

**Title: Integrated spatial model estimates the fish distribution using environmental DNA and catch data**

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**Abstract**

**Keywords**

# 1 Introduction

2 Understanding of spatial distribution of species and underlying its mechanism is a major goal  
3 in ecology. Field surveys using environmental DNA (eDNA) are widely used for detecting  
4 invasive or rare species and hotspot of biodiversity because the surveys of eDNA are easy to  
5 detect occurrence of target species, non-invasiveness, and high cost effectiveness rather than  
6 previous direct sampling method (Rees et al. 2014; Thomsen & Willerslev 2015) However,  
7 uncertainty of the occurrence of eDNA is a issue in eDNA studies because various factors,  
8 such as biological and environmental features, intricately affect the shedding (i.e.,  
9 production of eDNA from organisms) and degradation (i.e., decay of eDNA from a system)  
10 of eDNA (Fig. 1). Therefore, it is necessary to consider the spatial uncertainty included in  
11 eDNA to infer the spatial distribution of species.

12 After the suggestion of the importance to understand about origin, state, transport, and  
13 fate of eDNA ("ecology of eDNA") by Barnes & Turner (2016), the studies which used  
14 laboratory experiments and numerical hydrological models have been increased to  
15 overcome the uncertainty of eDNA. For example, the relationship between production rate  
16 of eDNA and biological factors (e.g., species and body mass) or environmental factors (e.g.,  
17 temperature), and between decomposition of eDNA and the state of eDNA (e.g., length of  
18 eDNA) or environmental factors were measured. In numerical hydrological models, spatial  
19 distribution of eDNA was simulated in aquatic area and obtain the production, transport and  
20 decay of eDNA (e.g., Fukaya et al. 2020). However, keeps for all focal species in laboratory  
21 are not realistic and low cost-efficiency when multi species studies such as biodiversity  
22 monitoring and fisheries management. Moreover, biologists monitoring species are not often

23 familiar with hydrological models and the simulation of eDNA seems to be hard for them.

24 Integrated species distribution models (IDMs) are now common spatial model to  
25 predict spatial pattern of species (Issac et al. 2020). The models combine the different type  
26 of data with strengths and weaknesses in a single model. For example, the model can use  
27 both scientific survey data, which is high quality but less abundant due to restriction of cost,  
28 and citizen data, which is widely collected and abundant but may be low quality due to not  
29 using consistent field methods in a model. Combining both types of data can capitalize on  
30 the strengths of each data and perform better prediction than models when using single data  
31 (Pacifi et al. 2017; Miller et al. 2019). Hence, if we develop a IDM that uses not only the  
32 occurrence data of eDNA but also the second data which contains the information that  
33 species exists at a location, as well as environmental factors as covariance in the model, then  
34 the inference from the model should represent the reduction of the spatial uncertainty of  
35 eDNA and improvement (Fig. 1).

36 In this paper, to infer spatial distribution of species from the occurrence data of eDNA,  
37 we first make a spatial distribution model which considers spatial uncertainty of eDNA by  
38 using an integrated spatial distribution model. We then applied the model to both eDNA data  
39 and catch weight data for four fish in Tokyo Bay, Japan, and predicted the spatial  
40 distribution of these fish. We finally compared the differences in (i) the predicted spatial  
41 distribution of eDNA among fish and (ii) the relationship between the occurrence of eDNA  
42 and environmental factors among fish to discuss the effects of the biological factors on the  
43 spatial uncertainty of eDNA.

44

## 2 Materials and Methods

### 2.1 A general model to estimate species distribution from eDNA

Integrated spatial distribution model that account for explicitly spatial autocorrelation in occurrence were built by Pacifici et al. (2017), which shows three approaches to predict the spatial distribution of species: the joint likelihood (shared), correlation, and covariate methods. The joint likelihood method uses multiple data types to simultaneously estimate a shared set of parameters with constraining that the likelihoods of shared set of parameters to be equal across. The correlation method connects multiple data types indirectly through a shared covariance matrix that captures similar patterns present in each data sources. The covariate method incorporates information from a added dataset via a fixed effect.

Although each methods estimate the spatial distribution of species using multiple data sets, we need to select method depending on the data features for analysis because there are strengths and weaknesses (Pacifici et al. 2017; Miller et al. 2018). The joint likelihood method may be problematic when the second data is of poorly quality compared to correlation and covariate methods because each data can directly inform the latent occurrence state (probabilities?) and the weight given to estimate the parameters is naturally determined by their relative size and quality. Thus, it is not the best method when our second data is low quality while it is the best method when our second data is high quality (vise versa). The correlation method is added robustness to the joint likelihood because the second data indirectly inform the occurrence state. Thus, it is the best method when our second data is low quality while it is inferior to the joint likelihood method when both data are deemed reliable. The covariate method does not make full use of the information in the

second data because the second data as a constructed covariate in the mean occurrence state. In addition, this method can reduce the computational cost because there are fewer parameters to estimate and the number of data locations can be reduced. Thus, it is the best method when the second data is low quality and/or there is computational limitation while it may not the best method when the information of the second data is needed.

When predicting the spatial distribution of species from eDNA using integrated species distribution model, the information that a species exists is needed as second data to consider spatial uncertainties of eDNA due to complex factors (Fig. 1). Hence, the second data is preferred to high quality as possible.

しかし、eDNA は直接的なモニタリングに比べて簡易的であるためより広い範囲で取得されている可能性が高く、eDNA のデータと同様の空間範囲で調査データのように質の高いデータを取得することは難しいかもしれない。その一方で、eDNA の空間的な不確実性を考慮するためには、種がいた証拠である 2 番目のデータの情報を eDNA のデータにしっかりと伝える必要がある。これらを考えると、integrated spatial distribution model を用いた eDNA からの空間分布の推定には、以下のような correlation method が適切である：

$$\begin{aligned} p_e(s_i) &= \alpha_e + \sum_k f_{e,k}(x_{e,k}(s_i)) + w\theta(s_i) + u_e(s_i) \\ p_a(s_i) &= \alpha_a + \sum_k f_{a,k}(x_{a,k}(s_i)) + \theta(s_i) + u_a(s_i) \end{aligned} \quad (1)$$

where  $\alpha$  and  $x_k(s_i)$  are the intercept and the covariates at sites  $i$  for occurrence probabilities at sites  $i$  of the added data ( $p_a$ ) and eDNA data ( $p_e$ ), respectively.  $u(s_i)$  is spatial error that is specific for each data following multivariate normal distributions  $MVN(0, \mathbf{R})$ , where the variance–covariance matrix  $\mathbf{R}$  is a Matérn correlation function.  $\theta$  which is shared between

87 two equations is the common spatial pattern between the two data, which cannot explain by  
88 each terms of the equations. That is,  $\theta$  can be interpreted as "true" spatial distribution of  
89 species.

## 90 **2.2 An application to a eDNA and catch data in Tokyo Bay**

### 91 **2.2.1 eDNA data**

#### 92 **Field surveys**

93 Field surveys were conducted by prefectural experimental station in Chiba, following the  
94 consistent sampling design at 14 sites in Tokyo Bay from April to December in 2018 (Fig.  
95 1). In each sites, seawater and environmental data were simultaneously collected. For eDNA  
96 analysis, two litter of bottom seawater was collected using a Niskin water sampler, and then  
97 it was separated for two 1L samples for replicate. Each samples filtered glass fiber  
98 membrane GF/F (0.7  $\mu m$  pore size; Cytiva, Sheffield, UK) onboard and then the filters were  
99 frozen on a block of dry ice. These frozen filters were stored at  $-30^{\circ}$  in the laboratory until  
100 eDNA extraction. To lower the levels of cross-contamination, equipments for eDNA  
101 sampling were changed new one or washed in each sites. During sampling the bottom  
102 seawater, seawater temperature, salinity, pH, and dissolved oxygen (DO) at the same depth  
103 of seawater sampling for eDNA were measured by CTD (メーカ一).

#### 104 **Laboratory experiments**

105 In laboratory, eDNA extraction, eDNA amplification, and eDNA sequence were conducted.  
106 Total eDNA was extracted from the frozen filters using a DNeasy Blood and Tissue Kit  
107 (Qiagen, Hilden, Germany) following Yamamoto et al. 2019. Mitochondrial 12S rRNA

gene was amplified using MiFish universal primers referring to Miya et al. 2015 with slight modification. The details was shown in Hongo et al. (受理されてないようだったら書くしかない). eDNA sequence were ....

### 2.2.2 Catch statistics

A part of catch statistics of small-scale bottom trawl fisheries recorded by several representative boats of Chiba Prefecture were provided by Chiba Prefecture. This data included date, geographic location, efforts (number of tows), gear, and catch weight (kg) in each fish. Almost of all gear was beam trawl although dredge net also used. The species which also detected by eDNA was *Conger myriaster* (マアナゴ), *Kareius bicoloratus* (イシガレイ), *Lateolabrax japonicus* (スズキ), and *Konosirus punctatus* (コノシロ). Thus, we estimated the spatial distribution of these four species using the eDNA-IDM. マコガレイ, カマス類, クロダイ, イシモチ類も解析できる??

### 2.2.3 Estimation of spatial distribution

To estimate the spatial distribution of four focal species using eDNA and catch data by considering with spatial uncertainties of eDNA, we fitted the model (equation 1) to the presence/absence of eDNA and of catch collected in Tokyo Bay as follows:

$$\text{logit } p_e(s_i) = \alpha_e + \sum_k f_k(x_k(s_i)) + w\theta(s_i) + u_e(s_i)$$

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$$\text{logit } p_c(s_i) = \alpha_c + \beta_i + \theta(s_i) + u_c(s_i)$$

where  $\alpha$  is the intercept, and  $x_k(s_i)$  is the covariates at sites  $i$  for occurrence probabilities of eDNA at sites  $i$ . In the study, seawater temperature, salinity, pH, and DO were used as



127 covariates which effect on the occurrence of eDNA (i.e.,  $k = 4$ ).  $u(s_i)$  is spatial error that is  
128 specific for each data following multivariate normal distributions  $MVN(0, \mathbf{R})$ , where the  
129 variance–covariance matrix  $\mathbf{R}$  is a Matérn correlation function.  $\theta$  which is shared between  
130 eDNA and catch is the common spatial pattern between the two data, which cannot explain  
131 by each terms of the equations. That is,  $\theta$  can be interpreted as the spatial distribution of  
132 species we want to know. 共変量の非線形性について書く Parameters in this model was  
133 estimated by Integrated Nested Laplace Approximation using using the R-INLA package  
134 (Lindgren, 2012) in R 3.6.1 (R Development Core Team, 2019).

135

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## 138 **Authorship**

139 YK conceived of the research idea. YH, YU, HM, MI, KA, and AK conducted field  
140 sampling. YH performed the laboratory experiments. YK, HO, and SN designed statistical  
141 analyses. YK wrote programs and performed the analyses. YK wrote the manuscript with  
142 input from all co-authors' comments.

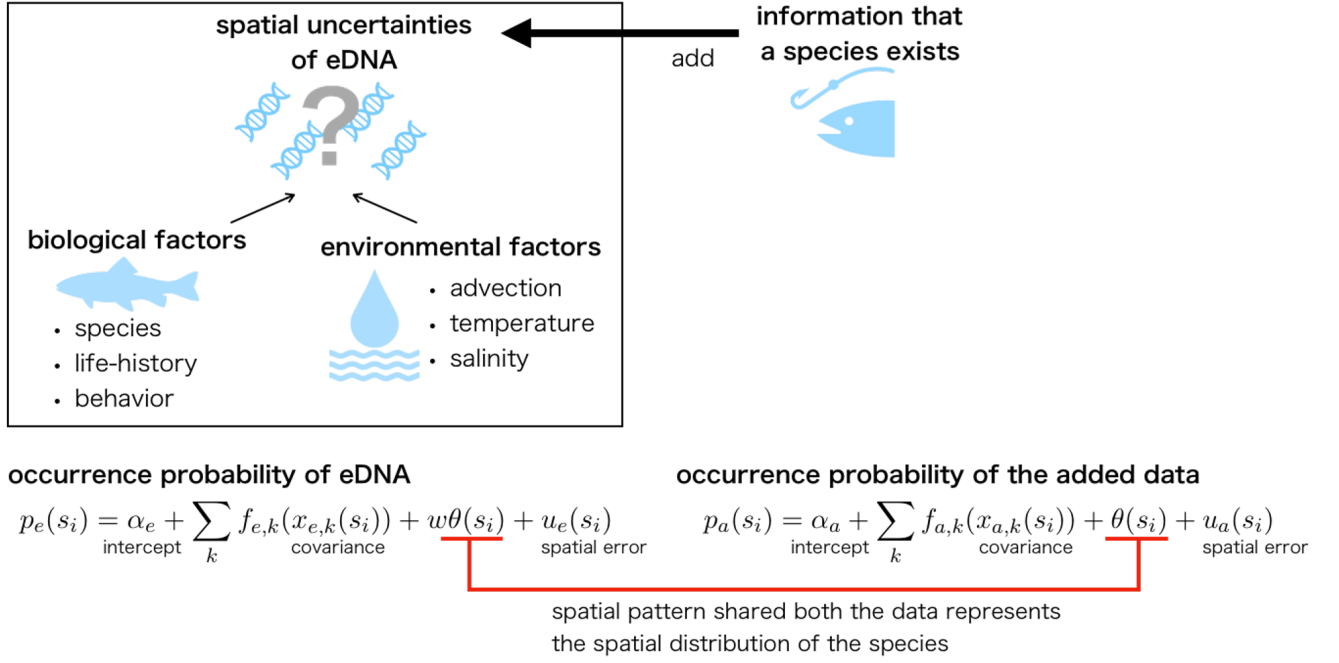


Fig. 1: Conceptual diagram of this study.