

Chapter 1

State-space Covariates

Underlying all spatial capture recapture models is a point process model describing the distribution of individual activity centers (\mathbf{s}_i) within the state space (\mathcal{S}). So far we have focused our discussion on the homogeneous binomial point process, $\mathbf{s}_i \sim \text{Uniform}(\mathcal{S})$, $i = 1, 2, \dots, N$, where N is the size of the population. This is a model of “spatial-randomness”¹ because the intensity of the activity centers is constant across the study area and the activity centers are distributed independently of each other.

The spatial-randomness assumption is often viewed as restrictive because ecological processes such as territoriality and habitat selection can result in non-random distributions of organisms. We have argued, however, that this assumption is less restrictive than may be recognized because the homogeneous point process actually allows for infinite possible configurations of activity centers. Furthermore, given enough data, the uniform prior will have very little influence on the estimated locations of activity centers. Nonetheless, the homogeneous point process model does not allow one to model population density using covariates—a central objective of much ecological research. For example, a homogeneous point process model may result in a density surface map indicating that individuals were more abundant in one habitat than another, but it does not do so explicitly. A more direct approach would be to model density using covariates as is done in generalized linear models (GLMs).

In this chapter we will present a method for fitting inhomogeneous binomial point process models using covariates in much the same way as is done with GLMs. The covariates we consider differ from those covered in previous chapters, which were typically attributes of the animal (*e.g.* sex, age) and were used to model movement or encounter rate. In contrast, here we wish to model covariates that are defined for all points in the the state-space, which we will refer to as state-space, or density, covariates. These may include continuous covariates such as elevation, or discrete covariates such as habitat type.

¹The phrase “complete spatial-randomness” is reserved for the homogeneous Poisson point process

Borchers and Efford (2008) were the first to propose an inhomogeneous point process model for SCR models, and our approach is similar to theirs with the exception that we will use a binomial rather than a Poisson model because the binomial model is easily integrated into our data augmentation scheme and is consistent with the objective of determining how a *fixed* number of activity centers are distributed with respect to covariates.

The method we use to accommodate inhomogeneous binomial point process models within our MCMC algorithm is simple—we replace the uniform prior with a prior describing the distribution of the N activity centers conditional on the covariates. Development of this prior, which does not have a standard form, is a central component of this chapter.

1.1 Homogeneous point process revisited

The homogeneous Poisson point process is *the* model of “complete spatial randomness” and it is often used in ecology as a null model to test for departures from randomness. Given its central role in the analysis of point processes, it is helpful to compare it with the binomial model that we use in our SCR models. The primary descriptor of the homogeneous point process model is the “intensity” parameter, μ which describes the expected number of points in an infinitesimally small area. Thus the intensity parameter can also be used to determine the expected number of points in any region of the state-space \mathcal{S} . To denote this, we say that the expected number of points in region $B \in \mathcal{S}$ is $n(B) = A(B)\mu$ where $A(B)$ is the area of region B . One property of the Poisson model is that if we divide the entire state-space into $k = 1, \dots, K$ disjoint regions, the counts $\{n(B_k)\}$ are independent and identically distributed, (*i.i.d.*). This is one of the distinctions between the Poisson model and the binomial model, for which the counts $n(B_k)$ are not *i.i.d.* as we will explain shortly. This difference is also related to more important distinction between the two models, namely that the binomial model conditions on the number of points to be simulated N ; whereas under the Poisson model N is random. Here is some simple **R** code to illustrate this point.

```

61 mu <- 4                                # intensity
62 Np <- rpois(1, mu)                     # Np is random
63 PPP <- cbind(runif(Np), runif(Np)) # Poisson point process
64
65 Nb <- 4
66 BPP <- cbind(runif(Nb), runif(Nb)) # Binomial point process

```

Note that in both models, the N points are independent of one another and distributed uniformly throughout \mathcal{S} . Thus, the intensity at any point $x \in \mathcal{S}$ is $\mu = 1/A(\mathcal{S})$ where $A(\mathcal{S})$ denotes the area of the state-space. For example, if the area of our state-space is 4 km², under a homogeneous model, the intensity is $\mu = 1/4$.

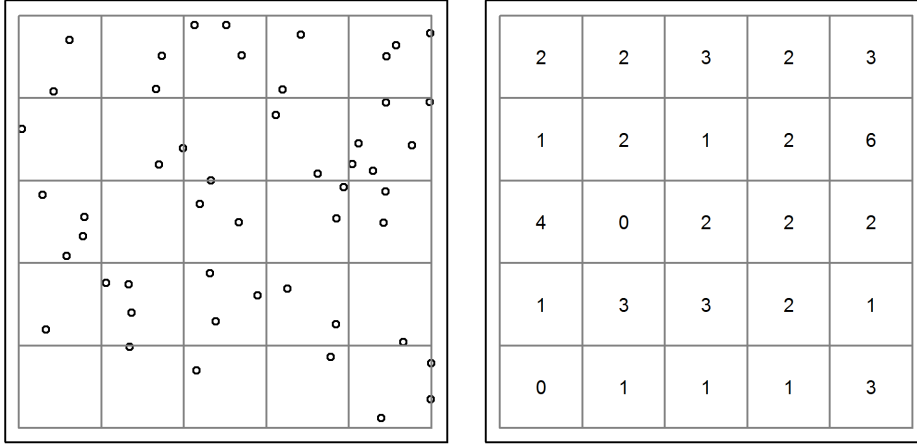


Figure 1.1: Homogeneous binomial point process with $N=50$ points represented in continuous and discrete space.

Although the Poisson model is typically described in terms of μ , the binomial model is not; rather, it is more common to consider a discrete state space, such as a grid with K pixels. Under the binomial model, the number of points in each region is $n(B_k) \sim \text{Bin}(N, p_k)$ where $p_k = A(B)/A(\mathcal{S})$, ie p_k is simply the fraction of the state-space area in B_k . This discrete space representation of the binomial point process is shown in Fig. 1.1. The state-space in this case is the unit square, and thus probability of a point falling in each of the 25 disjunct regions is $p_k = 1/25$ and thus the expected counts are simply $\mathbb{E}(n(B_k)) = Np_k$. In the figure $N = 50$ and thus we would expect 2 points per pixel, which happens to be true in this case. Note also that these counts are not independent realizations from a binomial distribution since $\sum_k n(B_k) = N$. Instead, the model for the entire vector is $\mathbf{n}(\mathbf{B}) \sim \text{Multinomial}(N, \pi = (p_1, p_2, \dots, p_K))$ (Illian, 2008). The dependence among counts has virtually no practical consequence when the number of pixels is large. For example, if we have 100 pixels, the number of counts in one pixels tells you very little about the expected count in another pixel. However, if there are only 2 pixels, then clearly the number of points in one pixel tells you exactly how many will occur in the remaining pixel. To gain familiarity with the multinomial distribution and the discrete representation of space, use the `rmultinom` function in **R** to simulate counts similar to those shown in Fig. 1.1, for example using a command such as:

```

n.B_k <- rmultinom(1, size=50, probs=rep(1/25, 25))
matrix(n.B_k, 5, 5)

```

95 The discrete space representation of the binomial point process is of practical
 96 importance when fitting SCR models because spatial covariates are almost
 97 always represented in a discrete format, often called “rasters” in GIS-speak. In
 98 such cases, we often need to change our definition of the prior for an activity
 99 center from $s_i \sim \text{Uniform}(\mathcal{S})$ to $s_i \sim \text{Multinomial}(1, \pi)$. In the latter case, the
 100 activity center is simply defined as an integer representing pixel “id”. Note also
 101 that the multinomial distribution with an index of 1 (*i.e.* `size=1` in `rmultinom`)
 102 is referred to as the categorical distribution, which we will often make use of in
 103 the BUGS language.

104 1.2 Inhomogeneous binomial point process

105 As with the homogeneous model, the inhomogeneous binomial point process
 106 model is developed conditional on N . The primary distinction is that the uni-
 107 form distribution is replaced with another distribution allowing for the intensity
 108 parameter to vary spatially. To arrive at this new distribution, define $\mu(x, \alpha)$
 109 to be a function of spatially-referenced covariates (α) available at all points of
 110 the state space. Subsequently we will drop the vector of coefficients from our
 111 notation to be concise. Since an intensity must be strictly positive, it is natural
 112 to model $\mu(x)$ using the log-link.

$$\log(\mu(x)) = \sum_{j=1}^J \alpha_j v_j(x), \quad x \in \mathcal{S}$$

113 where α_j is the regression coefficient for covariate $v_j(x)$. To be clear, $v(x)$ is
 114 the value of any covariate, such as habitat type or elevation, at location x . This
 115 equation should look familiar because it is the standard linear model used in
 116 log-linear GLMs. Note, however, that we have no need for an intercept because
 117 it would be confounded with N . This should be intuitive since an intercept
 118 would represent the expected value of N when $\alpha = 0$, but we already have a
 119 parameter in the model for expected abundance, namely $\mathbb{E}[N] = \psi M$. Thus an
 120 intercept would be redundant, and without it we are still able to achieve our
 121 goal of describing the distribution of N activity centers as a function of spatial
 122 covariates.

123 Now that we have a model of the intensity parameter $\mu(x)$, we need to
 124 develop the associated probability density function to use in the place of the
 125 uniform prior used in the homogeneous model. Remembering that the integral
 126 of a pdf must be unity, we can create a pdf by dividing $\mu(x)$ by a normalizing
 127 constant, which in this case is the integral of $\mu(x)$ evaluated over the entire
 128 state-space. The probability density function is therefore

$$f(x) = \frac{\mu(x)}{\int_{x \in \mathcal{S}} \mu(x) \, dx} \quad (1.1)$$

129 Substituting this distribution for the uniform prior allows us to fit inhomoge-
 130 neous binomial point process models to spatial capture-recapture data. We can

also use this distribution to obtain the expected number of individuals in any given region. Specifically, the proportion of N expected to occur in any region B when heterogeneity in density is present is $p(B) = \int_B f(x) dx$. These are also the multinomial cell probabilities if the regions are disjoint and compose the entire state-space.

As a practical matter, note that the integral in the denominator of $f(x)$ is evaluated over space, and since we almost always regard space as two-dimensional, this is a two-dimensional integral that can be approximated using the methods discussed in refChXXX. These methods include Monte Carlo integration, Gaussian quadrature, etc... Alternatively, if our state-space covariates are in raster format, *i.e.* they are in discrete space, the integral can be replaced with a sum over all pixels, which is much more efficient computationally.

We now have all the tools needed to fit inhomogeneous point process models. Before doing so, we note that this results in another point process model for the observation process, $\lambda(x)$. As a reminder, $\lambda(x)$ is the expected number of captures for a trap at point x . As was true for the homogeneous model, this intensity function is a convolution of the point process intensity ($\mu(x)$) and the encounter rate function, $\lambda(x) = \mu(x)g(x, s)$.

In the next section we walk through a few examples, building up from the simplest case where we actually observe the activity centers as though they were data. In the second example, we fit our new model to simulated data in which density is a function of a single continuous covariate. In the last example, we model the intensity of activity centers for a real dataset collected on jaguars (*Panthera onca*) in Argentina +cite some paper by Augustin.

1.3 Examples

1.3.1 Simulation and analysis of inhomogeneous point processes

In SCR models, the point process is not directly observed, but in other contexts it is. Examples include the locations of disease outbreaks or the locations of trees in a forest. Fitting inhomogeneous point process models to such data is straight-forward and illustrates the fundamental process that we will later embed in our MCMC algorithm used to fit SCR models.

Suppose we knew the locations of 100 animals' activity centers. To estimate the intensity surface $\mu(x)$ underlying these points, we need to derive the likelihood for our data under this model. Given the pdf $f(x)$, and assuming that the points are mutually independent of one another, we may write the likelihood as the product of R such terms, where $R = 100$ is the sample size in this case, *i.e.* the observed number of activity centers.

$$\mathcal{L}(\alpha|\mathbf{x}_i) = \prod_{i=1}^R f(x_i)$$

169 Having defined the likelihood we could choose a prior and obtain the posterior
 170 for α using Bayesian methods, or we can find the maximum likelihood estimates
 171 (MLEs) using standard numerical methods as is demonstrated below.

172 First, let's simulate some data. Simulating data under an inhomogeneous
 173 point process model is often accomplished using indirect methods such as rejection
 174 sampling. Rejection sampling proceeds by simulating data from a standard
 175 distribution and then accepting or rejecting each sample using probabilities
 176 defined by the distribution of interest. For more information, readers should
 177 consult an accessible text like Robert and Casella (2004). In our example, we
 178 simulate from a uniform distribution and then accept or reject using the (scaled)
 179 probability density function $f(x)$. Note that we first define a spatial covariate
 180 (elevation) that is a simple function of the spatial coordinates increasing from
 181 the southwest to the northeast of our state-space.²

182 The following **R** commands demonstrate the use of rejection sampling to
 183 simulate an inhomogeneous point process for the covariate depicted in Fig. 1.3.1.

```

184 # spatial covariate (with mean 0)
185 elev.fn <- function(x) x[,1]+x[,2]-1
186
187 # 2-dimensional integration over unit square
188 int2d <- function(alpha, delta=0.02) {
189   z <- seq(delta/2, 1-delta/2, delta)
190   len <- length(z)
191   cell.area <- delta*delta
192   S <- cbind(rep(z, each=len), rep(z, times=len))
193   sum(exp(alpha*elev.fn(S)) * cell.area)
194 }
195
196 # Simulate PP using rejection sampling
197 set.seed(300225)
198 N <- 100
199 count <- 1
200 s <- matrix(NA, N, 2)
201 alpha <- 2 # parameter of interest
202 while(count <= 100) {
203   x.c <- runif(1, 0, 1); y.c <- runif(1, 0, 1)
204   s.cand <- cbind(x.c,y.c)
205   elev.min <- elev.fn(cbind(0,0))
206   elev.max <- elev.fn(cbind(1,1))
207   pr <- exp(alpha*elev.fn(s.cand)) / int2d(alpha)
208   Q <- max(c(exp(alpha*elev.min) / int2d(alpha),
209             exp(alpha*elev.max) / int2d(alpha)))
210   if(runif(1) < pr/Q) {
211     s[count,] <- s.cand
212     count <- count+1
213   }

```

²Such functional forms of covariates are rarely available, which is why continuous spatial covariates are more often measured on a discrete grid.

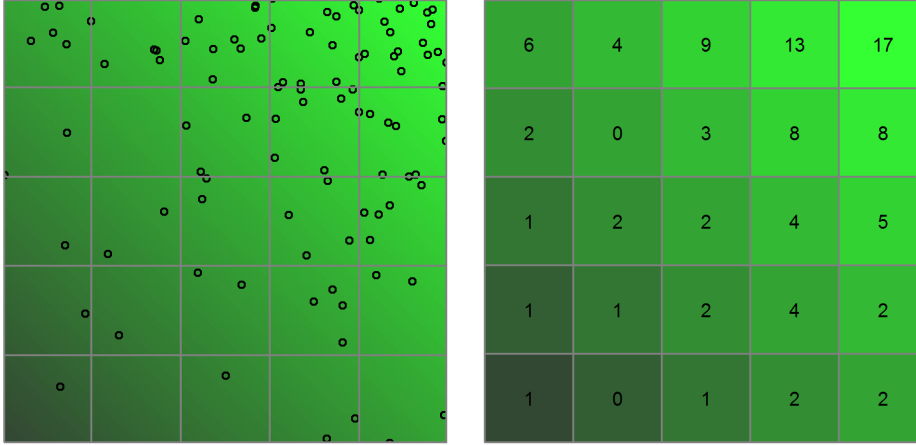


Figure 1.2: An example of a spatial covariate, say elevation, and a realization of a inhomogeneous binomial point process with $N=100$ and $\mu(x) = \exp(\alpha \text{Elev})$ where $\alpha = 2$.

214 }

215 The simulated data are shown in Fig 1.3.1. High elevations are represented
 216 by light green and low elevations by dark green. The activity centers of one
 217 hundred animals are shown as points, and it is clear that these simulated animals
 218 prefer the high elevations. The underlying model describing this preference is
 219 $\log(\mu(x)) = \exp(\alpha \times \text{Elevation}(x))$ where $\alpha = 2$ is the parameter to be estimated
 220 and $\text{Elevation}(x)$ is a function of the coordinates at x , as displayed on the map.

221 Given these points, we will now estimate α by minimizing the negative-log-
 222 likelihood using R's `optim` function.

```
223 # Negative log-likelihood
224 nll <- function(beta) {
225   -sum(beta*elev.fn(s) - log(int2d(beta)))
226 }
227 starting.value <- 0
228 fm <- optim(starting.value, nll, method="Brent",
229             lower=-5, upper=5, hessian=TRUE)
230 c(Est=fm$par, SE=sqrt(1/fm$hessian)) # estimates and SEs
```

231 Maximizing the likelihood took a small fraction of a second, and we obtained
 232 an estimate of $\hat{\alpha} = 2.47$. We could plug in this estimate to our linear model at
 233 each point in the state-space to obtain the MLE for the intensity surface.

234 This example demonstrates that if we had the data we wish we had, *i.e.*
 235 if we knew the coordinates of the activity centers, we could easily estimate
 236 the parameters governing the underlying point process. Unfortunately, in SCR

models, the activity centers cannot be directly observed, but spatial re-captures, that is captures of individuals at multiple locations in space, provide us with the information needed to estimate these latent parameters.

1.3.2 Fitting inhomogeneous point process SCR model

One of the nice things about hierarchical models is that they allow us to break a problem up into a series of simple conditional relationships. Thus, we can simply add the methods described above into our existing MCMC algorithm to simulate the posteriors of α conditional on the simulated values of \mathbf{s}_i . To demonstrate, we will continue with the previous example. Specifically, we will overlay a grid of traps upon the map shown in Fig. 1.3.1. We will then simulate capture histories conditional upon the activity centers shown on the map. Then, we will attempt to estimate the activity center locations as though we did not know where they were, as is the case in real applications.

Here is some R code to simulate the encounter histories under a Poisson observation model, which would be appropriate if animals could be detected multiple times at a trap during a single occasion.

```
# Create trap locations
xsp <- seq(-0.8, 0.8, by=0.2)
len <- length(xsp)
X <- cbind(rep(xsp, each=len), rep(xsp, times=len))

# Simulate capture histories, and augment the data
ntraps <- nrow(X)
T <- 5
y <- array(NA, c(N, ntraps, T))

nz <- 50 # augmentation
M <- nz+nrow(y)
yz <- array(0, c(M, ntraps, T))

sigma <- 0.1 # half-normal scale parameter
lam0 <- 0.5 # basal encounter rate
lam <- matrix(NA, N, ntraps)

set.seed(5588)
for(i in 1:N) {
  for(j in 1:ntraps) {
    distSq <- (s[i,1]-X[j,1])^2 + (s[i,2] - X[j,2])^2
    lam[i,j] <- exp(-distSq/(2*sigma^2)) * lam0
    y[i,j,] <- rpois(T, lam[i,j])
  }
}
yz[1:nrow(y),,] <- y # Fill
```

Now that we have a simulated capture-recapture dataset y , and we have augmented it to create the new data object yz , we are ready to begin sampling

from the posteriors. A commented Gibbs sampler written in **R** is available online. There are two small parts of the **R** code that distinguish it from previous code we have shown to fit homogeneous point processes. First, we need to update the parameter α conditional on all other parameters in the model. The code to do so is:

```

287 D1 <- int2d(beta1, delta=.05)
288 beta1.cand <- rnorm(1, beta1, tune[3])
289 D1.cand <- int2d(beta1.cand, delta=0.05)
290 ll.beta1 <- sum( beta1*elev.fn(S) - log(D1) )
291 ll.beta1.cand <- sum( beta1.cand*elev.fn(S) - log(D1.cand) )
292 if(runif(1) < exp(ll.beta1.cand - ll.beta1) ) {
293   beta1<-beta1.cand
294 }
```

Next, we need to put the new prior on the activity centers:

```

296 #ln(prior), denominator is constant
297 prior.S <- beta1*cov(S[i,1], S[i,2]) # - log(D1)
298 prior.S.cand <- beta1*(Scand[1] + Scand[2]) # - log(D1)
299 if(runif(1)< exp((ll.S.cand+prior.S.cand) - (ll.S+prior.S))) {
300   S[i,] <- Scand
301   lam <- lam.cand
302   D[i,] <- dtmp
303 }
```

We can apply this modified sampler to our data using the code shown in the following panel. We obtain posterior distributions summarized in Table 1.1. Mixing is good, and as usual, life is very nice when we are working with simulated data.

```

308 library(scrbook)
309 fm1 <- scrIPP(yz, X, M, 3000, xlims=c(-1,1), ylims=c(-1,1),
310             tune=c(0.002, 0.1, 0.25, 0.07) )
311 plot(mcmc(fm1$out))
```

Table 1.1: Posterior summaries from inhomogeneous point proces model

	Mean	SD	2.5%	50%	97.5%
$\sigma = 0.10$	0.1026	0.0048	0.0935	0.1025	0.1123
$\lambda_0 = 0.50$	0.4419	0.0493	0.3496	0.4400	0.5390
$\psi = 0.66$	0.6826	0.0554	0.5762	0.6820	0.7923
$\beta = 2.00$	2.1601	0.3390	1.5193	2.1583	2.8043
$N = 100$	102.7696	6.2689	92.0000	102.0000	117.0000

We can also fit these models using maximum-likelihood. Let's try using **secr**.

Fitting continuous space versions of these of these models is somewhat difficult in **BUGS** because our prior $f(x)$ is not one of the available distributions³

³It is possible, if somewhat cumbersome, to add new distributions in **BUGS**.

However, discrete space versions are straight-forward. This is not really an important limitation of **BUGS**, since most covariates are represented as rasters not continuous functions. To fit the discrete space models, we follow the same steps as outlined in Chapter 5—we define s_i as pixel id, and we use the categorical distribution as a prior. A good example of this is in `+citeKery capricaille`. Here we present an analysis of the simulated data shown in the right panel of Fig. 1.3.1. The **BUGS** code to fit the model is shown in the following panel.

```

323 model{
324   sigma ~ dunif(0, 1)
325   lam0 ~ dunif(0, 5)
326   beta ~ dnorm(0,0.1)
327   psi ~ dbeta(1,1)
328
329   for(j in 1:nPix) {
330     theta[j] <- exp(beta*elevation[j])
331     probs[j] <- theta[j]/sum(theta[])
332   }
333
334   for(i in 1:M) {
335     w[i] ~ dbern(psi)
336     s[i] ~ dcat(probs[])
337     x0g[i] <- Sgrid[s[i],1]
338     y0g[i] <- Sgrid[s[i],2]
339     for(j in 1:ntraps) {
340       dist[i,j] <- sqrt(pow(x0g[i]-grid[j,1],2) + pow(y0g[i]-grid[j,2],2))
341       lambda[i,j] <- lam0*exp(-dist[i,j]*dist[i,j]/(2*sigma*sigma)) * w[i]
342       y[i,j] ~ dpois(lambda[i,j])
343     }
344   }
345
346   N <- sum(w[])
347   Density <- N/1 # unit square
348 }

```

A complete script to conduct the analysis is presented in the **R** package .

1.3.3 The jaguar data

Estimating density of large felines has been a priority for many conservation organizations, but no robust methodologies existed before the advent of SCR. Distance sampling is not feasible for such rare and cryptic species, and traditional capture-recapture methods yield estimates that are highly sensitive to the subjective choice of the effective survey area. In this example, we demonstrate how readily density can be estimated for a globally imperilled species using SCR. Furthermore, we show how inhomogeneous point process models can be used to test important hypotheses regarding the factors affecting density.

[describe study]

A few aspects of this design are noteworthy. First, the dimensions and configuration of the trap array differed among the regions of the trap array. This fact alone could explain variation in the number of animals exposed to sampling, which would have no biological meaning. Furthermore, the area of inference is an irregular polygon that was not sampled uniformly. Only by estimating density can we hope to extrapolate our estimates from the sampled region to get what we are after. In this case, this is readily accomplished since the entire state-space can be classified as one of the 3 levels of protection from poaching. Of course, in general it is always preferable to sample more uniformly throughout the area of interest in case some unmeasured covariate biases the extrapolation.

To assess the influence of poaching on jaguar density, we considered 2 metrics of poaching pressure, one political and one continuous measure of accessibility (Fig xxx).

1.4 MLE

Maybe its easy to adapt the MLE code from chapter 5 for doing a spatial covariate? For completeness it might be worth having that.

1.5 Other ideas

Should have some discussion on some ideas for building flexible models. Might be cool to use the Ickstadt/Wolpert as a model for the inhomogeneous point process. Dont have to do it, just mention it. Also some kind of a spline model or similar.

1.6 Summary

When state-space covariates are available, we can model density by replacing the uniform prior on the activity centers with a prior based on a log-linear function of covariates.

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