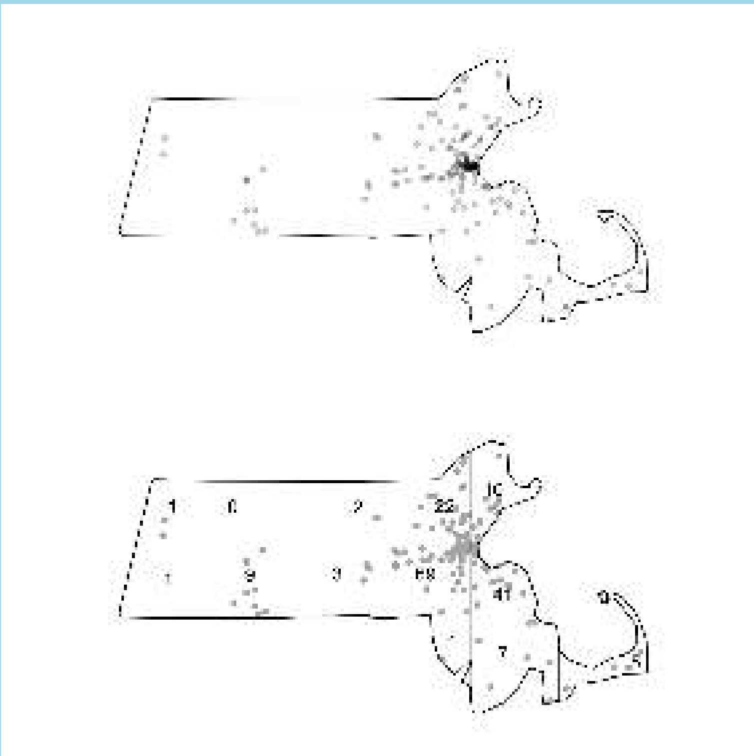
Expected values and hypothesis testing

- Considering each outcome as the realization of a process allows us to generate expected values
- The simplest spatial process is Completely Spatial Random (CSR) process
- **First Order** effects: any event has an equal probability of occurring in a location
- **Second Order** effects: the location of one event is independent of the other events



From Manuel Gimond

Generating expectations for CSR



- We can use quadrat counts to estimate the expected number of events in a given area
- The probability of each possible count is given by:

$$P(n, k) = \binom{n}{x} p^k (1 - p)^{n-k}$$

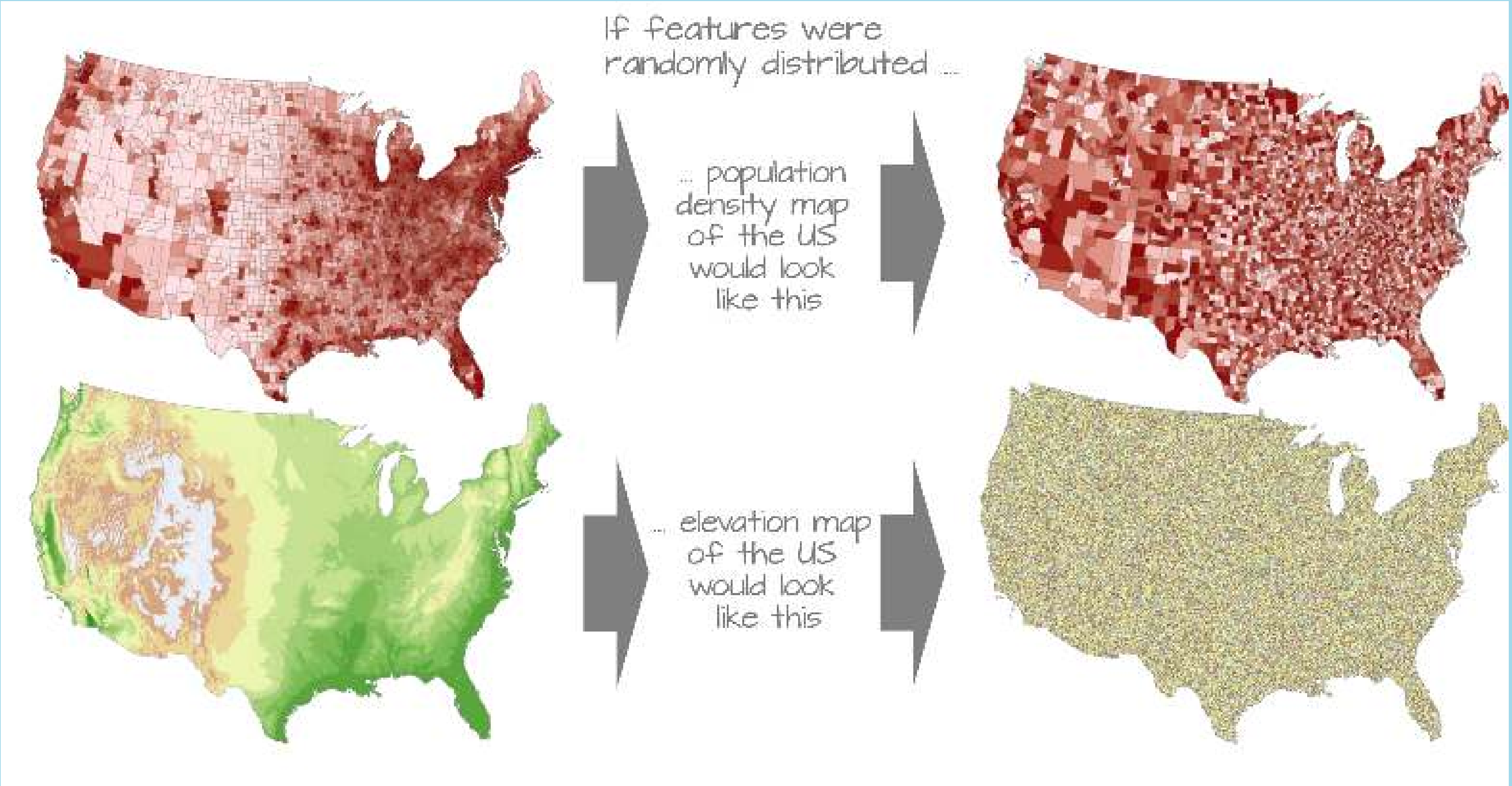
- Given total coverage of quadrats, then $p = \frac{\frac{a}{x}}{a}$ and

$$P(k, n, x) = \binom{n}{k} \left(\frac{1}{x}\right)^k \left(\frac{x-1}{x}\right)^{n-k}$$

Tobler's Law

> ‘everything is usually related to all else but those which are near to each other are more related when compared to those that are further away’.
> Waldo Tobler

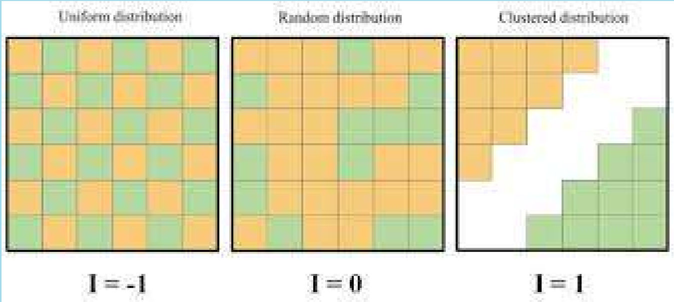
Spatial autocorrelation



From Manuel Gimond

(One) Measure of autocorrelation

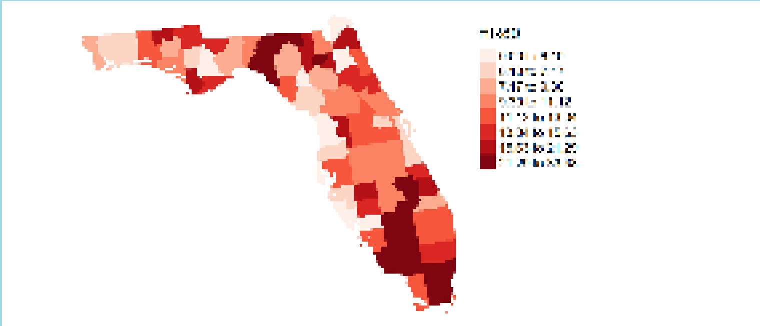
- Moran's I



$$I(d) = \frac{\sum_{i}^{n} \sum_{j \neq i}^{n} w_{ij} (x_i - \bar{x})(x_j - \bar{x})}{S^2 \sum_{i}^{n} \sum_{j \neq i}^{n} w_{ij}}$$

Moran’s I: An example

- Use spdep package
- Estimate neighbors
- Generate weighted average



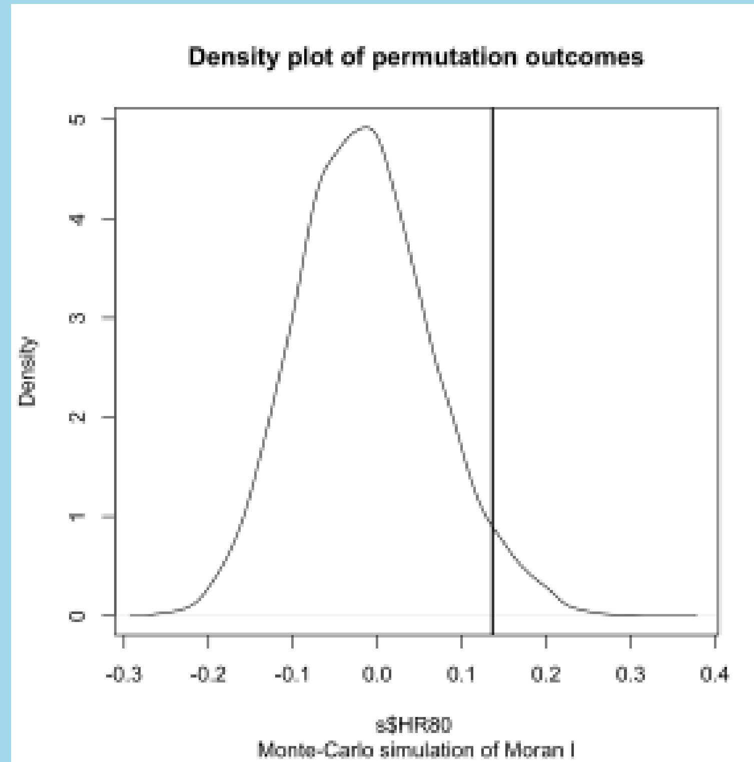
```r
set.seed(2354)
# Load the shapefile
s <- readRDS(url("https://github.com/mgimond/Data/raw/gh-pages
# Define the neighbors (use queen case)
nb <- poly2nb(s, queen=TRUE)
# Compute the neighboring average homicide rates
lw <- nb2listw(nb, style="W", zero.policy=TRUE)
#estimate Moran's I
moran.test(s$HR80,lw, alternative="greater")
```

```
    Moran I test under randomisation

data:  s$HR80
weights: lw

Moran I statistic standard deviate = 1.8891, p-value = 0.02944
alternative hypothesis: greater
sample estimates:
Moran I statistic       Expectation          Variance
      0.136277593      -0.015151515       0.006425761
```

Moran’s I: An example

```r
M1 <- moran.mc(s$HR80, lw, nsim=9999, alte



# Display the resulting statistics
M1
```

```
    Monte-Carlo simulation of Moran I

data:  s$HR80
weights: lw
number of simulations + 1: 10000

statistic = 0.13628, observed rank = 9575, p-
value = 0.0425
alternative hypothesis: greater
```



The challenge of areal data

- Spatial autocorrelation threatens *second order* randomness
- Areal data means an infinite number of potential distances
- Neighbor matrices, $\boldsymbol{W}$, allow different characterizations

Interpolation

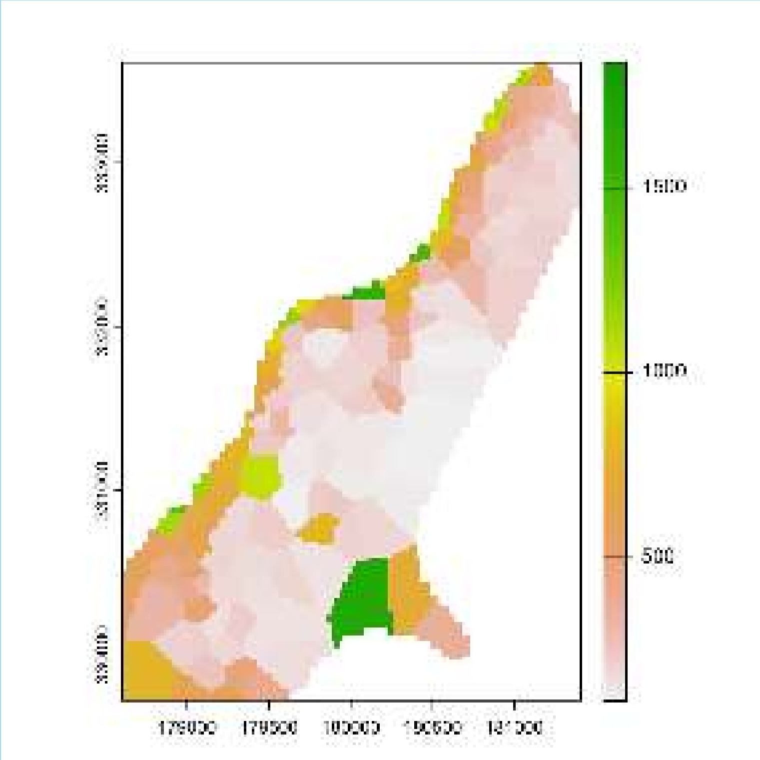
Interpolation

- Goal: estimate the value of z at new points in $\mathbf{x_i}$
- Most useful for continuous values
- Nearest-neighbor, Inverse Distance Weighting, Kriging

Nearest neighbor

- find i such that $|\mathbf{x}_i - \mathbf{x}|$ is minimized
- The estimate of z is z_i

```r
data(meuse)
r <- rast(system.file("ex/meuse.tif", package="terra"))
sfmeuse <- st_as_sf(meuse, coords = c("x", "y"), crs=crs(r))
nodes <- st_make_grid(sfmeuse,
                      cellsize = 25,
                      what = "centers")

dist <- distance(vect(nodes), vect(sfmeuse))
nearest <- apply(dist, 1, function(x) which(x == min(x)))
zinc_nn <- sfmeuse$zinc[nearest]
preds <- st_as_sf(nodes)
preds$zn <- zinc_nn
preds <- as(preds, "Spatial")
gridded(preds) <- TRUE
preds.rast <- rast(preds)
r.resamp <- resample(r, preds.rast)
preds.rast <- mask(preds.rast, r.resamp)
```



Inverse-Distance Weighting

- Weight closer observations more heavily

$$\hat{z}(\mathbf{x}) = \frac{\sum_{i=1} w_i z_i}{\sum_{i=1} w_i}$$

where

$$w_i = |\mathbf{x} - \mathbf{x}_i|^{-\alpha}$$

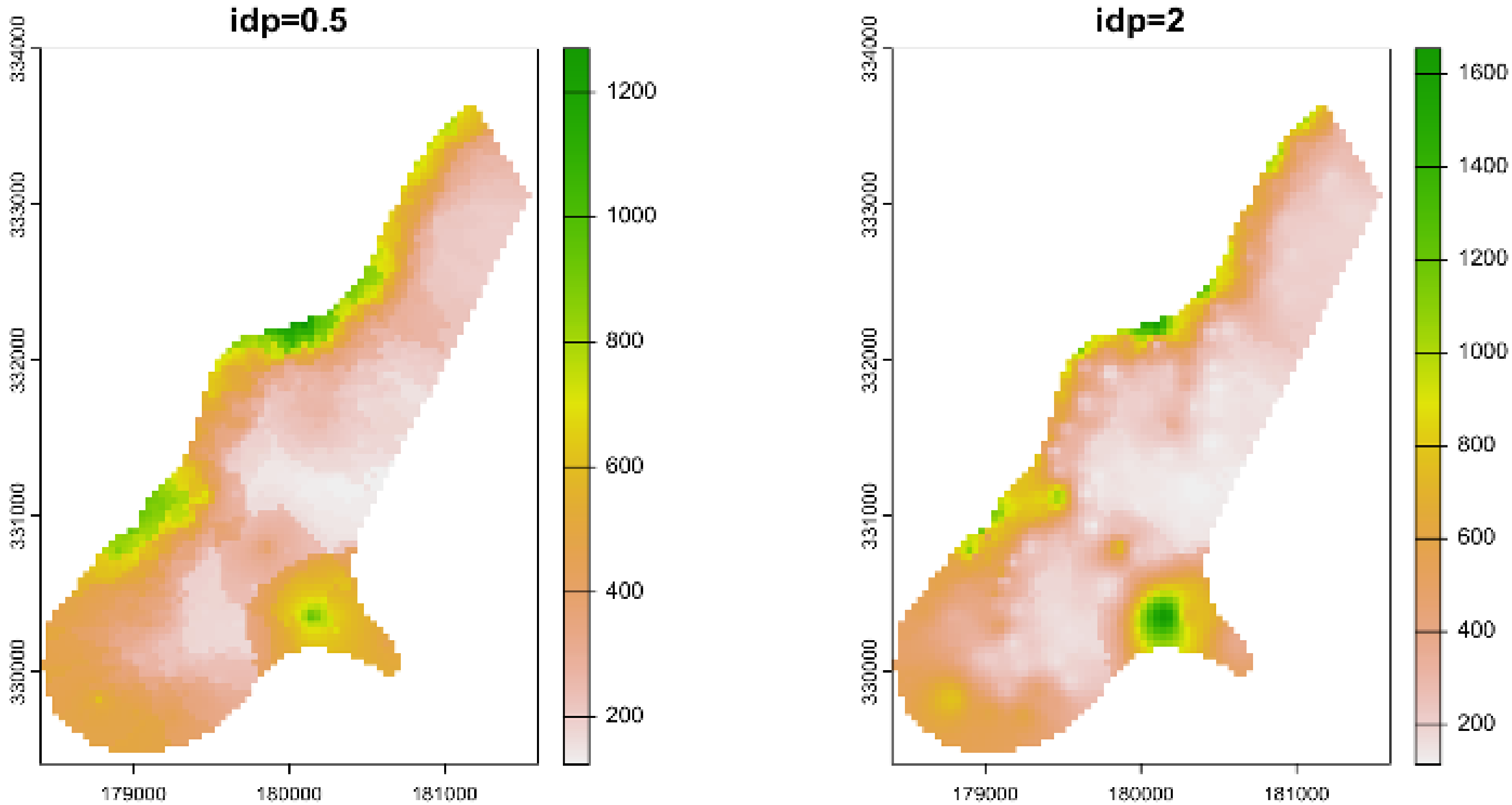
and $\alpha > 0$ ($\alpha = 1$ is inverse; $\alpha = 2$ is inverse square)

Inverse-Distance Weighting

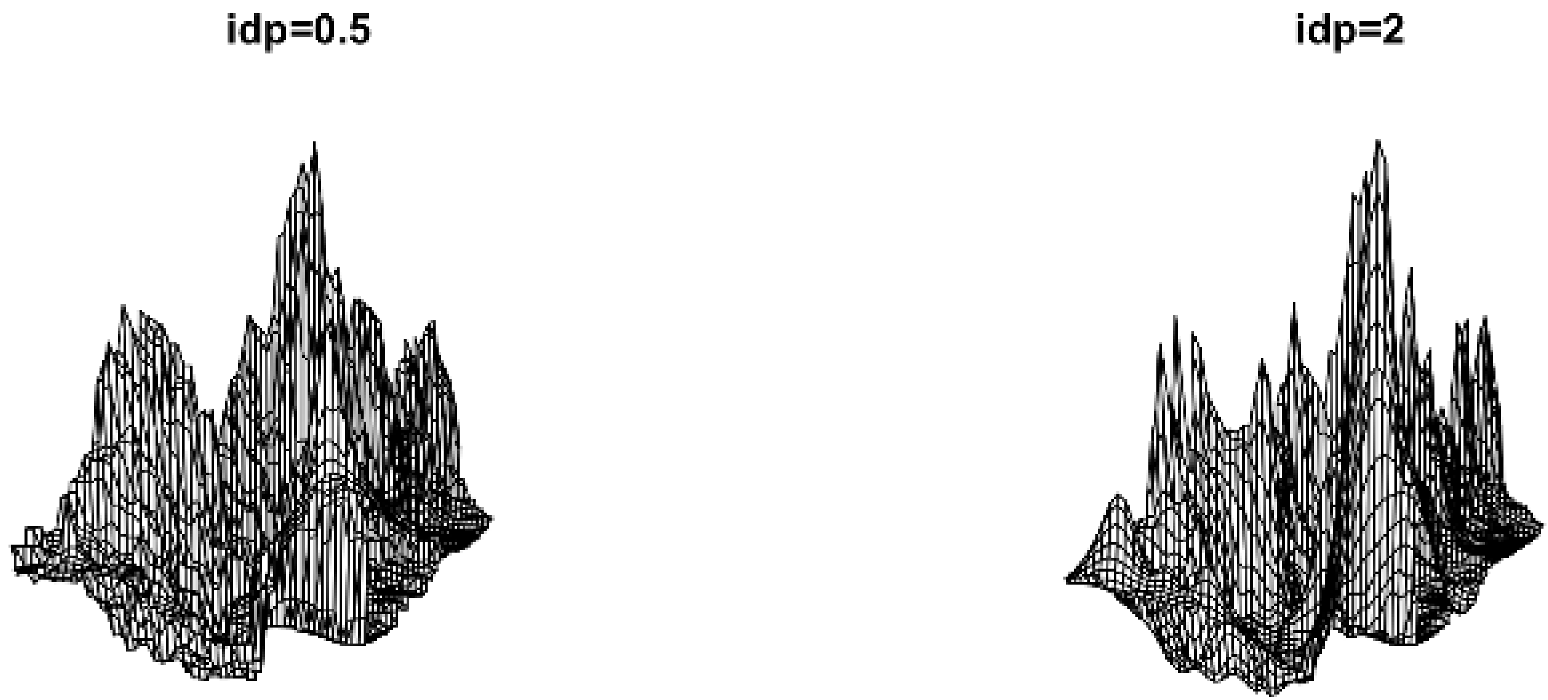
- `terra::interpolate` provides flexible interpolation methods
- Use the `gstat` package to develop the formula

```
mgsf05 <- gstat(id = "zinc", formula = zinc~1, data=sfmeuse,  nmax=7, set=l
mgsf2 <- gstat(id = "zinc", formula = zinc~1, data=sfmeuse,  nmax=7, set=li
interpolate_gstat <- function(model, x, crs, ...) {
    v <- st_as_sf(x, coords=c("x", "y"), crs=crs)
    p <- predict(model, v, ...)
    as.data.frame(p)[,1:2]
}
zsf05 <- interpolate(r, mgsf05, debug.level=0, fun=interpolate_gstat, crs=c
zsf2 <- interpolate(r, mgsf2, debug.level=0, fun=interpolate_gstat, crs=crs
```

Inverse-Distance Weighting



Inverse-Distance Weighting



Kriging

- Previous methods predict z as a (weighted) function of distance
- Treat the observations as perfect (no error)
- If we imagine that z is the outcome of some spatial process such that:

$$z(\mathbf{x}) = \mu(\mathbf{x}) + \epsilon(\mathbf{x})$$

then any observed value of z is some function of the process ($\mu(\mathbf{x})$) and some error ($\epsilon(\mathbf{x})$)

- Kriging exploits autocorrelation in $\epsilon(\mathbf{x})$ to identify the trend and interpolate accordingly

Autocorrelation

- **Correlation** the tendency for two variables to be related
- **Autocorrelation** the tendency for observations that are closer (in space or time) to be correlated
- **Positive autocorrelation** neighboring observations have ϵ with the same sign
- **Negative autocorrelation** neighboring observations have ϵ with a different sign (rare in geography)

Ordinary Kriging

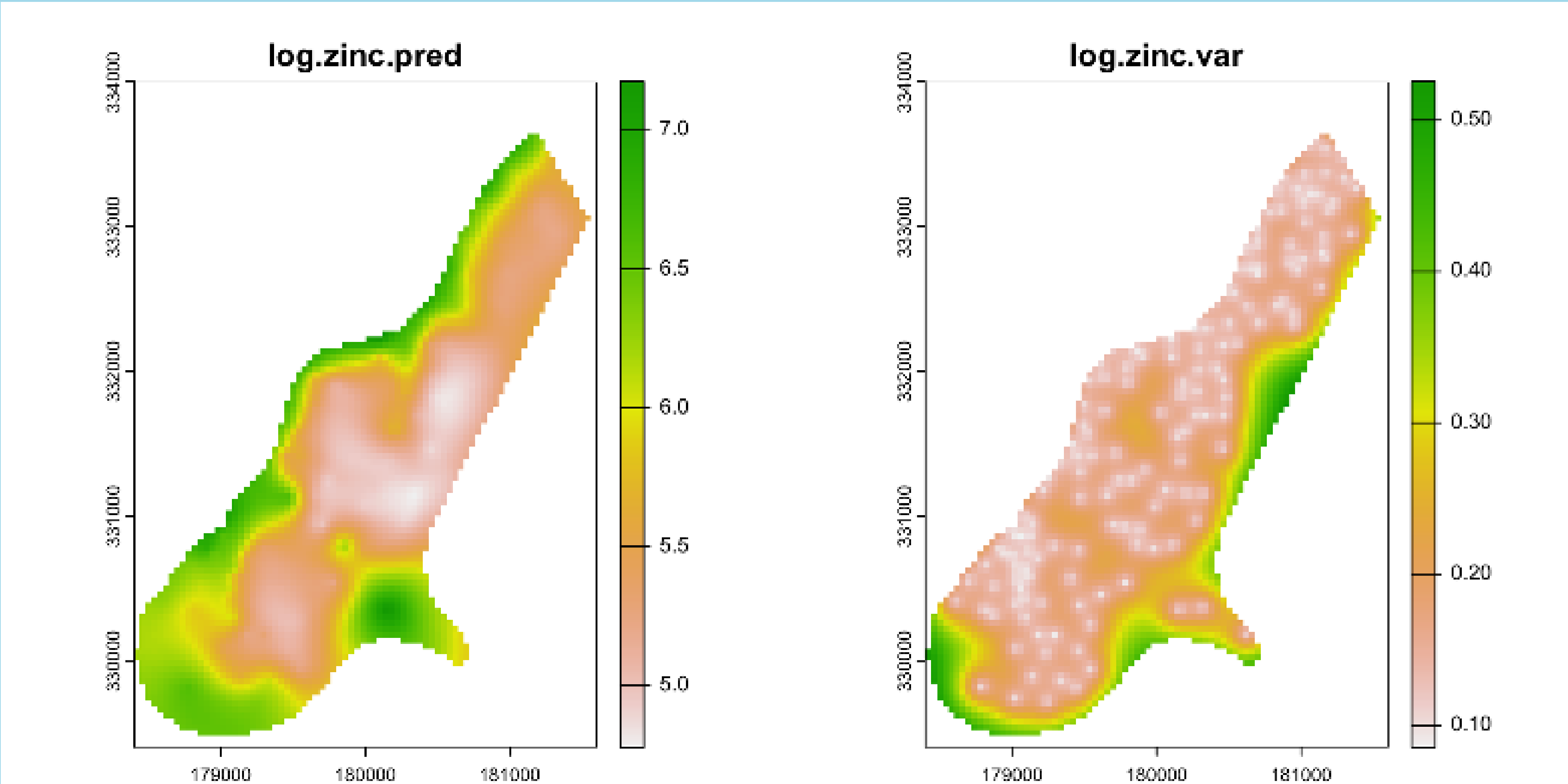
- Assumes that the deterministic part of the process ($\mu(\mathbf{x})$) is an unknown constant (μ)

$$z(\mathbf{x}) = \mu + \epsilon(\mathbf{x})$$

* Specified in call to `variogram` and `gstat` as `y~1` (or some other constant)

```
v <- variogram(log(zinc)~1, ~x+y, data=meuse)
mv <- fit.variogram(v, vgm(1, "Sph", 300, 1))
gOK <- gstat(NULL, "log.zinc", log(zinc)~1, meuse, locations=~x+y, model=mv
OK <- interpolate(r, gOK, debug.level=0)
```

Ordinary Kriging

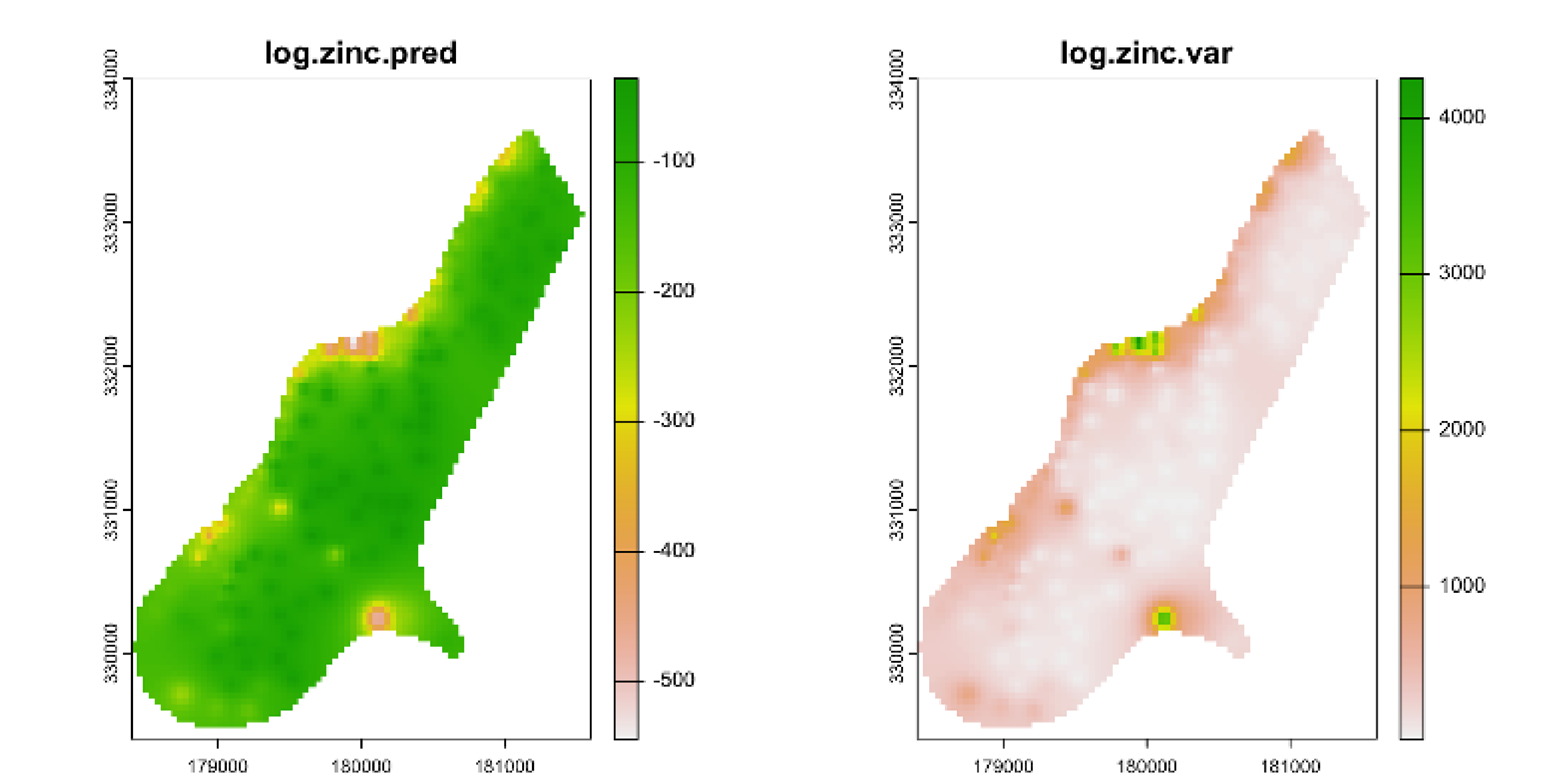


Universal Kriging

- Assumes that the deterministic part of the process ($\mu(\mathbf{x})$) is now a function of the location $\mathbf{x}$
- Could be the location or some other attribute
- Now y is a function of some aspect of x

```
vu <- variogram(log(zinc)~elev, ~x+y, data=meuse)
mu <- fit.variogram(vu, vgm(1, "Sph", 300, 1))
gUK <- gstat(NULL, "log.zinc", log(zinc)~elev, meuse, locations=~x+y, model
names(r) <- "elev"
UK <- interpolate(r, gUK, debug.level=0)
```

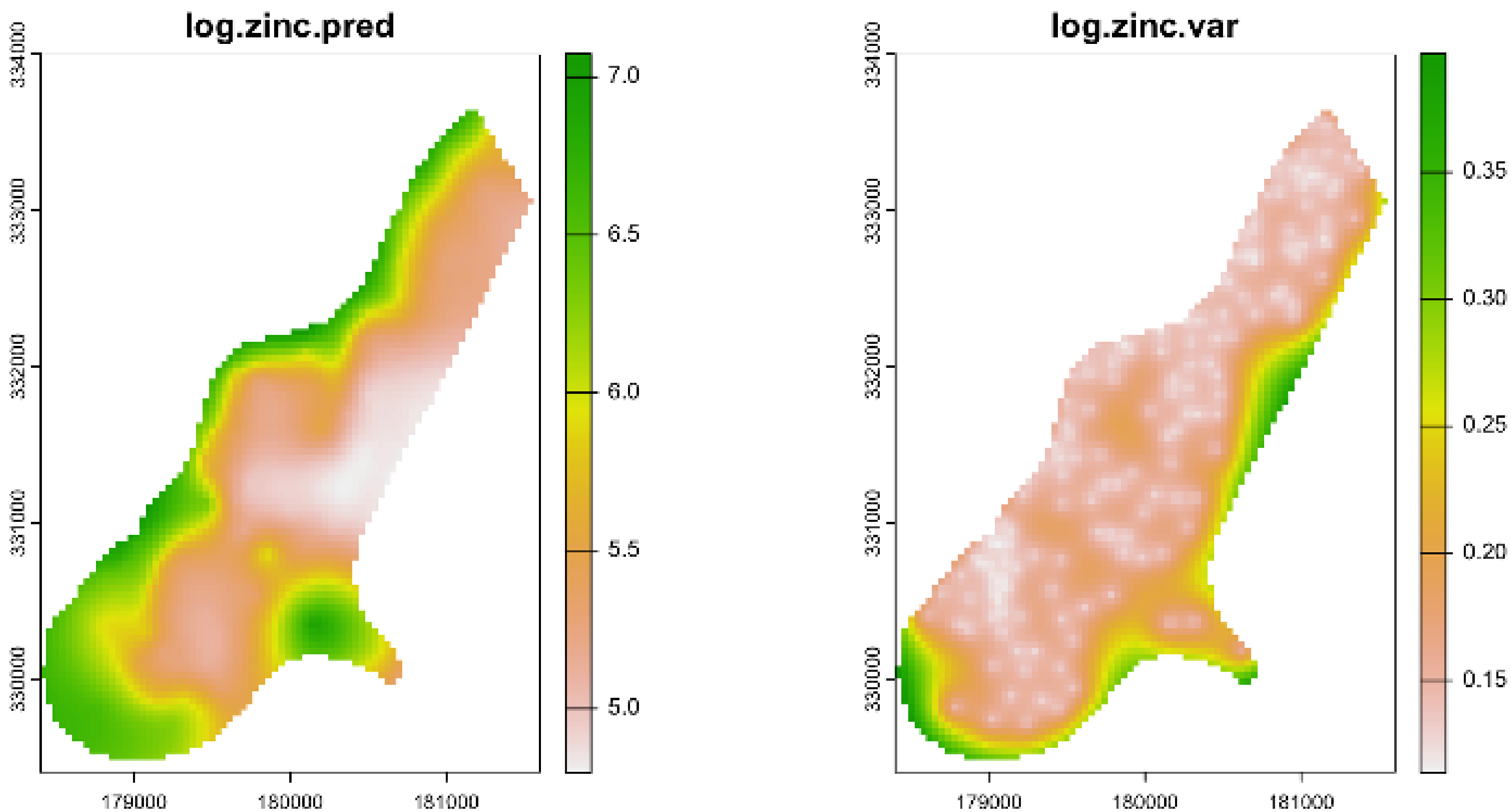
Universal Kriging



Universal Kriging

```
vu <- variogram(log(zinc)~x + x^2 + y + y^2, ~x+y, data=meuse)
mu <- fit.variogram(vu, vgm(1, "Sph", 300, 1))
gUK <- gstat(NULL, "log.zinc", log(zinc)~x + x^2 + y + y^2, meuse, location
names(r) <- "elev"
UK <- interpolate(r, gUK, debug.level=0)
```

Universal Kriging



Co-Kriging

- relies on autocorrelation in $\epsilon_1(\mathbf{x})$ for z_1 AND cross correlation with other variables ($z_{2\ldots j}$)
- Extending the ordinary kriging model gives:

$$z_1(\mathbf{x}) = \mu_1 + \epsilon_1(\mathbf{x})$$
$$z_2(\mathbf{x}) = \mu_2 + \epsilon_2(\mathbf{x})$$

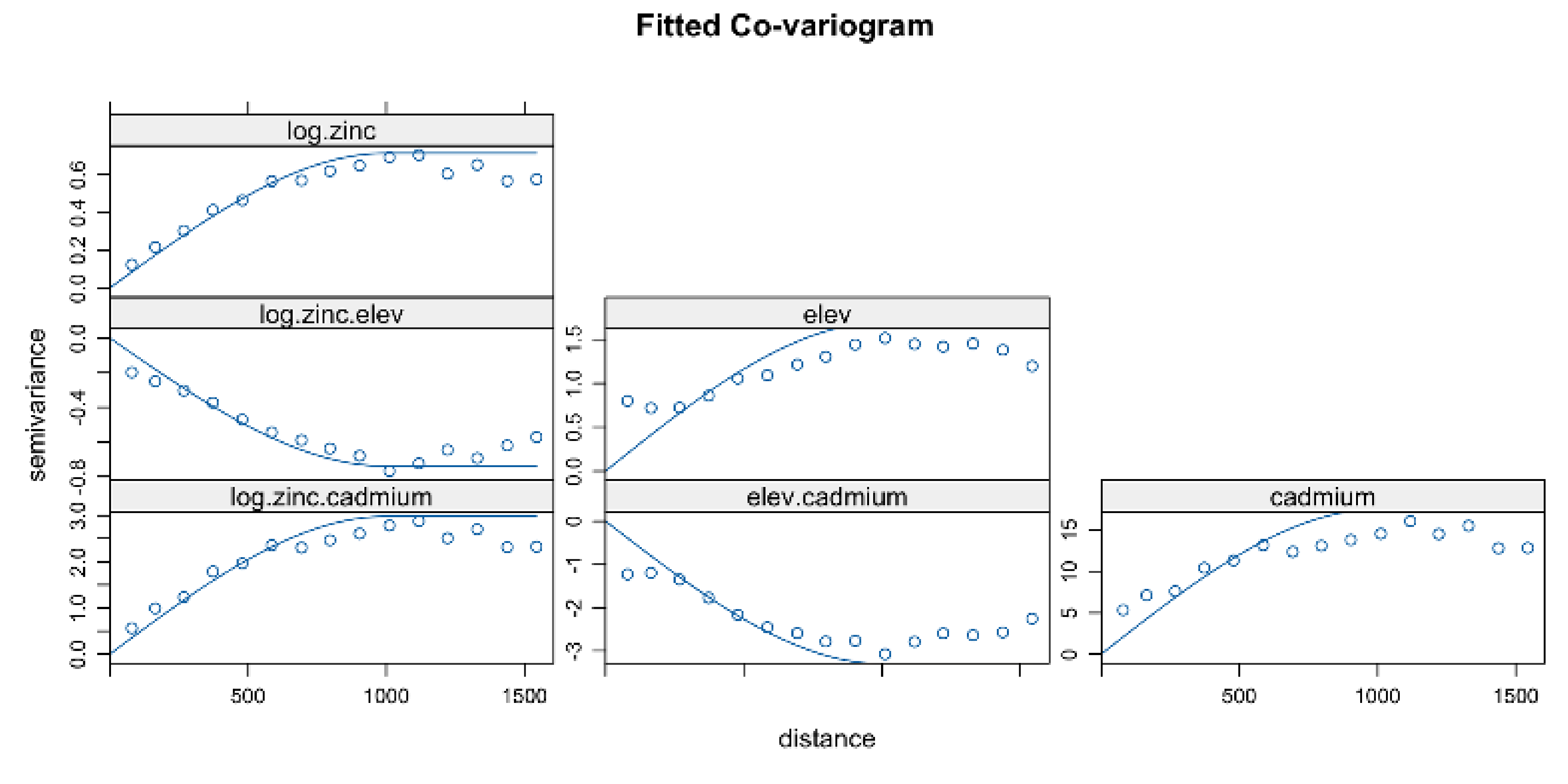
* Note that there is autocorrelation within both z_1 and z_2 (because of the ϵ) and cross-correlation (because of the location, $\mathbf{x}$)

Co-Kriging

- Process is just a linked series of `gstat` calls

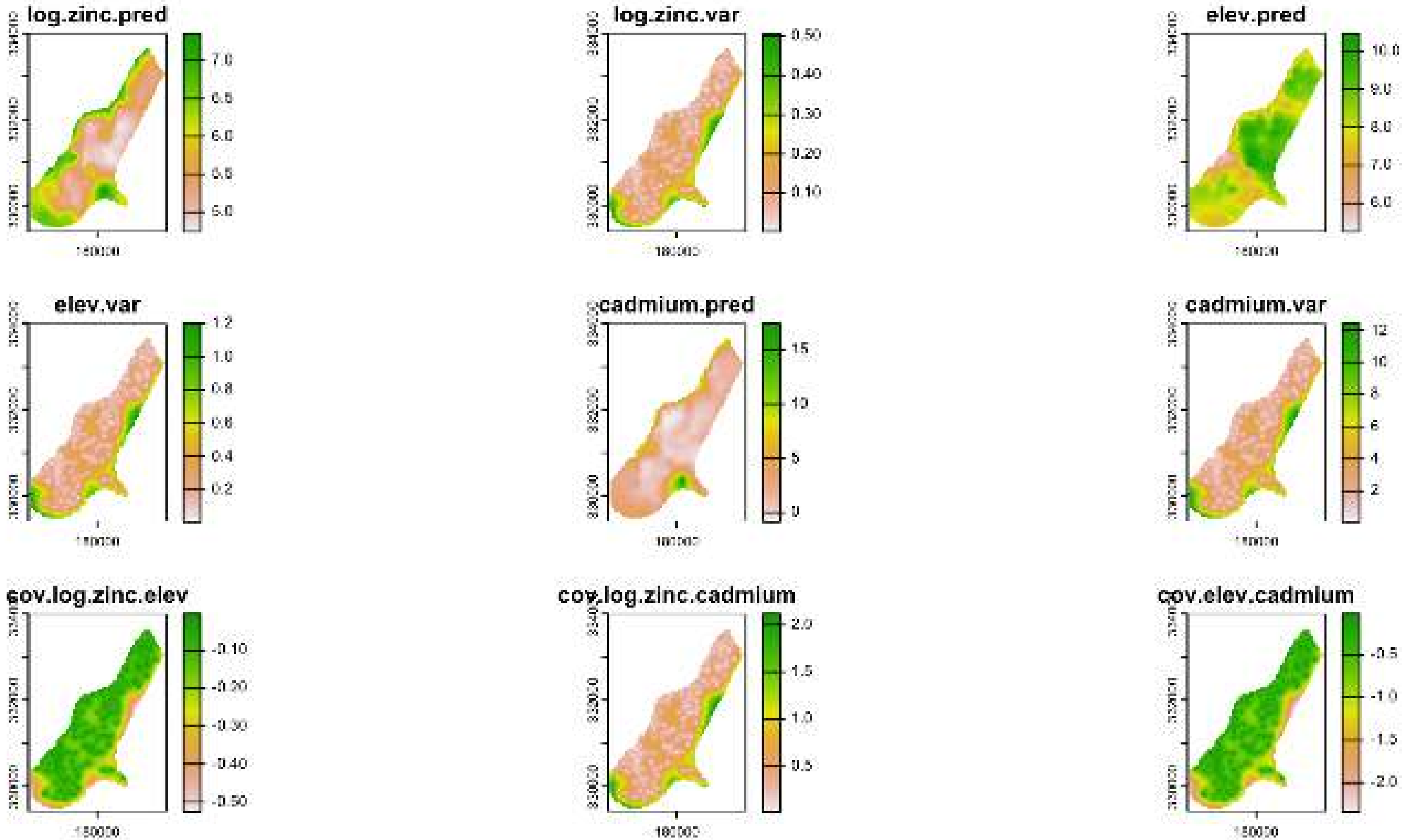
```
gCoK <- gstat(NULL, 'log.zinc', log(zinc)~1, meuse, locations=~x+y)
gCoK <- gstat(gCoK, 'elev', elev~1, meuse, locations=~x+y)
gCoK <- gstat(gCoK, 'cadmium', cadmium~1, meuse, locations=~x+y)
coV <- variogram(gCoK)
coV.fit <- fit.lmc(coV, gCoK, vgm(model='Sph', range=1000))

coK <- interpolate(r, coV.fit, debug.level=0)
```

Co-Kriging



Fitted Co-variogram
log.zinc
log.zinc.elev
log.zinc.cadmium
elev
elev.cadmium
cadmium
semivariance
distance
0.0 0.2 0.4 0.6
0.0 -0.4 -0.8
0.0 1.0 2.0 3.0
0.0 0.5 1.0 1.5
0 -1 -2 -3
0 5 10 15
500 1000 1500

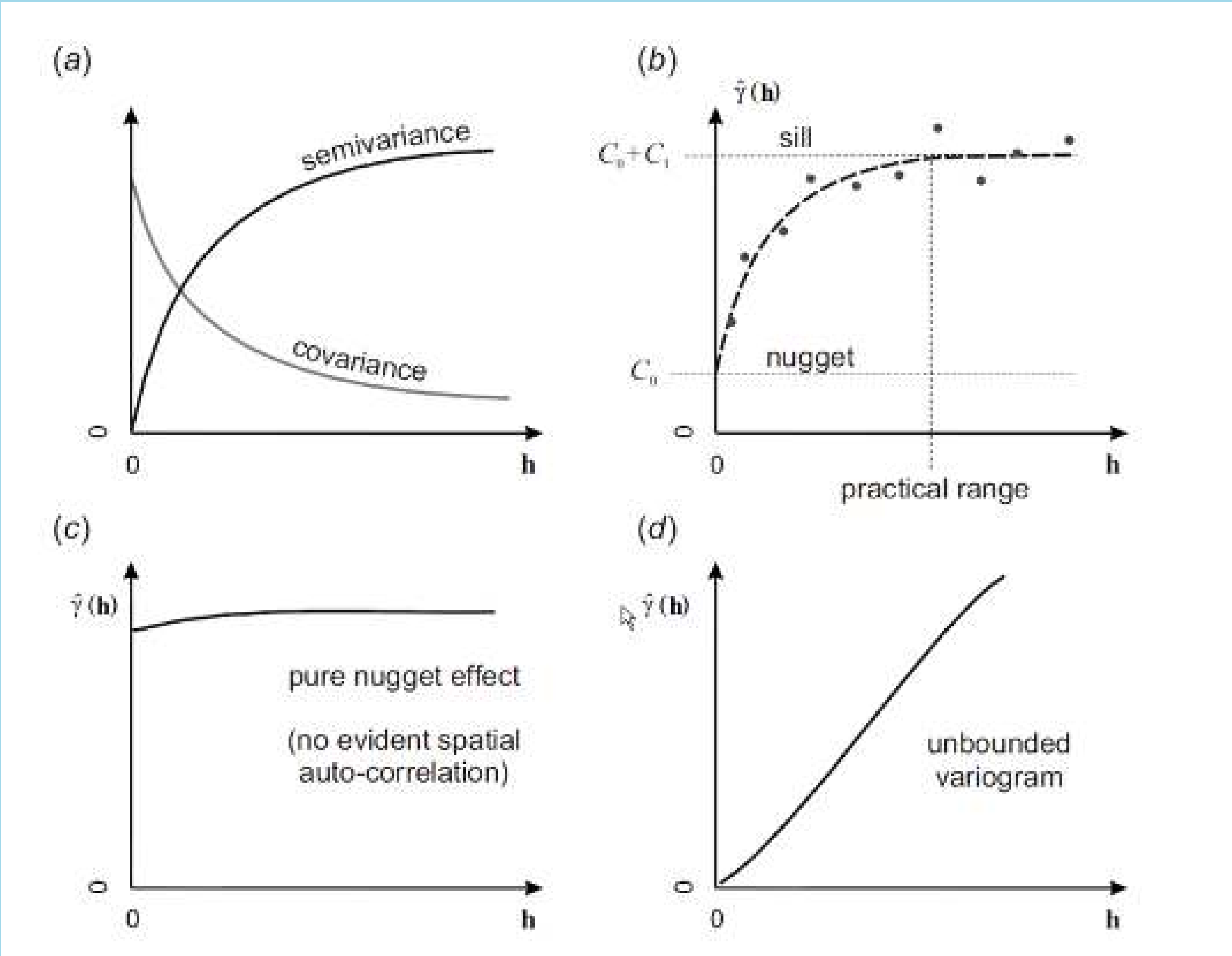
Co-Kriging


log.zinc.pred
log.zinc.var
elev.pred
elev.var
cadmium.pred
cadmium.var
cov.log.zinc.elev
cov.log.zinc.cadmium
cov.elev.cadmium

A Note about Semivariograms

- **nugget** - the proportion of semivariance that occurs at small distances
- **sill** - the maximum semivariance between pairs of observations
- **range** - the distance at which the **sill** occurs
- **experimental** vs. **fitted** variograms

A Note about Semivariograms



Fitted Semivariograms