

# Apportioning seabirds to breeding colonies

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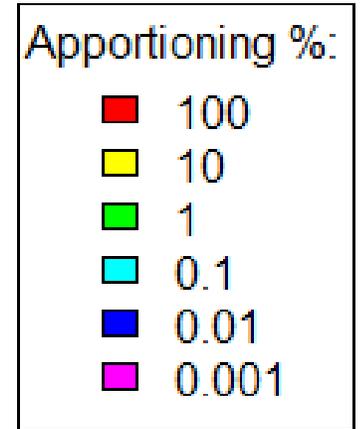
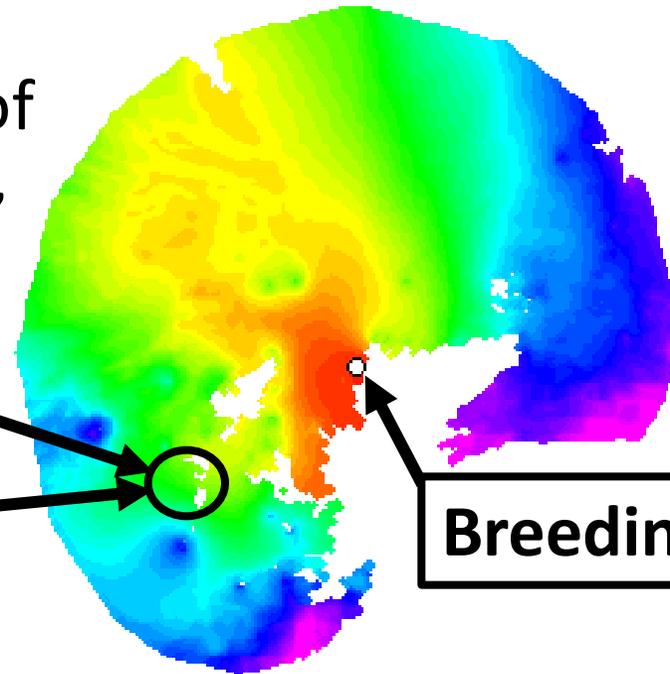
**Glen Tyler** - Scottish Natural Heritage

# Overview

1. The problem
2. The SNH apportioning tool
3. The MSS apportioning tool
4. Possible alternatives
5. Comparisons
6. Conclusions

# 1. The problem

**At sea survey** data count the number of birds seen at sea, from a boat or plane, and are widely used in quantifying the baseline population when assessing impacts of offshore renewables



**Breeding colony: Handa**

However, legislation protecting seabird populations relates largely to **breeding colonies**

If we use at sea data to estimate the number of birds within a particular area of sea, how do we know the **proportion** of these that originate from each breeding colony?

## 2. SNH Apportioning Tool

In practice, a rule-based approach called the “**SNH Apportioning Tool**” is currently widely used

This tool says that the proportion of birds at location  $i$  that arise from colony  $j$  will be proportional to:

**(Size of colony  $j$ ) \* (1 - proportion of the area within the foraging range of colony  $j$  that is sea) / (Distance from location  $i$  to colony  $j$ )<sup>2</sup>**

- A key advantage of the tool is that it is very straightforward to apply in practice
- It also has no minimum data requirements
- However: since this approach does not use empirical data – it therefore implies that the distributions of all species decline with distance from colony **at the same rate**, which does not seem biologically realistic...
- It also ignores the effects of **competition**, and **environmental heterogeneity**

# 3. MSS Apportioning Tool

**Wakefield *et al.* (2017)** assume that the **colony-specific UD** (e.g. the proportion of birds from colony  $j$  that are in area  $i$ ) is a mathematical function of the effects of: accessibility (e.g. distance to colony), competition-related variables, and a range of different environmental variables

They estimate the parameters of this model for four species (kittiwake, guillemot, razorbill, shag) from **GPS tracking data**

The **MSS apportioning tool** provides an R interface for calculating apportioning proportions using the outputs from Wakefield *et al.* (2017), and for calculating proportions using the SNH apportioning tool

How does the **MSS Tool** calculate apportioning proportions using the Wakefield *et al.* (2017) outputs? This is straightforward:

A basic mathematical theorem (**Bayes theorem**) tells us that:

**Proportion** of birds within area  $i$  that originate from colony  $j$

= **Proportion** of birds from colony  $j$  that are in area  $i$  \* **size** of colony  $j$ ,

renormalized so that these values sum to one across all colonies

## 4. Possible alternative methods

The Wakefield *et al.* (2017) approach is very powerful... ...but:

It relies on having **extensive GPS tracking data** from multiple colonies, and is relatively time-consuming and challenging to implement

What do we do for species where this is **not feasible**? (e.g. because there are no, or insufficient, GPS tracking data)

Currently investigating the potential to stick with a probabilistic approach, but to consider **simpler models** for the UD...

We are considering a range of **simple probabilistic models...**

**Probability** a randomly selected bird from colony  $j$  is at location  $i$

is proportional to:

**SPM1:**  $1 / (\text{distance to colony}^2)$

This assumes the same decay relation as in the SNH tool...

**SPM2:**  $1 / (\text{distance to colony}^\theta)$

**SPM3:**  $\exp(-\theta * \text{distance to colony})$

**Semi-empirical:**  
We estimate  $\theta$  so that it matches the published ratio of max to mean foraging ranges (Thaxter et al., 2012)

**No data requirements:**

**SNH tool**

**SPM1**

**Minimal data requirements:**

(mean & max foraging  
ranges only)

**SPM2**

**SPM3**

**Requires extensive GPS tracking data:**

**Wakefield model**

Increasing  
level of  
scientific  
defensibility

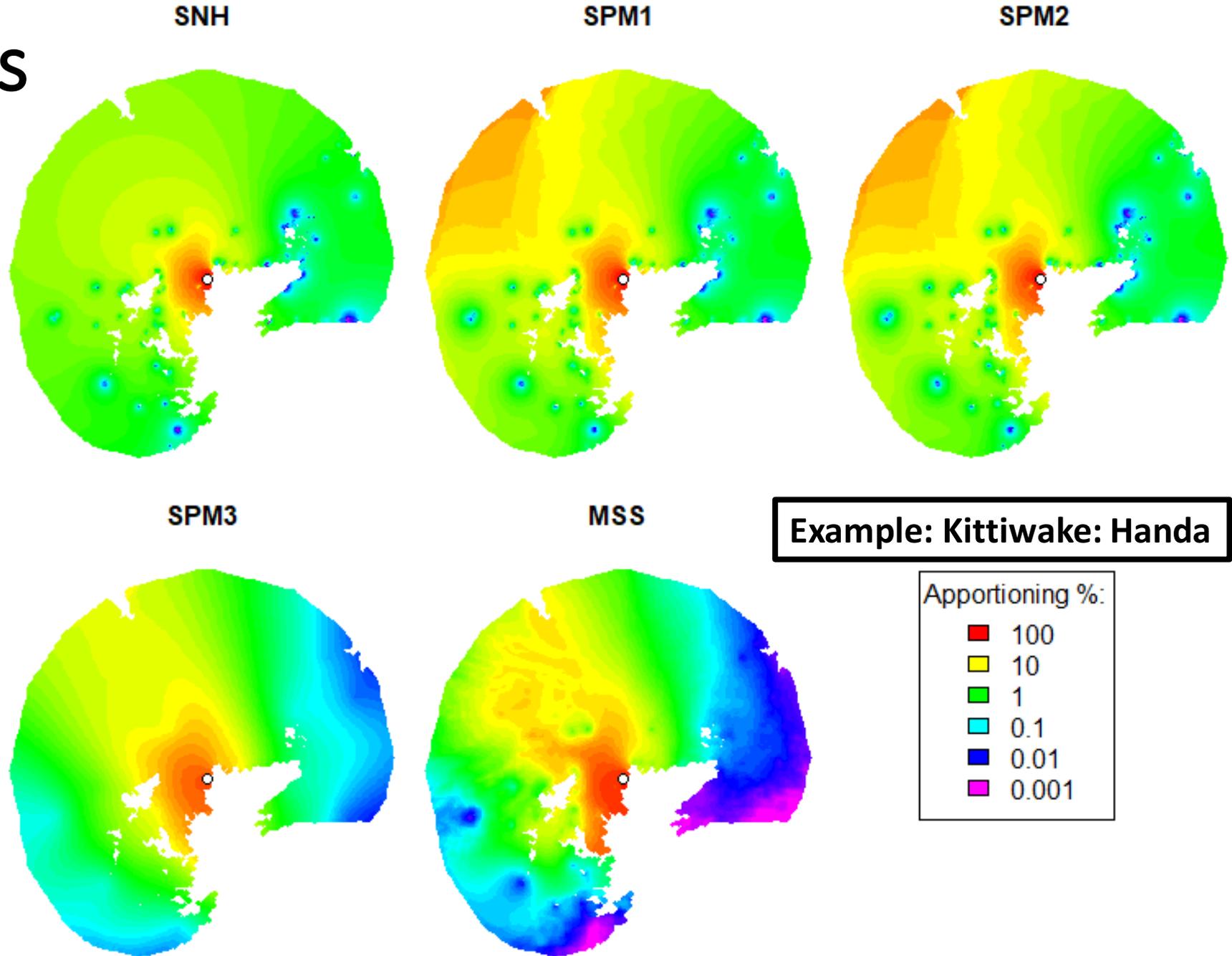
Increasing  
time &  
resource  
required to  
apply the  
method



# 5. Comparisons

How different are the apportioning probabilities estimated using the different methods?

We focus on two species (**kittiwake** and **guillemot**) that were modelled by Wakefield *et al.* (2017)



Example: Kittiwake: Handa

In order to compare the different methods more generally, we focus on all locations within the **UK EEZ** & all breeding colonies within the **British Isles**

We compare the apportioning probabilities estimated using pairs of methods using the **Bhattacharyya distance**,

$$BA = \frac{1}{n} \sum_{i=1}^n \sum_{j=1}^m \sqrt{p_{ij}q_{ij}}$$

where  $p_{ij}$  and  $q_{ij}$  denote the estimated apportioning probabilities derived from each of the methods being compared, and where  $i = 1, \dots, n$  are locations (cells on a regular grid) and  $j = 1, \dots, m$  are breeding colonies

## National results: Kittiwake

0 = no similarity  
1 = perfect similarity

	<b>SNH tool</b>	<b>SPM1</b>	<b>SPM2</b>	<b>SPM3</b>	<b>Wakefield</b>
<b>SNH tool</b>		0.59	0.59	0.55	0.52
<b>SPM1</b>			1.00	0.94	0.90
<b>SPM2</b>				0.94	0.90
<b>SPM3</b>					0.96
<b>Wakefield</b>					

# National results: Guillemot

0 = no similarity  
1 = perfect similarity

	<b>SNH tool</b>	<b>SPM1</b>	<b>SPM2</b>	<b>SPM3</b>	<b>Wakefield</b>
<b>SNH tool</b>		0.75	0.76	0.74	0.65
<b>SPM1</b>			1.00	0.95	0.86
<b>SPM2</b>				0.96	0.85
<b>SPM3</b>					0.86
<b>Wakefield</b>					

## 6. Conclusions

- **Apportioning of birds to breeding colonies** is a key practical problem in relation to assessing the impacts of offshore renewables on seabirds
- The **rule-based approach** that is currently used in practice has considerable limitations
- For species with sufficient **GPS tracking data**, sophisticated statistical modelling (e.g. Wakefield *et al.*, 2017) can be used to estimate apportioning probabilities in a substantially more defensible way
- For species which lack sufficient GPS data, our work tentatively suggests that there is potential to use **simple probabilistic models** in place of the SNH tool
- **Initial results** suggest that these will be less defensible than the Wakefield approach, but more defensible than the current rule-based approach ...

# Acknowledgements

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## Further information

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# Extra slides

(in case of questions...)

# Technical details: estimation for SPM2 & SPM3

1. From the values in **Thaxter *et al.* (2017)** calculate

$D = (\text{Mean foraging range} / \text{Maximum foraging range})$ , for each species

2. Now, take a fine **regular grid** of points  $i = 1, \dots, n$  covering a circle of radius 1; each point has distance  $0 < d_i < 1$  from the origin

3. Estimate  $\theta$  to be the value of  $\theta$  which **minimizes**

$$\left( \left( \sum_{i=1}^n d_i p(d_i | \theta) \right) - D \right)^2$$

where  $p(d|\theta) = d^\theta$  (for SPM2) or  $p(d|\theta) = \exp(-\theta d)$  (for SPM3)

# Technical details: apportioning

For all five methods apportioning values are calculated using the same **2x2km grid** as that used in Wakefield *et al.* (2017)

For all methods apportioning values are assumed to be zero for grid cells whose distance to colony  $d_{ij}$  exceeds the **foraging range**  $R$  used by Wakefield *et al.* (2017)

For SPM2 and SPM3, the models are applied to **standardized distances**,  $(d_{ij}/R)$

# Possible further work

- Do the decay parameters of the simple probabilistic models (SPM2, SPM3) that are estimated from GPS tracking data differ from those estimated using the published foraging ranges in Thaxter *et al.* (2012)?
- Quantifying **uncertainty in the estimation of the UDs** – within both the simplified models (SPM2, SPM3) and within the Wakefield *et al.* (2017) model
- Accounting for **uncertainty in estimation of colony size**, and accounting for change in colony size over time
- Are there other “simple” probabilistic models that could be considered?