1

bases

## Supporting Information

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## - A The Paris 12 dataset - Presentation and estimation results

| Name of the street | Abbreviation | Number of tree bases |
| :--- | :---: | :---: |
| Rue Baron le Roy | BARO-1 | 40 |
|  | BARO-2 | 19 |
| Boulevard de Bercy | BERC-1 | 22 |
|  | BERC-2 | 37 |
| Rue de Charenton | CHAR-1 | 69 |
|  | CHAR-2 | 70 |
| Rue Daumesnil | DAUM-1 | 102 |
|  | DAUM-2 | 44 |
|  | DAUM-3 | 39 |
| Rue Joseph Kessel | KESS-1 | 36 |
|  | KESS-2 | 33 |
| Rue Montgallet | MONT | 48 |
| Rue Pommard | POMM-1 | 17 |
|  | POMM-2 | 22 |
| Quai de la Rapée | RAPE-1 | 49 |
|  | RAPE-2 | 25 |
| Rue de Bercy | RBER-1 | 22 |
|  | RBER-2 | 18 |
| Rue de Reuilly | REUI-1 | 36 |
|  | REUI-2 | 42 |
| Rue Taine | TAIN-1 | 33 |
|  | TAIN-2 | 29 |

Table A.1: List of the portions of streets taken into account in this study


Figure A.1: Map of the study area, adapted from OpenStreetMap. The full street names are listed in Table A.1.


Figure A.2: Illustration of the relation between the local extinction risk (as quantified by the LER metric, and averaged over all streets for each species) and two biological traits for which a borderline significant correlation was identified: (a) the maximal height ( p -value $=0.01918$ ), and (b) the beginning of the flowering period ( p -value $=0.061$ ). See Table 1 for more details on the biological traits and the correlation tests used.

| Name of the plant species | Monitoring in 2013 | Number of portions of streets | List of portions of streets |
| :---: | :---: | :---: | :---: |
| Bromus sterilis | No | 2 | BERC-1, KESS-2 |
| Capsella bursa-pastoris | Yes | 16 | BARO-1, BARO-2, BERC-1, BERC-2, CHAR-1, CHAR-2, DAUM-1, DAUM-2, DAUM-3, KESS-1, KESS-2, POMM-1, POMM-2, RBER-1, RBER-2, REUI-1 |
| Chenopodium album | Yes | 4 | BARO-1, BERC-1, RAPE-1, REUI-1 |
| Conyza sp. | Yes | 20 | BARO-1, BARO-2, BERC-1, BERC-2, CHAR-1, DAUM-1, DAUM-2, DAUM-3, KESS-1, KESS-2, MONT, POMM-1, POMM-2, RAPE-1, RAPE-2, RBER-1, RBER-2, REUI-1, REUI-2, TAIN-1 |
| Geranium molle | No | 3 | BARO-1, CHAR-1, CHAR-2 |
| Hordeum murinum | Yes | 16 | BARO-1, BARO-2, BERC-1, BERC-2, CHAR-1, CHAR-2, DAUM-1, DAUM-2, DAUM-3, KESS-1, KESS-2, RAPE-1, RBER-1, RBER-2, REUI-1, REUI-2 |
| Lactuca serriola | Yes | 1 | BARO-1 |
| Lolium perenne | No | 4 | DAUM-1, DAUM-2, DAUM-3, KESS-2 |
| Parietaria judaica | No | 2 | BARO-1, REUI-2 |
| Plantago lanceolata | Yes | 1 | RAPE-1 |
| Plantago major | Yes | 5 | BARO-1, POMM-2, RAPE-1, REUI-1, REUI-2 |
| Poa annua | No | 22 | BARO-1, BARO-2, BERC-1, BERC-2, CHAR-1, CHAR-2, DAUM-1, DAUM-2, DAUM-3, KESS-1, KESS-2, MONT, POMM-1, POMM-2, RAPE-1, RAPE-2, RBER-1, RBER-2, REUI-1, REUI-2, TAIN-1, TAIN-2 |
| Polygonum aviculare | Yes | 11 | BARO-1, BARO-2, BERC-1, BERC-2, CHAR-1, CHAR-2, DAUM-1, DAUM-3, RAPE-1, RAPE-2, REUI-1, REUI-2 |
| Senecio inaequidens | Yes | 2 | BARO-1, BERC-2 |
| Senecio vulgaris | Yes | 6 | BARO-2, KESS-1, POMM-1, RAPE-1, RBER-2, REUI-1 |
| Sisymbrium irio | Yes | 7 | BARO-1, BARO-2, BERC-1, BERC-2, DAUM-1, KESS-1, MONT, REUI-1 |
| Sisymbrium officinale | No | 2 | BARO-1, REUI-1 |
| Sonchus oleraceus | No | 13 | BARO-1, BARO-2, BERC-1, BERC-2, DAUM-1, KESS-1, KESS-2, MONT, POMM-1, POMM-2, RAPE-1, RAPE-2, RBER-2 |
| Stellaria media | Yes | 22 | BARO-1, BARO-2, BERC-1, BERC-2, CHAR-1, CHAR-2, DAUM-1, DAUM-2, DAUM-3, KESS-1, KESS-2, MONT, POMM-1, POMM-2, RAPE-1, RAPE-2, RBER-1, RBER-2, REUI-1, REUI-2, TAIN-1, TAIN-2 |
| Taraxacum sp. | Yes | 19 | BARO-1, BARO-2, BERC-1, BERC-2, CHAR-1, CHAR-2, DAUM-1, DAUM-2, DAUM-3, KESS-1, KESS-2, MONT, POMM-1, RAPE-1, RAPE-2, RBER-1, RBER-2, REUI-1, REUI-2 |
| Veronica persica | Yes | 1 | RAPE-1 |

Table A.2: List of the plant species taken into account in this study. The taxonomic reference used is the French Flora Reference TAXREF v8.0 (2014). For each species, the portion of streets which were taken into account in this study were the ones in which the focal species was observed in an average of at least $10 \%$ of the patches per year over the monitoring period (2009-2018 for species monitored in 2013, 2014-2018 otherwise).

|  | Estimate | Standard error | p-value |
| :---: | :---: | :---: | :---: |
| (Intercept) | 0,127 | 0,161 | 0,4339 |
| Species | Estimate | Standard error | p-value |
| Capsella bursa-pastoris | -0,111 | 0,158 | 0,4852 |
| Chenopodium album | 0,706 | 0,182 | 0,0002 |
| Conyza sp. | -0,093 | 0,157 | 0,5525 |
| Geranium molle | 0,129 | 0,195 | 0,5087 |
| Hordeum murinum | -0,118 | 0,158 | 0,4554 |
| Lactuca serriola | 0,841 | 0,259 | 0,0014 |
| Lolium perenne | 0,386 | 0,182 | 0,0353 |
| Parietaria judaica | 0,378 | 0,214 | 0,0790 |
| Plantago lanceolata | 1,003 | 0,261 | 0,0002 |
| Plantago major | 0,725 | 0,179 | 0,0001 |
| Poa annua | -0,146 | 0,157 | 0,3521 |
| Polygonum aviculare | 0,587 | 0,162 | 0,0004 |
| Senecio inaequidens | 0,856 | 0,213 | 0,0001 |
| Senecio vulgaris | 0,054 | 0,174 | 0,7590 |
| Sisymbrium irio | 0,067 | 0,167 | 0,6893 |
| Sisymbrium officinale | 0,797 | 0,212 | 0,0003 |
| Sonchus oleraceus | 0,606 | 0,160 | 0,0002 |
| Stellaria media | -0,146 | 0,157 | 0,3522 |
| Taraxacum sp. | -0,145 | 0,157 | 0,3574 |
| Veronica persica | 0,074 | 0,261 | 0,7770 |
| Street | Estimate | Standard error | p-value |
| BARO-2 | 0,129 | 0,086 | 0,1370 |
| BERC-1 | -0,110 | 0,084 | 0,1955 |
| BERC-2 | 0,035 | 0,085 | 0,6781 |
| CHAR-1 | -0,027 | 0,092 | 0,7725 |
| CHAR-2 | 0,080 | 0,096 | 0,4045 |
| DAUM-1 | 0,002 | 0,086 | 0,9791 |
| DAUM-2 | 0,056 | 0,097 | 0,5634 |
| DAUM-3 | 0,039 | 0,093 | 0,6778 |
| KESS-1 | 0,003 | 0,089 | 0,9738 |
| KESS-2 | 0,038 | 0,091 | 0,6794 |
| MONT | 0,127 | 0,101 | 0,2132 |
| POMM-1 | 0,060 | 0,097 | 0,5340 |
| POMM-2 | 0,050 | 0,101 | 0,6232 |
| RAPE-1 | -0,129 | 0,086 | 0,1337 |
| RAPE-2 | 0,053 | 0,101 | 0,6042 |
| RBER-1 | 0,038 | 0,101 | 0,7112 |
| RBER-2 | -0,006 | 0,093 | 0,9509 |
| REUI-1 | -0,078 | 0,081 | 0,3354 |
| REUI-2 | 0,049 | 0,091 | 0,5911 |
| TAIN-1 | 0,002 | 0,132 | 0,9876 |
| TAIN-2 | 0,020 | 0,157 | 0,9005 |

Table A.3: Summary of the results of the regression of MaxGER on species and portions of streets. For the species, estimates are expressed relative to Bromus sterilis. For the streets, estimates are expressed relative to BARO-1. The species in bold are the ones for which a significantly higher extinction risk was identified.

| Biological trait | p-value |
| :--- | :---: |
| Dispersal mechanism | 0.6899 |
| Flowering duration | 0.002677 |
| Seed mass | 0.5479 |
| Heat preference | 0.763 |
| Pollination vector | 0.5634 |
| Maximal height | 0.004763 |
| Beginning of flowering period | 0.00915 |

Table A.4: Summary of the results of the correlation tests of the global extinction risk (as quantified by the MaxGER metric and averaged over all streets for each species) with the species traits listed in Table 1. The biological traits in bold are the ones for which a significant correlation was identified (when accounting for multiple testing using the Holm-Bonferroni method).

|  | Estimate | Standard error | p-value |
| :---: | :---: | :---: | :---: |
| (Intercept) | 0,745 | 0,091 | 0,0000 |
| Species | Estimate | Standard error | p-value |
| Capsella bursa-pastoris | -0,053 | 0,090 | 0,5552 |
| Chenopodium album | 0,009 | 0,103 | 0,932 |
| Conyza sp. | -0,010 | 0,089 | 0,9107 |
| Geranium molle | 0,022 | 0,111 | 0,8465 |
| Hordeum murinum | -0,254 | 0,090 | 0,0054 |
| Lactuca serriola | 0,124 | 0,147 | 0,3993 |
| Lolium perenne | 0,078 | 0,103 | 0,4508 |
| Parietaria judaica | 0,012 | 0,121 | 0,9210 |
| Plantago lanceolata | 0,065 | 0,148 | 0,6599 |
| Plantago major | 0,109 | 0,102 | 0,2847 |
| Poa annua | -0,578 | 0,089 | 0,0000 |
| Polygonum aviculare | -0,071 | 0,092 | 0,4381 |
| Senecio inaequidens | 0,062 | 0,121 | 0,6096 |
| Senecio vulgaris | 0,111 | 0,099 | 0,2633 |
| Sisymbrium irio | 0,004 | 0,095 | 0,9625 |
| Sisymbrium officinale | 0,034 | 0,120 | 0,7797 |
| Sonchus oleraceus | 0,022 | 0,091 | 0,8103 |
| Stellaria media | -0,110 | 0,089 | 0,2164 |
| Taraxacum sp. | -0,267 | 0,089 | 0,0032 |
| Veronica persica | -0,045 | 0,148 | 0,7602 |
| Street | Estimate | Standard error | p-value |
| BARO-2 | 0,077 | 0,049 | 0,1182 |
| BERC-1 | -0,045 | 0,048 | 0,3518 |
| BERC-2 | 0,046 | 0,048 | 0,3377 |
| CHAR-1 | -0,014 | 0,052 | 0,7915 |
| CHAR-2 | 0,076 | 0,054 | 0,1635 |
| DAUM-1 | 0,008 | 0,049 | 0,8677 |
| DAUM-2 | 0,041 | 0,055 | 0,4634 |
| DAUM-3 | 0,033 | 0,053 | 0,5351 |
| KESS-1 | -0,038 | 0,051 | 0,4494 |
| KESS-2 | -0,022 | 0,052 | 0,6724 |
| MONT | 0,082 | 0,057 | 0,1544 |
| POMM-1 | 0,083 | 0,055 | 0,1326 |
| POMM-2 | 0,066 | 0,057 | 0,2509 |
| RAPE-1 | -0,085 | 0,049 | 0,0833 |
| RAPE-2 | 0,071 | 0,057 | 0,2197 |
| RBER-1 | 0,118 | 0,057 | 0,0418 |
| RBER-2 | -0,001 | 0,053 | 0,9786 |
| REUI-1 | -0,046 | 0,046 | 0,3121 |
| REUI-2 | -0,009 | 0,052 | 0,8639 |
| TAIN-1 | 0,163 | 0,075 | 0,0308 |
| TAIN-2 | 0,229 | 0,089 | 0,0109 |

Table A.5: Summary of the results of the regression of LER on species and portions of streets. For the species, estimates are expressed relative to Bromus sterilis. For the streets, estimates are expressed relative to BARO-1. The species in italic are the ones for which a significantly lower LER was identified. The portions of streets in bold are the ones for which a significantly higher LER was identified.

| Biological trait | p-value |
| :--- | :---: |
| Dispersal mechanism | 0.2049 |
| Flowering duration | 0.2748 |
| Seed mass | 0.3375 |
| Heat preference | 0.814 |
| Pollination vector | 0.3371 |
| Maximal height | 0.01918 |
| Beginning of flowering period | 0.061 |

Table A.6: Summary of the results of the correlation tests of the local extinction risk (as quantified by the LER metric and averaged over all streets for each species) with the species traits listed in Table 1. No significant correlation was identified when accounting for multiple testing (using the Holm-Bonferroni method).

| Value of $H_{\text {inf }}$ | Species |
| :---: | :--- |
| $H_{\text {inf }}=0$ | Plantago lanceolata <br> Sisymbrium officinale (*) |
| $H_{\text {inf }}=1$ | Chenopodium album <br> Polygonum aviculare <br> Senecio inaequidens <br> Veronica persica |
| $H_{\text {inf }}=2$ | Parietaria judaica <br> Sonchus oleraceus |
| $H_{\text {inf }}=3$ | Plantago major <br> Poa annua |
| $H_{\text {inf }}=4$ | Lactuca serriola <br> Sisymbrium irio <br> Bromus sterilis <br> Geranium molle <br> Lolium perenne |
| $H_{\text {inf }}=5$ | I |
| $H_{\text {inf }}=6$ | Conyza <br> Hordeum murinum <br> Senecio vulgaris <br> Taraxacum |
| $H_{\text {inf }}=7$ | Capsella bursa-pastoris <br> Stellaria media |
| $H_{\text {inf }}=8$ |  |

Table A.7: Value of $H_{\text {inf }}=\min \left\{h \in \llbracket 0, H_{\text {max }} \rrbracket: \mathbb{P}(H \leq h \mid \mathrm{Obs}) \geq 0.05\right\}$ for each species listed in Table A.2. The posterior distribution of $H$ was obtained by performing parameter inference simultaneously on all portions of streets listed in Table A.2, assuming that only $p_{\text {ext }}$ and $s$ differed from one portion of street to another. Species in bold are species for which the absence of a seed bank was identified (that is, for which $\mathbb{P}(H=0 \mid \mathrm{Obs}) \geq 0.95)$. The asterisk indicates species for which neither the absence (see above) nor the presence (defined as $\mathbb{P}(H \geq 1 \mid \mathrm{Obs}) \geq 0.95)$ of a seed bank was identified.

(a) Distribution of the quotients of the average SMDs inside a street and between streets, grouped by species.

(b) Distribution of the quotients of the average SMDs inside a street and between streets, grouped by street.

Figure A.3: Comparison of the average Standartised Mean Differences (SMDs) of the posterior distributions of patch extinction probabilities computed between portions of the same streets or of different streets. The plots correspond to the distribution of the quotients of the mean SMDs inside a street and between streets, grouped by species (a) or by street (b).
We recall that the SMD measures the difference between two probability distributions. Therefore, a quotient smaller than one indicates that posterior distributions of patch extinction probabilities are on average closer between portions of a same street than between portions of different streets, while a quotient larger than one indicates the opposite.

## B The BOA Process: Mathematical formulation and estimation procedure

## B. 1 Formal definition of the BOA process

Formally, the BOA process for a street with $N$ patches observed for $T$ years involves three dependent random variables:

1. The seed age $L=\left(L_{n, t}\right)_{n \in \llbracket 1, N \rrbracket, t \in \llbracket 1, T \rrbracket} \in \mathbb{N}^{N \times T}$.

The random variable $L_{n, t}$ gives the age of the youngest seeds in patch $n$ at the beginning of generation $t$. These seeds are viable (i.e., they can germinate and grow into plants) if and only if their age is below the maximal dormancy duration $H$.
2. The extinction events $E=\left(E_{n, t}\right)_{n \in \llbracket 1, N \rrbracket, t \in \llbracket 1, T \rrbracket} \in\{0,1\}^{N \times T}$.

We have $E_{n, t}=1$ if an extinction event occurs in patch $n$ during generation $t$, and $E_{n, t}=0$ otherwise.
3. The observations of standing vegetation $O=\left(O_{n, t}\right)_{n \in \llbracket 1, N \rrbracket, t \in \llbracket 1, T \rrbracket} \in\{0,1\}^{N \times T}$.

We have $O_{n, t}=1$ if plants are observed in patch $n$ during generation $t$, after potential patch extinction events and before the seed production step, and we have $O_{n, t}=0$ otherwise.

At $t=1$ (initial condition), each patch is randomly chosen to contain viable seeds with probability $s \in[0,1]$. In that case, the age of the youngest viable seeds is chosen uniformly at random in $\{0, \ldots, H\}$. Then, during each generation $t$, we follow these five steps.

1. Germination step: In all patches $n$ such that $L_{n, t} \leq H$ (i.e., in all patches containing viable seeds), some of the viable seeds germinate and grow into plants.
2. Extinction step: Each patch containing plants is affected by an extinction event with probability $p_{\text {ext }} \in[0,1]$, independently of other patches. This extinction event kills all the plants in the patch. Formally, the random variables $\left(E_{n, t}\right)_{1 \leq n \leq N}$ are i.i.d. and follow a Bernoulli distribution with parameter $p_{\text {ext }} \in[0,1]$. The patch $n$ is affected by an extinction event during generation $t$ if, and only if $E_{n, t}=1$.
3. Observation step: The observer records which patches contain standing vegetation. For each patch $n, O_{n, t}$ is set to 1 if the patch contain plants, and to 0 otherwise.
4. Seed production step: For each patch such that $O_{n, t}=1$, we set

$$
L_{n, t+1}=L_{\max (1, n-1), t+1}=L_{\min (N, n+1), t+1}=0
$$

For all remaining non-affected patches $n^{\prime}$, we set $L_{n^{\prime}, t+1}=L_{n^{\prime}, t}+1$.
5. All remaining plants die, for instance due to the action of gardeners.

The BOA process is thus characterised by three parameters:

- The initial proportion of occupied patches $s \in[0,1]$,
- The maximal dormancy duration $H \in \mathbb{N}$,
- The patch extinction probability $p_{\text {ext }} \in[0,1]$.


## B. 2 Bayesian framework used

## B.2.1 Model likelihood

With the above description of the BOA process, we can now write the probability $\mathbb{P}\left(O, L \mid s, p_{\text {ext }}, H\right)$ that the observations $O$ and the seed ages $L$ are produced by the process, given that the true parameters are $s, p_{\text {ext }}$ and $H$. Let us introduce the shortcut notations $O_{t}=\left(O_{1, t}, \ldots, O_{N, t}\right)$ and $L_{t}=\left(L_{1, t}, \ldots, L_{N, t}\right)$.

As a first remark, note that the age $L_{t}$ of the seeds at times $t>1$ is a deterministic function of the initial age of the seeds $L_{1}$ and the previous observations $O_{1}, \ldots, O_{t-1}$. This function defines the seed production process; it can be written recursively as:

$$
L_{n, t+1}= \begin{cases}L_{n, t}+1 & \text { if } O_{\min (1, n-1), t}=O_{n, t}=O_{\max (N, n+1), t}=0 \\ 0 & \text { otherwise }\end{cases}
$$

As a consequence, we only need to compute the probability $\mathbb{P}\left(O, L_{1} \mid s, p_{\mathrm{ext}}, H\right)$, since the remaining values $L_{2}, \ldots, L_{T}$ are a deterministic function of $L_{1}$ and $O$. This probability can be decomposed as:

$$
\mathbb{P}\left(O, L_{1} \mid s, p_{\mathrm{ext}}, H\right)=\mathbb{P}\left(L_{1} \mid s, p_{\mathrm{ext}}, H\right) \times \mathbb{P}\left(O \mid L_{1}, s, p_{\mathrm{ext}}, H\right)
$$

At time $t=1$, under the definition of the process introduced in the previous section, the seeds $L_{1}$ are either non viable (which we represent with a seed age equal to $H+1$ ), or viable, with an age chosen uniformly in $\{0, \ldots, H\}$. Therefore, for all $1 \leq n \leq N, L_{n, 1} \in\{0, \ldots, H+1\}$ and

$$
\mathbb{P}\left(L_{n, 1}=\ell \mid s, p_{\mathrm{ext}}, H\right)= \begin{cases}\frac{s}{H+1} & \text { if } \ell \leq H \\ 1-s & \text { if } \ell=H+1\end{cases}
$$

As $L_{1,1}, \ldots L_{N, 1}$ are independent, we can then compute $\mathbb{P}\left(L_{1} \mid s, p_{\text {ext }}, H\right)$ as

$$
\mathbb{P}\left(L_{1} \mid s, p_{\mathrm{ext}}, H\right)=\mathbb{P}\left(L_{1,1} \mid s, p_{\mathrm{ext}}, H\right) \times \cdots \times \mathbb{P}\left(L_{N, 1} \mid s, p_{\mathrm{ext}}, H\right) .
$$

The probability $\mathbb{P}\left(O \mid L_{1}, s, p_{\text {ext }}, H\right)$ can be decomposed under the form

$$
\mathbb{P}\left(O \mid L_{1}, s, p_{\mathrm{ext}}, H\right)=\prod_{t=1}^{T} \mathbb{P}\left(O_{t} \mid L_{t}, s, p_{\mathrm{ext}}, H\right) .
$$

This equation expresses the fact that the random variables $O_{t}$ only depends on the quantity $L_{t}$ (which is itself a function of $O_{1}, \ldots, O_{t-1}$, as described above). Then, each term in this equation can be expressed separately, as follows:

$$
\mathbb{P}\left(O_{n, t}=1 \mid L_{t}, s, p_{\mathrm{ext}}, H\right)= \begin{cases}1-p_{\mathrm{ext}} & \text { if } L_{n, t} \leq H \\ 0 & \text { otherwise }\end{cases}
$$

This equation expresses the fact that plants can only be observed in patch $n$ during generation $t$ if 1) $L_{t} \leq H$ (i.e., if the youngest seeds present in the patch are viable) and 2) if no extinction event occurred (which happens with probability $1-p_{\text {ext }}$ ). As $O_{n, t}$ is $\{0,1\}$-valued, we also obtain $\mathbb{P}\left(O_{n, t}=0 \mid L_{t}, s, p_{\text {ext }}, H\right)$ as $1-\mathbb{P}\left(O_{n, t}=1 \mid L_{t}, s, p_{\text {ext }}, H\right)$.

A consequence of the above observation is that conditionally on $L_{t}$, the random variables $O_{1, t}, \ldots, O_{N, t}$ are independent. Therefore, we can compute $\mathbb{P}\left(O_{t} \mid L_{t}, s, p_{\text {ext }}, H\right)$ as

$$
\mathbb{P}\left(O_{t} \mid L_{t}, s, p_{\mathrm{ext}}, H\right)=\mathbb{P}\left(O_{1, t} \mid L_{t}, s, p_{\mathrm{ext}}, H\right) \times \cdots \times \mathbb{P}\left(O_{N, t} \mid s, p_{\mathrm{ext}}, H\right) .
$$

We can combine these expressions to obtain the complete likelihood of the model, which is given by $\mathbb{P}\left(O, L_{1} \mid s, p_{\text {ext }}, H\right)$. Note that this quantity is different from the marginal likelihood of the observations $\mathbb{P}\left(O \mid s, p_{\text {ext }}, H\right)$. The latter would be ideally the one to use in practice (since $L_{1}$ is unknown), but is unfortunately impossible to compute: formally, it writes as sum over all the $(H+2)^{N}$ possible configurations of seed ages at time $t=1$, and the number of such configurations grows exponentially with $N$. As a consequence, we need to estimate $L_{1}$ along with the model parameters $s, p_{\text {ext }}, H$.

## B.2.2 Bayesian methodology

Since the observed data only spans a period of ten years, our estimation necessarily comprises a certain amount of uncertainty. In the context of complex hierarchical statistical models (of which the model
considered here is an example), Maximum Likelihood estimations only give the most likely value for $s, p_{\text {ext }}$ and $H$, and cannot be used to obtain confidence regions around the estimated values. For this reason, methods like the EM are not suited to our study.

Instead, we propose to work in a Bayesian framework. It consists in determining the posterior distribution $\mathbb{P}\left(s, p_{\mathrm{ext}}, H \mid O\right)$ of the parameters $s, p_{\mathrm{ext}}, H$ given the observed data $O$ using Bayes' rule:

$$
\mathbb{P}\left(s, p_{\mathrm{ext}}, H \mid O\right)=\frac{\mathbb{P}\left(O \mid s, p_{\mathrm{ext}}, H\right) \mathbb{P}\left(s, p_{\mathrm{ext}}, H\right)}{\mathbb{P}(O)}
$$

As we will see in the following sections, this formula can be used to draw samples from the distribution $\mathbb{P}\left(s, p_{\text {ext }}, H \mid O\right)$, even though it may not be computed explicitly in practice. These samples are then used to approximate the distribution. For instance, if we have $M$ samples $\left(s^{(m)}, p_{\text {ext }}^{(m)}, H^{(m)}\right)_{1 \leq m \leq M}$ of the posterior distribution, the expectation of $p_{\text {ext }}$ given $O$ can be computed with a Monte-Carlo approximation:

$$
\mathbb{E}\left[p_{\mathrm{ext}} \mid O\right] \simeq \bar{p}_{\mathrm{ext}}=\frac{1}{M} \sum_{m=1}^{M} p_{\mathrm{ext}}^{(m)}
$$

Similarly, the uncertainty on $p_{\text {ext }}$ can be measured by computing its posterior variance

$$
\operatorname{Var}\left(p_{\mathrm{ext}} \mid O\right) \simeq \frac{1}{M} \sum_{m=1}^{M}\left(p_{\mathrm{ext}}^{(m)}-\bar{p}_{\mathrm{ext}}\right)^{2}
$$

Prior distribution In a Bayesian framework, the model parameters $s, p_{\text {ext }}$ and $H$ are considered as random variables. In order to apply Bayes' rule and obtain the posterior distribution that we are interested in, their distribution a priori $\mathbb{P}\left(s, p_{\text {ext }}, H\right)$ must be defined in a way that reflects our (prior) knowledge of the model parameters. In this paper, we do not make any initial assumption on the model parameters, and consider the following simple, uninformative prior distributions:

- The initial proportion of occupied patches $s$ follows a uniform distribution over $[0,1]$.
- Similarly, $p_{\text {ext }}$ also follows a uniform distribution over $[0,1]$.
- The maximal dormancy duration $H$ follows a uniform distribution over the set of integers $\left\{0, \ldots, H_{\max }\right\}$ :

$$
\mathbb{P}(H)= \begin{cases}1 /\left(H_{\max }+1\right) & \text { if } H \in\left\{0, \ldots, H_{\max }\right\} \\ 0 & \text { otherwise }\end{cases}
$$

The pre-defined upper bound on the maximal dormancy duration is a consequence of the fact that with a limited number of years of observation, identifying long maximal dormancy durations (compared to the length of the observation window) can be an ill-posed problem and lead to identifiability issues.

In order to compute the GER and the MaxGER extinction metrics, we need samples from the posterior distribution $\mathbb{P}\left(p_{\text {ext }}, H \mid O\right)$. As explained earlier, this distribution takes an intractable form: using the law of total probabilities it writes as

$$
\mathbb{P}\left(p_{\mathrm{ext}}, H \mid O\right)=\sum_{L_{1} \in\{0, \ldots, H+1\}^{N}} \int_{0}^{1} \frac{\mathbb{P}\left(O, L_{1}, s, p_{\mathrm{ext}}, H\right)}{\mathbb{P}(O)} d s,
$$

which is a sum over an exponential number of terms. We overcome this hurdle by focusing instead on the posterior distribution of $\left(L_{1}, s, p_{\mathrm{ext}}, H\right)$ given $O$, which writes as:

$$
\mathbb{P}\left(L_{1}, s, p_{\mathrm{ext}}, H \mid O\right)=\frac{\mathbb{P}\left(O, L_{1}, s, p_{\mathrm{ext}}, H\right)}{\mathbb{P}(O)} .
$$

We can then combine the different priors to obtain the complete prior distribution.

## B.2.3 Markov Chain Monte-Carlo sampler

the

Since this probability distribution is known up to a normalising constant, the method presented in the next section can be used to draw samples from it. This method will provide us with samples $\left(L_{1}^{(m)}, s^{(m)}, p_{\mathrm{ext}}^{(m)}, H^{(m)}\right)_{1 \leq m \leq M}$, which then give the marginal distribution samples $\left(p_{\mathrm{ext}}^{(m)}, H^{(m)}\right)_{1 \leq m \leq M}$ of the posterior distribution $\mathbb{P}\left(p_{\text {ext }}, H \mid O\right)$ that we are interested in.

In practice, we will use a Markov Chain Monte Carlo (MCMC) sampler to draw approximate samples from the posterior distribution of $\mathbb{P}\left(L_{1}, s, p_{\text {ext }}, H \mid O\right)$. Such methods rely on simple and fast iterations which generate a Markov chain whose invariant distribution is the target distribution we wish to sample from. After a certain amount of iterations, the samples of the Markov chain are very close from being true samples of the target distribution; they can thus be used in Monte-Carlo estimators to compute the GER and MaxGER metrics. Note that consecutive MCMC samples are correlated by definition, which increases the variance of Monte-Carlo estimations compared with independent samples, but does not affect the expectation of the estimator, which is unbiased as the number of samples grows large.

## B.2.4 Metropolis-Hastings within Gibbs sampler

In this section, we detail the MCMC implemented in practice. For an introduction to classical MCMC methods, we refer the reader to (Robert and Casella, 2010). In this paper, we use the MetropolisHastings within Gibbs (MHwG) sampling algorithm, which is designed to draw samples from a general probability distribution $\pi\left(x_{1}, \ldots, x_{d}\right)$ in a high-dimensional space. The general MHwG procedure is recalled in Algorithm 1. In the algorithm, $x_{-k}$ denotes the vector $x$ where component $k$ has been
removed: the term $\pi\left(x_{k} \mid x_{-k}\right)$ thus refers to the conditional distribution of $x_{k}$ given the remaining components of $x$. The algorithm mainly relies on the so-called proposal distributions $q_{k}^{m}$ : at each step $m$, the distribution $q_{k}^{m}$ proposes, given the $m$-th value of $x_{-k}$, a random candidate for the next value of $x_{k}$. Then, this candidate is accepted as the next value of $x_{k}$ with probability $\alpha$.

```
Algorithm 1: The Metropolis-Hastings within Gibbs algorithm
    input : Target distribution \(\pi\left(x_{1}, \ldots, x_{d}\right)\); number of samples \(M\)
    Initialize \(x_{1}^{0}, \ldots, x_{d}^{0}\)
    for \(m=1\) to \(M\) do
        for \(k=1\) to \(d\) do
            Sample a candidate variable \(y_{k}^{m}\) from a proposal distribution \(q_{k}^{m}\).
            Define the acceptance ratio \(\alpha=\min \left[1, \frac{q_{k}^{m}\left(y_{k}^{m}\right) \pi\left(x_{k}^{m-1} \mid x_{-k}^{m-1}\right)}{q_{k}^{m}\left(x_{k}^{m-1}\right) \pi\left(y_{k}^{m} \mid y_{-k}^{m}\right)}\right]\)
            Sample \(B_{k}^{m} \sim \operatorname{Bernoulli}(\alpha)\).
            If \(B_{k}^{m}=0\), set \(x_{k}^{m}=x_{k}^{m-1}\). Otherwise, set \(x_{k}^{m}=y_{k}^{m}\).
        end
    end
    return \(\left(x^{m}\right)_{1 \leq m \leq M}\)
```

MHwG for the BOA process In this paper, we are interested in the distribution $\mathbb{P}\left(L_{1}, s, p_{\text {ext }}, H \mid O\right)$. In the MHwG algorithm, we will thus alternatively be sampling from $s, p_{\text {ext }}, H$ and the components of $L_{1}$. Since $L_{1}$ has $N$ components, at each step of the algorithm we only update a single coordinate $L_{n, 1}$ for a patch $n$ chosen at random. This allows spending more time on sampling the model parameters $s, p_{\text {ext }}, H$ rather than the seed ages $L_{n, 1}$, which in practice only contribute marginally to the likelihood. In order to obtain a complete algorithmic procedure, we need to specify the proposal distributions $q_{k}^{m}$ used at each step.

- For $H$ : the new value of $H$ is chosen uniformly at random in $\left\{0, \ldots, H_{\max }\right\}$.
- For $L_{n, 1}$ : the random value is sampled uniformly in $\{0, \ldots, H+1\}$. Values between 0 and $H$ produce viable seeds, and the value $H+1$ produces non-viable seeds.
- For $p_{\text {ext }}$ and $s$ : instead of working with $p_{\text {ext }}$ and $s$, we represent them as $p_{\text {ext }}=h\left(\xi_{p}\right)$ and $s=h\left(\xi_{s}\right)$, with $\left.h(x)=(1+\exp (-x))^{-1} \in\right] 0,1[$ a sigmoid function. In the algorithm, the proposal value for $\xi_{p}$ at step $m$ is drawn from a Gaussian distribution $\mathcal{N}\left(\xi_{p}^{m-1}, \sigma_{p}^{2}\right)$. Similarly, the proposal value for $\xi_{s}$ is drawn from a Gaussian distribution $\mathcal{N}\left(\xi_{s}^{m-1}, \sigma_{s}^{2}\right)$. The corresponding values for $p_{\exp }$ and $s$ are then obtained by applying $h$. The sigmoid representation allows sampling values very close to 0 or 1 as well as more centered values using a common proposal variance $\sigma_{p}^{2}$ or $\sigma_{s}^{2}$.

In the form we just described, the algorithm currently has a practical issue: a change in the value of $H$ can change the initial state of some seeds from viable to non-viable, and conversely. Although
this is not a problem in itself, we noticed that it hinders the convergence in practice. Our intuition is that it is due to the fact that frequent changes in the value of $H$ prevent the distribution of $L_{1}$ from converging, as the viability of the seeds varies not only with the value of $L_{n, 1}$, but also with $H$.

We overcome this issue by defining a duplicate $L_{1}^{h}$ of $L_{1}$ for each value of $h \in\left\{0, \ldots, H_{\max }\right\}$. For each $h$, we impose that $L_{1}^{h} \in\{0, h+1\}$; the distribution of $L_{1}$ given $H=h$ corresponds to $L_{1}^{h}$. In other words, by definition:

$$
L_{1}=\sum_{h=1}^{H_{\max }} \mathbb{1}_{\{H=h\}} L_{1}^{h}
$$

In practice, at each step of the MHwG algorithm, a random patch $n$ is selected, and the variables $L_{n, 1}^{0}, \ldots, L_{n, 1}^{H_{\max }}$ are updated. Theoretically, these variables should be updated using the conditional distribution $\mathbb{P}\left(L_{n, 1}^{h} \mid s=s^{(m)}, p_{\text {ext }}=p_{\text {ext }}^{(m)}, H=H^{(m)}, O\right)$. However, it must be noted that, if $h \neq H^{(m)}$, the value of $L_{1}^{h}$ does not play a role in the distribution of $O$. In other words, the variables $L_{1}^{h}$ and $O$ are independent conditionally on $H=H^{(m)}$, and the conditional distribution of $L_{1}^{h}$ thus simplifies to a fixed base distribution over $\{0, \ldots, h+1\}$. As a consequence, if $h \neq H^{(m)}$, the variable $L_{1}^{h}$ is randomised to a distribution that does not depend on $O$. In order to bypass this hurdle, we change the conditional distribution $\mathbb{P}\left(L_{n, 1}^{h} \mid s=s^{(m)}, p_{\text {ext }}=p_{\text {ext }}^{(m)}, H=H^{(m)}, O\right)$ in the MHwG to $\mathbb{P}\left(L_{n, 1}^{h} \mid s=s^{(m)}, p_{\text {ext }}=p_{\text {ext }}^{(m)}, H=h, O\right)$. This modification results in an approximate MHwG procedure, which provides significantly better performances than the base algorithm.

As a last point, the multiple variables $L_{1}^{0}, \ldots, L_{1}^{H_{\max }}$ must be modelled by distinct values of $s$ : the proportion of viable seeds may vary depending on the value of $h$. In practice, $s$ is thus replaced with a vector $\left(s^{0}, \ldots, s^{H_{\max }}\right) \in[0,1]^{H_{\max }+1}$, and the probability distribution of $L_{1}^{h}$ is defined using $s^{h}$.

Remark B.1. The variances $\sigma_{p}^{2}$ and $\sigma_{s}^{2}$ for the proposal distributions of $\xi_{p}$ and $\xi_{s}$ are tuned throughout the convergence of the MCMC in order to obtain an average proportion of accepted samples around $30 \%$. Larger variances lead to larger transitions, which are thus rejected more often; smaller variances lead to smaller transitions, which are easier to accept.

## B. 3 The noisy BOA process

The noisy BOA process adds a new parameter $\varepsilon \in[0,1]$, which controls the probability of what can be interpreted as external colonisation (but was introduced to model noise in observations). Compared to the standard BOA process, patches containing non-viable seeds or affected by an extinction event can now contain plants with probability $\varepsilon$. This only changes the probability $\mathbb{P}\left(O_{n, t}=1 \mid L_{t}, s, p_{\text {ext }}, H, \varepsilon\right)$ :
it now expresses as

$$
\mathbb{P}\left(O_{n, t}=1 \mid L_{t}, s, p_{\text {ext }}, H, \varepsilon\right)= \begin{cases}1-p_{\mathrm{ext}}(1-\varepsilon) & \text { if } L_{n, t} \leq H \\ \varepsilon & \text { otherwise }\end{cases}
$$

As with $s, p_{\text {ext }}$ and $H$, the posterior distribution of the parameter $\varepsilon$ can be sampled from with the MHwG algorithm. As the parameter $\varepsilon$ was introduced to provide a buffer against noise in the dataset rather than to model an actual biological phenomenon, we expect it to take very small values. Therefore, we take a slack and slab prior distribution for $\varepsilon$, that is to say, a mixture of two uniform distributions:

$$
\varepsilon \sim \frac{1}{2} \mathcal{U}\left(\left[0, \varepsilon_{m}\right]\right)+\frac{1}{2} \mathcal{U}\left(\left[0, \varepsilon_{M}\right]\right)
$$

In practice, we choose $\varepsilon_{m} \ll \varepsilon_{M}$, e.g., $\varepsilon_{m}=1 \%$ and $\varepsilon_{M}=5 \%$. The idea is to obtain a prior distribution concentrated around relatively small values, with a spike on very small values.

We perform Metropolis transitions on the inverse sigmoid of $\varepsilon, \xi_{\varepsilon}=h^{-1}(\varepsilon)$, with a Gaussian proposal with variance a $\sigma_{\varepsilon}^{2}$ tuned adaptively throughout the MCMC convergence.

## B. 4 Handling multiple streets

Finally, the method introduced in the previous sections seamlessly transposes to the case of observations of a given species in multiple streets, denoted $O_{1}, \ldots, O_{K}$. We assume that for each species, the maximum dormancy duration $H$ and the noise intensity $\varepsilon$ are identical across all streets, but the initial proportion of occupied patches $s_{k}$ and the extinction probability $\left(p_{\text {ext }}\right)_{k}$ depend the street $1 \leq k \leq K$. As in the previous case, we are interested in sampling from the distribution

$$
\mathbb{P}\left(\left(p_{\mathrm{ext}}\right)_{1}, \ldots,\left(p_{\mathrm{ext}}\right)_{K}, H, \varepsilon \mid O_{1}, \ldots, O_{K}\right)
$$

and, as in the previous case, we tackle this problem by instead sampling from the complete posterior distribution

$$
\mathbb{P}\left(\left(L_{1}, s, p_{\mathrm{ext}}\right)_{1}, \ldots,\left(L_{1}, s, p_{\mathrm{ext}}\right)_{K}, H, \varepsilon \mid O_{1}, \ldots, O_{K}\right),
$$

which, up to the normalising constant $\mathbb{P}\left(O_{1}, \ldots, O_{K}\right)$, is proportional to the function

$$
\mathbb{P}\left(O_{1}, \ldots, O_{K},\left(L_{1}, s, p_{\mathrm{ext}}\right)_{1}, \ldots,\left(L_{1}, s, p_{\mathrm{ext}}\right)_{K}, H, \varepsilon\right) .
$$

The MHwG can then be transposed to the multiple streets setting, by updating $H, \varepsilon$ and the parameters $\left(L_{1}, s, p_{\text {ext }}\right)_{k}$ of each street $k$ at each MHwG step.

Using multiple streets at the same time allows reducing the uncertainty on the parameters $H$ and $\varepsilon$, which benefit from the combination of all the observations; this is verified in our numerical experiments (see Supporting Information C.4).

## C Assessment of the performances of the estimation procedure

## C. 1 Parameter sets

| Parameter | Values |
| :---: | :--- |
| Number of patches $N$ | 50,100 |
| Number of years of observation $T$ | 5,10 |
| Initial proportion of occupied patches $s$ | $0.2,0.8$ |
| Patch extinction probability $p_{\text {ext }}$ | $0.1,0.2, \ldots, 0.9$ |
| Maximal dormancy duration $H$ | $0,1,2,5$ |
| Noise intensity $\epsilon$ | $0.00,0.01,0.02,0.05$ |
| Additional parameter sets $-H=0$ |  |
| Patch extinction probability $p_{\text {ext }}$ |  |
| Additional parameter sets $-H=1$ |  |
| Patch extinction probability $p_{\text {ext }}$ | $p_{c}(1)+x, x=-0.1,-0.08, \ldots, 0.08,0.1$ |
| Additional parameter sets $-H=2$ |  |
| Patch extinction probability $p_{\text {ext }}$ | $p_{c}(2)+x, x=-0.1,-0.08, \ldots, 0.08,0.1$ |
| Additional parameter sets $-H=5$ |  |
| Patch extinction probability $p_{\text {ext }}$ | $p_{c}(5)+x, x=-0.1,-0.08, \ldots, 0.08,0.1$ |

Table C.1: Parameter sets used to compare the performances of the MaxGER and GER metrics. For each parameter set, we simulated 30 BOA processes, and computed the average MaxGER and GER over the 30 simulated processes.

| Parameter | Values |
| :---: | :--- |
| Number of patches $N$ | 50 |
| Number of years of observation $T$ | 10 |
| Initial proportion of occupied patches $s$ | $0.2,0.8$ |
| Patch extinction probability $p_{\text {ext }}$ | $0.1,0.35,0.55,0.75$ |
| Maximal dormancy duration $H$ | $0,1,2,5$ |
| Additional parameter - False positives |  |
| False positive rate $\epsilon_{\text {pos }}$ | $0.00,0.01,0.02,0.05$ |
| Additional parameter - False | negatives |
| False negative rate $\epsilon_{\text {neg }}$ |  |
| Additional parameter - External colonization |  |
| External colonization rate $\epsilon_{\text {col }}$ |  |

Table C.2: Parameter sets used to compare the performances of the MaxGER and GER metrics on corrupted datasets (containing false positives, false negatives or external colonization). For each parameter set, we simulated 30 BOA processes and computed the average MaxGER and GER over the 30 simulated processes.

| Parameter | Values |
| :---: | :--- |
| Number of patches $N$ | 30,50 |
| Number of years of observation $T$ | 5,10 |
| Initial proportion of occupied patches $s$ | $0.2,0.8$ |
| Patch extinction probability $p_{\text {ext }}$ | $0.1,0.35,0.55,0.75$ |
| Maximal dormancy duration $H$ | $0,1,2,5$ |
| Noise intensity $\epsilon$ | $0,0.01,0.02,0.05$ |
| Number of streets $M$ | $1,2,5,10$ |

Table C.3: Parameter sets used to assess the effect of performing the estimation simultaneously on multiple streets on the quality of the estimation of $H$. For each parameter set, we generated 30 simulations and performed parameter inference assuming that $H$ and $\epsilon$ were constant across streets.

## C. 2 Comparison of the performances of the GER and MaxGER metrics

## C.2.1 Performances of the GER metric

The following figures show the evolution of the GER metric as a function of the patch extinction probability $p_{\text {ext }}$. For each parameter set listed in Table C.1, we simulated 30 datasets and performed parameter inference under a noisy BOA process. We then computed the average GER across the 30 simulations. The black vertical line indicates the critical patch extinction probability $p_{c}(H)$.

$$
(N, T)=(50,5)
$$



Figure C. 1

$$
(N, T)=(50,10)
$$



Figure C. 2


Figure C. 3

$$
(N, T)=(100,10)
$$



Figure C. 4

The following figures show the evolution of the MaxGER metric as a function of the patch extinction probability $p_{\text {ext }}$. For each parameter set listed in Table C.1, we simulated 30 datasets and performed 157 parameter inference under a noisy BOA process. We then computed the average GER across the 30 158 simulations. The black vertical line indicates the critical patch extinction probability $p_{c}(H)$.

$$
(N, T)=(50,5)
$$



Figure C. 5
$(N, T)=(50,10)$


Figure C. 6


Figure C. 7

$$
(N, T)=(100,10)
$$



Figure C. 8


The effect of the introduction of false negatives on the assessment of the MaxGER metric is mostly visible when $H=0$, for high patch extinction probabilities and when parameter estimation is performed under a BOA process without noise.

- $\varepsilon_{\text {neg }}=0.0$
$\nabla \varepsilon_{n e g}=0.01$
- $\varepsilon_{\text {neg }}=0.02$
$+\varepsilon_{\text {neg }}=0.05$ $-p_{c}(H)$

Figure C.9: Effect of the introduction of false negatives on the assessment of the MaxGER metric, when estimation is performed under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. For each parameter set listed in Table C.2, we simulated 30 datasets and performed inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. The black vertical line indicates the critical patch extinction probability $p_{c}(H)$.

The introduction of false positives has a very different outcome depending on whether the estimation is performed under a BOA or noisy BOA process. This is particularly visible when $H=0$ or 1 and for high patch extinction probabilities.









| $\bullet$ | $\varepsilon_{p o s}=0.0$ |
| :--- | :--- |
| $\nabla$ | $\varepsilon_{p o s}=0.01$ |
| $\square$ | $\varepsilon_{p o s}=0.02$ |
| + | $\varepsilon_{p o s}=0.05$ |
| $\square$ | $p_{c}(H)$ |

Figure C.10: Effect of the introduction of false positives on the assessment of the MaxGER metric, when estimation is performed under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. For each parameter set listed in Table C.2, we simulated 30 datasets and performed inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. The black vertical line indicates the critical patch extinction probability $p_{c}(H)$.

The same observation can be made in the presence of low rates of external colonization.


Figure C.11: Effect of the introduction of external colonization on the assessment of the MaxGER metric, when estimation is performed under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. For each parameter set listed in Table C.2, we simulated 30 datasets and performed inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. The black vertical line indicates the critical patch extinction probability $p_{c}(H)$.

## C. 3 Performances of the estimation of $p_{e x t}$ and $H$



$$
\begin{array}{ll}
- & \varepsilon_{\text {neg }}=0.0 \\
\nabla & \varepsilon_{\text {neg }}=0.01 \\
\square & \varepsilon_{\text {neg }}=0.02 \\
+ & \varepsilon_{\text {neg }}=0.05
\end{array}
$$

Figure C.12: Root Mean Square Error (RMSE) on the estimation of $p_{\text {ext }}$ in the presence of false negatives, when performing parameter inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. For each parameter set listed in Table C.2, we simulated 30 datasets and performed inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$.








$$
\begin{array}{ll} 
& \varepsilon_{p o s}=0.0 \\
\nabla & \varepsilon_{p o s}=0.01 \\
& \varepsilon_{p o s}=0.02 \\
+\quad \varepsilon_{p o s}=0.05
\end{array}
$$

Figure C.13: Root Mean Square Error (RMSE) on the estimation of $p_{e x t}$ in the presence of false positives, when performing parameter inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. For each parameter set listed in Table C.2, we simulated 30 datasets and performed inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$.


Figure C.14: Root Mean Square Error (RMSE) on the estimation of $p_{\text {ext }}$ in the presence of external colonization, when performing parameter inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. For each parameter set listed in Table C.2, we simulated 30 datasets and performed inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$.


Figure C.15: Average value of $\left|H_{i n f}-H\right|$ in the presence of false negatives, false positives or external colonization, when performing parameter inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$. For each parameter set listed in Table C.2, we simulated 30 datasets and performed inference under a BOA process or a noisy BOA process with $\epsilon_{\max }=0.1$.
C. 4 Handling multiple streets


Figure C.16: Effect of performing the estimation simultaneously on multiple streets on the quality of the estimation of $H$, when the maximal dormancy duration $H$ and the noise intensity $\epsilon$ are constant across streets. The parameter sets used are listed in Table C.3.

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