Comparison of short range spatial predictive policing forecasts

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Abstract

We work within the framework of spatial "predictive policing": the generation of short range (for example, the next day) predictions or forecasts of crime locations within, say, a city. We survey methods of comparing such predictions as given by predictive policing algorithms. We discuss a framework for thinking about the problem, and provide some new comparison methods. We develop the framework with a "toy" model, via computer simulation of synthetic data, and with a case-study using real data.

Conclusions???

1 Introduction

We are interested in spatial "predictive policing" algorithms (see [23] for an overview, or [1, 4, 9, 15, 19, 21, 26]) and in particular, how to assess the match between "prediction" and reality. As [23, Summary] argues, the word "forecasting" is better suited to the objective, reproducible, and ultimately probabilistic algorithms we study, but unfortunately the word "predictive" is by now in common usage. We shall concentrate upon predicting the likely spatial locations of future crime over short time ranges, of the order of one day into the future. In the language of [23] we look only at "Methods for predicting crimes: These are approaches used to forecast places and times with an increased risk of crime." Notice already that we need to be careful with language. This quote says "an increased risk of crime", but it is not entirely clear what such an "increase" is to be measured against. All of the predictive methods we have looked at actually attempt merely to predict where there is a "risk" that crime will occur.

As input, we take a list of past crime events, typically longitude and latitude coordinates projected in a suitable way, and a time-stamp. This data is run through an algorithm whose aim is to forecast the "risk" of crime in different spatial locations, for a short time range into the future (typically one day, and perhaps not more than a week). Typically we lay a grid over the study area, and ask that the algorithm produce an estimate of risk in each grid cell, with a higher risk indicating that a crime in that grid cell is more likely. A "continuous prediction" can be approximated by a very small grid size. We shall deliberately view the algorithm as a "black-box" and make as few assumptions as possible about how it functions. We then wish to compare our prediction to the set of crime events which

did actually occur in the prediction window. As our time window is small, such a set of events is typically rather small, maybe 5 to 20 events. This is consistent with our case study using data from the North side of Chicago, Section 6.

Such a technique is often termed "hot-spotting" in the literature; see for example [23], or [4]. We regard this as slightly misleading, as a "hot-spotting" technique can also be assessed in terms of the visual output, or by some measure of how "practical" the hotspot is from an operational police perspective, see [4, 1]. Instead, we seek assessment methods which look only at how "closely" the prediction or forecast matches reality.

The "hit rate" is by far the most common assessment method in the literature, see for example [1, 4, 21], [23, Chapter 5]. As such, this paper can thought of as an exploration of alternative assessment techniques, rather than a simple survey. We have turned to meteorology for inspiration. A probabilistic forecast, often derived from an ensemble forecast, gives a forecast of the form, for example, "There is a 10% chance of rain tomorrow." Such a forecast is meant to mean that, over a large number of such predictions, it does indeed rain in around 1 in 10 cases, [16, Chapter 7]. This is at least superficially similar to our interpretation of "risk". We also look at comparison methods motivated by Bayesian statistics and information theory, [13, 20].

There has in fact been relatively little consideration of quantitative comparisons of "hot-spot maps". For example, the relatively recent [19] writes "Until now, users had evaluated hotspot methods by how they looked, rather than by an objective measure that allowed comparison between different methodologies, crime types, and time periods."

In the next section, we introduce our assessment techniques in the setting of a toy model, which allows us to explore the ideas with the minimum of technical fuss. We then fully explain the methods, and compare them with a real geographical test area, but using completely artificial data (which both produces the "real events" to test against, and the predictions). In the final section, we use both real-world data, and a number of genuine prediction algorithms, to illustrate our methods.

1.1 Summarising the distributions

In the crime prediction literature, it is common to simply present numerical or graphical summaries of results (for example, [4, 9]) or to compute "p-values" (for ex-

ample, [1, 5]). We do not feel that computing p-values is always appropriate.

For example, we might be tempted to test if "hit rates" (for a given coverage, see Section 3.1 below) for two predictions show "statistically significant differences". One test to use here would be the Wilcoxon signed-rank test (see [27, Test 6]). Here the formal statistical test is, supposing we have hit rates $(h_i^{(1)})$ and $(h_i^{(2)})$, we ask "Does the sample $(x_i) = (h_i^{(1)} - h_i^{(2)})$ come from a population where the median is 0". This test is valid under the assumption we are taking a sample from a population, and that the population distribution is symmetric. It is not fully clear to us that such assumptions are warranted.

There is by now substantial criticism of the use of p-values alone, see for example [2]. In the Wilcoxon signed-rank test, suppose we obtain a p-value of 3% and so reject the null hypothesis that the median is 0. What this means is exactly that, if the median actually were 0 and we could repeat the experiment a large number of times, then we we would expect to see a test statistic this extreme or more extreme only around 3% of time. As [7, Section 2.3.3] notes, a layperson's interpretation is often that "the probability that the median is 0 is just 3%", but this is simply not the case.

We prefer to take a more graphical approach, and to try to summarise the full distribution. At the end of the paper, we quickly present a Bayesian approach to hit-rate comparison, and also a Hierarchical model, which attempts to take some account of the possibility that hit rates vary day by day due to external factors beyond simply the prediction algorithm in use.

1.2 Computing environment

This paper grew out of our work to provide an open source implementation of different crime prediction methods, in the Python programming language. The prediction algorithms used later in the paper, and all of the comparison methods discussed in this paper, are implemented in the open_cp package [24].

1.3 Acknowledgements

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2 How to compare a forecast to reality

We are in an unusual situation, compared to many spatial data studies: our "predictions" are deliberately considered as being atheoretical, not based upon any one given statistical model, and the "reality" we wish to compare to forms a sparse, stochastic point pattern. That is, we are trying to predict where a small number of random events will occur, where the probability of such events is rather small.

Our situation seems to differ from much of the literature in quantitative geography. It is still common to aggregate data up to large administrative areas (which runs the risk of the ecological fallacy) or to large regular grids (which runs the risk of the modifiable areal unit problem), see criticism in [8, 28]. A more serious problem for us is that we simply do not have enough data from "reality" to form a sensible map- almost all grid cells would be empty of data. Similar problems apply to kernel density estimation (although we do pursue this below). Once we have formed a map, there is then the problem of comparing the "prediction" map to the "reality" map. One can of course apply various standard tests (correlation tests, conversion to categories and then computing e.g. the Kappa statistic, [14]) but this would seem to completely ignore the fact that we are making a *probabilistic* prediction/forecast.

Let us think more about what we are trying to predict. We will assume that the "validation period" (typically one day) is sufficiently short that the locations of crime events in that time can be well modelled by an inhomogeneous Poisson process, with an unknown intensity. See for example [3, Chapter 8], [22, Chapter 3] or [11, Chapter 8]. Over a longer time period, there are highly likely to be feedback mechanisms giving rise to a process having dependence on its history—this is, after all, what most prediction algorithms attempt to capture.

Let the study region be Ω , a subset of the plane \mathbb{R}^2 . Typically Ω will be a grid intersected with a geographical outline, see for example Figure 9. An *inhomogeneous Poisson process* with an intensity function $\lambda: \Omega \to (0,\infty)$ is a random selection of points $(x_i)_{i=1}^N$ such that:

• for each (measurable) subset $U \subseteq \Omega$ let N(U) be the number of points which occur in U. Then N(U) is distributed as a Poission distribution with parameter $\lambda_U = \int_U \lambda$. That is,

$$\mathbb{P}(N(U) = k) = \frac{\lambda_U^k}{k!} e^{-\lambda_U} \qquad (k = 0, 1, 2, \cdots).$$

• For disjoint sets U_1, \dots, U_j the random variables $N(U_1), \dots, N(U_j)$ are independent.

In particular, with $\mu = \int_{\Omega} \lambda$, we see that the total number of events N is distributed as a Poisson distribution with parameter μ , and so $\mathbb{E}(N) = \mu$. It is common to define $f = \lambda/\mu$ so that f is a probability density function on Ω , governing the relative probability of seeing an event as location varies across Ω , and μ is the *total rate*, governing the expected number of events seen.

This gives us a way to *simulate* an inhomogeneous Poisson process. We first draw N from a Poisson distribution of parameter μ , and then, independently, decide upon the locations $(x_i)_{i=1}^N$ from the density f.

For us, μ will be small number, around 5–10. None of the prediction methods we are interested in attempt to estimate μ , and so we shall treat it as a "hidden variable" or a "nuisance parameter". We do not have

access to f, but only a "sample" or "realiation" of the process, namely the points $(x_i)_{i=1}^N$.

We shall consider a prediction as a "best guess estimate" of the unknown f. A little care is required here, as some prediction algorithms aim only to give a "relative" notion of risk, which we can think of as an indication that f(x) is greater than f(y), for given locations x, y, but without information as to the absolute value of f(x) or f(y). We will return to this issue below.[1]

We shall work exclusively with grids, assuming that f is continuous, so that it can be arbitrarily well approximated by taking a sufficiently fine grid. For the moment, we assume that each grid cell is of equal area A_{cell} . Let the grid cells be $(C_k)_{k=1}^K$ so that the C_k are pairwise disjoint and cover Ω . The probability that an event occurs in C_k is then just

$$p_k = \int_{C_k} f.$$

That is, the cell into which an event falls follows a categorical distribution. By independence, conditioned upon N, the probability of seeing n_k events in the cell C_k hence follows a multinomial distribution,

$$\mathbb{P}((n_k)|N = \sum_k n_k) = \frac{N!}{n_1! \cdots n_K!} \prod_{k=1}^K p_k^{n_k}.$$

See for example [17]. Thus our task can be summarised by saying that our prediction algorithm gives an estimate of the values (p_k) , we then observe (n_k) , and we wish to assess how good the estimate was.

Essential to this analysis is the independence assumption. Being interested in e.g. burglary crime, we think of criminals as agents who make decisions, and respond to e.g. perceived risk. As such, perhaps it is not entirely reasonable to say that the risk of crime in two adjoining areas is independent– perhaps any burglary event tomorrow is likely to be down to one individual, who might, say, burgle at most just one property, viewing more action as too risky. If there were a number of burglars all operating a similar strategy in overlapping regions, we would find that knowledge that a burglary did occur in one region does tell us something about the risk in an adjoining region. We note, however, that none of the prediction algorithms even begin to try to predict such dependence. As such, while the model of an inhomogeneous Poisson process may be at best a simplification of reality, it does seem to be the model underlying all predictions. Nevertheless, we will consider "multi-scale" techniques below, which attempt to capture dependence between spatial regions.

3 The assessment methods

In this section we describe the assessment techniques we shall study.

3.1 Hit rate

We pick a "coverage level", say 10%, and select this fraction of the grid cells, picking the most "risky" cells, according to the prediction. We say that an event x_i is "captured" if the event falls into one of the selected grid cells. We report the "hit rate", which is the fraction of captured events. This is by far the most common technique in the literature, [4], [15, page 20], [1, Section 3.1], [21, Section 5]. Clearly the hit rate will increase monotonically with the coverage level. As such, it is important to standardise the coverage level to, say, either select by area covered, or to scale the hit rate by area covered (leading to the "predictive accuracy index", see [9]).

The hit rate has an obvious interpretation, is easy to explain to an end user of the algorithm, and seems to directly capture what we care about most—namely, finding the areas where crime will occur. A drawback is that it gives a range of values, one hit rate for each coverage level. Often a realistic coverage level might be more dictated by operational policing concerns than anything else. There is hence a risk of conflating the formation of "hot spots" (or more broadly, the production of something like a "patrol plan", for practical use, from a prediction) with the assessment of the prediction itself.

A variation on the hit rate is the Prediction Accuracy Index (PAI) which is defined, [1, 9], as the hit rate divided by the coverage level. As [19] notes, this is equivalently the density of crime events in the "hot spot" divided by the density of crime events in the whole area. The PAI still depends upon the chosen coverage level, and once the coverage level is fixed, the PAI and the hit rate are proportional. We thus choose to work just with hit rates (and vary the coverage level).

3.2 Rank ordering

In [5] the authors take a prediction $f: \Omega \to [0, \infty)$, converted to a grid prediction $(p_k)_{k=1}^K$ as above, and convert this to a "percentile" distribution,

$$p_k' = \frac{1}{K} \sum_{i=1}^{K} \left[p_k \ge p_i \right],$$

where $[\cdot]$ is the Iverson bracket. That is, p'_k is the fraction of the grid cells which have value at most p_k ; so $p'_k = 1$ when k is the "most risky cell".

Given actual events $(x_i)_{i=1}^N$ we consider the values $(a_i)_{i=1}^N \subseteq (0,1]$ given by $a_i = p'_k$ for the k such that x_i is in cell C_k . The authors then work directly with the values (a_i) . For example,

- Compute a summary statistic, such as the mean $\frac{1}{N} \sum_{i=1}^{N} a_i$;
- Given two predictions $(p_k^{(1)})$ and $(p_k^{(2)})$, we form $(a_i^{(1)})$ and $(a_i^{(2)})$, and then compare these sequences, e.g. by looking at the statistic

$$\delta = \frac{1}{N} \sum_{i=1}^{N} \left[a_i^{(1)} > a_i^{(2)} \right].$$

¹Where? Do we??

The authors use a z-test with these statistics, but we are not certain that this is entirely appropriate—is it reasonable to suppose that the (a_i) are uncorrelated with common mean and variance, of a large enough sample size?

An advantage of this method is that it explicitly recognises that the prediction method may not assign a consistent probability to each grid cell, but rather may just give a relative estimate of how risky one grid cell is compared to another. This method is related to the hit rate method, but has the advantage of not requiring the specification of a "coverage".

Notice that the rank ordering "rounds up": if there are two (or more) grid cells with the exact same p_k value, then p'_k will be rounded up. The hit rate, in particular, does not deal well with exact repeats of p_k , as this leads to situations where for certain coverage levels, there is no unique selection of cells with the "greatest" risk. For this paper, we will always add a very small amount of noise to our predictions to ensure that each p_k is unique, while also making sure that we do not alter the ranking, except to break ties. (This is not always possible, due to finite floating point precision, but in practise seems to work well enough; see the discussion in Section 6.) [2]

3.3 Likelihood

This technique has been used in the crime prediction literature when choosing parameters for models, [26] or [21, Section 5] where the authors write "...cross validation used to select the bandwidth".

We compute the normalised log likelihood, as

$$L = \frac{1}{N} \sum_{i=1}^{N} \log p_{k_i}$$

where again, k_i is the cell containing x_i , namely $x_i \in C_{k_i}$, for each i.

Assuming our inhomogeneous Poission model, conditioned on N, the likelihood of seeing $(x_i)_{i=1}^N$ is exactly $\prod_{i=1}^N f(x_i)$ which is approximated by $\prod_{i=1}^N p_{k_i}$. We have normalised L as a slightly ad hoc way of removing the condition upon N.

L takes explicit account of the actual values of (p_k) , and not just their ordering. As such, it should reward predictions which attempt to make an accurate assessment of the probabilities. On the other hand, notice that values of (p_k) where events do not occur play no part in L.

3.4 Kernel density estimation

In [12], in the context of Biology, the authors propose using a (fixed bandwidth, Gaussian kernel based) kernel density estimation (KDE) to compare point patterns. Once we have kernel estimates, the squared error (L^2 distance) can be computed. In this context, some analytic simplifications occur, and the authors of

[12] use these to find suitable p-values for hypothesis testing.

In our case, we already have a prediction, and we use the KDE technique on the real events (x_i) to obtain a density function $g:\Omega\to [0,\infty)$. We then integrate this over each grid cell to obtain $(g_k)_{k=1}^K$ say. We can then estimate

$$\int_{\Omega} |f - g|^2 \approx A_{\text{cell}} \sum_{k=1}^{K} |p_k - g_k|^2.$$

When forming the KDE for g, we take account of edge effects, following [18]. For grid regions, the computational techniques in [18] yield an acceptably fast algorithm.

A critical issue with KDE methods is the choice of bandwidth. For us, we already have an issue as standard "plug-in" choices of bandwidth need at least 3 data points, and we do not always have this many points available. In our study, we will limit to cases where there are at least 3 events, and will mostly use a fixed bandwidth.

Despite these difficulties, the KDE method has a clear advantage of using the exact coordinates of the events. Varying the bandwidth can be compared with multi-scale methods to be discussed below.

3.5 Scoring rules

We proceed by analogy with the notion of a "probability forecast" in meterology, [16, Chapter 7]. A genuine probability forecast is of the form "tomorrow there is a 40% chance of rain in Leeds". This carries two key pieces of information:

- The "reliability" of the forecast. Over a long run of such "40% chance of rain" predictions, it should indeed rain around 4 in 10 times the next day.
- The "resolution" of the forecast. Suppose in Leeds that it actually rains around 4 in 10 days each year. Then a constant prediction of 40% chance of rain would be reliable, but useless as a forecast. The resolution of a forecast measures the ability of a forecast to separate cases which are more or less likely than the long term average.

To adapt this framework to our setting seems difficult. Even assuming independence of each grid location (which is seemingly assumed in e.g. [16, Section 7.3.1]) our forecasts are not "probability forecasts" in this sense, as our forecasts give no indication of the overall rate of crime (a perfectly reliable forecast, in the above sense, carries information on the average rate of the event in question).

Instead we follow an idea from [25] and work with the *Fractional Brier Score*. This is a multi-scale method (compare [10]) but we first describe it at the first level. Define

$$F = \frac{1}{K} \sum_{k=1}^{K} \left(p_k - \frac{n_K}{N} \right)^2,$$

²Check we do discuss this!

where recall that n_k is the number of actual events we see in cell C_k . We can compare this with the worst possible score,

$$F_{\text{worst}} = \frac{1}{K} \sum_{k=1}^{K} p_k^2 + \frac{1}{KN^2} \sum_{k=1}^{K} n_K^2,$$

which leads to the Fractional Brief Skill Score,

$$F_S = 1 - \frac{F}{F_{\text{worst}}} = \frac{\frac{2}{N} \sum p_k n_k}{\sum p_k^2 + \frac{1}{N^2} \sum n_k^2}.$$

Then $F_S \in [0,1]$ and the closer to 1, the better the forecast.

This becomes a multi-scale method when we start to aggregate cells. At the nth level, we look at a moving window of size $n \times n$ cells, and compute the average of (p_k) and (n_k/N) over these cells. If we started with a rectangular array of size $K_1 \times K_2$ we will now have a derived array of size $(K_1 - n + 1) \times (K_2 - n + 1)$, from which we recompute F_S as above.

We typically work with a grid of cells which is not rectangular (having been clipped to some geographical region, compare Figure 25). In such a case, we need to be careful about appropriate normalisations and edge effects. Suppose we have grouped the original cells into (in general, overlapping) regions $(C'_k)_{k=1}^{K'}$, and then the sum (not average) of the (p_k) over each region is $(p'_k)_{k=1}^{K'}$; similarly for (n_k/N) leading to $(q'_k)_{k=1}^{K'}$. We now want to compute F_S as if these regions actually were disjoint. An appropriate normalisation is then to define

$$p_k^{\prime\prime} = \Big(\sum_{\mathbf{k}} p_k^\prime\Big) p_k^\prime, \quad q_k^{\prime\prime} = \Big(\sum_{\mathbf{k}} q_k^\prime\Big) q_k^\prime.$$

Then, taking account of area, we define

$$F' = \Big(\sum_{k} |C_k'|\Big)^{-1} \sum_{k} |C_k'| (p_k'' - q_k'')^2,$$

where $|C_k'|$ denotes the area of C_k' , and similarly for F_{worst}' hence leading to F_S' .

Notice that F is very closely related to the squared error calculation for the KDE method, when the bandwidth chosen for the KDE is very small. Similarly, F' is related to the KDE method with increasing bandwidth.

An alternative to the fractional score is to regard "the number of crime events which occurred in a given grid cell" as a "continuous" prediction, and then use known methods to score such a prediction, [16, Section 7.5.2]. Our idea here is to scale the prediction (p_k) by N, the observed number of events, and then to model the "predicted" number of events in C_k as being Poisson distributed with mean Np_k . Then the cumulative density function of our prediction becomes

$$F(x) = \mathbb{P}(\operatorname{Pois}(Np_k) \le x) = \sum_{i=0}^{\lfloor x \rfloor} \frac{(Np_k)^i}{i!} e^{-Np_k},$$

where $\lfloor \cdot \rfloor$ is the floor function. If the observed count is n then, following [16, Section 7.5.2], the *continuous ranked probability score* is

$$\int_0^n F(x)^2 \ dx + \int_r^\infty (F(x) - 1)^2 \ dx.$$

For our F this becomes the infinite sum

$$\begin{split} \sum_{j=0}^{n-1} & \Big(\sum_{i=0}^{j} \frac{(Np_k)^i}{i!} e^{-Np_k} \Big)^2 \\ & + \sum_{i=n}^{\infty} \Big(1 - \sum_{i=0}^{j} \frac{(Np_k)^i}{i!} e^{-Np_k} \Big)^2. \end{split}$$

As the sum over i converges quite rapidly to 1, as j gets large, in practise we can very well approximate this with a finite sum.

3.6 Bayesian inference and information theoretic ideas

Imagine in our setup that for a given day, we observe no actual crime events. In that case, (and unlike in strict probabilistic forecasting) we can say nothing about our prediction. If we observed one event, we might feel we can say a little about the prediction. And if we observed, say, 100 events, we would feel that for the prediction to be "good", we would want a close match. That is, intuitively, we feel that as N increases, we gain more information about the real distribution of crime, and so more sense as to whether our prediction is good or not. None of the above techniques have any such dependence on N, so we know turn our attention to ideas from Bayesian inference and information theory, [13, 20].

We have been modelling the total number of events observed, $N = \sum n_k$, as a Poisson distribution with unknown mean. The combined probability of seeing counts $n = (n_k)_{k=1}^K$ from events $x = (x_i)_{i=1}^N$ is

$$p(n) = \frac{\mu^N e^{-\mu}}{N!} \frac{N!}{\prod_k n_k!} \prod_k p_k^{n_k} = p_1(N) p_2(n),$$

say, where $n=(n_k)$. Working in a Bayesian inference framework, suppose that $p_1(N)=p_1(N|\mu)$ depends upon a parameter μ ; note also that $p_2(n)=p_2(n|p)$ depends on the parameter vector $p=(p_k)$. Let μ have prior distribution $f_0(\mu)$, and similarly let p have prior distribution $f_1(p)$. We wish to know p(p|n) the posterior distribution of p given the data n. We can integrate out the unknown μ ,

$$p(p|n) = \int p(p, \mu|n) \ d\mu.$$

By Bayes' Theorem this is proportional to

$$\int p(n|p,\mu)p(p,\mu) d\mu$$

$$= \int p(n|p,\mu)f_1(p)f_0(\mu) d\mu$$

$$= \int p_1(N|\mu)p_2(n|p,N)f_1(p)f_0(\mu) d\mu$$

$$= p_2(n|p,N)f_1(p) \int p_1(N|\mu)f_0(\mu) d\mu$$

$$\propto p_2(n|p,N)f_1(p) \int p_1(\mu|N) d\mu$$

again by Bayes' Theorem. As p_1 is a probability density, we find that

$$p(p|n) \propto p_2(n|p, N)p(p),$$

so there is no dependence on the prior we chose for μ . We now consider a suitable prior for (p_k) . As (n_k) follows a multinomial distribution, it is natural to use a Dirichlet distribution for (p_k) , see [13, Section 3.5], as this is a conjugate prior. The Dirichlet distribution is parametrised by $(\alpha_k)_{k=1}^K$ strictly positive numbers, and

$$p((p_k)|(\alpha_k)) = \frac{1}{B(\alpha)} \prod_{k=1}^{K} p_k^{\alpha_k - 1},$$

where $B(\alpha) = \prod_k \Gamma(\alpha_k)/\Gamma(\alpha_0)$ is the normalising factor, with $\Gamma(\cdot)$ the Gamma function, and $\alpha_0 = \sum_{k=1}^K \alpha_k$. Given this prior, the posterior is also a Dirichlet distribution, with parameters $(\alpha_k + n_k)_{k=1}^N$. We can therefore think of the α_k as "pseudo-counts", representing the number of counts we have "already seen".

In our setting, we are actually given definite values of (p_k) from our prediction algorithm, say (\hat{p}_k) to distinguish from the random variables (p_k) above. We shall set $\alpha_k = t\hat{p}_k$ for some t>0, which we think of governing our "confidence" in the prediction. A larger t means that the prior has more weight than the data; whereas a very small value of t lets the data dominate the posterior. Under this prior,

$$\mathbb{E}(p_k) = \hat{p}_k, \quad \text{Var}(p_k) = \frac{\hat{p}_k(1 - \hat{p}_k)}{t + 1}.$$

To further illustrate this, consider the posterior predictive distribution, [13, Chapter 1]. Our posterior is a distribution on (p_k) , and each value of (p_k) gives a multinomial distribution. By marginalising out (p_k) we obtain the posterior predictive distribution, which in this case is a Dirichlet-multinomial distribution, which gives a (complicated) distribution of possible event counts (\tilde{n}_k) subject to $\sum_k \tilde{n}_k = \tilde{N}$. If we fix $\tilde{N} = 1$ (and so effectively look at just the relative chance of a single event occurring in each grid cell) we obtain the categorical distribution, the same as a multinomial with sample size 1. That is, the probability of picking cell C_k is β_k , where (β_k) is a probability vector. In our setting, the posterior predictive distribution has

$$\beta_k = \frac{\alpha_k + n_k}{\alpha_0 + N} = \frac{t\hat{p}_k + n_k}{t + N},$$

whereas the *prior* predictive distribution has

$$\beta_k = \frac{\alpha_k}{\alpha_0} = \hat{p}_k.$$

If t is very large, then $(t\hat{p}_k+n_k)/(t+N)\approx\hat{p}_k$ regardless of the values of n_k , while as $t\to 0$, the posterior will limit to the categorical distribution with probabilities n_k/N .

In summary then:

- We start with a prior distribution which is influenced by our prediction; a Dirichlet distribution parametrised by $\alpha_k = t\hat{p}_k$;
- We observe the actual event counts (n_k) ;
- We form the posterior distribution, which is a Dirichlet parametrised by $\alpha_k = t\hat{p}_k + n_k$.

To assess the prediction, we wish to compare the prior and posterior distributions.

To compare distributions, we shall use the Kullback-Leibler divergence, [6, Section 2.1]. Given the prior distribution Q and the posterior P, the Kullback-Leibler divergence $D_{KL}(P||Q)$ measures the information lost when Q is used to approximate P. By definition,

$$D_{KL}(P||Q) = \int p(x) \log(p(x)/q(x)) \ dx,$$

where P, Q have densities p, q, respectively.

We shall start by comparing the Dirichlet prior and posteriors. This is computationally messy, see Appendix B.

An easier computation is to compare the prior and posterior predictive distributions, again in the form of categorical distributions. Here

$$D_{KL}(P||Q) = \sum_{k=1}^{K} \frac{t\hat{p}_k + n_k}{t + N} \log\left(\frac{t + n_k/\hat{p}_k}{t + N}\right)$$
$$= \sum_{k=1}^{K} \frac{\hat{p}_k + q_k N/t}{1 + N/t} \log\left(\frac{1 + (q_k/\hat{p}_k)(N/t)}{1 + N/t}\right),$$

where $q_k = n_k/N$. Let s = 1/(1+N/t) so that 1-s = (N/t)/(1+N/t), and so

$$D_{KL}(P||Q) = \sum_{k=1}^{K} \left(s\hat{p}_k + (1-s)q_k \right) \log \left(\frac{s\hat{p}_k + (1-s)q_k}{\hat{p}_k} \right).$$

So we are linearly interpolating between \hat{p}_k and q_k , with parameter s. The KL divergence is also known as the relative entropy, [20], and the above sum can be understood in this way. The log term measures the difference between the prior and posterior estimates for the fraction of events to occur in cell k (e.g. if $\hat{p}_k = q_k$ then we obtain $\log(1) = 0$). We then weight these by the posterior probability of an event occurring in that cell (meaning, for example, that the prediction is allowed to be less accurate is a low probability region).

It hence seems reasonable to fix s; say s = 1/2 perhaps, equivalently t = N. Notice that in practice N is random, and so we might take t to be the mean of N. If N is larger than average, then s will be smaller, and so we will put more weight on q_k , i.e. the data, over the prediction. This is as we had hoped, in the introduction to this section. The KL divergence for the Dirichlet prior and posterior, Appendix B, is (seemingly) not parameterised by s, but by analogy we shall also take t to be the average value of N.

4 A toy model

Let us suppose that our grid is so coarse that we actually have only two grid cells, labelled H and T, of equal size. Any prediction is simply an assignment of two non-negative numbers, one to each cell, where a larger number is meant to indicate greater risk of a crime event. By rescaling, we may suppose that we have a probability distribution, say assigning probability p to cell H, and probability q = 1 - p to cell T. We should note that not all prediction algorithms are necessarily designed to report consistent probabilities.

The "reality" with which to compare our prediction to is the crime events which occur in the next day (or other time period). In this model, we obtain two counts, the number of events which occurred in cell H, say n_H , and the count in T, say n_T . Set $N = n_H + n_T$.

As a thought experiment (and often via computational experiments) we consider the following. We fix a real probability $p_{\rm r}$ and $\lambda > 0$. For each trial, we simulate N as a Poisson random variable with mean λ , and then simulate n_H (with $n_T = N - n_H$) as a Binomial random variable ${\rm Bin}(N,p_{\rm r})$. For each trial, we see how the proposed assessment method scores a prediction with value p. We hence have three variables, $\lambda, p, p_{\rm r}$, and we wish to see how the methods capture p being close to $p_{\rm r}$ (or not) and what effect increasing λ (which should increase our confidence in assessing a prediction) has on the result.

4.1 Hit rate

There is only one coverage level to consider: 50%. This will select H if and only if p > 1/2, and in such a case, we obtain the hit rate n_H/N . Thus there is a rather crude dependance on p. This could be seen as an advantage, however, if our prediction method doesn't aim to assign exact probabilities, but only a relative risk ranking.

If we perform our simulation study, then by symmetry, we can restrict to the case p > 1/2. The expected

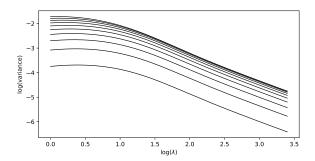


Figure 1: Variance in hit rate for the toy model, on a log-log scale. We plot $p_{\rm real} = 0.05, 0.1, 0.15, \cdots, 0.5$. Variance decreases monotonically with $p_{\rm real}$.

hit rate is

$$\begin{split} \mathbb{E}\frac{n_H}{N} &= \sum_{N \geq 1, 0 \leq n_H \leq N} \frac{n_H}{N} \mathbb{P}(N) \mathbb{P}(n_H|N) \\ &= \sum_{N \geq 1} \frac{1}{N} \mathbb{P}(N) \sum_{0 \leq n_H \leq N} n_H \mathbb{P}(n_H|N) \\ &= \sum_{N \geq 1} \frac{1}{N} \mathbb{P}(N) \mathbb{E}(n_H|N) = \sum_{N \geq 1} \frac{1}{N} \mathbb{P}(N) Np \\ &= p \sum_{N \geq 1} \mathbb{P}(N) = p(1 - e^{-\lambda}). \end{split}$$

We limit to $N \geq 1$ as we cannot perform an evaluation with no events. Thus for λ not too small, the expected hit rate is close to p. Thus here the hit rate tells us about the underlying random process but not the prediction.

The variance is harder to calculate analytically, see Figure 1.

4.2 Rank ordering

When p > q, we have p' = 1, q' = 1/2, and so $a_i = 1$ for n_H cases, and 1/2 for n_T cases. (When p = q we have that $a_i = 1$ for all i, though here this is an uninteresting silly case.) The mean rank is then

$$\frac{1}{N} \Big(n_H + \frac{1}{2} (N - n_H) \Big) = \frac{n_H}{2N} + \frac{1}{2},$$

so directly proportional to the hitrate.

The only interesting cases of comparing predictions is when one prediction has p>q and the other p<q. The first prediction will have $(a_i)=(1,\cdots,1,\frac{1}{2},\cdots,\frac{1}{2})$, where 1 occurs n_H times, and the second will have $(a_i)=(\frac{1}{2},\cdots,\frac{1}{2},1,\cdots,1)$ where now the $\frac{1}{2}$ occurs n_H times. Thus $\delta=\frac{n_H}{N}$ which is, again, just the hit rate.

4.3 Likelihood

We calculate that

$$L = \frac{1}{N} (n_H \log p + n_T \log q).$$

For the simulation, the expectation is

$$(1 - e^{-\lambda})(p_{\text{real}}\log(p) + (1 - p_{\text{real}})\log(1 - p)).$$

Notice from this, and the form of L, then as p gets closer to 1/2 we learn less; indeed, if p = 1/2 then $L = \log(1/2)$ constantly.

The value of p which maximises the likelihood is n_H/N . However, notice that if p is fixed, say p>1/2, then as $\log(p)>\log(1-p)$ we have that L is maximal when $n_H=N$. Some care is hence required when interpretting L. See Figure 2 for examples. Here for each plot we fix our prediction p and plot results as $p_{\rm real}$ varies. We use the same scale on each plot; the plots would all look alike if we chose the natural scale for each one.

As $\lambda = \mathbb{E}(N)$ increases, the variance decreases, in a very similar way to the hit rate.

4.4 Kernel density estimation

To explore this properly, we would have to specify coordinates for our events. The end result, however, will be to "mix" the events which fall in H with those that fall in T. In our simulation study, we use a grid of size 10×10 units, and assign points uniformly at random in each cell. We cannot use the "plug-in" bandwidth estimator, as occasionally, for small values of N, the bandwidth ends up being so small that our monte carlo integration method assigns 0 risk to both cells.

The result of the KDE, following by intergration over the grid cells, is to give values g_H, g_T , which are somehow "averaged" versions of n_H/N and n_T/N . As we have a probability distribution, $g_T = 1 - g_H$, and so the score is (up to some constant reflecting the area of the grid)

$$|p - g_H|^2 + |q - g_T|^2 = 2|p - g_H|^2$$
.

The results for bandwidths of 1/2 grid cell width, and 2 grid cell widths is show in Figure 3. The larger bandwidth behaves much like the likelihood, but the smaller bandwidth shows more interesting behaviour, in that the smallest ("best") score does now occur approximately when $p=p_{\rm real}$.

Increasing λ again leads to smaller variance, but no change in the overall shape of the result.

4.5 Scoring rules

There is only one scale to consider here, that of not aggregating the cells together. The fractional Brier score, F, is the same as the KDE score when we use a very small bandwidth, namely,

$$F = \left(p - \frac{n_H}{N}\right)^2,$$

and results are similar to the top row of Figure 3. The skill score is interesting, see Figure 4, in that the plots are very similar, if we imagine them as "windows" onto a symmetric plot of width 2, each plot being centred on $p = p_{\rm real}$. Unlike the scores we have seen so far, it

hence makes sense to directly compare the *score* for any choice of p and p_{real} . As before, increasing $\lambda = \mathbb{E}(N)$ again leads to smaller variance, but no change in the overall shape of the result.

For our Poisson model, a closed form does not exist. The simulation study, Figure 5, gives results similar to the skill score. Increasing λ here increases the value of the score, but if normalised, see Figure 6, has the effect of both decreasing the variance, and of increasing the score when p and $p_{\rm real}$ differ. We will see shortly that the KL divergence score for the Dirichlet prior behaves in a similar way.

4.6 Information

For the Dirichlet prior and posterior see Figure 7, and for the divergence between the predictive distributions, see Figure 8. In both cases we have run our experiment twice, once with $\mathbb{E}(N)=10$ and then again with $\mathbb{E}(N)=50$. Motivated by our analysis in Section 3.6, we have set $t=\mathbb{E}(N)$ in all cases. For the predictive distributions, as we expected from our analysis in Section 3.6, we see that the resulting curves are very similar, but when $\mathbb{E}(N)=50$ we have a smaller variance. For the Dirichlet distribution case, the curves agree when $p_{\rm real}=p$ but as $\mathbb{E}(N)$ increases, both the variance decreases, and the absolute score increases. This is somewhat as expected, because we had hoped that given "more evidence", i.e. a larger N, we would expected a "worse" score if p and $p_{\rm real}$ differ.

In both cases, this scoring method seems to capture well when $p_{\rm real}$ is close to p. Furthermore, the value of the scoring method seems to have a good absolute interpretation, correlating well with distance between $p_{\rm real}$ and p (that is, like the Poisson based Continuous Brier Skill score, and unlike the likelihood, for example).

4.7 Conclusions

The hit rate and the rank ordering methods are perhaps hampered by the very artifical nature of this experiment (just two grid cells), but it fails to tell us much about how p and p_{real} compare. The likelihood method, perhaps as we might expect by considering the utility of maximum likelihood techniques, allows us to estimate p_{real} well. However, as a comparison method, it does not well distinguish between p and p_{real} . The KDE method, with a *suitable* bandwidth (here, half the grid cell size) performs much better than the likelihood in distinguishing between when $p = p_{\text{real}}$ and when p and p_{real} differ. The Brier skill score, and the Poisson based CRPS, both perform well, better than the KDE method (for example, when p and p_{real} are small). The KL divergence score for the predictive distributions performs similarly well. Finally, the KL divergence score for the Dirichlet distributions also assigns a higher (that is, "worse") score to the $p \neq p_{\text{real}}$ case when $\mathbb{E}(N)$ increases; the Poisson CRPS does this as well, but only with some re-scaling.

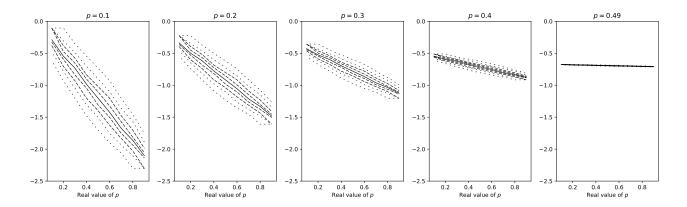


Figure 2: Distribution of values of L. For 1000 simulations with $\lambda = 10$, we plot estimates of the median (solid line), the 30, 40, 60 and 70% percentiles (dashed lines) and 10, 20, 80 and 90% percentiles (dotted lines).

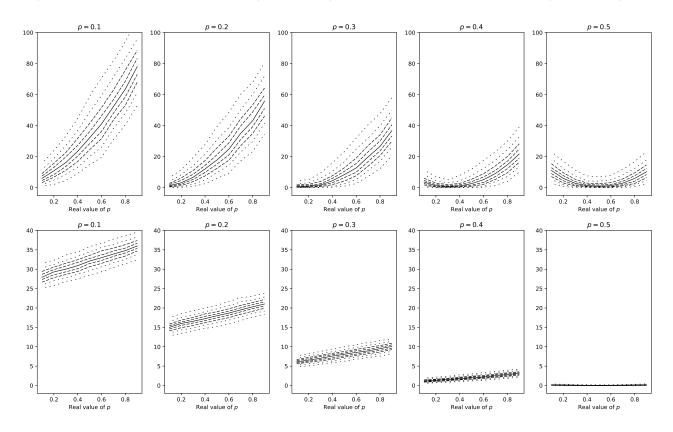


Figure 3: Distribution of values of the KDE score; otherwise as Figure 2. Top row is with a bandwidth of 1/2 grid cell width, and bottom row with a bandwidth of 2 grid cells.

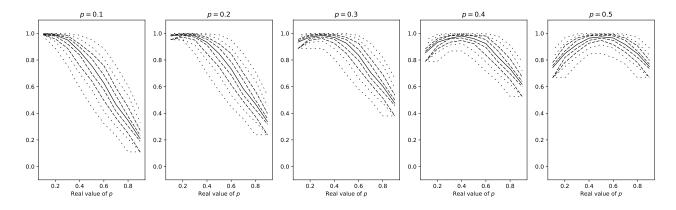


Figure 4: Distribution of values of the Brier Skill score; otherwise as Figure 2.

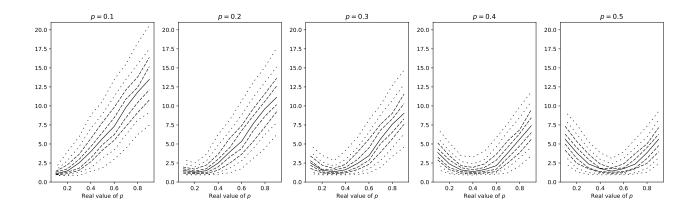


Figure 5: Distribution of values of the Poisson based Continuous Brier Skill score; otherwise as Figure 2.

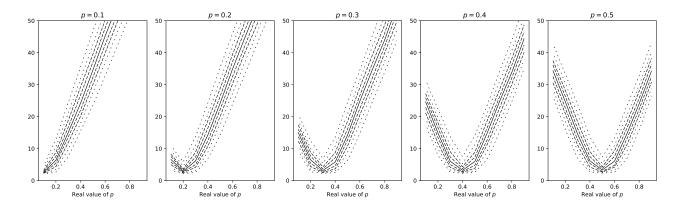


Figure 6: As Figure 5 but with $\mathbb{E}(N) = 50$ instead of 10. The y-axis scale is changed so that the minimal value is, on the plot, comparable to that in Figure 5.

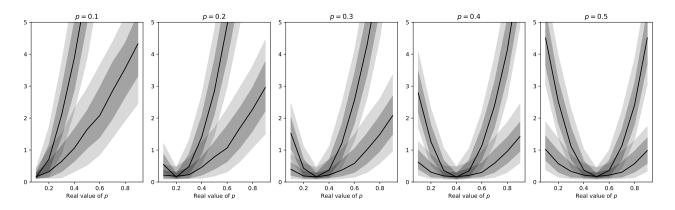


Figure 7: Distribution of values of the KL divergence for the Dirichlet prior. As Figure 2, but here the solid line shows the median values for $\mathbb{E}(N) = t = 10$ and $\mathbb{E}(N) = t = 50$, shaded area the inter-quartile range, and lightly shaded area the 10–90% region.

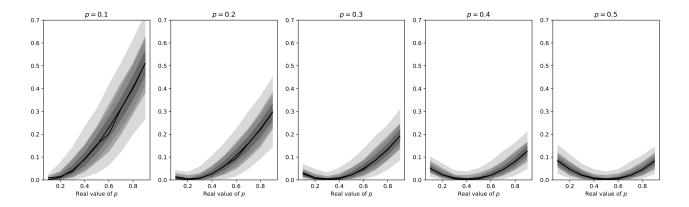
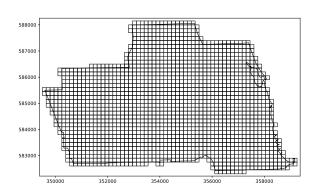


Figure 8: Distribution of values of the KL divergence for the predictive posterior and prior; otherwise as Figure 7.



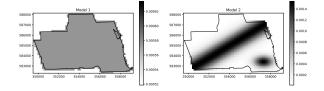


Figure 10: Intensity (value of p_k) for the two models.

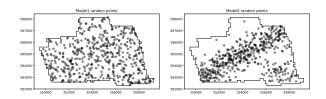


Figure 9: The grid we use for making predictions, over- Figure 11: 500 points drawn at random from each model. layed on the North Side of Chicago.

5 Comparison with artificial data

We now look at our comparison methods by using a "real" geometry with some artifical data. We will use the outline of the North Side of Chicago, with a grid size of 150m square. We include any grid square which intersects with the outline of the geographic area, see Figure 9.

We will compare two models:

1. Complete spatial randomness, that is, a homogeneous Poisson process. This is equivalent to setting $p_k = 1/K$ for all k. When making a prediction, we add to each p_k a uniformly random number between 0 and 10^{-7} , and then renormalise. Some algorithms (e.g. selecting 10% coverage) do not cope well with many cells having exactly equal p_k values.

2. An inhomogeneous Poisson process. We linearly scale the rectangle containing the grid to $[0,1]^2$, and use the intensity

$$f(x,y) = \frac{1}{100} + \exp\left(-30(x-y)^2\right) + \exp\left(-100\left((x-\frac{8}{10})^2 + (y-\frac{2}{10})^2\right)\right).$$

We evaluate f at the mid-point of each cell C_k , and then normalise so that the resulting (p_k) sums to 1. The fraction 1/100 ensures that $p_k > 0$ for all k.

See Figure 10 for a visualisation of these intensities, and see Figure 11 for example samples of points (500 in each case) from the model. As an exercise, it's worth thinking about what the corresponds plots would look like for, say, 10 points, and whether you could distinguish them by eye.

For each model, we select N from a Poisson distribution with mean 10 (which is the same order of magnitude as the real data used in Section 6) and then select N points according to the intensity given by the model. This forms our collection of crime events which we then compare with the prediction made from the models.

5.1 What we hope to learn

There are two things we wish to learn from an "assessment method":

- Is the prediction algorithm "good"?
- Given two or more prediction algorithms, which is "better"?

We can often reduce the question of comparing multiple algorithms to simply comparing their scores given by an assessment method.

In our experiment, we generate trial data from both models, and then make predictions from both models, leading to four experiments in total, for each prediction method. Notice that as we have complete control over the statistical process which leads to the trial data, it is impossible to "predict" better than the generating model from which the data is actually drawn.

We have two graphical ways of comparing the results:

• A scatter plot. For each trial, we compute the "score" from the assessment method for the two predictions, and plot these. We also look at the marginal distributions and plot estimated densities for these. A method which is good at discrimiating the models will have most of the trails scattered at one side of the line of equality. A method which has a tightly peaked marginal distribution gives us confidence that looking at the score alone will tell us if the assessment is "good"; a flat distribution suggests that we will have a harder time spotting outliers.

For example, see Figure 14. Here there are two scatter plots, one for each generating model (the model from which samples of events are taken from). For each trial, we compute the score (in this example, the hit rate at 20% coverage) for the two predictions, and plot a point.

• The empirical "cumulative density" from the tri-For each trial, we look at the difference between the scores from the assessment method, and then we compute the cumulative density from these. For example, Figure 13 shows that with events generated from Model 1, the solid line, around 20% of the time, both predictions give the same score. That the density appears symmetric suggests (correctly, in this case) that this assessment method does not discriminate well between the predictions.

5.2Hit rate

It is usual (compare [1, 26, 21]) to present a graph Model 1 assigns the same probability to each cell, and of coverage level against hit rate, or if predictions are so the likelihood is always the same, and hence the

made for many (say) days, to report the mean hit rate. [21] also gives the standard error. Figure 12 shows such a curve, together with the 25% and 75% quartiles. We note immediately some curious features of the hit rate. If the crime events are actually distributed at random (from model 1) then it doesn't matter which cells we flag for attention: on average we expect to see x fraction of the events if we flag x fraction of the area.

Similarly, if we flag x fraction of the cells at random, then it doesn't matter how the events are distributed, on average we will see x fraction of the events; see Appendix A for a proof.

Finally, we note that when model 2 is used to predict data from itself, the curve is super-linear. This is to be expected, as the top, say, 20\% of cells account for much more intensity that the bottom 20% of cells.

We are also interested in directly comparing the "score" different predictions assign to a given instance of simulated crime events. To do this, we fix coverage at 20%, and produce plots as in Figure 13. The patterns in the scatter plots are due to the discrete nature of the score (for a small number of events, only a small number values of x can be the hit rate percentage). The estimated densities show that, as expected, for data from model 1, both predictions perform the same, on average. For data from model 2, the prediction from model 2 leads to a higher hit-rate, but there is a large variance.

The CDF plot shows that for model 1 there is no difference in the hit rate (as we know) but a large spread. For model 2, the prediction using model 2 is far superiour to randomly guessing, as we might hope.

As we change the coverage level, the plots do not qualitatively change. The distributions in the scatter plots move up and right, towards higher hitrates. The CDF plot also keeps the same shape, with model 2 increasingly outperforming model 1 at predicting data from itself.

Rank ordering 5.3

As in Section 3.2 we think of this method as being some sort of "summary" of the hit rate. The results shown in Figure 14 reflect this, in that when the events are entirely random, both predictions perform equally well, but for events sampled from model 2, the prediction from model 2 is better around 98% of the time.

The estimated densities for data from model 2 show, for example, that if we obtain an average ranking score ≥ 0.7 then it is very likely the prediction came from model 2. It is worth noting that this is not hugely different from the hit-rate, although the average ranking seems better "separated".

The " δ statistic" as in Section 3.2, see Figure 15, is similar.

5.4Likelihood

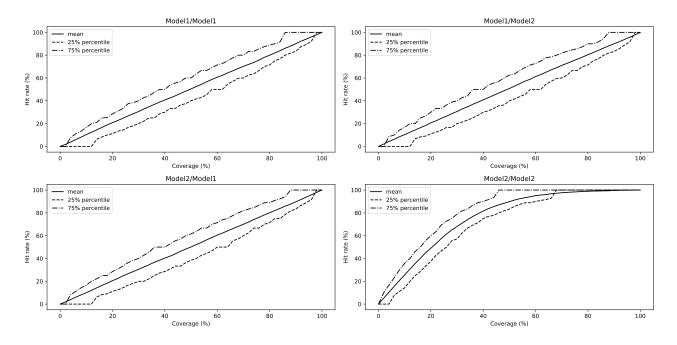


Figure 12: Coverage against hit rate. The top row shows points sampled from model 1, and the bottom row points from model 2. The left column shows predictions from model 1, and the right column predictions from model 2.

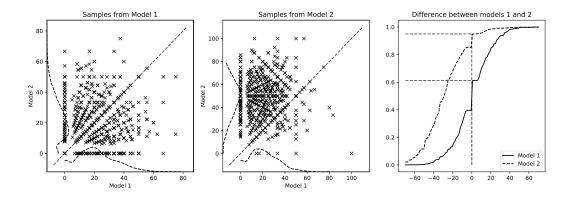


Figure 13: Hit rate for 20% coverage. See Section 5.2.

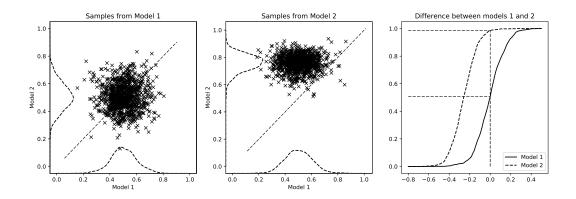


Figure 14: Mean value of ranking. See Section 5.3.

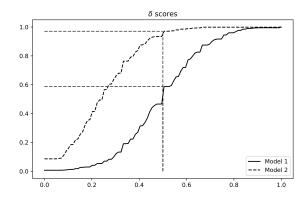


Figure 15: The δ statistic from ranking. See Section 5.3.

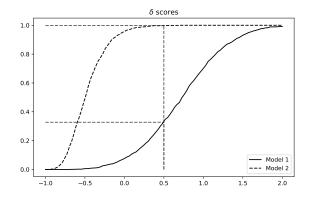


Figure 16: Likelihood. See Section 5.4.

scatter plots are not very informative here. The cumulative density plots, Figure 16, show that the models fit the data from themselves much better than the alternative model, in both cases. However, this is far more pronounced for data from model 2. The likelihood method only evaluates the prediction at points where events actually occur; thus if events occur completely at random, model 2 will be expected to assign a higher probability some of the time.

5.5 Kernel density estimation

For the kernel density estimation method we have to choose the bandwidth. One approach is simply to use a "plug-in" bandwidth estimator (which is simply a "rule of thumb", not expected to work well here due to the small sample size). The results, shown in Figure 17, are partly expected, recalling that the "score" here is squared-error, so a lower score means a better match. Thus, for data from model 1, the vast majority of trials give a "better" score to the model 1 prediction. For the data from model 2, it is a 50–50 split, which is unexpected.

If we select a fixed bandwidth (remember that this is applied to the kernel estimation from the data, which is on average only 10 points) then we see optimal distrimination at around a bandwidth of 300m (2 grid

cells), Figure 18. Notice that the scatter plots are dispersed, with the points forming a rough straight line. Hence we expect that knowing just the score from one prediction to not be terribly useful for this assessment method.

5.6 Scoring

The Brier score, Figure 19, is essentially mean squared error, and so a smaller score is "better". So the CDF plot is as we might hope. The scatter plots show a huge amount of correlation, so knowing just the score will be essentially useless.

The skill score, Figure 20, is "reversed" from the Brier score, in that a better prediction has a higher score, a score closer to 1. The skill score fails to discriminate for the data from model 1, but works very well for data from model 2. The scatter plot also shows that the raw value will be useful.

The Poisson model backed continuous ranked probability score performs much like the straight Brier score, Figure 21.

We originally introduced the Brier score in the context of a multi-scale measure. The scatter plots (not shown here) do not change qualitatively as cells are aggregated; the Brier score decreases in absolute terms, while the Skill score increases and becomes more clustered. Figure 22 shows the CDF plots at different aggregations levels (from 1 cell, so no aggregation, through to 35 cells; the study area is 39 cells high). Initially there is very little difference (the 1 cell aggregated plots are of course identical to Figures 19 and 20) but for the Brier Score we see a monotonic decrease in the discrimination between the models (which is completely expected: at a high aggreation level, model 2 will look fairly uniform, like model 1). For data from model 2, the Skill score behaves similarly, but for data from model 1, the skill score improves in its ability to discriminate up to moderate aggregation levels.

5.7 Information theoretic

We compare both the Kullback-Leibler divergence for the Dirichlet prior and posterior distributions, and for the predictive distributions. We will set t=10, as this is about the value of $\mathbb{E}(N)$, as above. The Dirichlet prior, Figure 23, shows good discrimination between the models from the CDF plot. However, the scatter plots show less separation than we might hope for. The CDF plot for the predictive distributions, Figure 24, is almost identical (except for scale), while the scatter plots are better separated.

5.8 Conclusions

The hit rate results are surprising, and essentially cannot distinguish between the models. The ranking method is useless for data from model 1, but works well for data from model 2 (either by looking at the mean ranking, or the δ statistic). The likelihood fairly well

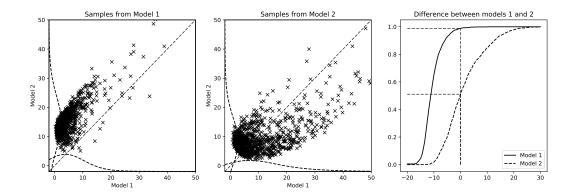


Figure 17: "Plug-in" bandwidth selection KDE. See Section 5.5.

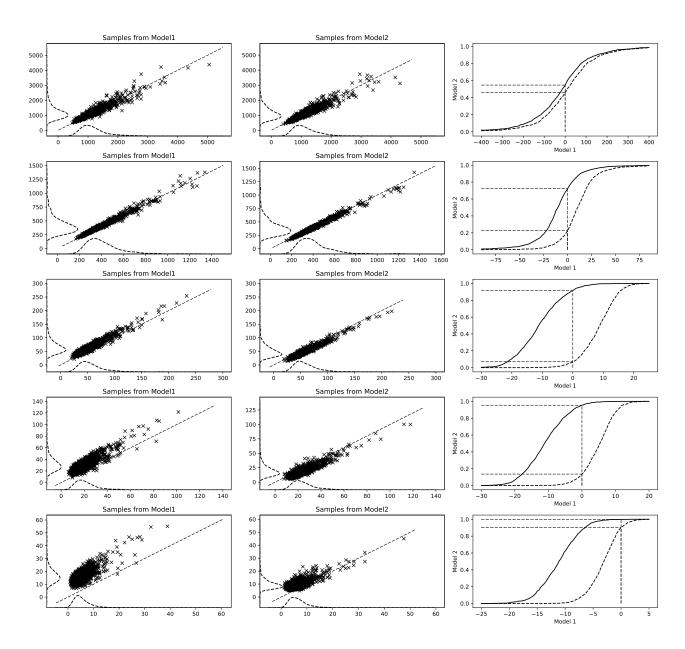


Figure 18: The KDE scoring method, with, from top to bottom, bandwidths of 50m, 100m, 300m, 500m and 1000m. See Section 5.5.

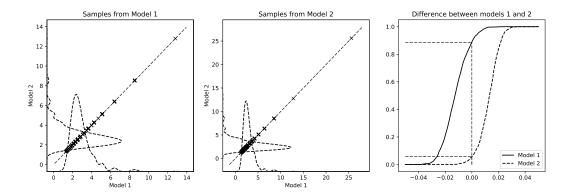


Figure 19: Brier score, multiplied by 10^9 . See Section 5.6

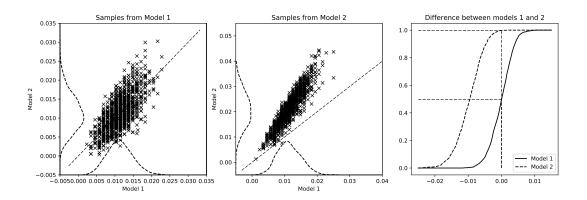


Figure 20: Brier skill score. See Section $5.6\,$

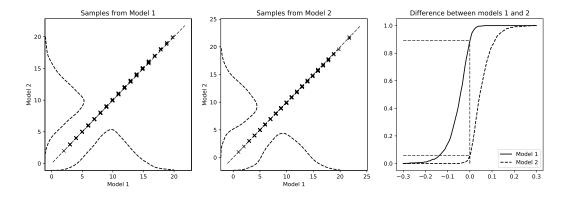


Figure 21: Poisson model based CRPS. See Section 5.6

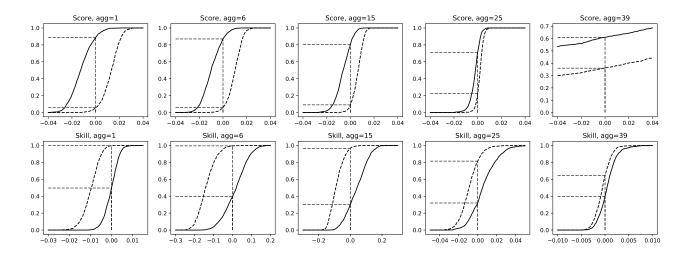


Figure 22: Multiscale Brier Score Skill. See Section 5.6

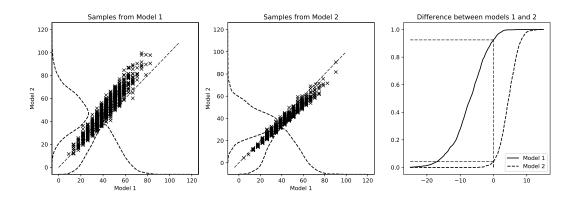


Figure 23: Information gain in Bayesian setting. The KL divergence between the prior and posterior Dirichlet distributions. See Section 5.7

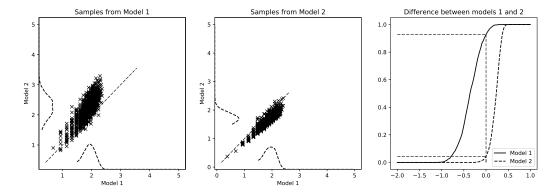


Figure 24: The KL divergence between the prior and posterior predictive distributions. See Section 5.7

distinguishes the models. Plug-in estimation of bandwidth gives unexpected results; a bandwidth of 300m (two grid cells) seemed to work best. The Brier score distinguishes well, but the skill score does not work with model 1. The Poisson CRPS again distinguishes well, but there is huge correlation between the predictions. The two information gain methods both distinguish well, with the predictive distribution method having better separated scatter plots.

6 Case study using Chicago data

We now turn our attention to real data and real prediction methods. As data, we shall use the publicly available dataset of crime events from Chicago. We will look at Burglary events in the North Side, for the year 2016. Figure 25 shows a plot of each location, and also a fixed bandwidth kernel density estimation (bandwidth of 300m) showing an estimate of the density of events. For each day in 2016 there are between 0 and 10 actual events which occur, with a mean of 3.3 events a day.

For this case study, we compare two prediction methods, as implemented in open_cp, [24]. For each day of September to December, inclusive, we make a prediction for that day, using data from January 2016 up to, but not including, that day, and then score the prediction using the events which actually occur on that day.

Our "baseline prediction" is what we term the "naive" predictor. We look at all the data in the past, count the number of events which occurred in each grid cell, and the normalise these counts to produce a risk surface. The alternative method we term the "KDE" method. This is based upon the "prospective" ideas in [4], but instead of working with grid cells, we first generate a continuous risk surface (essentially using some sort of kernel density estimation method, with a time component) and then sample to a grid. This follows the grid based method outlined in [26], for example. We shall see that neither method performs terribly well, but this gives us a good opportunity to highlight differences in the comparison methods.

Two example predictions are shown in Figure 26. The naive prediction, as we might expect, is quite "random" in appearance; we suspect it might suffer from the MAUP, in that if we moved the offset of the grid slightly, we might see a different pattern. The KDE predictions are much smoother, and tend to change more in time, as they weight recent past events more than distant past events. As is typical of this dataset, on each day, we have rather few actual events occur.

The hit rates, Figure 27, show that for small coverages, the two methods perform rather similarly (and that, as we know, crime is quite clustered). For higher coverage levels (and probably unrealistically high coverage levels, from a policing perspective) the KDE method performs a little better. The cumulative density plots shows that for a large number of days, there is no difference between the methods.

The ranking method, Figure 28, can be thought of, loosely, as a way of "averaging" the hit-rate across all coverage levels. For the mean rank, this shows little difference between the predictions (but a lot of variation). The δ score is a direct measure of which prediction assigns a higher rank to each point (but not taking account of difference); here it weakly favours the KDE method.

The "naive" prediction method, being based upon counts, often ends up assigning the same p_k values to multiple cells k. As discussed before, this can lead to problems with the hit rate and ranking methods, as it is not clear how to deal with "ties". We have added noise to predictions to stop this from being a problem—without doing this, the ranking results were somewhat different, favouring the "naive" method.

The likelihood, Figure 29, shows something a little unexpected. The likelihood for the KDE method varies somewhat less than that for the "naive" method. A larger likelihood means a better match, and so that the CDF plot shows 80% of the mass in the negative region means that the KDE prediction often has a greater likelihood than the "naive" prediction.

We present only the results for the fixed bandwidth KDE method, Figure 30. As the bandwidth ranges from 40m to 100m (i.e. less than the grid cell size) the scatter plots show increasing correlation, but the CDF plots do not change much in shape. As a smaller score is "better", these favour the KDE method around 60% of the time. For larger bandwidths, 250m and 1000m, the KDE prediction is always better than the naive prediction. This is rather different behaviour to that seen in Figure 18. It is not clear that this tells us much more than what a visual examination of the examples in Figure 26 show, namely that the KDE predictions are much "smoother" than the "naive" predictions.

The scoring rules, Figure 31, again show a lot of correlation in the scatter plots (so much so that we have chosen to plot the differences for the Brier score and Poisson CRPS). A smaller Brier score is "better", while a larger (closer to 1) Skill score is better. So the two scoring methods favour the KDE prediction around 65% of the time, while the Skill score favours the naive prediction around 55% of the time.

The multi-scale Brier scores are perhaps more informative than for the synthetic data study, see Figure 32. Again, we plot only 5 aggregation levels, but the omitted plots are all very similar. For the Brier score we have kept the aspect ratio constant; the way we interpret the plots is that for either prediction, the Brier score becomes much more clustered, while the relative difference between the two prediction methods increases. Figure 33 showing the CDF plots somewhat confirms this. Notice the jump in quality of the naive prediction at aggregation level 2 (this also holds for level 3). This seems to be telling us something useful, and perhaps expected: if we "blur" or "smooth" out the naive prediction by aggregating over nearest neighours, then it improves, which isn't surprising, given that the naive prediction takes no account of possible spatial interaction (unlike the KDE prediction).

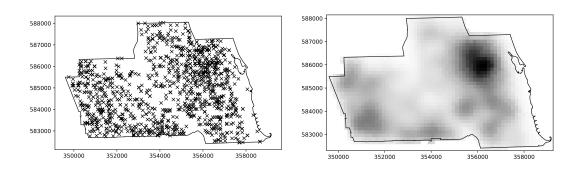


Figure 25: Chicago North Side Burglary events for 2016.

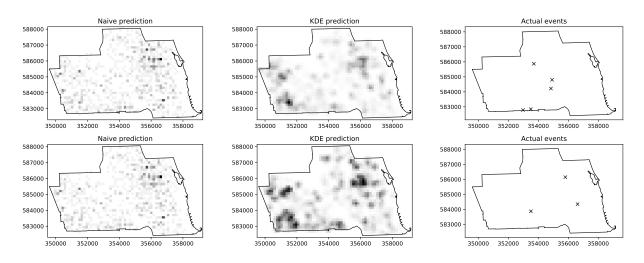


Figure 26: Example predictions, and actual events. Top row is 5th November 2016, while the bottom row is 23rd October 2016.

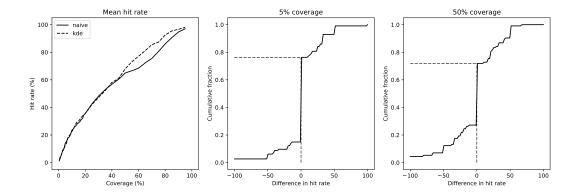


Figure 27: Hit rate for Chicago Northside data.

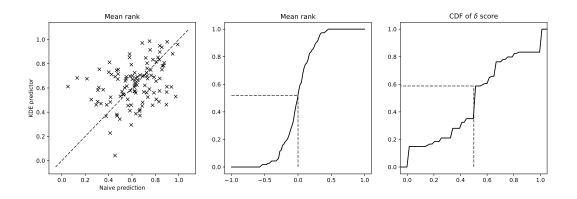


Figure 28: Ranking scores: mean ranking, and δ score.

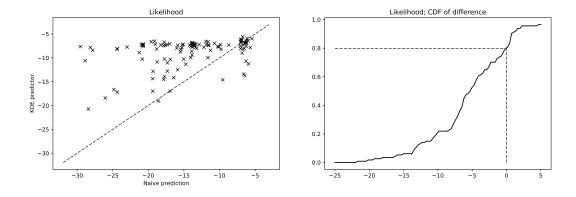


Figure 29: Likelihood.

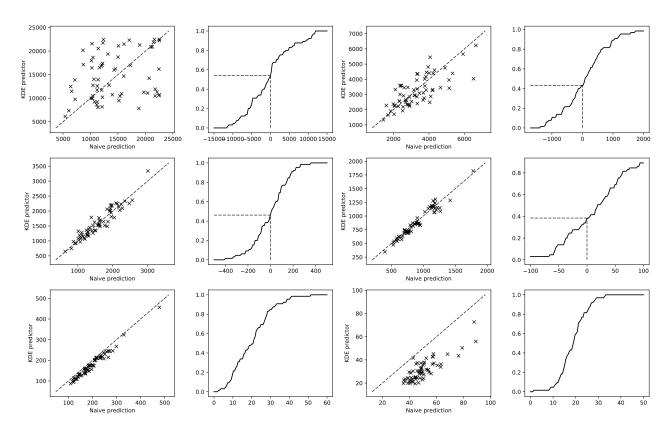


Figure 30: KDE comparison (squared error). From top to bottom, left to right, the bandwidths used are 10m, 40m, 70m, 100m, 250m and 1000m.

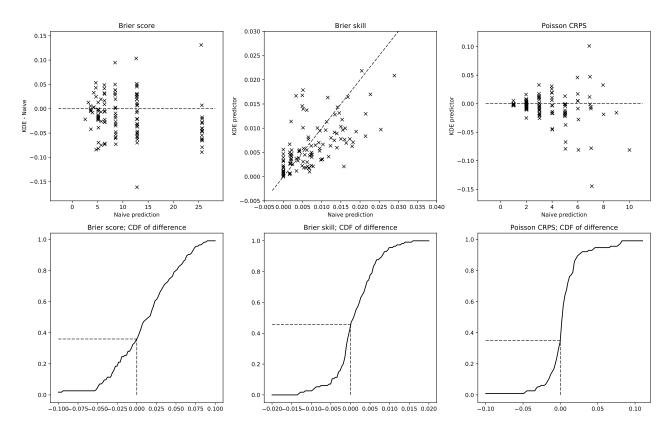


Figure 31: Brier score $\times 10^9$, skill score and Poisson CRPS. For the Brier score and Poisson CRPS we plot the difference between the score, instead of a true scatter plot, as there is such a strong correlation that the points just form a line.

At higher aggregation levels the naive method again seems to lose ground. However, notice that the x axis scale becomes rather narrow (relative to the associated scatter plots). Hence the "real" gradient of the CDF plot is becoming large, indicating a great deal of uncertainty as to whether there is really any difference between the two predictions.

The Skill scores again increase as the aggregation level increases, as expected. The CDF plots do not change terribly much in how they discriminate between the two predictions; but here the x axis scales increase and then decrease again. If plotted with the same scale, this would indicate that there was much more certainty at a middle aggregation level than at either end.

We can perhaps see a little more closely what is happening by looking at estimated densities of the scores at differing aggregation levels, Figure 34. We have plotted these only for one prediction, such is the correlation between the scores that the plots are essentially idential for the other prediction. The Skill score is perhaps most interesting, showing that as the aggregation level increases, the skill increases, but becomes much more dispersed.

Turning now to the information theoretic ideas, we recall that a smaller Kullback-Leibler divergence means a "better" match between prediction and observed data. Thus that we see most of the mass on the positive side in Figure 35 shows that the "naive" prediction has a larger divergence than the KDE prediction. The results for the predictive distributions are rather similar

For this real-world data and predictions, we had no particular *a priori* feeling for which was the "better" prediction. The classical measure, hit rate, suggests that actually they perform quite similarly, except at large (and unrealistic) coverage levels. An alternative way of computing the "average" hit rate, again using Bayesian ideas, see Section 7 below, suggests that the naive method is slightly better than the KDE method, at small to medium coverage.

From our synthetic data study, we were distrustful of the Likelihood and ranking methods; the KDE method seemed to be sensitive to bandwidth choice; the skill score methods gave mixed results; and the information gain technique worked fairly well. Thus these results would probably suggest that, on balance, the KDE technique is superior, but not overwhelmingly so.

7 Bayesian modelling of difference

We criticised the Wilcoxon signed-rank test above. Here we offer a simple Bayesian approach which, under some assumptions, tries to capture the actual probability that two sequences (x_i) and (y_i) have different mean. We will firstly attack the problem of comparing two hit-rate sequences. The hit rate actually comes from scoring a number of trials, each trial having n_i events of which we capture $x_i^{(1)}$ and $x_i^{(2)}$ from our two

prediction algorithms. Let us model this by assuming that $x_i^{(l)}$ is distributed binomially with parameters p_l and n_i . Here p_l is assumed to depend only on the prediction algorithm, and not on i. That is,

$$\mathbb{P}(x_i^{(l)}) = \binom{n_i}{x_i^{(l)}} p_l^{x_i^{(l)}} (1 - p_l)^{n_i - x_i^{(l)}}.$$

The conjugate prior is a Beta distribution, say $B(\alpha_0, \beta_0)$ for some hyper-parameters α_0, β_0 . We will always have sufficient data that the exact choices do not matter; we could take $\alpha_0 = \beta_0 = 1$ for a uniform prior.

Upon observing $(x_i^{(l)})_{i=1}^I$ the posterior distribution is

$$B(\alpha_0 + \sum_i x_i^{(l)}, \beta_0 + \sum_i n_i - \sum_i x_i^{(l)}).$$

Let $N = \sum_{i} n_i$ and $x_l = \sum_{i} x_i^{(l)}$. Then the posterior probability of p_l is

$$\frac{\Gamma(\alpha_0 + \beta_0 + N)}{\Gamma(\alpha_0 + x_l)\Gamma(\beta_0 + N - x_l)} p_l^{\alpha_0 + x_l - 1} (1 - p_l)^{\beta_0 + N - x_l - 1}.$$

This has

$$\mathbb{E}(p_l) = \frac{\alpha_0 + x_l}{\alpha_0 + \beta_0 + N},$$

which is close to the average x_l/N . Note that this differs from the average hit rate, which is $I^{-1} \sum_i x_i^{(l)}/n_i$.

Given say p_1, p_2 we can compute for example $\mathbb{P}(p_1 > p_2)$. Or we can find the inter-quartile range and graphically plot this. Figure 36 shows this technique applied to the Chicago case study. We note that the estimated probabilities follow closely the shape from the left-hand plot of Figure 28. Actually here we see a good match with the Wilcoxon signed-rank test (we note that in this case there is no evidence of auto-correlation in the difference sequence $(h_i^{(1)} - h_i^{(2)})$). The inter-quartile range gives an estimate of the likely range of the success probability.

7.1 A Hierarchical approach

A key statistical assumption in the Wilcoxon signedrank test is that the samples are iid from a population: in practise, this translates into the belief that each and every day is the same, so we can treat the hit rate for one day as being a sample from the same population as a hit rate for another day. Our Bayesian model above makes the same assumption.

There is plenty of reason to doubt this assumption: it seems likely that external factors (weather, day of the week, other unknown factors affecting offender movements) could well make each day slightly different to the next. One way to account for such changes is to construct a Hierarchical model, [13, Chapter 5]. We again suppose $x_i^{(l)}$ is distributed binomially with parameters $p_{i,l}$ and n_i . However now we allow $p_{i,l}$ to be a random variable itself, drawn from a Beta distribution with parameters (α_l, β_l) . We now seek a prior on (α_l, β_l) , for l = 1, 2.

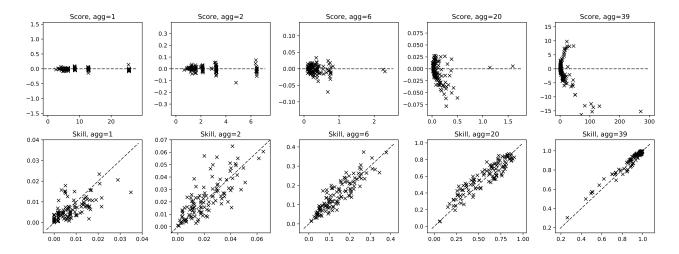


Figure 32: Brier score $\times 10^9$ and Skill score. Aspect ratio of the Brier score plots is kept constant; plots show score for naive prediction against difference to score for KDE prediction.

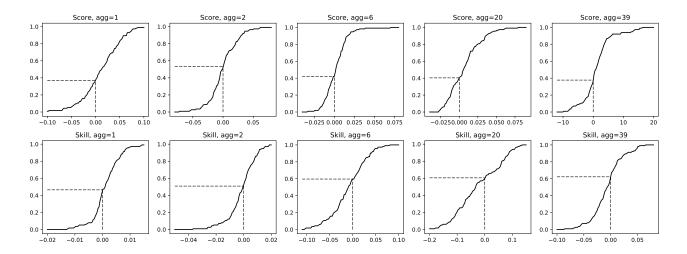


Figure 33: Brier score $\times 10^9$ and Skill score; cumulative densities.

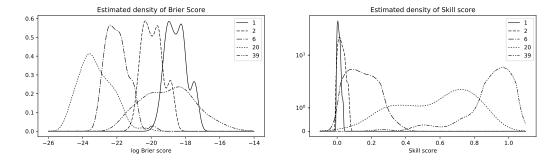


Figure 34: Estimated densities for the Brier score and Skill score at different aggregation levels.

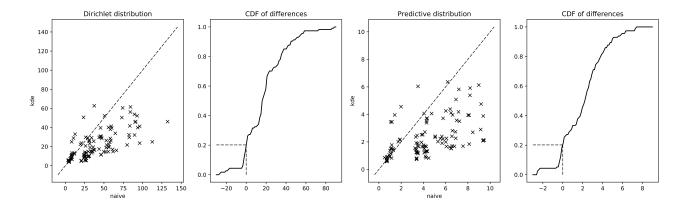


Figure 35: Bayesian information gain.

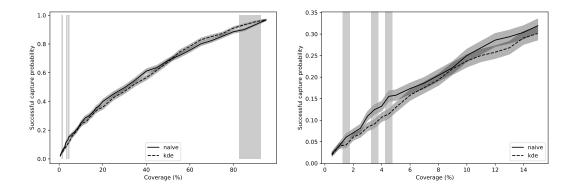


Figure 36: Fitted binomial distribution to the hit-rates from the Chicago case study. Lines show the median of the predicted probability, while shaded regions show the inter-quartile range. Shaded backgound indicates where the Wilcoxon signed-rank test has a p-value ≤ 0.2 .

Following [13, Chapter 5] we parameterise a Beta distribution by the mean $\alpha(\alpha+\beta)^{-1}$ and the "sample size" $\alpha+\beta$. We then use a logit transform on the mean, noting that logit $\left(\frac{\alpha}{\alpha+\beta}\right) = \log(\alpha/\beta)$, and a log transform on the sample size. A natural noninformative prior to take is

$$p\left(\log\left(\frac{\alpha}{\beta}\right),\log(\alpha+\beta)\right) \propto \alpha\beta(\alpha+\beta)^{-5/2}.$$

We may then use numerical techniques to sample from the posterior distribution for (α, β) and then for p. We found that tuning Markov-Chain Monte Carlo methods to be hard, but we can follow [13, Chapter 5] and compute the posterior density on a grid, and then sample from this

The result is, for l=1,2 and a fixed coverage level, a sample of values for p_l . The resulting graphs, an analogue of Figure 36, is shown in Figure 37. The findings are somewhat similar to the non-Hierarchical case, excepting that the inter-quartile range is larger, reflecting the decreased certainty we have. This model provides even less evidence that there is much difference between the two prediction methods.

A Random choices from a multinomial

Our model is that counts $(n_k)_{k=1}^K$ come from a multinomial distribution with $\sum_k n_k = n$ and $\mathbb{E}(n_k) = np_k$. Fix $0 \le m \le K$ and uniformly at random choose $A \subseteq \{1, 2, \dots, K\}$ of size m. Let H be the "hit-rate of A", that is,

$$H = \frac{1}{n} \sum_{k \in A} n_k.$$

We claim that $\mathbb{E}(H) = m/K$ that is, the fraction of the cells chosen.

Given a fixed choice of A, we have that

$$\mathbb{E}(H|A) = \frac{1}{n} \sum_{k \in A} \mathbb{E}(n_k) = \sum_{k \in A} p_k.$$

Thus

$$\mathbb{E}(H) = \mathbb{E}(\mathbb{E}(H|A)) = {K \choose m}^{-1} \sum_{A} \sum_{k \in A} p_k.$$

The normalisation factor occurs as this is the number of ways to choose a subset of size m from K choices. In the double sum, consider the number of times p_k occurs. There are $\binom{K-1}{m-1}$ sets which contain p_k , and so

$$\mathbb{E}(H) = {K \choose m}^{-1} {K-1 \choose m-1} \sum_{k} p_k.$$

Using $\sum_k p_k = 1$, and cancelling out the binomial coefficients, we indeed find that $\mathbb{E}(H) = m/K$ as claimed.

B Divergence for the Dirichlet Prior

As in Section 3.6 we use a Dirichlet distribution,

$$p((p_k)|(\alpha_k)) = \frac{\Gamma(\alpha_0)}{\prod_k \Gamma(\alpha_k)} \prod_{k=1}^K p_k^{\alpha_k - 1},$$

where by convention $\alpha_0 = \sum_{k=1}^K \alpha_k$. The prior has $\alpha_k = t\hat{p}_k$ and the posterior has $\alpha_k = t\hat{p}_k + n_k$. Set $N = \sum_k n_k$. An alternative way to write the posterior is

$$\alpha_k = (t+N)\frac{\hat{p}_k + n_k/t}{1 + N/t},$$

which emphasises the "counts" t+N and the relative probabilities $\frac{\hat{p}_k+n_k/t}{1+N/t}$.

The Kullback-Leibler divergence is $\int p \log(p/q)$ where the prior Q has density q and the posterior P has density p. We can rewrite this as

$$D_{KL} = \mathbb{E}_P(\log p) - \mathbb{E}_P(\log q).$$

Using that the expectation is linear, this is

$$\log \Gamma(t+N) - \sum_{k} \log \Gamma(t\hat{p}_{k} + n_{k})$$

$$+ \sum_{k} (t\hat{p}_{k} + n_{k} - 1) \mathbb{E}_{P}(p_{k})$$

$$- \log \Gamma(t) + \sum_{k} \log \Gamma(t\hat{p}_{k})$$

$$- \sum_{k} (t\hat{p}_{k} - 1) \mathbb{E}_{P}(p_{k}).$$

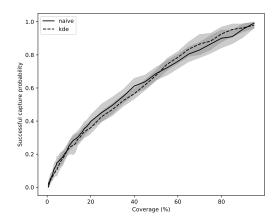
Finally, we use that $\mathbb{E}_P(p_k) = \psi(t\hat{p}_k + n_k) - \psi(t+N)$ where ψ is the digamma function (the derivative of $\log \Gamma(\cdot)$). This simplifies to

$$\begin{split} \log \Gamma(t+N) - \log \Gamma(t) \\ - \sum_{k} \log \Gamma(t \hat{p}_k + n_k) + \sum_{k} \log \Gamma(t \hat{p}_k) \\ + \sum_{k} n_k \psi(t \hat{p}_k + n_k) - n \psi(t+N). \end{split}$$

Further simplifications are possible by exploiting the functional relations which the gamma and digamma functions possess.

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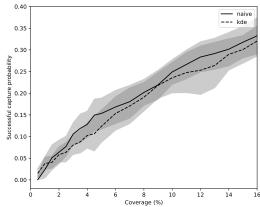


Figure 37: Fitted Hierarchical Model as described in Section 7.1. Lines show the median of the predicted probability, while shaded regions show the inter-quartile range.

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