Improved Corona incidence maps via kernel density estimates

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A typical Corona incidence map

Incidence= (no. of infections in 7 days/ no. of inhabitants) x 100000





	Kreis	Fälle	Inzidenz
1	SK Hamm	180	100,5
2	SK Berlin Neukölln	187	56,5
3	SK Remscheid	62	55,9
4	SK Berlin Mitte	213	55,5
5	SK Berlin Tempelhof-Schöneberg	166	47,2
6	SK Berlin Friedrichshain-Kreuzberg	136	47,0
7	SK Frankfurt am Main	329	43,7
8	SK Duisburg	212	42,5
9	SK Berlin Charlottenburg-Wilmersdorf	141	41,3
10	SK Bremen	231	40,6
11	LK Rhön-Grabfeld	31	38,9
12	SK Schweinfurt	21	38,9
13	LK Oberbergischer Kreis	103	37,8
14	SK Leverkusen	61	37,2
15	SK Gelsenkirchen	94	36,1



- Make infection numbers comparable across regions with different population sizes
- Show regions with low and high incidence figures (Range)
- Identify local clusters with high incidences (Spatial distribution)
- Temporal development of spatial distribution (Animated maps)



• Disease maps

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- Regional voting results
- Poverty maps, social atlases



Standard incidence maps via Choropleths

- Based on reference areas. Usually Counties, federal states, etc.
- Area value: (no. of new infections within a week/ no. inhabitants) × 100000 in area
- Temporal development of spatial distribution (Animated maps)
- But:
- For different area systems quite different maps are generated
- Unrealistic assumption of uniform local incidence within area
- Information reduction by discrete display of levels (6 colours)
- Discontinuities at borders avoid identification of clusters



- Density is independent from reference areas
- Kernel density estimates are smooth and flexible
- However: Individual geo-coordinates are needed!
- Only local aggregates are known!
- Approach: Use statistical missing data techniques, like EM algorithm.



- Density of infections $f_I(x_1, x_2)$ for geo-coordinate (x_1, x_2)
- Density of population $f_P(x_1, x_2)$ for geo-coordinate (x_1, x_2)
- Total number of infections N_I
- Total number of population N_P
- Definition of local incidence at coordinate (x_1, x_2) :

$$f_{I|P}(x_1, x_2) = \frac{N_I}{N_P} f_I(x_1, x_2) / f_P(x_1, x_2) \times 100000$$



Estimation of local incidence in case of known geo-coordinates

• Replace $f_I(x_1, x_2)$ and $f_P(x_1, x_2)$ by kernel density estimates:

$$\hat{f}_{NW}(x_1, x_2) = \frac{N_l \hat{f}_l(x_1, x_2)}{N_P \hat{f}_P(x_1, x_2)} \times 100000$$
 (1)

This is the nonparmetric Nadaraya/Watson estimator, see for example, Härdle (1991).

 Use a joint smoothing factor from the distribution of infections!



The estimation of incidences with aggregates for areas

- Compute f_{NW}(x₁, x₂) by an iterative procedure: Simulated Expectation Maximation (SEM) algorithm
- S-Step: Sample from the actual distributions $\hat{f}_P^{(n)}$ for the population and $\hat{f}_I^{(n)}$ for the infected persons.
- M-Step: Estimate new densities $\hat{f}_P^{(n+1)}$ from the population sample and $\hat{f}_I^{(n+1)}$ from the infection sample.
- Calculate incidence for each iteration $\hat{f}_{NW}^{(n)}(x_1, x_2)$
- Repeat the iterations *B*-times for a burn-in phase and then *R*-times for a replication phase.
- Compute the final incidence $\hat{f}_{NW}(x_1, x_2)$ by:

$$\hat{f}_{NW}(x_1, x_2) = \frac{1}{R} \sum_{r=1}^{R} \hat{f}_{NW}^{(B+r)}(x_1, x_2)$$

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(2)

Realisation with the R-Package Kernelheaping

- Drawing a population sample in each area of size $N_{P,a}$ on a fine grid \mathcal{G} in each area. Sampling is proportional to size with $\hat{f}_P^{(n)}$ as size variable. This generates the population sample $s_P^{(n)}$.
- Sampling of infected persons is with replacement from $s_P^{(n)}$ with sample size $N_{I,a}$ in area a. Sampling is proportional to size with $\hat{f}_I^{(n)}$ as size variable. This generates $s_I^{(n)}$.
- The smoothing factor h for the kernel estimation is calculated by a data driven procedure of Wand/Jones (1994) on the basis of the infection sample $s_l^{(n)}$.
- The estimated densities for the population and the infected persons are consistent with the area totals for the population and the number of infected persons.
- The R-Package *kernelheaping* for density estimation with "heaped" data is freely available.

A comparison of maps of Corona-incidences at 3. October 2020. Left: Official Choropleth map of German counties by the RKI. Right: Map computed via Kernelheaping algorithm based on the county figures of the RKI



- Though based on the same data (RKI county aggregates) differences due to the joint analysis of neighbouring counties for Kernelheaping map.
- Scattered incidence regions (Choropleth) are united to a smooth region in the west of Germany (Northrhein-Westfalia).
- A high incidence region in the north-west of Germany is detected, which remains a stable high incidence region during the entire second pandemic wave in Germany.



Spatial and temporal comparisons of incidence clusters

- The daily infection numbers exhibit a strong seasonal pattern over the workdays: use of 7-day moving averages!
- For each day a new 7-day moving average is used to display the spatial and temporal development of incidence clusters.
- An internet application uses the RKI county data to display the Corona pandemic in Germany since the start of the second wave in October 2020.

Link: https:

//www.inwt-statistics.com/read-blog/covid-19_

heat-map_of-local_7-day_incidences_over_time.html

• Similar presentations with Choropleths fail: Despite the temporal smoothing by the moving averages we get only an erratic and spurious impression of the temporal development of incidences!

Link:https://interaktiv.tagesspiegel.de/lab/ corona-analyse-in-welchen-regionen-die-zahlen-wieder

The temporal development of infection rates in Saxony and in the city of Bautzen (Blue mark).



Incidence (cases per 100.000 population)

≤ 10 ≤ 20 ≤ 35 ≤ 50 ≤ 100 ≤ 150 ≤ 200 ≤ 300 ≤ 500 > 500
Left: 30. Oct. (Separate Clusters) Middle: 12. Nov (Merge of clusters) Right: 17. Dec. (Entire region infected)

• The level of aggregation often depends on the available data.

- Corona data: RKI data at county level
- Berlin: 12 Bezirke (BZK City districts), 97 Ortsteile (ORT), 447 Neighbourhoods (LOR) Only incidences at BZK-level are delivered from RKI, despite local government (Senator für Gesundheit) asked for data at LOR-Level.
- Level of incidences? The lower, the better?
- Impact of regional data on incidence risks?



Regional Corona analysis for Berlin

Analysis at the level of 12 city districts:

Abbildung 7:

Anzahl der COVID-19-Fälle je 100.000 Einwohnerinnen und Einwohner in den Berliner Bezirken im Zusammenhang mit dem Anteil der Einwohnerinnen und Einwohner (EW) mit einfacher Wohnlage (a) und der durchschnittlichen Wohnfläche je Einwohnerin und Einwohner (b). (Stand: 29.10.2020)



(Datenquelle: RKI-COVID-19-Dashboard, SenStadtWohn, AfS / Berechnung und Darstellung: SenGPG - I A -)

Conclusion: Densely populated districts with low quality housing increase Corona incidences!



A simulation study for Berlin

- How are local true incidences estimated?
- Scope: Comparison of maps (Choropleth vs Kernel density procedure) in case of known infection cases. Need for simulation data!
- Comparison of RMSE over city area.
- Simulation design
 - Start with infection clusters proportional to population density. Total infection numbers according to official records.
 - Generate infections according to official R-values via Poisson distribution.
 - Dispersion: On neighbouring grid points proportional to population density.
 - Duration: Over 16 weeks (approx. duration of the second wave in Berlin)
- Different levels of aggregation for map construction: 12 Districts (BZK), 97 so-called Ortsteile (ORT), 447 Neighbourhoods (LOR).





(a) True density

(b) True incidence

The Kernel density of simulated cases (true density) and the resulting local incidence (true incidence).

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(c) Choropleth incidence(LOR)

(d) Kernel heaping incidence(LOR)

Aggregation level LOR: Choropleth map (left) and Kernel heaping map (right).



(e) Choropleth incidence(ORT)

(f) Kernel heaping incidence (ORT) $\,$

Aggregation level ORT: Choropleth map (left) and Kernel heaping map (right).



(g) Choropleth incidence(BZK)

(h) Kernel heaping incidence(BZK)

Aggregation level BZK: Choropleth map (left) and Kernel heaping map (right).

Comparison of RMSE over 16 simulation weeks

Choro(BZK) Semel(BZK) Choro(ORT) Kernel(ORT) Choro(LOR) Kernel(LOR)



Upmost lines: ORT level (Red=Choropleth, Lightblue=Kernel), middle lines: BZK level (Green=Choropleth, Orange=Kernel) LOR level for Choropleths (Violet), bottom line: LOR level of the Kernel heaping map (Darkblue)

- Kernel heaping map has at all levels and at all times smaller RMSE values than the Choropleth map.
- It does **not** hold: the smaller the area level the better the map.
- RMSE of Choropleth maps: There is almost no difference between the LOR level and the BZK level!



• Extension of approach to 3-dim Kernel densities:

- Longitude, latitude and time
- Longitude, latitude and age
- **Geostatistics**: Smoothing by Kriging of area centroid values. Ignores the shape of the areas!
- A complain: Public media in Germany + RKI: 100 percent use of Choropleth maps!
 I tried to contact newspapers (Spiegel, Tagesspiegel) and the RKI. No reaction!



References incidence maps

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https://www.inwt-statistics.com/read-blog/covid-19_ heat-map_of-local_7-day_incidences_over_time.html

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