Interpolation

HES 505 Fall 2023: Session 19

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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

But first…

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 produce the same outcome

$$z = 2x + 3y$$

- Results in a spatially continuous field

Deterministic vs. stochastic processes

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

Deterministic vs. stochastic processes

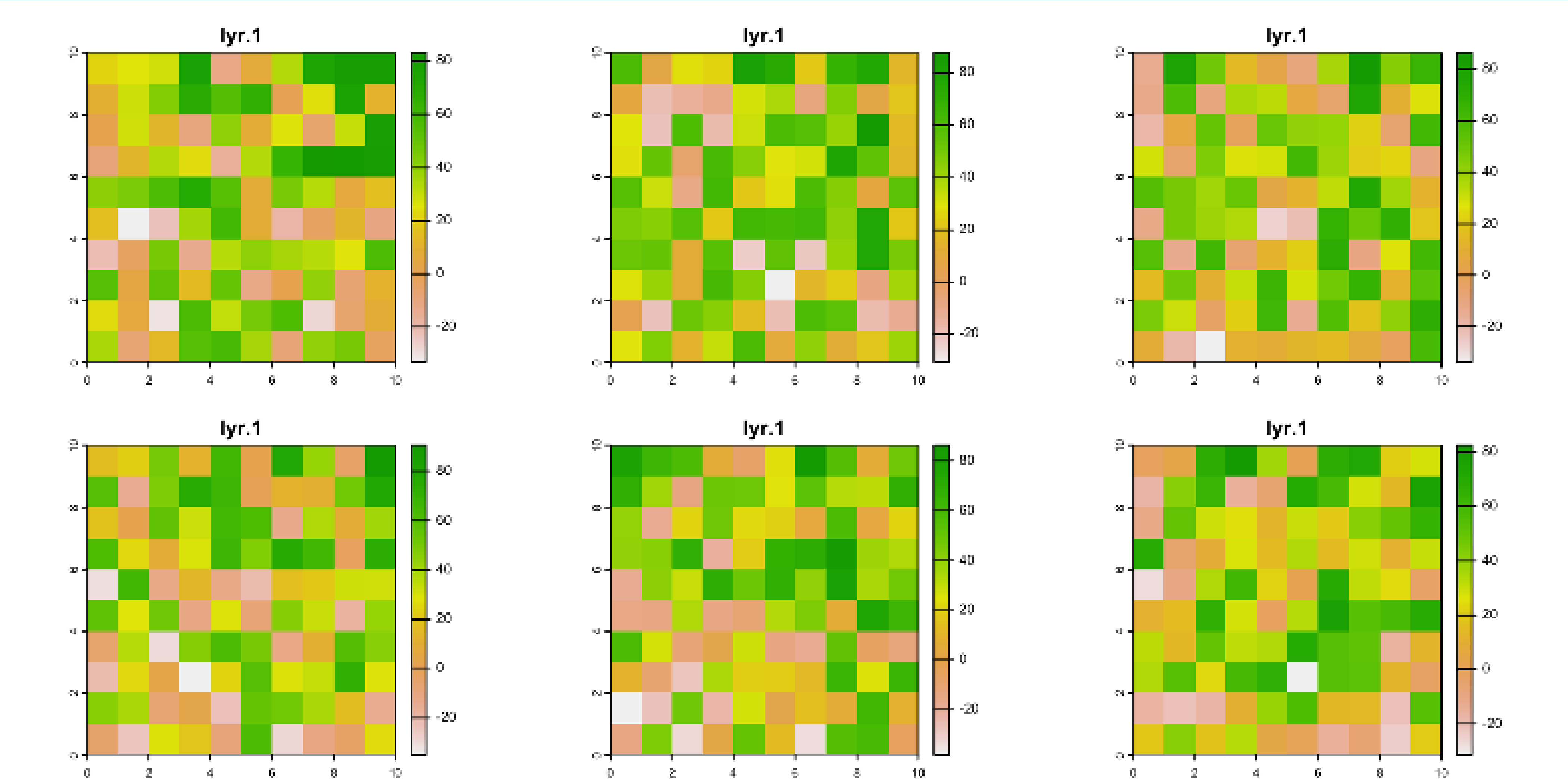
- Stochastic processes: variation makes each realization difficult to predict

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

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

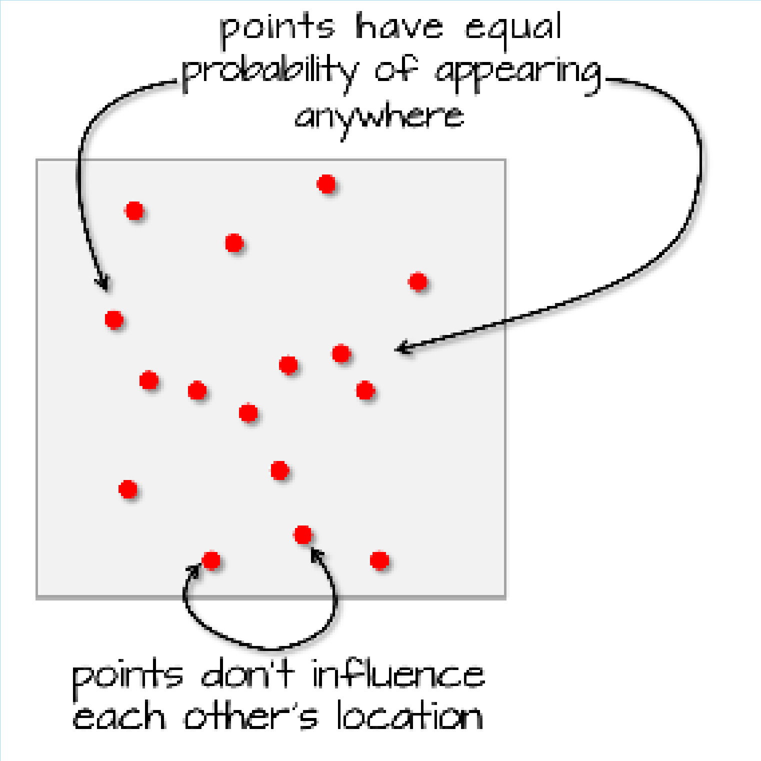
```r
x <- rast(nrows = 10, ncols=10, xmin = 0,
values(x) <- 1
fun <- function(z){
a <- z
d <- runif(ncell(z), -50,50)
values(a) <- 2 * crds(x)[,1] + 3*crds(x)[,
return(a)
}

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

Deterministic vs. stochastic processes



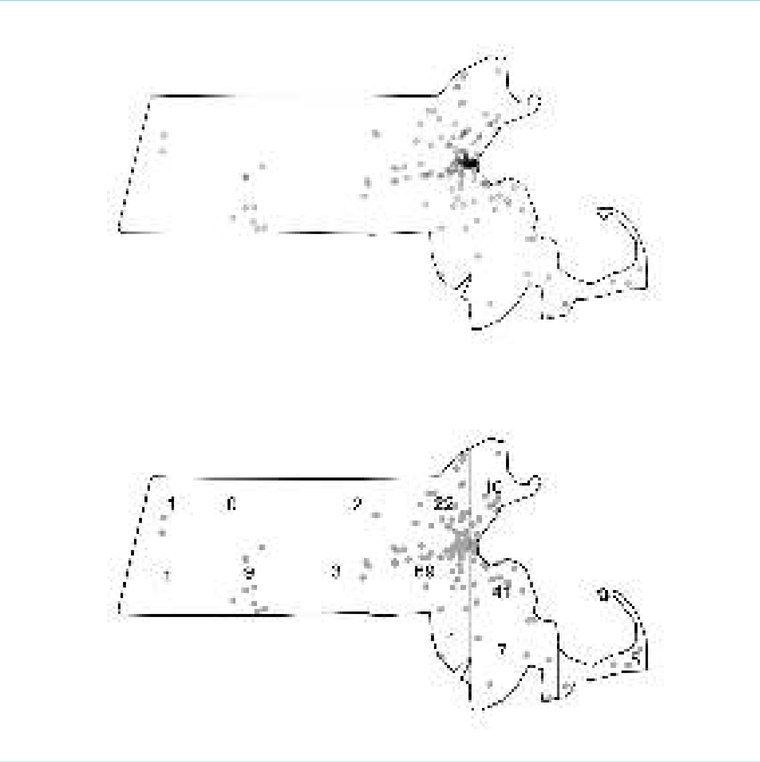
Expected values and hypothesis testing

- 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


points have equal probability of appearing anywhere
points don't influence each other's location

From Manuel Gimond

Generating expactations 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

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

Revisiting Ripley's K

- Nearest neighbor methods throw away a lot of information
- If points have independent, fixed marginal densities, then they exhibit *complete, spatial randomness* (CSR)
- The *K* function is an alternative, based on a series of circles with increasing radius

$$K(d) = \lambda^{-1} E(N_d)$$

- We can test for clustering by comparing to the expectation:

$$K_{CSR}(d) = \pi d^2$$

- if $k(d) > K_{CSR}(d)$ then there is clustering at the scale defined by d

Ripley's K Function

- When working with a sample the distribution of K is unknown
- Estimate with

$$\hat{K}(d) = \hat{\lambda}^{-1} \sum_{i=1}^{n} \sum_{j=1}^{n} \frac{I(d_{ij} < d)}{n(n-1)}$$

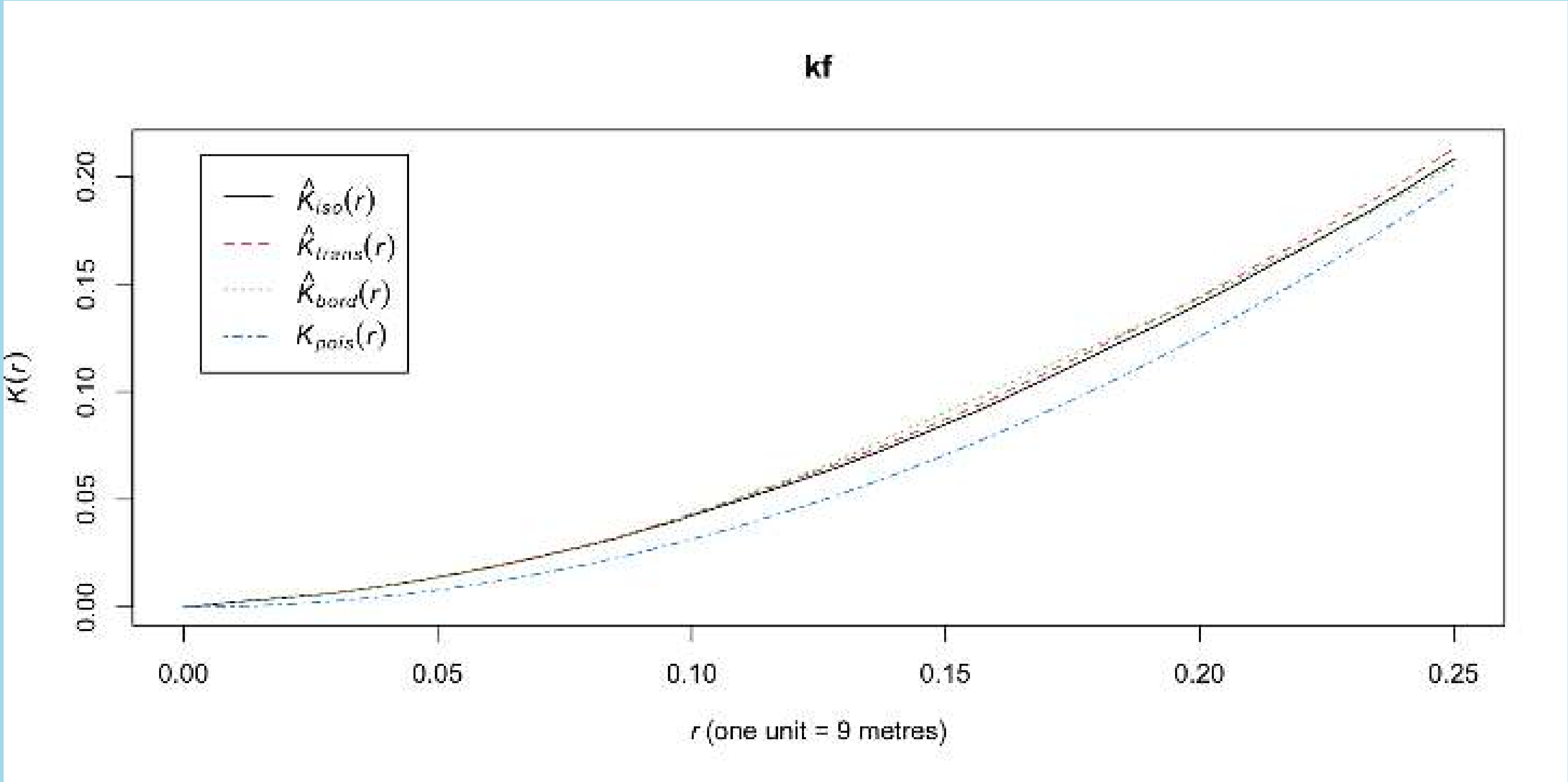
where:

$$\hat{\lambda} = \frac{n}{|A|}$$

Ripley’s K Function

Ripley’s K Function

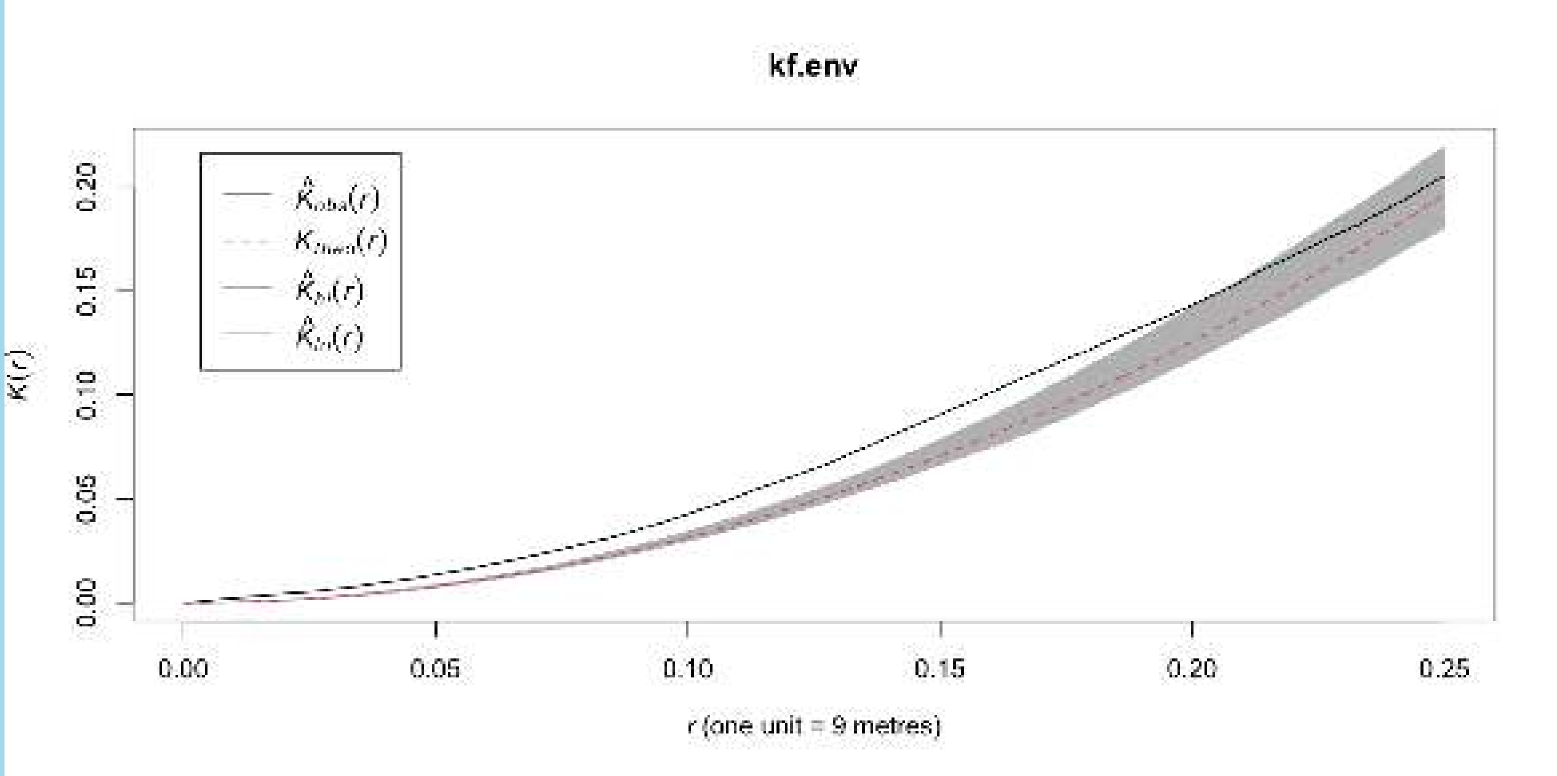
```
kf <- Kest(bramblecanes, correction-"border")
plot(kf)
```



Ripley’s K Function

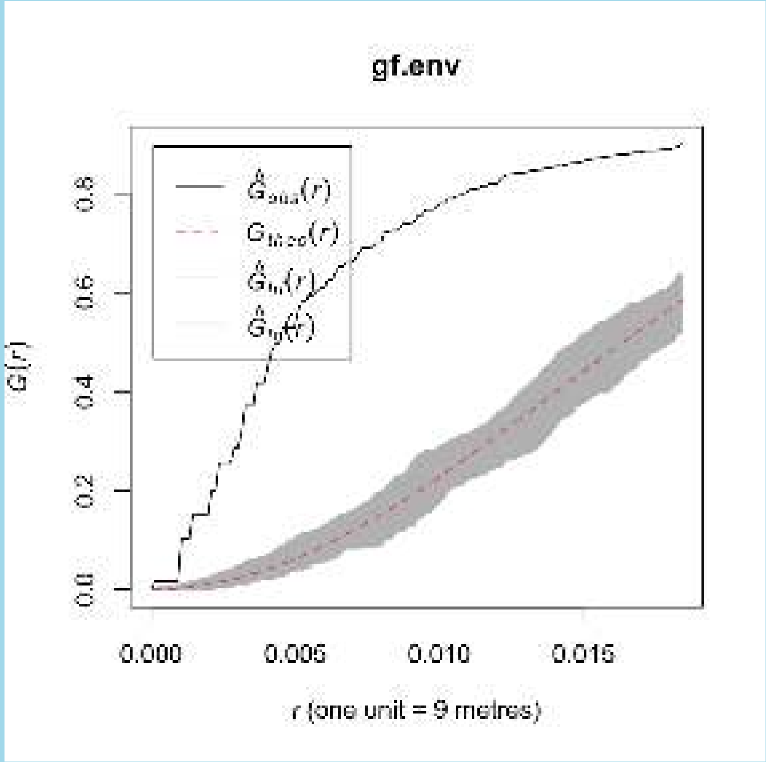
- accounting for variation in d

```r
kf.env <- envelope(bramblecanes, correction="border", envelope = FALSE, ver
plot(kf.env)
```



Other functions

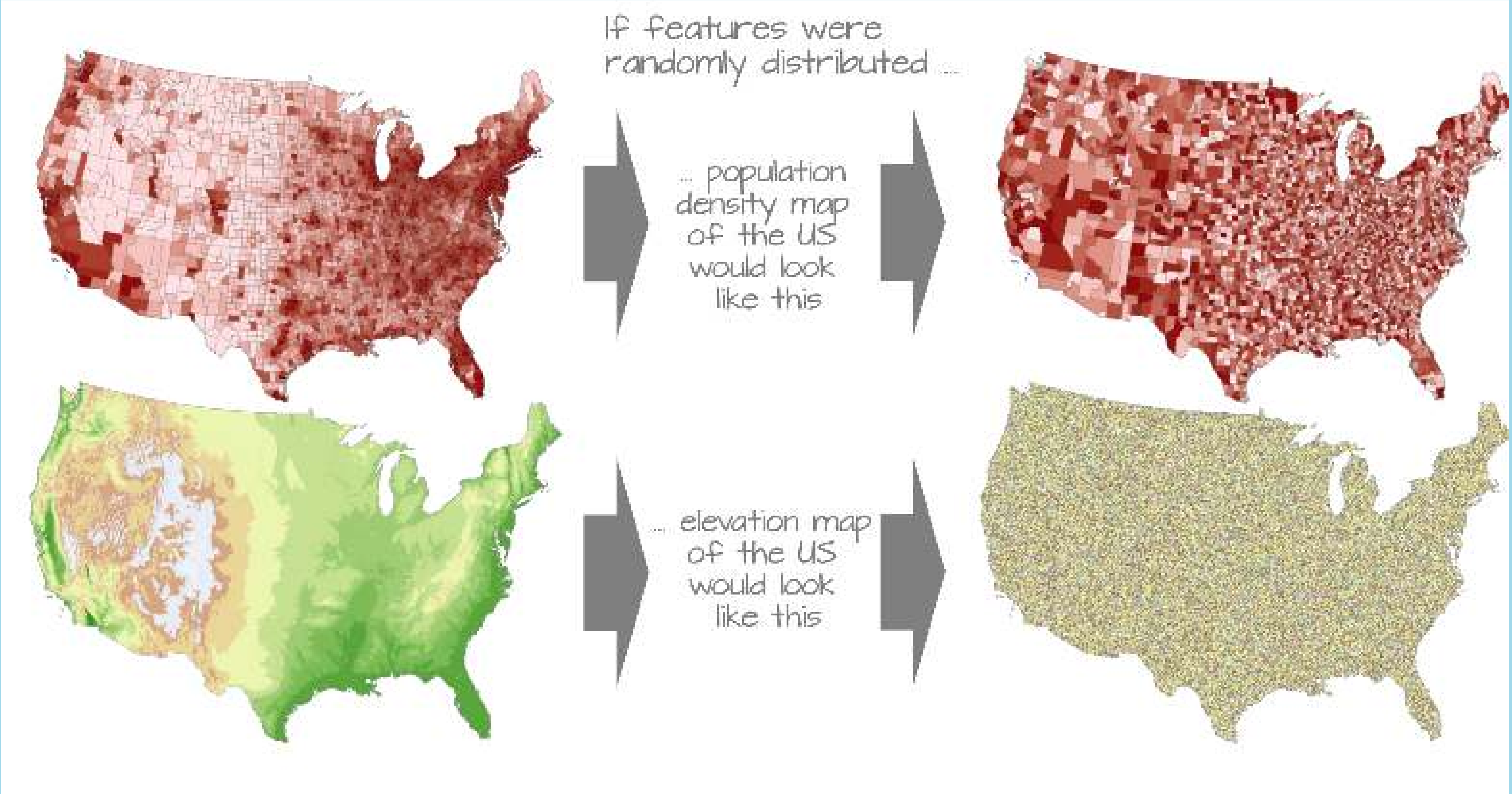
- L function: square root transformation of K
- G function: the cummulative frequency distribution of the nearest neighbor distances
- F function: similar to G but based on randomly located points



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



If features were randomly distributed ...

... population density map of the US would look like this

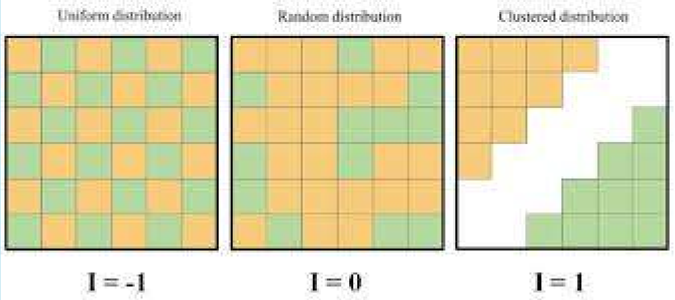
... elevation map of the US would look like this

From Manuel Gimond

(One) Measure of autocorrelation

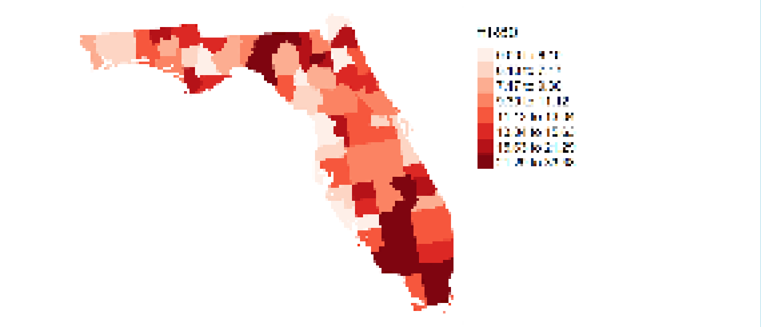
- Moran’s I

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



Moran’s I: An example

- Use spdep package
- Estimate neighbors
- Generate weighted average



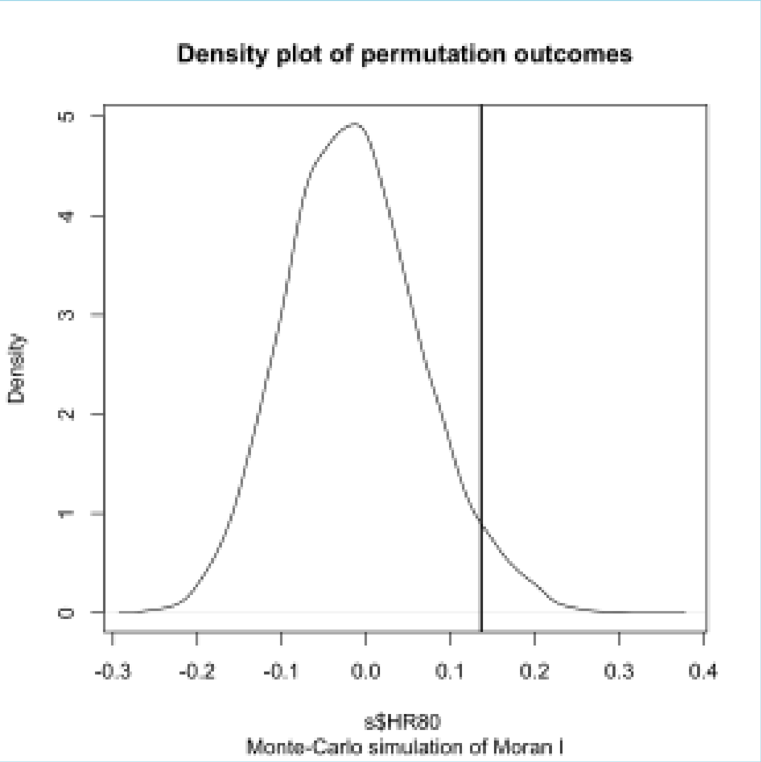
```r
set.seed(2354)
# Load the shapefile
s <- readRDS(url("https://github.com/mgimond/Data/raw/gh-pages
                                                                                            
# Define the neighbors (use queen case)
nb <- poly2nb(s, queen=TRUE)

# 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

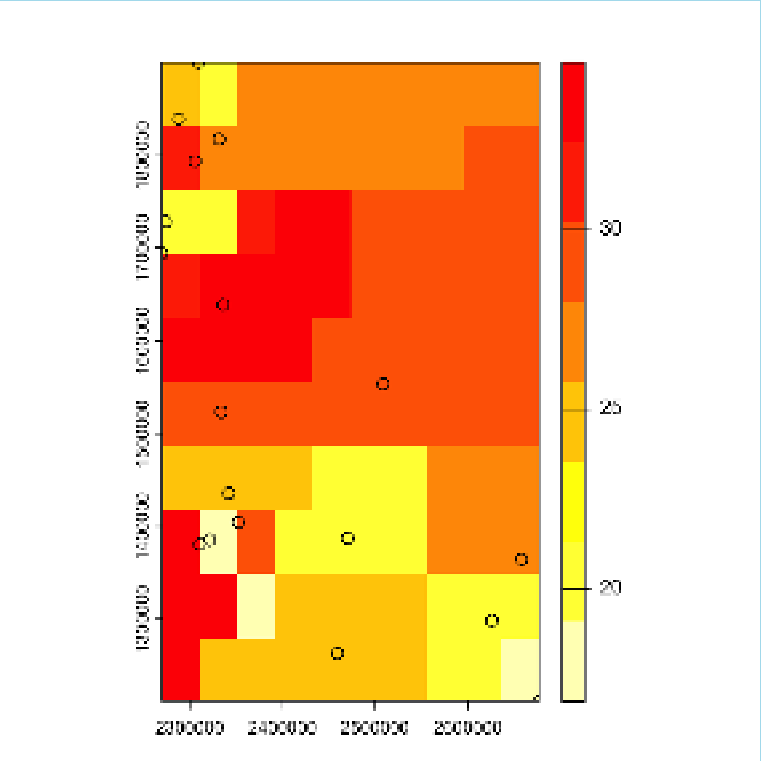
Interpolation

- 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
aq <- read_csv("data/ad_viz_plotval_data.csv") %>%
  st_as_sf(., coords = c("SITE_LONGITUDE", "SITE_LATITUDE"), c
  st_transform(., crs = "EPSG:8826") %>%
  mutate(date = as_date(parse_datetime(Date, "%m/%d/%Y"))) %>%
  filter(., date >= 2023-07-01) %>%
  filter(., date > "2023-07-01" & date < "2023-07-31")
aq.sum <- aq %>%
  group_by(., `Site Name`) %>%
  summarise(., meanpm25 = mean(DAILY_AQI_VALUE))

nodes <- st_make_grid(aq.sum,
                      what = "centers")

dist <- distance(vect(nodes), vect(aq.sum))
nearest <- apply(dist, 1, function(x) which(x == min(x)))
aq.nn <- aq.sum$meanpm25[nearest]
preds <- st_as_sf(nodes)
preds$aq <- aq.nn

preds <- as(preds, "Spatial")
sp::gridded(preds) <- TRUE
preds.rast <- rast(preds)
```



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

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

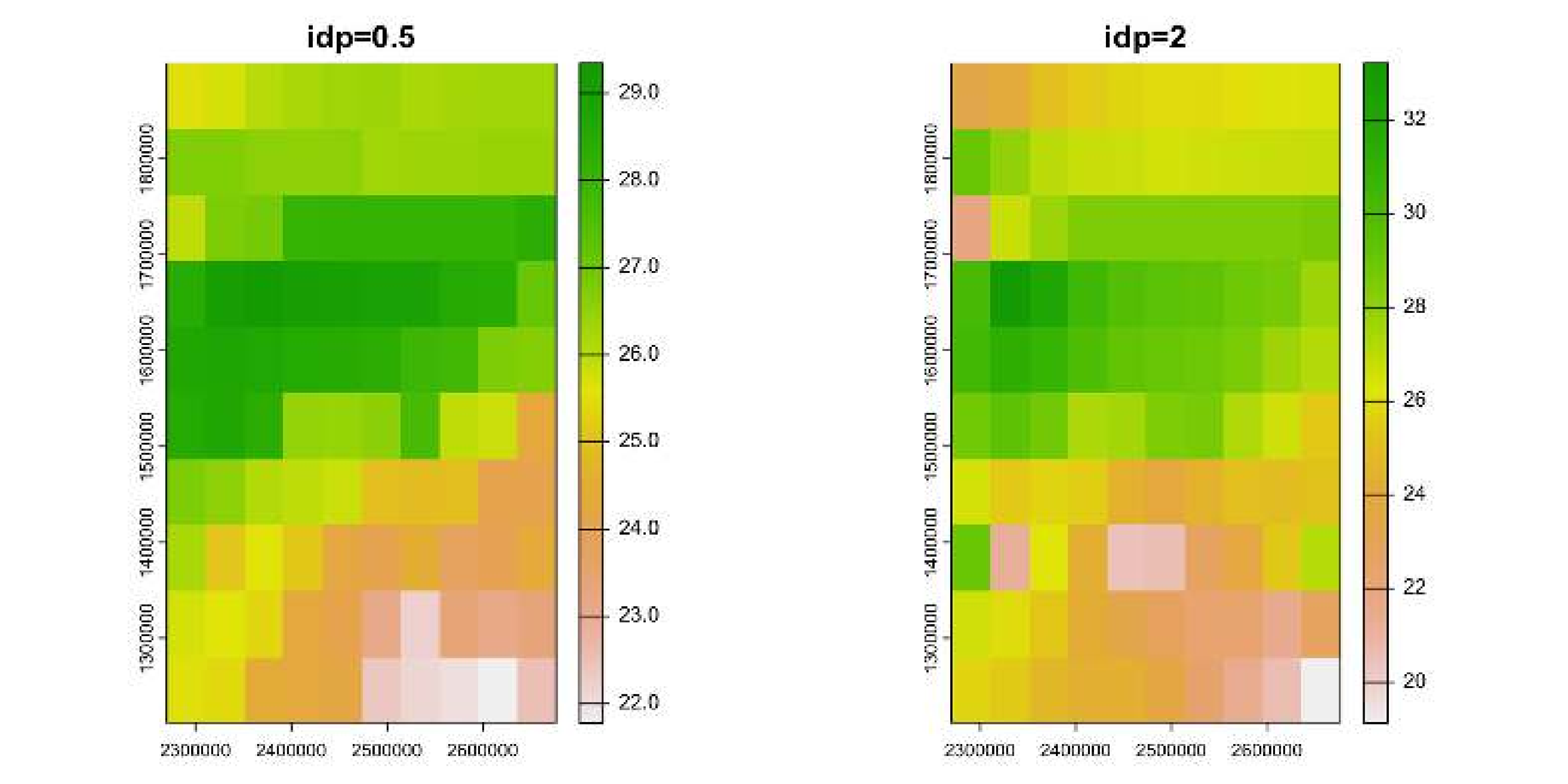
and $\alpha > 0$ ($\alpha = 1$ is inverse; $\alpha = 2$ is inverse square)

Inverse-Distance Weighting

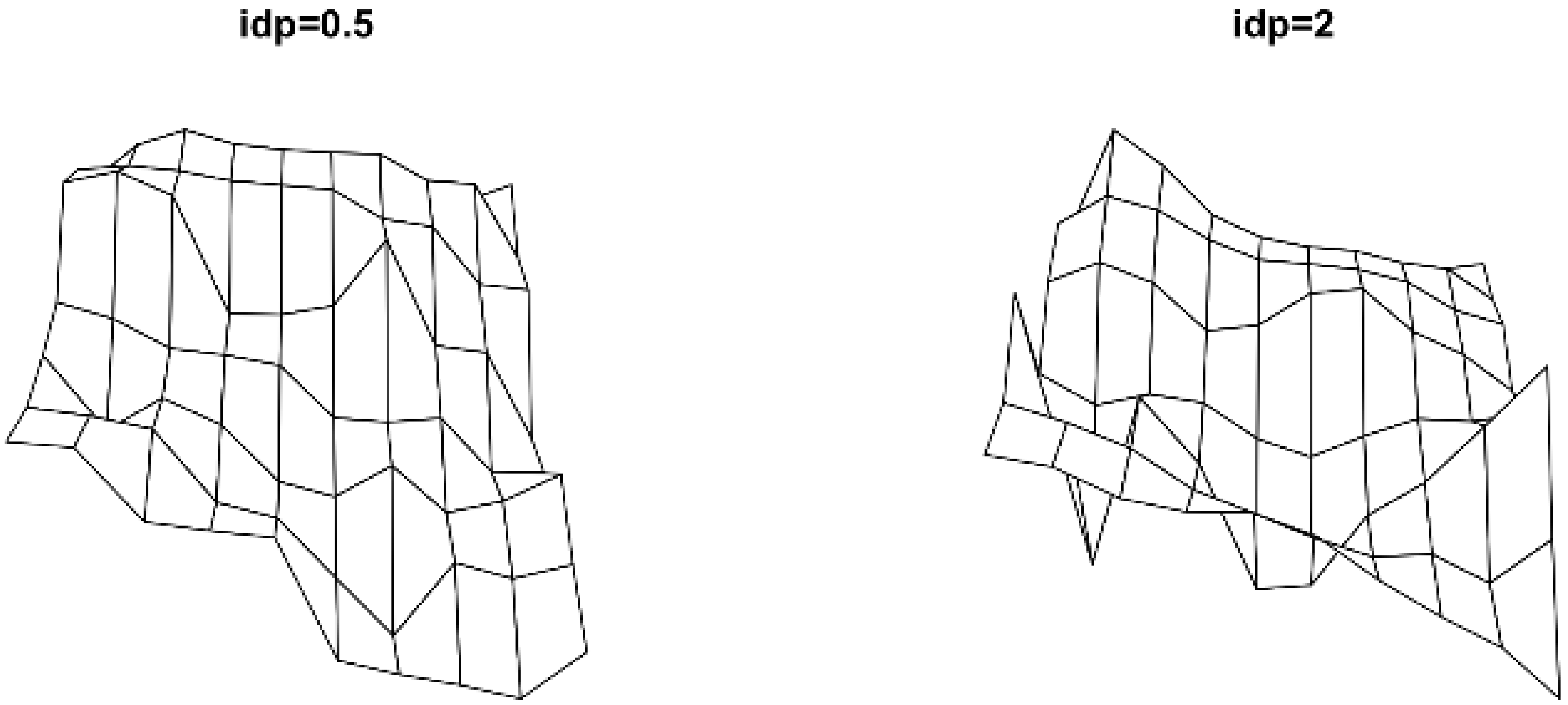
- terra::interpolate provides flexible interpolation methods
- Use the gstat package to develop the formula

```
mgsf05 <- gstat(id = "meanpm25", formula = meanpm25~1, data=aq.sum,  nmax=7
mgsf2 <- gstat(id = "meanpm25", formula = meanpm25~1, data=aq.sum,  nmax=7,
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(preds.rast, mgsf05, debug.level=0, fun=interpolate_gst
zsf2 <- interpolate(preds.rast, mgsf2, debug.level=0, fun=interpolate_gstat
```

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)

```r
library(sp)
data(meuse)
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 **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

```r
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 ($z_{2...j}$)
- 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

```r
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)
```

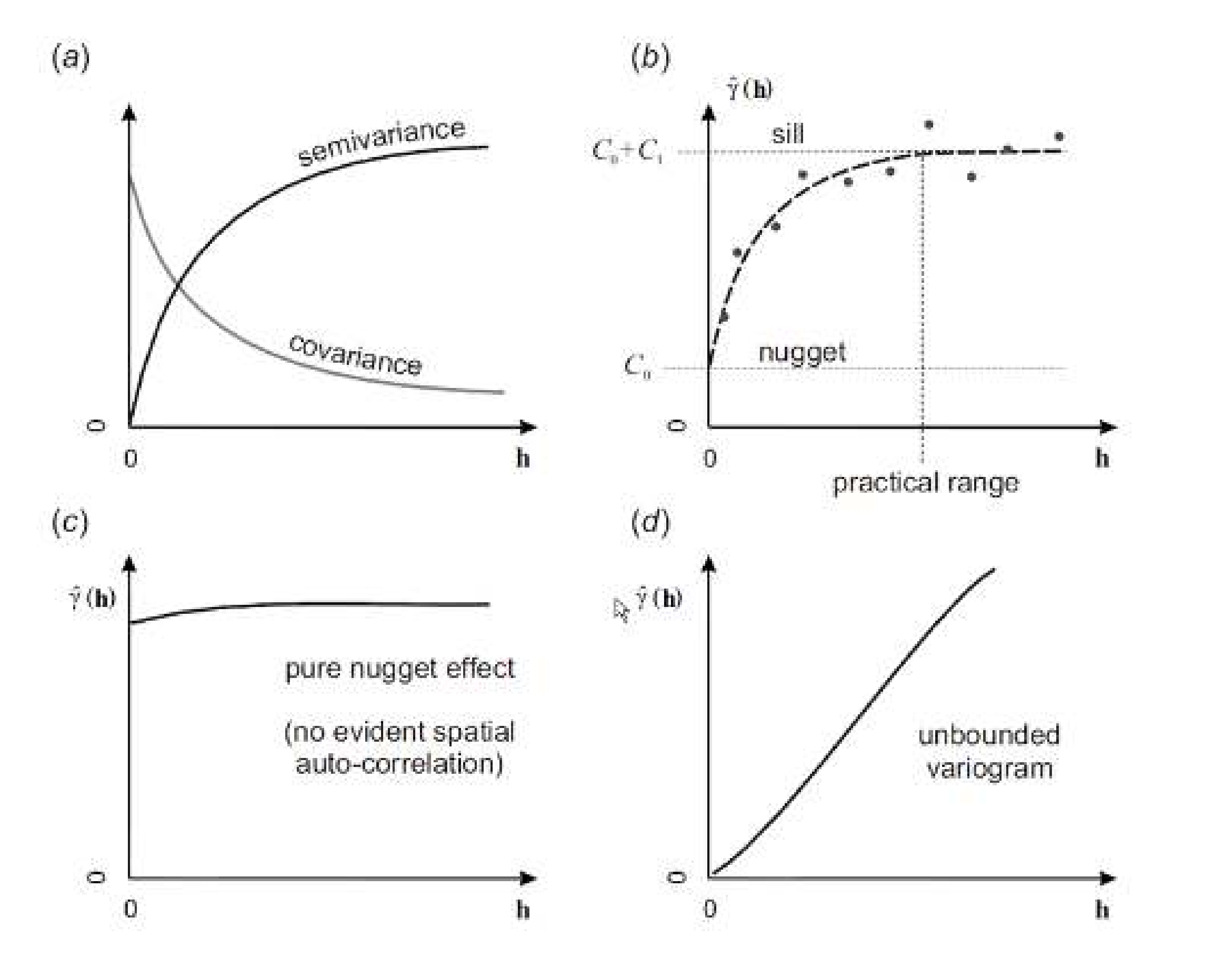
Co-Kriging

Co-Kriging

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